PROGRAM OF THE
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MARCH 20-23, 2024

To be held at the

JW Marriott LA Live
900 W Olympic Blvd, Los Angeles, CA 90015

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MESSAGE FROM THE VP & PROGRAM CHAIR

Welcome!

It is my great pleasure to welcome you to the 2024 meeting of the American Association of Biological Anthropologists. This year we are convening in Los Angeles, California for our 93rd annual meeting. Several of our events will be available to virtual meeting attendees. However you participate, we hope you find the conference vibrant and intellectually stimulating!

The full AABA 2024 program includes 765 peer-reviewed scientific presentations by authors from all over the world. Of these, 733 are scheduled to be presented in Los Angeles and the remaining 32 presentations will be presented online only.

The abstracts illustrate the remarkable breadth of our discipline, covering a range of research topics and approaches, and with global reach and incredible time depth. A total of 13 invited symposia (146 abstracts) are included in this year's program: six podium symposia will take place in Los Angeles and be live-streamed via Zoom, six poster symposia in Los Angeles, and one symposium will be exclusive to the online program. There are 620 contributed abstracts. By subfield, these include Bioarchaeology (n=123, ~20%), Dental Anthropology (n=29; ~5%), Education in Biological Anthropology (n=14; ~2%), Forensic Anthropology (n=35; ~6%), Functional Anatomy & Tissue Biology (n=67, ~11%), Genetics & Genomics (n=63; ~10%), Human Behavior (n=22; ~4%), Human Biology (n=48; ~8%), Paleoanthropology (n=108; ~17%), and Primatology (n=110; ~18%).

This Program provides an overview of the activities planned for the Los Angeles meeting. More details are available on AABA's annual meeting website. The conference hotel is the JW Marriott LA Live, which is centrally located in downtown LA. I'm excited to be hosting the conference in my home town and serving on the Local Arrangements Committee. Many thanks to the other LA Local Arrangements Committee members, Stephanie Meredith and David Raichlen, for helping AABA articulate with the local community. We have put together a wonderful list of Los Angeles attractions; check it out on our website!

Vaccination Requirement

Vaccination is required for attendance at AABA 2024, with very few allowable exceptions. We ask that all attendees be up-to-date on COVID boosters currently available to them. Exemption requests can be directed to AABA President, Leslea Hlusko, at bioanthpresident@gmail.com. Anyone granted an exception must submit a negative PCR test taken within 72 hours of the first day of the conference.

Masking Policy

Indoor masking is strongly recommended for all attendees (vaccinated or unvaccinated) at the AABA 2024 conference. KN95 masks will be available for all AABA attendees at the registration desk. A limited number of medical-grade N95 masks will also be available. Disinfectant wipes and hand sanitizer will be provided at each podium. We encourage attendees to eat and drink outdoors when possible. Fortunately, our venue has several large outdoor areas available.

The Scientific Program

We are pleased to be joined in Los Angeles by our partner organizations: the **American Association for Anthropological Genetics** (AAAG), the **Dental Anthropology Association** (DAA), the **Human Biology Association** (HBA), the **Paleoanthropology Society** (PAS), and the **Paleopathology Association** (PPA).

AABA 2024 programming in Los Angeles begins on Wednesday, March 20 with the **Committee on Diversity Undergraduate Research Symposium** (open to everyone from 6:00-8:00pm) and the **Opening Reception** (8:00-10:00pm). On Thursday, March 21, scientific sessions begin. This portion of the program includes six invited podium symposia, six invited poster symposia, one invited virtual symposium, and 46 contributed sessions (22 poster and 24 podium sessions). All six of the invited podium symposia, the Business Meeting, and the President's Panel will be live-streamed on Zoom and recorded so that attendees can participate in these events either in-person or online, synchronously or asynchronously.

MESSAGE FROM THE VP & PROGRAM CHAIR

Overview of Session Schedule and Presenter Information

Morning podium sessions begin at 8:00am and end by 12:00pm. Afternoon podium sessions begin at 2:30pm and end by 5:00pm (with a few exceptions). We have a few quarter-day podium sessions (half-morning or half-afternoon); be sure to check the Program for start times. The 2.5 hour lunch break allows for dedicated time to view posters as well as attend a variety of mid-day events including workshops and committee meetings between 12:15pm and 2:15pm. **New this year, contributed poster sessions will only be on Thursday and Saturday from 5:00-7:00pm.**

As in previous years, podium presentations need to be uploaded onto a central secure server in the Speaker Ready Room no later than a half day before the presentation. This server will then "push" presentations to the appropriate meeting room and will be available for the session. To ensure accessibility of presentations, we will be using voice-to-text subtitles in Powerpoint and ask all presenters to follow accessibility guidelines posted on the AABA website. Please note that all Invited Podium Symposia will be held in Platinum D and live-streamed via Zoom.

Contributed poster sessions and exhibitors booths will all be held in the Diamond Ballroom. Poster set-up will begin at 7:30am and should be completed by 8:00am. Posters should be taken down by 7:30pm. **Even-numbered poster presenters will stand by their posters from 5:00-6:00pm, with odd-numbered presenters attending from 6:00-7:00pm.** Invited Poster Symposia are held in Platinum H-I and are assigned to a morning or afternoon time.

Joint sessions

The joint **HBA/AABA invited podium symposium**, *Terminology, Theory, and Method for the Study of Inequality of Health: Breakthroughs or Barriers?*, organized by Heather J.H. Edgar & Lexi O'Donnell, will be held on Saturday afternoon.

On Saturday at 12:30pm, we will hold the ***Presidential Panel***, *Funding our Priorities: Past, Present, and Future of the AABA*. Please come with your questions and opinions as to what AABA's future funding priorities should be.

Workshops

This year we have planned 20 exciting and innovative workshops throughout the week that occur in conjunction with our annual meeting. Because of space limitations, some of the workshops and events may require pre-registration (information is available on our meeting website; pre-registration closes March 1). Our workshops provide professional development, science communication, and methodological training that should be of broad interest to our membership. Most workshops are held over the lunch hour from 12:15-2:15, but there are a few exceptions. Be sure to check the schedule.

Special Events

The **American Anthropological Association Commission for the Ethical Treatment of Human Remains** is approaching the completion of a two-year effort to canvass global representatives of descendant communities and professional organizations regarding the ethical treatment of human remains, samples, and images. Drs. Michael Blakey (College of William & Mary) and Sabrina Agarwal (University of California, Berkeley) will host a panel session on Thursday at 12:15pm to debrief colleagues who may be affected by the Commission's recommendations and provide an opportunity for comment.

On Thursday afternoon we are excited to hold our annual **Auction**! Each year the auction raises thousands of dollars to support Pollitzer Student Travel Awards and Cobb Professional Development Grants. Please participate through donations (of items or cash!) and by bidding on our array of tempting auction items (please contact co-organizers Amy Rector and Anne Grauer if you are interested in donating or learning more).

On Friday, following the conclusion of the scientific sessions, we will hold the **Annual Business Meeting and Awards Presentation** (6:30-8:30pm). This meeting is where the association comes together to review business of the past year (including annual reports from AABA Officers and committee chairs) and make a plan for the future. If you want to have a say in the organization, come to the business meeting! We strongly encourage and welcome attendance by all members and those interested in applying for membership. Join us as we celebrate this year's Cobb Professional Development Grant, Pollitzer Student Travel award, and COD Undergraduate Research travel award winners. We will also recognize this year's recipients of the Charles R. Darwin Lifetime Achievement Award (awarded to **Laurie Godfrey**), the Gabriel W. Lasker Service Award (awarded to **Steven Leigh**), and the AABA and Leakey Foundation Communication & Outreach Award in Honor of Camilla Smith (awarded to **Tina Lasisi**). Please join us in celebrating this year's outstanding winners!

This year we will have a dedicated **In Memoriam** session on Saturday to remember colleagues who passed away over the last year. This stand-alone session will allow more time to learn about and remember our colleagues.

Saturday evening brings our annual meeting to a close, with the **Student Awards Closing Reception** and **Hooding Ceremony** from 7:00-9:00pm. Please join us for a last-chance to network in person, say goodbye to new and long-time colleagues, and to learn who won the 2024 Student Presentation Awards!

As we approach the conference, we will be publicizing additional information regarding special events. These will be listed in the final meetings program and on our website.

Acknowledgements and Appreciation

I sincerely thank everyone who helped organize the 2024 program. Tremendous thanks are due to our extraordinary business partners, Annual Meeting Executive Director Lori Strong and her team from Burk & Associates.

I am immensely grateful to the 67 dedicated members of our Program Committee who conducted and completed symposium and abstract reviews thoughtfully, thoroughly, and expeditiously. Additional thanks go to the 25 members of the Program Committee who took on the task of organizing the contributed sessions.

Many thanks to the Advance Team who met in Los Angeles to set the schedule for the scientific program. Thank you to Eduardo Amorim, Steve Leigh, Stephanie Meredith, David Raichlen, Amy Rector and to the extraordinary student volunteers Katie Beachem, Chloe Coulter, Cassie Croasmun, Alexandria Koedel, and Anamika Nanda! I also want to thank Michelle Bezanson for designing the beautiful AABA 2024 logo!

Of course, none of the program organization would be possible without the immense effort of Ed Hagen, our website and abstract database developer. The Program Assistant Amber Jaeger has been a tremendous help and I am very grateful for her outstanding organizational skills. I also want to thank the AABA Officers and members of the Executive Committee for their year-round hard work that makes our annual meeting possible.

The annual meeting would not be possible without the help of all these individuals, and I hope you will join me in thanking them when you see them in Los Angeles!

Kristi L. Lewton
AABA Vice President and Program Chair

ABSTRACTS

Cultural Marxism, Anthropology, and Social Media

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Cultural Marxism is a far-right conspiracy theory predicated on the idea of an elite (typically antisemitic accusations of a Jewish elite) pushing progressive ideas into broader culture, particularly using universities as a tool of influence. This concept is often associated with Antonio Gramsci's theory of cultural hegemony. Modern discussions of cultural Marxism can often be seen regarding political correctness, "woke ideology," and indoctrination in higher education.

Given anthropology's close relationship to topics of gender, sex, sexuality, and race (concepts particularly of interest in cultural Marxism), this presentation analyzes the intersection of cultural Marxism and anthropology in far-right online communities.

Collected as a part of a larger investigation of the relationship between anthropology and extremism, nearly 3000 YouTube channels' videos and comments were examined for mentions of "cultural Marxism" and "Frankfurt School" (often associated with cultural Marxism) to evaluate how users discussed these concepts, the connection to anthropology, and perceptions of academia broadly.

This presentation will address the ways in which cultural Marxism is discussed but will focus on how biological anthropology, in particular, is used to paradoxically bolster and deconstruct a cultural Marxist conspiracy of academia. For instance, modern anthropology is typically referred to as "Boasian anthropology," a targeted, antisemitic dog whistle, that includes antisemitic accusations of individuals that reject biological race. Anthropologists, among other social sciences, are "blamed" for the spread of critical race theory and indoctrination of "woke" ideals. Simultaneously, anthropological practice (e.g., forensic ancestry estimation) is utilized as a tool to combat the spread of cultural Marxism.

This project was supported by a Wenner-Gren Post PhD Research Grant (Gr. 10255).

Why terminology matters: Exploring structural inequities in forensic recovery time

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First used by John Galtung (1969) and later utilized by Paul Farmer (1996; 2004), structural violence describes a form of violence that exists interwoven throughout society, exacerbating societal discrepancies that persist within a population and manifest physical impacts that are detrimental to marginalized individuals through sociocultural and socioeconomic biases. Building upon the ramifications of structural violence, structural vulnerability, which is more often used in contexts related to public health, describes the risk of adverse outcomes relating to a group or individual's health and well-being due to factors that exacerbate social or political constraints, including unequal distributions of power and a lack of funding for impoverished communities. But what about in cases of missing persons or medicolegal death investigations? Does an individual's status as a missing person mean they are vulnerable or the product of structural violence? Does death, arguably the absence of health, warrant an examination to identify systematic barriers leading to extended recovery times of certain groups of individuals?

We argue that the answer is yes, especially in the Southeastern United States. Sociocultural and socioeconomic inequalities do impact factors relating to missing and unidentified persons because systematic and structural barriers, perpetuated by historically held ideologies of racism, sexism, and discrimination, are still present throughout the U.S. Structural systems, including a decentralized medicolegal field, inequitable access to proper forensic funding, sociopolitics, and sociocultural stigmas, all play a role in understanding the inequalities that cause discrepancies in forensic recovery times and the importance of terminology when identifying these disparities.

Using DMTA to Reveal Dietary Shifts Among the Ancient Mongolians of the Bronze Age

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The mobile pastoral lifeway has been characterized as relatively uniform, with a correspondingly general lack in food diversity (i.e. meat and dairy products), in contrast to broad spectrum diets of foragers, or even as compared to farmers. However, Inner Asian steppe peoples were known to engage in mixed economy practices including foraging and trade from agricultural societies. Dental microwear texture analysis (DMTA) is a useful tool in distinguishing characteristics among various modes of subsistence in human groups. This study focuses on DMTA analysis of samples from three key periods of cultural transformation among people of ancient Mongolia: Bronze Age (c. 2000-500 BC), when the pastoral lifeway emerged in the region; the Iron Age nomadic confederation of the Xiongnu polity (c. 3rd century BC-2nd century AD); and Medieval period that includes the Mongol Empire (12th -14th century AD).

Comparing our DMTA analysis to contemporary groups, we have identified a dietary transition during the Bronze Age. Beach determined the Late Bronze Age/Early Iron age diet in Mongolia likely included plant-based foods, meat, and dairy, while new data from the current study shows that harder foods were a more common aspect of the diet than previously thought. This likely indicates dietary variation during the Bronze Age in Mongolia. In contrast, comparing the Mongolian medieval texture signatures to a contemporary population in England indicates dietary similarities for Europeans and Mongolians of this time, suggesting increased similarity in food availability across Eurasia.

This work is supported by the National Science Foundation (BCS-2141844), (#0922930).

Body size differences between modern and fossil eastern African mammal assemblages suggest increased predatory pressures in Pliocene paleocommunities

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Body mass is an important biotic variable in modern and fossil mammal assemblages, and early hominins have been potentially implicated in the demise of megaherbivores that began around 4.6 Ma. We explored structural differences between body mass distributions of predatory and nonpredatory mammals at hominin-bearing Pliocene sites in eastern Africa and compared them with assemblages from 168 modern African game parks, representing all major habitats/environments. This allowed us to infer potential competitive and predatory pressures in fossil communities, presumably before anthropogenic landscape modification, and relate these pressures to those experienced in modern continental systems. Sampled fossil sites included Hadar, Laetoli, Tulu Bor Member of Koobi Fora Formation, and Woranso-Mille, including recently published Leado Dido'a and Nefuraytu collection areas. A correspondence analysis separated modern and fossil sites almost completely based on differences in the number of species represented in predator and nonpredator body size categories. Body size means at modern sites were typically about half those at fossil sites, where there were higher numbers of predator species exceeding 100 kilograms and nonpredators larger than 150 kilograms. The first axis was closely associated with mean body size of sites, and the second axis reflected differences between dominance of smaller predators or nonpredators. Hadar had the largest predators among all sites, but broadly overlapped with Woranso-Mille. Though differences in mean body mass between modern and fossil sites may also be partially attributed to depositional or collection differences, Pliocene paleoenvironments included larger numbers of predators capable of feeding on sympatric hominins.

Comparison of fracture characteristics in paired human ulnae loaded at two distinct loading rates

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Skeletal trauma interpretation is an important duty of forensic anthropologists. The objective of this study was to investigate differences in fracture characteristics within pairs of ulnae loaded at two distinct rates to explore the predictability of loading velocity from observed fracture outcomes.

Ten ulna pairs from unembalmed adult female post-mortem human subjects were dissected from the forearm and ends potted. All ulnae were experimentally loaded to failure in a controlled 3-point bending test with blunt point of impact at 50% of bone length. The left ulna in each pair was loaded quasi-statically at 0.64 mm/min (SLOW), and the right was loaded dynamically at 2 m/sec (FAST).

Nine ulnae in the SLOW group experienced a single fracture and one had two fractures. The FAST group was more variable with four ulnae having one fracture, four with two fractures, and two with three fractures, resulting in significant differences in fracture number between loading rates (Marginal Homogeneity Test, $p=0.025$). All ten SLOW tests resulted in simple fracture types, whereas only three of the FAST tests experienced simple fractures and the remaining were more complex (four wedge and three multifragmentary). Fracture type within pairs significantly differed between SLOW and FAST loading rates (Marginal Homogeneity Test, $p=0.008$).

Ulnae loaded at a realistic, dynamic rate resulted in more fractures of greater complexity than those loaded quasi-statically. Despite repeatable dynamic loading there were more variable fracture outcomes within the FAST group, and this may result in challenges with interpretation of blunt force trauma in forensic casework.

Tracing Down the Genetic History of Vadnagar Archaeological Complex in India Using Genomics and Palaeoanthropology

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Vadnagar is a prominent archaeological site in India and has held prestigious status through the five dynasties of Gujarat during ancient and medieval times. Vadnagar is located in the Mehsana district of Gujarat, India, a strategic location that has served as a melting pot for trade, and cultural and religious activities. The location of the town makes it a rich cultural heritage site. The Vadnagar archaeological complex includes five locations- Vadnagar, Taranga, Anaj Godown, Kota Ambaji Lake and Sharmistha Lake. This study focuses on exploring the genetic ancestry of the Vadnagar locality in Gujarat and investigating any possible migratory pattern in the area through excavated skeletal remains, and anthropological and archaeological evidences. Ancient DNA analyses of skeletal remains (N=4), using PCA and ADMIXTURE analysis indicate that the genetic affinities of the skeletal remains are local along with some visible migration. Genetic analyses from relics retrieved from the Taranga archaeological complex point towards the possible migration and the growth of Hinayana Buddhism around the 4th century CE during the pinnacle of Buddhist spread in the region.

Network insights of tuberculosis infection and social behavior of free-ranging long-tailed macaques in Thailand

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Group living plays a significant role in the evolution of many primate species. However, socializing can increase the risk of exposure to infectious agents, such as *Mycobacterium tuberculosis* (Mtb) bacteria that causes an airborne disease tuberculosis (TB). In particular, group-living nonhuman primates like long-tailed macaques (*Macaca fascicularis*) may act as asymptomatic carriers of TB, but little is known about the socio-ecological factors that may influence Mtb infection and transmission among these wildlife populations. In this study, we investigate the demographic, ecological, and social factors that influence TB exposure and transmission among long-tailed macaques in Thailand. We collected behavioral observations and non-invasive biological specimens (freshly defecated feces and rope-baited buccal cells) from 98 free-ranging long-tailed macaques in Wat Khao Tamon, southern Thailand, between August 2021 and February 2022. Eleven out of 98 monkeys (11.22%) were detected Mtb antigen for active TB using IS6110 nested-PCR method. Interestingly, many of the infected monkeys were found residing in the periphery of the grooming network. A logistic regression analysis demonstrated that macaques receiving grooming from many partners (high in-degree) had a significantly lower chance of TB infection ($\beta = -3.75$, $p = 0.05$). This suggests that individuals with higher network connectivity may benefit from the stress-relieving effects of allogrooming, reducing their susceptibility to active Mtb infection. These findings shed light on the complex interplay between social behavior and disease transmission in wildlife populations.

This project was supported by the Leakey Foundation, the American Society of Primatology, the UC Davis Wildlife Health Center Fellowship, and the National Primate Research Center of Thailand Chulalongkorn University.

(Bi)Pedal Predicaments: Osteoarthritis in the hallucal metatarsophalangeal joint

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Although the hallucal metatarsophalangeal joint is recognized as the pedal joint most frequently affected by osteoarthritis, the distribution of osteoarthritic changes within the joint has yet to be explored. To address this gap in the literature, distribution of osteoarthritic changes (lipping, porosity, eburnation, and osteophytes) across the distal articular surface of the hallux was analyzed by dividing the articular surface into four quadrants for scoring. The sample utilized for this project is comprised of 71 individuals from the Bass Donated Skeletal Collection. Distribution of osteoarthritic changes was determined via a suite of statistical tests, including Kruskal-Wallis rank sum tests and Dunn's tests. ANCOVAs were used to determine whether these differences between the quadrants were statistically significant even when accounting for age, sex, stature, BMI, tibial robusticity, and occupation as covariates. The results indicate that only porosity scores differ significantly between quadrants, and these differences are still statistically significant when accounting for all covariates. Specifically, there are statistically significant differences in porosity degree score between the second quadrant (dorsolateral) and all other quadrants. This dorsolateral quadrant has the greatest porosity degree scores of all quadrants. These results indicate that specific joint mechanics may make this aspect of the joint surface most susceptible to osteoarthritic changes, perhaps related to the medial shift of center of pressure toward the hallux as the forefoot contacts the substrate and participates in toe-off. Further characterization of these joint mechanics may show how gait changes, as well as footwear changes, can reduce the incidence of hallucal osteoarthritis.

The use of multiple foot bones to estimate sex in human archaeological and fossil populations

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Sex estimation is one of the main steps in the construction of the biological profile. When working with osseous human remains, this task could be impaired by a poor conservation state of the remains due to taphonomic processes, especially in fossil populations. Metric methodologies allow to estimate sex from different bones, which is why in recent decades studies that offer discriminant functions for different skeletal elements have become increasingly popular. Foot bones are generally well preserved due to their small size, and various foot bones have already demonstrated their capability to create these functions, with good results when applied to fossil remains.

The objective of this work is to present new multivariate discriminant equations for sex estimation from a combination of foot bones: navicular, talus, and calcaneus; that can be applied in different human populations, both modern and fossil. To generate these functions, we have used 44 linear variables among the three bones, all measured from the Hamann-Todd Osteological Collection (HTOC). The obtained equations were applied to fossil individuals, with a previous morphologic sex estimation, of different fossil populations (Middle Paleolithic *Homo sapiens*, Upper Paleolithic *H. sapiens*, and *H. neanderthalensis*) to check the accuracy of these formulae in these population groups.

The discriminant analysis carried out yielded several new equations with a cross validated range of accuracy between 80.2% and 95.6% for the HTOC. These equations maintained high allocation percentages in the fossil groups, reaching 100% for some of them, including the one with higher accuracy in the HTOC.

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Human Mobility in the first millennium AD of Asia Minor: An Archaeogenomic Approach

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The first millennium AD witnessed profound cultural shifts in the Mediterranean region, marked by the rise and fall of the Western Roman Empire and the emergence of the Byzantine Empire. In the quest for a comprehensive understanding of human mobility, I employ a multidisciplinary approach, combining ancient DNA analysis, archaeological, and historical data. This study aims to unearth the genetic imprints of human mobility and diversity within coastal and inland regions of Anatolia, unveiling population dynamics across centuries and illuminating migration and settlement patterns. I analyze a dataset comprising ancient genomes encompassing the Mediterranean region, including Asia Minor, to shed light on historical connections both within and beyond the ecoregions of the Anatolian Peninsula, extending to Western Eurasia.Our findings underscore the intricate population structure and regional connectivity within Anatolia, which commenced prior to the Roman period. Systematic analyses of the data reveal interactions beyond Anatolia, highlighting that there was no massive population replacement in the region during this era. Northern western Anatolia exhibits a diverse gene pool, influenced by both eastern and western contributions, while central, western, and southern Anatolia's populations remained closely clustered until the end of the Roman Era. Later during Byzantine period, a few Western Mediterranean outliers emerge within the local population structure, which remains largely unaffected. The southern eastern ecoregion presents a distinct gene pool with affinities to Persian populations, demonstrating that the interaction sphere extended beyond western influences, aligning with historical records.

This study was supported by the Scientific and Technological Research Council of Türkiye (TUBITAK) ARDEB 1001 Grant No 121Z485.

Somatic Mutation and Adaptive Flexibility: Neural Plasticity and the *NF1* Gene in Hominin Evolution and Beyond

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The unique, wild-type hominin variant of the *NF1* gene displays a strong association with skills fundamental to oral knowledge systems. The sequence of the *NF1* protein product has also shown remarkable utility in distinguishing phylogenetic relationships between primate species. Further study now suggests that *NF1* mutations play significant roles in adaptation at both the germline (intergenerational/speciation) and somatic (individual lifespan; e.g., acclimation, learning) levels.

First recognized for its role in the human tumor disorder Neurofibromatosis Type 1, homologs of the *NF1* gene have since been identified and studied in a diverse array of organisms including social amoebae, fruit flies, cephalopods, pigs, rodents, canines, and non-human primates. The *NF1* gene is associated with development of the nerve sheath and the regulation of cellular growth, proliferation and signaling. In fruit flies, rodents, and humans, germline defects in the *NF1* gene have been linked to deficits in communication, learning, and spatial reasoning.

In response to environmental factors, the social amoeba transitions between unicellular and multicellular structure, and asexual and sexual reproduction. *NF1* knockout amoebae are able to greatly expand their dietary options, at some expense to chemotactic motility. The fully-motile phenotype can be rescued through transition to a multicellular state, or through sexual reproduction. We describe here the somatic mechanism by which certain *NF1* alleles provide comparable adaptive neural flexibilities. These enable a plasticity in neural pathways that is especially enhanced by the paralogous *NF1* mutations of social, intelligent, and/or broadly-dispersed (flexibly-adapted) species and which produce, arguably, the greatest adaptive flexibilities in hominins.

None to disclose.

The primate gut microbiota contributes to interspecific differences in host metabolism

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Because large brains are energetically expensive, they often result in an energetic trade-off within and across primate species that result in storing less energy as adipose tissue. The biological underpinnings of these metabolic differences are not known. However, the gut microbiota (GM) has been shown to causally influence host metabolism in disease, and its composition and function are distinct across primate species. As a result, interspecies variation in the GM represents an unexplored mechanism through which primate metabolism could be shaped to support different brain energetic requirements. To test this hypothesis, we inoculated groups of germ-free mice (n=10 mice each) with the GMs of relatively large-brained (LB) (*Homo sapiens, Saimiri boliviensis*) and small-brained (SB) primates (*Macaca mulatta*). LB primate-inoculated mice exhibited a metabolism shifted toward energy production and away from energy storage. They exhibited significantly lower percent body fat ($F_{2,23}=3.9$, p = 0.03) despite consuming more food on average ($F_{2,8}=370.6$, p < 0.001) and had increased fasting blood glucose ($F_{2,23}=7.5$, p = 0.003), alkaline phosphatase ($F_{2,23}=6.1$, p = 0.008) and alanine aminotransferase ($F_{2,23}=7.8$, p = 0.003), the latter of which is a key enzyme involved in gluconeogenesis. Functional analysis of liver transcriptome data revealed an enrichment for amino acid, lipid, and fatty acid metabolism in the liver of LB primate-inoculated mice. These data suggest that the GM plays a causal role in differentially programming the metabolisms of primate species in ways that are consistent with brain energetic requirements with important implications for understanding human brain evolution.

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The Genetic History of Roman Dacia

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Dacia (present-day Romania) witnessed various cultural transformations over time, culminating in its integration into the Roman Empire under Trajan in 106 AD. Currently, there is limited bioarcheological research on the inhabitants of Roman Dacia. This study focuses on the Apulum area (located in today's Alba Iulia), strategically chosen by the Romans for a military camp, where Legio XIII Gemina was stationed until its withdrawal in the 3rd century AD. The history of the area, along with the prosperous civilian settlements in its vicinity, especially the social and demographic shifts leading to its emergence as a pivotal Dacian center, remains relatively unexplored. Teeth specimens from 34 individuals from the main necropolis Dealul Furcilor (ADF) were sampled to generate whole genome shotgun sequencing data. Following strict quality controls, 21 samples were selected for the downstream analyses, and their genetic variants were filtered based on the 1240K SNP panel. We performed PCA, F-statistics, and admixture modeling to compare ADF's genome-wide variability against coeval and present-day populations. The genetic variation observed in ADF aligns with broader European patterns, revealing two distinct clusters. While most ADF individuals exhibit genetic affinities with Mediterranean populations, a subset demonstrates closer ties to Eastern European groups. These findings enhance our understanding of the Romanization process in the area, shedding light on the genetic legacies of those who arrived in Apulum as legionaries, in contrast to individuals who migrated from surrounding areas, whose genetic makeup is expected to differ from that of the former military personnel.

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Effects of Prenatal Stress on Bone Development of the Offspring

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Introduction: Anthropologists have had a long-standing interest in how events in early life affect the long-term development of an individual. Retrospective studies done in a cross-sectional design have provided significant insights. Given the significant long-term impact that intrauterine environment has on an individual's life, we hypothesized that maternal stress during pregnancy will have negative effects on the offspring's bone development.

Methods: Twenty-eight female and seven male Wistar rats (*Rattus norvegicus*) were bred to produce 176 offspring. During pregnancy, dams were randomly divided into four groups (n=7, per group) and immobilization stress induced as follows; Group 1 (GW1): immobilization stress on days 1-7 of pregnancy, Group 2 (GW2): on days 8-14, Group 3 (GW3): on days 15-21, Group 4 (Controls): left undisturbed. Pups were raised under normal laboratory conditions and sacrificed at ages: 4, 8, 12, and 16 weeks to determine the effect of prenatal stress. At necropsy, femurs were removed and preserved for image analysis. Femurs were scanned using the XCT Research SA+ peripheral Quantitative Computed Tomography (pQCT). Mixed models were fit to the data to assess the effects of maternal stress on offspring. Analyses were performed in R.

Results: Cortical density, thickness, area and total bone density increased with age regardless of the treatment group. The measured parameters were higher in males compared to females after week 4.

Conclusion: Exposure to high levels of cortisol in-utero did not affect the growth trajectory of the offspring compared to the control group. This could be an example of the thrifty phenotype.

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A New Method for the Study of Activity Indicator Facets on the Distal Tibia

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Activity indicator facets (AIFs) are extra facets in the skeleton that develop from habitual activities and body postures. This study proposes a new method—the "An-Sandoval Method"—to evaluate AIFs on the anterior surface of the distal tibia, which develop from habitual ankle dorsiflexion, using a Late Classic (AD 600-900) Maya skeletal assemblage from Midnight Terror Cave, Belize. Our method recognizes two types of facets, accessory and extending, and requires the margin and surface of the facet to be scored. From 77 tibiae, 40 had the distal end preserved, and of these 40, sex could be estimated in 23 (10 females, 13 males). The type of facet and the degree of facet expression are sexually dimorphic in our sample, indicating that the sexes repeatedly engaged in different activities involving ankle dorsiflexion. Accessory facets are more common and pronounced than extending facets among females, while facet type and degree of expression are more variable in males. Moreover, the degree of expression in accessory and extending facets has an inverse relationship among males. Patterns in AIF type and degree of expression suggest that females were regularly engaged in more stereotypical activities involving more stabilized ankle postures, whereas males were engaged in a wider range of activities with more dynamic ankle dorsiflexion. Our method is an improvement over the "present/absent" scoring method because it considers qualitative and quantitative aspects of a facet, which provides a more nuanced perspective.

Impacts of locomotor mode and limb dominance on carpal and tarsal scaling

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The hands and feet are serially homologous structures, often performing similar functions in locomotion (e.g., weight bearing, propulsion). In primates, increased reliance on the hindlimb during locomotion is thought to have allowed increased functional differentiation of the forelimb, causing these homologous structures to diverge from one another. We test the hypothesis that non-locomotor selective pressures on the forelimbs have led to more functional differentiation. We do this by comparing the morphological diversity of carpal bone configurations to tarsal bones. We predict that comprehensive sampling of primate species will show hands to (1) be morphologically distinct from feet, consistent with distinct functions between the two extremities; and (2) exhibit a larger interspecific range of values, indicating a larger range of functions. The present study addresses these predictions using a taxonomically diverse sample of haplorrhine and strepsirrhine primates (n = 26 genera) and volumetric measures of all carpal and tarsal bones. Individual bone size was scaled to overall wrist/ankle size. In support of prediction 1, hands and feet occupy distinct regions of the morphospace. Regarding prediction 2, while hands do not exhibit a larger interspecific range of values, taxa do cluster according to locomotor mode, while feet do not. Thus, preliminary results suggest that variation in carpal proportions reflect increased interspecific variability in function of the hand relative to the foot. Addition of further taxa is needed to better address these trends.

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Assessing intra-regional biological affinities among Middle Neolithic populations in Switzerland

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The relationship between the development of social complexity in Switzerland during the 5th-3rd millennium BCE (Middle Neolithic to Early Bronze Age) and population movement has been a longstanding question. Biological affinity analyses were used to explore demographic dynamics, and specifically to test the hypothesis that similarities in material culture and burial practices were accompanied by a concomitant biological change. The Arizona State University Dental Anthropological System was used to record 36 crown, root, and intraoral osseous discrete traits in 191 dentitions from four regional Middle Neolithic samples (Chamblandes, Corseaux, Barmaz I and II). These data were compared using the Mean Measure of Divergence Statistic and Principal Components Analysis to yield intersample phenetic affinities and the identification of traits driving intersample variation. These biological distance estimates suggest the following: 1) dental phenetic heterogeneity is evident among the samples; 2) the populations retained a degree of cultural autonomy and genetic divergence from one another; 3) phenetic homogeneity is evident among the broad northern and southern regional groups and, 4) the similarity in burial practices may be linked to differences in social boundaries and exchange networks. The comparative results suggest that these groups represent biologically distinct intra-regional northern and southern populations; thus, the hypothesis is not supported. A degree of population discontinuity among these broad intra-regional groups is implied, inhabitants were participants in wide-reaching exchange networks, and gene flow among these groups was likely influenced by strict social boundaries between neighbors and rigid group identities between northern and southern populations.

Comparing Three Non-Invasive Methods for Assessing Seasonality of Insectivory in a Community of Nigeria-Cameroon Chimpanzees in Mbam & Djerem National Park, Cameroon

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Insects are an important chimpanzee dietary resource for which chimpanzees devote considerable time and effort to acquire. However, there is considerable inter-individual and inter-community variation in insect prey targets, frequency, and degree to which insects are consumed by chimpanzees. Several methods have been used in to examine this variation in chimpanzee insectivory. In this study, we compare three non-invasive methods that explore seasonal variation in termite and ant consumption in an unhabituated community of Nigeria-Cameroon chimpanzees (*Pan troglodytes ellioti*) located in central Cameroon: 1) tool assessment (T), 2) macroscopic fecal assessment (M), and 3) fecal DNA assessment (D). We periodically collected chimpanzee tools and fecal samples opportunistically along 10 2-km transects near Ganga Research Station in Mbam & Djerem National Park, Cameroon from 2016 to 2022. Tools were catalogued based on species and prey target. A subset of fecal samples were washed and analyzed macroscopically for insect parts. The remaining fecal samples were analyzed with primer sets targeting hymenopteran and termite DNA. There was greater correlation between the three methods for ants (T-M: r^2 = 0.757, T-D: r^2 = 0.199, D-M: r^2 = 0.439) compared to termites (T-M: r^2 = 0.179, T-D: r^2 = 0.517, D-M: r^2 = 0.315), potentially because mound building termites are a seasonally accessible resource in this region. Additionally, it is important to recognize each of these methods has its own bias and benefits. Overall, a multi-method approach can provide greater coverage and potentially more accurate results for examining seasonality in chimpanzee insectivory.

Data collection for this project was funded in part by The Leakey Foundation through a Leakey Foundation Research Grant.

Primates and other mammals from Tipton Buttes, Great Divide Basin, Southwestern Wyoming: Biochronology and Systematics of an Early Eocene fossil community

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The early Eocene (ca. 56-50 MA) represents a critical period in primate and mammalian evolution and has been best documented in the Rocky Mountain states of the American West. The Great Divide Basin of SW Wyoming has yielded a variety of fossil mammals (including euprimates, microsyopoids, plesiadapiforms) since the pioneering work of Smithsonian paleontologist C.L. Gazin in the 1950s. Gazin described Eocene mammals from three different areas within the Great Divide Basin, including Tipton Buttes. We have relocated and collected larger samples from each of Gazin's original localities to better characterize evolutionary transitions among euprimate lineages. Here we report on the biochronology and systematics of the fossil mammals from Tipton Buttes based on recent, intensive collecting. Gazin reported a total of seven Eocene mammalian taxa from his sample of fewer than 100 fossils and suggested that the Tipton Buttes fossil assemblage was either Lysitean (Wa6) or Lostcabinian (Wa7) in age. Our sample from Tipton Buttes includes nearly 1800 mammalian specimens, with the great majority being isolated teeth from a series of extraordinarily productive anthills. Nine mammalian Orders are represented in our sample including 25-30 genera. Euprimate taxa include both omomyids (*Steinius*, *Anemorhysis*, *Absarokius*) and adapids (*Cantius*). Our sample of *Cantius* (N = 50) is metrically (lower M1 occlusal area) and morphologically (hypocone and stylar shelf development, entoconid notch) indistinguishable from Bighorn Basin *Cantius abditus*. This and the presence of *Heptodon calciculus* demonstrates that the Tipton Buttes fauna is Lysitean in age, confirming Gazin's initial but poorly supported conclusion.

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Characterization of pre-Hispanic oral microbiomes among marine and agricultural diets in coastal populations from the Atacama Desert

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Early populations in the Atacama Desert (northern Chile) such as the Chinchorro people relied mainly on marine resources of the Pacific coast. Yet, around 3,500 years ago, agriculture started to be more predominant and a higher prevalence of oral pathologies associated with carbohydrate-rich diets has been observed. Thus, this study aimed to assess the impact of agriculture on the oral microbiome of these populations over the last 9,000 years.

We collected archaeological dental calculus samples from coastal sites (n=30, Archaic Period (9,000-3,500 years BP)) and inland sites (n=35, Agricultural Periods (3,500-1,000 years BP)) in northern Chile. DNA was extracted from a subset of samples (n=14, 7 from each period) followed by library preparation and shotgun sequencing. The microbial community for each sample was taxonomically profiled using SourceTracker analysis and MetaPhlAn4, and DNA damage patterns were assessed using MapDamage2.

Our results show well-preserved ancient microbial DNA, but low host (human) DNA. We also found changes in the microbial communities after the agricultural transition. For example, strains associated with environment and oral microbiota (*Desulfobulbus sp., and Staphylococcus sp.*) are more abundant in the Archaic Period. In contrast, strains associated with oral diseases (*Pseudoramibacter alactolyticus, Desulfobulbus sp.,* and *Tannerella forsythia*) are more common in the Agricultural Period. Interestingly, *P. alactolyticus* and *T. forsythia* have been reported in pre-Hispanic populations from the U.S. and Mexico, but not in South America. Currently, we are assessing phylogenetic origins of specific oral microbial strains in this population.

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Brace yourself: Investigating the advantages of subtalar joint mobility during walking on an uneven surface

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The human subtalar joint allows for inversion-eversion motion that was likely retained from an adaptation for arboreal locomotion in our ancestors. Retention of this mobility presents the risk of trauma, like common ankle sprains, but may represent an adaptive tradeoff. Subtalar joint mobility could aid in walking across uneven surfaces, where it could assist with adjusting foot posture to help maintain balance without necessitating costly changes in stance width. To determine the advantages of subtalar joint mobility during bipedal walking, we used ankle braces to reduce subtalar joint mobility, thereby observing how frontal plane mechanics during walking were perturbed. We collected three-dimensional kinematic and kinetic data from ten subjects (6 males, 4 females; 29±3 years, 1.7±0.7 m, 67.8±12 kg) who walked barefoot across an uneven surface with and without ankle braces. These braces had stabilizing splints designed to limit inversion-eversion motion. The uneven surface consisted of tiered blocks of stiff EVA foam that caused a repeating 1-2 cm height variation. On average, the brace reduced inversion-eversion motion during walking by 19%, driven by a 68% decrease in maximum eversion. Participants wearing ankle braces increased their stance width by 23.5% and experienced 13.4% higher maximum medial ground reaction forces. Previous research has shown that increasing stance width during walking beyond the preferred width significantly increases the metabolic cost of walking. Thus, our results suggest that an advantage of subtalar joint mobility is to reduce walking costs on naturally uneven surfaces as well as reduce medial loads on the lower limbs.

Inferences from the radius of *Ardipithecus ramidus*

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The morphology of the primate forelimb reflects its use in positional behaviors and can be used to reconstruct locomotor behavior in fossils. Although the human forelimb is largely freed from a locomotor role, some fossil hominins seem to have engaged in climbing and suspensory behaviors. Here we test whether the radius may be a reliable indicator of locomotion and locomotor ancestry in fossil hominins.

Comparative shape data were collected from radii of *Homo sapiens* (n = 57), six species of extant apes (n = 210), two species of cercopithecoids (n = 59), and fossil hominins Ardipithecus *ramidus* (ARA-VP 6/500), *Australopithecus afarensis* (A.L. 288-1), *Australopithecus sediba* (U.W.88-85), and the "Little Foot" *Australopithecus* (StW 573). Whole bone shape of the radius was quantified using elliptical Fourier analysis.

As predicted, radial morphology partitioned the sample into humans, knuckle-walkers, and brachiators, with digitigrade cercopithecoids and orangutans overlapping with one another. The radii of the knuckle-walking African apes are robust proximally and distally and curved ventrally, contrasting with the straight radial shafts of Asian apes and cercopithecoids. The unique pattern of robusticity and curvature expressed in African ape radii may relate to stabilizing the arm during knuckle-walking. The radius of *Ardipithecus ramidus* exhibits unique characteristics among hominins, falling exclusively within the gorilla morphospace. Although *A. ramidus* seems to have been a habitual biped on the ground and was proposed to lack features suggestive of African ape-like ancestry, this study adds to the growing body of evidence suggesting that humans likely evolved from a knuckle-walking ancestor.

Reconstructing and evaluating morphological differences in the upper and lower limbs of *Australopithecus*, *Paranthropus*, and early *Homo*, using non-homologous fragments

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Our understanding of the early stages of human evolution is constrained by the increasing discovery of a wide diversity of sympatric hominin populations, often represented by fragmentary remains. This limitation significantly impacts the study of postcranial remains, not only due to the difficulties in finding homologous bone fragments, but also in identifying their taxonomic allocation.

While various reconstruction techniques are available, these approaches have primarily been applied to cranial remains, and have also raised several methodological questions concerning the use of modern specimens or single fossil individuals. To address this issue, we have developed a novel approach for reconstructing hominin long bones, utilizing morphological variables extracted from modern anatomical data. Our approach implements a technique called the 'Reverse Engineering' method, which leverages landmark-based information to predict the morphology of entire bones, based on morphological variables extracted from the portions of preserved bone represented by each fossil fragment. We have then applied this technique to the fossil record, reconstructing several femoral and humeral fragments from *Australopithecus*, *Paranthropus*, and early *Homo* (non-*erectus*).

Our reconstructions reveal a more ape-like morphology for *Australopithecus* in both its upper and lower limbs, while indicating certain differences when compared to the *Paranthropus* femur, which exhibits an anatomy that does not entirely align with either the chimp/orangutan cluster, or the human morphology. In contrast, non-*erectus* early *Homo* is reconstructed with a clearly bipedal femur while retaining ape-like features in its humerus. These results concur with previous interpretations, implying differences in the locomotor repertoire among these three genera.

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Systematics and population genetics of a high-altitude primate in the Himalayas

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Taxonomy is replete with groups where the species identity and classification remain unresolved. One such group is the widely distributed Himalayan langur (Colobinae: *Semnopithecus*). For most part of the last century, the Himalayan langur was considered to be a single species with multiple subspecies or was subsumed into other species. This traditional classification was mainly based on morphology, which was one of the issues creating the ambiguity in taxonomy. We used an integrative taxonomy approach wherein morphological, molecular, and ecological data was used to resolve the taxonomy of Himalayan langur. We do not find any support for the currently recognised three species, therefore, we suggest subsuming these three species into a single species *Semnopithecus schistaceus* Hodgson, 1840. Further, we also studied the population genetic structure of *S. schistaceus* in the Indian Himalayas. We hypothesised the complex topography and varied climatic conditions across the Himalayas, resulted in genetic structure across different populations of *S. schistaceus*. We used the mitochondrial cytochrome *b* gene with a combination of phylogeographic analysis and palaeodistribution modelling to test this hypothesis. Here we show that the deep river valleys in the Indian Himalayas act as a barrier to gene flow between different populations. Further, we found that *S. schistaceus* in the Indian Himalayas is nested within the *S. schistaceus* populations from the eastern Himalayas. This was corroborated by the statistical phylogeographic and niche modelling analysis, suggesting an east to west dispersal of these langurs after the last glacial maximum.

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New Late Miocene cercopithecid fossils from the Lemudong'o Formation, southern Kenya

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The Lemudong'o Formation (5.8-6.1 Ma; southwestern Kenya) has previously yielded fossils of three distinct colobine taxa: the medium-sized *Paracolobus enkorikae*, a large indeterminate colobine species, and a small indeterminate colobine species. Renewed collection efforts at the main fossil sites from 2019-2023 recovered 42 additional cercopithecid specimens confidently attributable to taxon. The three previously described colobine taxa are represented, along with a previously undocumented papionin monkey. A partial female cranium preserving most of the face and palate is referred to *P. enkorikae*, representing the first definitive facial morphology for this species and one of the few colobine crania from the Miocene. The face demonstrates a relatively long rostrum, large orbits, and narrow interorbital pillar, distinguishing it from the type species of the genus, *P. chemeroni*, but somewhat similar to other late Miocene colobines such as *Libypithecus* and *Sawecolobus*. Additional isolated teeth are attributable to the indeterminate small and large colobine species at the site.

A papionin is also reported from the Lemudong'o Formation for the first time, identified by two M_3s, anterior molar fragments, and a partial upper incisor. These specimens are distinguished from the colobines by their taller crowns and lower, rounded cusps. The M_3s also have well-developed hypoconulid lobes, further distinguishing them from cercopithecins (guenons). The Lemudong'o papionin is similar in size to *Parapapio lothagamensis* from the late Miocene at Lothagam and *Parapapio* cf. *ado* from Kanapoi, ca. 4.2 Ma. At 6 Ma, these specimens add to a meager late Miocene papionin fossil record.

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Ontogeny of jaw muscle fiber types in tufted and untufted capuchins

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Myosin heavy-chain isoforms–or muscle fiber types–in the jaw muscles of primates are highly variable, providing a range of contractile properties. Further, primate jaw muscle fiber-type phenotype has been linked to variation in feeding behavior. Currently, however, the fiber-type phenotype of primates during development is unknown. Here, we report preliminary analyses using immunohistochemistry to determine fiber-type expression in the masseters of an ontogenetic sample of tufted (*Sapajus*, n=13) and untufted (*Cebus*, n=13) capuchin monkeys. We predict that fiber-type phenotype will change as primates transition from suckling to an adult diet. Additionally, ontogenetic changes in fiber-type phenotype will vary between primate species with different feeding behaviors. Capuchins are an excellent model for these analyses as *Sapajus* demonstrate a mechanically challenging diet compared to *Cebus*. Three antibodies were used to determine the presence/absence of Type-I (NOQ7.5.4), Type-I alpha-cardiac (MyH6), and Type-II (MY32) myosins. Age groups were divided by dental eruption into infant, juvenile, subadult, and adult. The majority of cells across age ranges and genera were hybrid cells (co-expressed multiple myosins). Fiber types varied between age groups;

notably, *Sapajus* increased Type-II expression by 25% while *Cebus* increased Type-I by 50% from infant to adult. Fiber phenotype was significantly different between *Sapajus* and *Cebus* within each age group ($p<0.001$, log-linear regression) and *Sapajus* consistently displayed a greater variety of hybrid-types across ontogeny. These novel results highlight the diversity of contractile properties in developing primate jaw muscles and suggest flexibility in feeding parameters across ontogeny.

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The evolution of vertebral shape throughout human evolution

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The evolution of bipedalism represents a pivotal step in human development, with a complex biomechanical process involving diverse musculoskeletal systems. This transformative shift is evident in skeletal alterations across the entire body, encompassing changes in bone size, shape, and orientation. The spine, serving as the principal weight-bearing component linking the head, upper limbs, trunk, pelvis, and lower limbs, plays a crucial role in this process.

However, the extent of changes in vertebral shape and size from chimpanzees to the earliest habitual bipedal hominins, the australopithecines, has generated conflicting interpretations within existing literature. Therefore, this research aims to elucidate the morphological transformations in the lumbar vertebrae, shedding light on the evolutionary journey of the hominin spine.

In pursuit of this goal, we conducted a comprehensive comparative analysis of lumbar vertebrae from chimpanzees, australopithecines, Neanderthals, and modern humans, employing both linear and 3D shape analyses.

Our findings indicates that Australopithecines display lumbar vertebral shapes and sizes that neither resemble modern humans nor chimpanzees. Instead, they form a distinctive group, highlighting their unique adaptation to bipedal locomotion. Neanderthal lumbar vertebrae, on the other hand, align closer with those of modern humans, indicating a convergent evolution in this regard.

Australopithecines exhibit a novel lumbar vertebral morphology, representing a biomechanical evolutionary solution for bipedalism. This uniqueness parallels their distinctive pelvic morphology, as suggested by Rak (1991). The concept of an intermediate evolutionary form should not be expected, as evolution offers a spectrum of morphological solutions to address various constraints.

Coevolution of modern humans hands and feet

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Modern human hands and feet can be distinguished from those of apes. Modern humans have distinctive hand proportions, characterized by long thumbs relative to fingers. Their feet feature a robust, fully adducted, and non-opposable hallux, as well as the absence of a tarsal break. These characteristics are viewed as adaptations to obligate bipedalism and responses to lithic manipulation behaviors.

However, some authors propose the possibility that both autopods did not evolve independently. They suggest that modern human hand proportions may be a by-product of morphological adaptations for bipedalism in the foot, due to pleiotropic effects. In this study, our aim is to shed light on the coevolution of hands and feet. To achieve this goal, we tested differences in the organization of their skeletal structures and calculated magnitudes and patterns of covariation between hands and feet to assess their ability to evolve independently.

To do so, we utilized nine linear variables for each of the 19 bony elements of the hand and foot (metapods and phalanges). Our preliminary results indicate that both autopods are not modularized structures, with the exception of the first digit acting as an independent element in comparison to the other digits. Additionally, all five digits exhibit a strong correlation with their homologous counterparts in the other autopod, especially the first digit, where size has exerted a positive influence. Finally, the analyses of evolutionary responses of the hand and foot digits to random selection gradients indicate a high degree of evolutionary constraint, mainly in the first digit.

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Modeling the impact of cultural processes and selection regimes on the fate of loci undergoing evolutionary mismatch

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Phenotypes that are adapted to ancestral environments may no longer be advantageous in a new environment, potentially leading to "evolutionary mismatch" and decreased fitness. This hypothesis has been popularized to explain rising rates of lifestyle-associated health issues in "Western" societies, which experience socio-ecological conditions that diverge from recent human evolutionary history. Mechanistically, evolutionary mismatch is predicted to manifest as one of two selection regimes: 1) a beneficial allele (thus historically under positive selection) in the population's ancestral environment becomes detrimental in the "mismatched" environment, or 2) a neutral allele in the population's ancestral environment becomes detrimental in a mismatched environment. However, no research has been conducted on the fate (extinction vs retention) of mismatched loci in their novel environments, or whether the selection regime impacts this fate. To study these loci, we developed an agent-based computational model to simulate fitness outcomes, incorporating cultural processes including migration, market integration that increases over time, horizontal and vertical knowledge transfer, and assortative mating. Our results suggest that migration rate is the most important factor for the fate of mismatched loci. In particular, mismatched loci are retained in populations while migration continues to occur, but then quickly approach extinction if migration ceases. Under different conditions, we then investigate whether the selection regime or the magnitude of selection pressure difference between environments is more important to changes in allele frequencies. Overall, this work sheds light on how migration and other cultural processes impact genetic loci and health traits around the world.

New paleoecological data from the middle Miocene of Maboko Island, Kenya reveals a humid subtropical local climate

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Over eight decades of paleontological fieldwork in the middle Miocene deposits on Maboko Island, Kenya, have yielded a rich mammalian fauna including at least six primate species, preserved within a long stratigraphic sequence. The diversity of primates from Maboko, including the first appearance of a large-bodied semi-terrestrial hominoid and a dominance of stem cercopithecoids, has generated interest in the environmental context in which these taxa evolved. Fieldwork at Maboko Island was renewed in 2022 with an emphasis on re-evaluating the stratigraphy and paleopedology of the Maboko Formation localities. Paleosol samples were collected for bulk elemental geochemistry, soil description, and phytolith analysis. Preliminary results of paleosol descriptions and phytolith analyses indicate landcover on Maboko Island and the adjacent mainland locality of Majiwa was mostly wooded and shows a transition between woodland habitat types. Paleoclimate estimates from elemental compositions of paleosol samples suggest a mean annual temperature (MAT) between 18 and 25°C and a mean annual precipitation (MAP) between 900 and 1800 mm yr-1, placing Maboko in the "humid subtropical" climate regime. These MAT and MAP results contrast with previous inferences of a much drier and hotter paleoclimate for Maboko. Overall, these results suggest that the Maboko fauna inhabited a relatively moist, woodland habitat. This aligns with recent herbivore enamel isotopic profiles that indicate foraging in open and closed woodland environments, with no consumption of C_4 or water-stressed C_3 vegetation. This new paleoclimatic and paleoecological data have implications for the paleoenvironmental context of middle Miocene primate evolution.

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Inflammation has opposing effects on heart and brain health in later life among the Tsimane and Moseten of lowland Bolivia

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Inflammation in later life has been implicated in health risk. However, studies among the Tsimane and Moseten in lowland Bolivia have complicated this relationship, as they experience repeated pathogen driven inflammation throughout life, yet cardiovascular disease and dementia are rare. Here we investigate these associations at the individual level within the population to further clarify the relationship between inflammation and health. Previous studies have found that infections and inflammation are associated with elevated metabolic rates and impaired child growth among the Tsimane, suggesting it is a significant energetic stressor. While this might be protective for cardiometabolic health, at the same time it might also compete with and constrain brain energetics, impairing function and health. To understand this complex relationship, we tested associations between a battery of immune measures (15 cytokines, C-reactive Protein, IgE) and CT-scan measures of epicardial adiposity, total brain gray matter, white matter, and overall brain volume (n = 885 – 1,013 depending on measure) in a sample of older Tsimane and Moseten (ages 39 – 94 years, mean = 60.4 years). Among the immune markers, those indicating inflammation in response to helminth infection (IgE and IL-5) were associated with better heart health and poorer brain health. IgE was negatively associated with epicardial adiposity and total brain white matter, while IL-5 was negatively associated with both gray and white matter as well as overall brain volume. Our findings indicate complex, opposing effects of inflammation on heart and brain health in later life among the Tsimane and Moseten.

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Dental arch shape and dimensions influence maxillary and mandibular third molar impaction

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Populations around the world suffer from the negative effects of third molar impaction. This research evaluates the hypothesis that certain dental arch dimensions could contribute to obstruction of an incoming third molar in both the upper and lower jaw, which would contribute to third molar impaction. We digitized landmarks on intraoral 3D scans of 61 dental casts, collected from populations in India in 1983-1984 and housed at the University of Oregon. The sample includes individuals from the Madia Gond, Maratha and Mahar populations, all between 18 and 30 years of age. The sample was further divided into one group with visible third molar impaction as determined by visible cross-impaction of a tooth, and a second group with no visible third molar impaction. Landmarks were used to calculate maxillary and mandibular arch length and were then processed using Generalized Procrustes and principal component analyses. No significant differences were observed in maxillary or mandibular arch length by sex or population based on ANOVA, although the first principal component (PC1) of maxillary arch shape was significantly different by population. However, with all populations and sexes pooled, third molar impaction significantly influences the relationship between maxillary and mandibular arch lengths. Both maxillary and mandibular PC1 scores were significantly different between non-impacted and impacted third molar groups. From these data, maxillary and mandibular arch shape and dimensions may contribute to third molar impaction and may therefore be useful tools for predicting impaction in humans.

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Genetic History and Population Structure of Kazaks in Jetisuu as Informed by Genome-wide SNP Data

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Kazaks have a social structure that is composed of three *Jüz*, and multiple clans comprise each of the *Jüz*. Previous studies revealed the maternal and paternal genetic profiles of Kazaks. However, no research has addressed the population structure of Kazaks through a holistic approach that utilizes genome-wide data and with special reference to the social structure and genealogy. We hypothesized that the social structure of Kazaks has a genetic basis and they descended from a common ancestor as informed by the folklore and genealogy of Kazaks. To test this hypothesis, we genotyped 80 individuals who belong to four clans of the *Great Jüz* using genome-wide SNPs (~750K) on the Geno 2.0 microarray. For comparative purposes, we genotyped 10 Kazak individuals from other regions using the same microarray platform. We found that, while paternal lineages were relatively homogenous, with most individuals sharing a common paternal ancestry, maternal lineages were intriguingly heterogenous. Despite the maternal heterogeneity, the autosomal SNPs did not reveal any pronounced genetic structure, implying Kazak populations formed through ancient admixture events followed by a homogenization process. These results contribute to our understanding of the social organization of historical nomadic societies from Central Eurasia, and provide new insights that complement the anthropological knowledge gained through the ethnographic and historical studies of these populations.

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Cognitive-locomotor interactions during human foraging

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Human foraging requires cognitive and physical demands that may influence how the brain and body interact during movement. For example, bipedalism in environments with uneven terrain challenges stability in ways that may require enhanced cognitive resources for motor control. Foraging combines these stability challenges, with higher order cognitive tasks. The concurrent combination of cognition and movement are known as cognitive-motor dual-tasks. Researchers have often used dual-task paradigms to investigate how cognitive resources are partitioned. However, the influence of cognitive-motor dual-tasks on locomotor performance have not been observed during foraging. Here, we test the hypothesis that locomotor mechanics will be associated with ecologically relevant dual-tasks - communication with others and while walking over uneven terrain. We tested this hypothesis using data collected during foraging bouts with the Hadza, a hunter-gatherer population living in northern Tanzania. Nine Hadza women were followed and recorded during nine separate foraging bouts. Dual-task behavior (engaged in communication while walking) and terrain unevenness were classified. Walking cadence (strides per minute) was quantified for each minute of foraging bouts. Participants engaged in communication during ~49% of bouts and walked over highly uneven terrain in ~16% of bouts. Dual-task behaviors and uneven terrain were associated with a ~6% ($F(1,428)=39.039$, $p<.0001$) and ~15% ($F(2,428)=19.056$, $p<.0001$) decrease in walking cadence, respectively. Our preliminary results indicate that during foraging, walking cadence may decrease when individuals engage in dual-tasks and navigate challenging terrain, possibly due to shared cognitive resources diverted away from speed and towards other important cognitive demands, such as maintaining stability.

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Looking within: Why race scientists easily exploit anthropological science

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In the early 20th century the conflation of physical anthropology with the burgeoning field of genetics crowned our subdiscipline as a scientific field concerned primarily with racial studies. Our methodological toolkit was deployed to enact eugenic policies, and physical anthropologists--understood to be race scientists--facilitated the Second and Third Reich's genocides in Namibia and throughout Europe. While contemporary biological anthropology is no longer considered a race science, it is continually appropriated to support racist agendas within science. Here we focus on normative practices within our subdiscipline that reflect how racial logics persist, and illustrate how they render our scholarship easily exploitable by race scientists. First, we describe how our naming practices convey samples as bounded biological entities, supporting an essentialized and typological understanding of human variation. Second, we demonstrate how using trees to depict evolutionary relationships allows racial purists to easily conceive of "populations" as end points of distinct and non-reticulating lineages. Finally, we explore what it means that biological anthropology conceives of humanity primarily through the lens of the past, a temporally distant space that allows for the flagrant use of reified populations and bifurcated relationships. Yet "the past" is not an innocent space; it often serves to naturalize the present. We end by challenging biological anthropologists to reflect on how historical events and traditional methods have shaped our contemporary discipline, and how we can shift methodological norms towards ones that do not as easily play into the premise of race science.

Habitual activity induced musculoskeletal stress markers among coastal prehistoric foragers in Yayoi Japan

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Rank ordering of musculoskeletal stress marker (MSM) scores from high to low is used to examine the utilization of sets of muscles as related to behavioral activity. Strong similarities in rank ordering suggest similar labor activities, while dissimilarities suggest distinctive activity patterns. Here, we test two hypotheses: 1) It is possible to determine if different prehistoric agricultural sites were doing different activities; 2) Earlier agricultural sites were taking part in a broad-spectrum subsistence economy, while later agricultural sites were relying heavily on farming. These hypotheses were tested by studying nine human skeletal collections that date to the Yayoi (2600-1800 BP) period in Japan, long considered to represent a large-scale rice agricultural society. These collections are curated in the Kyushu University Museum. This MSM study modifies the Hawkey and Merbs (1995) method to score three morphological traits (robusticity, stress lesions, and ossification exostosis) with intermediate scores. A total of 72 muscle attachments (36 per side) from the upper and lower limbs were used to assess the MSMs of 191 individuals. Hypothesis 1 was supported by our results, however hypothesis 2 was refuted. Instead of all the sites becoming more reliant on rice farming with time, we discovered that the coastal sites continued to participate in a broad-spectrum subsistence economy, while the inland sites relied heavily on rice farming. Geography played a significant role in what types of subsistence activity were present in Yayoi Japan rather than the entire region universally becoming a rice agriculture society.

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Implications of the australopithecine diet for the emergence of unique hominin subsistence strategies and social structures

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Australopithecus afarensis, Australopithecus africanus, and Australopithecus sediba are the three best-represented members of the genus Australopithecus, which is widely accepted as the direct ancestral group of the genus Homo. In order to understand subsistence patterns and their influence on social structures within this group of hominins, I compared data on their diet, habitat, and anatomy to corresponding data and behavioral observations on modern human hunter-gatherers and chimpanzees who occupy habitats similar to reconstructed australopithecine paleoenvironments. In many ways, the anatomy and diet of australopithecines are mosaic between those of modern great apes and modern humans. Therefore, it may be inferred that their subsistence strategies, and therefore social structures, were similarly mosaic- perhaps becoming more similar to those of the genus Homo over time. These three australopithecine species evolved during a period of intense climate fluctuations trending towards aridification in eastern and southern Africa. In the face of these new environmental conditions, the lineage made a shift towards exploitation of savanna resources much different from those used by modern savanna chimpanzees, exemplifying the ingenuity of the lineage. This adoption of novel, more complicated subsistence methods likely fostered a growing division of labor- although it likely did not resemble the somewhat stricter sexual division of labor present in many modern human cultures- accompanied by increasingly complex social grouping patterns in australopithecine communities. I argue that climate-related dietary pressures are the main driving force behind the emergence of unique hominin subsistence strategies and social structures beginning with Australopithecus.

Frontal bone allometry and differentiation in *Homo erectus* and other archaic *Homo* fossils

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The aims of the current study are threefold: 1) characterize the 'common allometric component' (CAC) for frontal bone shape in *Homo erectus* s.l. and other archaic-looking *Homo* species; 2) assess whether the CAC constrained population and species differentiation; and 3) evaluate the influence of brain size, face size and temporalis size on frontal bone allometry. The latter aim is in keeping with William Jungers' position that allometric patterns are descriptive and require explication.

Variation in frontal bone size accounts for 15% of differences in frontal bone shape across the sample. The CAC reflects a wide and superiorly expanded frontal squama combined with a narrower supraorbital torus in larger individuals and most closely reflects brain size variation. However, a multiple regression model of shape on the natural logs of endocranial volume, temporalis size and bi-orbital breadth indicates roles for all three factors in determining frontal bone shape. A size-shape PCA suggests that population and species differentiation diverged from the CAC in many cases. Asian groups of *Homo erectus* diverge along PC 2, which is influenced by the size of the temporalis muscle whereas African *Homo erectus* as a group are distinguished on PC 3, a dimension that is partially affected by upper facial breadth. Thus, frontal bone allometry (shape change associated with frontal bone size variation) reflects changes to endocranial volume, but does not strongly constrain population and species differentiation. Temporalis muscle size and upper facial breadth influence frontal bone shape independently of endocranial volume and relate to population divergence.

Characterizing variation in black-and-white ruffed lemur (*Varecia variegata*) allomaternal care

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Ruffed lemurs (*Varecia* sp.) are unusual among primates in their suite of reproductive strategies: females bear litters of altricial young, which are nested during their early development; young are sometimes communally créched; and litters receive extensive allomaternal care (AMC) from members of their extended social community. Nevertheless, details of their AMC, including the identities and relationships of care providers and the amount and types of care they provide, remain unclear. Here, we synthesize observational data collected during four birth seasons (2008, 2019, 2021, 2023) to characterize patterns of allomaternal care (AMC) observed at the nest in one black-and-white ruffed lemur community. We combined 5-minute instantaneous focal nest sampling (n = 2,200h) with long-term demographic, social network and relatedness data (2007-2008, 2017-present; 15 microsatellites) to characterize *Varecia* AMC, as well as the social and genetic relationships among mothers, infants, and their allomaternal caregivers. We found that the number of helpers at the nest varied among mothers (range, 1-5; mean2.75, n=16), and included members of all age-sex classes except subadult males. Adult males provided the majority of AMC (76.19% of care observed), followed by adult (23.44%), and subadult females (0.36%). AMC included grooming, huddling, playing and nest guarding. Helpers were often, though not always, a mother's preferred male partner and her close female relatives (R > 0.25). Our results build upon earlier work examining the importance of communal nesting among mothers, and expands this to include the extensive AMC exhibited by non-mothers in this taxon.

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The Woodland Cemetery and African American Burial Ground Historic Preservation Project: Researching the Complicated History of Clemson University's On-Campus Burial Ground

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Clemson University's Woodland Cemetery resides on a landscape with a complicated history that began well before the establishment of the University. In 1826, the former vice president John C. Calhoun established Fort Hill Plantation and created Cemetery Hill, now known as Woodland Cemetery, as the burial ground for those enslaved on area plantations and members of the Calhoun family. While the cemetery was officially re-established in 1924 for white university faculty, it has served as the final resting place of enslaved peoples, sharecroppers, tenant farmers, convict laborers, and wage workers and their families. Due to the variety of people buried upon Cemetery Hill, Woodland Cemetery encapsulates not only the Antebellum Period, but the totality of the burial populations of the region through to the current day. Much of the history of the cemetery has been intentionally hidden; however, in 2020 with the aid of archaeological survey and ground penetrating radar, university faculty, students and community members identified over 500 unmarked African American graves.This discovery led to the creation of the Woodland Cemetery and African American Burial Ground Historic Preservation Project which now leads the process of revealing the complete history of Woodland Cemetery and telling the story of those who are buried in this sacred space. The project now navigates the arduous task of identifying the burial populations through a multidisciplinary approach including bioarchaeology, archival research, genealogy and community engagement. Through this project Clemson University is dedicated to the long-term preservation and memorialization of Woodland Cemetery.

Crafty women: Life and death of a potter from Kerma period Sudan

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Although feminist archaeology originated in the 1980s, women's roles in craft production often remain overlooked due to biased assumptions about gendered labor and who possessed requisite skills. This presentation highlights the lived experiences of an innovative female potter in ancient Sudan. Located 25 m downslope of other graves at Site ASU 09-01 near al-Qinifab, Sudan, her grave was reopened in antiquity, disturbing the skull, neck, and shoulders. Like most, the body was flexed on the right side and wrapped in a hide (radiocarbon dated to 1751-1619 cal BCE, 95.4% probability). A bone tool with a tapered end was found along the upper back. Several potsherds from the superstructure and shaft fill showed vessel shapes and decoration unlike local styles, with similar sherds found in some other graves. Lesions on visceral surfaces of ribs, small calcified plaques, and a calcified nodule (granuloma) indicate a chronic respiratory disease, potentially tuberculosis or silicosis, an occupational hazard of miners and potters. Together, the tool and respiratory infection suggested this individual was a potter. The granuloma was negative for *M. tuberculosis* DNA and micro-CT scanning showed no necrosis, supporting a non-infectious origin and diagnosis of silicosis. The few remaining teeth are severely worn. Both humeri have well-developed deltoid tuberosities with osteoarthritis of the left elbow and left wrist pathology. The pelvis contained tissue and four molariform, fully rooted teeth, accompanied by straightened right ribs 8-9, indicative of an unusually large teratoma. Strontium isotope analyses suggest she grew up locally, despite production of unusual ceramics.

Biocultural analyses lend insights into local population histories in ancient Fuegian-Patagonians

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Paleogenomic data are commonly used to test archaeological questions, but paleogenomics best informs ancient population histories when applied using a biocultural approach that contextualizes genomic analyses within a socio-historic framework. In this study, we focus on hunter-gatherer populations from southern Patagonia and Tierra del Fuego (Fuego-Patagonia) who have inhabited the region for more than 10,500 years. These groups practiced subsistence strategies that relied on either marine or terrestrial resources, or a mix of both. Some prior studies suggest that Marine and Terrestrial groups descended from the same ancestral group, while others indicate they had distinct ancestries.

Here, we examined genome-wide data from 40 newly sequenced and 30 previously reported ancient Fuegian-Patagonians spanning 6,800 years, as well as sociocultural evidence from archaeological, ethnohistorical, and linguistic sources. Previous analyses of the newly sequenced individuals suggested that Marine and Terrestrial groups had distinct ancestries that diverged ~14,000 years ago. To further elucidate the genetic relationships among Terrestrial, Marine, and Mixed Economy groups, we examined population substructure using PCA, ADMIXTURE, tests of genetic distances, and *f*-statistics. We found that some Marine and Mixed Economy individuals from the Middle Holocene shared ancestry with Late Holocene Terrestrial groups, while Terrestrial and Marine groups from the Late Holocene showed distinct ancestries and limited admixture until Historic times. We contextualized these paleogenomic results with evidence from sociocultural sources, adding further nuance and justification to our conclusions. This study highlights the complexities of local population histories and demonstrates the importance of including sociocultural data in paleogenomic studies.

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Investigating the admixture history of humans in the Indian Himalayas using ancient genomics

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The Himalayan arc has played a crucial role in molding the genetic, cultural, and ethno-linguistic diversity of human populations in the region. Archaeological evidence suggests long-term cultural connections across the Himalayan region, such as the trans-Himalayan cist burial culture found in Tibet, Nepal, India, and Northwest Pakistan and dated to the first millennium BCE through historical times. Paleogenomics studies have reported gene flow into the Tibetan plateau and Central Himalayas (Nepal) from Central Asia and South Asia as early as 2,300 years ago, supporting archaeological findings of cultural connections across the broader trans-Himalayan region. However, little is known about past and present-day admixture dynamics on the western end of the Himalayan arc.

We characterized genetic variation over time in the Indian trans-Himalayas by generating genome-wide data from three ancient individuals dated to the last ~1,500 years from Spiti Valley, located in the state of Himachal Pradesh in the Indian Himalayas. All three ancient individuals are from high-altitude (4,270-4,650 masl) cist burial contexts. The ancient individuals, sequenced to 0.5-15X, exhibit the greatest genetic similarity to present-day Central and West Himalayan populations, consistent with genetic continuity in the region. Furthermore, we found evidence of lowland South Asian admixture in the ancient individuals, which suggests that genetic connections between high-altitude and lowland regions in the Indian Himalayas date back to at least 1,500 years. Our results provide the first insights into the human genetic history of the Indian Himalayas using ancient genomics.

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Phylogenetic Analysis of the Lukeino Molar (KNM-LU 335) using Occlusal Morphology

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KNM-LU 335, known informally as the Lukeino molar, is a hominoid mandibular molar collected in 1973 from the Lukeino Formation, Kenya, and dated to approximately 6 million years old. Paleoanthropologists have since debated its taxonomic attribution, with some finding morphological affinities with modern *Pan* and others finding similarity to early hominins, perhaps even representing *Orrorin tugenensis* directly.

Given the ambiguity of the molar type ID of Lukeino, variation was assessed by collecting 2D landmark coordinate data on photographs of the occlusal surface of M_1 and M_2 of *Pongo, Gorilla, Pan, Australopithecus*, *Homo habilis,* modern humans, and the Lukeino molar. Analyses of variance (ANOVAs) were performed on the cusp area ratios to test for significant differences between groups. Landmark data were subjected to principal component analyses. The landmark coordinate data together with cusp angles (derived from cusp apex to morphological constants) and cusp area ratios were analyzed in TNT to reconstruct the phylogenetic position of KNM-LU 335 using parsimony.

ANOVA and principal component results show low separation among the groups, with the Lukeino molar placed in various positions within the overlapping ranges of *Pongo*, *Gorilla*, and *Homo* morphospace, depending upon the data employed. Interestingly, the Lukeino molar did not overlap with chimpanzees. Phylogenetic analyses using parsimony recovered the Lukeino molar as sister taxon to either fossil hominins or crown hominines, contingent on character source.

These results underscore the uncertain taxonomic status and tooth position of this specimen. Expanding this work to include Miocene hominoid mandibular molars may further clarify our findings

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Aiding and abetting racism in the biological and behavioral sciences

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As overt racism has become increasingly unacceptable in the academy, race science has shape-shifted. While some full-blown race science continues to flaunt itself unapologetically, there is also work that is not explicitly racist, but that aids and abets race science indirectly. This can occur even when the researchers themselves disavow racist intentions, often through negligence (acting without knowledge of potential harms) or recklessness (acting while knowing that harmful effects might occur). Here I review several areas of recent anthropological research that can and have been used to bolster racist projects. I theorize these indirect effects using the framework of epistemic and ethical risk. I present data from a cross-cultural study of moral judgment which shows that negligent and reckless actions are widely considered blameworthy, reflecting a value of a *duty to know* about the potential consequences of our actions. While many researchers in today's scientific and political climate believe they can insulate themselves from responsibility by claiming good intentions, lack of knowledge, or inability to control the potential effects of their research, I argue that researchers expose themselves and others to risk of harm by turning a blind eye to the potential uses of their work. I offer a taxonomy of mechanisms whereby such indirect complicity can occur, despite the (sometimes) good intentions of researchers. I conclude with thoughts on how we can employ analyses of ethical risk in the design, execution, and communication of our research.

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Application of regular equivalence blockmodeling to identify epidemiological roles associated with hookworm infection in rural Madagascar

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The social patterning of infectious disease transmission depends on *whom* you interact with and *how* you interact with them. Role analysis via equivalence-based blockmodeling identifies latent roles in a social system from multiple interaction patterns in a network. We used this method to identify epidemiologically meaningful roles among 159 adults (≥18 years old) in a rural agricultural community in northeast Madagascar. Roles were determined using five types of relations involving social interactions and providing/receiving food and farm help. We used logistic regression models to investigate the association between role membership and infection with two species of hookworm (*Necator americanus* [a human hookworm] and *Ancylostoma ceylanicum* [a zoonotic hookworm shared with dogs]). We identified three distinct roles. Role one (n=58) and two (n=65) had the highest mean total degree centrality scores, and role three (n=36) had more isolates across relations. Individuals in role one often named individuals in role two as people they provided farm help to and received food help from, while individuals in role two helped fewer people with farmwork, and those they helped tended to also be in role two. Role two members had higher odds of infection with *A. ceylanicum* than role one members (OR [95% CI]: 2.20 [1.05-4.64], p=0.038), but role membership was not significantly associated with *N. americanus* infection. This analysis suggests that having more people work your land in this setting—likely a higher status role—is associated with a greater risk of zoonotic hookworm infection, which is commonly associated with low socioeconomic status.

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Biomechanics of stone tool production: a novel approach to percussive force measurement in flintknapping experiments

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Increasing studies of stone tool production by Plio-Pleistocene hominins are focusing on the relationship between the biomechanics of stone knapping and the evolution of human anatomical structures. A key component of this research is understanding the generation and application of percussive force during flaking in relation to the functional morphology of the hominin upper limb. However, there is currently a lack of experimental capability to directly measure force variables in the knapping process, such as the net force applied by flintknappers to detach flakes through hammer impact. This study presents a new instrumental design involving a synthetic hammerstone consisting of a custom-designed 3D-printed deformable pneumatic chamber that is encased within a 3D-printed handle and a stone-milled hammer tip. The device uses a pressure sensor to record the pressure change during percussion. This pressure signal is used to estimate force, based on a calibration model developed using force plate measurements. Validation using an anvil-supported knapping setting shows that the hammer device is capable of accurately recording the percussion forces under variable hammer striking angles while detaching flakes. Our research provides a new versatile method for quantifying hammer percussion force during flintknapping experiments. This innovation enables future studies to directly investigate the role of percussion force in flake formation and the biomechanics of stone knapping, allowing a new range of research possibilities in the study of tool use behavior in relation to human anatomical evolution.

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Regional and Temporal Patterns of Dental Disease in Prehistoric Central California

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Archaeological research in prehistoric Central California reported temporal declines in foraging efficiency reflected in the temporal increase in the use of smaller, more costly game and lower-ranked plant foodstuffs. Regional dietary differences have also been noted between inland and bayshore shore environments. This study examines regional and temporal patterns of dental disease among foragers from Central California as a window into oral health. The study comprises 511 adults from six Central Valley (CV) and four San Francsico Bay Area (SFB) sites, dating to 4950-200 B.P. Each tooth position was inventoried and scored for carious lesions, antemortem loss, postmortem loss, and occlusal attrition. Caries prevalence was calculated for the total number of scorable teeth, and burials were aggregated by region, time period, and sex. Dental caries prevalence was significantly higher in CV sites vs. SFB sites for all time periods (p<.001). Caries rates in CV males declined from 7.6% to 5.9% between the Early and Middle period, and then increased to 6.6% in the Late period (p<.001); among females, caries rates declined from 23.3% to 13.0% between the Early and Middle period (p<.001) and then increased to 19.3% in the Late period (p=.005). Dental caries prevalence in SFB males was <1% for all time periods, whereas female caries rates increased from 3.0% to 5.6% between the Early and Middle period, and then declined to 2.2% in the Late period (p=.018). Sex differences were most marked in the CV, where female caries rates were two or three-fold higher compared to males.

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Contrasting evidence of a short-term scarring effect following two synergistic epidemics of measles and scarlet fever: Investigation of age-cause-specific contributions to life expectancy change

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Previous research identified a synergistic pattern of overlapping epidemics of measles and scarlet fever (SF) in Victoria, Australia in 1866–1868 and 1874–1876, with mortality peaks in 1867 and 1875. Here we consider potential mortality impact of these diseases beyond the immediate epidemic period and test the hypothesis that changes in life expectancy (LE) could indicate the presence of a short-term scarring effect. We use annual age- and cause-specific death statistics and census population data to construct abridged period life tables for a baseline period, combined mortality peak year, and post-crisis year for each of the two periods and compare LE at birth using Z-tests (following Sawchuk et al., 2022). We decompose age-cause-specific mortality according to Arriaga's method to identify age- and cause-specific contributions to LE change.

LE at birth in 1869 (47.6 ± 0.26) was not significantly different from the 1864–1865 baseline (47.7 ± 0.35); however, LE at birth in 1878 (47.5 ± 0.22) was significantly lower (p<.00001) than the 1871–1873 baseline (49.1 ± 0.24). Measles and SF contributed more than twice the impact on LE in 1875 (4.44 years of life out of 7.42) compared to 1867 (2.05 years of life out of 3.06), but it was a lower proportion of the LE drop. This suggests the larger and longer LE drop in the 1870s may be explained by the impact of other causes of mortality, either acting independently or as part of a previously unidentified synergistic or syndemic relationship with measles and/or scarlet fever.

Virtual reconstruction of the StW 573 *Australopithecus* skull

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The specimen StW 573 ("Little Foot"), dated to 3.67 million years old, represents the oldest occurrence of *Australopithecus* in southern Africa. StW 573 is remarkable for the exceptional degree of preservation of its skeleton, which includes a nearly complete skull with only a small area of bone missing in the basicranium. However, post-depositional damage resulted in the lower face being displaced upward into the frontal and left zygomatic bones, while the frontal squama has been pushed downward. Additionally, the supraglabellar and the temporal line regions are fragmented and buckled. Here we present the first digital reconstruction of the StW 573 skull. The skull of StW 573 was scanned in 2019 by propagation phase-contrast synchrotron X-ray micro-computed tomography at the I12 beamline of the Diamond Light Source (United Kingdom) with an isotropic voxel size of 21.23 μm. Semi-automated segmentation was performed to digitally separate bones and teeth from the matrix and isolate bone fragments using smart interpolation in Biomedisa (https://biomedisa.org/). Digitally and physically (i.e., using 3D prints), pieces were assembled manually according to their anatomical position and natural breaks and sutures. Because StW 573 is the most complete adult southern African *Australopithecus* skull to date, comparative shape analysis of the reconstructed skull is crucial to track evolutionary changes and address long standing questions on the timing and process of the evolution of the hominin head (e.g., integration versus modularity, neutral evolution versus adaptive evolution).

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Structural vulnerabilities and Indigenized harm reduction strategies for missing and murdered Indigenous peoples, Idaho

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The Missing and Murdered Indigenous Persons (MMIP) crisis necessitates urgent, culturally sensitive solutions amid reporting discrepancies and a lack of cooperation between law enforcement, forensic practitioners, and tribal leaders. These issues are deeply rooted in colonial violence, racism, and discrimination, creating structurally embedded vulnerabilities within Indigenous communities. Forensic anthropologists should specialize their practice with culturally-informed and contextualized strategies to better support the populations they serve.

We present a Global Information System (GIS) database and map of MMIP cases in Idaho. Mapping is merged with spatial and homicide/health data to understand whether socioeconomic status, availability of social/health services, and locations of police departments impact MMIP cases in Idaho. Next, Indigenous-created and led (Indigenized) harm reduction strategies were adopted to guide medico-legal practitioners in best practices for MMIP cases. Indigenized harm reduction, incorporating traditional knowledge and community-driven methods and reflecting cultural norms and social structures, were sourced and prioritized in developing this guide.

Results demonstrate spatial patterning of MMIP correlated to the county population size, social services, and law enforcement presence. An anonymized MMIP case study is presented to demonstrate proof-of-concept for practice of Indigenized harm reduction strategies. Unlike conventional Western methods, Indigenized harm reduction is intersectional, centers community history, community engagement, and culturally-grounded knowledge of missing individuals. Overall, contextualizing MMIP cases and incorporating Indigenized harm reduction can create lasting impact by amplifying Indigenous voices and addressing systemic issues, driving a shift towards a safer, culturally informed environment for Indigenous peoples in Idaho.

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Reconstruction of Amud 7 baby Neandertal, and its implication for Neandertal evolution

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Neandertal infant remains, especially those within the 0-2-year age range, are exceedingly rare in the archaeological record, with only a few documented cases. One such discovery is the infant skeleton, Amud 7, unearthed in 1991. This specimen was identified as Neandertal based on cranial features, with an estimated age of around 10 months, determined by incisor tooth eruption. Despite its significant implications for understanding Neandertal growth and development, a comprehensive 3D reconstruction of Amud 7 is lacking.

This study aims to create a detailed 3D reconstruction of Amud 7, encompassing both cranial and postcranial elements. Micro-CT scans of Amud 7 were conducted in 2011 by the Max Planck Institute. The reconstruction process involved three key steps: re-identifying virtual scanned osteological elements, positioning them in their anatomical position, and replicating missing components from their contralateral counterparts. Endocranial volume was determined using a warped virtual endocranium, equivalent to that of a 10-month-old human.

Nearly all attributed bones and fragments of Amud 7 were successfully integrated into the 3D reconstruction. The endocranial volume, measuring 753cc, aligns with that of a 6-8 month-old modern human infant. However, the length of long bones suggests an age closer to 12-14 months. This intriguing disparity suggests significant differences in Neandertal growth and development compared to modern humans, emphasizing the need for further research to elucidate the distinctive aspects of Neandertal ontogeny and their broader implications for human evolution.

Geometric morphometric analyses of the enamel-dentine junction of the premolars and molars of the Miocene hominine *Anadoluvius turkae*

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Hominid fossils from the 8.7 Ma site of Çorakyerler (central Anatolia, Türkiye), originally attributed to *Ouranopithecus*, have been recently re-assigned to the new taxon *Anadoluvius turkae*. Multiple cladistic analyses recognize the clade including *Anadoluvius, Ouranopithecus,* and *Graecopithecus* (graecopithecins) as stem hominines, but the origin of hominines remains unclear. Some analyses recover dryopithecins as stem hominines broadly ancestral to graecopithecins. Others recover dryopithecins as stem hominids, with the ancestry of graecopithecins more likely represented by *Nakalipithecus.* Here we investigate the morphology of the enamel-dentine junction (EDJ), a dental structure recognized as a reliable taxonomic and phylogenetic proxy. We analyzed the EDJ shape of maxillary and mandibular premolars and molars of *Anadoluvius* in comparison with other Eurasian Miocene apes, Plio-Pleistocene hominins (*Australopithecus* and *Paranthropus*), and extant great apes (*Pan*, *Gorilla* and *Pongo*) using geometric morphometrics. Our results indicate that *Anadoluvius* and *Ouranopithecus* show similar EDJ molar shapes, resembling both pongines and hominins, but differing from dryopithecin and African ape morphologies. However, dryopithecins also overlap with *Pan*, *Pongo,* and the hominins, sharing similar overall EDJ proportions and occlusal pattern, which complicates the interpretations of phylogenetic relationships. The EDJs of *Anadoluvius* premolars classify most commonly with *Pan* in comparisons with extant apes and variously with diverse hominids when fossil taxa were included. Our results support *Anadoluvius* and *Ouranopithecus* as closely related. Additional analyses including hominins and other Miocene apes are required to further clarify patterns of EDJ shape among hominines.

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Morphology of the early Upper Paleolithic Zlatý kůň mandible, Czech Republic

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The Zlatý kůň (ZK) human remains were found in the 1950s in Koněprusy Cave (Czech Republic). After their discovery the skeletal remains were consolidated with bovid collagen biasing radiocarbon dating methods. Currently, the most conclusive evidence for the ZK age comes from a recent analysis of the length of Neandertal DNA sequences in the ZK genome which confirmed its early Upper Paleolithic attribution (ca. 45 ky BP). This makes the ZK individual, consisting of an incomplete cranium, mandible, and vertebral and rib fragments, the best-preserved early *Homo sapiens* specimen from Europe. Here, we describe the morphology of the ZK mandible, and we present geometric morphometrics analyses of its shape using samples of extant modern humans and Middle and Upper Paleolithic fossil samples. The ZK mandible is moderately large with highly worn teeth and substantially flattened condylar processes. The specimen shows a modern suit of discrete traits characteristic of Middle and Upper Paleolithic *Homo sapiens*, and it is characterized by massive mandibular body, oblique mandibular angles, broad rami, and a low position of the coronoid processes. The overall shape of the ZK mandible falls outside the variation of extant modern humans and is closer to Middle Paleolithic and early to middle Upper Paleolithic *Homo sapiens*. The morphological affinities of the ZK mandible align with its previous paleogenetic analysis.

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Skeletons in the Closet: reanalysis of mammalian fauna from the early Pleistocene site of ‘Ubeidiya, Israel, and the implications for early *Homo* dispersals from Africa

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The site of 'Ubeidiya, Israel, 1.4 ± 0.2 million years ago, has a rich collection of Acheulean lithic and vertebrate fossils. Initially, the fauna was believed to have a high percentage of endemic species from various biogeographic regions. As a result, the Levant was considered a cul-de-sac, implying that the early dispersals of *Homo* may have led to a demographic dead-end rather than continuous dispersals. However, since the seminal publication in 1986 and other studies in the early 2000s, there have been significant changes in our understanding of taxonomy, new comparative material has been discovered, and new analytical methods have been developed.

Here, we updated the taxonomy, biochronology, and biogeography of the 'Ubeidiya mammalian fauna. The revised biochronology is consistent with the earliest Biharian or the later phases of Odessian faunal units, suggesting a date of 1.5 to 1.8 mya which is older than previously estimated. Moreover, the study suggests that some species (e.g., *Parapodemus jordanicus*) could not be sustained, while new species have been discovered (e.g., *Cricetus nanus*). The number of endemic species, a hallmark of previous studies, has significantly decreased. While the fauna of 'Ubeidiya includes elements from different zoogeographic regions, the high relative proportion of African taxa is reduced. The results of this study suggest that the Levant is a biogeographic corridor. While these findings do not rule out the possibility that isolated *Homo* populations became extinct, the case of continuous dispersal of populations as early as 1.8 million years ago is now open.

Preliminary Results of Quantitative Measurements for Age-at-Death Estimations of Three Pelvic Joints

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Age-at-death estimations of human skeletal remains are essential for reconstructing individual identities, as well as modern and past populational demographics. Many methods for age-at-death estimations rely on practitioner experience to accurately assign a score of phases to a particular set of traits. To mitigate subjective biases that occur with macroscopic analysis, this project aims to quantify age-related changes observed on three pelvic joint surfaces: the pubic symphysis (PS) and the iliac and sacral auricular surfaces (IAS and SAS, respectively). As individuals age, feature variability on joint surfaces increases; Dirichlet normal energy (DNE) was implemented as a shape characterizer to quantify the age-related variation of the three joint surfaces. A total of 110 paired os coxae and sacra, aged 18-102 years ($\bar{x}$ = 64.8 years), from the Texas State University Donated Skeletal Collection were scanned with an Artec Space Spider to acquire three-dimensional meshes. The isolated joint surface meshes were imported into R Studio and DNE values were calculated from the mola(r) statistical package. A Pearson’s correlation coefficient was used to assess the relationships between the calculated DNE values and age individually for the PS, IAS, and SAS. Results indicate low correlations between DNE values and age: $r = 0.287$ (PS), $r = 0.257$ (IAS), and $r = 0.0858$ (SAS). While previous research found positive correlations between DNE with age for the PS, the low correlations for three pelvic joints from this study suggest alternative quantitative methods should be explored for quantifying change related morphological changes observed on pelvic joint surfaces.

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A high incidence of antemortem rib fractures in a historical Chinese population

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Excavations at the Ming period (A.D. 1368-1644) tombs at Upper Xuwucun, Shaanxi, recovered twenty-three adult skeletons from one family, who were members of the local gentry class. Of the ten male individuals, four exhibited healed fractures of the ribs. This paper investigates the possible causes of such a pattern. We consult the epitaphs of these specific individuals recording the events of their lives, other patterns of trauma (or lack thereof) in this group of individuals, modern clinical data on injury patterns, and sources on Chinese social and economic history. Based on all these lines of evidence, we conclude that the healed rib fractures were likely the result of working in close contact with draft animals. Despite their relatively high status in their local community, these men engaged in agricultural labor and trade which necessitated close contact with large domesticated animals, and the consequences of that work seem to be clearly reflected in the 40% incidence of rib fractures among them. We also discuss the sequelae of rib fractures and the possible impact they had on these men’s subsequent morbidity and mortality.

The excavation of these individuals was funded and conducted by the Shaanxi Archaeological Academy.

A Comparison of Inter-State Human Skeletal Remains Trafficking Laws: Case Studies from Washington State and Recommendations for Improved Protections

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In the United States the sale and purchase of human skeletal remains are largely governed by state laws. While 38 states currently have laws of this nature, they are varied in content and enforcement. Washington State has one of the most progressive sets of laws in the United States governing the discovery and investigation of human skeletal remains. The law dictates how human skeletal remains – both forensic and archaeological/historic – are handled, and by whom, from discovery to disposition. However, the law notably lacks clear provisions governing the trafficking of human skeletal remains within the state. Because the initial jurisdiction of human skeletal remains finds/cases falls to individual county coroners and medical examiners, the lack of an explicit state law necessitating their investigation has resulted in mixed legal application. This has been further complicated by clandestine internet sales where the identification of and location of individuals involved in the sale are difficult to identify. Here, we present data on 23 case studies from Washington and how individual counties have handled them. Case outcomes under Washington State law are compared to that of other states and suggestions for improvement to Washington State law are offered. This research illustrates how this problem plays out in one state, the lessons – positive and negative – that can be learned from other states, and brings this issue to the attention of the biological anthropological community.

A transdisciplinary, bioculturally sensitive and sustainable approach towards inclusive prosthetic design

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The vast majority of the ~31.6 million lower-limb amputees (LLAs), worldwide, live in low- and middle-income countries (LMIC). A range of lower-limb prosthetics exist for high-income countries (HICs) to account for user variability, but few exist for LMICs, suggesting there is more sociocultural, economic, and demographic variability within HICs than between LMICs. Working with a local prosthetic and orthotic (P&O) centre in northern Sri Lanka, we developed a transdisciplinary approach to quantify user needs for the co-design of culturally relevant, sustainable prosthetic devices for LMICs. Statistical analyses of an anonymized database from the centre (30 years, 3,665 patients) revealed most amputees seen by the centre were transtibial and male, and >90% of all patients were LLAs. A global literature review revealed results are largely consistent with other LMICs, pointing highlighting gender gaps in P&O provisioning. Wear analysis on broken prosthetic feet from the P&O centre revealed excessive wear under the end of the keel and around the edge of the foot, being particularly high at the heel and under the toes: these failure mechanisms are not captured by western prosthetic design standards (ISO 10328). This because of cultural differences with how the prosthetics are being used. Ethnography (surveys, interviews, and observations) of LLAs revealed issues with prosthetic function and cosmesis due to a lack of biocultural flexibility in the prosthetic design. Combining multiple fields (biocultural anthropology, anthroengineering, prosthetics, data science) has helped create criteria for the design and development of culturally relevant, sustainable prosthetic feet in northern Sri Lankan.

The project has been funded by the Global Challenges Research Fund (GCRF), London South Bank University, and the British Council.

Guidelines for Forensic Anthropology in Northern France. Where Medicolegal Significance Meets Archaeological Relevance

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Establishing medicolegal significance from skeletal remains is a pivotal aspect of forensic anthropology practice or casework. This work examines a structured flowchart of steps and coordinated cooperation between multiple institutions for the proper management of inadvertent discoveries of human skeletal remains within the criminal jurisdictions of Northern France. In a region where over 38,000 archaeological sites are listed in the Ministry of Culture's geo-referenced database, the existence of a structured, systematic, and multi-partner cooperation is necessary for guiding experts and for assessing the archaeological susceptibility of an area and the medicolegal relevance of human skeletal remains. By presenting the flowchart and organization of the structure, we highlight the importance of integrating the efforts of the forensic experts, the French judicial system, the law enforcement agencies, the war graves organizations and the archaeological authorities.

At the interface of the French Penal Code and the Heritage Code, the flowchart serves as the linchpin, guiding stakeholders through a meticulously designed sequence of actions and decisions from the moment the law enforcement officer is notified of the discovery of skeletal remains until the presentation of findings through a standardized report. This protocol also emphasizes the response at the scene using advanced techniques such as precision imaging laser scanner to conduct documentation of the scene and describes the routine implementation of analytical methods for determining the post mortem interval of the remains. Through tangible examples, this presentation demonstrates the mutual benefit for archaeological heritage and the criminal justice system.

This project has received funding from the Hauts-de-France Region (France)

Stress in transition? A diachronic analysis of population health in Hellenistic and Roman Anatolia

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Although the Roman Empire has been depicted as a homogeneous political, economic, and social landscape, recent archaeological research indicates that it was instead a patchwork, with different ethnic groups reacting differently to the imposition of imperial rule. In this way, while some populations experienced deleterious physiological effects as a result of their subjugation, there is ample evidence to suggest that individuals of differing social status, age, and geographic origin experienced the physical effects of these changes in diverse ways. The goal of this study is to understand how the transition from Hellenistic to Roman rule in southwestern Anatolia impacted overall population health. The skeletal remains of Hellenistic (n=30) and Roman (n=76) individuals from the archaeological sites of Kibyra, Myndos, and Patara (N=106) were assessed for skeletal indicators of stress as a proxy for overall population health. Each individual was then evaluated using the Skeletal Frailty Index, which is based on clinical frailty indices for modern living populations that measure health sequelae of life-long stressors. After assigning each individual a skeletal frailty score and calculating crude prevalence rates of pathological conditions, comparisons of overall health status were made between cohorts at the intra-site, inter-site, and temporal levels. Preliminary results suggest that overall population health (as proxied through the skeletal frailty index) remained largely unchanged from the Hellenistic to the Roman period. Therefore, while the Roman conquest of southwestern Anatolia initiated a notable shift in civic, religious, and political life, it was insufficient to impact the physiological condition of the local populations.

Investigating the relationship between elemental fluctuations and seasonality in baboon teeth

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Baboons are an excellent proxy for investigating questions about human evolution due to their generalist diet and habitat overlap with early hominins. Previous analyses of baboon teeth show fluctuating patterns of strontium and barium, nonessential metals. Similar elemental fluctuations were reported in *Australopithecus africanus* teeth and were causally linked to seasonality. Here we further assess this in baboons using tooth histology, laser ablation-inductively coupled plasma-mass spectrometry of calcium-normalized strontium and barium (Sr/Ca and Ba/Ca), and high-resolution ion microprobe analyses of oxygen isotopes to discern rainfall variation and timings of Sr/Ca and Ba/Ca changes. Three baboon taxa from three localities were analyzed: *Papio ursinus* from Cape Peninsula, South Africa (n = 5 individuals, 6 teeth), *Papio hamadryas x anubis* (*hybrids*) from Awash, Ethiopia (n = 3 individuals, 8 teeth), and *Papio anubis* from Rubirizi, Uganda (n = 1 individual, 2 teeth). Seasonal dietary variation is notable in Cape and Awash baboons, leading to predictions that Cape baboons would show increased strontium in the wet season and Awash baboons would show increased strontium in the dry season (barium was also expected to vary in response to seasonal changes in rainfall). However, co-plots of Sr/Ca, Ba/Ca, and oxygen isotope ratios show variable patterns for each tooth, including teeth from the same individual. Increases in strontium and barium in these baboons are not consistently linked to wet or dry seasons. Additional studies are needed to test associations between elemental variation in teeth and seasonality, particularly suggestions that such patterns are due to dietary stress.

Energy limitation during early life impairs fat oxidation: evidence from children and adolescents in Vanuatu

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Evidence suggests that limited dietary energy intake during childhood and adolescence can increase risk of obesity in adulthood, but the underlying mechanisms remain unclear. In this study, we tested the hypothesis that early life energy limitation leads to a lower metabolic rate and impaired fat oxidation, factors that have been shown to be predictive of later gains in body weight and fat tissue. To do so, we used data collected from 60 children and adolescents (aged 6-15 years; n=31 females) living in Vanuatu. Relative leg length, calculated as the ratio of leg length to stature, was used as a surrogate measure of each individual's early life energy availability, with a short relative leg length considered indicative of energy scarcity. Fasting resting metabolic rate (RMR) and respiratory quotient (RQ) were measured with indirect calorimetry, and a high RQ value was considered indicative of a low rate of fat oxidation. We found that in a general linear model controlling for sex, age, body weight, and village, relative leg length was not significantly associated with RMR ($p=0.88$). However, in a separate model, relative leg length was found to be significantly negatively correlated with RQ ($p=0.049$), after controlling for sex, age, and village. The latter finding suggests that energy limitation during early life leads to impaired fat oxidation, which has the potential to increase risk of obesity later in life. This finding might partially explain the so-called double burden of malnutrition (the co-occurrence of undernutrition and obesity) currently affecting many low- and middle-income countries.

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The DOMINA project: revisiting the condition of women in Milan over 2,000 years through their skeletal remains

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The DOMINA (Donne Milanesi Nascoste – Hidden Women of Milan) project aims to revisit the condition of women of Milan over the last 2,000 years in an interdisciplinary approach including bioarchaeology, paleopathology, history, and paleoepidemiology, centered around the study of skeletal remains. The project started with 200 skeletons from the Anthropological Collection of the LABANOF, equally divided by sex and historical periods, representing a continuum of 2,000 years in Milan (25 females and 25 males from Roman, Medieval, Modern and Contemporary periods). The sample has now increased to over double its original size (n=484). Results showed that female skeletons tend to be less complete than those of males (ANOVA, $p=0.01$) regardless of age-at-death or post-mortem interval and that male and female stature did not significantly vary across historical periods in Milan ($p<0.001$). Mann-Whitney U and ANOVA tests showed robusticity of entheseal changes varied significantly with sex and historical period. Kaplan-Meier survival analyses and Gompertz hazards analyses indicated decreased survivorship and higher risks of death for females compared to males in the Roman ($p=0.014$, $p=0.037$) and Modern ($p=0.039$, $p=0.079$) samples, but increased survivorship and lower risks of death for females in the Contemporary sample ($p=0.001$, $p=0.009$). These first results are starting to shed new light on the life experiences and history of women in Milan over the last 2,000 years with different patterns of lifestyle and survivorship.

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Misinterpretations of admixture regression in racial hereditarian research

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A major focus of racial hereditarian research is to estimate the degree to which mean differences in phenotypes between "racial groups" are driven by a mean difference in their genetic value. Racial hereditarian researchers have recently published several 'admixture regression' studies that try to exploit admixture, which 'mixes' genetic variation between groups, to test whether individuals carrying more alleles from one group have a higher average trait value than individuals carrying more alleles from the other group. We explore how the interpretation of admixture regression can lead to erroneous conclusions about the etiology of phenotypic differences between groups that are actively harmful when applied to the study of health disparities and variation in 'cognitive ability'. We address the misapplication of admixture regression using bottom-up generative models and simulations. We show that trait-ancestry correlations can arise without a difference in mean genetic value between groups, and even when a trait has no heritability, as a result of environmental factors that are correlated with ancestry (e.g. structural racism). This kind of confounding obscures any real correlation between ancestry and genetic value, the direction of which may be in the opposite direction of the correlation between ancestry and trait. We demonstrate that efforts to correct for such environmental confounders using noisy proxies (e.g. socioeconomic status) are insufficient. Researchers, especially those studying racial health disparities, should exercise caution, acknowledge the multifaceted nature of group differences, and integrate various disciplines to avoid reinforcing the genetic essentialism that allows racial hereditarian research to prosper.

The HUMANITY exhibition: a model for decolonizing human evolution museum displays

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As human beings we are fascinated with our origins, and there is no greater story than our evolution. This story is, however, too often filtered through a colonial lens, both in the media and museums. Within these spheres of public discourse, the legacy of racist science persists, as does the centering of the Great (White, Western) Explorer narrative of discovery. This does a disservice to science and the public and impedes the transformation and progress of our discipline. Here we discuss the process by which we produced a new permanent museum exhibit at the Iziko South Africa Museum titled *HUMANITY*, where we attempted to decolonize the narratives of human evolution and decenter Whiteness. This exhibit represents many voices and was created through active community engagement, including input from researchers, curators, artists, community leaders and museum visitors. All exhibition components, from research to design principles, were developed to create a welcoming, inclusive space that shares our origin story as a collective. We focus on the diversity of people in South Africa today and delve into how this diversity came to be. In doing so, we explore themes of cultural identity, genetic relatedness, human variation, and the deep evolutionary and archaeological past. The thread of complex human interconnectedness runs through the exhibit and is consistent with our current understanding of the braided stream narrative for human origins. Finally, the exhibition acknowledges the negative legacies of paleoanthropological practice and encourages critical reflection on race, skin color variation and privilege.

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Nutritional supplements 'biscuits' increase regurgitation and reingestion behavior in captive gorillas (*Gorilla gorilla gorilla*)

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Regurgitation and reingestion (R/R) remains a poorly understood behavior observed in apes in human care. Animal welfare management goals include reducing stereotypic behaviors while providing nutritionally adequate diets. We quantified R/R behavior of the Santa Barbara Zoo's two male Western lowland gorillas (*Gorilla gorilla gorilla*), Bangori and Nzinga (January – May 2021). When the gorillas arrived at the zoo in 2016, Nzinga exhibited frequent R/R behavior. Upon arrival, the gorillas transitioned to a low starch and high fiber diet to reduce R/R prevalence. We tested if the subsequent reintroduction of nutritional supplements 'biscuits', due to weight management and husbandry considerations, would cause increased R/R behavior. Observers recorded all occurrences of R/R behavior in 1-hour sessions (n=93). Gorilla diet types, in order of occurrence, were 1) 0% biscuits, 2) 2% biscuits, 3) 4% biscuits, 4) 2% biscuits, and lastly, 5) 0% biscuits. Bangori rarely performed R/R behavior during the study. We developed a Bayesian model to estimate Nzinga's R/R occurrence by diet type. Nzinga's highest R/R rates occurred during the second 2% biscuit diet (exponentiated posterior mean: 27.4, 89% CI: 11.8, 65.3). No R/R behavior was observed during the baseline 0% biscuits. Informal keeper review of gorilla videos revealed a temporal component to R/R behavior. R/R behavior occurred frequently between 10am-noon after morning feeding, which may explain the higher R/R frequency during the second 2% biscuit diet based on sampling protocols. Biscuits resulted in increased R/R behavior with implications for behavioral management of gorillas in human care.

New auditory ossicles of *Homo naledi* (Rising Star Cave, South Africa)

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A previous study analyzed three incudes from *Homo naledi* and found them to show ancestral features for the genus *Homo*. The present study describes the morphology and dimensions in several new specimens. A series of linear, angular and areal measurements were taken on these specimens following previously developed protocols and compared to fossil hominins and extant hominids. UW101-0633 is an isolated incus retrieved when sieving sediments from the site. UW101-0633 resembles the previously discovered *H. naledi* incudes in the dimensions that could be directly compared, including a relatively closed angle between the crurae. Four additional ossicles were virtually reconstructed from microCT scans of the temporal bones, including an associated partial malleus and incus (UW101-396) and two nearly complete stapes (UW101-231 and UW101-1044). The partial preservation of the associated malleus and incus limits the comparative analysis of these two bones. However, the limited measurements possible suggest the malleus is human-like, while the incus resembles extant African apes more closely. The two *H. naledi* stapes fell outside of the range of variation in *H. sapiens* in a principal components analysis of size-adjusted variables, but were within the 95% confidence ellipses of African apes. These results are consistent with previous studies of early hominins and *H. naledi*, suggesting this species shows a combination of a human-like malleus while the incus and stapes more closely resemble African apes. This study contributes new data to our understanding of *H. naledi* middle ear morphology and taxonomy.

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Dietary stress, tooth characteristics and the Patterning Cascade Model

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We examined relationships among crown size, principal cusp spacing, and accessory cusp expression from maxillary dental casts of nutritionally supplemented (n=34) and non-supplemented (n=39) individuals from Tezonteopan, Mexico. The groups profoundly differ in nutritional status. We hypothesized that non-supplemented individuals would have smaller molars and reduced principal cusp spacing. Based on previous studies, we expected the non-supplemented individuals to have greater frequency and expression of Carabelli trait and cusp 5. We predicted that anterior tooth crowns of the non-supplemented individuals would be smaller with fewer tuberculum dentale. Finally, we investigated whether the presence of accessory traits followed predictions of the Patterning Cascade Model (PCM).

We found that principal cusp spacing differed more than crown size between the two groups. The non-supplemented group showed little evidence of increased Carabelli trait frequency, but some evidence of greater trait scores. As predicted, the non-supplemented group showed some evidence of greater frequency and expression of cusp 5. Also, following our prediction, the non-supplemented group had reduced central incisor and canine crown sizes with fewer tuberculum dentale. Lateral incisors did not conform to these predictions. With respect to the PCM, we found strong evidence of a decrease in mesiodistal distances between principal cusps in molars with Carabelli trait or cusp 5. These findings are consistent with the PCM and suggest there are many possible configurations among principal cusps that can favor the initiation and growth of later-forming cusps. It may then be useful to consider the impact nutritional stress might have on accessory cusp expression.

As the bones churn: efficiency and observer reliability in documenting highly fragmented, burned human remains

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Prolonged and/or high temperature thermal damage, such as vehicle fires, plane crashes, explosions, etc., can diminish a body to small bone fragments which are brittle, warped, shrunken, commingled, and in other ways, taphonomically altered. The complexities of documenting such remains are particularly tedious and time consuming for practitioners with limited resources and crew. Forensic field recovery protocols have been refined for efficient, complete, and detailed recoveries at fatal fire scenes. Yet, there is no comparable forensic guidance for documenting highly fragmentary, burned bones/teeth once they reach the laboratory, particularly if they were not systematically recovered.

A case study of highly fragmented, burned skeletal remains analyzed from a vehicle fire lasting 14 days, which were subsequently churned, is presented. Responding to the complexities of this case, a qualitative, multi-method scoring guide was developed for efficient documentation. Fleiss' kappa and intraclass correlation coefficient were calculated to assess observer agreement and reliability using this guide among 5 observers who recorded burning modification traits from 45 photographs of fragments.

Results show that this approach increased documentation time of highly fragmented, burned bone by 70%+ when focused on identification classes, zonation, size class, color categories and locations, and surface modifications (texture/fractures, warping, adherences, etc.). Overall, observer agreement was highest related to experience level ($\kappa = 0.61$ to 0.80), but combined parameters demonstrated high inter-rater reliability (ICC > 0.75). This guide is adaptable to individual case needs and laboratory resources and is time efficient and user-friendly for a range of experience levels.

Pinniped-derived *Mycobacterium tuberculosis* strains along the pre-conquest Osmore Drainage Valley, Perú

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Tuberculosis (TB) in pre-conquest South American humans was caused by a *Mycobacterium tuberculosis* complex (MTBC) strain that today primarily infects seals and sea lions, suggesting that people contracted TB while hunting, consuming, and processing pinnipeds. Although pinniped exploitation was limited to coastal regions, ancient *M. pinnipedii* genomes have been recovered from pre-conquest skeletons from inland Colombia, suggesting that this zoonotic strain became human-human transmissible. We seek to understand the evolutionary mechanisms underlying the introduction, diversification, and replacement of *M. pinnipedii* in human populations. To do this, we have targeted archaeological sites within the Osmore Drainage Valley of southern Perú representing a time transect from 385 BCE to 1476 CE, encompassing the Huaracane, Tiwanaku, Tumilaca, and Chiribaya cultures. The interconnected population centers span 50 miles from the coast to the Osmore Mid Valley, composing an ideal sample to determine how pinniped-derived strains entered and spread among human populations. We extracted DNA from vertebrae (n = 64), ribs (n = 14), ilia (n = 4), sacrum (n =1), ulna (n = 1), and teeth (n = 21) from 85 individuals with skeletal lesions indicative of tuberculosis. We built 81 DNA extracts into 81 single-stranded, dual-indexed libraries, which were shotgun sequenced to 4-50 million reads on the Illumina NovaSeq X Plus. We screened the sequencing data for evidence of MTBC DNA using a competitive mapping approach (MALT) and a k-mer based approach (Kraken2), and we identified 16 candidates for whole genome capture. We discuss the discrepancies in positive assignments between the two approaches.

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Multiple Component Sulci Form the Chimpanzee Lunate Sulcus

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One of the major hallmarks of hominin brain reorganization is the loss of the occipital operculum and its border the pongid lunate sulcus (LS), which in apes are major functional and organizational landmarks. Allen et al. (2006) showed that the human sulcus labeled as the lunate is made up of multiple lesser sulci and suggested that it is therefore not homologous to the chimpanzee LS. We used BrainVisa to quantify sulcal patterns, surface area, and depth in the occipital lobe of over 200 chimpanzee brains and show that the chimpanzee LS is also composed of multiple lesser sulci, so having component sulci cannot be a basis for discounting homology. Our study of intraspecies variation suggests that the chimpanzee LS is composed of a shorter, more medial sulcus and a longer, more lateral sulcus, likely homologous to the sulci Duvernoy (1999) labeled in humans as the transverse occipital sulcus and the sulcus lunatus.

Bone modeling and remodeling: similar response to mechanical loading?

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Haversian bone remodeling (HR) responds to mechanical loads by replacing discrete amounts of damaged tissue, representing a valuable proxy for reconstructing patterns of physical activities of past populations. However, the microscopic response to loading is not straightforward, and HR is also influenced by several other factors (e.g., age, sex, diet).

This study aims to investigate the microscopic bone responses to mechanical loading by analyzing the correlation between cross-sectional geometry parameters (CSGP) and HR in human second metacarpals. To control for confounding factors, we used residual asymmetry between pairs of metacarpals instead of raw values. Since humans tend to use their upper limbs asymmetrically, we hypothesized that right-left asymmetry of CSGP would be positively correlated with that of HR. We prepared histological sections from 126 pairs of second-metacarpal midshafts from two archaeological populations (Euro-Canadian and Inuit). Mechanical loading was quantified using the CSGP I_{max}, I_{min}, J, and cortical area. HR was estimated by calculating the Osteon Population Density (OPD) across the entire cross-section. Percentage of directional asymmetry (%DA), controlling for body mass and bone length, was calculated for each variable and correlations between %DA of CSGP and OPD were tested. Against expectations, our results showed that %DA-OPD was significantly negatively correlated with %DA-CSGP, with the more robust side experiencing fewer remodeling events than the smaller side.

These results suggest that, in metacarpals, bone turnover is slowed under higher loads. These results further underscore the complexity of skeletal response to loads, and the difficulty of inferring activity directly from Haversian remodeling.

The subfossil occurrence and paleoecological implications of the small mammal fauna at Tsimanampesotse, SW Madagascar

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We describe the subfossil vertebrate fauna from Tsimanampesotse National Park (TNP), southwestern Madagascar. At TNP, we recovered bones from 12 extinct species and >40 endemic extant taxa. Five of the latter are locally extirpated, including a Vulnerable euplerid (*Fossa fossana*) never previously been collected in the dry west or subarid southwest, and a rare nesomyid rodent (*Macrotarsomys petteri*). *Fossa fossana* is restricted today to the humid eastern rainforest and parts of the Central Plateau. The TNP vertebrate assemblage shows a dramatic shift in taxonomic composition over time. Prior to ~2000 cal yr BP, the assemblage consists of endemic species that are today extinct, locally extirpated, or surviving in the park. After ~2000 years ago, rainfall decreased, and species dependent on freshwater resources disappeared. Drought conditions became severe by 1600 cal yr BP and remained so until ~900 years ago. All TNP vertebrate dates between 2000 and 900 cal yr BP belong to smaller-bodied, endemic species, such as extant lemurs or bats, although indirect evidence supports local survival of some larger-bodied extinct taxa until ~1000 years ago. After 900 cal yr BP, we begin to see introduced taxa such as cats, rats, and cows alongside small-bodied endemic extant species. Our data support the "subsistence shift hypothesis" of megafaunal extinction. However, we also document local extirpation events almost certainly driven by climate change. This allows us to understand how climate may have impacted smaller vertebrate species and how climate change may have made megaherbivores more vulnerable to the impacts of agropastoralism.

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Strontium isotopes track female dispersal in Taï chimpanzees

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Chimpanzees (*Pan troglodytes*) are patrilocal, meaning males remain in their natal group and females usually disperse upon reaching sexual maturity. Female dispersal is difficult to assess, with origin and distance traveled unknown even in habituated chimpanzees. Strontium isotope ($^{87}Sr/^{86}Sr$) analysis allows the differentiation of local and non-local individuals in geologically heterogeneous landscapes. In this study, we present $^{87}Sr/^{86}Sr$ ratios of tooth enamel from habituated male and female chimpanzees (n = 34) and corresponding environmental samples (n = 35) from five neighboring communities in Taï National Park in Côte d'Ivoire. We tested the $^{87}Sr/^{86}Sr$ ratios measured in environmental samples from the different territories, as well as the $^{87}Sr/^{86}Sr$ ratios measured in enamel of resident males from these communities for isotopic differences. We then compared the $^{87}Sr/^{86}Sr$ ratios within North Group residential males and females, to females with unknown origin, and evaluated the potential origins of these females within and immediately outside of the Taï chimpanzee project (TCP) study area. We found significant differences between North Group residents and unknown females; however, we show that most females (n = 6) possibly emigrated from within the TCP study area, while some are local to North Group (n = 4). Based on this baseline dataset, we estimate that only one female with unknown birth community came from areas outside of the TCP study area. Our data provides novel insights into a largely unknown yet crucial phase of female chimpanzee life history.

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Hand use in Gorilla based on asymmetry of first metacarpal entheses

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A species-wide preference for right handedness is a defining feature of modern humans, but this pattern has not been observed in non-human primates, including *Gorilla spp*. Studies on *Gorilla* hand use have found conflicting results on hand use frequencies, though there is currently no evidence for species or even population-level hand preference within the taxon. *Gorilla spp*. use their hands in a wide variety of activities and *G. beringei* have been observed using an array of power and precision grips, all of which heavily recruit muscles of the hand. The *m. opponens pollicis*, located on the first metacarpal, is responsible for abduction and adduction of the thumb and is heavily recruited across many activities and grip types, which should elicit asymmetrical patterns of development if *Gorilla* habitually engage one hand over the other. This study analyzed asymmetry in the opponens pollicis muscle enthesis on the first metacarpal of *G. beringei* (n=4, 2 from each side) and *G. gorilla* (n=12, 2 each side) to test for bilateral asymmetry based on possible differential hand use. Three dimensional renderings derived from laser scans were used to generate elevation maps in the CloudCompare v12.2 software and individual asymmetry scores were calculated based on the distances obtained between sides. Results of paired t-tests comparing the right to left sides showed significant differences between sides, and further tests revealed left-directional asymmetry within the sample. This study highlights the need for further research into *Gorilla* hand use to better understand manual lateralization outside of modern humans.

Women's Health in Industrial-Era London

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Women's health in the past is poorly understood because of the historical processes of sexism and gender discrimination whose legacies continue to impact women's health in the present. We integrate skeletal samples (St. Bride's Fleet Street and New Bunhill Fields) and archival documents (*London Bills of Mortality* and *General Register Office Reports*) from industrial-era London to examine women's health across the life course, focusing on the relationship between adverse health experiences in childhood (growth disruption, infection, and nutritional deficiency) and their impact on respiratory disease burden in adulthood (inferred using visceral surface periosteal rib lesions). Using Bayesian modeling, we found that, contrary to expectations, the posterior odds of presenting rib lesions were lower among individuals with evidence of early life stress compared to individuals without such lesions after adjusting for age-at-death, biological sex, and social class ($\mathrm{OR}_{\text{cribra orbitalia}}$: 0.38, 95%CI:0.15-0.90; $\mathrm{OR}_{\text{enamel hypoplasia}}$: 0.28, 95%CI:0.12-0.64). Furthermore, neither sex nor class mediated the relationship between early life stress and respiratory disease burden, although being from the middle/upper class was associated with a lower odds of presenting rib lesions. Given previous evidence of a survival differential between individuals with and without rib lesions, these findings suggest that females and males who experienced early life stress were better able to physiologically respond to respiratory system stress as adults. We argue that women are not necessarily absent from all bioarchaeological research. Rather, inequalities other than those related to sex and gender may have a greater impact on morbidity and mortality in certain historical contexts.

Vertical jumping agility as a key measure of performance in strepsirrhine primates

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Though leaping is considered critical for strepsirrhine evolution, we lack sufficient leaping performance data to evaluate its adaptive role. Here, we examine vertical jumping agility (VJA) in four strepsirrhine species at the Duke Lemur Center: a specialized leaper (*Propithecus coquereli,* ~ 4.13 kg), two intermediate leapers (*Varecia variegata,* ~ 3.55 kg and *Eulemur coronatus,* ~ 1.82 kg), and a generalist (*Cheirogaleus medius,* ~ 0.20 kg). VJA – jump height divided by takeoff duration + flight duration – represents how much and how quickly an animal changes vertical position. VJA is tied to mechanical power density (*i.e.,* power per unit mass), which generally scales with negative allometry. We collected force data for 309 jumps and found absolute VJA was greatest in *Propithecus* (1.45 m/s, vs. *Eulemur*: 1.09 m/s, *Cheirogaleus*: 1.03 m/s, and *Varecia*: 0.957 m/s). However, adjusted for target height, VJA was greatest in *Cheirogaleus* (1.68 m/s, vs. *Eulemur*: 1.50 m/s, *Propithecus*: 1.14 m/s, and *Varecia*: 0.993 m/s). *Propithecus* generated the greatest absolute power densities (168 W/kg, vs. *Cheirogaleus*: 128 W/kg, *Eulemur*: 106 W/kg, and *Varecia*: 98 W/kg). But, *Cheirogaleus* had the greatest relative power densities adjusted for target height (200 W/kg, vs. *Eulemur*: 118 W/kg, *Propithecus*: 111 W/kg, and *Varecia*: 78.7 W/kg). Small-bodied strepsirrhines may require greater VJA and power density to reach a given target height because their small size affords them less time to achieve takeoff velocity, highlighting how key aspects of leaping performance vary in this clade.

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Using micromammal faunal analysis to contextualize vegetation structure local to the development of early human behavior in Pleistocene Morocco

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Contrebandiers Cave, a late Pleistocene site on the coast of Morocco preserves the remains of early anatomically modern humans, and is unique for its bone tool assemblage used in the preparation of leather and fur, representing some of the earliest evidence of clothing production in the human archaeological record. Reconstructing paleoenvironmental conditions local to this site should provide insight as to when and why anatomically modern *Homo sapiens* evolved such modern behaviors. Micromammal faunal analysis is a preferable method for cave sites because they are typically abundant and have the ability to provide a fine scale, local paleoenvironmental signal unique to the immediate surrounding area. Analysis of all present rodent genera (*Meriones*, *Mus*, and *Gerbillus*) produces a Gerbillinae:Murinae ratio indicative of an arid and open local habitat (399:133 = 3.0). A comparison of overlapping genera present at Contrebandiers and the nearby cave site El Harhoura 2 (*Meriones* and *Mus*) shows a difference between sites (G:M = 2.9 and 3.2, respectively). El Harhoura 2 has yielded micromammal assemblages richer in biodiversity, suggesting that there may be more to uncover at Contrebandiers with a larger sample size of rodents. Ongoing work in this study will utilize 13 previously un-analyzed collections of micromammals from Aterian levels to reconstruct the environment around Contrebandiers. Future work will assess how vegetation structure might have interacted with local climatic variables in a manner that may have necessitated novel human behaviors.

First macaque fossils from Sudan

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Macaques have the broadest geographic range among all living non-human primate genera. Today, *Macaca* includes more than 20 species, which collectively span a diverse array of habitats, behaviors, and morphologies. Among these, the only extant species outside Asia is *M. sylvanus* (the Barbary macaque), with natural populations restricted to small forest patches in Algeria and Morocco and an introduced population in Gibraltar. The macaque fossil record is rich across Europe but is limited to a handful of occurrences in northern Africa. Here, we significantly expand the known fossil distribution of macaques by describing two specimens from later Pleistocene sediments of the middle Atbara River in eastern Sudan. We compare these fossils – one partial maxilla and one partial mandible – to extant cercopithecids and fossil macaques using linear metrics and qualitative features of the dentition, cranium, and mandible. We refer both individuals to *Macaca sylvanus* based on morphological affinities to extant and fossil representatives of this species. Fossils described here provide the first and only record of *Macaca* in sub-Saharan Africa and indicate the importance of the Nile Valley as a north-south faunal dispersal corridor. The specimens have inferred ages of ~160 ka and ~90 ka, which suggest that this taxon was a persistent inhabitant of the middle Atbara valley during the later Pleistocene. The presence of *M. sylvanus* in Sudan reaffirms the importance of the fossil record for reconstructing faunal distributions in the relatively recent geological past, and opens a new window onto the last quarter million years of *Macaca* evolution.

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Beer, Bones, and Biomechanics: Investigating the Impacts of Alcohol Use Patterns on Femoral Cross-Sectional Geometry in Young Adult Males

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Alcohol consumption and reliance is common in humans. While most studies evaluating the effects of alcohol consumption patterns on bone biology have largely focused on factors affecting material aspects of bone, it is critical to ascertain how alcohol consumption patterns may affect bone geometry and biomechanical properties to better contextualize environmental factors impacting human biology studies of bone biomechanics. The aim of this study was to ascertain whether young adult males with high-risk alcohol use patterns have lowered cross-sectional geometric property values at the subtrochanteric and midshaft femoral sections in comparison to their peers who use alcohol in a low-risk fashion, or not at all. Through the evaluation of the postmortem full-body computed tomography scans of seventy-five individuals, as accessed through the New Mexico Decedent Image Database, this study ultimately found that individuals who use alcohol in a high-risk manner tend to exhibit significantly decreased biomechanical cross-sectional geometric properties in the femur. These effects are more frequently significant at the midshaft of the femur compared to the subtrochanteric location. These results are likely due to reduced bone formation and remodelling in high-risk alcohol users, in addition to the possible uncoupling of bone formation and resorption. The effects of alcohol are likely more frequently significant at the midshaft due to biomechanical canalization at the subtrochanteric location. Human biology studies considering long bone biomechanical properties should take alcohol use risk into account when selecting study individuals, as it can be a confounding variable in assessments of how physical activity affects bone geometry.

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Histotaphonomy as a proxy for post-mortem treatment in archaeological contexts: how can it help?

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The application of histological analysis of bone diagenesis, known as histotaphonomy, has emerged as a valuable tool in archaeological research with the potential to shed light on complex mortuary practices globally. This method involves assessing the degree and type of microscopic modification in thin sections of cortical bone and considering this alongside other evidence from the burial context. However, interpretation depends on the origin of the osteolytic microorganisms: that is, whether bacterial bioerosion is caused by putrefactive gut bacteria (enteric) or by soil microbiota (exogenous). Experimental studies using buried and exposed porcine carcasses in Britain have shown an enteric aetiology is likely, thus there is a direct relationship between early post-mortem treatment of a corpse and histological preservation. This model is further supported by the wide range of variation in histological preservation of bone samples from prehistoric burials across Britain resulting in an increasing number of archaeological studies employing histological analysis to inform on multi-phase mortuary practices.

This poster focuses on sites from prehistoric Britain and explores the problems and potential of histotaphonomic analysis. It examines how histotaphonomy has the potential to advance our understanding of post-mortem treatments such as mummification, inhumation, disarticulation and deposition environment(s) when used as part of a multi-scalar study including archaeology, osteological and taphonomic analyses.

Using Human Mitochondrial DNA Genomes to Reveal Patterns of Migration of the haplogroup L1b1a3

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The genetic history of post-colonial North and South America is closely tied to that of Europe and in many cases North and SubSaharan Africa. Researchers have suggested that the human mitochondrial DNA (mtDNA) L1b haplogroup originated in central Africa, dispersing from there at different moments in history. Today, it is largely found in the Americas, West and Central African, and Western European countries associated with colonization.

MtDNA functions as a vital phylogeographic tool, informing about lineage origins and movement, due to its steady yet slower mutation compared to other DNA types. In the following analysis, we analyzed data collected from National Geographic's Genographic project, FamilyTreeDNA, and published manuscripts, where we delve into the ancestral migratory connections between Africa, Europe, and the Americas. The data allows us to investigate how haplogroup L1b1a3 can serve as a model to trace movements between the three continental regions.

Haplogroup L1b1a3 was identified in 23 individuals from 13 countries including four countries in Africa; three in South America; four in the Caribbean; and two in Europe. L1b1a3 individuals were selected because their mtDNA was described as "good" quality. Our data shows that the South American lineages share branches, unique from those of the Caribbean, suggesting a possible distinct origin for them. Lineages identified from Portugal were shared with those from Brazil suggesting a strong colonial connection between the two. The other lineage found in Western Europe, namely the United Kingdom, was part of the ancestral type, shared with Ecuador, Cameroon, Jamaica, and Puerto Rico.

An assessment of the craniodental and postcranial material from juvenile *Homo naledi* recovered in the Rising Star Cave System

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Several localities in the Rising Star cave system have yielded remains of *Homo naledi* subadult individuals. These provide the opportunity to study the progression of juvenile life stages, which requires clear assessment of the association and ontogenetic age of individuals. In this study we examine craniodental and postcranial *Homo naledi* remains from the early juvenile stage, defined by first molar eruption, and the late juvenile stage, defined by second molar eruption, roughly from 4–6 years up to 15–17 years at death. From dental attrition, interproximal and occlusal facets, eruption/developmental ages and size of 76 teeth, and analyses of developmental stages and spatial locations of 148 skeletal elements, we refine the total number of juvenile individuals recovered for *Homo naledi*. A revised MNI of seven early juveniles are represented from different localities in the system: the Dinaledi Chamber, the Lesedi Chamber, the Hill Antechamber, and U.W. 110. A revised MNI of three late juveniles are represented in Dinaledi Chamber, with an additional two late juveniles newly reported on from the Hill Antechamber. The increasing number of non-adult specimens recovered from the Rising Star cave system provides a robust paleodemographic profile of 12 juvenile *Homo naledi*, laying the foundation to study this localized hominin population's growth and development.

Presence of vancomycin resistance gene *vanA* in a declining population of mantled howler monkeys (*Alouatta palliata palliata*) at La Pacifica, Costa Rica

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Antimicrobial resistance is a growing threat to the health of human populations globally; however, little is known of health impacts on wild primates. Primates living in agricultural habitats with high levels of anthropogenic activity are at particular risk for exposure to antibiotic resistant bacteria. The mantled howler monkeys (*Alouatta palliata palliata*) at La Pacifica, Costa Rica inhabit a fragmented forest surrounded by livestock ranching and other human activity. The once-stable population is in sharp decline, but the causes are unknown. As part of a larger study evaluating broad health parameters in the La Pacifica monkeys, our objectives were to determine whether individuals from this population were harboring antibiotic resistant bacteria in their gut. We assessed the presence of vancomycin resistance gene *vanA* in microbial DNA isolated from fecal samples from 42 individuals. Vancomycin is considered a last resort drug to treat antibiotic-resistant Gram positive bacterial infections. Samples were collected opportunistically between 2009-2017, initially immersed in 96% ethanol and stored in silica for desiccation. We extracted bacterial DNA using commercially available kits, and tested for the presence of the *vanA* gene by PCR using primers internal to the *vanA* sequence. Results revealed that 12 of the 42 samples tested positive for *vanA*. These preliminary results highlight a possible role for these primates as reservoirs for antibiotic resistant bacteria, and warrant further investigation into how antibiotic resistant bacteria may play a role in overall primate health. Additionally, these data may ultimately serve to inform conservation management strategies for declining primate populations.

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Bioarchaeology of Care: A Case Study from Nineteenth Century Mississippi

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Here, we interpret the pathologies evident on the skeleton of a deceased human individual, identified as Burial One and exhumed from the historic Gale Cemetery, within the Bioarchaeology of Care approach (BoC). The once-marked Gale Cemetery, located in Yazoo County, Mississippi, was associated with an elite, planter-class family in the 19th century. Four grave shafts were identified during mitigation archaeology in 2012, though excavations yielded only two individuals within cast iron coffins. Burial One is estimated to be female and 30-45 years of age-at-death. Following the BoC and employing the Index of Care (IoC) we estimate that pathologies shown by Burial One (e.g., long bone spindling, bilateral asymmetry in post-cranial morphology, scoliosis, osteoarthritis) are indicative of physical impairment, such as possible partial paralysis. Integrating this finding within contextual historical evidence, mortuary data (e.g., burial markers, cast iron coffin style), and family archival records, we propose that the living individual represented by Burial One experienced disability and required long-term health-related caretaking for several aspects of daily life. We consider Burial One's social identity (e.g., age, gender, socioeconomic status) and agency, as well as their family resources and social position, relative to the inferred caretaking needs and the likely provision of care by enslaved individuals within the plantation system of the antebellum South.

Combining direct and indirect contests to compare intergroup relationships in sympatric primates

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Relationships between neighboring social groups of primates consist of both face-to-face encounters as well as more distant interactions, where the latter are often based on auditory cues and allow groups to avoid direct contests while monitoring neighbors and resources. We investigated close-range and distant encounters among six groups each of red-tailed monkeys (*Cercopithecus ascanius*; N=232 encounters) and grey-cheeked mangabeys (*Lophocebus albigena*; N=93) at the Ngogo site in Uganda from 2008 through 2015. We used permutation analyses and Bayesian mixed modeling to identify, classify, and explain intergroup interactions from the location data. A greater proportion of redtail group-dyads interacted at expected frequencies (6 of 7 dyads) than mangabeys (5 of 11 dyads), and encounters ending in a draw were common for both species. Encounters ending in wins/losses were only predictable for mangabeys and occurred mostly in distant interactions. For redtails, winning was more likely for large groups and when encountering neighbors in less-frequented areas of the overlap zone. For mangabeys, winning occurred when focal group males were not distracted by mating competition over females, when groups had recently arrived at the encounter location and not yet depleted local resources, and when they had a history of frequent use of the site. Using elo ratings, only one dyad in each species showed consistent dominance relationships; other dyads flipped ranks or had none. In sum, simultaneous movement data provide a holistic picture of intergroup relations and despite their similar ecologies, the two study species express very different patterns of between-group relationships.

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Energetic and Social Factors of Habituation Behaviors in Wild Bornean Orangutans (*Pongo pygmaeus wurmbii*) in Gunung Palung National Park, Indonesia

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While group-living apes rely on the social cues of conspecifics during habituation, orangutans face this challenge alone as the only semi-solitary ape. Despite this distinctive behavioral ecology, there are no published studies on orangutan habituation behavior. We analyzed 8,383 follows and 82,413 observation hours of wild Bornean orangutans. We gave each follow a score of 1-10, based on the number of human-directed alarm vocalizations. A GLMM, controlling for individual and food availability, revealed that individuals with the highest vocalization scores spent a greater percentage of time traveling ($b=40.5$, $p < 0.0001$) and less time eating ($b=205$, $p < 0.0001$). Furthermore, we calculated a normal range of time spent eating and traveling for habituated adult orangutans. If the percent of time spent in these behaviors fell outside two standard deviations of this normal range, this behavior was considered extreme. This analysis, using chi-square test for proportions found that flanged males were more likely to excessively travel than adult females ($p = 0.0142$). We discuss these results within an energetic context. Both adult females and flanged males may have high energetic needs. Adult females are often lactating and caring for offspring. Hiding may be a better option, so that the mother can continue eating to meet the energetic needs of lactation, and to protect offspring more easily. Flanged males may be able to afford temporarily expending more energy, while females with offspring cannot. These findings demonstrate that orangutan responses to human presence are complex and contextual, with various energetic and social considerations.

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Preliminary Investigation of Regional Clavicle Cortical Porosity using Pore Extractor 2D

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Microstructural variation in the human clavicle, a critical component of the pectoral girdle, remains underexplored despite this bone's contribution to overall function of the upper limb. Cortical porosity can provide evidence of loading history, bone quality, and insight into functional adaptation. This pilot study aimed to investigate regional patterns in clavicle porosity using Pore Extractor 2D. Un-decalcified midshaft cross-sections from the clavicles of 5 female modern post-mortem human subjects aged 50-75 years were used in this study. Analyses were conducted with the custom ImageJ macro Pore Extractor 2D, which facilitates computer-assisted isolation of pores using thresholding and binary operations. Quantifications in each anatomical quadrant included pore number, pore density, mean pore area, and percent porosity. Most pores were automatically captured, and pore number and density for the entire cross-section ranged from 324-932 and 7.02-12.87 $1/mm^2$, respectively. Additionally, mean pore area and percent porosity ranged from 4,235-8,507 μm^2 and 4.7-9.7%, respectively. The considerable variation between individuals warrants further inter-individual comparisons to understand possible contributors and functional implications. While mean pore area was greatest in the superior region, the greatest pore numbers, pore densities (relative numbers), and percent porosities (relative areas) were found in the anterior and inferior regions, suggesting regional adaptation at the clavicle midshaft. Further exploration of porosity will improve understanding of the underlying mechanisms that produce these distributions and their contributions to functional adaptation in the human clavicle. Additionally, these findings highlight the utility of Pore Extractor 2D for efficiently analyzing variation in clavicle porosity.

The effect of hybridisation on variation: a macaque model

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The ability of *Homo sapiens* to colonise almost all terrestrial ecosystems is fundamental to what defines our species. Interbreeding with now-extinct resident hominins may have eased *H. sapiens* dispersals into novel habitats. Hybridisation increases variation, potentially facilitating adaptability in dispersing groups where founders' effects can reduce standing variation. Since the paucity of fossils generally prevents quantification of intra-population variation, we use non-human primate (NHP) samples to elucidate the effects of hominin hybridisation. Here, we quantify and compare coefficients of variation in size within Chinese / Indian *Macaca mulatta* (MMU) full-breds and hybrids (n = 134). MMU are a valuable proxy for hominin hybrids because their split time (generations) approximates that of *H. sapiens* / Neanderthals. The sample is captive-bred, multigenerational, and of known pedigree. Using visualisation and T-tests, we show low size variation in hybrid MMU compared to full-breds, in contrast to expectations from studies with other NHPs. As the variables governing the influences of hybridisation on primate morphology are poorly understood, we evaluate the suitability of MMU as hominin analogues. We compare size variation within our MMU and a parvorder-wide sample of wild-shot catarrhines (n = 163) and find levels to be comparable. We discuss the influences effecting the morphological outcomes of interbreeding between different taxa. We question which NHPs may make successful hominin proxies and how to proceed in using NHP to compliment fossil and aDNA analyses to better understand the role of hybridisation in human evolution.

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Cranial Modification and Social Identity in Early Islamic Rural and Urban Populations of Central Asia

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Cultural cranial modification (CCM) is documented in Eurasian populations from the Bronze Age (c. 2000-1000BCE), Iron Age (c. 700-500BCE), and medieval period (c. 700-1300CE). However, few studies examine the cultural dynamics behind CCM in Central Asia, especially during the medieval period. We present data on two samples: one from Kalmyk-krylgan (12th-13th c. CE, n=17), a nomadic burial ground, and one from Bukhara (c. 10th-14th c. CE, n=19), one of the largest urban oases of the time. Macroscopic, and linear and 3D geometric morphometric analyses document three types of CCM in these populations: occipito-to-parietal flattening (present in both samples), occipito-parietal-frontal flattening (present at Kalmyk-krylgan), and annular (present at Bukhara). CCM is nearly ubiquitous at Kalmyk-krylgan (88.2% of individuals), and common in Bukhara (42.1% of individuals). Presence or type of CCM is not correlated with sex, and biological distance based on principal components analysis indicates these individuals were not genetically distinct populations. In addition, the burials of all studied individuals conform to normative Islamic prescriptions. While some early Islamic legal documents discourage permanent body modification, there have been no studies on how Islam, brought to Central Asia in the 7th c., impacted CCM. The chronology of the cemeteries suggests that CCM was practiced across multiple generations of Muslims. CCM at Kalmyk-krylgan may reflect a tradition that survived beyond urban Islamic strongholds. Its presence in Bukhara could be from migrants from rural communities like Kalmyk-krylgan. However, it could have also been a method to publicly signal group membership in an increasingly cosmopolitan society.

Comparing the performance of double-stranded vs. single-stranded DNA library protocols on ancient microbial DNA recovery and microbiome reconstruction

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Ancient DNA library construction can affect the recovery of endogenous DNA, thus influencing downstream taxonomic assessment. While studies have shown that single-stranded library generation outperforms double-stranded when applied to highly degraded eukaryotic host DNA, no systematic studies have examined the impacts on ancient microbial communities. To examine the impact, we assessed sequencing characteristics and taxonomic composition of the reconstructed microbial communities from double- and single-stranded libraries produced from the same extracts of dental calculus of seventeen Neanderthals and other Pleistocene-era humans sequenced with identical Illumina sequencing chemistry. To observe bias in the sequencing effort, we compared differences in the read length, GC content, and number of sequences processed from both protocols. Further, we compared the taxonomic profile as determined by three programs–Kraken2, MALT, and MetaPhlAn4–to explore how sequencing biases affect the identification of authentic, ancient oral species. Results show that the sequencing of double-stranded libraries produces a greater number of significantly longer and GC rich reads. Additionally, a significantly greater number of species were identified in the double-stranded samples, but after selecting specifically for oral species, comparable alpha diversity is seen. Nevertheless, though a single-stranded sample is more similar to its double-stranded counterpart than a random sample, there is still variation in beta diversity between samples from the same individual, indicating differences in species abundance. In sum, comparable microbial community composition indicates that other factors such as cost or the feasibility of recovered fragments to perform well in *de novo* assembly may be important in library protocol selection.

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Examining the Dental Morphology of Donors within the JAW Collection

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Dental morphological traits can be difficult to score without proper training and experience in examining the differences among trait expression, especially continuous variables. In this pilot study, inter- and intra-observer error rates for traits within the Arizona State University Dental Anthropology System (ASUDAS), as well as those defined by Pilloud (2019) and Pilloud and colleagues (2018), are examined between a novice and more experienced scorer to add to the literature on these difficulties with scoring dental morphology. The John A. Williams (JAW) Human Skeletal Collection at Western Carolina University was utilized to score dental morphology on a sample of 10 donors. An additional purpose of this study is to begin collecting these data as part of the standard inventory for donors within the JAW Collection for future research and teaching uses. Donors with at least 50% dentition were scored for 37 dental morphological traits twice by each author, with at least one week between sessions. Raw scores for the highest expression for nine of these traits on the key tooth in at least five donors by the second author were selected for preliminary observer error analyses: shoveling, interruption grooves, *tuberculum dentale*, premolar accessory ridges, premolar accessory cusps, hypocone, Carabelli's trait, mandibular enamel extensions, and premolar cusp number. Cohen's kappa scores are high (above 0.7) for the more experienced scorer, while several scores for the novice scorer fall below 0.5. Interobserver error scores were low, supporting the results in the literature regarding experience and training to consistently record dental morphological traits.

Limited dietary energy intake during growth has long-lasting negative effects on limb bone diaphyseal strength in capuchin monkeys

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It is well established that low levels of physical activity during the growing years can negatively affect limb bone diaphyseal strength in adulthood. Less is known about whether limited dietary energy intake during growth has long-lasting negative consequences for diaphyseal strength. Here, we examine the enduring effects of dietary energy deficiency on diaphyseal strength using a longitudinal series of radiographs originating from a study of nutritional influences on capuchin monkey growth. Starting at 8 weeks of age, monkeys (*Cebus albifrons*) received either a standard laboratory diet *ad libitum* (n=10) or the same diet at 67% of normal *ad libitum* consumption (n=5). Then, at 28 weeks of age, the monkeys with the energy-limited diet transitioned to *ad libitum* feeding like the other monkeys for the rest of the experiment. Full-body radiographs were collected at ages 8, 26, and 52 weeks. At each age, we measured mid-diaphyseal strength (polar moment of area) in the humerus. We found that throughout the experiment, diaphyseal strength increased among all monkeys, regardless of diet. However, limited dietary energy intake between 8 and 26 weeks of age significantly diminished increases in diaphyseal strength. Moreover, significant differences in diaphyseal strength remained evident between the experimental groups at 52 weeks of age, long after monkeys with the energy-limited diet transitioned to *ad libitum* feeding. Our findings underscore the importance of sufficient dietary energy intake for developing strong limb bone diaphyses, as well as the long-term negative consequences of inadequate energy intake.

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The Genomic and Oral Histories of the Lipan Apache

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The Lipan Apache Tribe are the descendants of the Apache people who migrated south from present-day Canada, approximately 1,000 years ago. Since the 1600s, the Tribe has called the plains of what is now Texas home. Over the next 400 years, the Lipan experienced various demographic events in response to other Tribes, contact with Europeans, changes in the environment, and the ultimate formation of the United States government, which resulted in displacement, warfare, and the onslaught of European-borne disease. Today, the Tribe exists as a sovereign Native American Tribe within Texas. Here, we present the Lipan Apache history as told from a genomic perspective and within the context of the Tribe's oral histories, which have been passed down for millennia. We find links to the Lipan Apache ancestry that stem from signals from ancient Northern and Southern Indigenous lineages, with an additional signal from a population that diverged before the ancestral North/South split. We also scanned the genomes of the Lipan for signs of positive selection and found pathways under adaptation that deal with detoxification of nutrients, which correlates with the historical nomadic lifestyle of the Tribe. However, the strongest signal of selection was associated with the formation of narrative memory in the hippocampus, which may have facilitated the transmission of Lipan knowledge, culture, and history for hundreds of generations.

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Characterization of infants' caregiving environments and their relationship to maternal investment: the MIMBE Study

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Humans are cooperative breeders who rely on assistance from others to raise children. Research has documented that greater allomaternal support is associated with a reduction in maternal caregiving investment, improved child outcomes, and increased maternal reproductive success. However, few studies have examined allomaternal investment from a cooperative breeding perspective in the United States (US). Between 2017-2018, we enrolled 51 maternal-infant dyads from the US pacific northwest in the Maternal-Infant Microbiome, Behavior, and Ecology Study

(MIMBES). Mothers were ≥18 years old. Infants were <6 months old and exclusively breastfeeding. We conducted naturalistic infant focal observations over a 12-hour period in 4-hour increments over multiple days, to characterize a day-in-the-life of infants and investigate the relationship between allomaternal support and maternal investment. Utilizing a human cooperative breeding framework, we hypothesized that the frequency of allomaternal investment would be negatively associated with maternal caregiving. Results indicate that infants had an average of 3.2 caregivers in physical contact and 3.4 caregivers within a forearms distance to them on a daily basis. Mothers provided the majority of infant care, whereas allomothers provided 16.7% of affection, 10.1% of holding, and 14.5% of physical contact that infants received. Linear regression models demonstrated that amount of allomaternal physical contact with infants was not associated with maternal-infant contact. In contrast to studies conducted in non-Western populations, allomaternal investment does not appear to reduce maternal investment. Our findings suggest that household structure and ecology, at least in this US population, may dampen the role of allomothers on maternal behavior.

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Sketching experience from osteomyelitis in Indigenous Californians of the Bay Area

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Excavations at a shell mound cemetery site that date to the Early/Middle Transition Period (500-200 B.C.) recovered eight adults with skeletal alterations consistent with osteomyelitis. While there are a number of bones impacted and causes for these infections, including secondary responses to traumatic injuries, there was healing present in all eight individuals. The presence of healing and extensive skeletal alterations suggest individuals were living chronically with systemic infections. Here, exploration of individuals' experiences with osteomyelitis provides insights to the various activities' individuals were engaging in, the relative risk associated, and community perception of infections related to osteomyelitis.

Eight adult individuals, three females and five males, were observed with skeletal alterations consistent with osteomyelitis. Using the bioarchaeology of care approach, these eight Early/Middle period individuals from the Bay Area of California are studied for differential experience of osteomyelitis. Seven of the eight individuals exhibit alterations consistent with osteomyelitis in leg bones, which likely impacted their short- and long-distance mobility. Through tracing the experience of probable osteomyelitis, including disease etiology, demographic profile, and necessity for health-related care, an understanding of the role infections play in day-to-day life as well as death are presented. Healing in skeletal remains and normative mortuary practices for these individuals suggest that trauma was not uncommon in adulthood. Therefore, secondary infections, like osteomyelitis, in response to traumatic injuries conferred health-related care for individuals but does not suggest difference that was archaeologically visible.

The efficacy of resin-based stereolithography 3D-printing of trabecular bone as a non-invasive option for mechanical testing

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Mechanical testing is an important component of trabecular bone research; however, testing primate samples is often not feasible due to the destructive nature of most procedures. 3D-printing has recently emerged as a non-invasive way to model trabecular bone samples for mechanical testing. Given the variety of 3D-printing technologies, it is critical to evaluate the ability of different methods to reliably print complex trabecular matrices. We printed trabecular bone imaged via µCT from femoral heads of 4 *Colobus polykomos* individuals in resin using a Formlabs Form2 stereolithography printer. Cubic volumes of interest were aligned with anatomical planes, centered within each femoral head and sampled at 0.3x head diameter. Samples were scaled to $2cm^3$ and printed 4 times. Each print was loaded in compression at a displacement rate of $0.1mms^{-1}$ using an MTS 858 axial testing machine. Elastic modulus was calculated from stress-strain curves. Kruskal-Wallis tests revealed differences in modulus among individuals (p=0.003). Data were collected for each individual to assess association of morphological variables with higher variation in modulus among replicated prints. Model II regression revealed positive correlation between modulus standard deviation and bone volume fraction ($R^2=0.99$, p=0.005) and negative correlation between modulus standard deviation and bone surface area to volume ratio ($R^2=0.91$, p=0.044). Modulus standard deviation did not correlate with trabecular thickness, number, spacing or anisotropy. These results suggest the potential efficacy of stereolithography to reliably print trabecular bone samples. However, future studies should account for heteroscedasticity in stiffness among replicate samples when comparing specimens with different morphologies.

Spatial approaches aid interpretations in Holocene Southern African Ancestral KhoeSan bioarchaeology

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Environmental variation may contribute to human diversity. Skeletal traits may be compared among groups from different regions to determine if specific environmental conditions associate with certain skeletal properties. For example, among Holocene Southern African Ancestral KhoeSan groups, some individuals have stable light isotopic properties indicative of intensive marine resource exploitation, and most individuals have lower limb biomechanical properties indicative of highly mobile lifeways. These variables relating to diet and terrestrial mobility have been compared between different Southern African regions, particularly along the southern and southwestern Cape coasts. Regional analyses may mask the influence of local site-specific factors, such as proximity to key coastal marine resources or terrain complexity. Here, spatial analyses were used to assess how skeletal variation is distributed across the Southern African Cape coast to determine how environmental variables, such as terrain or coastal access, affect skeletal properties. Biomechanical variables indicative of high terrestrial mobility and stable light isotope values associated with high trophic level protein sources, likely marine sources, are unevenly distributed across the Cape coast. These distributions do not necessarily overlap with regional biome classifications. Distance to the coast may be less informative than a locality's specific ecological and archaeological context in shaping marine resource consumption. The terrain encountered, for example, mountainous terrain rather than complex, rocky shorelines, may shape observed lower limb biomechanical variables. Future work seeks to further clarify how site-specific or local environmental factors may have affected the diets, physical behaviours, and consequently skeletal traits of these individuals.

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Ontogenetic changes in experimental feeding behavior in tufted capuchins

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Primate feeding behaviors represent a multilayered blend of social and morphological factors. In wild settings, food access may be limited by social hierarchies and chewing durations possibly shortened under heightened predator threats. Under experimental settings, we may control these influences, thus better targeting age/sex class-related patterns. Here, we test whether chewing sequence durations, chewing frequencies, and chew numbers differ across age/sex categories and food material properties in tufted capuchins (*Sapajus* spp.) at the Núcleo de Procriação de Macacos-Prego Research Center (Araçatuba, Brazil). Twenty-nine captive and semi-wild juveniles (*n*=2), subadults (*n*=12), older subadults (*n*=4), and adults (*n*=11) were briefly trapped and offered foods representing a range of toughness and elastic modulus values: almonds, halved-peanuts, sunflower seeds, popcorn kernels, and gummy bears – all of which fall well under published maximum toughness and elastic modulus values for *Sapajus*. Feeding was video recorded and coded frame by frame using a Python GUI. Across all individuals, higher toughness and elastic modulus foods were associated with longer chewing sequence durations (p<0.001). For chewing frequency, all age groups differed (p<0.01), with adults having shorter frequencies and fewer chew numbers than younger groups. By sex, only subadults differed in chewing frequency (p=0.02), with males yielding shorter frequencies. These results align with ontogenetic changes in body size and the feeding system, with younger individuals having reduced food processing abilities. Further, methods of quantifying feeding behaviors in controlled environments (e.g., tracking durations) can be applied to wild primates, facilitating feeding behavior comparisons from captive and wild taxa.

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What does it take to refer iconically?

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Matt Cartmill's work on the evolution of language and human cognition weaves together evidence across disciplines and time periods, leading to insights often overlooked by others. His work encourages others to think more deeply, read more broadly, and take a humbler approach to their own theories. Inspired by Cartmill's insights about linguistics, philosophy, hominin evolution, and art, I critique the idea that iconicity played a key early role in the evolution of language. Theories proposing a gestural origin of language argue that iconicity provided a way to understand the meanings of signs before the emergence of conventional symbols. But iconic reference is difficult (for minds that aren't modern adult humans). Iconicity requires understanding analogical relationships between the form of the sign and that of the referent. This mapping is more difficult than the associative learning that underlies conventions (i.e., symbols). Evidence from early childhood, extant great apes, and the archeological record all suggest that iconicity comes late. Iconic gestures emerge later than other gestures in childhood, and are nearly absent from the gestures of great apes. Apes and children under three have difficulty understanding iconicity in gestures, drawings, and 3D models, but do not have difficulty learning conventional symbols. Abstract or symbolic markings on caves and animal bones appear around 70,000 years ago, and arguably as far back as 500,000 years ago on Java; but iconic (figurative) drawings did not appear until around 45,000 years ago. These lines of evidence all suggest that symbols preceded icons in our evolutionary past.

The use and misuse of proxy phenotypes in genotype-phenotype research

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Many behavioral traits like intelligence, temperament, and industriousness are hard to measure and are not easily defined. However, biobanks are stocked with weakly correlated proxies for traits of this nature (e.g., educational attainment), facilitating Genome Wide Association Study (GWAS) and Polygenic Score (PGS) research and ultimately, publications that proliferate concepts of biological essentialism. Research on the genetic architecture of quantitative complex traits (e.g., height) has repeatedly demonstrated that predictability of trait expression is limited even for highly heritable traits. It's possible that poor prediction reflects underlying selection bias or data quality associated with biobank database development. Here, we present analyses of the UK Biobank genetic, environmental, and phenotypic data that exemplify current limitations in the predictive and explanatory power of GWAS and PGS results. We investigate the data quality of a directly phenotyped trait (height), assess standard quality control procedures for population genetic analyses using array data, and examine how the intersection of discrete ethnicity labels and genetic affinities influences downstream results. For example, participants with South Asian genetic ancestry (n = 8188) who have DXA imaging data tend to be significantly taller, younger, and of higher socioeconomic status than participants of the same self-identified ethnicity and sex without DXA images (p-values <0.001 to <0.05). In this manner, we demonstrate that even canonical complex traits like height still require careful efforts to untangle the nuances of environmental and genetic contributions, and argue that extreme caution is warranted when conducting and interpreting GWAS/PGS of less tangible traits.

Protocol for application of traditional points and measures to digital crania

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The growing use of virtual databases and 3D skeletal material requires methods that will ensure the accuracy and precision of results. While methods are available describing the handling of skulls, using callipers and acquiring craniometric data from dry bone, these descriptions transfer poorly to placing traditional landmarks in a virtual environment and rely on physical handling. Previous literature using virtual crania does not explain their methodology for point placement in detail.

This research presents an overview of the proposed protocol, which leverages the benefits of free, open-source visual analysis software for the placement of 60 points on the crania. Of these, 26 are traditional craniometric points on virtual crania (14 placed bilaterally) and 20 additional points placed to enable the acquisition of all traditional measurements. These cranial measurements have been in use for decades and applied in forensic programs like CranID FORDISC, as well as applied to any number of research questions in biological anthropology using dry bone. Future biological and forensic anthropology necessitating these points and measures requires such a protocol to ensure consistency of data acquisition and precise results.

The collection of 37 measurements using the protocol has been conducted on 12 crania (6 CT-scanned crania and 6 scanned with a structured light scanner). The preliminary result has been an intra-observer error with an average relative Technical Error of Measurement (%TEM) value below 1.5% and an average Coefficient of Reliability (R) of .96 among all 37 measurements.

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An Examination of Vertebral Osteoarthritis in Victims from the Midnight Terror Cave, Belize

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The Midnight Terror Cave (MTC) osteological assemblage containing over 10,000 commingled skeletal fragments of at least 118 sacrificial victims from the Classic Maya Period (250 CE - 925 CE) was excavated between 2008-2010. Previous research has explored how sacrificial victims were recruited and the identity of the victims at MTC. To learn more about the adult victims, we examined the patterning and severity of vertebral osteoarthritis and found an unusually high level of osteoarthritis in the cervical region when compared against the expected progression from the lumbar and thoracic regions following expected aging patterns. Such a heavy stress around the cervical region may indicate the possible use of tumplines by the victims. We also found that the most severe osteoarthritic cases were located in Operation VII of the cave, despite having a comparatively small quantity of human remains. The differences in osteoarthritic severity as divided by operation may indicate a spatial separation within the cave by types of ceremonial sacrifice or at least, which individuals were selected for sacrifice. This follows the previously proposed hypothesis that the cave was used for various rituals, both private and public, as part of a ritual circuit that moved through the cave.

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Phylogeography and demographic history of *Varecia variegata* using mitochondrial DNA sequences

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Understanding how biological and environmental factors shape the distribution of animal genetic diversity is fundamental to biodiversity conservation. To understand how genetic diversity was partitioned in a critically endangered lemur, *Varecia variegata*, we analyzed 173 publicly available partial (564 bp) D-loop sequences of mitochondrial DNA. Individuals derive from 18 geographically representative localities across the existing *V. variegata* range. Previous studies, identified two distinct genetic populations, one north of the Mangoro River and the other south. Using this designation, we found that the northern population retained higher levels of nucleotide diversity ($\pi = 0.029$) than the southern population ($\pi = 0.001$). Using a Bayesian approach, our phylogenetic tree showed that the northern population diverged around 0.23 mya (95% HPD 0.12-0.89 mya) and had a large historical female effective population size (N_{ef}, ~32,000). While the southern sites diverged around 0.018 mya (95% HPD 0.005 - 0.34 mya) and had a significantly lower N_{ef} size (~720). Furthermore, the northern most sties in our study grouped closely with *V. variegata's* sister taxa *V. rubra*. The higher levels of genetic diversity and large ancestral N_{ef} suggest that the *Varecia* genus likely evolved in the north and migrated down Madagascar's eastern humid rainforest corridor.

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Engineering algorithms for camera trap data: recent advances and new challenges for primate identification in the savannas of Sénégal

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With the integration of camera trapping in field primatology and the concomitant demand for big data management, there is an emerging need to automate image processing and analysis. However, automation methods to analyze camera trap imagery of wild primates are still in their infancy. Detection methods locate a bounding box surrounding each animal in the image, and classification methods identify the animal species inside the box. Despite considerable progress, these methods are unreliable when applied to new imagery data collected in new environments. Methods in these novel contexts require a significant number of manually labeled images, and method performance is notoriously brittle without extensive data training. In this study, we collected over 55,000 videos and 122,000 images from 287 cameras between 2020 and 2022 at the Assirik and Fongoli study sites in Sénégal. 8000 bounding boxes that were automatically detected by the Microsoft MegadetectorV4 were manually labeled with animal species. Of these, 2586 were deemed to be false detections (e.g., rocks, branches), yielding a detection accuracy of 67%. We then applied a specially designed animal classifier tool that mitigates the problems of few manually labeled images and the mismatch between species used in training and species encountered in implementation. With a stricter (versus more lenient) setting, the classifier rejected 93% (versus 69%) of those false detections and achieved an overall accuracy of 55% (versus 67%). More algorithm development is required for primatologists to apply existing automation tools to environments and to primate species that were excluded from model training processes.

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Using anthropological ethics frameworks to inform museomics research on natural history museum collections

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Within the emerging field of museomics, the study of genomic data sequenced from museum specimens, museum collections are seen as a window into past genomic diversity for researchers studying conservation-related questions. However, much of this work has proceeded without proper understanding and acknowledgment of museums as institutions rooted in imperialism and colonialism with dubiously acquired collections. This is particularly the case with natural history collections. In contrast, much informative discussion has centered on the use of human remains from anthropological collections in research. Here, we examine the ethical best practices for research with human remains in museum collections to inform guidelines on working with natural history collections with violent colonial histories. Specifically we present the case study of narwhal tusks collected as part of the Crocker Land Expedition (1913-1917) to northwestern Greenland, now housed in the Illinois State Museum. The colonial violence that occurred during this expedition resulted in the death of an Inughuit guide. Greenland is still impacted by colonial science to this day, and as a result of conservation research used to support hunting quotas without community engagement, culturally important food species like the narwhal are now increasingly inaccessible to Greenlandic Inuit. This project aims to create frameworks for researchers using natural history museum collections to help them consider the context of these collections and engage with the potential social impacts of their research. We propose guiding questions and recommendations based in anthropological best practices for museomics researchers, using the Crocker Land Expedition case study as an example.

Fine-scale Analysis of Population Genetics and Signatures of Selection in Central Asian pastoralists

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Ancient Central Eurasia is known for genetic heterogeneity and large-scale human migrations and interactions. This research presents genome-wide SNP data from ancient individuals associated with various archaeological cultures of Central Eurasia ranging between the Bronze Age and the first Millennium CE. Central Eurasia is known to have undergone several distinct large-scale migration events, however, the nature and specific timing of these processes is not well understood. We generated genome-wide capture data for N=99 individuals ranging from the Iron Age until the first millennium CE from modern day Kazakhstan and Kyrgyzstan. We investigated the general population genetic structure of these individuals, and performed IBD sharing analysis together with published individuals from Central Eurasia. We imputed and processed N=309 published ancient individuals from modern-day Kazakhstan, Mongolia, Russia, Uzbekistan, Turkmenistan, and Kyrgyzstan ranging between Bronze Age until the 1st millennium, which were analyzed together with our unpublished data to identify IBD networks and clusters of more closely related groups. Lastly, we performed frequency- (PBS) and haplotype-based scans (XP-EHH, iHS) for signatures of natural selection in our population. We identified genes and pathways associated with immune (HLA genes, *MUC22*) and metabolic pathways (*MTCH2*, *HMGCR*), as well as phenotypic variation. Our findings shed light on the nature of the transition from Bronze to Iron Age, and from Iron Age to the 1st millennium CE, and help us understand the nature of the underlying admixture processes. Moreover, our results inform us of the selective pressures that have been experienced by the Central Eurasian populations through time.

Adult Body Mass Estimation using Femur Cross-Sectional Properties

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Variation in long bone cross-sectional geometric properties is often attributed to differences in load history experienced by individuals over a lifetime. Increased body mass will cause relatively greater mechanical loading of the weight-bearing bones, such as the femur, resulting in changes to the geometric cross-sectional properties of the bone shaft. If changes to cross-sectional properties are patterned with increased mass, then they can be used estimate body mass (or body mass index, "BMI") from the skeleton.

Computed tomography (CT) scans of eighty femora from the Texas State University Donated Skeletal Collection were used in this study. Inclusion criteria for this sample consisted of an equal distribution of male and female representation, as well as equal distribution of "Moderate" (≤ 30) and "High" (> 30) BMI classifications. Two-dimensional CT slices, perpendicular to the femur shaft, were interpolated at five-percent increments from 20-80%. From the individual slices, six measures of cross-sectional properties used for comparison between BMI classifications using Mann-Whitney U tests.

Statistically significant differences ($p < 0.05$) were detected in 72 out of 78 properties investigated between Moderate and High BMI classification. Non-significant differences were only present in the lower portion (65-80%) of the femoral shaft for total area and the upper portion (20-25%) for the second moment of area in the medial-lateral direction. Random forest modeling achieved a testing accuracy of 84.62% for estimating BMI classification. Results of this study demonstrate the potential for cross-sectional properties of the femur to aid in BMI estimation in forensic casework.

Funding for this project was provided by the National Institute of Justice (NIJ 2020-R2-CX-0048).

On the verge of greatness: Preliminary remarks from isotopic investigation into the foundation of the kingdom of Alwa

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By the mid-sixth century AD the territory of modern Sudan was divided between three kingdoms of Nobadia, Makuria and Alwa. The foundation of Soba, the capital of the southernmost kingdom of Alwa, is still shrouded in mystery. During the British excavations at the site in the 1980s and 1990s, a number of cemeteries associated with local churches were uncovered. The remains are considered those of upper class citizens (i.e. local elites) and may represent the first generations of founding fathers and mothers. Samples of dental enamel from the British Museum Wendorf Collection were analyzed for carbon, oxygen, and strontium ratios to elucidate the origins and associated subsistence strategies of the local inhabitants. Results indicate local background for the studied individuals, having profound implications for the research on the establishment of the city. According to some researchers, first settlers might have been the legacies of the late Meroitic kingdom, who relocated further south after its final downfall. The founders of the future metropolis might have also shared ancestry with founders of the kingdoms of Nobadia and Makuria, the Nuba people from Kordofan region to the south and south-west of Soba. Despite no evidence of occupation pre-dating the foundation of the city in 6th c., the obtained results speak not only to local roots of city's inhabitants, but also to the economic reliance on enduring agro-pastoral symbiosis. This presentation explores the application of isotopic research to uncover the social dynamics at the foundation of the medieval African metropolis.

This research was co-founded by the University of Warsaw and the Max Planck Society.

Trends in tooth development and eruption in a world-wide sample: the foundation of a generalized dental age estimation method

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The trend in the subadult dental age estimation literature of population-specific methods (e.g., sex-specific, or ancestry-specific) means few methods have generalized application. The presumed benefit of greater precision in population-specific methods has not been adequately demonstrated nor justified over methods that favor accuracy for individuals from unknown populations common in forensic work, or groups not represented in the samples.

This research explores the development and eruption timing of all permanent teeth using a world-wide, generalizable sample. Dental development stages were recorded on a sample of radiographs and CT scans from 2,664 modern individuals from 10 countries, and eruption stages recorded on 1,183 individuals from seven countries. For each stage of development and eruption, mean age-at-stage and the age interval associated with that stage (the minimum and maximum age recorded) were calculated by tooth. The median stage of development and eruption were also recorded by tooth for one-year interval cohorts (i.e., age 0.00-0.99 years, 1.00-1.99 years, etc.).

Most teeth followed the same general trends: variation increased as the tooth approached complete development, while variation decreased as the eruption stages progressed. Several teeth exhibit an abrupt change in median stage of development or eruption between age cohorts that is not captured at one-year intervals, indicating periods of accelerated development that are not adequately represented using this traditional mode of uniform categorization. Raw descriptive statistics for this pooled sample are presented for immediate general use with the intention of continuing to expand the sample for increased representation.

Exploring genome-wide DNA methylation changes following glucocorticoid exposure in iPSC-derived neuroprogenitor cells

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Prenatal psychosocial stress has significant and lasting effects on health, potentially through epigenetic pathways early in development. Exposure to cortisol, a key stress hormone, can alter DNA methylation of genes related to the hypothalamic pituitary adrenal axis, particularly *in utero*. However, epigenetic effects in the key target tissue of the brain are particularly understudied, given difficulties accessing neuronal tissue early in life. Our aim is to address these gaps through a novel series of experiments measuring methylation using neural progenitor cells (NPCs) derived from human pluripotent stem cells exposed to a synthetic version of the cortisol stress hormone, dexamethasone. We first examined methylation in stress-related genes *FKBP5* and *SLC6A4* using bisulfite pyrosequencing to determine the appropriate dosage and timing of dexamethasone exposure. Next, we repeated the experiment with optimized exposure conditions and examined genome-wide methylation differences in the NPCs exposed to dexamethasone versus control, using Illumina's MethylationEPIC BeadChip. We also tested if epigenetic effects of dexamethasone exposure varied in NPCs from individuals with major depression disorder, including those who respond to serotonin reuptake inhibitors (remitters; n=3) and those who did not (non-remitters; n=3), relative to healthy individuals (n=3). No methylation differences were detected in response to dexamethasone exposure after adjusting for genome-wide significance, but microscopically visible changes to cell growth were evident. While we failed to detect an epigenetic effect of dexamethasone exposure, this study provides a model of how iPSC-derived NPCs can be used to further explore effects of varying hormones, dosages, cell types, and timings of exposure.

This study was funded by a seed grant to Drs. Non and Marchetto from the Altman Clinical and Translational Medicine Institute at University of California, San Diego.

Sexual Selection and the Interaction between Facial Breadth and Canine Dimorphism

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Across primates there is great variation in both craniofacial form and tooth morphology. Evolutionary changes to dental morphology can be associated with changes in facial morphology based on the interdependence between tooth and jaw mechanics. While there are many factors that influence evolution of the face and teeth, such as diet, the effect of sexual selection on the canine teeth is of particular interest. Previous research has found a negative correlation between canine height dimorphism and facial breadth dimorphism (Weston et al. 2004), suggesting that facial breadth is associated with threat display and intrasexual competition in males, such that facial breadth replaces canine teeth in agonistic threat displays. Weston et al. (2004) uses a ratio of facial breadth (bizygomatic width) and facial height to correlate against canine height dimorphism, with the inclusion of facial height to protect against facial geometric confounds. Here an alternative hypothesis that facial breadth increases as canine height decreases reflects an interaction between facial length, canine tooth size, and gape requirements. Craniofacial and dental data (Plavcan 1990; 2002; 2003; 2004) were evaluated for 195 primate species using standard regression and PGLS. The results of this analysis support the hypothesis that facial dimorphism is associated with canine tooth size as a consequence of gape size preservation and not sexual selection.

Ancient Mitogenomes from Belize Provide Insights into the Mobility and Migration of Ancient Communities in Mesoamerica and the Caribbean

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Genomic research regarding paleodemography in Mesoamerica to date has often been conducted as part of large-scale studies of North and South America. Mesoamerica, as a result, has not been a sustained focus of paleogenomic-scale studies of population history at the regional level. Poor preservation of ancient DNA in the neotropics, among other difficulties, has limited ancient genomic studies of mobility in Mesoamerica. Here, we present mitogenomic data of ancient and contemporary individuals from across Mesoamerica and the Caribbean to reconstruct paleodemographic and mobility patterns of maternal lineages through time. We present mitogenomic data sequenced from Ancestors recovered from burial contexts at ancient Maya archaeological sites. The seven Maya Ancestors recovered were interred in the ancient Maya city of Caracol, located in the Maya Mountains of present-day Belize. These data were combined with 63 previously published ancient mitogenomes spanning Mesoamerica and the Caribbean and 55 contemporary mitogenomes from Corozal, in Northern Belize, for analysis. This work was conducted with authorization from the Belize Institute of Archaeology in and collaboration with Maya partners in Corozal. Haplogroup frequencies and median joining haplogroup networks were generated using Haplogrep2 v2.1.18 and PopArt v1.7.2, respectively. Bayesian fixed molecular clock models were used to estimate matrilineal phylogenetic relationships between community members included in this study. Bayesian Skyline Plots were generated to infer dynamics in matrilineal effective population size. Models resulting from these 125 mitogenomes are used here to reconstruct paleodemographic events temporally and geospatially to gain a more robust understanding of the demographic history of the region.

This project was not funded through external resources.

Were Fewer Boys Born in the US During the COVID-19 Pandemic: A test of the Trivers Willard Hypothesis

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The Trivers-Willard evolutionary hypothesis predicts that parents in poor environmental conditions will favor the offspring sex with more reliable chance of reproductive success, which in humans is female offspring. For example, red deer mothers in adverse conditions show a reduction in the male: female sex ratio of offspring, due to increased loss of male fetuses. The sex ratio in humans at birth (male births/total live births) is typically 0.510 globally. In line with this hypothesis, the sex ratio at birth has been observed to briefly decrease within a few months after large-scale, unexpected stressful events, such as the 9/11 terrorist attacks. Around 3 months following the onset of the Covid-19 pandemic quarantine, the sex ratio at birth decreased to 0.499 in South Africa, and a smaller decrease was also observed in England and Wales. Using publicly available natality data from the National Center for Health Statistics, we examined the sex ratio of all singleton births in the United States (U.S.) from 2015 through 2021. We utilized an autoregressive integrated moving average (ARIMA) model to compare predicted versus actual sex ratios for April 2015 through December 2021, with controls for seasonality. We found no statistically significant decrease in the sex ratio at birth following the onset of the COVID-19 pandemic in the United States in the total population, nor when stratified by race or other socioeconomic factors. Differences from patterns identified in other countries may be due to varying maternal environments and perceived impacts of the pandemic.

This work was funded by the UC San Diego Triton Research and Experimental Learning Scholars (TRELS) program.

Stress Chronologies in a Late Ottoman Bedouin Cemetery from Tall Hisban, Jordan: A Histological Evaluation of Stress during the Tanzimat Land Reforms

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This research reconstructs the chronology of episodic stress experienced by individuals interred at a 19th-century Bedouin cemetery at Tall Hisban, Jordan. The cemetery was established under Late Ottoman rule during the implementation of the Tanzimat, a series of political and economic reforms that targeted the Bedouin way of life, forcing land privatization and agricultural sedentism. Previous studies report that those under two years of age experienced remarkable frailty during this period of heightened stress at Hisban. This research uses cross-sectional histology to identify and estimate the chronology of accentuated striae (AS) in the permanent first molar enamel sampled from six individuals (n=6). The chronology of these enamel growth disruptions was calculated by dividing the distance between defects by the daily secretion rates of enamel. The earliest disruptions occurred at ten weeks, and the latest around 2.4 years of age. On average, more defects formed in the first year of life compared to the second. Moving average peaks in weekly AS frequency occurred at weeks 10, 15, 24, 57, and 73, all within the first two years of life. Episodic stress was recorded during the expected period of exclusive breastfeeding as well as weaning, reflecting both maternal and infant stress patterns. Correlating with the increased mortality risk in late infancy at the Hisban cemetery, the chronology of AS suggests that even among those who survived infancy, the first two years of life were a precarious developmental period subject to greater vulnerability to stress and heightened disease risk.

Homo naledi and the evolution of infancy

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Infancy is a critical developmental window between birth and the cessation of nursing. Human infancy is distinguished by large body size at birth and relatively slow growth rates, among other things, compared to other apes. Aside from a wealth of later Middle Pleistocene Neandertal remains from Eurasia, an otherwise scant fossil record of immature individuals leaves the evolutionary origins of human infancy in the dark. We bring new light to this life history question by analyzing infant remains from the Dinaledi Chamber of Rising Star Cave, South Africa. Dating to around 300,000 years ago, the provenience, morphology, and state of development of these remains are consistent with a single individual around 2 years of age. We compare these remains with homologous elements of adult *Homo naledi*, as well as human infants of known age and body size. Regression equations based on the human comparative sample predict the body mass of the Dinaledi infant to be 5 kg (95% prediction interval: 1.5–8.5 kg) and its stature to be 62 cm (95% prediction interval: 53–71 cm). We use a simulation-based approach to estimate body mass growth rates from birth to three years in *Homo naledi*, which we compare with empirical data from humans, chimpanzees, and bonobos. Growth rates of humans and chimpanzees are higher than those for bonobos and the simulated *Homo naledi* distribution. Comparing infant body mass as a percentage of neonatal size indicates relatively less size change in humans, bonobos, and *Homo naledi* compared to chimpanzees.

Histological and micro-CT perspectives on the regionality of porosity in the human rib

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Localized strain on bone tissue influences the extent of bone remodeling, which produces some net bone loss through the formation of a Haversian canal. Under particularly low strains remodeling resorbs more bone than is subsequently formed, further increasing porosity. Regional patterns of porosity should reflect bone remodeling activity and allow inference about local mechanical loading history.

In the midshaft midthoracic human rib, the cutaneous cortex and the pleural cortex are thought to experience opposing strain modes in bending during respiration. Histological analysis of an age series of midshaft ribs (n=124, 22—97 years, mean=57.4) found the cutaneous cortex was significantly more porous than the pleural cortex across the lifespan ($p<0.001$). Since cortical pores are complex, highly interconnected systems, and a 2D cross-section may not fully capture 3D variation, a protocol was developed for micro-CT imaging of the same ribs previously embedded in methyl methacrylate for histological sectioning. A region-of-interest technique corrected for X-ray attenuation, allowing higher-resolution (7.94 µm voxel size) 3D pore visualization. Preliminary micro-CT analysis of a sub-sample (26, 43, 67, 83 year old males) confirmed higher percent porosity in the cutaneous cortex than the pleural (+ 2.3—8.7%), either matching or exceeding histological findings (+ 0.4—4.2%). One individual with higher pleural porosity in 2D cross-section (+ 2.2%) was found to have marginally higher cutaneous porosity in 3D (+ 0.5%). Continuing micro-CT on this age series will further explore regional patterning in pore system morphometry and connectivity with increased precision and to complement histological results.

Age-related physiological dysregulation progresses slowly in semi-free-ranging chimpanzees

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Lifestyle factors have widespread effects on human health and aging. Small-scale subsistence populations—who puzzlingly experience relatively low incidence of chronic disease yet short life expectancies—exhibit a slightly faster pace of biological aging compared to industrialized human groups. To better understand the evolutionary context for these differences, we examined how analogous lifestyle factors associated with different living environments affect rates of aging in closely related chimpanzees (*Pan troglodytes*). We used LMMs to compare *physiological dysregulation*, an index of biological aging, in semi-free-ranging chimpanzees in an African sanctuary (N=426 measurements from 47 individuals) versus captive chimpanzees in US laboratories (N=3,351 measurements from 325 individuals). If the pace of aging is accelerated by high calorie diet and sedentary lifestyle, we predicted greater age-related dysregulation in laboratories. But if costs of a wild lifestyle accelerate aging, we expected greater age-related dysregulation at the sanctuary, whose environment better approximates the wild. We found that semi-free-ranging chimpanzees exhibited lower overall dysregulation (x2=70.67, p<0.001) and lower age-related change in dysregulation (x2=6.25, p=0.01). Age slopes in sanctuary chimpanzees (0.06) were lower than laboratory chimpanzees (0.22), as well as previously published slopes for industrialized humans (0.14) and forager-horticulturalists (0.17). We further found that although neither population show significant differences in dysregulation by sex, they exhibit distinct aging profiles across different body systems (p<0.001): while sanctuary chimpanzees showed fastest dysregulation in immune system biomarkers, laboratories dysregulated fastest in circulatory and liver/renal markers. This provides some insights into the specific ways that different lifestyles impact aging outcomes.

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Modularity and mosaic evolution in the macaque skull: A study of multivariate shape variation in phylogenetic context

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Mosaic evolution of the primate skull is expected to be facilitated by the skull's modular organization, where relatively-autonomous anatomical modules are determined by genetic, developmental, and functional factors. In this preliminary study, we used craniometric data to explore patterns of modularity and mosaic evolution in the skulls of 14 living species of the genus *Macaca*.

We analyzed 66 linear skull measurements, collected from one representative adult male specimen for each species. The measurements were transformed to dimensionless log-shape variables (where a specimen's "size" was defined as the log-transformed geometric mean of its measurements) and then standardized to z-scores. Our working phylogeny for *Macaca* was drawn from published molecular studies. To explore the data for evidence of modularity and mosaic evolution, we employed the Parins-Fukuchi clustering procedure, using the program *greedo*. In addition to identifying evolutionary modules, *greedo* can estimate relative rates of shape change across a phylogeny.

Surprisingly, the Parins-Fukuchi algorithm only finds a single, well-delineated module (essentially, the entire skull) in our best-fitting model. This result suggests that modular autonomy within the *Macaca* skull is not as clear-cut and pronounced as we might expect from theory or from published studies that have been carried out at higher taxonomic levels. Our examination of relative rates of shape change revealed that rates were highest within the *fascicularis-arctoides* species groups, while rates in the *silenus* species group (including Sulawesi taxa) were considerably lower.

Support for data collection was provided by the University of Missouri-Kansas City's Funding for Excellence program.

Microstructure and Homology in the Human Upper and Lower Limb

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Whether the fore- and hindlimbs of tetrapods are serially homologous elements or developmentally and evolutionarily distinct remains a point of contention among researchers. Additionally, organisms that display functional divergence between the fore- and hindlimbs, such as humans, show less integration of morphological traits. This study analyzes the microstructure of long bones from the upper and lower limbs of humans to establish any relationships in vascularization and bone proportion in paired elements (ulna/fibula and humerus/femur). We predicted that due to functional divergence of the upper and lower limbs in humans compared to quadrupedal organisms and the different developmental trajectories of fore- and hindlimbs, there will not be a similarity between the paired elements, but that fore- and hindlimb elements will show differences in microstructure. A modern American cadaveric sample of 9 females and 10 males (15–105 y.o. (sd=29.87)) was evaluated using histologic samples from the midshaft of the ulna, humerus, fibula, and femur. Osteon population density, porosity area percentage, and bone area percentage were collected. Data were analyzed using an ANOVA and Tukey's HSD to evaluate the cross-sectional microstructure relationship between paired and unpaired elements. Results from both tests indicate that there is no significant difference in tested variables among any of the elements since paired "homologous" elements were as similar to each other as they are to other unpaired counterparts. While homology may be contributing to the similarities between appendages, microstructural features do not support any divergence due to functional differences.

Birthing Across the Diaspora: Making Sense of Embodiment through Black Parenting and Pregnancy

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Low birthweight (LBW) is tied to a wide range of both long- and short-term adverse health outcomes including increased risk of infant mortality, and cardiovascular diseases and metabolic diseases in adulthood. Currently, about 13% of Black infants are born LBW annually, compared to the national average of 8.5%, with the overall LBW rate increasing steadily over the last decade. While it is hypothesized that exposure to systemic and cultural racism have made Black women and their infants especially vulnerable to adverse outcomes in pregnancy and birth, the particular biocultural mechanisms that drive the high rates of LBW have yet to be fully elucidated. Using cohort data from the National Longitudinal Study of Adolescent to Adult Health study, we find that Black women experienced statistically significant rates of LBW (P <.001), and that they were significantly likely to have been diagnosed with high blood pressure (p <.001) and diabetes (p <.001), as well as reporting recent experiences of "feeling blue" (p =.026). Notably, these self-diagnoses of poor mental health are not accompanied by increased formal diagnoses of depression, anxiety, or PTSD. Black feminist theory reimagines the relationship between Black women's bodies, subjectivities, and experiences of oppression and resistance—a useful framework for further theorizing biocultural embodiment for biological anthropologists working with Black women. This presentation engages Black feminist scholarship to contextualize the subjective experiences of Black women navigating pregnancy amidst disproportionately high experiences of poor mental and physical health, highlighting the social contexts and political stakes of LBW outcomes.

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An analysis of cranial and pelvic covariation, with implications for the evolution of cephalopelvic disproportion in non-human primates

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Cephalopelvic disproportion and its potential impact on human pelvic evolution has been a focus of anthropological research for over 70 years. Recent research on anthropoid primate sexual dimorphism has indicated that obstetric selection may affect multiple primate lineages rather than being a hallmark of the hominin lineage alone. Additionally, the proposed method of selection, mismatch between the size of the cranium and the size of the pelvic canal, implies that the cranium and pelvis may be coevolving and that traits in these two skeletal regions may therefore covary. While covariation between the adult cranium and pelvis has been shown in humans, this has yet to be explored in many non-human primate lineages. Here, we test patterns of covariation between the cranium and pelvis of four genera with different hypothesized levels of cephalopelvic disproportion: *Hylobates* and *Cebus* (high cephalopelvic disproportion), *Alouatta* (low cephalopelvic disproportion), and *Lophocebus* (expected average cephalopelvic disproportion) using two-block partial least squares analysis. Results indicate high rates of covariation between the cranium and pelvis (r-PLS>0.9, p=0.0001) across all taxa, with bigger pairwise differences among taxa when genera with high cephalopelvic disproportion (*Hylobates*, *Cebus*) are compared to genera with low (*Alouatta*) or average (*Lophocebus*) cephalopelvic disproportion. This supports the idea that the cranium and pelvis covary and that this relationship may be stronger in lineages with high levels of reported cephalopelvic disproportion. Our results have implications for the role that obstetric selection may have played in shaping cephalopelvic disproportion across multiple anthropoid lineages.

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An archaeogenetic and paleopathological evaluation of an early medieval Iberian community at La Olmeda (Spain, 6th – 11th c. CE)

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The period spanning Late Antiquity and the Early Middle Ages in the Iberian Peninsula was characterized by social, political, and economic shifts. Urbanization and widespread migration are thought to have altered the genetic landscape of the local post-Roman population. While mobility can be closely tied to the spread of infectious disease, limited historical sources from this period in Iberia hinder the reconstruction of the epidemiological landscape.

Here we present molecular and morphological analyses of human remains from the Roman Villa at La Olmeda (Palencia, 6th – 11th c. CE). We studied 49 individuals spanning 500 years and evaluated them for 1) changes in genetic ancestries over time, 2) ancient pathogen DNA, and 3) skeletal evidence of infectious disease. Our results contribute to the debate on the timing of the introduction of African ancestry into NW Iberia, with genetic data indicating that North African ancestry was already present in this area before the arrival of Islamic peoples, alongside an individual with a genetic profile similar to modern-day Basques. Despite an absence of contemporary written references, tuberculosis, brucellosis and malaria were identified in this population. All of these diseases may offer insight into the mysterious fevers mentioned in contemporary historical sources from this region. Additionally, the genetic identification of malaria disproves a published hypothesis that malaria was absent in early medieval Iberia.

This interdisciplinary study offers a new perspective on the timing of the introduction of African ancestry into Iberia and challenges previous understandings of the epidemiological landscape in early medieval Iberia.

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Cultural World Heritage Sites: An imbalance of conservation techniques and funding between the global north and global south using Laetoli, Tanzania, East Africa animal and human trackways as a case study

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A critique of UNESCO's Global Strategy for a Balanced, Representative, and Credible World Heritage List is given, representing the disproportion of sites in the global north and the global south. The global north currently holds the majority of sites on the World Heritage List, with a substantial proportion of funding being fueled into maintenance and conservation of these sites. This leaves sites in the global south highly neglected and at a higher risk for damage and/or destruction due to inadequate funding and unsubstantial conservation efforts. In order to scrutinize this problem, a case study of the animal and human trackways in Tanzania, East Africa will be employed. The current state of the Laetoli footprints show signs of weathering, erosion, and anthropogenic damage. Locality 7, Site A presently exhibits severe cracking and water runoff depreciation. This is irreparably damaging both hominin and animal footprints. Hominin footprints from 3.6 million years ago are incredibly important since they assist paleoanthropologists in answering one of the fundamental questions in anthropology – the evolution of bipedal locomotion. Animal trackways are significant because they assist anthropologists in constructing paleoecologies and assess evolutionary pressures. Encouraging conservation techniques could be implemented at Laetoli that would address the degradation of the trackways, while benefitting the locals and economy.

The variation of maternal and fetal energy requirements and their role in birth timing

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The traditional view that bipedalism-related pelvic constraints and larger brain size are the primary cause of human birth difficulties has been challenged numerous times in recent years. As an alternative, the "Energetics of Gestation and Growth" (EGG) hypothesis proposes that maternal metabolic limitations and fetal energy requirements play a central role in the neurological immaturity and secondary altriciality observed in human neonates. According to the EGG hypothesis, labour is initiated when exponentially increasing fetal energy requirements surpass the maximum maternal metabolic capacity, suggested at around 2.0–2.1×basic metabolic rate (BMR). However, our analysis of 11 additional studies on pregnant females with varying geographic and socioeconomic backgrounds revealed an enormous variability in maternal metabolic scope that also partly exceeded the 2.1xBMR threshold. Further, recent data from athletes indicate a sustained metabolic ceiling of about 2.5×BMR that cannot realistically be crossed by fetal energy demands. Via calculating fetal energy requirements during pregnancy based on weight data of over 25 million livebirths, we found rapid growth until week 35 with substantial tapering thereafter. This finding contradicts the exponential growth pattern of fetal energy requirements towards the end of pregnancy and the starvation of the fetus immediately before birth posited by the EGG hypothesis. Rather, it supports recent research indicating a more intricate interplay of factors affecting birth timing, e.g., fetal membrane senescence and decidual inflammation. Birth timing thereby requires more complex explanations which consider the balance between cephalopelvic fit, energy demands, and biological clocks rather than those focused exclusively on fetal energetic demands.

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Nutrition transition and food insecurity: Stable isotopes (carbon and nitrogen), anthropometry, and diet in the Brazilian Amazon

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Previous research suggests that riverine Amazonian populations are going through a nutrition transition. This term describes the diet changes accompanying economic, demographic, and epidemiological shifts, specifically those taking place when developing countries abandon traditional diets, high in fiber and micronutrients, in favor of diets high in sugar, salt, and fat. To investigate this process, we combined fingernail stable isotopic analyses with anthropometric measurements and in-depth dietary and ethnographic questionnaires on 66 individuals, 32 women and 34 men, from a riverine population in the eastern Amazon, Brazil. Preliminary findings confirm a negative linear relationship between carbon and nitrogen isotopic values, $F(1,64) = 53.9$, $p < 0.001$, $R^2 = 0.45$, wherein the higher carbon isotopic values and lower nitrogen isotopic values belong to the more market-integrated communities, due to a higher consumption of C_4-based industrialised foods and a lower consumption of river fish. In addition, the women's (but not the men's) mean BMI (26.5 ± 5.1) and waist circumference (80 cm ± 9.7) denote a slightly overweight population at increased risk for non communicable diseases – a known risk of the nutrition transition. However, the dietary and ethnographic questionnaires detected the joint consumption of traditional and ultraprocessed foods, as well as the persistence of food insecurity. We argue that to fully understand this "double burden of malnutrition", we need in-depth, multi-method, and case-appropriate studies, but that stable isotopic analyses offer an non-invasive approach to track ongoing dietary changes.

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Limited age-related trabecular and cortical bone loss in chimpanzees differs from patterns of loss in humans

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Investigation of age-related bone loss in nonhuman primates is critical to better understand whether osteoporosis in humans is a recent phenomenon or a deeper evolutionary pattern. We ask: Do chimpanzees exhibit cortical and trabecular changes in bone geometry in response to aging? We test the predictions that as chimpanzees age: 1) trabecular bone volume fraction (BV/TV) will decrease, and bone orientation will become more anisotropic; 2) diaphyseal bone will undergo periosteal expansion and have a decrease in relative cortical area (CA/TA) but increase in torsional rigidity (*J*). The proximal femur (n=10) and first lumbar vertebrae (n=8) of chimpanzees from Gombe, Tanzania (ages 21-53) were scanned using microCT. Cubic ROIs were extracted and analyzed in Dragonfly, ImageJ using MomentMacro, and BoneJ. Linear regressions with age and ANOVA comparisons of age categories were used for statistical analysis.

There were no significant differences in trabecular BV/TV of either the femoral head or lumbar vertebrae. There was a slight, non-significant, increase in femoral head BV/TV with age. Degree of anisotropy remained consistent across age in both bones. In the diaphysis, when grouped by age categories (young adult (YA), mature adult (MA), old adult (OA)) there was an 8% increase in total area and *J* between YA and OA, and an 8% decrease in CA/TA from YA to OA. Although a limited sample, these data suggest that chimpanzee cortical bone exhibits greater changes than trabecular with age. This differs from the pattern in humans, where trabecular loss occurs earlier and at greater rates than cortical.

Alternative biomechanical strategies of Neandertals and *Homo sapiens* femora during the Pleistocene

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Neandertals and early *Homo sapiens* exhibit similar femoral robusticity that is interpreted as a shared mobility pattern in Pleistocene hunter-gatherers. However, their respective femoral cortical distribution and curvature pattern highlight biomechanical distinctiveness even in Middle and Late Pleistocene populations that shared a common environment and lifestyle. We hypothesized that these biomechanical features represent alternative responses to bending loads during bipedal locomotion. In that case, a potential link between femoral cortical distribution pattern and sagittal curvature would indicate that these features can be considered as biomechanically equivalent.

To test this hypothesis, we evaluate the correlations between these parameters on 136 femoral diaphysis from Middle Pleistocene to the present. We employed ratio of anteroposterior to mediolateral cross-sectional bending rigidity and strength to assess cortical distribution. Also, we proposed an original method for sagittal curvature measurement at the local scale on the diaphysis that enables its measurements on incomplete femora.

Our results reveal that neither Neandertals nor *Homo sapiens* femoral diaphyses display a significant correlation between curvature and cortical distribution. However, both features exhibit substantial differences between the two species and show variations within *Homo sapiens* subsamples.

These findings indicate that Neandertals and *Homo sapiens* developed independent physiological responses to bending loads rather than similar ones. To respond to the biomechanical demands of bipedalism, Neandertals femora exhibited an increased-curvature model, while *Homo sapiens* femoral diaphyses displayed anteroposterior cortical reinforcement associated with relatively low sagittal curvature. These findings suggest that both Neandertals and *Homo sapiens* developed distinct biomechanical strategies during the Pleistocene.

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Whole blood gene expression patterns associated with osteoporosis-like bone loss in a free-ranging rhesus macaque

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Osteoporosis is an age-associated disease characterized by reduced bone mineral density (BMD) and increased fracture risk. Although the major cellular mechanisms are in bone, identifying biomarkers in more accessible tissues enables research on molecular contributions to disease pathogenesis. Many species experience age-related BMD changes, but the extent to which these molecular processes are conserved is unclear. We identified molecular signatures of osteopenia in leg joints of the free-ranging Cayo Santiago rhesus macaques (*Macaca mulatta*), a common animal model for human disease. We used linear mixed models to test for association between maximum trabecular bone volume (BV/TV) of the proximal femur and tibia and peripheral whole blood gene expression in one social group (n=42). Similarly, we interrogated the relationship between osteopenia (1SD below prime age BV/TV mean) and expression. 17 genes were positively, and 51 negatively, associated with femur BV/TV (FDR 5%). Gene ontology enrichment revealed an overrepresentation of genes (e.g., *BLVRB)*, involved in riboflavin metabolism, implicated in bone health. Two genes were also associated with tibia BV/TV, including *HIVEP3*, an osteoblast suppressor. Femur osteopenia-associated genes (n=203) were enriched for Fc-gamma receptor mediated functions. Shared tibia osteopenia-genes included *EIF4E*, which is linked to BMD variation in humans. Of note, riboflavin and Fc-gamma receptors impact RANKL osteoclast signaling, and macaques with lower BV/TV showed lower expression of osteoclast suppressors, like *IRF9* and *SH3BP5L*. These results reveal conserved mechanisms underlying osteogenic pathways in primates, and highlight potential biomarkers of bone loss in whole blood.

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From photogrammetry to micro-CT analysis, application of Virtual Anthropology techniques to the new human burials discovered at Cabeço da Amoreira (Final Mesolithic, Portugal)

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The Tagus valley in Portugal represents one the last areas of occupation by the Mesolithic populations in Europe. 13 shellmiddens, located near the village of Muge (District of Santarém) were identified since 1863. However, the archaeological excavation techniques of the previous centuries and the taphonomic alterations have limited conclusions both from cultural and biological aspects on the nearly 300 individuals previously recovered.

Since 2008, a new series of excavations has been underway at Cabeço da Amoreira and have led to the discovery of 7 new individuals with ages at death spanning from the perinatal period to elderly adulthood. These newly discovered burials have benefited from a combination of modern techniques of excavation and the application of various Virtual Anthropology techniques, ranging from on-site photogrammetry to micro-CT analysis at the laboratory.

Those methodologies have enabled the collection and preservation of data on funerary practices with the creation of photogrammetric models of some burials but also with virtual excavation using CT-scan images of burial 5 removed en bloc. 3D reconstructions revealed post mortem movements of bones that explain the observed burial position.

Beyond cultural aspects, (micro)CT scan permitted to investigate various bone changes in order to determine their etiology: pathological, growth-related, or taphonomic. For instance, the cranial remains of burial 2 displayed pathological depressions on the calvaria with remodeling of the diploe and the presence of vascular canals visible on the CT slices, whereas porosities found on the long bones of burial 6 were attributed to normal growth patterns.

This research beneficiated from the funding and support of the European Commission, the Fyssen Foundation, the Fundação para a Ciência e a Tecnologia, the Earthwatch Institute and the Casa Cavadal.

Latent group biological variation in inflammation related biomarker trajectories over 30 days

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Inflammation is a protective response to an immune challenge. Dysregulation can increase both acute and chronic inflammation, producing negative health outcomes. Because inflammation contributes to processes in infectious disease, injury response, and chronic health conditions, most of the research in inflammation is within pathological states. Assessing baseline human variation in inflammation across daily life through intrinsic and extrinsic predictors may clarify how these pathological states arise and function.

This project uses existing data collected from first void urine samples from 117 Polish and Polish American regularly menstruating adults across one menstrual cycle. Intrinsic participant factors include age, length of follicular menstrual phase, and the presence of IL-6. Trajectories of CRP, C-peptide, and cortisol were examined for latent groups using latent class mixture modeling to avoid researcher bias. Group number was selected using BIC while maintaining groups of n>4. Distributions of intrinsic factors within groups were examined via Kruskal-Wallis tests.

Modeling produced three trajectory groups for cortisol and C-peptide, and four for CRP. Age was significantly different between CRP groups (p=0.04, group means: 28, 31, 33, 36). Follicular phase length and IL-6 presence were significantly different between c-peptide groups (p=0.02, p=<0.01). C-peptide group three (high, variable values) had a significantly shorter follicular phase (mean: 11 days) and the highest proportion of IL-6 presence.

Understanding base human variation in inflammation provides further information on short-term predictors of human health, but also indicates the potential for longer term impacts on human evolutionary change due to heterogeneity of risk and selective mortality.

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Contour Analysis of Stone and Steel Tool Cut Marks

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Distinguishing stone tool cut marks from anatomical and taphonomic features on ancient bones is necessary to determine, for example, the antiquity and scope of stone tool use. This study aims to improve profilometry-based methods for distinguishing ancient cut marks. The current study uses contour analysis to explore cut-mark cross-sectional geometry to discern the type of tool that made the marks. This approach provides a way to quantitatively discern the micromorphological features of cut marks made in antiquity from experimentally created cuts and vascular grooves to ascertain their distinctive shapes. The study used high-resolution resin replicas of archaeological-context cut marks (n = 7), vascular grooves from human bones (n = 5), and pig bones experimentally incised with modern steel trowels (n = 9). Cut mark 3D replicas were made with a white-light confocal profiler at 10X; this study used Digital Surf's Mountains9 software to generate an averaged cross-section analyzed via the contour analysis module. Cut marks measurements included kerf maximum width, maximum depth, angles where kerf walls met the bone surface, and the angle of the kerf floor. Multivariate discriminant models successfully classified 90.5% of the grouped cases. This updated approach to contour analysis holds promise for distinguishing ancient cut marks from incisions made by archaeological tools and anatomical features.

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Exploring life course through diet: Breastfeeding and weaning in medieval Croatia

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Archaeological reconstructions of breastfeeding and weaning have the potential to address central themes in anthropology including personhood, subsistence, demographics, and social structure. Dietary reconstructions may demonstrate cultural differences in timing of weaning according to sex, social status, or other factors. This allows for a deeper interpretation of identity and embodiment throughout the life course. The archaeological site of Đurđevac-Sošice appears to have been a religious center and trading district throughout the Middle Ages. This study explores early life diet among the medieval Croatian community through the use of commingled remains interred within the church of St. George.

Carbon and nitrogen stable isotopes of incremental dentin collagen were used to reconstruct patterns of breastfeeding and weaning. Longitudinal central slices of dentin were removed from the M_1 of twelve individuals. 1mm increments of dentin collagen were then extracted beginning from the crown and ending at the root using a biopsy punch method. This method improves temporal resolution and age-alignment accuracy by considering the anatomical structure of dentin. δ^{15}N data were entered into WEAN, a program designed to generate an age estimation for weaning completion using regression analysis.

The data demonstrate that weaning was typically completed by approximately 2.9 years, after which gradual shifts were observed, possibly indicating a transition to an adult-like diet. These results are consistent with available historical records. Although the archaeological context of commingled remains is greatly limited, this isotopic sampling method has allowed for detailed longitudinal reconstructions of diet that illustrate nutritional transitions throughout the life course.

A gene selection analysis of the umami taste receptor encoded by TAS1R1 and TAS1R3 within humans and *Pan* species

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The umami taste receptor, which is encoded by the TAS1R1 and TAS1R3 genes, enables humans' perception of the savory flavor commonly associated with meat through the receptor's detection of proteinogenic molecules. Whilst meat consumption is widespread in humans, meat eating is thought to be relatively rare and primarily opportunistic in non-human primates. However, there is evidence that some primates have systematically adapted meat into their diets, such as chimpanzees (*Pan troglodytes*), who consume a range of prey and employ varied strategies in their hunting behaviors. Given the hypothesized importance assigned to meat consumption during human evolution, and the recognition of hunting amongst chimpanzees, we have chosen to explore sensory adaptations that would support this behavior, such as increased sensitivity to the flavors present in meat. This work examines the selection patterns of the TAS1R1 and TAS1R3 genes in the *Homo*/*Pan* clade, which includes humans, chimpanzees, and bonobos (*Pan paniscus*). Sequences were downloaded from Ensembl and NCBI and manually aligned, and a maximum likelihood tree was generated in PAUP* and analyzed using codeml in PAML. Our results indicated no positive selection in TAS1R1 in the clade of interest, though we did infer positive selection in TAS1R3 on the branch ancestral to the *Homo*/*Pan* clade but not on the *Homo* branch. This suggests that protein taste perception as facilitated by TAS1R3 holds special significance to the *Homo*/*Pan* clade and the common ancestor of both chimpanzees and humans rather than being of unique significance to humans alone.

Virtual female primates in B3GET have highest reproductive success in medium-sized groups

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"Why do primates live in groups?" That remains an important yet unresolved question in understanding the evolution of primate social behavior. In this study, we investigated how group size affects the number of offspring – a major factor thought to influence primate sociality – using B3GET, an agent-based model built to simulate primates living in a range of environmental conditions. In 288 simulations over 100,000 timesteps, we simulated four virtual primate species – chimpanzees, geladas, hamadryas baboons, and olive baboons – that vary in their dispersal patterns, mating behaviors, and within-group and between-group spatial and interactive dynamics. This resulted in 370,199 agents that were virtually born and died in these simulations. We recorded group size and reproductive success in two ways: (1) with agent data, showing exact information about each female agent's number of offspring and size of her group at birth and death; (2) with scan data, by periodically scanning each group for group size and offspring born since the previous scan. We analyzed both datasets using linear mixed-effects models to test the relationship between group size and reproductive success. In both datasets, we found a quadratic relationship suggesting that medium-sized groups had the highest reproductive success in all four virtual species (▯ (group size^2) < 0; P < 0.001, for all). Our results support a longstanding hypothesis that group-living primates must compromise between having a larger group to minimize between-group competition and a smaller group to minimize within-group competition.

µCT scan data unveil previously undocumented morphology in the oldest known plesiadapiform cranium

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The partial cranium of the palaechthonid plesiadapiform *Plesiolestes nacimienti* (KUVP 9557) from the early Paleocene was described and evaluated a half century ago to infer the ecology of the ancestral primate. While additional plesiadapiform crania have since been recovered, this specimen remains the best-preserved palaechthonid cranium and the oldest known partial cranium of any plesiadapiform. Thus, this specimen has potential to help reconstruct the cranial anatomy of the oldest primate relatives. Novel µCT scan data of this specimen allowed us to document previously unknown internal anatomy, evaluate previously described cranial morphology, and make new comparisons with crania of other plesiadapiforms and euarchontan mammals (primates, colugos, treeshrews). While several of the original cranial descriptions were correct (e.g., posterior expansion of nasal bone), µCT data have helped resolve other previous morphological interpretations, such as the position of the olfactory bulbs, and the inferred presence of a postorbital process and premaxilla-maxilla suture. The olfactory bulbs have a more posterior position than previously inferred, which is like that of microsyopid and plesiadapid plesiadapiforms but differs from the more anterior position found within paromomyid plesiadapiforms and extant euarchontans. The postorbital process is absent, and its inferred presence was likely in part due to dorsoventral compression of the specimen, and an artificial edge created by matrix. µCT data indicate the premaxilla-maxilla suture is not preserved as previously described. Overall, the cranial anatomy of *P. nacimienti* appears to be very plesiomorphic like that of other plesiadapiforms and lacks clear cranial synapomorphies with crown primates, colugos, or treeshrews.

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Do fur isotopes detect weaning in dwarf lemurs?

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Juvenile primates relying on milk tend to have higher nitrogen ($\delta^{15}N$) and distinct carbon ($\delta^{13}C$) and oxygen ($\delta^{18}O$) isotope values than their mothers. However, once juveniles begin consuming solid foods, their isotopic profiles converge towards adults. We analyzed carbon, nitrogen, and oxygen isotopes in fur samples from wild dwarf lemurs (*Cheirogaleus crossleyi* and *C. sibreei*) from central Madagascar to determine if a "nursing" signal is obscured for species that wean quickly. Dwarf lemurs are obligate hibernators; juveniles undergo fast growth and development and likely wean during their first three months. We compared five mother-juvenile pairs, with juveniles ranging from one to three-month-olds. We divided fur samples into 0.5 cm sections and calculated the isotopic difference between base and tip sections ($\Delta_{tip\text{-}base}$) to capture recent dietary shifts. With the expectation that juveniles nursed in the weeks to months preceding sampling, we anticipated they would be isotopically distinct from their mothers and $\Delta_{tip\text{-}base}$ values would be largest for older juveniles. Contrary to expectations, there were no consistent isotopic differences between juveniles and adults. Positive $\Delta_{tip\text{-}base}$ values for carbon (ca. 1.5‰) and oxygen (2-3‰) support recent weaning for 2-3-month-olds. However, only the youngest individual (1-1.5 months) had a $\Delta_{tip\text{-}base}$ value larger than ±0.2‰ for nitrogen, and it was opposite the direction expected (-1‰). Lack of a clear nursing signal suggests dwarf lemurs may introduce solid foods during their first month of life. The nursing period may be too short to be captured in their fur.

Fraught (re)conceptions: Diasporic decedents and paths to commemoration

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Historic human remains occupy a contested status both within biological anthropology and culturally, such that the same set of remains can be conceived of as a complex former person or as a disembodied anatomical object without depth. Stewards of historic human remains have the power to act on these conceptions to determine, alter, or reverse burial conditions and socio-scientific constructs of these deceased individuals. This study critically reviews the contested status of Black decedents, for whom unmarked graves and the displacement and use of their remains are salient. We present a process of objectification for Black decedents. Objectification relies on intentional omission, a means of strategically silencing the complexity and value attached to human remains that comprise one's kin, to effectively position ancestors as nonsacred objects for scientific consumption. We apply this concept to two case studies: reproductions of violence in the use of unclaimed and non-consensually dissected Black decedents in anatomical collections, and conflicting stakeholder dynamics at the enslavement era burial site at Rupert's Valley, St. Helena. In both cases, power struggles and apathy contributed to the objectification and eventual renegotiation of these ancestors' value and treatment. Evolving engagements with these contexts, such as kinship identifications and increased protections, have worked to upend conceptions of disvalue for these decedents. These two instances of contestation highlight the complexity of navigating the contexts that espouse contradictions in perceiving Black decedents. They also present a critical consideration of the role of human remains work as it relates to stewardship.

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A Case Study of an Enlarged Mandibular Condyle from the Phaleron Cemetery in Athens

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An individual from the large, complex cemetery of Phaleron, which dates from the Archaic Period (c 7th-4th C BCE), near the old port of Athens, exhibits maxillofacial and mandibular asymmetry as well as malocclusion of the dentition caused by an enlargement of the right mandibular condyle. This presentation of pathological features is associated with multiple conditions, including: osteochondroma, mandibular condylar hyperplasia, and trauma. To perform a differential diagnosis for these conditions, the authors examined the exposed trabeculae of the hyperplastic condyle and found no abnormalities consistent with neoplastic disease, which is inconsistent with osteochondroma. Additionally, this individual exhibits multiple signs of interpersonal violence, including a healed depression fracture on the cranium and healed fracture, dislocation, and fusion of the pubic symphysis. This suggests that trauma was common in this individual's life and thus may have caused the hyperplasia. However, because the causes of mandibular condylar hyperplasia are not fully understood, developmental issues cannot be ruled out. Overall, the high incidence of interpersonal violence seen in this cemetery population, as well as the evidence of healed trauma on this individual suggests that traumatic injury may be the most likely cause.

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Differences in adult human femoral external shape and cortical and trabecular bone structure associated with body mass index

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Estimation of adult body mass from skeletal remains in a forensic context is plagued with inaccuracy and imprecision and therefore is infrequently provided in the biological profile. However, information regarding obesity status could contribute to the identification of unidentified decedents. Bone is a dynamic tissue that responds to mechanical loading by changing whole bone external shape and cortical and trabecular bone geometry and size. This study examines differences in femur external shape, cortical bone geometry, and trabecular bone architecture between obese and nonobese individuals. X-ray computed tomography (CT) scans of eighty human femora from the ethically-sourced and well-documented Texas State University Donated Skeletal Collection were used in the study. The sample was divided evenly into moderate (<30) and high (≥30) BMI males and females. Triangular mesh surfaces were generated from the CT scans and femoral shape variation was summarized using principal component analysis. Two-dimensional slices were interpolated from 20-80% of the shaft and trabecular bone was extracted as a single volume of interest of trabecular bone from the femoral head. In high BMI individuals, the femur has greater proximal diaphyseal breadth and a lower anteversion angle (males reached significance [$p<0.5$] and females approached significance [$p=0.065$]). For both sexes significant differences were observed in most cortical bone cross-sectional properties. Trabecular bone exhibited no significant differences except for trabecular spacing in females. The results demonstrate the potential for estimating BMI category in medicolegal death investigations from external shape and shaft cross-sectional geometry.

Systematic review of same-sex sexual behavior in non-human primates

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There has been a recent resurgence in evolutionary analyses of same-sex sexual behavior (SSB) that rely on data on the phylogenetic distribution of this trait; however, these studies have been limited by inconsistent terminology, species bias, discrepant methodologies, and the overall dearth of research on SSB. We address this problem head-on by examining: 1) What historical, taxonomic, or methodological biases exist among studies of SSB in non-human primates (hereafter primate)? 2) How widespread is SSB in primates? 3) How do these behaviors vary within and between sexes, populations, and species? To answer these questions, we conducted a systematic review of the primate literature examining how studies have discussed and researched SSB in this taxon. We extracted data on publication year, terminology, methodology, taxa, and population from screened publications. As expected, preliminary results show that publications on SSB in primates have increased since the late 1960s, with a peak in publications in 2006. Out of 5,105 publications returned after a search for studies on primates, we identified only 610 on SSB after an initial title and abstract screening. Taxonomically, bonobos were the most studied (12% of studies), closely followed by Japanese macaques (11%), other macaque species (11%), and chimpanzees (8%). SSB is documented in capuchins and spider monkeys but rarely studied (2.5% and 1.1% of studies respectively). As queer scientists, we highlight the biases that exist in the study of SSB and discuss how addressing these biases will provide opportunities for the production of novel knowledge.

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Plants as agents of bone surface modifications: Root-etching and implications for the fossil record

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Taphonomic analyses of bone surface modifications (BSMs) are used to elucidate conditions of depositional environments, which then inform our interpretations of ecological conditions and site formation processes. While root-etching on bone surfaces is a frequently cited BSM, there are few experimental studies regarding the specific ways roots modify surfaces and how root-etching varies with different parameters. Here the results of a year-long experiment on plants grown in substrates containing skeletal remains are presented to provide data on root-etching BSMs. Twenty skeletal specimens were buried in temperature, humidity, and lighting-controlled conditions and experimental parameters varied by types of plants grown, substrate types, bone types, burial depths, length of internment, ages of bone, and weathering stages of specimens.

Specimens presented various BSMs from small round pits, to long, deeply incised striations that could be confused with trampling or cut-marks. Fine, fibrous roots result in dendritic etching while thicker feeder roots produce linear striations. Increased pitting is found in lower pH substrates. Roots are able to penetrate deeper into juvenile/woven bone than mature bone. Root-etching is difficult to differentiate in higher weathering stages. Etching occurs in higher densities on flat and long bones than on irregular bones or dentition. Deeper incisions are found on bones in shallower substrates and on specimens that had been buried for longer.

These results allow for finer extraction of ecological information from taphonomic conditions. Future experiments will focus on varying root and substrate types to increase the use of this BSM as an ecological proxy.

Annular Ring Size and Position in *Australopithecus*

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The annular ring is a secondary ossification center in the spine which forms the connective anchor between two adjacent vertebrae and the cartilage of intervertebral discs, offering postural stability for the head and neck in the cervical spine. This study examines the size and position of the annular ring on the superior and inferior surfaces of the subaxial cervical vertebrae in humans, non-human primates, and extinct fossil hominins. The sample in this study included 13 *H. sapiens*, 25 *Pan,* 37 *Gorilla,* six *Hylobates,* and three *Papio* individuals, as well as sixth cervical vertebrae of fossil hominins, AL333-106 (*Australopithecus afarensis*) and UW88-83 (*Australopithecus sediba*). Measurements were obtained of the overall vertebral body articular surface area, the surface area inside the annular ring, and the anterior and posterior mid-sagittal length of the annular ring using Image J. Results show that the annular ring to overall vertebral body surface area ratio is significantly smaller in *H. sapiens* compared to non-human primates and *Australopithecus*. It was also found that *Australopithecus* ratios of the annular ring are more similar to great apes, and in some cases are larger than in African great apes.

Additionally, the anteroposterior placement of the annular ring follows a distinct pattern caudally along the cervical spine in humans compared to extant taxa. The differences in the annular ring across taxa may be related to locomotor and postural differences. Hominin fossils appearing more ape-like in this feature of the cervical vertebrae may offer more future insight into functional morphology of human ancestors.

Birth seasonality peak corresponds with detrimental health and mortality outcomes in modern Mexico

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Human populations cross-culturally are characterized by birth seasonality in which birth rates peak at specific, predictable, and relatively stable times of the year. Similarly, a large literature has identified strong seasonal patterns in neonatal health outcomes. However, we know much less about how these two seasonal processes interact, especially outside of wealthy nations at higher latitudes. Are neonates born in seasonal peaks healthier and less likely to die young compared to those born outside these periods, suggesting an adaptive origin to birth seasonality patterns? Or do "peak" neonates face neutral or even detrimental effects at birth and during infancy, suggesting that birth seasonality is simply a byproduct of human phylogeny or energetic constraints? Here we investigate the effects of birth seasonality on newborn birth weights and infant mortality risk for over 27 million recorded births and 13 million deaths in Mexico from 2004-2021. We find that newborns born during the peak birthing season (AUG-OCT) experience the *lowest* average birth weights across Mexico. Furthermore, being born in this peak window was associated with a significantly higher mortality risk across the first five years of life when compared to births during "trough" months (state-specific HRs between 1.4-2.0, $p < 0.001$). Taken together, these results suggest that (1) birth seasonality in Mexico does not match optimal timing for the maximization of child health and survival, and (2) human birth timing more generally likely reflect essential life-history trade-offs governed by energetic or environmental constraints.

Discriminating between taxa of Cercopithecid primates using morphometric analysis of landmark data

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Mandibles are well represented in the cercopithecid fossil record but are often challenging to allocate to species or even genus. To address this, we used geometric morphometric (GM) analysis to explore the shape variation within and among cercopithecid species based on a protocol with 32 3D landmarks. We analyzed a sample of 197 mandibles from 11 species of cercopithecid monkeys in 9 genera taken from the PRIMO database. To investigate the ability to distinguish among closely related species, one of us also digitized 82 mandibles from three species of *Macaca* (*M. fascicularis, M. mulatta, M. nemestrina*) from the University of Oregon Comparative Primate Collection using a Microscribe-3DX digitizer. Generalized Procrustes Analysis was performed in Morpheus. We performed Principal Components Analysis (PCA), Linear Discriminant Analysis (LDA), MANOVA and ANOVA in PAST. Our analyses showed that mandibles from different genera and species were distinct in both form and shape. According to MANOVA, all genera and species were distinct in shape with and without the natural log of centroid size (lnCS) included as a dependent variable ($P < 0.0001$). The LDA found that with lnCS included, mandibles had a jackknife classification rate for genera and species of 96%. Using only shape data, the jackknife classification rates were lower for genera at 92% and species at 79%. While more work needs to be done, especially analyzing individual regions of the mandible such as the corpus and the symphysis, GM analysis holds promise for distinguishing cercopithecid taxa.

Unraveling the Evolutionary Threads: insight into the polygenic adaptations to pathogens across human history

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Pathogens exposure is recognized as one of the strongest selective forces faced by humans through time. Large-scale genome-wide association studies (GWAS) related to the adaptations to pathogens in present-day individuals demonstrated that the genetic predisposition to these complex traits is likely due to the contribution of several thousand loci across the genome. To model this polygenic inheritance, it is possible to combine the effects of multiple variants in polygenic risk scores (PRS), an estimate of an individual's genetic potential for a trait. By combining present-day GWAS data with ancient genomes, we estimated the genetic contributions to the traits in the archeological record, accounting for their variation through time. Our analyses on the variation of the polygenic architecture of ID-related traits through time scrutinized more than 3,500 ancient individuals from Western Eurasia. Our study provides evidence that major events occurring in human pre- and historical times might have modulated the polygenic architecture of ID-related traits, impacting the biological processes to modulate the host-pathogen interaction. Three events - Justinian Plague, Antonine Plague, and Measles outbreaks - seem to be related to evidence of significant changes in the polygenicity of the ID-related traits. The enrichment analyses advocated multiple biological processes consistently involved in the associations of the polygenic liability for ID-related traits and the periods. Specifically, they underlined the role of lipid metabolism and the clearance of lipoproteins; the differentiation and development of the megakaryocytes; and the response to hormone stimuli, specifically insulin, highlighting the involvement of the body at a systemic level.

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The Impact of Case Protocol and Decedent Demographics on Positive Identification in Forensic Anthropology

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Variation in the percentage of unidentified remains cases curated across facilities ranges from less than 1% to 24.4%. However, these figures only reflect case admissions and do not account for the accumulation of long-term unidentified remains, especially at academic institutions where forensic anthropologists serve as consultants and curators until positive identifications are made. Consequently, it is informative to review the operational framework of casework and the intrinsic attributes of decedents that influence identification rates. For instance, social statuses, such as "migrant" and "unhoused," have led to an increased likelihood of anonymity in death. This study conducted an analysis of casework (N=73; 18 identified, 55 unidentified) at the Forensic Anthropology Center at Texas State University (FACTS), focusing on parameters including biological profile, chain of custody, missing persons data, media coverage, the presence of personal effects, and other factors relating to social vulnerability. This review showed that among positively identified individuals, the average amount of time in FACTS custody prior to identification was 12 months, with the most common identification method being dental records. The length of curation for unidentified individuals included in the study ranged from less than one to over 20 years. Sex and population affinity differences between groups were tested for significance with Chi Square tests; there were significantly more unidentified males ($P=0.025917$) and minorities ($P=0. 036338$). Understanding these variables and other factors contributing to long-term unidentified status is imperative for the development of targeted interventions to mitigate these issues in identification.

Identified sources of interobserver error in ASUDAS trait definitions: An investigation of the persistent inconsistency in dental morphology scoring

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Despite the formalization of dental morphology definitions, few studies have evaluated the levels of interobserver error impacting the method. Subjective ASUDAS definitions rely heavily on formal training and experience. To investigate the specific sources and levels of error in the method, observations from four workshops were coupled with quantitative data from an interobserver agreement study.

Two experienced and one inexperienced observer scored 17 traits on subsets of 52 skulls from the Atkinson Collection housed at the University of the Pacific, AA Dugoni School of Dentistry. A weighted Cohen's kappa (k) demonstrated the highest agreement in UI2 shoveling (0.64-0.86), UM2 hypocone (0.74-0.84), UM1 Carabelli cusp (0.79-0.92), and LM1 cusp number (0.74-0.84), and lowest agreement in canine DAR (0.03-0.21), UI2 *tuberculum dentale* (0.10-0.53), and LM2 deflecting wrinkle (0.11-0.15). Seven traits showed improved rater agreement in relation to experience level. Conversely, the deflecting wrinkle showed decreased agreement with greater observer experience. When limited to experienced observers, only 65% of tooth-specific traits resulted in k >0.6, and 20% in k >0.8, suggesting increased training does not necessarily resolve issues of rater disagreement.

Observations during the workshop trainings from three different instructors were consistent with these results. Difficulty in identifying anatomical features central to the definitions, and disagreement over subjective scoring based on individual experience and interpretation of vague definitions, were experienced in all four observed workshops. This research highlights particularly problematic traits that need revised definitions to enhance observer agreement and suggests approaches to training in dental morphology to minimize disagreement.

Sex-biased sampling may influence *Homo naledi* tooth size variation

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A frequent source of debate in paleoanthropology concerns the taxonomic unity of fossil assemblages, with many hominin samples exhibiting elevated levels of variation that can be interpreted as indicating the presence of multiple species. In contrast, the large assemblage of fossils from the Rising Star cave system, assigned to *Homo naledi*, exhibits a low degree of variation in many skeletal elements. Many factors can contribute to low sample variation, including genetic drift, strong natural selection, biased sex ratios, and sampling of closely related individuals. In this study, we tested for potential sex-biased sampling in the Rising Star dental sample. We compared coefficients of variation for the *Homo naledi* teeth to those for eight extant hominoid samples. A resampling procedure was used to generate samples from the extant taxa that matched those of the fossils in sample size for each possible Rising Star dental sex ratio. We found that variation at four *Homo naledi* tooth positions—I_2, M_1, P^4, M_1—is so low in the current sample that the possibility of one sex representing few or no individuals cannot be excluded. Additional evidence is needed to corroborate this inference, such as ancient DNA or enamel proteome data, and our study design does not address other potential factors that might contribute or cause low variation. Nevertheless, our results highlight the importance of considering the taphonomic history of a hominin assemblage, and suggest sex-biased sampling is a plausible explanation for low level phenotypic variation in some aspects of the current *Homo naledi* assemblage.

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Evaluating the Efficacy of Artificial Neural Networks in Classifying Isotopic Signatures: Applications for Forensic Provenancing

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The United States and Mexico border has become one of the deadliest diasporic regions in the world with over 3,000 people reported dead or missing within the last five years. Due to the isolated nature of border crossings and the extreme weather conditions present in the region, remains are often found skeletonized, complicating identification. Identification is further complicated by the undocumented nature of these crossings, limiting contextual information that could aide an investigation. Isotopic ratios that become engrained within human tissues over the course of life provide a means for estimating an individual's geographic region-of-origin and are particularly applicable in these cases. Isotopic datasets, however, exhibit a high degree of nuance in their spatial distribution making high-resolution classification challenging for many traditional analytical methods. Advanced machine learning methods that are more capable at distinguishing patterns in complex and multi-dimensional data have the potential to increase the resolution of these classifications, making region-of-origin prediction more accurate and reliable. Here, we evaluated the efficacy of an artificial neural network (ANN) in its ability to classify water isotope values into six geographic regions spanning from Mexico to Colombia and compared it to five other machine learning algorithms. Overall, the ANN outperformed each algorithm achieving accuracies up to 85% while the next best performing algorithm – the support vector machine – achieved a maximum accuracy of 77%. This highlights the utility of advanced machine learning algorithms in distinguishing nuanced patterns in complex datasets and in their potential for provenancing unidentified human remains.

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Higher latitude is associated with lower bone mass and higher remodeling in the midshaft femur of Medieval humans

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Cold exposure can increase bone remodeling and decrease bone strength via chronic sympathetic activation. Here we used archaeological skeletons of humans from different latitudes to test the effects of frequent cold exposure on bone.

We studied adults of European ancestry from two Medieval sites: Haffjarðarey, Iceland (1200-1563 CE), and Mistihalj, Bosnia and Herzegovina (1300-1500 CE), which differ by ~20° in latitude and ~20° F in mean high and low temperatures. The prediction was that bone mass would be lower at colder Haffjarðarey vs. warmer Mistihalj. We measured femoral midshaft cortical cross-sectional geometry by computed tomography (45-64 µm, N=9-13 per sex and site). Scans were reconstructed in Dragonfly and measured using MomentMacro in Fiji (2.14.0). Outcomes included total area (TA, mm^2), bone area (BA, mm^2), bone area fraction (BA/TA, %), cortical thickness (Ct. Th, mm), moments of inertia (Imax, Imin, and J, mm^4), and cortical porosity (%). In males, Imax (+31%), J (+25%), TA (+8%), BA (+10%), and BA/TA (+12%) were higher at Mistihalj than Haffjarðarey (all $p<0.05$). Estimated male body mass was also higher at Mistihalj (+10%, $p=0.041$); after adjustment for body mass, significance remained for BA ($p=0.034$). In females, Imax (+24%, $p=0.045$) was higher at Mistihalj than Haffjarðarey. Cortical porosity >2% was present in 45% of femora from Haffjarðarey vs. 24% of femora from Mistihalj. These initial results are consistent with our hypothesis that chronic cold exposure at high latitudes decreases bone mass and increases bone remodeling. Ongoing analyses focus on trabecular bone microarchitecture.

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Frailty or resilience? Hazards-based and cumulative phenotype approaches to discerning signals of health inequality in human skeletal data

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Since Wood and colleagues' (1992) influential paper detailing the osteological paradox and highlighting how heterogenous frailty complicates attempts to reconstruct variation in health in the past, numerous bioarchaeological studies have addressed the topic by differentially conceptualizing and quantifying frailty. Following Wood et al., frailty often is operationalized as increased risk of mortality; recent bioarchaeological re-conceptualizations of frailty consider it as a cumulative phenotype. These differing, but complementary, approaches have demonstrated that skeletal and dentoalveolar markers of stress may represent either frailty or resilience. Given recent developments in assessing frailty in both the living and the long deceased, we outline a research methodology for assessing skeletal frailty within and between populations that integrates hazards-based and indexical/cumulative phenotype approaches. Using data from several medieval London cemeteries, we estimated the risk of mortality (using Cox proportional hazards analysis) and survivorship (using Kaplan Meier survival analysis) associated with stress markers commonly used in bioarchaeology (either in isolation or as part of frailty indices). We found that some markers associate with elevated mortality and lower survivorship (linear enamel hypoplasia, short femur length), whereas others associate with lower mortality and higher survivorship (osteoarthritis, periosteal new bone formation, cribra orbitalia). We used these results to construct separate, context-specific mortality and resilience indices for medieval London samples. Applying these indices to adult individuals, we evaluated the possible existence of the male-female morbidity-mortality paradox in this urban Medieval context. Our findings suggest that the male-female morbidity-mortality paradox observed in modern populations may not have existed in this medieval setting.

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Metabarcoding of Environmental DNA from Soil: A Promising Tool for Assessing Mammalian Community Composition

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Metabarcoding of DNA extracted from environmental samples is emerging as a promising tool for rapid, cost-effective assessment of biodiversity. We evaluated the viability of this approach for inferring mammal species presence in two different habitats: tropical rainforest and human-impacted urban spaces. We collected and air-dried soil samples from mineral licks at the Tiputini Biodiversity Station in Amazonian Ecuador and from several sites in Austin, Texas, two of which we seeded with exogenous mammalian feces or hair (ferret, dog, human). We extracted eDNA from ~250 mg of dried, pulverized soil and amplified, via PCR, a ~120 bp fragment of the mammalian mitochondrial 16S rRNA gene using conserved primers. We then constructed DNA libraries for four samples -- one from a mineral lick where we had extensive camera-trap data on mammalian visitors plus three Austin sites -- and sequenced them on an MinION Mk1C portable sequencer. For each library, we selected ~45K to ~200K reads, ran a custom assembly algorithm to cluster and generate consensus sequences, and used BLAST to assign taxonomic identity to each consensus. The Ecuador sample yielded several mammal species known to regularly use the mineral lick (spider monkeys, sloths, pacas), although we did not detect DNA of other common visitors (howler monkeys, tapir). Mammals detected in the Austin samples included suids in both unseeded and seeded samples plus exogenous taxa in the seeded samples. Our results suggest that soil eDNA metabarcoding might be effective for surveying mammal communities with relatively low sampling effort and cost.

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Mitonuclear Discordance and Metabolic Function in Admixed Polynesian Populations

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Over 1,000 nuclear genes encode proteins essential for mitochondrial function. Decreased mitochondrial function has been linked to adverse health effects, including increased risk of metabolic-related diseases such as gout, type 2 diabetes, and chronic kidney disease. One possible cause of decreased mitochondrial function is mitonuclear discordance, a situation in which the mitochondrial and nuclear genomes do not cooperate optimally due to having differing ancestral backgrounds within the same individual. To assess the potential impact of these inter-genomic interactions on metabolic-related diseases, we estimated mitonuclear discordance from a cohort of 2,297 individuals with self-identified Polynesian ancestry living in Aotearoa New Zealand. The risk of gout and type 2 diabetes was found to decrease in this cohort as mitonuclear discordance increased, indicating that differing mitochondrial and nuclear backgrounds may instead provide a protective effect against metabolic-related diseases. Conversely, chronic kidney disease positively associated with mitonuclear discordance, indicating individuals with higher mitonuclear discordance were at higher risk for chronic kidney disease. There were no overall different patterns between the 86.16% of the study cohort with the B4a1a mitochondrial haplogroup and those with other haplogroups. These findings suggest that the Polynesian ancestral nuclear genome may have a greater impact on disease outcome than mitonuclear discordance. This result further complicates our understanding of mitonuclear interactions, particularly in its effects on mitochondrial pathways and disease outcomes in admixed populations.

Investigating biological and social factors in epidemic spread in an institutionalized population: A modeling study

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Institutionalized populations of persons with disabilities frequently experience high rates of morbidity and mortality during epidemics due to biological and social factors, including increased risk of infection and disproportionate access to health care and other services. Simulation modeling is a useful tool for teasing apart potential independent or interacting contributions from such factors. In this presentation, I will describe an agent-based model of a residential school for deaf children developed from Norwegian archival sources and data from the 1918 influenza pandemic. Previous analyses of the model show that observed differences in outcomes between students and staff could be explained by social factors alone. New analyses presented here incorporate potential biological factors related to disability status, age, and individual variation. Modeled scenarios involve adjusting the transmission and mortality probability parameters for different subgroups based on available historical data; additionally, those parameters are modeled as constants and as distributions from which agents pull individual values. Results indicate that, while expected differences in the number of cases or deaths are observed, there are few other emergent or non-linear patterns. There are few to no practical differences between experimental scenarios, indicating diminishing returns from more complex modeling of subgroup and individual variation. Rather, results comparing simulations of epidemics begun by student vs. staff first cases reinforce earlier findings that suggest differential epidemic outcomes in this modeled population are strongly influenced by – and thus could be prevented or reduced through – the social setting and associated behaviors rather than variation in biological disease parameters.

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Childhood frailty and mortality in medieval and early modern Aberdeen, Scotland

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The medieval and early modern periods (900-1800 CE) in Scotland were characterized by drastic political, economic, social and climactic changes. This study examines the relationship between cribra orbitalia (CO) (used as an indicator of frailty) and an increased risk of death during these turbulent periods in history. To do this, human skeletal remains that date to the 12th-15th centuries (n=228) and the 15th-18th centuries (n=91) from the Kirk of St Nicholas in Aberdeen, Scotland were assessed. Survival analysis and odds ratios (OR) were conducted to explore the relationships between CO, age-at-death and time period. The overall prevalence of CO was higher in preadults (45%) than in adults (9%) and preadults were significantly more likely to die with CO than adults (OR=4.57, $p < 0.0001$). Preadult individuals that died during the 12th-15th centuries were equally at risk of dying with CO than those that lived during the 15th-18th centuries. Though the odds of adults from the 12th-15th centuries having CO (17%) were higher than those that lived during the 15th-18th centuries (9%), this was not a significant difference (OR=1.99, $p = 0.1668$). There was no difference in CO risk between adult males and females. These results indicate that CO is associated with increased mortality risk and frailty for preadult individuals but not for adults. The increased mortality risk in children, as a highly vulnerable subset of the population, likely reflects the adversity experienced by northern communities as the result of ongoing conflict, social upheaval and climate deterioration.

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Using Uniparental DNA to Recover the Colonial Population History of Nuestra Señora de Belén, New Mexico

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Nuestra Señora de Belén church was first established in Belén, New Mexico in 1793 by the Spanish arch diocese to serve a community known as Genízaros. Descended from Indigenous peoples in what is now the US Southwest, Genízaros were captured, enslaved, indentured, and ultimately assimilated by Spanish settlers. Their history has since been subject to cultural and material erasure. In Belén, the original church was destroyed, and neighborhoods were built over the original plaza and cemetery where Genízaros and others from the surrounding region were buried. However, memories of the church, plaza, cemetery, and the Ancestors interred within have been carried by the descendant community to the present day. In collaboration with descendants, historians, and archaeologists, the goal of this project is to recover the population history of Belén. The genetic phase of this project was supported by the State Historic Preservation Division in NM and the IRB at GMU (Protocol: 2047389-1), and the research aims were co-developed with the descendant community. Small portions of dental and skeletal remains from 30 Belén Ancestors and 50 saliva samples from Belén descendants were obtained for genomic analysis. DNA was obtained and Illumina libraries were constructed and enriched using the TWIST ancient DNA and complete mitogenome panels. Resulting NRY and mitogenomic sequence data were evaluated using principal component and haplotype network analyses. Consistent with community knowledge, we recover genetic relationships between Ancestors recovered from the colonial cemetery and descendants, as well as sex-biased gene flow between Spanish settlers and Indigenous peoples.

This material is based upon work supported by the National Science Foundation under Grant No. 2051184 as well as by George Mason University's Mentoring for Anti-Racism and Inclusive Excellence program.

Phenotypes of Pigmentation and Vitamin D Metabolism in Ancient Individuals from Central Eurasia

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Although more than a hundred loci associated with pigmentation of skin, hair and eyes have been identified, only few common SNPs with large phenotypic effects are used for ancient genomes analysis. Regarding Eurasian ancient genomes, most studies have been focused on Europe, Siberia and South Asia, whereas Central Eurasia populations were poorly described.

This study focused on published genome-wide data from 225 ancient individuals from the territory of Central Eurasia, dating from the Eneolithic to early Middle Ages. Here, we present analysis of 19 SNPs in genes *SLC24A5, MYEF2, HERC2, OCA2, DCT, KITLG, TYR, GRM5, TYRP1, SLC45A4, MC1R,* *APBA2*, *ASIP*, and *DHCR7* characterizing pigmentation phenotypes in individuals associated with different archaeological cultures. The analysis revealed the dominance of ancestral alleles of 19 SNPs for Sakas, Savromo-Sarmatians, Huns and populations of the early Middle Ages. However, time-dependent changes in selective pressure on derived alleles could be identified for at least 6 SNPs. Selective advantage of *EDAR* rs3827760 ancestral allele is specific for all the relevant periods. Regarding *MC1R* rs2228479, *SLC24A5* rs1426654, and *SLC45A2* rs16891982, potential selective pressure on the derived alleles was detected for Saka, Savromo-Sarmatians, and Early Middle Age individuals, but not for Hunnic individuals. In the Hun population, high derived allele frequencies of *APBA2* rs4424881 were detected. The selective pressure for rs4424881 polymorphism was also found in the individuals from the early Middle Ages. Among all the relevant cultures, the Savromo-Sarmatians demonstrate the highest frequencies of derived alleles in polymorphisms *MC1R* rs2228479, *SLC24A5* rs1426654 and rs2470102, and *SLC45A2* rs16891982.

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Suggested influence of management and social environment features in captive squirrel monkey (*Saimiri*) gut microbiome

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The gut microbiome crucially impacts the fitness, life history and health of primates. Housing, diet, management and human interactions of captive scenarios have been suggested to affect the gut microbiome of primates maintained in captivity, although detailed characteristic investigations have not yet been published. This study is the first to investigate the influence of captive management and the social environment on the gut microbes of squirrel monkeys (*Saimiri*). Fecal samples (n=395) were collected from the Austin Zoo (n=46), San Antonio Zoo (n=93) and the KCCMR (n=256) for DNA extraction and microbiome sequencing in the Carlos-Shanley lab at Texas State University to determine whether gut microbiomes are differently affected by various animal care protocols, caretaker contact types, social housings, group sizes and group compositions. All studied characteristics showed significant values: group size alpha diversity Chao1 index (p=3.0394e-32), group sex composition beta diversity (p=5.174e-09), alpha diversity Chao1 of group sex composition (p=1.2323e-24), protocol-type alpha diversity (p=1.2259e-24) and contact-type beta diversity (p=2.8576e-09). Regressions indicate there is an influence of gut composition and protocol type on the variation observed in the *Saimiri* samples. Each of these features has significant p-values, demonstrating there is a link either within (alpha) or between (beta) groups with the captive feature and the diversity of the gut microbiome. These values suggest the management and social environments of captive scenarios affect the gut microbiome of squirrel monkeys. These relations and interactions should be considered when developing protocols and social groups in captive facilities.

Identity expression among Upper Paleolithic foragers through cheek plugs? Dental evidence from Arene Candide, Liguria

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The Pleistocene deposit of Arene Candide Cave, Liguria (north-western Italian coast) yielded one of the most important Late Upper Paleolithic (LUP) skeletal series in Europe (the Epigravettian “necropolis” ca. 12,900-11,600 cal BP). The complex funerary behavior at the cave, consisting of multiple phases of burial manipulation, suggests that the long-term transmission of values and identity was important among these foragers. Some ways through which LUP groups at Arene Candide expressed their identities may have been by means of tattoos, hairstyles, piercings, and other forms of body modification. All these important cultural features are virtually invisible in the archaeological record. However, cheek plugs, as reported in sites like Prédmostí, Dolní Věstonice and Pavlov, appear to leave visible macro and microscopic signs of non-dietary dental wear. Arene Candide 12, an adult male, shows an unusual wear pattern on the buccal surfaces of maxillary right premolars and molars, along with deep grooves in the mesial-buccal margins of the lower first and second molars of the same side. SEM analysis of micro-wear on dental replicas reveals differences in the orientation and number of scratches on the buccal enamel surfaces between the left dental arches and the right ones, where the peculiar wear pattern is present. We propose that this divergence can be attributed to the presence of a hard object—likely an ornament—that came into contact with both the upper and lower right dental arches, resulting in the polishing of the buccal surfaces and the removal of enamel flakes in the lower molars.

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Muscle activation patterns over the life course among the Tsimane

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This study aims to determine the extent to which muscle activation patterns during small scale subsistence activities differ between juveniles and adults among the Tsimane- a contemporary horticultural population of lowland Bolivia. Previous research has shown differences in muscle performance (e.g., size-normalized strength, power, and endurance) between children and adults, suggesting children do not fully recruit higher-threshold motor units to the same extent as adults. Electromyography (EMG) measures the electrical activity of muscles reflecting the summation of motor units recruited. We hypothesized that Tsimane children have lower muscle activation than adults due to this inability to recruit specific motor units. To test this hypothesis, muscle activation data were collected for 72 individuals ranging in age from 10 to 67 during a variety of activities including archery, rice pounding, and using a machete. Muscle activation for biceps, triceps, and posterior and anterior deltoid muscles were collected bilaterally using surface EMG, and data was standardized to everyone’s maximum voluntary contractions. Results from archery did not show significant difference in muscle activation between children (10-15 years old) compared to adults (>15 years old). Tsimane children start playing with bow/arrows when they are young, even by age 4. Future work should explore to what extent starting activities at a young age impact when children are able to recruit motor units to the same extent as adults. Ongoing analysis of the remaining activities will clarify if muscle activation patterns remain consistent between children and adults or if archery is an exception.

UMass Amherst Graduate School Fieldwork Grant; NSF Grant: Brigitte Holt and Jonathan Stieglitz, PIs, Bone Strength and physical activity over the life course in a physically active contemporary pre-industrial population

Learning from casts? Testing assigned ancestry using FORDISC

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The use of natural bone skeletons is becoming increasingly complicated in academia. Whether considering the decreasing supply, increased cost, or ethical considerations, teaching using human remains is problematic. To continue effective training amid these challenges, a shift to using high quality casts is often necessary. However, are these cast a viable alternative? When learning about the physical differences between ancestral groups, are casts appropriate? In this study, we tackled these questions using a set of casts marketed for this purpose.

Utilizing the digitization software 3Skull and the statistical software FORDISC, we assessed six skulls. These skulls were marketed as three males, three females with each sex having one skull of European, African, and Asian ancestry. Each skull was accompanied by a biological profile including a visual, gross assessment of ancestry.

Our results were perplexing. After numerous runs through FORDISC, measurement checks, and reassessment, we were unable to confidently assign any of the six to their suggested ancestral group. After contacting the company, we learned that all but one of the specimens were from unknown individuals. Upon further investigation, we learned that the ancestry for each was assigned and marketed due to their relatively clear adherence to historical morphological traits (i.e. shovel shaped incisors indicates Asian ancestry).

Casts will continue to be needed as Biological Anthropology and other fields struggle with the ethics and problematic history of using human remains. However, exemplars used in casting need to be vetted using current requirements of the field including using known samples.

Sex differences in the positional behavior of chimpanzees (*Pan troglodytes schweinfurthii*) living in the dry and open habitat of Issa Valley, Tanzania

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A shift from forest to savanna habitat has been linked to increased sexual dimorphism and, accordingly, increased sex-differences in the positional behavior of early hominins. However, reconstructions of early hominin positional behavior are limited by a lack of studies of extant, savanna-dwelling apes. Here, we describe sex-differences in adult chimpanzee positional behavior in the Issa Valley, Tanzania, as the first test of the hypothesis that open habitat drives sex-differences in ape positional behavior. We quantified (using instantaneous focal sampling) and compared male and female chimpanzee locomotor and postural behavior over 15-months across the riparian forest (closed) and miombo woodland (open) vegetation, and discuss results in comparison to forest-dwelling chimpanzee communities. We found that males and females showed similar postural and locomotor behavior on the same substrates and reduced arboreality in open vegetation ($F=7.75$, $p<0.05$). Examining only locomotion, Issa females were however significantly more arboreal than males ($F=29.65$, $p<0.001$) and compared to females from other communities, whereas males showed similar levels of arboreality across communities. Results suggest that open habitats may increase sex-differences in positional behavior by driving female arboreality. While more data are needed on chimpanzee behavior, ecology, and habitat structure, we suggest high arboreality is linked to high predator risk and nutritional demands associated with an open habitat, which are exaggerated for females caring for dependent infants. Our findings have implications for the interpretation of how sexual dimorphism may influence reconstructions of locomotor behavior in the past, and the role of open habitat in shaping hominin evolution.

The effects of castration on the skeleton: a case study from the Linglong Lane Cemetery in Beijing, China

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In recent years, bioarchaeologists have focused their attention on intersecting forms of identity through the contextualized study of human remains recovered from archaeological contexts. Despite this recent turn, fewer bioarchaeological studies have examined the intersecting identities of people who experienced permanent bodily modifications in the form of castration. Moreover, the physical effects of castration on the skeletal are relatively unknown and a novel area of study in the field of bioarchaeology. Eunuchs, castrated males who served within royal courts in ancient societies, hold historical prominence in contexts around the world, including China. The Linglong Lane Eunuch Cemetery located in Beijing, China dates to the Ming and Qing periods, and represents the final period of eunuch presence in Chinese history. Despite the centuries-long history of the practice of castration, comprehensive data concerning eunuchs' physiological attributes and health remains notably limited. This research examines skeletal remains recovered from an archaeological excavation of the cemetery which was initiated in 2014. This study examined the skeletal remains of 137 individuals and sought to elucidate the consequences of castration on the skeleton. Evidence of the procedure was present in form of growth disruptions to various long bones across the skeleton. This study contributes to broader bioarchaeological discussions related to sex estimation, the life course, and skeletal development patterns. By delving into these areas of inquiry, a deeper understanding of the lives and physical impacts to eunuchs in Chinese history can be interrogated.

The More the Merrier? Re-examining Health Outcomes of Urbanization from the European History of Health Project Database

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Health is a multifaceted phenomenon that is significantly influenced by environmental exposures to stressors and pathogens. These contextual elements of health inform both the individual's lived experience, as well as the fluctuations observed over time in terms of changes in social history and the associated physical and sociocultural environments. Given the dynamic nature of health, settlement patterns shape health outcomes in different ways, usually with poorer health observed in denser, larger settlement patterns. Here, we test the hypothesis that urbanization over the course of European social development created overall adverse health. The prevalence of skeletal markers representative of various aspects of health, including infection (osteoperiostitis (OP), antemortem tooth loss (AMTL), dental abscesses, and dental caries), and inflammation (osteoarthritis (OA)) were selected for analysis from the European History of Health Project (EHHP) dataset. Kruskal-Wallis tests were used to test differences in prevalence of health indicators between three settlement sizes across European history (3rd to 19th century CE). Large urban settlements showed the highest prevalence of AMTL (12.22%) and dental caries (16.28%), as expected. However, these same settlements showed the lowest prevalence of OA (15%) compared to other settlement sizes, and a lower prevalence of abscesses (2.23%) and periostitis (28.9%). All Kruskal-Wallis tests returned p-values of <0.001. These differential health outcomes dependent on settlement size across history suggest that urbanization does not universally reflect a decline in health. Further analysis of ecological, demographic, and biocultural factors is needed to better understand the contexts that influence the differential health outcomes observed.

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Reconstructing the Demographic History of Neolithic and Megalithic Populations of Burzahom, Kashmir: Insight into Ancient Genome

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Burzahom, the Neolithic archaeological site in Kashmir demonstrates transitions from the Neolithic era, to the Megalithic era, to the early historic period. However, today five decades after the excavation have passed, question on the genetic identities and interactions of these individuals are still unanswered. This study utilizes ancient DNA analysis to analyze the genetic ancestry of these individuals. Petrous bones and teeth of seven individuals were used for DNA extraction, which were sequenced on the Illumina HiSeq platform. Five out of the seven samples confirmed authentic ancient DNA using the software MapDamage. Further, two could be proceeded for downstream analyses. The genetic sex identified both samples as male individuals. One sample was dated using Accelerator Mass Spectrometry to around 1927 BCE, while the other belonged to around 563 AD. These individuals were assigned the mitochondrial haplogroups M65a and U2b. Both these haplogroups are present in south Asia today. Haplogroup U2b was reported previously in an ancient individual from the Harappan site of Rakhigarhi, India. Autosomal data analyses for both samples will help us further understand the genetic ancestry and migratory history of residents as well as their genetic relationships to contemporary and later populations in South and Central Asia. This study represents one of the oldest ancient genomic datasets from South Asia thus far and is a milestone for ancient DNA analysis in the Indian as well as south Asian context.

Lessons from Anthro-Cast: Ethical Futures in Casting, Curation, and Repair

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From 1962 until 1976, the Wenner-Gren Foundation's Anthro-Cast Program manufactured and sold replicas of over 900 fossil discoveries, contemporary humans, and non-human primates from around the world. These high-quality casts were distributed to over 300 institutions mostly in the global north, including but not limited to medical schools, universities, and museums. Although the Anthro-Cast Program represents a well-intentioned endeavor towards accessible anthropology education, a critical reflection on the legacy and impact of the Anthro-Cast Program reveals that bio-colonial and bio-capitalist violence remains embedded within anthropological curation and collection.

This presentation uses the legacy of the Anthro-Cast program to illustrate the ethical dilemmas of casting and replicating humans and human ancestors, and the necessity of biocultural curation and collecting practices. Building upon the work of the 2023 seminar "Grappling with The Legacies of Anthro-Cast: The Work of Bones in the Age of Mechanical Reproduction", this critical review draws parallels between the Anthro-Cast Program and current issues of decolonizing paleoanthropology, reparative efforts in natural history museums, and the complexity of consent in the use and replication of contemporary human ancestors in the era of 3D imaging and printing.

As biological anthropology continues to grapple with the use of unethically obtained human remains in research and teaching, digitization and casting emerge as promising alternatives. This presentation proposes a model for the ethical use and production of casts that privileges the expertise of community stakeholders, departs from colonial curation practices, and holds casts to the same ethical standards as osteological collections.

This material is based upon work supported by the Wenner-Gren Foundation.

Revaluating evidence for *Theropithecus darti* from the Luangwa Valley, Zambia, during the Pliocene

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A fossil femur discovered in the Luangwa valley, Zambia, in 2001 was attributed to *Theropithecus cf. darti*. This species identification is important because it is the only evidence for *Theropithecus* in Zambia and expands the known geographic distribution of the species, revealing a potential biogeographical link between sites in eastern and southern Africa where *T. darti* is well documented. However, the Zambian femur was found in a secondary sedimentary context and its geological age and primary context are unknown. Several traits used to assign the Zambian femur to *Theropithecus* are difficult to quantify and compare across taxa when using linear measurements and angles. Additionally, extant baboons from the Luangwa valley, which are hybrids, have not been included in previous assessments of papionin femoral morphology.

Here, we used 3D geometric morphometric techniques to test whether proximal and distal femur morphology can distinguish among nine extant papionin species (n = 96 individuals) and six extinct papionin species (n = 8 individuals). Importantly, we include an extant *Papio* femur collected 3 kilometers from the Zambian fossil femur. Our results reveal that: 1) extant *Theropithecus* is morphologically distinct from *Papio*, 2) fossils attributed to *Theropithecus* share proximal and distal morphology with extant *Papio* and not extant *Theropithecus,* and 3) the Zambian fossil is most similar in shape to the extant *Papio* femur collected from the Luangwa Valley. We argue that the Zambian fossil is not attributable to *T. darti* and most likely represents *Papio*.

Data collection was funded by the American Philosophical Society, Earthwatch, and Sturgis International Fellowship.

Stress by any other name? Terminology, Theory, and Method for the Study of Inequality of Health

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Biological anthropologists in many subfields are interested in the causes, manifestations, and consequences of inequality. Human biologists and bioarchaeologists have long focused on these issues; interest among forensic anthropologists and geneticists is more recent but quickly growing. Terms have proliferated to describe the theoretical and practical components of research in the area, such as allostatic load, embodiment, frailty, morbidity, resilience, social determinants of health, stress, structural violence, structural vulnerability, and weathering.

Are these terms just different ways of saying the same thing, each native to their own field? To address this question, we examined the use of these 10 terms in abstracts and titles of papers published between 2014-2023 in the American Journal of Biological Anthropology, American Journal of Human Biology, Human Biology, and the Journal of Forensic Science (n=463). Papers were discovered through searches of Ovid/Medline and Web of Science. Unrelated uses of terms were excluded, such as biomechanical stress or taphonomic weathering. Stress was by far the most used term (70%), followed by morbidity (15.1%) and frailty (6.5%). Human biology papers used stress most often (53.2%), followed by bioarchaeology (37.6%), genetics (6%), and forensics (3.2%). There was no clear change in the use of any term over time. Perhaps less commonly used terms that are now familiar in the biological anthropology lexicon appear more often in journals directed to specialized audiences, which may serve to silo research advances, hinder consistent information retrieval, and complicate communication. We use this text investigation as an introduction to this symposium.

Exploring the effects of European colonization on Khoe-San descendent communities in South Africa

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European colonization and the Dutch East India slave trade have played a large role in shaping the genetic diversity of present-day South African populations. As a result, many individuals in Cape Town have ancestral contributions from European, West African, South and East Asian populations, and indigenous Khoekhoe and San populations introduced during the 17th-18th centuries. However, there is limited knowledge about how colonization impacted the genetic ancestry of indigenous populations outside of Cape Town. In this study, we aimed to characterize the impact of European colonization on Khoe-San and Khoe-San descendant populations outside of Cape Town and examine environmental and geographical factors that additionally contributed to the genetic structure observed.

We sampled 827 individuals with high Khoe-San ancestry in South Africa and genotyped them across ~2 million SNPs using the Illumina H3Africa Array. We used ADMIXTURE to analyze global patterns of population structure and infer relative levels of recent admixture among sampled communities. We then used SPRUCE to predict environmental and geographic factors contributing to population structure observed within Khoe-San and Khoe-San descendent communities. ADMIXTURE results demonstrate a cline of Khoe-San ancestry with distance from the Cape Colony; from an average of 40% in individuals sampled closer to Cape Town, to 80% in individuals sampled in the southern Kalahari. This project advances our knowledge of population history and spatial genetic structure in Khoe-San and Khoe-San descendent communities for whom few historical records are reliable.

Habitat Selection and Home Range Composition of the Buraiga Chimpanzee Community, Kibale National Park, Uganda

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Chimpanzee (*Pan troglodytes*) populations face many threats, including increasingly fragmented habitats. Understanding how chimpanzees respond to anthropogenic pressures requires data from communities occupying habitat fragments of different sizes and compositions across their range, yet few studies document chimpanzees living along boundary zones of protected areas (PA). We present the first habitat composition and selection results for the Buraiga chimpanzee community that occupies a section of Kibale National Park's (KNP) eastern boundary region. Utilizing 15 months of GPS data (3,139 relocations), we calculated percent home range land-cover in QGIS and analyzed overall and seasonal habitat selection using Manly's selection ratios. Land-cover was comprised of 67.92% forest, 6.17% grassland, 12.82% riverine swamp, 8.19% agricultural, 1.43% eucalyptus plantation, 0.28% tourism facilities, and 3.19% roads. Overall Buraiga chimpanzees selected for forested areas within KNP (Manly's selection ratio Wi = 1.242; p = 0.00). In rainy season months they selected only forest (Wi = 1.286; p = 0.000). In dry season months they selected for forest (Wi = 1.219; p = 0.001) and riverine swamp habitats (Wi = 1.524; p = 0.029) within and outside of KNP, revealing use of the Kanyanchu swamp corridor outside KNP. Seasonal use of the swamp corridor to access agricultural land may reveal a lower-risk strategy for crop foraging than crossing through more open areas. Data on chimpanzee behavioral adaptations to anthropogenic pressures along PA boundaries are needed to inform conservation strategies at a time when great ape habitats are being altered at an unprecedented rate.

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Restoring identity: A paleopathological examination of deceased individuals from a human osteological teaching collection

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Identity, humanity, and lived experience are all aspects of life that can be gleaned through bioarchaeological analysis. Caretakers of osteological teaching collections, in particular, are positioned to acknowledge and uphold the personhood of deceased individuals with whom they teach. Examination of 250 postcranial and cranial elements from the Department of Biology (University of Louisville) revealed a collection of minimally 36 adult individuals purchased or acquired through legacy collections. All remains were observed for evidence of childhood and adulthood stress. On 130 teeth (five observable skulls), 18 manifested minimally one caries, 53 presented calculus, one manifested an enamel defect, 29 alveoli displayed periodontal disease, and eight teeth were lost antemortem. Additionally, dental attrition was moderate, and two incisors presented scooped, wave-like patterns consistent with habitual use wear.

Although few individuals were represented by multiple elements, observable conditions at the time of death were recorded. Cribra orbitalia and porotic hyperostosis were absent in the five skulls. Two of eight tibiae presented healed periosteal reactions. No osteoarthritis or joint disease was observed on appendicular synovial joints. Two antemortem fractures were observed macroscopically, one at the distal end of a fibula and one at a sternal rib end. These pathological conditions, evidence of embodied lifetime experiences and stressors, are essential to recognizing these dissociated skeletal elements as once living people. Although osteobiographical analysis is limited here by commingling and skeletal representation, paleopathological profiles contribute to our broader understanding of who became absorbed and victimized in the 19th and 20th century global skeletal exchange.

Contact aggression differently predicts injury risk in male and female chimpanzees

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Risk of injury is expected to constrain competition, shaping individual strategies. However, data on injuries in wild primates are sparse, and it is often assumed that injury risk corresponds with the rate of receiving aggression. Here, we examine this assumption by analyzing patterns of injury in the Kanyawara community of wild chimpanzees (*Pan troglodytes schweinfurthii*) in Kibale National Park, Uganda. Injuries were recorded over 14 years from 100 unique chimpanzees. We recorded 613 injuries, the majority of which were open wounds. In linear mixed models controlling for age, adult males received 2.7x more injuries than adult females ($t = 4.7, p < 0.001$) despite being less often the victims of contact aggression. While female injury rates were predicted by rates of received contact aggression (LMM, $t = 0.8$, $p = 0.44$), male injury rates were instead predicted by how often they attacked others ($t = 4.4$, $p < 0.0001$). Injury risk increased with rank in males but was unrelated to rank in females (sex*rank, $t = 3.1$, $p = 0.003$). Females were injured disproportionately while cycling (ChiSq = 28.5, $p < 0.0001$). Both sexes received wounds most often on their hands, followed by the back for males and hindquarters for females. These patterns are consistent with increased frequency of biting in conflicts among males and an unexpectedly high risk of injury from retaliatory aggression. These results add to evidence that high-ranking chimpanzee males incur significant costs associated with competition for status and mating opportunities.

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Bioarchaeological analysis of an elite Xiongnu site, Yamaan us, in western Mongolia

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Recent archaeological investigations in the Zavkhan province of Mongolia uncovered an elite burial at the site of Yamaan us, attributed to the Xiongnu polity, the first large confederation of mobile pastoralist peoples in Inner Asia (3rd c. BCE to 1st c. CE). Although looted, the site revealed numerous mortuary features similar to other known Xiongnu elite square-ramped tomb complexes. These burial types are considered representative of upper status individuals and recovered material culture from these site types can range from chariots and horse-riding equipment to gilded bronze horse decorations, items covered in gold, bronze utensils, and jade objects, among others. Notably from Yamaan us, the skeletal remains of an adult female were found in the elite central main tomb, designated Burial 61. Three satellite burials (61-1, 61-2, 61-3) associated with the main tomb revealed the remains of younger adolescent and juvenile individuals.

An in-depth bioarchaeological analysis of these individuals offers valuable insights into the health and lifeways of those who appear to be of upper elite status in Xiongnu society, particularly since studies of individuals from these site-types are relatively rare. Early results of comparative bioarchaeological analyses reveal variation in demographic attributes and dental disease of those interred in square-ramped vs. satellite burials. In addition, health and dietary characteristics of the Yamaan us individuals are compared to those derived from similar and comparative contexts across the steppe region in order to place the findings into a broader perspective.

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Facial fluctuating asymmetry in three species of colobus monkeys

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Fluctuating asymmetry (FA) in biological structures are deviations from perfect bilateral symmetry. Inbreeding and exposure to environmental stressors are associated with FA. Consequently, in primates, FA has historically been used as a proxy for developmental instability (DI), and therefore stress in development. Facial bones are of interest for FA analysis as they are subject to comparatively fewer biomechanical stresses. To better understand the impact of environmental stressors on morphology, facial FA was quantified in three colobus species representing a gradient of stress. Two species (*Piliocolobus badius* [n=63] and *Colobus polykomos* [n=17]) inhabit the Taï Forest, Côte d'Ivoire while a third (*Colobus angolensis palliatus* [n=23]) is from southern Kenya. Multiple indicators suggest red colobus are more sensitive to stress than the more resilient black and white colobus. We hypothesized this differentiation would be reflected in degree of FA. Landmarks were imposed on primate crania using Viewbox 4 software; using geomorph and morphoJ, a generalized Procrustes analysis was performed and relative differences in FA were quantified through Principal Component Analyses and FA component variance tests. The PCAs reveal that facial morphologies diverge by species and illustrate a gradient in FA by species. We found significant evidence ($p=0.035$) suggesting Taï *P. badius* demonstrate a greater response to stress than the population of *C. angolensis palliatus*. Given recent trends in *P. badius* conservation, future work comparing responses to stress among various populations and species of *Piliocolobus* is desired.

Photos from the past illuminate the complexities of flanging in historic captive orangutans (*Pongo* spp.)

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Orangutan males can develop secondary sexual characteristics called "flanges" at the same time as sexual maturation or postpone flange development to a range of possible ages. Captive studies have found males remaining unflanged up to age 18 and some wild studies find unflanged males in their 20s or even older. The range of possible ages at which males can remain unflanged is difficult to assess, as a large-scale captive study has yet to be undertaken, and wild studies can face challenges assessing age. Using the 2015 International Studbook, we investigated the first 2,400 historic orangutans, selecting males of at least seven years of age who died in US, Canadian, or European Zoos (N = 486) whom had photographs of their faces in a newspaper database (newspapers.com) to determine flanging status (N = 175; born 1914-1991). A total of 152 (87%) of males had photographs in which their faces were flanged. For those who survived into adulthood (n=149; 54 wild-born), flanging appeared as early as age seven. Unflanged males in captivity reached ages of 19, 20, 30, and even 40. All of the males who remain unflanged past age 18 were either wild-born or neutered. These results challenge current reported age ranges achieved by unflanged males in captivity. The future inclusion of additional data into this analysis, such as offspring tracking, heredity, enclosure style, social groupings, and transfer events, will help reveal new information on the contexts in which captive orangutan males either flange or delay flanging.

Phenetic Evidence of Social Change: Using population affinity to investigate social networks and mobility from the Iron Age to Early Medieval period in Wessex, England

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Despite an increase in isotopic and genetic studies in recent years, the nature and scope of migration among the Iron Age (800 BCE-43 CE), Roman (43-410 CE), and Early Medieval (410-1066 CE) periods in Britain remains contentious. Studies investigating these transitions have frequently focused on urban environments and eastern regions, and social frameworks underpinning regional and material variation are often overlooked. The current study investigates population affinity and mobility through these cultural transitions in southwest England ("Wessex"). Dental morphological traits were recorded for 765 individuals across 22 sites following the Arizona State University Dental Anthropology System. Population affinity was analysed with the Mean Measure of Divergence (MMD), using 25 uncorrelated traits with good intra-observer agreement.

MMD values among the Iron Age samples indicate significant ($p<0.05$) differences between geographically proximate sites thought to be part of the same tribal networks, while geographically distant 'central place' sites (Maiden Castle and Danebury) were phenetically more similar. A homogenising effect is seen during the Roman period, with greater correlation between MMD and geographic distance than in other periods, consistent with wider, more accessible networks (though this relationship was non-significant, $p=0.18$). Strong affinity was detected among the western sites across the Roman and Early Medieval periods, but little correlation with geographic distance was identified among the eastern sites. These findings demonstrate a complicated picture of population affinities across the region with shifting patterns of social interactions within the region of Wessex. These findings also contextualise the evidence for migration across these periods.

How wet is "wet": Comparing pluvials in southern Madagascar

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Madagascar experienced a dramatic turnover of vertebrate species between 1200 and 700 cal BP affecting ~40 endemic species, some replaced by invasive, human-introduced taxa. In the subarid spiny thicket (ST) ecoregion of the southwest, climate change (slow drying after 2000 BP followed by a severe, prolonged drought between 1600 and 900 BP) appears to have played a triggering role. There is little evidence of early human impact. In contrast, vertebrate population collapse began under wetter conditions in the dry deciduous forests of the northwest, with strong evidence of human agency. To better understand the roles of climate change and human activities, particularly in the ST, we documented the climate and vegetation history of this region prior to and after the arrival of humans. We studied the stable carbon and oxygen isotopes of 11 stalagmites from the ST covering the past 70,000 years. Throughout this time, the ST was consistently dry (likely drier than other parts of Madagascar), and changes in rainfall were correlated with changes in vegetation. Even during the apparently wettest periods, severe and sometimes prolonged droughts occasionally occurred. Some droughts extended well north of the ST, while others did not. The drought between 1600 and 900 BP was, by no means, the most severe, nor was it the most geographically expansive. However, this drought appears to have made large endemic species more vulnerable to subsequent human activities and may have triggered an earlier and more rapid collapse of vertebrate populations in the ST.

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Behavioral drive during human evolution

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Behavior is viewed as an important driver of morphological traits, a theoretical concept termed behavioral drive. Detecting behavioral drive in the fossil record is challenging because it is difficult to measure behavior in a way that is independent of the morphological trait under consideration. To remedy this problem, we focused on a puzzling behavior of primates during the Plio-Pleistocene: eating graminoid plants (graminivory). Here we report carbon and oxygen isotope ratios from cercopithecid monkeys and/or temporal intervals that were unrepresented or under sampled in prior analyses. We combined these data with published values from graminivorous monkeys and hominins to calculate (i) a preference-aversion function for graminoid plants and (ii) an equid-normalized measure of dietary water sources. We detected concordant shifts in dietary behaviors—exemplified by an increased preference for ^{18}O-depleted C_4 graminoid tissues in hominins—through change-point analysis, and we show that such behavioral shifts preceded those of dental morphological shifts by ca. 0.7 Ma, a result that corroborates the predictions of behavioral drive. Decoupling feeding behaviors and corresponding morphologies in time is essential to determining when, and exploring why, dietary ecologies changed, and it motivated us to consider and disambiguate the types of graminoid tissues that propelled human evolution.

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Locomotor signals in the clavicle of *Australopithecus afarensis*

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The emergence of hominins is characterized by the transition to bipedalism, but debates continue on the importance of arboreal behaviors during and after this shift. Uncertainties regarding the locomotor regime of *Australopithecus* are due, in part, to their mosaic traits, with lower limb features largely indicating bipedality and upper limb morphology considered 'primitive'. Analyses of internal bone structure may provide new insight in this regard. Here, we use cortical cross-sectional geometry to identify the functional signal in the internal geometry of the clavicle of an adult and juvenile *Au. afarensis* (KSD-VP-1/1 and DIK-1-1) and interpret it within the ape context. Previous investigations of the cortical distribution in the hominoid clavicle through ontogeny have supported the utility of cross-sectional geometry in characterizing locomotor adaptation and distinguishing between *Pan, Gorilla,* and *Homo*, with implications for our understanding of *Australopithecus*. Using micro-CT scans of the fossil hominin clavicles, alongside wild-origin extant hominoids for comparative context, we calculated the minimum (I_{MIN}) and maximum (I_{MAX}) area moments of inertia, as well as the moments of inertia in the dorsoventral (I_{DV}) and craniocaudal (I_{CC}) planes at 20 evenly spaced cross-sections across the diaphysis. Results indicate a unique clavicular cortical geometry in *Au. afarensis*, unlike what has been quantified in extant apes. I_{CC}/I_{DV} suggests forceful or habitual dorsoventral bending of the clavicle, and I_{MAX}/I_{MIN} supports a shift in locomotor regime during ontogeny in *Au. afarensis.* Our results suggest that more changes in clavicular morphology occurred within the hominin lineage than previously hypothesized.

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Reproductive aging patterns in wild female geladas

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Reproductive performance varies across the lifespans of female primates. Fertility and offspring survival are often lower early in life, when females have yet to reach adult body size, and late in life, when physical condition declines. However, recent comparative studies have revealed substantial between-species variation in reproductive aging patterns, perhaps due to underlying differences in ecological and social risk. Here, we quantified age-related changes in interbirth intervals and infant survival in wild female geladas (*Theropithecus gelada*), which experience high rates of male-mediated fetal loss and infanticide that could obscure aging patterns. Interbirth intervals were generally longer in younger mothers than in older mothers, but the oldest females studied often died many years after the birth of their last offspring – much longer than the average interbirth interval in the population. Contrary to our expectations, infant survival decreased linearly as females aged. Thus, although young mothers took longer to recoup the costs of lactation and resume reproduction, their presumed energetic deficits did not also compromise offspring survival. These results point to a potential role of geladas' high infanticide rates and/or graminivorous diets in selecting for cautious and compensatory reproductive strategies in young females (e.g., the Vandenbergh effect). Although many mothers continued to reproduce into old age, their subsequent deaths often resulted in either long and unclosed interbirth intervals or high rates of mortality for orphaned offspring. In sum, our data from geladas demonstrate that reproductive aging trajectories can remain apparent even when extrinsic threats to reproductive success are high.

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Dental microwear of late Paleogene/Neogene primates from the Turkana Basin of Kenya

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Dietary reconstructions of fossil primates from the Turkana Basin, Kenya, help us understand patterns of regional ecology and evolution over the past 30 Myr. Inferences of available food choices during periods of environmental/habitat fluctuation may be especially important. Here we compare molar microwear textures of primates from five sites in the Turkana Basin (Topernawi, late Oligocene; Locherangan, early Miocene; Buluk, early Miocene; Lothagam, late Miocene; and Pliocene sediments at Napudet) to one another and to extant baseline samples. Of 165 candidate specimens without obvious postmortem damage, 33 preserved antemortem microwear and were included in this study. We used a white-light confocal profiler to scan surfaces of high-resolution molar replicas, calculated microwear texture attributes for each specimen, and compared individuals by site. Results indicate that none of the locality samples were dominated by individuals that predominantly ate mechanically challenging foods (e.g., hard objects, tough leaves) in the days or weeks before death, though there was significant variation in the sample. The primates examined from Lothagam and Buluk (cercopithecoids) tend toward higher anisotropy and lower complexity, indicating a less hard but tougher diet. Inversely, those from Locherangan (non-cercopithecoid catarrhines) and Napudet (cercopithecoids) tend toward lower anisotropy and higher complexity. Finally, primates from Topernawi have both higher complexity and anisotropy, suggesting a diet of comparatively harder and tougher foods. These results indicate that there are no clear or simple temporal or taxonomic dietary trends for the Turkana Basin fossil primates, at least for the small samples available today.

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Socially integrated female chimpanzees have lower offspring mortality

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In a number of species, females that are more socially integrated, or have stronger social bonds, have higher reproductive success. Yet little evidence links female sociality with offspring production or survival in species with female dispersal. Because many evolutionary explanations of the direction of sex-biased dispersal emphasize the adaptive value of social bonding among kin in the philopatric sex, an important but less studied question is whether female sociality relates to reproductive success in species that lack female philopatry. Here we examine the relationship between female social integration and offspring survival in chimpanzees, a species with male philopatry and female dispersal. Females that were more socially integrated with other females in the year before giving birth had higher offspring survival to age 1 (GLM: OR = 3.41, 95% CI = [1.27 – 11.38]), and age 5 (OR = 2.42, CI = [1.01 – 6.64]). Furthermore, social connectedness with other females before giving birth predicted such social connectedness after giving birth (Pearson correlation = 0.580), demonstrating that female social environments were consistent across critical periods relevant to offspring survival. Finally, in a path analysis, although females with close female kin in the community tended to be more socially integrated, only maternal social integration with other females was directly associated with offspring survival. This adds to a small set of results linking sociality with adaptive benefits in the dispersing sex. Like in humans and other mammals, more socially connected female chimpanzees have higher reproductive success, despite usually residing with non-kin.

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Scales of fragmentation in the Lower Danube: subsistence of late antique and early medieval populations

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The territory of modern Eastern Romania faced gradual changes in the ethnic and economic landscape between 4th and 7th c. CE. The arrival of Slavs, Avars, and Bulgars changed the political dynamic and put some pressure on the Eastern Roman Empire. Furthermore, the expulsion of the Romans from Scythia Minor and later from most of the Balkan territories resulted in the exclusion of these populations from the imperial economy, thereby necessitating their self-sufficiency.

The "Scales of Fragmentation" project aims to highlight those changes through bioarchaeological analysis of subsistence, among others, by incorporating state-of-the-art carbon and nitrogen stable isotope analysis of human remains.

The stable isotope values were obtained for 59 individuals from four sites: Nufăru (4th-7th c.), Noviodunum-Isaccea (4th-5th c.), Boldești-Grădiștea (4th-5th c.), and Histria Capul Viilor (8th-9th c.). The δ^{13}C values of human individuals varied between -19.2‰ and -12.5‰, while the δ^{15}N values - between 9.5 and 14.7‰. There were significantly higher δ^{13}C values (F(3,55)=5.48, p=0.002) in Histria compared to Nufăru (p=0.036) and Noviodunum-Isaccea (p=0.001). This shift coincides with the arrival of Bulgars in Scytia Minor and can be interpreted as a shift in the subsistence between the ancient and early medieval economies, where the cultivation of millet was more significant.

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Biological Interaction Patterns in the Colonial Lambayeque Valley Complex, Peru: New Perspectives on Colonial-Era Population Structures from Dental Phenotypic Variation

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Until recently, little was known about population structures and histories on the north coast of Peru. Initial studies of dental phenotypes of local Muchik peoples living in Mórrope (Lambayeque Valley Complex, 1532-1750 CE) suggested broadened Indigenous mating networks following European conquest - linked to population aggregation and the breakdown of pre-Hispanic Muchik sociopolitical organization that was a barrier to frequent exogamy. Yet, did this process occur throughout the Lambayeque region? With new data from the contemporaneous site of Eten 45 km from Mórrope, we test the hypothesis of a valley-wide postcontact increase of Indigenous genetic diversity. Mesiodistal and buccolingual tooth measurements were collected from 173 individuals from Mórrope and Eten and submitted to an R Matrix analysis. Compared to previously published late pre-Hispanic Lambayeque (F_{ST} = 0.041), the postcontact Mórrope/Eten sample (F_{ST} = 0.026) demonstrates an increase in homogeneity (greater panmixis) consistent with altered Colonial biological interaction patterns. However, a D^2 matrix and residual values (relative gene flow) indicate that Mórrope and Eten were not likely exchanging mates. Analyzed independently, geographically isolated Mórrope (F_{ST} = 0.052) appears far more heterogeneous (genetically isolated) than the economic hub of Eten (F_{ST} = 0.008). Residual values indicate both communities experienced negative extralocal gene flow following conquest, but positive extralocal gene flow followed during the Middle/Late Colonial period. We partially accept the hypothesis. Re-structing (widening) of regional biological interaction patterns seems clear at both sites, but this phenomenon unfolded differently in Mórrope and Eten where many other biocultural dissimilarities have been documented.

Long-tailed macaque populations and community interactions in Cebu, Philippines

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Long-tailed macaques, *Macaca fascicularis*, are widespread and occupy various roles throughout the Philippines. They are kept as pets, viewed as pests, and used for tourism, trade, and food. Despite their reclassification as "Endangered" by the International Union for Conservation of Nature (IUCN) Red List of Threatened Species in 2022, many people in the Philippines perceive their populations as abundant. Nonhuman primates are understudied in the Philippines; however, with declining macaque populations, it is necessary to examine the threats they are facing. The goals of this preliminary project were to locate and describe existing macaque populations, and identify the concerns of communities in the province of Cebu, Philippines. From July-August, 2023, three Filipino researchers and I located macaque populations in Alcoy, Toledo City, and Oslob, Cebu. All macaque observations were nonintrusive and prior to our visits, we met with local officials (e.g., Barangay Captain, Mayor, Environmental Officer). Mining corporations near Alcoy and Toledo City have reported increasing human-macaque interactions in the mining area and near one university. Oslob is a known tourist site where macaques are habituated and provisioned; however, since it is located along a busy highway, there are concerns about potential accidents. These early results contribute valuable information about long-tailed macaque populations in Cebu and provide insight into continued human-macaque conflict. This project lays the groundwork for future projects and generating solutions for these communities, including the mining, tourist, and protected areas.

Who made early stone tools? Assessing the overlap of hominins with Oldowan assemblages

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The appearance of the first stone artifacts in the geological record represents a significant adaptive shift in hominin evolution that may have enabled toolmakers to access new food resources and expand into new environments. Historically, early tools were attributed to genus *Homo*. However, the oldest assemblages now predate the appearance of *Homo* and there is growing evidence to suggest that other hominin taxa also engaged in tool use. Species belonging to *Homo, Australopithecus, and Paranthropus* are present within the timeframe and regions where Oldowan and Lomekwian tools are known. Here I evaluate the chronological and geographic overlap of Oldowan sites with hominin taxa. *Paranthropus bosei, Paranthropus robustus, Homo habilis,* and *Homo erectus* are most frequently associated with Oldowan tool assemblages. Fossils attributed to *Homo* and fossils attributed to *Paranthropus* are recovered at an equal number of archaeological localities (n=12). Often both genera co-occur (n=8). However, at some archaeological localities, only *Homo* (n=4) or *Paranthropus* (n=4) are known. The presence of hominin taxa alongside stone tools varies by region and latitude. Artifacts are associated exclusively with genus *Homo* north of the Omo-Turkana basin. The taxonomic identity of the early tool users remains uncertain, and it is possible that both *Paranthropus* and *Homo* practiced tool-assisted foraging. While much attention has been paid to the implications of tool manufacture for genus *Homo*, an integrated technological perspective should also be considered when evaluating the diet and behavior of robust australopiths.

Tamarins lost in translation: using machine learning to search for convergence and divergence in vocalization repertoires across Neotropical primate species

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Neotropical monkeys (platyrrhines) use unique vocalizations in a large diversity of associated behavioral contexts, and each species uses a different vocal anatomy and vocalization technique to produce highly differentiated vocal repertoires. This creates a rich diversity of produced vocalizations across the platyrrhine suborder. For this project, we assembled vocalization profiles for four platyrrhine species (*Pithecia pithecia*, *Sapajus robustus*, *Leontopithecus chrysomelas*, and *Saguinus imperator*) across three families using recordings from captive animals housed at the Santa Ana Zoo. We then processed the repertoires using a bioinformatic pipeline involving unsupervised machine learning to evaluate the similarity between produced vocalizations. We found that a phylogeny created from character data derived from the morphology of individual vocalizations is not congruent with an evolutionary history phylogeny, indicating that vocalization repertoires have diverged within some species.

Using "narrative" in an introduction to biological anthropology course to improve student understanding of human evolution and support anti-racist pedagogies

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Four decades ago, Landau (1984) analyzed the structure of evolutionary narratives. Inspired by Landau's work, I selected "narrative" as a framework for restructuring my introductory course in biological anthropology. My new course covers standard introductory material but centers narrative throughout by investigating both the current scientific understanding of human evolution and the stories that scientists tell about it.

Using data from the fossil record, modern human biology, and our primate relatives, my students gain familiarity with the scientific evidence for human evolution. Students utilize narrative analyses to explore how scientists communicate stories about human evolution in both the scientific literature and "popular science" contexts. Further, students investigate how scientific narratives become part of popular culture understandings about evolution by examining evolutionary iconography and trends such as the "paleo-diet." Students also consider examples of how the cultural background of scientists shapes their research and who is given a voice in their narratives.

Compared to my standard approach of teaching introduction to biological anthropology, exam data and course surveys reveal improvements in student learning in the restructured course. In particular, students are more likely to avoid common misconceptions about evolution such as thinking of evolution as having a "goal". Additionally, students are better able to articulate how evolutionary stories can reinforce existing power structures and stereotypes of marginalized groups. This improvement has facilitated deeper student reflections about the impacts of systemic racism and other forms of discrimination in the sciences.

All work was performed as part of my regular position with Colorado College.

Funky Monkeys: Aberrant Stereotypy in New World Primates at Jungle Friends Primate Sanctuary

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Living through a recent period of isolation highlighted the issues of lockdown beyond infectious disease for many. As anthropogenic forces continue to destroy non-human primates' ecosystems, captive environments play a larger role in their survival. Our environmental stewardship should endeavor to improve standards of care at varying degrees of captivity outside of zoological societies like animal sanctuaries. Some captive animals exhibit aberrant stereotypies, or repetitive behaviors with no adaptive purpose, which are likely related to their captive environments. This project includes two 30-minute interval recordings of each enclosure, to be rewatched when switching between each (n=266) focal animal, of five New World primate species at Jungle Friends Primate Sanctuary in Gainesville, Florida utilizing an all-occurrence method to sample for stereotypic behaviors. Preliminary data analysis indicates that enclosure size, group composition, enrichment opportunities, medication, species, and prior history may play a critical role in the number and frequency of the ten stereotypic behaviors. Results indicate that a higher encephalization quotient is correlative with more frequent bouts of stereotypic behavior. Results show that 24.67% of single primates exhibited one or more behaviors. Aberrant behavior by species is 15% for Capuchins, 9% for Spiders, 7% for Squirrels. We used a comparative model to evaluate the socioecological factors that affect the primates exhibiting these behaviors. Given that freedom is not an option for most captive animals like it was for humans who experienced similar feelings of entrapment during the pandemic, then we should strive to provide the healthiest environment for them to thrive.

Embodied DNA: Towards a Theoretical Conceptualization of Community Engagement in Ancient DNA Research

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While there have been many published guidelines on the best practices for engaging Descendant Communities and other relevant stakeholder groups in Ancient DNA (aDNA) research, developing an underlying theoretical approach allows for a critical examination of the multifaceted contexts that aDNA research exists within. Here, Feminist and Indigenous Science frameworks are employed to reflect upon the pluralistic perceptions of DNA through the lens of subjectivity and/or objectivity. Within this discussion, we examine how research becomes entangled in discourses of genetic essentialism, which feed into biosocial realities and critical reclamations of the future. Lastly, relational frameworks of embodiment theory and Black Feminist approaches in archaeology are used to think about positionality and responsibility in the evolving relationship between 'researcher' and 'community'. In this way, persons carrying out aDNA research can better understand how existing engagement guidelines can be more conscientiously exercised in different community landscapes and socio-political contexts.

Recent work conducted at the 19th century First Baptist Church in Williamsburg (Virginia, USA), is presented to explore how this theoretical approach can be applied within established community engagement models. The Colonial Williamsburg Foundation, in collaboration with the Let Freedom Ring Foundation, and researchers from William & Mary and Dartmouth College, carried out community engagement following the Clientage Model. This paper discusses the theoretical perspectives which informed the community engagement surrounding aDNA testing on three burials from 2021 to 2023. Overall, this work seeks to explore how an embodied understanding of aDNA can facilitate community engagement.

The scaling of axon diameter to skeletal muscle volume as a framework for understanding functional adaptation and evolution

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Previous work on functional anatomy relies on long established scaling relationships from experimental and morphological evidence. However, there are many unexplored relationships between neuromuscular composition and function. Motor unit density and nerve fiber scaling may provide a novel framework for asking questions about human and non-human primate evolution. Previous work has shown a higher axon count in motor nerve fibers supplying flexor pollicis longus (FPL) compared to flexor hallucis longus (FHL) in a human sample. This result suggests a potential for adaptation to fine motor tasks in the upper extremity and gross recruitment for locomotor tasks in the lower extremity.

This study builds on this work by exploring the difference in diameter of axons (including their Schwann cell) between FHL and FPL in a cadaveric sample (n=6). All nerve branches supplying each muscle were sampled, placed in 10% formalin, stained with potassium ferricyanide, and scanned for virtual microscopy. Feret's diameter of each axon-Schwann cell unit was measured using ImageJ. Our results suggest that FPL axons have a larger diameter scaled to muscle volume than FHL ($p<0.001$). Greater axonal diameter predicts greater responsiveness in FPL compared to FHL. These results add further evidence for neuromuscular adaptation for task differentiation in the upper and lower extremities in humans. Examination of motor unit density and axonal diameter provides a new, and relatively unexplored, approach to the study of functional and comparative anatomy.

Funding was provided by Campbell University School of Osteopathic Medicine.

Social tolerance as a component of relationship quality among wild female chimpanzees, *Pan troglodytes schweinfurthii*

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In group living species, individuals may negotiate stable, selectively tolerant relationships with a subset of conspecifics to mitigate the costs and risks of sharing space when direct competition is undesirable. Here, we investigate dyadic social tolerance among adult female chimpanzees, a species where females rarely engage in strong, affiliative relationships. We test the hypothesis that variation in dyadic spatial association does not occur by chance but is evidence of selective social tolerance among female dyads. Accordingly, we predict that dyadic association rates are stable over time and correspond with infrequent aggression and frequent cofeeding. We analyzed 10 years (2010-2019) of behavioural data on N=30 adult female chimpanzees in Kibale National Park, Uganda (N=20280 focal hours). We measured dyadic spatial association using the frequency of five-meter proximity and found that rates of association were more differentiated than expected at random. Using LMERs, we found that dyadic association strength predicted relationship stability over years ($\beta=0.404$, $p<0.001$), and females exchanged less aggression with frequent associates ($\beta=-0.156$, $p<0.001$). Using an additional one year of targeted behavioral data (2019-2020, N=17 females, N=682 focal hours), we found that frequent association predicted cofeeding ($\beta=0.256$, $p<0.001$) and dyads who associated often actively maintained associations using following and waiting behaviour ($\beta=0.0514$, $p<0.001$). Further investigation indicated that association rates better predicted social tolerance than dyadic grooming rates. Selective tolerance may be a stable attribute of dyadic relationships that can predict and explain patterns of behaviour and social network structure, distinct from, or in the absence of, affiliation.

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Genomic insights on mobility, integration, and regional contact across Bronze Age Eurasia

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The past decade of ancient genomic research concerning prehistoric populations of Central Eurasia has reshaped many debates concerning social and material dynamics of steppe communities. This paper provides a synthetic view of the growing genomic data of the steppe region and situates the range of datasets in light of past and current models of social interaction, human mobility, and technological participation among diverse populations from the 4th to 1st millennia BCE.

Skeletal Health and Pathology in Cayo Santiago Rhesus Macaques – A Contextualization of Individual, Familial and Population History

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The Cayo Santiago Rhesus macaque (*Macaca mulatta*) colony is one of the most useful anthropological and biomedical resources in the world. A vast colony-derived skeletal collection harbors the potential to reveal the colony's history and hardships over the past 85 years. Using this collection, we reconstruct the health history of the rhesus colony by incorporating familial, colony-management, and climatic information into one comprehensive database. In total, skeletons of 2789 individuals (Age range: 0 – 31yrs), housed in the Caribbean Primate Research Center (CPRC) and the New York University-CPRC collection, were screened for pathological and abnormal signs, in addition to measurements of bone size and density. A range of diseases and defects were detected – including degenerative (enthesopathies:10.54%), inflammatory (joint disease:2.76%), oral (periodontitis: 4.33%), and congenital (craniosynostosis: 0.21%). Sex-based differences were found to be significant across multiple diseases/defect types ($p < 0.05$) as were differences between known matrilines ($p < 0.05$), indicating a genetic influence. A correlation matrix between diseases also demonstrated positive associations between those known to share etiological process, such as bony fracture and limb synostosis, and those that are not, such as periodontitis and cribra orbitalia. A preliminary glance at the impact of major hurricane events further pointed to a reduction in bone mineral density and an increase of skeletal pathologies ($p < 0.05$) clustered around these climatic disasters. Further contextualization of the skeletal health of the Cayo Santiago Rhesus colony is warranted to assess genetic vs environmental determinants of pervasive diseases.

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Craniofacial Complex of Cleft Palate in Newborn *Callithrix jacchus*

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Cleft palate is a congenital anomaly characterized by lack of fusion of the palatal tissues resulting in confluence of the oral and nasal cavities. Extensive clinical literature on this defect exists in humans and animal models; however, there is limited documentation of cleft palate in non-human primates. Here, we present the first known detailed report of soft tissue correlates of cleft palate in a newborn pygmy marmoset (*C. jacchus*) using a combination of nano-CT (computed tomography) and diffusible iodine contrast-enhanced CT (diceCT) imaging. We used a buffered I_2KI (B-Lugol) solution to visualize soft tissues of the craniofacial complex and avoid tissue shrinkage.

Using 3D Slicer, an open-source software, we segmented and visualized velopharyngeal elements such as tensor veli palatini, levator veli palatini, and salpingopharyngeus muscles. To provide structural context, we visualized bones of the skull and cartilage and mucosa of the auditory tube. We present this comparative dataset in three dimensions, highlighting analogous structures in typical specimens (N=7) to the variants evident in the cleft (N=1) newborn primate. Findings in the cleft individual include a shallow pharyngeal recess posterior to the torus tubarius and a distinct separation between bilateral levator veli palatini at the distal insertion on the palatine aponeurosis. Due to the unification of the oral and nasal cavities, structural abnormalities are evident throughout the midface, notably a prominently ventroflexed tongue. With this dataset, we provide valuable insight into the relationship between cleft palate and associated structures of the soft palate, affecting functions for deglutition and middle ear aeration.

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A shared pattern of facial growth in present-day humans

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Human facial shape, size, and morphology are remarkably variable. Whether this variability is attributable to phenotypic plasticity, natural selection, or neutral genetic variation is unclear. Quantitative genetic studies on adult craniofacial morphology have shown that population-wide differences in features that are directly involved in mastication (e.g., mandible) better reflect subsistence strategy than neutral genetic variation. What remains unclear is whether the differences observed between different subsistence groups are attributable to phenotypic plasticity or natural selection because these studies were limited to adult individuals. Periosteal bone modeling (i.e., patterns of resorption and formation) provides direct evidence of bone growth activity, and, together with sutural growth, is a key mechanism that underlies morphological variation. This study analyzed the bone modeling patterns on the periosteal surface of facial skeletons (maxilla, zygomatic, brow ridge, and mandible) in a cross-sectional ontogenetic sample of 48 individuals from three geographically diverse populations with differing subsistence strategies: Western Europe (France and Germany), Greenland (Inuit), and South Africa (San and/or Khoe). Epoxy replicas of the bone were imaged using a digital microscope, and bone resorption was identified and quantified to create digital bone modeling maps. The results indicate a shared bone modeling pattern in the facial skeleton between diverse regional groups throughout ontogeny, with subtle population differences. These results suggest a degree of phenotypic plasticity in facial growth during ontogeny, possibly related to subsistence strategy. This study expands on our understanding of the underlying biological mechanisms involved in facial evolution.

Histological human bone identification based on drifting osteon prevalence

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Histotaxonomic methods utilize principles of bone biology to characterize the microscopic appearance of taxonomic groups. In archaeology, histological analysis can be a valuable tool to classify small fragments of bone to taxa when morphological, proteomic, or genetic methods are inapplicable. While there are established histological characteristics to distinguish nonprimate mammalian bone from human, there is currently no histological pathway to positively distinguish human bone. Here we present a new method to identify human bone fragments using the prevalence of drifting osteons, an atypical secondary osteon morphotype found in primate long bones and normally absent from common mammalian domesticates. In developing this method, we surveyed undecalcified transverse sections of multiple skeletal elements from 25 species (human n=221; nonhuman primate n=24; nonprimate n=169) to quantify the number of drifting osteons present. Results indicate that drifting osteons represent a higher percentage of all secondary osteons) in human bone (mean prevalence =0.72%, SD=0.910) compared to nonprimate mammalian bone (mean prevalence=0.06%, SD=0.290). We developed a quantitative histological method that can positively discriminate human bone from nonprimate mammalian bone in archaeological contexts using four criteria: 1) The sample is a rib or long bone sample; 2) unlikely to be from a nonhuman primate given the archaeological context; 3) at least two drifting osteons are present in the cross section; and 4) the drifting osteon prevalence (or as a percentage of total secondary osteons) is ≥ 1%. Future research expanding the nonhuman primate dataset will be required to expand our method to include other primate groups.

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Investigating the influence of taxon, body size, and sex on shape variation in African ape distal femora

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Distal femur morphology of African apes reflects the range of knee joint movement and loading during tree-climbing and knuckle-walking. Early hominin distal femora exhibit features that may reflect some degree of tree-climbing; however, these features are difficult to interpret because distal femur variation in African apes is still poorly understood. We explored this variation and its potential links with locomotor behaviour using 3D geometric morphometrics on a sample of 20 chimpanzees, 24 bonobos, 20 eastern gorillas, and 11 western gorillas. We used PCA to visualize shape variation, and Procrustes ANOVA to measure the effects of taxon, sex, and centroid size on distal femoral morphology.

Species was a significant factor ($p=0.001$; 34% of the total variance). This was reflected in the PCA, with *Pan* and *Gorilla* separated along PC1, and bonobos and western gorillas separated from chimpanzees along PC2. As size was also significant ($p=0.007$), some subsequent analyses were performed using allometry-corrected data. Landmark subsets were then used to test the following predictions based on previous literature: 1) Femoral condyle shape is taxon specific; 2) The shape of the intercondylar fossa reflects body size; and 3) Femoral trochlea shape is sexually dimorphic and reflects differences in tree-climbing frequency. Prediction one was supported as species was significant ($p=0.001$). Prediction two was partially supported because species, and size were significant. Prediction three was supported with significant differences between groups with varied tree-climbing frequencies, and between male and female gorillas. These findings have the potential to improve our understanding of early hominin postcranial variation.

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It's Biocultural all the way down: Understanding The Pleistocene hominin niche

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A niche is the structural, temporal, and social context in which a species exists. Current evidence supports a biocultural niche in the evolutionary ecology for middle and later Pleistocene hominins. In at least the last 300,000-500,000 years there is uncontested material evidence of cultural behavior associated with the genus *Homo* including use of ochre, fire, complex lithics, and wooden tools/artifacts. In this same time frame, there are also contested claims of mortuary behavior, engravings/etchings and other forms of materially evident meaning-making behavior. Here we present the most up-to-date comprehensive overview of this entire material record. Given the structural and technological details characterizing these materials, we argue that the underlying emotional, cognitive, and social capacities necessary to produce them must lie deeper in time than the materials' current first appearances in the archeological record, and result from interplay of biological, social and cultural dynamics. To arrive at this argument we also reviewed the evidence for extended social-coordination in caretaking, foraging, and the creation if material items in the genus *Homo*, and expanded complexity in inter-group dynamics. The results of these dual analyses indicate that models for, and theoretical framings of, Pleistocene hominin behavior and morphology can, and should, include cultural behavior/dynamics as a baseline capacity/variable in hominin evolution not as an alternative hypothesis. We conclude that the accumulated evidence for a hominin biocultural niche in the Pleistocene is robust and offer methodological approaches that add to our ability to better understand the long biocultural durée of the hominin experience.

Gouging and non-gouging callitrichid primate canine morphospace

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Morphological correlates for the exploitation of exudates shed light on processes of craniodental adaptation and bear implications for the reconstruction of this ecologically significant behavior in fossil taxa. Here, we apply a novel implementation of a power law method for registering conical morphological shapes to a sample of callitrichid lower canines. This method creates a two-axis morphospace of cones using aspect ratio (height/maximum radius) and the slope of a line relating the change in radius to the distance from the tip of a cone in log space. Specimens representing three species (the non-gouging *Saguinus oedipus* and*Leontocebus fuscicolis* and the gouging *Callithrix jacchus*) were microCT scanned and mesh files analyzed using a Blender script created to take automated measurements on slices fit through surface vertices based on their geodesic distance from the canine tip, a procedure robust to a wide range of canine curvatures and orientations. Surface and cross-sectional areas measured from consecutive slices were used to estimate the parameters of the power model based on their best-fitting RMA regression coefficients. In the resulting power law morphospace, the gouging *C. jacchus* occupies distinct space of relatively high aspect ratio and slope. A linear discriminant model constructed using power law parameters correctly reclassified 89.5% of specimens to gouging or non-gouging categories using leave-one-out cross validation. Power law descriptors represent a potentially powerful method for distinguishing gouging from non-gouging primates. Gouging callitrichids appear to have canines with higher heights relative to maximum radius and more dramatic taper from base to tip.

Remote fossil prospecting in the Cradle of Humankind: Assessing variable importance for cave site prediction using Random Forest models

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The purpose of this study is to determine which geomorphological controls most significantly affect the spatial distribution of cave sites within the Cradle of Humankind, South Africa, in order to train accurate machine learning models for remote fossil prospecting. LiDAR point cloud data covering 70% of the Cradle, multispectral satellite imagery, and geological maps were converted into raster (pixelated matrix) images in a GIS environment to denote varying aspects of the local topography, including elevation, slope, aspect, curvature, drainage, spectral reflectance, vegetation cover, fault proximity, and underlying geology. The rasters were stacked and overlaid with point locality data of roughly 500 cave sites and 500 random non-cave sites in the study area. Variable values associated with these point localities were input into a Random Forest model in Python for training and evaluation using k-fold cross validation. The model performed with 77.3% accuracy and an F1 score of 78.6%. Variable importance for prediction was evaluated by measuring the increase in prediction error when variable values were shuffled. Fault proximity, elevation, and dolomite occurrence exhibited the highest importances for model accuracy, whereas Enhanced Vegetation Index, low-resolution drainage, and certain geological formations all exhibited less importance than two randomly generated variables. Removing these variables may improve model efficiency for future iterations that apply the model to the entire region for novel site prediction.

Bone Health Among Ancient Maya Females from the Midnight Terror Cave, Belize

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Osteoporosis is a metabolic disease caused by the imbalance between bone formation and resorption resulting in bone loss, microarchitectural alterations, compromised bone strength, and an increased risk of bone fracture. Age-related osteoporosis has been well-studied in the bioarchaeological record, but secondary osteoporosis, which can occur as a result of poor nutrition, disease, and trauma, has received less attention. This study investigates bone health in Late Classic (AD 600–900) young adult females (N=7) and males (N=4) from the Midnight Terror Cave, Belize. The os coxa was selected because molecular sex is known from several samples and sex and age, two important variables to consider in osteoporosis, can be estimated with high accuracy, which is critical since this assemblage is commingled. Standard methods were used to estimate age-at-death and sex for individuals with no molecular sex data. Bones were X-rayed, images were imported into Fiji (ImageJ), and regions of interest (ROIs) (100 × 100 pixels) were selected at the anterior superior and inferior iliac spines, acetabular fossa, and greater sciatic notch. Fractional bone area (bone area [BA]/total area [TA]) and the mean of trabecular thickness (Tb.Th), which assess bone quantity and quality, respectively, were measured on binarized ROIs using the BoneJ plug-in. Given the limited sample size, general patterns were explored between sexes and across ROIs within individuals. Females show greater BA/TA and Tb.Th than males at all four ROIs. Within individuals, BA/TA tends to be similar across ROIs while Tb.Th is variable. Results are discussed within a biocultural framework.

An improved approach to the taxonomic assignment of hominins using molar crown outlines: Algorithmic crown outline reconstruction

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Traditionally, when portions of a tooth's crown outline are absent due to interproximal wear, they are reconstructed through a qualitative assessment of the tooth's remaining morphology. In this study, we address two key objectives: first, we compare two methods of data acquisition employed to quantify molar crown outlines, and second, we juxtapose the qualitative assessments made by researchers with estimations generated by an algorithm. Our study samples include permanent lower first molars representing *Homo erectus* (n=3), Middle-Pleistocene *Homo* (n=5), *H. neanderthalensis* (n=14), early *H. sapiens* (n=10), Upper Palaeolithic *H. sapiens* (n=7), and recent *H. sapiens* (n=6). Our findings reveal that the two data acquisition methods, while fundamentally equivalent, are not interchangeable. Furthermore, the use of our algorithmic approach for reconstructing the missing portion of the crown outline consistently situates specimens within the taxonomic group's range of variation, irrespective of the reference sample employed. Importantly, the algorithmic reconstruction outperforms manual reconstruction by either researcher. As such, future studies involving worn teeth may be improved by incorporating an algorithmic framework to estimate the missing crown outlines.

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Patterns of juvenile vulnerability at three Bronze-Iron Age sites in the Turpan region, Western China

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Children's skeletons bear a wealth of information about childhood biological and social lives, hence the collective patterns of juvenile vulnerability in a population would suggest the overall environmental and social stress levels. In this study, skeletal remains of 74 juveniles from three cemeteries used during Bronze-Iron Age in the Turpan region, western China (10th to 2nd centuries BCE) were investigated for abnormal porosity, enamel hypoplasia, abnormal new bones, limb and rib deformities, and other signs of lesions. All three sites belong to the Subeixi Culture in the Western Regions. Results demonstrated that children of the Shengjindian (250–100 BCE) and Jiayi (800–400 BCE) mortuary populations had a higher overall prevalence in signs of pathology and developmental stresses than the earlier children of the Yanghai (1,000–700 BCE) mortuary population, suggesting an increase of juvenile vulnerability in the Western Regions, which might be related to environmental changes and increased interpersonal conflicts in a transitional zone between nomadic and settled populations. The regional socio-cultural evolution might have a significant impact on the health and mortality of children and adults alike.

Predicting the intermembral index of *Ardipithecus ramidus*: new insights from phylogenetic regression modeling on a large comparative sample

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The Intermembral Index (IMI) is well-correlated with locomotor modes in extant primate taxa. While this relationship is well-understood in living primates, reconstructing the IMI in fossil taxa is more difficult. This is particularly true of fossil hominins, as many have unique combinations of adaptations for both arboreal and terrestrial locomotion. Despite this uncertainty, limb ratios have been used to suggest that *Ardipithecus ramidus* lacked adaptations to suspensory and climbing behaviors seen in modern apes, with limb proportions more akin to arboreal quadrupeds. However, due to missing elements, this claim was based on a radius/tibia (RT) ratio, an index that has not been studied as extensively as IMI. Here, we model the relationship between RT and IMI with a large sample of extant catarrhine primates (n=310 individuals; 48 species), and phylogenetic least squares regression analysis using the *caper* package in R. This approach accounts for phylogenetic relationships that may contribute to observed similarities between taxa. We determine the RT ratio is, in fact, well-correlated with IMI and locomotor mode, and accurately predicts known fossil hominin IMIs. We use this model to predict the IMI of *Ardipithecus,* which returned a value of 91, falling within the range of cercopithecoids/arboreal quadrupeds, and supporting some previous suggestions in the literature. However, with a locomotor mode likely distinct from that of any extant taxa, we still need to be cautious in drawing conclusions about *Ardipithecus* locomotor behavior from limb proportions alone.

Evaluating Deep Learning Networks for the Identification of Secondary Osteon in Human Cortical Bone

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Cortical bone histomorphometry has been used for estimating the age of unknown individuals, with secondary osteons being the main parameter under consideration. To resolve issues related to time consuming data collection protocols, specialized training, and observer error, this study explores the use of various deep learning architectures for the automated identification of secondary intact and fragmentary osteons.

The sample under study consists of 99 photomicrographs from human ribs. A total of 1,415 intact and secondary osteons as well as their complete or partially complete canals were annotated manually using VGG Image Annotator. Seven different U-shaped neural network architectures were trained to segment photomicrographs into regions corresponding to intact osteons, fragmentary osteons, and background (non-osteon). They were evaluated using cross-validation with metrics including intersection over union (IoU) and Dice coefficient.

A U-Net architecture with an *EfficientNet B5* backbone was found to perform best of those tested. Its ability to segment osteon from non-osteon was quantified by the background IoU which was 0.795. Intact and fragmentary osteons had IoU values of 0.715 and 0.468, respectively, indicating that intact osteons were more successfully segmented than fragmentary osteons. The inclusion of canals in the models did not improve osteon identification.

The automatic segmentation of osteonal structures tested here suggests that, with further improvements, the technique could be promising as a platform for automatic identification of osteons in the future. Larger image datasets for training and testing as well as exploring other skeletal elements will help to corroborate our findings.

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Divergent trajectories between the Neanderthal and modern human ribcage development: paleobiological implications

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The study of the development of the ribcage has attracted the interest of the scientific community for decades because of the importance of the ribcage for clue biological aspects such as respiratory physiology, bioenergetics, or even body shape. The adult Neanderthal ribcage is caudally wider and antero-posteriorly deeper compared to the ribcage of our species, which is probably linked to a high ventilatory and/or total lung capacity because of the elevated energetic demands of the Neanderthals. Recent studies have proposed that the adult Neanderthal morphology is partially observed at birth since newborns and children already present a wide and deep ribcage. However, there is a need to study the complete ontogenetic trajectory of the Neanderthal ribcage in a comparative framework with modern humans to explore potential divergences in the trajectories. In this work, we compare entire ontogenetic trajectories of 30 modern human ribcages and 5 Neanderthals ranging from newborns to fully adults. Our results show that the development of ribcage is divergent in both species since most of the differences observed in adults are already observed at birth and the ontogenetic changes apply to both species in almost the same way. Also, we observed that the Neanderthal ribcage is larger than the modern human's during the trajectory, which is especially evident at birth. These results have important implications for understanding Neanderthal energetic demands and paleo-physiology since this fossil hominin lineage could have a larger energetic demand as well as a different respiratory pattern compared to modern humans.

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Neighbor-net analysis of extant apes supports reliability of fossil hominin results

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The reliability of hominin phylogenetic hypotheses has been debated in the literature for decades. In some cases, analytical methods used in these reconstructions have failed to reproduce known molecular relationships among extant primates, thus calling into question their validity when applied to hominin data. Exploratory data analysis can potentially help resolve some of these issues and is a process that involves the identification and visualization of incongruencies and phylogenetic signal conflict in a dataset. Network-based methods are often emphasized in exploratory data analysis because of their ability to reflect non-tree-like patterns in the data. One such method, Neighbor-net, is a distance-based method of constructing phylogenetic networks that has been used to analyze phylogenetic signal conflict among fossil hominin taxa. In these analyses, Neighbor-net has produced anomalous results regarding the placement of the taxon *Sahelanthropus*. Here, the Neighbor-net algorithm is applied to a dataset including extant members of Hominoidea to test whether it accurately reproduces known molecular relationships among those taxa. The results of the analysis indicate that Neighbor-net does accurately reproduce those relationships. This suggests that the anomalous findings in previous studies could be the result of limitations in the available character data for *Sahelanthropus* rather than issues with the Neighbor-net algorithm.

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Disappearing Trackways: Assessing of Erosion at Laetoli Site A Trackways Using UAV and DSLR Photogrammetry

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The Plio-Pleistocene Laetoli in northern Tanzania is renowned for the 1976 discovery of hominin trackways at Site G, which were preceded by the discovery of the enigmatic A prints at Locality 7. Recently McNutt et al 2022, securely identified the A prints as hominin prints, morphologically different from the G prints. Equally important at Site A are nonhominin footprint trackways which provide important snapshots of fauna composition useful in paleoecological reconstruction. During the 2023 field season, extensive photogrammetry work was conducted by our team to create a three-dimensional digital model of the site and evaluate the erosional history of the fast-disappearing animal trackways. Using an Unmanned Aerial Vehicle (UAV) and DSLR cameras, we collected data (photos and videos) of the site and post-field processed them to create a high-resolution 3D model of the site. Photogrammetric comparison of multiple sources of data and recent photos of site A trackways were used to create the current 3D model, which provides insight into the rate of deterioration of the trackways (degree and speed of erosion) and can be used to guide future conservation efforts. This project highlights the utility and effectiveness of photogrammetry as a method for tracking fossil footprint preservation which is both sustainable and easily accessible. This method can be employed at other sites that preserve fossil footprint trackways.

Updated analysis of fossil cercopithecid monkeys from Kromdraai B

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Deposits at Kromdraai B (KB) have been intermittently excavated since the discovery of *Paranthropus robustus* in 1938. Cercopithecid primates are abundant at KB and are represented by a large proportion of subadults. The most recent assessment of the old (pre-1990) KB collections identified at least two cercopithecid taxa: *Papio* cf. *robinsoni* and *Cercopithecoides coronatus*. Here, we studied all available KB cercopithecids, including ~380 catalogued specimens from the old collections and ~490 undescribed specimens from recent excavations in the new extension area including Unit P.

Our analysis identifies the same three taxa in both the old KB and new Unit P collections: *P. robinsoni*, *C. coronatus*, and *Theropithecus oswaldi oswaldi*. An additional large papionin is possibly present. The novel identification of *T. o. oswaldi* is cemented by craniodental specimens in Unit P and a hand skeleton with a diagnostically elongated first metacarpal from the old KB collections (corresponding to Units Q-R). The Unit P and old collections also share a distinctively high proportion of subadults. The shared taxonomic and demographic profiles of the old KB and new Unit P collections suggest they represent a single, broadly contemporaneous assemblage across sedimentary units and perhaps have the same accumulating agent.

Unit P *T. o. oswaldi* teeth are similar in size and enamel complexity to those at Swartkrans Member 1 (SK1), providing a mean age estimate of ~1.8 Ma. Additionally, all cercopithecid taxa known from Unit P and the old KB collections are found at SK1, suggesting they are broadly similar in geological age.

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Differences in regional bone mineral density with age in NHANES

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Bone mineral density (BMD), a critical measurement of overall bone health, relies on a dynamic remodeling process of concurrent deposition and resorption of bony matrix. BMD increases throughout childhood, reaching peak levels in early adulthood, then gradually decreases with age. Bone remodeling is sensitive to several nutritional, hormonal, immunological, lifestyle, and genetic factors, which can impact the rate of BMD loss with aging. Further, bone remodeling responds to repetitive mechanical loading by increasing bone mineral deposition, suggesting that differences in bone loading could modify associations between age and BMD by buffering weight-bearing regions against resorption. This study examines the association between age and BMD in 13 anatomical regions using survey, DXA, and laboratory data from adult NHANES participants (2007-2018 cohorts; n=12,260). In a linear regression adjusted for BMI, gender, race/ethnicity, and sedentary time, among other health and lifestyle variables, females have lower BMD than males in all regions regardless of age. Individuals who identified as non-Hispanic Black have significantly higher BMD in every region than the non-Hispanic White group. Proxies for socioeconomic status are positively associated with BMD in high-stress regions of the lower limb (i.e., total femur, femoral neck, trochanter, and the inter-trochanteric region) only. In the same regions, heavy smokers have lower BMD than non-smokers. Increased sedentary time is associated with lower BMD only in the arms (all p<0.01). Our presentation will further discuss how more rigorous statistical modeling may help identify and investigate the biological mechanisms underlying age-BMD associations and their impact on bone health and aging.

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Reconstructing the Genetic Relationship between Ancient and Present-day Siberian Populations

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Human populations across a vast area in northern Eurasia, from Fennoscandia to Chukotka, share a distinct genetic component often referred to as the Siberian ancestry. Most enriched in present-day Samoyedic-speaking populations such as Nganasans, its origins and history still remain elusive despite the growing list of ancient and present-day genomes from Siberia. Here, we reanalyze published ancient and present-day Siberian genomes focusing on the Baikal and Yakutia, resolving key questions regarding their genetic history. First, we show the long-term presence of a unique genetic profile in southern Siberia, up to 6,000 years ago, which distinctly shares a deep ancestral connection with Native Americans. Second, we ascertain that Yakutian hunter-gatherers, rather than their Baikal counterparts, exhibit a closer genetic affinity to Nganasan. This finding suggests that the origin of Siberian ancestry may be traced back to Yakutia. Third, we identify the Middle Neolithic individual from Yakutia, belonging to the Belkachi culture, as a crucial source in understanding the spread of the Siberian ancestry into Uralic and Yeniseian-speaking populations. These findings shed light on the genetic legacy of the Siberian ancestry and provide insights into the complex interplay between different populations in northern Eurasia throughout history.

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Archaeotoxicological findings in the 17th century *Ca' Granda* crypt: mercury, opium and cannabis as medical remedies

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The *Ca' Granda* hospital was a major healthcare institution dedicated to the care of the poor of Milan during the Modern Age. It became a European model during the Renaissance with its specialized doctors, surgeons, daily medical rounds, and strict hygiene protocols. About 10,000 patients were deposited in the hospital crypt: males and females of all ages with various pathological and traumatic signs. Notably, some hospital archives have been preserved up to today, including a very detailed and specialized pharmacopeia. The aim of the study was to evaluate the consumption of medicinal remedies and compare them with the patient's biological profile and medical practices of the time. The archaeotoxicological investigation was focused on searching plants alkaloids and trace elements in bones and well-preserved brain tissue with LC-MS/MS and ICP-MS instrumentations. The analytical evidence showed the presence of mercury in two subjects with tertiary syphilis, a metal widely used in the treatment of this disease. Several active principles of opium, a plant well-described in the pharmacopeia, were detected in six patients; one of whom had a blunt force trauma on the cranium. Alkaloids of cannabis were detected in two subjects. This plant was absent in the pharmacopeia suggesting recreational purposes according to written sources, although self-medication, occupational exposure, administration by healers not practicing in the *Ca' Granda* are possible alternatives. The diversity of the biological samples examined provided a partial toxicological history of the subjects, providing precious information about the health and lifestyle of this archaeological population.

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Poorer growth at 1 year among HIV exposed uninfected children compared to HIV unexposed children in Kenya

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Effective treatments have decreased vertical HIV transmission and most infants born to women living with HIV (WLH) are HIV-exposed but uninfected (HEU). HEU infants suffer greater morbidity and mortality than HIV-unexposed uninfected children (HUU). Data on growth outcomes among HEU in the era of optimized ART treatment is limited. We recruited mother infant pairs at infant age 6 weeks as part of a larger study on 3-year HEU outcomes in Nairobi and Western Kenya (n= 2000, n=1000 HEU/HUU). Weight and length for age and weight for length WHO Z-scores (WAZ, LAZ, and WHZ) were estimated at 6 weeks, 6 months and 1 year. We used linear mixed effects models to compare growth trajectories and determine correlates of growth. HEU mothers were more likely to be older, less likely to be married, have lower education, more anxiety symptoms and had higher food insecurity. HEU infants had lower birthweight and were more likely to be exclusively breastfed ($p<0.05$ for all).

In unadjusted analysis, at 6 weeks, 6 months and 12 months, HEU had lower WAZ compared to HEU and lower LAZ at 6 and 12 months. Adjusting for birth weight, maternal age, and infant sex, HEU infants had significantly lower LAZ at 6 months (-0.20 [-0.32, -0.08], p= 0.0011) and 12 months (-0.19 [-0.29, -0.09], p = 0.0001). Maternal illness was associated with lower LAZ overall and among HUU. Infant hospitalization was associated with lower WLZ overall and among HEU. Among HEU, ART regimen (dolutegravir versus efavirenz) was not associated with growth.

The genomic tales of early medieval steppe populations settled in Central Europe

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Recent genomic studies showed that during the Migration Period and Early Middle Ages, people carrying Central or East Asian ancestries appeared in the Carpathian basin during different time periods. The first evidences involve only a handful of individuals from the 5th century CE. Historically, this corresponds to the Hunnic period that in Europe lasted only few decades leaving a limited archaeological record testifying direct eastern or central Asian steppe connections. The scarcity of the genomic and archaeological evidences leaves open questions on the trans-Eurasian connections during the Hunnic period.

It is only a century later, in the late 6th century CE during the Avar period, that a substantial influx of people carrying East Asian ancestry appear in the Carpathian Basin. According to historical records, the Avars settled the Carpathian Basin in 568 CE, where they established their “Qaganate” that lasted over 250 years. Alongside, the Avar period left a large and culturally diverse archaeological record of trans-Eurasian connections.

Here we analyze the genomic composition of 424 Avar period individuals from four complete cemeteries showing cultural and biological connections to the steppe. Combining genomic data, archaeological, anthropological and historical contextualization, we investigated the social structure of these communities and if or how it changed in their descendants during the course of Avar period. This allowed us to infer extended multigenerational pedigrees that revealed unique features of their social structure and descent system and uncovered patterns of local mobility and community replacements that were not possible to asses before.

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Mortality and cause of death in 19th/20th century Americans from the Hamann-Todd collection

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Socioeconomic status and structural racism impact health and survival in marginalized groups. This study examined mortality rates and cause of death information in a large sample of historic adult individuals identified as Black/African American and White/European American from Cleveland Ohio. All individuals represent low socioeconomic status, allowing for a comprehensive analysis of health and mortality between sex and race/ethnicity over time.

A multinomial logistic regression tested for the effects of sex, race/ethnicity, and birthdate (categorized as during the Antebellum, Reconstruction, and Great Migration periods), with cause of death (degenerative, general infection, lung infection, and neoplastic) as the outcome variable. Relative Risk Ratios (RRR) compared risks of dying of those causes between groups.

Results indicated selective mortality was present as all individuals were significantly more likely to die younger from infectious disease than degenerative diseases. Males from both racial/ethnic identities were significantly more likely than females to die of general infectious causes compared to degenerative, while lung disease was not significantly different between sexes of either race/ethnicity. When comparing races/ethnicities within sex, people identified as White/European American males were 1.4 times more likely than individuals identified as Black/African American males to die of lung infections and 3.6 times more likely to die of neoplasms compared to deaths from degenerative causes. No significant differences were found between females, but changes over time were present.

In sum, individuals in the collection suffered poverty and marginalization, resulting in varied exposure to disease, especially higher levels of general infection compared to degenerative or neoplastic disorders.

Reconstructing behavior in large-bodied, extinct *Cryptoprocta* species and their impact on Malagasy lemurs past and present

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Today, the largest mammalian predator of Malagasy primates is the fosa (*Cryptoprocta ferox*), a member of the endemic family Eupleridae. Its larger congener, *C. spelea*, became extinct sometime during the past 2000 years. In this study, we reconstructed the behavior and ecology of extinct *Cryptoprocta* from Mitoho Cave at Tsimanampesotse National Park, southwest Madagascar, and other nearby locations. We analyzed postcrania of numerous *C. spelea*, subfossil and modern *C. ferox*, 30 additional extant carnivoran species (including euplerids), and a humerus from Mitoho Cave belonging to a new, even larger, species of *Cryptoprocta*. The latter was dated to >8.3 kyr BP on the basis of this fossil's location and the reconstructed flooding chronology of the cave. We employed multivariate and bivariate analyses of linear postcranial measurements to reconstruct the locomotor and positional behavior of both *C. spelea* and the new species of *Cryptoprocta*, and stable isotope analysis to test the hypothesis that sympatric, large-bodied, arboreal lemurs were likely preferred prey. Results of postcranial analyses indicate that both taxa were arboreal. Our conservative body mass estimate for the new species is 27-32 kg (considerably larger than either *C. ferox* or *C. spelea*). The contraction of the Malagasy predator guild during the Holocene was greater than previously thought. All *Cryptoprocta* species likely preyed on lemurs, with the larger ones targeting some of the largest-bodied extinct lemurs, such as *Megaladapis*. The existence of multiple large-bodied species of *Cryptoprocta* may explain mammalian carnivoran damage to the largest extinct lemurs in the southwest.

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Incremental dentine microsampling: Reconstructing weaning age in rural Medieval Italy

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Early infant nutrition, including weaning age has become an increasingly important line of research in bioarchaeology because it provides information about the demography, health, and social customs of past populations. Bioarchaeological knowledge of sex-based weaning differences in Medieval Europe is often based on urban samples and suggests that male nutrition is better in the crowded conditions of urban environments. This geographic bias calls for more research of rural cemetery samples that reflect the ecological variation of the time. Isotopic evidence from a few rural Medieval skeletal samples suggest that weaning age occurred later in rural populations (ca. 2-2.5 years) and may have been beneficial to infant health. Incremental microsampling allows for high resolution of isotopic ratios of nitrogen from ancient tooth dentine. This paper reports on the first isotopic data of juveniles from the San Paragorio church cemetery (10th-13th AD) in Noli, Italy on the Ligurian coast. This is the first isotopic study to provide genetic data for the sex of each skeleton (N=22) and confirmed age at death using micro-CT scans. $\delta^{15}N$ results show a later weaning age for Noli boys (mean=1.89 years, N=11) than for girls (1.48 years, N=11). $\delta^{15}N$ values are also more variable for girls, suggesting possible gender-based differences in weaning age and practices. Although Noli was a rural population, these preliminary results do not support a later age at weaning. Ongoing analysis focuses on the potential impacts of early weaning age on morbidity and mortality for girls and boys in the Noli population.

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Exploring the impacts of physiological stress on cortical bone through novel statistical modeling

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Bone is an intermediary tissue that is sensitive to physiological biorhythms, meaning that macroscopic structural changes related to health can be understood as the accumulation of cellular changes in response to metabolic, dietary, and activity-related factors. Currently, there are no methods for identifying the cellular impact of physiological stressors in cortical bone. Utilizing a novel statistical approach in histological research, multilevel structural equation modeling (MSEM), this presentation demonstrates how latent variable analysis can be used as a powerful tool for exploring relationships between microstructural variation and physiological stress.

This research analyzed the anteromedial, anterior, and anterolateral regions of interest (ROIs) of 70 femoral cross-sections from three modern skeletal populations with known demographics and available medical histories. Data collection yielded 2,169 demographic datapoints, 280 cross-sectional geometric measurements, and 4,297 histomorphometric parameters (including 204,500 osteons and over 5 million osteocyte lacunae) over 630 ROIs. MSEM analysis was used to model "cortical bone health" as a latent variable that was informed by individual demographics and influenced histomorphometrics across ROIs.

Results indicate cortical bone health explained 86.7% of the overall model variance ($p < 0.01$), supporting a strong model specification. Fragmentary osteon density was found to have a significant fixed factor effect on health (0.784), suggesting a relative sensitivity to physiological stressors. MSEM highlighted multiple medical histories (e.g., the presence of parasitic and/or infectious diseases) that explain significant proportions of model variance. Collectively, this exploratory approach allows for a theory-driven model of biological variation to provide meaningful suggestions for future research.

Beyond the Report: The Disparities Facing the Missing and the Invisible Unmissed

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The percentage of missing and unidentified persons in systematically marginalized communities (i.e., BIPOC, LGBTQ+, economically disadvantaged) has risen and is largely unnoticed, specifically in Mississippi. These communities are at greater risk of going missing as they are less represented in media coverage, less likely to be reported missing, and have fewer resources allocated to their cases. These issues are further compounded by socioeconomic and health disparities impacting these communities. By examining structural inequality, we can better understand how individuals remain missing and unidentified. Furthermore, it is essential to implement a biocultural approach that provides a more accurate identification profile within a framework that can be adopted into the medicolegal system. Using a comprehensive public database, like the Mississippi Repository for Missing and Unidentified Persons, we can show systemic inequalities in medicolegal, economic, and health disparities between Black and White Mississippians. For example, along with poorer health outcomes, we found that Black men and women in Mississippi were twice as likely to be found deceased after being reported missing compared to their White counterparts. Our goal with this discussion is to raise awareness of the disparities evident in the higher rate of missing and unidentified persons and what factors play into the data. Combining missing persons data with socioeconomic and health factors will provide answers about who goes missing and how we can help identify and resolve these cases.

Zooarchaeological Analysis at Area 8A Fossil Assemblage at Koobi Fora, Kenya

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Meat consumption is hypothesized as an important factor in major evolutionary developments within our genus. This includes encephalization and increased body size in species such as *Homo erectus*. Here we report on a recently discovered fossil assemblage in Area 8A, in the Ileret subregion of the Koobi Fora Formation, situated within the KBS Member (1.87-1.56 Ma). This assemblage contains a rare combination of hominin fossils, stone artifacts, and bones with evidence of butchery. The faunal sample consists of over 1,000 specimens, of which 558 are identified to taxonomic family, dominated by ungulates of size class 2, and include 5 hominin teeth. We offer an overview of the taxonomic makeup, distribution of ungulate size classes, stages of weathering, prevalence, and location of surface alterations, representation of skeletal parts, and ratios of epiphyses to shafts. High epiphysis-to-shaft ratio and low frequencies of carnivore damage suggests that carnivores played little role in the accumulation and modification of the assemblage. These results differ from later Okote Member assemblages associated with possible hominin modification (1.56-1.39 Ma.), suggesting variation in carcass acquisition strategies through time. The frequency of hominin butchery marks is low compared to experimental models in which hominins are the primary agents of accumulation. Nevertheless, the frequency of cutmarks on long bone midshafts indicates that hominins had predominantly early access to carcasses. This study expands our understanding of hominin carcass processing behavior at a critical time in human evolution and fills a temporal gap in our comprehension of early hominin carnivory in East Turkana.

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Paleoecological and Temporal Context of Area 123 Hominins in East Turkana, Kenya

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To better understand the evolutionary pressures driving high hominin diversity in the Early Pleistocene, it is imperative to contextualize the environments they inhabited. Area 123 in the Bura Hasuma region of the Koobi Fora Formation in Northern Kenya provides an ideal case study. It has yielded numerous significant hominin fossils, including the well-preserved cranium of *Homo habilis* (KNM-ER 1813), and a diverse mammalian community. However, a systematic assessment of the faunal community has not been conducted. The age of the assemblage in the southern portion of Area 123, where KNM-ER 1813 was recovered, has also been debated. We analyzed the historic mammalian collections and conducted additional faunal surveys to characterize the local paleoenvironment and provide a biochronological age estimate of this region. Our results favor an older age estimate for southern Area 123, as the mammalian fossils occur in or below a gastropod-bearing sandstone bed marking the end of the upper Burgi Member, and the presence of *Notochoerus scotti, Kolpochoerus limnetes,* and *Metridiochoerus hopwoodi* brackets the age of the assemblage between 1.79 and 2.1 Ma. The abundance of reduncine bovids, *Kobus,* and *Menelikia*, aligns with consistently well-watered conditions throughout the region. However, the presence of grazing bovids like *Megalotragus* and the cercopithecid *Theropithecus oswaldi* within the same context also indicates patches of drier habitats. This broader perspective from the mammalian community expands our understanding of the paleoenvironments available for hominins during the upper Burgi Member.

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Quantifying human body surface area: A comparison of photogrammetry and CT scanning to estimation techniques

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Research into ecogeographic variation in human form focuses extensively on Allen's and Bergmann's rules, which relate body surface area (BSA) to body volume. While body volume is readily assessed through water displacement, accurate quantification of BSA is more challenging due to the body's complex surface topography. Indeed, few studies actually measure BSA, relying instead on formulae that estimate BSA from height and weight. Accordingly, this study employed 20 human subjects to assess photogrammetry and CT scanning as viable methods for directly quantifying human BSA. Approximately 1,500 photographs were taken of each participant from multiple perspectives while they stood in standard anatomical position. 3D photogrammetric models were then generated in Agisoft Metashape, with BSA subsequently measured in Geomagic Wrap. Whole-body CT scans were also collected from participants, with BSA calculated in Avizo. Five published formulae were then used to estimate BSA from each participant's height and weight. The photogrammetric methods employed in this study were generally inadequate, returning only 6 models complete enough to be assessed. Photogrammetry consistently produced the smallest BSA values (mean=16554 cm^2), with regression formulae (mean=19019 cm^2) and CT scanning (mean=20888 cm^2) producing larger values. The small photogrammetric BSA values are likely attributable to correctable data collection parameters (e.g., lighting, camera specifications). Larger CT values compared to formula estimations may reflect the high scanning resolution, permitting quantification of minute surface details. Further research into methods capable of accurately assessing BSA is required. Photogrammetry appears particularly attractive for anthropological fieldwork as it is inexpensive, safe, and transportable.

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Locomotion and habitat use of forest-living olive baboons (*Papio anubis*)

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Studies of olive baboons derive predominantly from savannah and woodland habitats. Not surprisingly these studies describe olive baboons as nearly entirely terrestrial (Rose, 1977). Here we present locomotor and habitat use data from forest living olive baboons. A troop of 13 baboons (2 adult and 2 subadult males; 8 adult and 1 subadult females) was studied from June to August 2023 in Kibale National Park, Uganda. We used instantaneous focal sampling to record activity state, locomotor behavior, and substrate use and height. A chi-square test was conducted in R to test for sex differences. The locomotor profile was approximately 92% quadrupedal walking, 3.5% running, 0.5% leaping, and 4% climbing, with no significant sex differences. Despite the widespread availability of arboreal substrates, the baboons spent only about 24% of their daytime in the trees, with the majority of that time feeding or resting (about 76%). By contrast, most travel occurred on the ground. We found no significant sex differences in arboreality, but there were significant sex differences in arboreal activity budgets, apparently driven by higher rates of feeding and social behavior among females. Our results demonstrate that (a) olive baboons are very capable arborealists despite normally being classified as terrestrial, (b) when traveling olive baboons in forests overwhelmingly prefer to do so on the ground, and (c) a characterization of a primate's locomotor behavior and habitat use from only a few study sites may lead to incomplete conclusions regarding the ability of that primate to adapt to different environments.

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Time-frequency analysis of hindlimb muscle electromyograms in bipedalism and quadrupedalism in Japanese macaque

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Bipedal walking (BW) uses only two hindlimbs to support the body, so the hindlimb muscles would be required to generate higher muscular tension than quadrupedal walking (QW). A potential adaptation to generate the high tension is to recruit fast twitch fibers within a muscle, which activates with higher firing rates, or higher signal frequencies, and higher tension than slow twitch fibers. To elucidate the adaptation in activities of muscular components in BW, the frequency of electromyograms (EMGs) of primary hindlimb muscles in a few Japanese macaques was compared between BW and QW. We used the same fine-wire electrode setting to measure the EMGs during BW and QW so that the EMGs were comparable between the two modes of locomotion. The continuous wavelet transform decomposed the EMG by frequency. The key finding was a relationship between the EMG amplitude and the median frequency. When the hindlimb muscles began to activate, the median frequency increased following linear relationships between the amplitude and frequency in each muscle: the higher the amplitude, the higher the frequency tended to be. The frequency during BW should be higher than during QW because the amplitudes during BW were significantly higher than during QW; however, it did not. The frequency in BW reached some upper limit of frequency and did not increase beyond the limit. These results suggested that the hindlimb muscles activated during QW within a range where the frequency of EMG effectively increased, and BW required the hindlimb muscles to activate beyond the range.

Investigating Patterns of Gene Flow in the Cranial Morphology of East and Southeast Asian Populations

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Phenotypic variance observed between populations tends to correlate strongly with decreases in gene flow and is significantly structured by isolation-by-distance processes. Concisely, biological differences tend to accumulate linearly between populations as a function of their geographic separation. However, in some areas of the world, human populations demonstrate varied rates of morphological differentiation given the geographic distances between them. Previous analyses of Eurasian craniometric variation using k-mean clusters highlighted regions that deviate from the expected rate of morphological differentiation. Specifically, Mediterranean populations show more biological similarities than expected given their geographic distances. Similar patterns are observed in East Asia, particularly in Japanese Archipelago populations, but not so in Southeast Asia, despite their shared biological relationships. Here, we explore the structure of morphological differences between human populations in East and Southeast Asia, to further contribute to our understanding the factors that influence gene flow in the region. Mahalanobis distances among 23 East and Southeast Asian groups (1149 male individuals) were calculated, and populations were classified in a progressive number of clusters (k=2 to 10) using k-means algorithms. Clusters were visualized via map projections onto geographic coordinates. Results demonstrate that island populations in East Asia (Hokkaido and Jōmon) and Southeast Asia (Andaman and Philippines) separate themselves early in the cluster analyses. Continental East and Southeast Asia show strong regional structures, although morphologically distinct from each other. These results support the effects islands have in reducing gene flow between human populations, suggesting that non-linear factors impact the structure of biological differentiation in modern humans.

First burials give insights into mortuary rites at Göbekli Tepe, Pre-Pottery Neolithic Türkiye

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The site of Göbekli Tepe (9500-8000 BC) is located in modern day Southeast Türkiye. The round-oval monumental stone structures with their characteristic T-shaped pillars suggest that the place was a ritual center for human hunter-gatherer communities. So far, 928 scattered bone fragments and small bones have been found during excavations of the special buildings. In 2022, the first two burials were investigated bioarchaeologically. A single burial next to a special building contained the primary inhumation of a gracile, possibly female young adult in crouched position. Overall, the bones showed poor preservation, a high grade of fragmentation and covering by adhering calcareous deposits. Fragmentation was more severe in the long bones, and, due to postmortem damage, the epiphyses, the spine, ribs, and pelvis were missing. In the southern area of the site, a multiple burial was found below a plasterfloor of a rectangular room. The skeletal elements of at least two adults (one male, one female), and an adolescent female had been removed secondarily, and the postcranial elements piled in the middle part of the pit; the skulls had been placed at the pit's southern end.

Investigations of the taphonomic features show clear similarities to those of the human bone assemblage collected from other parts of the site. which, until the discovery of the burials, was the only evidence for human remains at Göbekli Tepe. Therefore, the burials are of great importance for our interpretations of human bone fragments found at the site, also providing information relating to site formation processes.

Kinematic strategies across substrates of varying risk and complexity in *Sapajus apella*

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Arboreal environments are complex, with substrates varying in size, inclination, compliance, and continuity, and arboreal animals have a high risk of injury when falls occur. Previous work has demonstrated primate arboreal gaits minimize whole-body center of mass movements to reduce the risk of falling. Overall head stability is a critical component of locomotion as it facilitates both visual and vestibular feedback required to navigate any naturalistic substrate. Here we hypothesize that because complex, arboreal substrates are riskier and more challenging than simple, terrestrial substrates, they require greater head stability to facilitate risk-mitigating visual and vestibular feedback. We tested this hypothesis in three adult female capuchins across a simple arboreal pole and a complex pole with obstacles. Gait cycles were filmed at 4K, 120fps. Two dimensional landmarks were digitized using SLEAP and angular motion calculated from landmarks using R. Linear mixed models were used to test for differences in 1) elbow flexion-extension, 2) knee flexion-extension, 3) head and trunk center of mass position, and 4) head-neck flexion-extension across substrates while accounting for repeated measuring the same individual. Results demonstrated a significantly more flexed elbow position (p=0.041) as well as a head and trunk positions closer to the substrate (p_{head}<0.0001, p_{trunk}=0.001) during complex, arboreal locomotion. However, there was no difference found in head or knee flexion-extension across substrates (p>0.05), indicating that head stability is maintained regardless of substrate complexity. Future work will explore gaze behaviors and the role of visual feedback in safe, efficient locomotion and head stability.

FACEFIT: Craniofacial morphology as a determinant of the fitted filtration efficiency of disposable respiratory protection

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Exposure to harmful aerosols is of increasing public health concern due to the SARS-CoV-2 pandemic and wildland fires. These events have prompted risk reduction behaviors, notably the use of disposable respiratory protection. This project investigated the role of craniofacial morphology as a determinant of the fitted filtration efficiency of commonly available face coverings (KN95, surgical masks, large KF94, medium KF94) in 100 participants (50 male, 50 female) between the ages of 18-55. Eighteen craniofacial measurements were collected using anthropological techniques and a 3D scan (Bellus3D Arc). Participants performed the modified quantitative Occupation Safety and Health Administration respirator fit testing procedure in a chamber supplemented with aerosolized sodium chloride particles. Each face covering was tested with and without an ear loop clip attached behind the head. Boosting and elastic net regression yielded five measurements (bizygomatic breadth, nose length, bizygomatic nasal arc, neck circumference, ear breadth) that were the best predictors of filtration efficiency based on overall model fit. Four groups with similar craniofacial dimensions were identified using k-means clustering. Participants in the group containing the smallest craniofacial dimensions (N=24) exhibited the lowest filtration efficiencies (KN95=62.3(2.4)%, surgical=48.8(1.6)%, large KF94=42.4(2.4)%, medium KF94=60.9(3.1)%) but averaged improvements of 17.5% when using a clip. In comparison, the best performing cluster (N=13) had efficiencies of: KN95=74.5(3.7)%, surgical=64.3(2.5)%, large KF94=67.1(4.0)%, medium KF94=73.6(5.1)% with an average clipped improvement of 7.4%. Overall, our results show that craniofacial morphology is a major determinant of fitted mask performance and should be considered when selecting disposable respiratory protection against exposures to harmful aerosols.

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Quality of Life, Religion/Spirituality, and Dementia Risk Among Black People in the US

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Objectives: Black people in the United States (US) are disproportionately more likely to be diagnosed with Alzheimer's disease and related dementias (ADRD) than people of other racial/ethnic groups. This study seeks to investigate how two sociocultural factors previously shown to impact age-related cognitive decline, quality of life (QoL) and religion/spirituality (R/S), may play a role in explaining racial disparities of ADRD risk. Specific aims include: 1) Examine if negative QoL and R/S measures affect ADRD risk among Black people in the US, and 2) Determine the extent to which differences in dimensions of R/S mediate the relationship, if at all, between QoL and ADRD risk.

Method: We conducted a secondary data analysis drawing from the Health and Retirement Survey (HRS), a nationally representative longitudinal dataset with an oversampling of Black adults.

Results: We used logistic regression analysis to demonstrate that higher levels of negative affect are correlated with increased ADRD risk while more frequent attendance of R/S services is correlated with decreased ADRD risk among Black people in the US. Further, a path analysis showed that those experiencing negative affect are less likely to attend R/S services, buffering the positive effect of R/S on ADRD risk.

Discussion: These findings demonstrate the importance of involving those experiencing negative affect in R/S for reducing ADRD burden among Black people. Future research should consider specific mechanisms by which R/S participation may ameliorate the relationship between negative psychological constructs and age-related cognitive decline.

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Is human birth really comparatively difficult? A review of dystocia among placental mammals

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Human childbirth is often argued to be difficult and risky compared to birth in other mammals, as judged by our tight fetopelvic fit, the incidence of obstructed labor, and relatively high rates of maternal and neonatal mortality and morbidity. To empirically evaluate the claim that human childbirth is comparatively difficult, I conducted a systematic literature review of the prevalence of dystocia, i.e. "difficult birth", and underlying causes in other placental mammals. Dystocia is common in many domesticated species, such as cows, horses, sheep, goats, dogs and even certain cat breeds, with prevalence rates ranging from ~2% to reportedly nearly 100% depending on the species and the breed. Common causes are fetal maldisposition ("incorrect" position or presentation of the fetus) and fetopelvic disproportion, i.e. obstructive dystocia. Obstructive dystocia is most prevalent in species with a single large offspring. Dystocia has furthermore been documented among captive animals of wild taxa, including several primates, rhinos, elephants, and various carnivorans. Importantly, dystocia, including fetopelvic disproportion, has also been documented among wild mammals, where it was even a common cause of death in certain populations of sika deer (7%), pronghorn (>13%), and fur seals (16%). My review of dystocia and underlying causes in humans and other mammals shows that human childbirth may be considered difficult compared to *some* but definitely not *all* mammals. Fetopelvic disproportion appears relatively frequent in many precocial species and may be difficult to completely "select out" given the many factors that influence fetal size and maternal pelvic form across individuals.

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How Mangabey Molar Form Differs Under Routine vs. Fallback Hard-Object Feeding Regimes

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Although the sooty mangabey *Cercocebus atys* and the grey-cheeked mangabey *Lophocebus albigena* are both durophagous, the former consumes hard objects year-round, while the latter relies upon them as dietary fallbacks. We hypothesized that these differences in feeding regimes would be associated with differences in molar form, with the molars of *Cercocebus atys* exhibiting greater fracture and wear resistance than those of *Lophocebus albigena*. We compared molars of both mangabey species to one another and to molars of *Cercopithecus*, a genus not known to feed on hard objects. Critical loads for margin fracture were estimated using measurements from 2D µCT slices of maxillary (n = 9 to 36 per taxon) and mandibular (n = 9 to 11 per taxon) molars. Nanomechanical properties (by nanoindentation) and decussation of enamel prisms (by SEM) in trigon basins of one upper second molar per taxon were also compared. Protocone and protoconid critical fracture loads were significantly greater in *Cercocebus atys* than *Lophocebus albigena* and greater in both than in *Cercopithecus*. Hardness and the elasticity index were greater in *Cercocebus atys* than in the other two taxa, particularly in outer enamel. Quantitative comparison of prism angles indicate that decussation in trigon basin enamel is more complex in *Cercocebus atys* than in either *Lophocebus albigena* or *Cercopithecus cephus*. These findings suggest that *Cercocebus atys* molars are more fracture and wear resistant than those of *Lophocebus albigena*, refining our understanding of associations between hard-object feeding and dental anatomy under conditions of routine vs. fallback hard-object feeding.

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Cellular aging of the prefrontal cortex and cerebellum in chimpanzees

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Humans and other primates, including our closest living relatives, chimpanzees, show cognitive decline and brain structural changes with age. Humans are also susceptible to more severe neurodegenerative conditions, like Alzheimer's disease (AD). Recent research has found that some chimpanzees also develop the pathological hallmarks of AD. Comparative research is of interest both for furthering our understanding of human brain evolution, as well as identifying promising therapeutic targets in treating neurodegenerative disease. In the current study, we generated and analyzed cell type-specific transcriptome data for chimpanzees (ages 0-57) for the PFC (n = 5) and the cerebellum (n = 8) using 10X single nuclei sequencing. For each brain region, we calculated the cell type proportions for each individual and, within each cell type (oligodendrocytes, neurons, microglia, and astrocytes), we identified genes showing differential expression with age and KEGG pathways enriched for differentially expressed genes. We found that the PFC, but not the cerebellum, shows a decrease in the proportion of neurons with age and many (>5000) genes that are differentially expressed with age. Astrocytes and microglia in both brain regions show several enriched pathways, whereas neurons in only the PFC show age-related functional enrichment. Moreover, several specifically neurodegenerative pathology-related KEGG pathways, including Alzheimer's disease and Parkinson's disease, are enriched in astrocytes in the PFC but not the cerebellum. In summary, we find greater evidence of age-related change in the chimpanzee PFC compared with the cerebellum, as well as greater neurodegenerative change, which is consistent with patterns observed in humans.

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Using µCT scans to assess R-L differences in tooth size for studies of fluctuating asymmetry

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Fluctuating dental asymmetry (FDA) refers to size differences in antimeres (right and left teeth of the same tooth type) that are random with respect to the side that is larger. The inconsistency of findings relating FDA to developmental stress may be a result of the high level of error (relative to right-minus left tooth size differences) involved in measurements taken with calipers at the outer enamel surface (OES). We hypothesized that measurements taken at the enamel-dentine junction (EDJ) on µCT scans would reduce measurement error when compared to measurements taken at the OES with calipers.

µCTs of deciduous upper second incisors from 10 individuals (20 total teeth) were made at Mass General Brigham at a resolution of 22µm. Using Dragonfly v.2022.2.0.1399 software, 2D virtual slices on mesio-distal and bucco-lingual axes were created. Mesio-distal and bucco-lingual EDJ maxima were taken on 2D virtual slices. For comparison, two caliper measures were taken at the OES: mesio-distal and bucco-lingual maximum. Average caliper OES measurement error was 0.14mm, while average EDJ µCT error was 0.107mm, a reduction in error of 0.033mm. The average difference of right-left EDJ measurements was 0.418mm. Thus, for µCT EDJ measurements, the magnitude of R-L differences was 3.9 times greater than measurement error.

This work suggests that µCT measurements at the EDJ can improve accuracy in FDA studies. Furthermore, measurements at the EDJ more directly reflect developmental events during crown morphogenesis than measurements at the OES, the latter of which are also affected by enamel thickness and surface wear.

Vole (Microtus guentheri) stable isotopes as proxies of MIS6 paleoenvironment: Implications for modern human and Neanderthals interactions in the southern Levant

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The environmental context of modern humans and Neanderthals in the Southern Levant has implications for understanding how these species interacted within a small geographic region with a sharp ecotone. In general, Neanderthals were believed to have inhabited cooler and more humid periods (MIS 6, MIS 4), while modern humans, were thought to occupy the warmer and dryer periods (MIS 5e). Previous studies have relied on rodent community structure as a means of reconstructing the environment. These studies found that the high abundance of voles indicated an open and dry environment. However, recent discoveries of Homo sapiens remains in Misliya Cave (ca. 200 - 170 ka) and micromammal community structure here pointed to a variable climate rather than a hot/dry or cold/humid one.

To further this discussion, stable isotope analyses of Microtus guentheri from Rantis (n = 9) and Hayonim E (n = 21) were conducted and compared to modern vole stable isotopes from across Israel (n = 39). Results suggest that Hayonim (d13C = -9.19 ± 1.70; d18O = 11.85 ± 14.33) and Rantis (d13C = -9.86 ± 0.25; d18O = 26.68 ± 0.24) were cooler and more humid than today (d13C = -15.47 ± 1.28; d18O = -1.38 ± 1.1). These results indicate that the climate and environment across the ecotone of the southern Levant were complex and that there was a more nuanced relationship between hominin species and preferred habitats. Moreover, it is necessary to look beyond community structure for a robust paleoecological indicator.

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Cute dogs bear the cost of dystocia: an analogy with the obstetrical dilemma in humans

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Dystocia, or "difficult birth", in humans is a global public health concern. The risk of dystocia can partly be explained by the evolutionary conflict in the pelvis between antagonistic selection related to bipedal locomotion and successfully giving birth to large-headed fetuses. Study of this 'obstetrical dilemma' has mostly centered around mediolateral width of the pelvic canal, although attention was originally on the shortening of the ilium during early hominin evolution. This reduction in hipbone length also reduced dorsoventral depth of the birth canal, yielding a tight fetopelvic fit. Nevertheless, the impact of reduced hipbone length on birth difficulties has scarcely been explored. The domestication and selection of dogs into highly disparate body sizes and shapes provides a natural experiment to test this. Based on all available data published between 1995 and 2023, we found a prevalence of dystocia of up to 26% in breeds selected for their "cuteness", specifically small body sizes and/or a short, broad face (e.g., certain bulldog, terrier or chihuahua breeds). About 15% of dystocic births could be directly related to a constricted bony birth canal and 8% to large puppy size, causing fetopelvic disproportion. Radiographic pelvimetry of 35 Scottish terriers and 55 Boston terriers showed that dystocic females had significantly shorter hipbones and reduced dorsoventral pelvic canal diameters relative to body size or pelvic width compared to normally whelping females, while transverse diameters were no different. This represents a remarkable analogy to the shortening of the hipbone and a concomitant tight fetopelvic fit in early hominins.

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To fight race science, double down on the genome: complex physiological and psychological phenotypes are determined by millions of regulatory interactions within the genome that are highly conserved in primates and universal in humans

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Human genetics, which has long investigated population history and structure using data on genetic differences, could exacerbate ethnic conflict by essentializing *phenotypic* population differences. A young white man who killed 10 Black people in 2022, for example, justified his murders by citing the human genetics literature. White nationalists use genetic ancestry tests to claim White bona fides, demonstrate the "purity" of Whites, and redefine genetic diversity to mean biological race. The emphasis of anthropologists and others on a concept of the genome characterized by admixture and drift is therefore understandable. An extensive review of recent research, however, supports a radically different conception of the genome: the biological (phenotypic) significance of highly conserved interactions *within* the genome vastly outweigh the biological significance of differences between genomes. Conserved interactions include: nucleotide interactions that determine the structures and activities of the 20k human proteins, only 16 of which are unique to humans; proteins and RNAs that bind specific sequences of DNA, RNA, and histones and other proteins to regulate gene expression; and cis-regulatory elements, 70% of which are conserved in primates. These interacting elements form conserved gene regulatory networks that determine hundreds of cell types as the zygote develops into an adult comprising 30 trillion cells, including over 100 billion brain cells. Like the musculoskeletal, circulatory, and immune systems, the genome should be conceptualized in teaching and research as an immensely complex, universal system of interacting elements profoundly involved in every aspect of biology and behavior that differs only trivially across human populations.

New fossil discoveries from Woranso-Mille and the status of *Australopithecus deyiremeda*

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The naming of *Australopithecus deyiremeda* based on dentognathic fossil remains from Woranso-Mille (Ethiopia), dated to 3.5–3.3 million years ago (Ma), provided further evidence supporting mid-Pliocene hominin diversity, and demonstrated that some early hominin species co-existed in close temporal and spatial proximity. However, the validity of this species has been questioned by some, mainly due to small sample size, and its similarity with *Australopithecus afarensis* in some primitive dentognathic features. Here, we present results from further comparative analysis of previously, and more recently, recovered dentognathic specimens from 3.6–3.3 Ma deposits at Woranso-Mille and test the validity of *Au. deyiremeda*. In addition to the isolated teeth previously recovered from the Burtele collection area (BRT) but not included in the hypodigm of *Au. deyiremeda* (n=7), we also included in our analysis newly discovered dentognathic specimens from BRT (n=8) and another nearby collection area (Badona Dululu (BDU); n=10). Our results from a detailed qualitative and comparative shape analysis confirm that *Au. deyiremeda* canines consistently lack prominent lingual relief, unlike *A. afarensis*; the P_3s have more oblique transverse ridge; and the occlusal outline of the P_4s is predominantly oval as in *Ar. ramidus* and some *Au. anamensis*. These findings suggest that *Au. deyiremeda* is demonstrably more primitive dentally than *Au. afarensis* and *Kenyanthropus platyops*. The proximity and stratigraphic context of the new specimens recovered from BRT also suggest that the partial foot (BRT-VP-2/73) probably belonged to the same species as the dentognathic remains from the locality, necessitating reassessment of the generic affinity of *Au. deyiremeda*.

Woranso-Mille project research was facilitated by permits from the Ethiopian Heritage Authority, the Afar Regional State, and financially supported by the National Science Foundation (BCS-1124705, BCS-1124713, BCS-1124716, and BCS-1125157).

Childhood stress explored through micro-enamel hypoplasia in two post-medieval Dutch populations of differing socioeconomic status

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Defects of dental enamel have been thoroughly explored as representations of stress during childhood. Micro-enamel hypoplasia allows for a more thorough investigation of childhood stress by assessing deviations in perikymata spacing (DPS) through microscopic analysis. This research presents an exploratory multi-tooth approach to the investigation of embodied childhood stress between two post-medieval Dutch populations of differing socioeconomic status (SES).

Mandibular canines and premolars were analysed from four high SES, and five low SES females, aged 20-35 at death. Widths of all visible perikymata were measured and counted, then fit to a quadratic trendline to find expected values. Residuals in the 90th percentile were identified as DPS. Differing frequencies of DPS events were identified per tooth type. The frequency of DPS was higher in the low SES individuals during canine development, yet higher in the high SES individuals during premolar development. Further, differences were found in the duration of stress events (i.e., consecutive affected perikymata). The high SES population had a higher frequency of long-term stress events, while the low SES population had more short-term stress events.

This research suggests that low SES populations were not experiencing an overall higher level of childhood stress than their high SES contemporaries. Rather, they experienced more frequent short periods of stress during canine development. However, this is complicated by the osteological paradox. For example, children of lower SES may not have survived more severe, long-duration illnesses that high SES children were buffered against, given access to medical care, nutritious food, and clean drinking water.

This research is part of the project "Embodied Inequality: Transforming Archaeological Knowledge of State Formation, Social Disparity, and Health Inequality" [VI. VIDI.201.153], which is financed by the Dutch Research Council (NWO).

Investigating skeletal stress and oral health among the working class in urbanizing Colombia: evidence from a cemetery in Bogotá

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The majority of the population of Colombia was rural until the mid-twentieth century. As Bogotá urbanized, working-class *bogotanos* experienced increased access to jobs, education, basic services, healthcare, and charitable aid alongside low wages, overcrowding, urban displacement, and disease. Meanwhile, rural farmers faced oppressive labor practices and displacement from large landowners and were largely without water, electricity, or sanitation. Further, two major civil conflicts at the turn of the century and midcentury were predominately fought in the countryside, creating additional pressure for people to leave for major cities.

To investigate the effects of urbanization on working class people from rural and urban backgrounds in Colombia, biogeochemical analyses of radiogenic strontium and stable oxygen from enamel were used to infer "local" versus "nonlocal" geographical origins of 119 adults in a skeletal sample excavated from Globo B of Cementerio Central in Bogotá, a section of the cemetery where people of low socioeconomic status were buried from the late nineteenth to mid-twentieth century. Skeletal indicators of stress (linear enamel hypoplasia, cribra orbitalia, porotic hyperostosis, and periosteal lesions) and oral health (dental caries and antemortem tooth loss) were then compared between local and nonlocal individuals. While there were no statistical differences in skeletal stress frequencies between locals and nonlocals, comparisons of oral health suggested that individuals who grew up in the city had higher dental attrition. The results of this study demonstrate how isotopic analysis can assist in the exploration of diverse experiences of urbanization within urban archaeological samples.

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Sr/Ca Ratios Indicate Dietary Categories of Early North American Primates

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Assessing contributions of frugivory and folivory to primate diets is critical across the evolutionary history of the primate clade. The rise of euprimates was almost certainly related to arboreality, but the debate over the relative importance of visual predation (insectivory) or coevolution with fruiting angiosperms continues. Dietary reconstructions of late-Paleocene, early-Eocene euprimates is highly variable and based primarily on morphology. Such adaptive proxies for diet are often confounded by phylogenetic issues, and non-adaptive reconstruction methods would be an important contribution to the paleontological toolkit. Studies in extant primates show frugivores have lower Sr/Ca ratios than folivores. It is unclear if such methods are transferable to samples spread across time and space. This pilot study presents trace element data gathered via non-destructive XRF measurements on early euprimates and plesiadapaformes from the collections at the University of Wyoming's Geology Museum including the genera *Microsyops, Cantius, Smilodectes, Notharctus, Teilhardina,* and *Tetonius*. Initial results show elevated Sr/Ca ratios in the likely-folivorous *Smilodectes* and *Notharctus* specimens compared to the likely-frugivorous *Cantius* specimens. However, Sr/Ca ratios of *Cantius* are not as low as the frugivorous *Hyracotherium*, and the likely-frugivorous *Microsyops* has ratios more similar to folivores than frugivores. Omnivorous *Teilhardina* and *Tetonius* have the most elevated Sr/Ca ratios, which could be consistent with insectivory, although modern analogous datasets are currently lacking. These findings are encouraging for future use of Sr/Ca ratios as a means of reconstructing diet even in complex datasets. Larger comparative modern samples and greater fossil samples sizes are necessary to resolve lingering questions.

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Morphological variation of the *Australopithecus afarensis* maxilla

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Central to discussions about hominin diversity in the mid Pliocene of eastern Africa is whether or not certain fossils should be attributed to *Australopithecus afarensis*, instead of representing *Kenyanthropus platyops* or *Australopithecus deyiremida* as separate species. Key to answering this question is a good understanding of the magnitude and pattern of morphological variation shown by *A. afarensis*. Maxillary characteristics are particularly important here, as these are at the heart of the species diagnoses of *K. platyops* and *A. deyiremeda*. We therefore explored maxillary variation among all nine available *A. afarensis* specimens. After CT-based virtual reconstruction, these were analyzed in the comparative context of 448 extant hominine maxillae, representing all currently recognized subspecies, large geographic areas, and both sexes. Maxillary morphology was captured by three-dimensional landmarks, and size and shape were examined using geometric morphometric methods. The main findings are that 1) *A. afarensis* has high degrees of size and shape variation compared with extant hominines, potentially linked with sexual dimorphism, 2) no allometry was found, despite the large size variation, 3) a temporal trend in maxillary size is suggested, but not in shape, and 4) the inferred patterns of sexual dimorphism in form and shape are different from those observed in *Homo sapiens*, *Pan*, and *Gorilla*. These results provide a greater understanding of *A. afarensis*, enable quantitative comparisons with contemporary maxillae attributed to *K. platyops*, *A. deyiremeda*, and *Australopithecus bahrelghazali*, and can help evaluate variation in other Plio-Pleistocene hominins, such as those assigned to species of early *Homo*.

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Capacity building in aid of long-tailed macaque conservation

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In 2021, we initiated the Long-Tailed Macaque Project (LTMP) (*Macaca fascicularis*). The increase in challenges to the species due to its synanthropic abilities and use in biomedical research required fast and efficient conservation initiatives. Long-tailed macaques fill many crucial ecological and cultural roles, having coexisted with humans for millennia, co- creating and co-shaping ecosystems and cultures. LTMP focuses on 1) understanding long-tailed macaque ecology, behavior and population dynamics through collection, analysis, and dissemination of scientific data, 2) collaborative work with researchers and practitioners across the world, 3) evidence-based conservation and coexistence measures locally and globally, 4) mediation of the above through habitat country researchers, NGOs, communities and management agencies taking a place-based capacity building approach to conservation.

LTMP now includes more than 150 individuals and institutions from more than 20 countries, including 13 LTM habitat countries. Our accomplishments include documenting the extirpation of LTMs in Bangladesh, finding only 600 individuals in Laos, and conducting surveys in Cambodia and Vietnam, which will soon be published. Our results informed the 2022 uplisting of the species to EN on the IUCN Red List. We also assessed all nine LTM subspecies, whereof six went from DD to EN or CR. We have published two peer-reviewed papers and are working on several more, for example, a Population Viability Analysis in collaboration with the IUCN SSC CPSG. In this poster we will present an up-to-date overview of the project data and outcome as of March 2024.

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Linking Bone Microstructure to Skeletal Trauma Analysis and Interpretation in the Tibia

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Tibia fracture characteristics (number, type, and group) have demonstrated variation in controlled experimental loading conditions. These results indicate that tibiae respond differently even in the same blunt force trauma event. Previous research has demonstrated this variation cannot be explained by individual (age, sex) or global bone (length, width) characteristics alone. The purpose of this research is to demonstrate how bone microstructure contributes to variation in fracture characteristics in the same skeletal element under the same loading scenario. Additionally, this research highlights the value of incorporating multi-scale methodologies in skeletal trauma analysis.

Fourteen human tibiae were experimentally loaded in a controlled lateral-medial bending scenario at 5 m/s. Resulting fractures were analyzed using the AO/OTA Fracture and Dislocation Classification Compendium. Observed fractures were classified as simple (n = 3), wedge (n = 8), or multifragmentary (n = 3). Cortical pores were morphometrically characterized on a histological cross-section at the 66% site using a custom ImageJ macro, Pore Extractor 2D. Compared to simple and wedge fractures, multifragmentary fractures had lower mean porosity and smaller mean pore size in all quadrants, and a higher pore density in the posterior quadrant. Larger, more convergent pore systems, concentrated posteriorly, may contribute to less complex fractures in this loading scenario.

Skeletal trauma interpretation relies on a thorough understanding of how bones respond to loading. Therefore, it is critical to ascertain the contributions of hierarchical variables (individual, global bone, bone microstructure) to allow for a more complete analysis to support accurate interpretations.

Introducing an “Indigenous-Life-History” approach: Supporting informed and informative bioarchaeology

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Bioarchaeologists have worked towards developing programs of academic decolonization by employing activist frameworks to reduce continued harms on marginalized communities. This project presents demographic data from IRB-approved surveys and interviews conducted among students and faculty of an anthropology department at a public research university. Data from fifty-one participants demonstrates the increasing awareness of the necessity for repatriation and collaborative relationships between Western-institution scholars and Indigenous communities and the need to continue developing undergraduate education about repatriation, Indigenous knowledge and history, and decolonizing methodologies within anthropology programs in the United States. To formulate a culmination of myriad theories and hybridized methods, the framework of Indigenous-life-history is proposed. This approach to bioarchaeology acknowledges the past failures and violences of the discipline and explores topics of concern directed by the research questions and restrictions provided by descendant collaborators. Indigenous-life-history makes it a priority to perform bioarchaeology as a deeply informed and involved science which practices respect towards Ancestors and their relations, whether this be through data-producing research or projects of repatriation. Synthesized activist motivations, intersectional frameworks, integrated bioarchaeological models, and collaboration with descendant communities are premises to Indigenous-life-history and the work it accomplishes. By reorienting research to consider repatriation and restitution of Indigenous life and land as the “discussion and conclusion” of scientific pursuits, this model can develop innovative project designs, methods, engagements, communication, and collaborative relationships that do not perpetuate frameworks established by modes of colonization. Through Indigenous-life-history, it is hoped bioarchaeology can narrate informed, informative histories and create new activist legacies.

Calcaneal trabecular structure in *Pan* and *Gorilla*

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While studies have investigated relationships between calcaneal trabecular structure and mechanical loading in bipedal humans, quadrupedal and climbing African apes have not been examined. Thus, there is limited available comparative context to fully understand trabecular bone functional adaptation in the human foot and among closely related extant and extinct taxa. Here we analyze whole-bone calcaneal trabecular variation among *Pan* (n=16) and *Gorilla* (n=22) as they differ in degree of arboreality and adopt variable foot postures during locomotion.

Calcanei were µCT scanned (30-53µm) and subjected to a three-dimensional geometric morphometric (3DGM) sliding semilandmark analysis. The 3DGM outputs were used to position 156 spherical volumes of interest (VOI). Bone volume fraction (BV/TV), trabecular spacing (Tb.Sp), and trabecular thickness (Tb.Th) were calculated using the BoneJ plugin for ImageJ and MATLAB. Non-parametric MANOVAs were run on all VOI results for each property. Parameter distributions were visualized using color maps and summarized using principal components analysis.

Pan significantly differs from *Gorilla* in whole-bone BV/TV, Tb.Sp, and Tb.Th ($p<0.002$ for all analyses). *Pan* exhibits relatively more Tb.Sp throughout the calcaneus and relatively higher Tb.Th in the calcaneal tuberosity than *Gorilla*. *Gorilla* exhibits relatively higher BV/TV and Tb.Th in the anterior calcaneus relative to the posterior calcaneus; this regional differentiation is not observed in *Pan*. The anterior-posterior gradation in *Gorilla* likely reflects a consistent loading pattern in these highly terrestrial apes, whereas the more evenly distributed pattern in the *Pan* calcaneus may be an adaptation for more variable foot positioning as a consequence of greater arboreality.

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Women of the North: A biocultural analysis of identity and social roles in the Arctic and Subarctic

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Synthesizing multiple datasets, we critically analyzed the roles that women held in society and the activities that they performed for their communities in the Arctic and Subarctic. Using a biocultural approach, we reinterpreted data collected from human skeletal remains of Indigenous people in Alaska, including the Iñupiat, Unangan, and Yup’ik cultures. The remains we analyzed included contract reports on isolated or scattered remains by Harrod, and numerus previously published articles on remains taken from Alaskan communities and housed for decades at the American Museum of Natural History or the National Museum of Natural History. There are hundreds of individuals at the museums, but since data was collected by different researchers, the number of individuals included in each report varies by research question. The biological data we assessed included body size estimates (robusticity and stature), pathological conditions (cribra orbitalia, enamel hypoplasia, non-specific infection, porotic hyperostosis, and traumatic injuries), and changes in dentition (chipping and wear). Cultural data we assessed included ethnohistorical records, oral traditions, contemporary accounts, and communication with Indigenous collaborators. Prior bioarchaeological work by Temple and colleagues analyzing robusticity found that strict sexual divisions of labor were not universal. Our reassessment of all the biological data supports what they found, and the cultural data provides context for why differences between the genders exist. The value of reassessing the decades of data published on the remains in museums is that we were able to weave in local Indigenous perspectives that provided context for the gender fluidity in women's roles and activities.

N/A

Comparative Reproductive Patterns and Seasonality Between Subspecies of Captive Rhesus Macaques (*Macaca mulatta*)

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Other than humans, rhesus macaques (*Macaca mulatta*) are the most dispersed primate species resulting in two main subgroups: Indian-derived from the west and Chinese-derived from the east. This divergence is estimated to have occurred 162,000 years ago. Since then, demographic models have suggested that the Chinese population expanded while the Indian population maintained its ancestral size. This study aims to compare the demographic patterns of these subgroups to identify trends that could explain this difference in population growth. Our study analyzed the breeding colony records from Tulane National Primate Research Center (Covington, LA) of 1136 Indian-derived and 324 Chinese-derived females between 2005 and 2019 and compared them to a previous study of three generations. We calculated crude birth rates (CBR), interbirth intervals (IBI), and seasonality based on circular statistics. We found that the Indian-derived population had significantly more infants per female (Cohen's $d = 0.169$; $p = 0.01$) and a higher average CBR (Cohen's $d = 1.34$; $p < 0.01$). However, the IBI was not significantly different ($p = 0.326$), but the Indian population continued fertility through age 20 while the Chinese population stopped at age 16. Interestingly, we found that the Chinese-derived population had significantly stricter seasonality than the Indian-derived population ($R = 0.819$ vs $R = 0.766$; $p < 0.001$). Our results show that Indian-derived rhesus macaques in this population have consistently higher population growth than the Chinese-derived indicating that the growth differences measured in wild populations cannot be explained alone by the parameters analyzed in this study.

DiceCT: an anatomical visualization method never used by Matt Cartmill, but that closely follows his fundamental teachings

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While Matt Cartmill established much of our field's foundational content, arguably, his deeper impact was imparting many fundamental theoretical rules about how we should approach our work. Some of these rules were formally codified: for instance, his work with Rich Kay codifying "the comparative method" that so many of us use for functional interpretation of our fossils. Even more importantly, Professor Cartmill imparted to his mentees many other subtle fundamental principles that guide our research today. Although he has never conducted studies using diffusible, iodine-based contrast-enhanced computed tomography (DiceCT), our work with it follows two of the many Cartmillian precepts: 1) Anatomical description almost always benefits from visualization, preferably including animation if it adds value. 2) Elaborate techniques should be avoided when questions can be answered as well using simpler approaches, and if elaborate techniques *are* used, they must impart a deeper understanding of the subject than would the simpler approaches. To this end, our use of DiceCT has given us deeper insight (literally and figuratively) into the myology of primates – allowing us to see fascicular structures in three-dimensions, yielding not only more thorough visualizations than are possible with the traditional dissection and cross-sectional analysis that Professor Cartmill taught so well, but also to be able to measure variables (namely fascicle compression and 3D angles) heretofore not previously measurable. This is but one example of how Professor Cartmill launched generations of anatomists to both study and teach beyond even his own methods in ways that enrich our understanding anatomy.

The role of the Eastern Mediterranean in human evolution: Recent results from Greece

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The Eastern Mediterranean region lies directly on the principal migration route through which past human groups dispersed across Africa, Europe and Asia. It also encompasses one of the major southern peninsulae of the European continent, the Balkans, where fauna and flora, as well as hominin populations, are thought to have persisted through the Pleistocene glacial periods. Based on this geographic position, the region's paleoanthropological record would be expected to be among the longest and most continuous, but also highly diverse, reflecting the complex processes of late survivals, new arrivals and, potentially, contact between different groups. While the record from the Near East meets these expectations, little evidence exists to support these ideas in other parts of the Easter Mediterranean. Indeed it is common for maps of Paleolithic Europe to indicate population dispersals as arrows that either entirely bypass or 'fly over' much of the southern Balkans. Here I present new evidence from our work over the last ten years in Greece, both in the laboratory and in the field. These new data highlight the regions' importance as both dispersal corridor and glacial refugium for human populations. Results strongly suggest that the paucity of currently available data is due to lack of research, and highlight the potential of the record to shed further light on the complex processes underlying human evolution and dispersals.

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Sensitivity of musculoskeletal models to changes in pelvic tilt

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Pelvic tilt (PT)—the orientation of the pelvis in the sagittal plane—is critical to maintaining the stability of the trunk on the lower limb in bipedal walking, but measuring PT in living humans is difficult. Recently, musculoskeletal modeling has become an important tool for studying evolutionary biomechanics, and ensuring that participants' anatomical and locomotory characteristics reflect reality is a critical modeling component. We aim to evaluate the sensitivity of musculoskeletal modeling to variation in estimates of PT.

We used previously collected kinematic and kinetic data from a single individual (male, 1.77m stature, 87.2kg mass) walking at their normal velocity and inverse dynamics to determine muscle and joint reaction forces (JRF) using an established musculoskeletal model (AnyBody Managed Model Repository AMMR v2.4.2). We established neutral pelvic orientation (0°) and created trials with altered PT ranging from -20°

(posterior tilt) to 20° (anterior tilt) in 10° increments. The trials were identical, excluding PT. When PT differed from neutral by 20°, the average changes in muscle forces were as much as -7.5%, 7.8%, 125%, 3.0%, and -12.1% in gluteus minimus, gluteus medius, gluteus maximus, gastrocnemius, and soleus, respectively. Changes in JRF were as much as 42.0% (x-axis), 82.7% (y-axis), and 19.5% (z-axis) in the hip, -15.1, 27.6%, and 11.0% in the knee, and 12.7%, -40.2%, and -8.9% in the ankle. These data suggest that PT influences JRF and muscle forces. Future research will include more participants.

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Feet apart: Using spatial analysis to model matches of commingled elements in a mass grave

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Establishing the number of individuals and which elements belong to which individual in a mass grave is a long-established challenge in anthropological research. Approaches that utilise DNA matching, a minimum number of skeletal elements (MNI), elemental matching, or anthropological expertise can have varying levels of success depending on depositional and taphonomic factors. In order to expand the toolkit available to correctly identify skeletal elements within a mass grave belonging to the same individual a novel spatial analytical approach to element matching is deployed within a mass grave of primary interments from Early Bronze Age Mesopotamia at the archaeological site of Başur Höyük. Within the mass grave 4,474 disarticulated skeletal elements were collected in 50cm grid squares alongside 143 individual clusters of articulated remains that were precisely geolocated. The distance between all individual elements of the skeleton was calculated to determine elements that, while potentially belonging to a pair, could not belong to the same individual because of their spatial position. This increased MNI calculated from all skeletal elements, allowing for increased accuracy in identifying the number of individuals interred and for a predictive spatial analysis model to be established.

Comparative analysis: Dentin, auditory ossicles, and petrous portion sampling for ancient human DNA

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Sampling ancient DNA (aDNA) from skeletal elements beyond the dentition in human remains is a new area of research. Historically, aDNA sampling has focused on dentin but scholars have recently begun examining other human skeletal elements that may be optimal for endogenous aDNA preservation, such as the petrous portion and auditory ossicles. However, many studies have been performed in ancient samples from Europe and few stem from sub-tropical locations (Hansen et al., 2017). This study addresses this gap in scholarship by comparing endogenous aDNA preservation in three skeletal elements (petrous portion, auditory ossicle, and dentin) from the same individual originating from a historic context in Palm Beach County, Florida. We sampled the skeletal elements in a clean lab, extracted DNA via a silica-based method, prepared both single and double stranded sequencing libraries, and performed shotgun Illumina sequencing. Preliminary analyses found that the ossicle was the best performing element, yielding nearly 1.5 times more reads that mapped to the human genome than the petrous portion and nearly 80 times more than the dentin. However, the dentin yielded over 5 times greater coverage of the mitochondrial genome and was the only sample to provide sufficient coverage for a preliminary haplogroup assignment of an L3 lineage. Previous scholarship on this topic has found similar results with both cranial elements yielding significantly more endogenous aDNA than the dentin (Sirak et al., 2017). Understanding this variation that exists between skeletal elements is a necessary step in optimizing protocols for sampling aDNA.

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Expanding assemblages of early Pleistocene hominin footprints at Koobi Fora, Kenya

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In 1978, a ~1.4 Ma hominin trackway was discovered alongside other animal footprints at site GaJi10 in Area 103 of the Koobi Fora Formation. This marked the first discovery of fossil footprints in the Turkana Basin of northern Kenya. In 2016 that excavation was expanded, and in 2023 we reopened it for further analysis. On the expanded surface are 16 additional hominin footprints, attributed to as many as seven more hominin individuals, and over 170 tracks of other animals. The hominin tracks are morphologically similar to others uncovered recently from another, slightly older site in Area 103, and distinct in important ways from modern human footprints and from some of the ~1.5 Ma tracks recorded at sites near Ileret. The overall footprint assemblage includes many taxa observed at other sites, as well as unique taxa. The expanded GaJi10 track assemblage offers an improved snapshot of hominin anatomy and locomotion, and of the animal community that lived in the immediate vicinity at ~1.4 Ma. Our renewed geological and sedimentological research also revealed new insights into the paleoenvironmental contexts of this site and others in Area 103. We documented an unexpectedly vast spatial extent of multiple footprint layers, spanning nearly 1.3 by 1.2 kilometers. All track-bearing surfaces occur in shallow, sub-aqueous lake margin environments, in transgressive or regressive sequences. This provides new data not only on the types of sedimentary deposits likely to preserve fossil footprints, but also indicates lake margin environments that were apparently attractive to multiple Plio-Pleistocene hominin species.

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The mismeasure of recent human endocranial volumes

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Recent studies have suggested that human populations in many parts of the world underwent reductions in endocranial volume (ECV) during the last 50,000 years. Changes in climate, social organization, and technology have all been proposed as explanations for this pattern. However, all analyses have relied mostly on a few secondary sources to assemble their ECV datasets, with little variation across studies. I undertook a survey of primary sources of ECV estimates used in published work. This survey revealed several important biases in recent datasets. Secondary sources from the 1950s through the 1990s omitted many well-preserved specimens that had been reported in primary sources. These omissions were not random: smaller endocranial volume estimates from primary sources were less often included in secondary sources ($p<0.01$). In the most extreme case, the site of Ofnet, Germany, only two of the three largest ECV estimates are included in recent datasets, excluding 11 smaller estimates, thereby inflating the sample average by more than 200 ml. In addition to these omissions, secondary sources generally failed to report the estimation method, thereby introducing systematic biases in comparison of samples from different time periods. Meanwhile many samples from the period between 50,000 and 6000 years ago are excluded from recent studies with no justification. I discuss the effects of these biases on recent research, and report an alternative dataset with consistent sample inclusion. These results challenge the interpretation of recent selection for smaller ECV in human populations.

Caught in the middle: Variation in the physical and behavioral development of male olive baboons (*Papio anubis*)

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Male baboons mature more slowly than females, reaching full adult maturity at around 10-12 years of age. After the onset of puberty at 5-7 years, the sub-adult period lasts 3-5 years while the male continues to grow, though there is considerable variation between individuals. Here, we present data on the behavioral changes that accompany the physical maturation of male olive baboons (*Papio anubis*) as they transition through each developmental stage. This research was conducted on a fully habituated wild troop at the Uaso Ngiro Baboon Project in Laikipia, Kenya. We use long-term grooming data (2018-2023) to show that males have significantly more grooming partners as they get older (n=48, p<.001). We then use behavioral data collected in June and July 2023 to compare the social behaviors of males from three developmental stages: juveniles (n=5), males who recently became sub-adults (n=4), and males who have been sub-adults for over a year (n=5). The differences between these three groups show the effect of puberty on behavior: juveniles were observed in social play significantly more often than sub-adults (p=.006), while males who recently underwent puberty tended to groom less often than either juveniles or older sub-adults (p=.091). Our focal data also revealed variation in the age at which males reached each developmental stage. Further research is needed to determine causes and consequences of the variation in age at puberty and the potential long-term consequences of this variation on the males' social behavior.

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Spina bifida occulta within the Archaic Greek cemetery of Phaleron

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This study reports the prevalence and demographic patterning of sacral spina bifida occulta (SBO) within the Archaic Greek Cemetery of Phaleron (700-480 BCE). Phaleron is among the largest Archaic Greek cemeteries, containing a variety of burial types including jars, pits, and "atypical" burials. While spina bifida occulta is a commonly reported developmental defect, little information exists from Archaic Greece.

Of the 382 burials currently analyzed, 105 individuals have sacra observable for sacral spina bifida occulta. Here a sacrum is considered observable if the posterior aspects of S1-S3 are present. Of 105 individuals, five exhibit various forms of sacral spina bifida occulta. Four of the individuals are classified as young adult (18-35 years) males, while the other is classified as an adolescent (14-18 years).

A case study of individual IV_683 is presented. IV_683's age-at-death is estimated to be between 14 to 18 years, based on a combination of dental development and epiphyseal fusion. A sex estimation was not conducted due to the young age of the individual. IV_683 exhibits a cleft fifth lumbar vertebra and complete sacral spina bifida occulta (S1-S5). Within Archaic Greece spina bifida occulta would not have been readily diagnosed. Athough this condition apparently was not the primary cause of death, it may have helped place this adolescent at risk of early death.

Phaleron Bioarchaeological Project. Project is supported by the Wiener Laboratory of the American School of Classical Studies in Athens and the Malcolm H. Wiener Foundation.

The Brain Is Not the Most Energetically Expensive Organ

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The brain is commonly believed to require 20% of an individual's daily energy budget; this figure has been cited as an energetic constraint in multiple hypotheses for relative brain size evolution not just in primates, but also multiple vertebrate taxa. This figure is based on estimates of the oxidative component of the resting energy expenditure of a 1350g brain in a 65kg human male. Intraspecific variation in energetic requirements of other high metabolic rate organs, such as the heart, kidney, and liver as well as the interspecific variation in these organs in primates or other taxa remains unaccounted for. I address this gap using comparative data on body, brain, heart, kidney, and liver masses collected from the same individuals as well as mass- and organ-specific metabolic rates to allometrically model the proportional and total organ-specific resting energy requirements in non-human primates and other mammals. Most mammal brains, including primates, require modest proportions of scaled resting energy expenditures, especially compared to the liver, which can be twice as 'expensive' as the brain. Comparisons with published data on daily total energy expenditure in primates demonstrates that brains require a small fraction of the total energy budget regardless of daily activity, while the energy required by other organs can vary widely depending on daily activity. For example, on a day the liver processes excess calories, the liver will require more energy, while the brain will require the roughly identical amount of energy as any other day.

Cosmopolitan Herculaneum? A multi-isotope study of the victims of Mt. Vesuvius (79 CE)

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During the late Roman Republic and early Empire, the Bay of Naples was a popular vacation destination with cosmopolitan cities such as Herculaneum. Despite an earthquake in 62 CE, Herculaneum maintained its popularity, evidenced by rebuilding efforts throughout the city. This all ended abruptly when Mount Vesuvius erupted in 79 CE, destroying the entire region. Hundreds of people managed to evacuate, but hundreds remained when the first pyroclastic surge hit, destroying everything in its wake.

Several teams of researchers have studied the individual remains recovered from Herculaneum and have described them in great detail. In this study, we present a multi-isotopic analysis to parse out locals and non-locals to the region using radiogenic 'heavy' isotope ratios of strontium (Sr) and lead (Pb) and oxygen (light) isotopes in tooth enamel of third molars. Radiogenic isotopes derive from bedrock with plant foods and local waters broadly consistent, although there are complications with anthropogenic lead. For example, evidence shows lead contamination in water due to lead pipes commonly used throughout the Roman Empire.

We know where/how these individuals died, but this study allows us to explore the heterogeneity of the region. The strontium isotopes (87Sr/86Sr) have an observed range from 0.7079 to 0.7094 and an average value of 0.7085 (±0.0003). Lead isotope averages for 208Pb/204Pb are 38.67

(±0.062), for 207Pb/204Pb are 15.65 (±0.005), and for 206Pb/204Pb are 18.52 (±0.057). The values are similar to those identified in a number of Roman isoscapes, and descriptive statistics underscore the notion of a cosmopolitan Herculaneum.

Back to the “cyrtodonty” in Upper Pleistocene hominin teeth: evidence from the Arcy-sur-Cure Neandertals

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Discussed since the early XXth century (e.g. Patte, 1962), "cyrtodonty" refers to the convexity of the buccal tooth profile in permanent lower/upper incisors, canines and premolars. This distinctive morphology is mostly described as functional (e.g. Brace, 1967), rather than arising from neutral selection or developmental constraints. Intriguingly, the term “cyrtodonty”, sparsely mentioned for Neanderthal fossils (Maureille et al., 2008; Garralda et al., 2023), is disregarded in the literature and absent from scoring protocols.

We focused on defining this specific qualifier using Neanderthal teeth (isolated and in dental arcades) from the Arcy-sur-Cure caves (Yonne, France). We examined 15 isolated teeth, of which 86% exhibited cyrtodonty.

To systematically describe this characteristic, we introduce a basic grading system, categorizing it into three levels: (0) Absence – no convexity on the buccal tooth profile; (1) Mild expression – slight convexity of the profile, with a bending of the apical structures (especially the distal mid sections of the root); (2) Pronounced expression – the tooth profile exhibits a regular and important convexity. These expressions have to be discussed with the potential development of hypercementosis at the apex of the teeth. Furthermore, our study revealed variations in cyrtodonty expression based on dental rank in the maxilla and mandible of Arcy.

Documenting cyrtodonty holds importance to evaluate its phylogenetic and/or biomecanic significance, particularly for the Neandertal lineage, among which we observed it more frequently than among Archaic Upper Pleistocene human taxa according to the published dental records (e.g. *H. erectus* from Zhoukoudian; archaic Modern Humans from Qafzeh).

The project is founded by a CNRS MITI PhD grant (Juliette Henrion) and the Région nouvelle Aquitaine (project ADNER, dir. Priscilla Bayle).

Gastrointestinal parasitism in capuchin monkeys: Effects of individual, social, and environmental factors in patterns of parasitic infection in a wild population

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Parasitic infectious diseases play a significant role in the evolution of primate sociality and continue to threaten wild populations today, especially as anthropogenic pressures increase. The complex diet, social behaviors, and parasite communities of white-faced capuchins (*Cebus imitator*) make them ideal models in which to examine principles of parasitology, namely the role of individual, social, and environmental characteristics in shaping patterns of parasite infection in host populations. We used morphological and molecular methods to study the diversity, prevalence, and infection patterns of gastrointestinal parasites in a wild population of white-faced capuchins at the Sector Santa Rosa field site, Área de Conservación Guanacaste (ACG), Costa Rica. We morphologically identified 9 parasitic morphotypes in our samples, including lungworms (*Filariopsis sp.*), threadworms (*Strongyloides sp.*), tapeworms (*Hymenolepsis sp.*), and others. Molecular identification of these parasites using the ITS-2 genetic marker revealed close genetic matches to heartworms, cyst-forming plant-parasitic nematodes, and other parasites of capuchins and their prey items. We found that host age affected our two most prevalent parasites differently, with younger individuals shedding fewer *Filariopsis sp.* larvae per fecal gram but more *Strongyloides sp.* eggs per fecal gram compared to adults. One capuchin social group had lower infection intensities than the other four, and the distance of a group’s home range from human-disturbed areas had a modest positive effect on parasite infection prevalence and parasites per fecal gram. This study’s multi-faceted and holistic approach reveals the complexity of host-parasite relationships and highlights the importance of studying entire parasite communities in primate epidemiology.

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Stature, frailty, and mortality in working class Americans: Evidence for structural racism

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This study analyzed mortality rates among adults identified as Black/African American and White/European American of low socioeconomic status from the Hamann-Todd Collection, to detangle the influence of racism, poverty, and sex-based bias. Because preexisting health conditions affect mortality risk, femur and fibula lengths were used to examine whether individuals who underwent increased stress during growth also experienced earlier mortality, i.e., selective mortality.

Survivorship and mortality were estimated with Kaplan-Meier analyses. Log rank tests indicated significant differences between the survivorship curves from all-cause mortality between racial/ethnic groups, indicating individuals identified as Black/African American suffered significantly higher mortality, but no sex differences within racial/ethnic groups. Logistic regression models tested for the effects of age-at-death, a variable of combined sex and race/ethnicity, and birthdate (categorized as Antebellum, Reconstruction, and Great Migration) on the outcome of bone length. Age and birthdate were not significant, suggesting there was no relationship between stunted stature and age-at-death (i.e., no selective mortality), which also did not change over time. However, odds ratios showed significant differences in prevalence between individuals identified as White/European American (22-33%) and Black/African American (5-7%), which is consistent with the literature that fewer people identifying as Black/African American were surviving to adulthood.

While all individuals in the collection suffered poverty and marginalization, the analyses show outcomes were significantly worse for individuals identified as Black/African American. The effects of systematic racism resulting in further socioeconomic marginalization significantly affected the health and mortality in the Black/African American community.

Early herders of Inner Asia

TAYLOR HERMES

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The Afanasievo culture in the Altai Mountains (ca. 3300-2800 BCE) has long represented the first herders to spread to Inner Asia and the spark for widespread subsistence transformations towards dairy pastoralism throughout the steppes. Despite its standing, the Afanasievo culture is known almost exclusively from mortuary contexts, giving an important record of paleogenomic, osteological, and material cultural data but lacking crucial subsistence and ecological information. This paper presents the results of research at the only known Afanasievo habitation site, Nizhnyaya Sooru. Though zooarchaeology, ZooMS, faunal stable isotope analysis, paleoethnobotany, human and animal paleogenomics, and radiocarbon dating, this paper documents adaptation to new community and environmental pressures in the Altai and critically fills long-standing gaps in the biosocial story of the first herders of Inner Asia.

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Recent biological distance assessments of the Green River Archaic burial sample from 15OH2

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The Green River Archaic period skeletal collections represent one of the largest regionally specific aggregate hunter-gatherer burial samples. These collections have been the focus of numerous studies on paleopathology, paleodemography, and biological distance. Indian Knoll, 15OH2, is the largest collection with over 1000 individuals spanning at least a 1200-year burial window. This study details the results of a biological distance assessment of a subset of the 15OH2 burial sample (n=319) using recent inter-individual Gower and Mahalanobis distance methods to discern any biological relationships within the burial population. A series of 42 traits were selected for analysis including 20 dichotomized cranial non-metric and 22 cranial metric traits from adult individuals. The cranial non-metric traits were collected by the first author and the metric data were obtained from Snow's 1948 osteological report. Mahalanobis-type D^2 and Gower distances are calculated following methods presented by Rathmann and colleagues (2019 and 2023). Distances are assessed relative to two spatial subsets of the burial sample (one by depth and one by site quadrant). In both analyses, distance to centroid measures by sample subset exhibit similar distributions. Permutation tests of the average and dispersions of the distance to centroid between subsets are not significantly different. The results are consistent with prior assessments of the 15OH2 burial sample as being derived from a morphologically homogenous population which has implications for the extensive Green River Archaic burial samples and interactions of Archaic populations across the southeastern US.

Malaria Mortality Favors Patriliny

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Demography likely constrains social and political organization. Moreover, infectious disease mortality has been, and remains, an important factor in demographic patterns across space and time. Malaria in particular has been shown to have substantial effects on both genetic and cultural evolution in high-endemicity areas. Ellison (1994) showed that patrilineal social organization is favored when male variance in reproductive success exceeds female variance, as agnatic lineages become shallower and more closely related. Based on the Standard Cross-Cultural Sample, patrilineal social organization is historically substantially more common than expected in Sub-Saharan Africa, a region where malaria is endemic. We hypothesize that the high, sex-biased mortality arising from endemic malaria results in shallower, more closely-related agnatic lineages and favors patrilineal social organization. To test this hypothesis, we employ demographic microsimulation (rsocsim), using malaria-calibrated mortality schedules and a variety of fertility schedules and marriage rules. Overall, patrilineal kinship resources are considerably higher than matrilineal kin in the malaria mortality condition. However, the asymmetry in kinship resources is sensitive to both the prevalence of polygynous unions and the overall rate of increase of the population. These results suggest that– to the extent that the size of coalitions is representative of power– the pattern of mortality characteristic to regions with endemic malaria favors patrilineal social organizations.

A fossil galagid from the middle Miocene of Napudet, northern Kenya

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Relationships among extinct lorisiforms are poorly understood compared to those among the living taxa, due in part to a paucity of middle to late Miocene fossils in Africa. Here, the taxonomic and morphologic affinities of a lorisiform mandible preserving the lower third molar from the middle Miocene (~13 Ma) of Napudet are assessed. Lower dentitions from a comparative sample of extant lorisiforms (10+ species), and several extinct Miocene lorisiforms (*Komba, Progalago,* and *Mioeuoticus*), were segmented from 3-D data available from Morphosource and scans of the original fossils, respectively. Scan surfaces were aligned and autolandmarked with a set of 1,024 correspondence coordinates using the auto3dgm algorithm. Variance in shape space was visualized using principal components (PC) analyses and heatmaps of minimum-maximum PC1 and PC2 scores. The m3 of the Napudet specimen differs from the crown galagid morphotype in its completely enclosed trigonid basin with both a well-developed paracristid and premetacristid, the latter of which ascends the metaconid, and in having a relatively gradual inclination of the postvallid shearing surface, with a protocristid that is strongly oblique relative to the tooth's long axis. Compared to extinct taxa, the Napudet specimen is most similar to the holotype of the early Miocene galagid *Komba walkeri* from Mfwangano, Kenya. This latter observation is confirmed by its close position to *Komba* in the PCA morphospace. The Napudet specimen is best interpreted as a late-surviving stem galagid. Analyses of m2s from other fossils will also be presented to help clarify relationships among Miocene lorisiform taxa.

The Simons Foundation

Hominid Taxonomy in the Omo, Ethiopia: New fossils and new analytical approaches for isolated teeth

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Sediments exposed by the Omo River produce an abundant fossil record of 1 to 3 million-year-old terrestrial faunas, when the genus *Homo* first evolved and the eastern African robust hominids first appear. The Omo Group Research Expedition (OGRE)'s fieldwork since 2006 has recovered dozens of new isolated dental specimens that add to those already known.

In order to infer taxonomic identifications, we developed a four-pronged approach based on the external crown morphology of postcanine teeth. First, we ran linear discriminant analyses of linear crown dimensions on a comparative dataset of 534 hominid teeth (with well-established taxonomic identifications) that were then used to predict the classification of 108 complete crowns from the Omo. For the second and third components, we ran a cluster analysis on the morphological scores and on the 2-dimensional cusp areas for these same teeth. The fourth part of our approach compared the three quantitative methods to reach a final decision on taxonomic identification.

Our results reveal a significant amount of overlap in size and morphology between the isolated post-canine teeth of *Australopithecus afarensis* and *Homo habilis*. This *A. afarensis*/*H. habilis* group dominates the dental assemblage in the earliest part of the Omo stratigraphic sequence, with the robust lineage gradually increasing in proportion. By 2.27 million years ago, we see clear evidence of teeth from genus *Homo* alongside those from the robust lineage. Near the top of the sequence, between 1.38 and 1.05 million years ago, we only find isolated teeth of *Homo*.

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The use of pose-estimation and large language models in decoding great ape communication

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Studying animal behaviour allows us to understand how different species and individuals navigate their physical and social worlds. Coding of video and audio behavioural recordings is a gold standard: allowing researchers to extract rich nuanced datasets, validate their reliability, and for research to be replicated. However, in practice, recordings are only useful if data can be efficiently extracted. Manually locating relevant signals in 10,000s of hours is extremely time-consuming, as is the manual coding of animal behaviour, which requires extensive training to achieve reliability. Machine learning approaches are used to automate pattern recognition, considerably reducing the time to extract data and improving reliability.. Tracking visual information to recognise nuanced behaviour is a challenging problem and, to date, the tracking and pose-estimation tools used to detect behaviour are typically applied where the visual environment is highly controlled. Animal behaviour researchers are interested in applying these tools to the study of wild animals, but it is not clear to what extent doing so is currently possible. In contrast, the automated detection and description of the audible features of vocalizations is well established. However, the recent application of large language models in speech decoding offers an interesting novel application of machine learning approaches to exploring meaning in nonhuman primates. I will describe preliminary findings from i) two pose-estimation models for tracking facial and whole-body movements in hand-held video of wild apes, and ii) a sentiment analysis of speech-to-text translation based on the use of chimpanzee vocalizations.

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Interdigit Variation in Proximal Phalangeal Curvature and Metacarpophalangeal Joint Dorsal Canting in *Homo sapiens, Pan paniscus, and Macaca mulatta*

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Paleoanthropologists have a long history of quantifying phalangeal morphology to help reconstruct locomotor behaviors of extinct primates. Higher degree of longitudinal curvature in the proximal manual phalanges correlates with habitual suspension, while a higher degree of dorsal canting of the metacarpophalangeal joint (MCPJ) correlates with quadrupedism with palmigrade and digitigrade hand postures. These patterns have previously been confirmed in studies of digit 3, but whether these hold true of others is unclear. In this study, interdigit variation in longitudinal curvature and MCPJ dorsal canting was assessed in three primate species that vary in locomotor behavior and habitual hand postures: *Homo sapiens, Pan paniscus*, *and Macaca mulatta.* 3D virtual models were made of proximal phalanges of digits 2-5 from µCT and laser scans, and eight landmarks were placed to quantify the included angle and dorsal canting angle. A repeated measures ANOVA was performed to test for significant differences among taxa and across digits. Results indicate that although there is variation in included angle across all digits within taxa, it does not negate the interspecific signal relating to locomotor behavior. Dorsal canting among digits exhibits somewhat more interdigit variation than included angle does within a species, but this variation is relatively small. Overall, the results uphold the utility of these angle variables for inferring locomotor behaviors irrespective of digit studied. Therefore, phalanges from different rays can be pooled for comparative analyses and accurate reconstruction of behavior in fossils is not reliant on the specific ray from which a proximal phalanx is derived.

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Ecology differentially constrains male and female sociality in wild chimpanzees

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The socioecological model uses differences in food availability and feeding competition to explain the wide variety of social systems exhibited by non-human primates. According to the model, food primarily determines female grouping which, in turn, determines male grouping. Confounding factors and additional varying pressures, such as predation, have made comparative tests of the model across species challenging. An alternative approach is to examine grouping patterns within one species under varying conditions. Chimpanzees are an excellent candidate species for this methodology as they experience seasonal fluctuations in food availability and have a fission-fusion social system in which party sizes are flexible. In this study, we leveraged 43 years of long-term behavioral data to investigate how food availability affected grouping patterns among the chimpanzees of Gombe National Park, Tanzania. We found that, as the proportion of feeding time spent feeding on non-fig fruit increased, party size increased for both sexes, although it increased more rapidly for males, and the probability of spending time alone decreased for both sexes, with females being, overall, more likely to spend time alone. However, unlike other sites, when food availability was particularly low, males and females had similarly small party sizes. While the socioecological model emphasizes the impact of food on female grouping, our results show that, in times of scarcity, there is also a direct effect of food on male grouping. These findings suggest that food availability differentially constrains male and female sociality and is likely an important factor contributing to behavioral variation across chimpanzee populations.

Natural terrain causes high variability in walking stride parameters in Semai horticulturalists

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The mechanics of human bipedal walking have been extensively studied in laboratories where participants walk on flat, even surfaces that allow for the characterization of consistent, representative features of human gait. However, humans evolved to walk on natural terrains with challenging, uneven surfaces, which are expected to require significant deviations from the more stereotyped stride parameters measured in labs. In this study, we investigated the effects of forest terrain on walking stride variability in 20 adults (6 female, 14 male; 54±10 kg; 18-48 yrs) from a Semai village located in Pahang in Peninsular Malaysia. The Semai traditionally rely on foraging and small-scale agriculture, and all study participants reported regularly walking through nearby forests during subsistence-related activities. We recorded 3-D gait kinematics in participants using inertial measurement units as they walked back and forth barefoot or in simple sandals on two surfaces: a 30-meter segment of even, hard-packed dirt trail, and an adjacent 30-meter transect through light forest characterized by leaves, sticks, roots, and sparse vegetation. Participant stride lengths and durations had 65% and 77% higher coefficients of variation (CVs), respectively, in the forest than on the trail ($p<0.001$, both). Participants also had 55% and 57% higher CVs in mediolateral center of mass excursion and step width, respectively, in the forest ($p<0.001$, both). Variability in these parameters has been shown in lab studies to correlate positively with metabolic energy expenditure. Thus, these results suggest that natural terrains entail greater walking costs and more varied loading patterns than human-made surfaces.

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Genetic structure in the Medieval coastal town of Noli (Liguria, Italy)

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Coastal Liguria in northwestern Italy has served as an important link between eastern and western Europe since the Paleolithic. Despite Liguria presenting a complex population history, its paleogenetic history remains under-represented. We present the first study of Medieval genomic diversity in a Ligurian town, Noli. Noli was known in Medieval times as an important navigation center and a maritime republic. Although Noli is located in a relatively isolated bay, circumscribed by hills and far from main roads linking it to larger centers, its trade routes extended throughout the Mediterranean. To assess genetic variation in Noli resulting from these historic contacts, we screened 58 ancient human bone samples from the San Paragorio church cemetery (10th - 13th CE). Of these, 23 samples passed our authentication criteria and were further shotgun-sequenced for population genetics analyses. We found that the mitochondrial and genome-wide genetic variation in Noli mirrored that of present-day and Medieval European samples, suggesting broader genetic continuity in the region. Moreover, we observed a genetic outlier whose mitochondrial haplogroup (L) and genome-wide affinities suggest similarities to present-day African populations. Ongoing analysis of strontium isotopes will help clarify lifetime mobility of the Noli individuals and demographic impacts of the trade connectivity of Noli. Finally, kinship analysis revealed varying degrees of relatedness among several individuals, including two brothers buried in the same area of the cemetery. Overall, our study presents an archaeo-genomic snapshot of under-represented Medieval Italy, adding to our growing understanding of genetic and mobility patterns in the Mediterranean.

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How does reproductive skew in humans compare to that of other mammals?

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Reproductive skew—inequality in reproductive success within each sex—is a fundamental variable that characterizes the mating system and social structure of animal societies. It also affects the strength of sexual selection for traits such as aggression, risk-taking, and competitiveness within each sex. In a recent collaborative, comparative, and cross-cultural study, we quantified reproductive skew in 90 human groups and 49 mammalian species. This study utilizes a measure of skew—the multinomial index—that allows direct comparison across populations despite substantial differences in group size, life history, sampling method, and mean reproductive success. The results of the analysis include the following. (1) Reproductive skew among human females is very close to the mean for other mammals. (2) Reproductive skew among human males, however, is significantly lower than the mean for other mammals. Consequently, (3) sex differences in skew are significantly smaller in humans than in most non-human mammals. (4) Across human groups, the extent of polygyny positively predicts skew among males and sex differences in skew. Even so, (5) human groups with the greatest extent of polygyny still have lower skew among males and smaller sex differences in skew compared to polygynous non-human mammals. These results help us understand how human-typical patterns of mating and reproduction are similar to (and different from) those of our closest relatives.

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Role of body proportions on thermoregulation during endurance locomotion in the heat

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Theoretical considerations and inter-population variation in body proportions indicate that a greater ratio of body surface area to body mass (BSA/BM) associated with a narrow pelvis should be advantageous for thermoregulation in the heat. However, the expectation that greater BSA/BM results in lower body core temperatures during physical activity in hot conditions was not supported by recent experimental studies. Here we aim to investigate the outlined contradiction using heat exchange modeling.

We modified the published heat exchange model to explore the effect of BSA/BM (250–310 $cm^2\ kg^{-1}$, constant body mass, varying pelvic breadth and stature) on endurance, body core temperature, and other heat exchange variables during walking and running across a range of velocities (1–5 $m\ s^{-1}$) and ambient conditions (25–50 °C, 30–80 % humidity).

Our model predicts that the effect of BSA/BM on body core temperature is negligible across most of the analyzed conditions. At physiologically compensable conditions (lower temperature, lower velocity), lower BSA/BM was offset by greater skin blood flow that resulted in higher skin

temperature and hence heat loss. However, just before the boundary where heat balance becomes physiologically unachievable, we identified a narrow range of conditions where the BSA/BM had a strong negative effect on core temperature. Moreover, greater BSA/BM allowed for achieving heat balance at more demanding conditions. Thus, the key advantage of a narrow pelvis and higher BSA/BM seems to be in achieving heat balance under greater activity-related heat stress, e.g., while carrying heavy loads or running at high temperatures.

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A trepanation case caused by surgery during the late Neolithic Age in the North of China

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Jijiazhuang Site is a Neolithic archaeological site located in Datong City, Shanxi Province. In the third district of the site, there was a tomb No. 4 in which two individuals were buried. The carbon-14 dating result of this tomb was about 4060 BP. One of the burials was a woman of 50-55 years of age. There was a perforation in the left parietal bone of this woman, the edge of which was smooth with signs of bone remodeling. The CT scan was used to create a 3D model, and the details were observed under the microscope, which showed the signs of healing at the trepanation site. The results indicated that the patient survived for more than about 6 months after the craniotomy, and the purpose of the operation could be the treatment of subdural hematoma. This case was the earliest trepanation case found in northern China. It reflected the level of civilization development of the late Neolithic period in China.

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Financial barriers to graduate student success in biological anthropology

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Graduate students in biological anthropology regularly make career-investment decisions with heavy financial burdens. To further the discussion with community-sourced data, a survey of current and recent graduate students collected quantitative data on debt, expectations, and resources and qualitative data on perspectives and proposed changes to alleviate financial stress.

Survey responses (n=104) highlighted financial strain beyond tuition; 82% of participants faced personal debt to cover graduate school fees (non-tuition) and 80% to cover conference attendance. The majority (64%) personally paid >50% of the cost of attendance, while 71% have declined conference opportunities they felt would significantly benefit their career because of financial hardship. Further, 89% felt directly pressured to attend conferences by their supervisor; greater pressure than reported for research opportunities, field schools, or internships.

Beyond academic/career costs, 50% of participants relied on government aid to afford healthcare, groceries, and/or utilities. Of all respondents, 29% accessed food pantries to meet their basic needs while enrolled in graduate school. These results suggest severe financial struggle and sacrifice beyond what is outlined in previous research. Qualitative data revealed feelings of exploitation, deception, regret, and desperation.

The outstanding financial struggle poses serious consequences for current and future academic practice in biological anthropology. These results underscore the need for tangible solutions based on areas of greatest concern: inadequate payment for graduate student labor, funding needs for expectations outside of the institution, an imbalanced ratio of students to resources, and the lack of advisor and peer support.

Shifting paradigms in facial approximation

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The twenty-first century is marked by the need for a paradigm shift within the forensic sciences. Techniques reliant on untested assumptions and subjective judgement should be replaced by robust methods based on relevant data, quantitative measurements, and statistical models. Traditionally, facial approximation has experienced targeted scepticism due to its reliance on visual arts, conflicting or limited and often fragmented guidelines, history with overconfident claims in accuracy, no error measurements, and insufficient validation testing. Despite these limitations, facial approximation has demonstrated relevance in raising the public profile and supporting successful recognition during unidentified person inquiries. Following a scoping review on current practice, this paper confronts lasting issues with existing guidelines and proposes potential solutions. A streamlined approach to protocol selection is needed, with improved accessibility to relevant supporting guidelines that effectively report method reliability and error margins. Given challenges in biological profile estimation, a call for a globalised approximation model determined by skull morphometrics is needed for adult and subadult individuals. Potential variances in sex, population, and age categories needs to be carefully scrutinised to determine true accounts of practical significance and to ensure influences from study design and sampling error are mitigated. Though developments in facial soft tissue thickness data are recognised, feature prediction protocols have not received the same level of attention and are notably lacking for subadults. There is furthermore a need for more transparent and reproduceable protocols that are intrinsically resistant to cognitive bias that follow a logical framework that has been calibrated and validated.

Examination of gene-by-environment interactions in primate skeletal cells

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Primates display a range of complex skeletal trait differences. In addition to morphological variation, different taxa appear to have different susceptibilities to skeletal diseases, including osteoarthritis which results in the degradation of cartilage and underlying bone in joints. The evolution of such skeletal pathologies was likely influenced by a combination of genetic and environmental factors, which can act through gene expression changes to impact resultant phenotypes. However, studying how gene regulation patterns dynamically change in response to environmental perturbations is challenging. This project begins to dissect gene-by-environment interactions in primates in the context of osteoarthritis by taking advantage of cell culture resources, functional assays, and genomic technologies. Specifically, a panel of 6 human and 6 chimpanzee induced pluripotent stem cells were differentiated into chondrogenic cells (the primary cells in cartilage) and exposed to mechanical stress and inflammatory cytokine treatments that induced a matrix-degrading, osteoarthritis-like phenotype in cells. RNA-seq data were collected from control and treatment conditions, and replicate data from 3 humans and 3 chimpanzees were collected to assess technical variation. Analyses to detect patterns of differential expression revealed a mixture of shared and unique gene expression responses across osteoarthritis treatments. Additionally, a mixture of conserved and divergent gene expression patterns was observed between humans and chimpanzees. These findings expend on prior work characterizing static regulatory variation in human and chimpanzee skeletal cells and provide evolutionary context for gene-by-environment interactions that may be relevant for osteoarthritis pathogenesis and other skeletal traits.

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Resource use for three sympatric Costa Rican primate species (*Alouatta palliata, Ateles geoffroyi, Cebus imitator*)

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Recent studies indicate reforestation and resource protection efforts worldwide have been initiated to ensure primate conservation. We consider resource use for sympatric Costa Rican primates (howler, spider, and capuchin monkeys) at La Selva Biological Station (LSBS). LSBS is a 1600 ha protected area transformed over the last 40 years including old growth wet tropical lowland forest and a variety of recovering areas (e.g., reforested secondary forests). Our aim was to understand how primates used environmental resources. We censused primates between January and February 2023 using a transect method. Subjects included 447 primates (197 howler monkeys, 146 spider monkeys, 104 capuchin monkeys). Resource use included land (forest type, forest canopy height, soil type, elevation, geology) and water (nearest water resource, nearest river, watershed) resource use. A chi-square test of independence was performed to examine the relationship between primate species and resource use (p<0.05). Results were significant for observed tree layer use (*X2* (4, *N*=447) = 14.84, *p*=0.005), geology (*X2* (4, *N*=447) = 12.63, *p*=0.0132), and forest canopy height (*X2* (8, *N*=447) = 24.02, *p*=0.0023). Primates preferred trees grown in alluvial terraces although capuchins and spider monkeys were also observed in trees grown in andesitic compositions. Primates preferred canopy areas although spider monkeys also used emergent tree levels and capuchins used shrub areas. Results suggest that primates used all available protected and transformed forest types, but preferred trees grown in alluvial deposits and showed conspecific differentiation in their use of varied tree layers within this tropical lowland forest.

There were symptoms since he was little. Looking for symptoms of renal medullary carcinoma before the cancer is diagnosed

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In its online sickle-cell trait information sheet, the CDC states "People with SCT usually do not have any of the symptoms of sickle cell disease (SCD) and live a normal life." However, SCT can be deadly for individuals who develop renal medullary carcinoma (RMC), an aggressive cancer manifested in late adolescence. This cancer occurs in SCT individuals, though it occasionally affects sickle cell disease patients. RMC is due to macromutations in the SMARCB1 gene (located in a fragile region of chromosome 22), which produces a core subunit of a chromatin remodeling complex (SWI/SNF) which regulates gene expression (Tourigny et al., 2022). The purpose of this paper is to demonstrate that even asymptomatic SCT individuals exhibit measurable symptoms which may be used for an early diagnosis, and to involve the RMC community in the question of why this has not been done. Using the CARDIA data set via the DBGAP depository, we downloaded data from 89 SCT and 3,053 non-SCT healthy participants and computed odds ratios for developing a clinical entity at the end of the study. SCT participants had an odds of developing kidney problems of 3.05 (2.5 CI=1.42-6.54, p=0.0040) and of developing diabetes of 5.4208 (2.5 CI = 1.45-20.25, p=0.0119). A community partner member, referring to his now-deceased son's health, noted that "...there were symptoms since he was little." RMC parents clamor for recognition that SCT is not benign because for them and their dead offspring, it is not. Will the medical community listen and re-write its textbooks?

No support for the V.A.G.G.I.N.A. hypothesis as an alternate explanation for pelvic sex differences

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The human pelvis is unusual for its female-biased dimorphism. Although the larger pelvis in females (relative to those in males) is traditionally explained as an adaptation facilitating the delivery of large neonates, this "obstetric pelvis hypothesis" receives mixed support as female-biased pelvic dimorphism is also found in species delivering small neonates. Recently proposed as an alternate hypothesis, the "Virile, Active Gonads & Genitalia In Nether Area (V.A.G.G.I.N.A.) hypothesis" suggests the larger female pelvis is partly derived from a need to spatially accommodate females' larger pelvic organs. Specifically, the "V.A.G.G.I.N.A. hypothesis" predicts that 1) females have volumetrically, mediolaterally, and anteroposteriorly larger pelvic organs than males and 2) a significant, positive correlation should exist between organ and (corresponding) pelvic cavity dimensions. These predictions are tested using morphometric data derived from pelvic MRI of 37 females and 41 males (cisgender) between 18 and 45 years old. Organ volumes and linear dimensions were obtained from segmented structures and pelvic cavity dimensions were calculated from bony landmarks. After adjusting for differences due to body mass, females have volumetrically (17%) and mediolaterally (12%) larger pelvic organs. However, correlations among all organ and pelvic cavity measurements are nonsignificant (r = -0.3 – 0.18, p > 0.05). Failure to find significant correlations between these structures does not support the "V.A.G.G.I.N.A. hypothesis," and indicates more work is necessary to resolve contradictions in the "obstetric pelvis hypothesis."

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What are bigger snouts for? Looking to non-primates for answers

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The generally pronounced midfaces of strepsirrhine primates are sometimes termed "olfactory snouts," due to the complexity of turbinals within the nasal cavity. Turbinals of the ethmoid bone (e.g., ethmoturbinals) are at least partially lined by olfactory mucosa, whereas the maxilloturbinal is solely lined by respiratory mucosa. In primates, respiratory surfaces of turbinals scale closer to isometry with head or snout size, whereas olfactory surfaces are negatively allometric. To see if this reflects a broader mammalian trend, we studied caviomorph rodents, mammals that vary broadly in body size like primates and share the functional distribution of nasal mucosae. Using iodine enhanced CT scan data of three rodents (capybara, agouti, and pacarana), we measured volumes of the maxilloturbinal and the fourth ethmoturbinal (ETIV), and then converted volumes by the cube root (CRV). We also measured palatal length as a proxy for midfacial length. Results show that CRV of ETIV is inversely related to its palatal length: 5% in the largest species (capybara) and 9% in the smallest species (agouti). In contrast, the CRV of maxilloturbinal is nearly the same percentage of palatal length in all species (11-12%). Such results are consistent with the prediction, based on primates, that olfactory structures do not scale as closely with body-size proxies as is the case for respiratory structures. Our results also emphasize that in mammals with widely varying body sizes, longer midfaces are associated with increased volume (and perhaps greater complexity) of respiratory turbinals in particular.

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Effects of two systematic collection protocols on faunal abundance and diversity: A cost-benefit analysis in the Koobi Fora Formation

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Recent research has confirmed that environmental changes played a critical role in the evolution of our ancestors. However, our understanding of past environmental changes depends on an incomplete fossil record. Researchers emphasize the role of taphonomy in structuring the fossil record, but the implications of variable collection protocols for paleoenvironmental reconstructions have been undervalued. Intense, standardized collection protocols are recommended, but spend time and labor resources.

We investigated the impact of collection methods on Pleistocene fossil assemblages by comparing proportional abundances of vertebrate taxa (i.e., mammal, reptile, fish) between dry-sieve (DS) and wet-sieve (WS) data. We also assessed the efficiency of each protocol by recording collection time (CT).

We collected DS and WS data from 2x2m grids in the Ileret and Karari Ridge subregions of the Koobi Fora Formation from Upper Burgi sediments (2.0-1.87 Ma). Chi-square analysis compared taxonomic abundance using the number of identifiable specimens (NISP) between squares within subregions and between DS and WS data within squares (n=2036). No significant differences were found in faunal abundance between squares by subregion ($X^2(5)<0.91$, $p>.60$), nor by sieve method within squares ($X^2(2)<0.89$, $p>.90$). We evaluated method efficiency by dividing DS and WS NISP by CT to calculate Fossils per Minute Worked (FMW). The mean FMW for DS and WS were 0.111 and 0.269, respectively, suggesting that WS was more efficient.

Although sieve method did not affect faunal abundances, WS could expedite fossil collection. These results demonstrate the importance of examining collection methods to determine when less intensive protocols may be appropriate.

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Genomic adaptation in ancient Brazilian shell mound builders

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The societies formed by shell mound builders, or Sambaqui, on the Atlantic coast, are one of the densest human groupings in America during the Holocene. Such societies comprised 8,000 years of human history in South America and are strongly connected with the marine environment. This scenario likely led to several cultural adaptations; however, whether these changes are related to biological adaptations at the genomic level is unknown. This study leverages genomic data from 62 ancient Native Americans to understand whether the niche constructed around the Sambaqui marine lifestyle could be one of the forces in the natural selection process for those ancient societies. Our results showed that genes related to diet and short stature were advantageous in this population, probably due to the transition to a diet based on collecting seafood and plants. In this sense, Sambaqui dwellers created a specific niche characterized by a strict relationship with the marine and coastal environment, leading to these individuals' genomic adaptation to this lifestyle.

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Geography and subsistence strategy and their relationship to human femur morphology

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Bone structure is determined by a number of factors including genetics, environment, physical activity, and diet. Previous research has shown that bone structure (particularly trabecular and cortical bone) is related to an individual's behavior. However, it is less clear how variation in a bone's gross morphology may be related to various extrinsic factors. The goal of this study is to analyze variation in overall shape of the femur for three groups of humans from different geographic regions and time periods. We hypothesize that femoral shape and size will differ in relation to the general subsistence strategy and geographic location of each group. Landmark-based 3D geometric morphometric analysis was used to quantify femoral shape for 30 individuals from three human groups. Following an intra-observer error study, Checkpoint was used to position and record coordinate data for 20 landmarks on each femur. Landmarks were selected to capture overall femur shape. A principal components analysis and Procrustes ANOVA were performed in MorphoJ. Variation along PC1, which accounted for 26%, shows little separation among groups. Variation summarized by PC1 likely reflects relative size. However, PC2, which accounts for 18% of variation, shows substantial separation between groups ($p<0.001$). Based on wireframe deformations, variation along PC2 likely reflects change in femoral shaft curvature. These results support our hypothesis that whole bone morphology does vary significantly between groups from distinct geographic regions and time periods. However, further investigation is required to better understand what factors drive variation in whole bone morphology among groups.

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Assessing inter- and intraspecific variation in carpal articular surface geometry in catarrhines

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Cineradiographic work on primate forelimbs has demonstrated strong functional and anatomical relationships between carpals. These relationships have been investigated through pairwise morphological comparisons between carpals or articulations, with the aim of inferring the dexterity or locomotor behavior of extinct taxa. A limitation of this approach, however, is that carpals are a tightly bound complex with interplay between multiple articulations simultaneously, suggesting that no single relationship is sufficient to infer dexterity. To tackle this limitation, we collected 3D scan data of each carpal (excluding pisiforms) from a sample of catarrhine taxa (*Homo* = 15, *Pan* = 15, *Gorilla* = 15, *Pongo* = 15, *Papio* = 10, *Macaca* = 13, *Nasalis* = 12) and isolated all articular surfaces. We then measured the size and curvature of each articular surface by calculating the number of size-standardized triangles and the Dirichlet normal energy of each mesh. We examined how these values vary inter- and intraspecifically, calculated carpal articular surface covariation, and measured covariation similarity between all taxa using the random skewers method. Centrally located articulations show less interspecific variation than peripheral ones, suggesting that peripheral articulations play an outsized role in range of motion. These data will help to formulate hypotheses related to overall wrist range of motion and shed light on which areas of the carpal complex have undergone recent selection in which taxa. Our understanding of these form-function relationships may prove useful in identifying adaptations related to the evolution of diverse locomotor behaviors in fossil hominoids and tool use in early hominins.

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Direct Assessment of Phytoload in *Cercocebus Atys* Diet to Further Identify Selective Agents of Thick Enamel

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Given that enamel thickness covaries both with dietary hardness and ingestion of abrasives such as grit and plant phytoliths, identifying the selective agents responsible for thick enamel in primates is difficult. The sooty mangabey, *Cercocebus atys,* is a thick-enameled cercopithecid whose diet is dominated by hard foods collected from the forest floor. Previous analyses indicate that phytoload in the *C. atys* diet is low based on family level estimates, increasing the likelihood that the selective agent(s) responsible for thick enamel in *C. atys* is grit or obdurate foods themselves. Here we provide a further test of these competing hypotheses by quantifying phytolith content in plants representing 64% of *C. atys* feeding time.

Plant foods consumed by sooty mangabeys were collected from Côte d'Ivoire's Taï Forest during the 2021-2022 field season. Dried plant material was washed and heated to 500 degrees C for at least 6 hours to remove organic material. Ashed plant material was bathed in 10% HCL and 15% H2O2 and centrifuged at 3500rpm for 5 minutes between chemical baths. The final sample was dried before obtaining a dry weight.

We obtained an average phytoload for *C. atys* of 0.0428 grams per gram of plant material, suggesting that *C. atys* phytoloads are indeed low. We conclude that thick enamel in *C. atys* is not likely related to abrasion caused by phytoliths but is instead more likely associated with the hardness of *Sacoglottis* seed casings and gritty adherents associated with these foods gleaned from the sandy forest floor.

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Identifying links between childhood diet, weaning practices, and IGD formation in adults from Tell Hisban, Jordan

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The Late Ottoman agropastoralists buried at Tell Hisban in Jordan have an unexpectedly high frequency of rickets during infancy and childhood. Approximately 60% of analyzed infants between 6 months and two years (MNI = 32) died with active vitamin D deficiency, or rickets. In addition, analysis of interglobular dentin (IGD) in adults (MNI=20) indicates that approximately 75% suffered from but survived at least one IGD-forming condition, usually attributed to vitamin D deficiency, during childhood. Although childhood rickets typically derives from a lack of sufficient UVR to synthesize the amount of vitamin D necessary for normal bodily functioning, the timing and duration of breastfeeding also can impact the risk for vitamin D deficiency in infancy. Carbon and nitrogen isotopic analysis of incremental dentin samples from 7 adult individuals from Hisban, three with evidence of IGD and four without, created a timeline of their childhood diet to identify dietary changes and age of weaning cessation. We discovered no clear differences in either the composition of the diet or weaning timing between those with IGD and those without, suggesting that conditions resulting in IGD formation, typically rickets, were not linked to diet or weaning practices. Future research will focus on the possibility of a genetic polymorphism or sociocultural practice that reduced access to UVR in pregnant females and infants as causes for rickets in this community.

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Ecological determinants of the multi-level society of gelada monkeys (*Theropithecus gelada*)

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Multi-level societies (MLS) in primates are thought to facilitate flexible social responses to variation in food availability and predation risk. The MLS of gelada monkeys (*Theropithecus gelada*) consists of four hierarchical levels (One-Male Unit (OMU), team, band, and community), but it has typically been regarded as relatively unaffected by food constraints due to the geladas' graminivorous diet. Here we combine remote sensing data and social network analysis to examine the relationship between seasonality, food availability, and social structure in geladas based on an 11-year dataset from Guassa, in northern Ethiopia. We found that Normalized Differential Vegetation Index (NDVI), a measure of food availability, was a reliable metric for predicting seasonal phenological dates and edible grass biomass. Mean monthly rainfall predicted both NDVI and grass biomass and drove much of the temporal variation in graminoid availability in Guassa. The band's social networks exhibited marginally higher densities and stronger associations between OMUs during periods of high food availability, though herd sizes did not differ. These results suggest that resource constraints may indeed influence the expression of MLS in geladas. This study prompts future consideration of the impact of ecological factors influencing MLS in primates.

Rearfoot Form and Function in Hominin Bipedalism: Insights from Finite Element Analysis

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The rearfoot is especially important in understanding the evolution of bipedalism in fossil hominins as it transmits high weight-bearing forces during locomotion. While many studies have utilized methodologies that describe and interpret rearfoot elements' morphology to infer function, few directly test form-function relationships. Therefore, many questions remain about fossil hominins' locomotor behavior and rearfoot function. Through the use of finite element analysis (FEA), it is possible to experimentally test the relationship between calcaneal form and function, improving our understanding of rearfoot biomechanics. This study aims to (1) investigate if there is a biomechanical association between different loading regimes and calcaneal morphology by modeling the rearfoot at heel strike using FEA and (2) infer fossil hominin locomotor behavior based on comparisons to modern taxa. FE models of *Homo sapiens*, *Pan troglodytes*, *Australopithecus sediba* (MH2), and *Homo neanderthalensis* (La Ferrassie) were generated under scaled loading conditions simulating human bipedalism at heel strike using body mass and material property parameters from the literature and previously collected force plate and high-speed 3D kinematic data from modern human subjects. The extant models considerably differ, with *P. troglodytes* models producing overall higher stresses, especially in the area anterior to the posterior talar facet. The MH2 and La Ferrassie models exhibit stress accumulation patterns most similar to modern human models. However, stress results in MH2 are subtly distinct from both human and Neanderthal models potentially indicating differences in heel strike mechanics.

Reconstructing the leaping ability of early fossil primates using hip and knee morphology

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Early fossil crown primates, the adapoids and omomyoids, are commonly reconstructed as grasp-leapers. Conversely, plesiadapiforms, proposed stem primates, are not characterized as leapers and are instead reconstructed as vertical clingers and claw climbers. The hip and knee joints are particularly important to leaping ability, as several features have been associated with leaping. We recorded 30 linear measurements of the innominate, proximal femur, distal femur, and proximal tibia for 16 fossil primate genera and 40 extant primate genera (171 total specimens) to reconstruct the locomotor behavior and leaping ability of early fossil primates. We compared innominate and tibial indices using one-way ANOVA and conducted principal component analyses (PCA) of femoral measurements, for which we had more complete fossil samples. There are no statistically significant differences among locomotor groups for acetabulum shape, ilium to ischium length, or relative tibial condyle width. These results contrast with those from prior studies and suggest that these features may not be helpful in reconstructing fossil primate locomotor behavior. Proximal and distal femoral morphospace is characterized by phylogenetic rather than locomotor groupings. Distal femur PC1 (40.1%) is primarily ordered by knee depth. The omomyoids, except for *Vastanomys*, group with VCL tarsiers, whereas adapoids such as *Notharctus* and *Cantius* align with the frequent leaping galagos and lemurs. Plesiadapiform femoral morphology is not similar to that of leapers, which is in agreement with prior studies. Future analyses will include larger fossil samples and detailed assessment of the phylogenetic signal in the traits under study.

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Variation in Distal Humerus Morphology Among Eastern Gorilla Populations

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Distal humerus morphology has been observed to vary with locomotor behavior among ape genera. Gorilla populations live in a range of habitats, presenting the opportunity to test whether variation in the distal humerus reflects ecological and locomotor variation within a hominoid genus. A previous analysis of distal humerus variation among gorilla subspecies found significant differences between *Gorilla gorilla gorilla*, which lives in lowland forests, and *G. beringei beringei*, which lives in montane forests and engages in less terrestrial and arboreal locomotion; however, only capitular width varied in the predicted direction. *Gorilla beringei graueri*, which occupies a range of altitudes, was predicted to show intermediate morphology but did not. In order to clarify the relationship between morphology and ecology in *G. beringei* (eastern gorilla), this study includes an expanded sample permitting analysis at the population level.

Three populations of *G. b. graueri* and one population of *G. b. beringei* were compared based on six linear measurements of the distal humerus, using comparisons of means and discriminant function analysis. The *G. b. graueri* samples included individuals from DRC lowlands (n=30), Itombwe (highland: n=15), and Tshiaberimu (highland: n=7), while the *G. b. beringei* sample was from the Virungas (highland: n=31). Populations were discriminated at medium to high rates, and significant differences were found between populations, both across subspecies and within *G. b. graueri*. Capitular width varied as predicted between DRC lowlands and the Virungas but not between lowland and highland *G. b. graueri*, and other measurements did not show consistent patterns of variation.

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Mentally Institutionalized African Americans During the 1918 Spanish Flu

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The 1918 influenza pandemic killed over 34,000 Missourians between 1918-1920, including a number of people undergoing inpatient treatment in Missouri's public mental health system.This poster will present some of the early findings of a project examining the impact of 1918 influenza on institutionalized African Americans in Missouri's public hospital system. Using a variety of historical resources, the authors have attempted to document the treatment and outcomes of African American Missourians during the pandemic. Data sources include death certificates, annual reports submitted by state hospitals to the state government, and other primary sources. The evidence, while sometimes sparse, points to a health system that underserved Black people and kept little evidence of their experiences. For example, though historical sources indicate segregated wards for white and Black patients at State Hospital #1 in Fulton, the only reporting on Black patients is a short record of patients held as "criminally insane", which may attest an emphasis to the lack of mental health care that was available to African Americans during this time. Meaning that the lack of evidence is evidence itself because it signifies the erasure of Black people from history and the significance of the roles African Americans played in communities during this time.

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Primate Social Organization Evolved from a Flexible Pair-Living Ancestor

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Explaining the evolution of primate social organization has been fundamental to understand human sociality and social evolution more broadly. It has often been suggested that the ancestor of all primates was solitary and that other forms of social organization evolved later, with transitions being driven by various life history traits and ecological factors. However, recent research showed that many understudied primate species previously assumed to be solitary actually live in pairs, and intra-specific variation in social organization is common. We built a detailed database from primary field studies quantifying the number of social units expressing different social organizations in each population. We used Bayesian phylogenetic models to infer the probability of each social organization, conditional on several socio-ecological and life history predictors. We show that when intra-specific variation is accounted for, the ancestral social organization of primates was inferred to be variable, with the most common social organization being pair-living but with approximatively 10-20% of social units of the ancestral population deviating from this pattern by being solitary living. Body size and activity patterns had large effects on transitions between types of social organizations. As in other mammalian clades, pair-living is closely linked to small body size and likely more common in ancestral species. Our results challenge the assumption that ancestral primates were solitary and that pair-living evolved afterwards emphasizing the importance of focusing on field data and accounting for intra-specific variation, providing a flexible statistical framework for doing so.

Gender and Health: Paleoepidemiology of an Institutionalized Population in Nineteenth-Century Colorado

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Nineteenth-century men and women were understood by both medical professionals and laymen to be differentially vulnerable to madness. Exploring the perceived causes of insanity listed in the admissions record of the Colorado State Hospital, in combination with wider social contexts, demonstrates that madness in nineteenth-century Colorado was understood to be deeply integrated with laboring bodies and physical health. Skeletal analysis of 150 individuals who died while institutionalized at the Colorado asylum provides osteological evidence of the lived experience of perceived madness in Colorado from 1879 to 1899. Comparison to another contemporary American West population sample from a low-socioeconomic but non-institutionalized environment suggests that the lives of these individuals were similar to other socioeconomically disadvantaged Americans. However, some population differences were observed. Vulnerabilities were differentially embodied through gender-typical labor and the health consequences of gendered behavioral expectations. Skeletal analysis reveals a high incidence rate of traumatic injury among the male Colorado asylum population sample with 82 out of 97 male individuals (84.5%) exhibiting at least one traumatic injury. The degree of remodeling suggests that some injuries likely occurred before institutionalization and may have been the cause of admission to the asylum while other injuries likely occurred during institutionalization. Skeletal indications of poor health, such as linear enamel hypoplasia and osteoperiostitis, as well as an unusual mortality pattern revealed in the admissions record, suggest that the women of this population sample faced exceptional challenges to their physical health.

Unveiling the human form: A multisegment model for estimating body surface area and volume

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Body surface area, volume, and their ratio are integral to understanding human thermoregulation, but the direct measurement is complicated by the human body shape complexity. Commonly used methods for estimating body surface area and volume from height, weight, and density may not fully reflect the influence of body proportions and composition. Multisegment models could offer a solution, although they were previously tested against estimates rather than measurements. A new multisegment model for estimating body surface area and volume from anthropometric measurements is proposed. Focusing on the trunk segment's significant contribution to body surface area and volume, three model variants are introduced featuring the trunk segment as a cylinder with a circular base, a cylinder with an elliptical base, and a cuboid. The remaining segments were modeled as spheres, cylinders, and conical frustums uniformly across model variants. Anthropometric measurements were taken from 60 full-body 3D surface scans. All model variant estimates were tested against measurements from corresponding full-body 3D surface scans. Model variants with circular and cuboidal trunk seem to provide an accurate estimation of body surface area with standard error of estimate, mean percentage difference, and mean absolute percentage difference under 5 %. For volume estimation, the cuboidal trunk variant outperformed the others, displaying the lowest standard error of estimate, mean percentage difference, and mean absolute percentage difference. A comparison of the three model variants suggests that modeling the trunk segment as a cuboid may provide better results in estimating volume, and hence body surface-to-volume ratio, than the cylindrical variants.

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Multi-Bone Micro-CT Scanning with a leap towards reproducibility and efficiency using automated tools

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Recent advancements in micro-CT technology now enable simultaneous scanning of multiple bones, boosting speed and cost-effectiveness in bioanthropological research. However, there are challenges in determining anatomical or mathematical homology for detailed analysis, such as processing cortical bone cross-sectional data or trabecular bone volumes, still acting to constrain sample sizes. Accurate 3D bone positioning to match homologous morphological counterparts is essential for comparative purposes, as is defining equivalent cross-sectional images for comparative cortical studies. Differentiating between cortical and trabecular bone during separation is also crucial for trabecular bone data preparation.

Addressing these challenges, we created a new automation tool (AT) for Amira3D software, requiring minimal user input. It is adept at efficiently separating multiple bones scanned together. After identifying and segmenting bones, the AT saves them separately, streamlining post-processing. It also has algorithms for user-specified alignment and cross-sectional positioning, allowing for standardized or custom images based on bone morphology. The AT can also differentiate the boundaries between cortical and trabecular bone.

Our tests show that when multiple users apply the AT to the same micro-CT data, they achieve consistent results. Without the AT, individual users introduce variability, increasing the effect of inter-observer errors. The AT reduces bone separation time and generates tailored image data, ensuring repeatability and reproducibility previously lacking in conventional cross-sectional and trabecular bone studies in biological anthropology. This tool has the potential for broad application in research using micro-CT bone imaging and analysis and for establishing a benchmark in promoting methodological efficiency and accuracy.

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Higher resilience and hope predict lower perceived stress in war refugees from Ukraine

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War and forced migration are highly traumatic events. People may experience trauma before leaving their homes, during the escape, and in the country of resettlement. There is significant inter-individual variation in responses to trauma, with some refugees being more resilient than others. We tested the hypothesis that Ukrainian war refugees with higher levels of resilience and hope for the future will experience lower levels of perceived stress.

146 mothers and grandmothers (ages 25 to 81) from 120 families of Ukrainian war refugees in Poland were surveyed at two time points six weeks apart. Surveys included the Perceived Stress Scale, the Resilience Measurement Scale, and the Adult Hope Scale, among others. Saliva and hair samples were collected for hormone and immune biomarkers, and buccal swabs for mitochondrial DNA damage analyses.

Participants with higher scores of resilience and hope for the future had significantly lower levels of perceived stress shortly after migrating to Poland ($p<0.0001$). Perceived stress levels measured 6 weeks later were also significantly predicted by their initial scores of resilience and hope ($p<0.0001$). Age and education, used as covariates, did not correlate with perceived stress.

Long-term stress has strong detrimental effects on health. Our findings suggest that resilience and hope in war traumatized refugees can mediate perceived stress. Resilience training should be an important element of help that refugees receive in host countries.

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An analysis of hominin fossil preservation at Hadar, Ethiopia using Uberon Ontology

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Taphonomic analyses are essential for reconstructing the faunal, environmental, and hominin histories of fossil assemblages. Faunal preservation and representation is at the forefront of taphonomic analyses leaving the preservation analyses of hominin fossils understudied. We examine hominin fossil preservation at Hadar to assess skeletal element biases in fossil representation. We developed a new method to systematically encode skeletal element preservation using a modified version of the Uberon multispecies anatomy ontology. Ontologies are widely used tools in information science to represent knowledge in specific domains (e.g. anatomy). Uberon documents all vertebrate anatomical elements and provides a comprehensive atlas of relational anatomical parts that we extended to include annotations for completeness. We compiled a dataset of 807 individual skeletal elements from 522 published Hadar fossil specimens. We observe that mandibles (n=64) are the most abundant element in the assemblage. We observed that dental elements at Hadar are significantly overrepresented compared to expected values. Using a resampling protocol programmed in R, we found that the abundance of Hadar fossil elements from five anatomical anatomical regions were significantly different ($p < 0.0001$) than expected if randomly sampled from a complete human skeleton. The highest percentage of complete elements was recorded in the dental region (86%) and the lowest in the axial (12%). Uberon allows for the creation of a fossil encoding system that accounts for individual skeletal element preservation for use in hominin preservation analyses.

Taxonomic and functional profiling of oral metagenomes from ancestral Maya reveals impacts of dietary transitions

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Interactions with our environments are directly negotiated through our mouths, from explorations as children grow to food selections throughout our lifespan. For ancestral populations, these interactions have quantifiable impacts on the oral microbiome that can persist through time and thus shifts in lifestyle and subsistence can be surveyed. In this study, we characterized the taxonomic diversity and functional capacity of oral microbiomes reconstructed from dental calculus of ancestral Maya individuals (n=23). They represent populations from a single geographic area who lived approximately 9600-1000 cal BP and who experienced a transition to agriculture with maize becoming a dietary staple based on previously published stable isotopic ratios. DNA extracted from calculus was partially uracil deglycosylase-treated and double-stranded libraries were sequenced with Illumina technology. Statistical comparisons of metagenomes from a staple maize diet (n=14) to those from a pre-maize diet (n=9) show that relative abundances of microbial functions related to carbohydrate metabolism, such as starch and sucrose metabolism, were significantly higher in staple maize diets. Clustering of metagenomes from staple maize diets was primarily driven by *Streptococcus sinensis* while separation of pre-maize diets was driven by *Pseudoramibacter alactolyticus.* This corresponds to a shift in taxa contributing to carbohydrate metabolism. Relative abundances of these functions from *P. alactolyticus* are significantly higher in pre-maize diets while *Streptococcus* species are largely absent but become the primary contributors in staple maize diets. A transition to agriculture impacted the functional potential of the oral microbiome, indicating its efficacy as a source to infer dietary constituents of our ancestors.

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Preliminary Geometric Morphometric Identification of Cercopithecoidea Teeth from Laetoli, northern Tanzania

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Teeth play a key role in the understanding of primate life histories, dietary behavior, and social structure. They provide important morphological evidence that can assist in taxic classification and species diversity in the fossil assemblages. Within the fossiliferous beds at Laetoli, fossil cercopithecoid teeth are the most abundant anthropoid skeletal elements in association with Pliocene hominins such as *Australopithecus afarensis*. Understanding the variation of fossil cercopithecoids is vital when attempting to reconstruct local (Laetoli) and regional (eastern Africa) paleoenvironments. The application of landmark data using Geometric Morphometrics (GM) can help statistically analyze taxonomic range of morphological variation and the generalized clusters of differences among species. Continued paleoanthropological research at Laetoli has expanded the collection of non-hominin primate craniodental material that can be used to infer taxic diversity and dietary adaptation among cercopithecoids during the Pliocene. The sample includes a nearly complete mandible (preliminarily attributed to *Rhinocolobus sp.*) as well as a maxillary fragment that has not yet been assigned to a specific taxon. In this study, we report preliminary comparative analyses of 3D-based GM analyses (dental crown shape and morphology) between extant and Pliocene cercopithecoids. Semi-terrestrial cercopithecines (i.e., *Parapapio ado*) are more abundant at Laetoli than arboreal colobines (i.e., *Rhinocolobus* sp). Preliminary identification of the new fossil cercopithecoids suggests that species diversity for a limited subset of Laetoli fossil localities may differ significantly.

The Misuse of Life History Theory in Racist Pseudo-Science

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Life history theory is the branch of evolutionary biology that attempts to understand patterns of investment in growth, reproduction, and survival across the life cycle. A key to the formal theory of life histories is the existence of trade-offs arising from either multi-objective optimization or budget constraints. Most applications of life history theory to human evolution, diversity, and behavior focus on trade-offs induced by budget constraints attributable to energetic allocation. In fact, life history theory in the behavioral sciences is often effectively synonymous with the application of trade-off logic. Starting with the writing of Rushton, trade-off models focused on the "pace of life hypothesis" have been implicated in racist pseudo-science. Using the formalism of life history theory, I show the shortcomings of this approach. I make three fundamental points: (1) trade-offs based on budget constraints require proper measurement of the budget, which is essentially never done, (2) trade-offs imply potential reallocation but many apparent trade-offs are actually constraints, where reallocation is not possible, (3) even if trade-offs exist, they are only measurable if the variance in the energy allocated within individuals is at least as great as the variance energy available between individuals. This is typically possible only in highly-controlled (and artificial) experiments. I show that when this condition is not met, the "trade-off" curves have a positive slope. Future studies of human life histories should focus on the primary source of variability in energy allocation, which is environmental.

Recovering Coahuiltecan Ancestors: A Collaborative Exploration of Texas' Prehistoric Populations using Ancient DNA

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The Tap Pilam Coahuiltecan Nation (Tap Pilam) and their non-profit American Indians in Texas at Spanish Colonial Missions (AIT-SCM), who are associated with San Antonio's mission-era American Indians, have worked for decades to bring awareness to tribal and familial links between their members and their ancestral homelands in central and south Texas and northern Mexico. However, the physical remains of many of the Coahuiltecan ancestors have been archaeologically designated as "culturally unaffiliated" or similar, making it extremely difficult for modern descendants to connect with their ancestors. In concert with Tap Pilam AIT-SCM, my objective for this study was to mitigate the adverse effects of these difficulties by identifying Coahuiltecan ancestors who are currently housed in institutional collections using ancient DNA. Whole-genome sequencing was completed for 29 individuals from culturally Coahuiltecan areas, six of whom had mitochondrial coverage over .8X. All six belong to mitochondrial haplogroups B and C and phylogenetic analyses reveal clustering with prehistoric individuals from Coahuila, Mexico and Central America. These results provide independent evidence in support of modern genealogically- and historically-determined Coahuiltecan cultural heritage.

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Sex ratio interpretation: An analysis of methods to estimate biological sex in a commingled and fragmentary skeletal assemblage from Midnight Terror Cave, Belize

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A biological sex ratio on the adult skeletal assemblage from Midnight Terror Cave was previously conducted using ancient DNA extracted from five pelvises. It is unclear if the sex ratio from the pelvis sample is representative of the assemblage given the small sample size analyzed. There is a large sample of femora in this assemblage, and the femoral head diameter can be used to estimate sex. A comparison of sex ratios derived molecularly from pelvises and skeletally from femora provides insight into potential methodological and sampling biases, which are critical to establish given the commingled and fragmentary nature and ritual significance of the assemblage. There were 45 femora (25 right, 20 left) each with a well-preserved femoral head to measure maximum femoral head diameter (FHD). The side with the larger sample size was selected for analysis so as not to double-count individuals. Using published discriminant functions for FHD to estimate sex in Maya populations, the resulting sex ratio of the assemblage is 56% female and 44% male. This sex ratio suggests a more modest overrepresentation of females compared to males than the paleogenomic analysis on the pelvises (80% female, 20% male). The significance of this paleodemographic profile is discussed. Given the greater number of femora, the skeletal method to estimate sex may give a more realistic reconstruction of the sex ratio in this assemblage. This is particularly important with skeletal assemblages from ritual contexts like Midnight Terror Cave.

The evolvability of *Paranthropus boisei* skull morphology in the context of feeding biomechanics

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The highly derived skull morphology in *Paranthropus* may have conferred advantages for processing hard/tough foods due to the adaptative features in their skull morphology. However, the distinctive characteristics related to the feeding apparatus might have limited their ability to respond to selection and evolve toward new adaptive peaks rapidly (i.e., evolvability). We used viability selection modeling, which simulates evolution over time based on probability of individual survival, to test this hypothesis in *P. boisei*.

We predicted that evolution would be slower from the morphologically derived *P. boisei* (OH 5) towards the peaks corresponding to the more generalized australopithecine and early *Homo* crania, represented by *Australopithecus afarensis* (A.L. 444-2) and *H. habilis* (KNM-ER 1813), respectively, than the inverse direction. We performed viability selection simulations using 29 biomechanically-informative linear distance measurements and a recent *H. sapiens* P (phenotypic covariance) matrix after controlling sex variation. The number of generations required to reach a new adaptive peak was considered as a measure of evolvability (e.g., fewer generations indicate higher evolvability). The number of generations from 100 simulations was compared using the Mann-Whitney U test ($\alpha=0.05$).

The differences were in the predicted direction: *P. boisei* required a larger number of generations to reach both the *Au. afarensis* and *H. habilis* cranial morphotypes than either did to reach the *P. boisei* morphotype, but the differences did not reach the level of statistical significance. These preliminary results indicate that biomechanical specializations in the *P. boisei* cranium had limited impact on its evolvability.

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Comparative functional analysis of the prostate-specific KLK3 enzyme in hominoids reveals the impact of sexual selection

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Humans and other hominoids experience varying modes and intensities of sexual selection, depending on their social structure and mating systems, resulting in anatomical, physiological, and molecular adaptations. Several male reproductive genes have evolved more rapidly in species with strong sperm competition while losing function in species with low sperm competition, including the prostate-specific enzymes KLK2 and KLK3. Although numerous studies have observed similar patterns of molecular evolution, they are almost always based on DNA sequence analysis only. To test the hypothesis that the KLK3 homologs of humans and chimpanzees differ functionally, and potentially in response to differing levels of sperm competition, we expressed and purified these enzymes as recombinant proteins in a mammalian cell culture system. We characterized their enzyme kinetics in vitro. In these functional assays, the chimpanzee KLK3 protein shows significantly greater activity than that of humans. Furthermore, we produced the recombinant protein corresponding to that of the last common ancestor of humans and chimpanzees (LCA-HC). This protein has nearly identical enzyme kinetics to the human homolog, suggesting that differences between humans and chimpanzees evolved in the latter. The increased efficiency of the chimpanzee KLK3 enzyme is therefore derived, and if it evolved in response to high sperm competition in this species, suggests that their other adaptions to sperm competition are also derived. Therefore, the LCA-HC likely experienced lower sperm competition associated with monogamy or single-male polygyny, with the caveat that it is not possible to reconstruct the entire complexity of a species' behavior from one gene.

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Estimating vertebral column length from contiguous vertebrae segments for anatomical stature reconstruction

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Stature estimation from skeletal elements is used in bioarchaeological, forensic, and paleoanthropological analyses. Several regression formulae exist for estimating stature from long bones and while these estimates typically have high accuracy, knowledge of sex and ancestry is necessary to achieve the best results. Anatomical stature, on the other hand, is independent of such knowledge as sex and population differences in stature are naturally included in the final estimate. As anatomical stature estimates require linear measurements of all skeletal elements that contribute directly to stature, incomplete skeletons make this assessment problematic. The axial skeleton, being unpaired, is especially susceptible to incompleteness. Here, we focus on total vertebral length (TVL), a large portion of the axial skeleton's contribution to an estimate of stature, as vertebrae are common missing elements in all bioanthropological contexts in which a stature estimate is desired. Using 62 (38 male, 24 female) individuals from the Texas State Donated Skeletal Collection (TXSTDSC), an ethically-sourced and well-documented human skeletal collection, we measured the midline height of C2-L5 following Raxter et al. (2006) and correlated four vertebral segments (C2-C7, T1-T6, T7-T12, L1-L5) to TVL. All four segments produced TVL estimates with an approximately 3.5% error. The correlations (R^2) for each segment are 0.48, 0.51, 0.56, and 0.53 with absolute errors of 17.6 mm, 17.2 mm, 16.6 mm, and 18.8 mm for C2-C7, T1-T6, T7-T12, L1-L5 segments, respectively. The study demonstrates that estimations of vertebral column length can be used when not all vertebrae are present.

My Evolving Understanding of Primate Communities with Kaye Reed

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I met Kaye Reed in 1998 as an undergraduate student in her Primate Paleoecology class. She was the first professor to introduce me to thinking about primates on broad evolutionary and ecological scales, including at the community level. This time was a couple of years after Kaye's publications on primate communities in PNAS and JHE and John Fleagle's second edition of his Primate Adaptation and Evolution book. Kaye generously gave the class reprints of her papers and proofs of John's book chapters. These readings were truly eye opening for me and cemented my interest in primate community ecology and evolution. This inspired me to attend graduate school, where Kaye's letter of recommendation supporting my application played an important role in me getting accepted to the doctoral program at Stony Brook. Her impact on my career did end there. After several years as a postdoctoral fellow, I obtained a position at Midwestern University in Phoenix. Kaye supported my adjunct position at ASU, which allowed me to co-teach a graduate course with her on quantitative methods. In addition to teaching opportunities, Kaye and I began to think about research projects that leveraged our strengths in primate ecology and evolution. This led to a successful NSF grant and subsequent publications on the evolution of primate communities. To say that Kaye played a critical role as a teacher and mentor to me is an understatement.

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Death end for a Hun warrior - A migration period (5^{th} -6^{th} cent. AD) burial from Eastern Austria

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Skeletal remains recovered from a Migration Period burial near an abundant *villa rustica* in Weiden am See (Burgenland, Austria) were examined using osteopathology, forensic anthropology, archaeozoological, genetic, and isotopic analyses to elucidate their origin, circumstances of death, and postmortem treatment.

The primary grave buried a 25-30 years aged male, with a robust build and relatively tall stature (174±5cm). He exhibited skull deformation (circular-erect type) and displayed stress markers from late childhood and adolescence, including Harris lines and cribra orbitalia. Bone analysis revealed perimortem injuries, indicating death by violent means, with cuts and stab wounds to the head and chest areas.

Ancient DNA analyses revealed an overlap with the genetic complexity of present-day groups from Eastern Europe. Together with stable isotopic examination ($\delta^{13}C$, $\delta^{15}N$, $\delta^{34}S$, $\delta^{2}H$, $^{87}Sr/^{86}Sr$), strong indications, that this individual originated in Eastern Europe, most probably from the Carpathian Basin. Further, stable isotope data suggests a prolonged residence in the Hungarian Plain, with a relatively short period in the region where he was finally unearthed. Dietary patterns reflected a significant reliance on terrestrial animal protein, in the form of either meat or dairy products, with a relatively low but significant proportion of millet (~35%).

Additionally, we attributed a well-preserved skull and extremity bones to a single horse. This discovery closely parallels equestrian graves or horse burials found in Hunnish and Sarmatian dominion areas. Most likely, the human remains belong to a "Hun" warrior who met his violent end far from home, but buried with all the trappings of honor.

Why is my tooth blue? Implications of dental enamel diagenesis in studies of health in the past

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Skeletal remains are integral to studies of health and disease in the past. Poor preservation in archaeological, palaeontological, and forensic contexts can hamper scientific investigation. Histotaphonomy, a discipline investigating post-mortem changes at the microscopic level, plays a crucial role in overcoming these challenges. Although dental enamel, primarily composed of inorganic material, is relatively resilient to post-mortem alterations compared to other skeletal tissues, it is frequently overlooked in histotaphonomic studies of diagenesis. Recognizing the effects of the burial environment on dental enamel is paramount to preventing premature exclusion of samples that may yield critical insights into enamel formation and/or disruption. This research draws on archaeological dental samples excavated from mid-late 19th century New Zealand colonial cemeteries. Skeletal preservation is highly variable, and many teeth exhibit heavy staining, enamel fracturing and loss of dentine, visible on the microscopic level. Of note, an individual interred in a green woollen blanket displays post-depositional blue staining up to 200µm into the outer enamel, likely from arsenic or copper in the blanket dye. This underscores the vulnerability of enamel to environmental modification in the post-depositional environment. Here we present common types of enamel diagenesis we have encountered in our own histological samples and propose strategies for mitigation. By addressing the types of diagenesis enamel is subject to in the burial environment, the presentation and interpretation of results in paleohistological studies can be enhanced.

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Expansion of primate neocortical visual areas is associated with improved visual acuity in crown haplorhines but not in Eocene stem haplorhines (Omomyoidea)

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Multiple lineages of primates have independently evolved increases in brain size relative to body size. These parallel increases in relative brain size may be attributed to the expansion of different brain regions in different primate lineages. For instance, relative to total brain size, haplorhines have expanded portions of the neocortex that are associated with visual functions. Here we show that combined expansion of the occipital, parietal, and temporal cortices (OPT) can be discerned on the exposed neocortical surfaces of brain endocasts, allowing study of this haplorhine characteristic using fossil endocasts. Using anatomical landmarks on endocast surfaces, neocortical surface areas were measured for 96% of all extant primate genera and 16 extinct primate taxa (N=103 genera, 241 specimens). Using phylogenetic comparative models, we find that, compared with strepsirrhines, extant haplorhine endocasts have larger summed OPT areas relative to frontal areas. Endocasts of Oligo-Miocene stem anthropoids, catarrhines, and platyrrhines likewise have expanded OPT areas, whereas Eocene strepsirrhines (Adapiformes) and haplorhines (Omomyiformes) do not. Expanded crown haplorhine OPT, especially the occipital area where primary visual cortex resides, join a suite of features related to refinements to the visual system, including postorbital closure and an increase in optic foramen/nerve size associated with the evolution of a retinal fovea and high visual acuity. By comparison, the Eocene taxa lack postorbital closure, have relatively small optic foramina, and exhibit strepsirrhine-like neocortical proportions. Independent increases in encephalization in catarrhines and platyrrhines are not accompanied by changes in neocortical proportions, possibly reflecting a conserved developmental program.

Human vs. animal bone: Less-destructive identification using scanning electron microscope

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In the medico-legal field of forensic anthropology, correctly determining whether a bone came from a human or an animal is a vital step in any case. Current best practices to differentiate human from animal on non-morphologically distinct bone fragments are destructive, requiring cross-sections or for the bone to be ground into powder. In an effort to create a less destructive procedure for bone fragment differentiation, I have been developing a method of bone cell analysis that utilizes a scanning electron microscope (SEM) to take images of the bone cell structures. Human bone cells are typically laid out in haversian systems, which appear circular in structure, while animal bones generally are laid in rectangular layers called plexiform systems. However, manual classification of these micrographs proves challenging to replicate or regulate. In response, we developed a machine learning algorithm to do this differentiation based solely on observable characteristics in SEM images. Preliminary results show up to an 88% accuracy rate for differentiation. Using an SEM, fragments can be directly placed inside the microscope for imaging and do not necessarily need to be thin or severely altered in order to image, thus leading to a less destructive (and often non-destructive) method of bone cell analysis. Destructive analytical techniques halt further analysis of a sample, which can run a case dry or impede the investigation process. As scientists and biological anthropologists, we have an ethical duty to maintain the integrity of remains out of respect for the individual and their culture and kin.

Animal management strategies at the Wari imperial site of Huaca del Loro, Nasca, Peru (A.D. 650-950) using isotopic analyses of camelid bone

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During imperial expansion, food resources, trade routes, and animal management can be affected by state needs in colonized regions. Camelids in prehistoric Peru were important for food, transportation of goods, and as ritual sacrifices. As an important state resource, camelids may have had their diet controlled for better management. If used in a sacrificial ritual, animals sometimes had their diet limited to special foods. The Wari state expanded into the southern Peruvian Nasca region (A.D. 650-950 C.E.) and built the large multicomponent site of Huaca del Loro. In this study, we examine if camelid diet was controlled or limited at this Wari imperial site. Using stable isotope analysis of bone, we analyzed approximately 30 camelids buried in various sectors of Huaca del Loro, including sacrifices near the D-shaped temple, midden remains in habitation areas, and within human burials. Camelid diet is mostly maize or C4-plant based but varies significantly (>5‰) in both carbon and nitrogen. Additionally, no clear dietary patterns are discerned between camelids buried in different sectors of the site, suggesting that diet was not restricted or controlled based on how camelids were used. In comparison with other Wari sites, including Conchopata, the secondary Wari heartland city, Nasca camelid dietary management seems to have been adaptable, especially in an arid environment like the Nasca region.

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Reconstructing woody cover in African habitats using Bayesian modeling and 3D shape variation of the bovid astragalus

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Ecomorphology of the astragalus, the ankle bone which forms the diagnostic double-hinge joint in artiodactyls, is a useful proxy for reconstructing paleoenvironments, particularly for comparing the extent of tree cover among habitats at hominin bearing sites. Existing work on bovids (Family: Bovidae) indicates that linear dimensions of the astragalus differ predictably between open-habitat and closed-habitat taxa, and these variables are useful for reconstructing paleoenvironmental variability during the Plio-Pleistocene. However, linear measurements are limited in discriminating among bovids associated with intermediate habitats. This restricts our ability to interpret subtle variations in tree cover within the heterogeneous, mosaic environments which hominins inhabited. This study presents a method for parsing apart tree cover variation in hominin paleoenvironments with additional nuance by examining the morphology of the bovid astragalus in greater detail. Habitat-related shape variation in extant bovid astragali is analyzed using 3D geometric morphometrics, then quantified through a principal components (PC) analysis. PC scores are subsequently applied as predictor variables in a Bayesian regression model, which reconstructs woody cover in modern African habitats in terms of percentages, rather than discrete categories. This approach represents a novel application of Bayesian modeling to ecomorphology, and by characterizing habitats in terms of percent woody cover, this model provides additional insight into subtle habitat variability. Additionally, the results of this project demonstrate the utility of combining 3D geometric morphometrics and Bayesian models for reconstructing hominin paleoenvironments with greater nuance than before.

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Assessment of Genetic Ancestry From a Captive Baboon Colony

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Hybridization studies of primates are of interest to anthropologists because they provide a comparative context to the gene flow between modern humans and archaic hominins in the past. Baboons (genus *Papio*), a member of the Cercopithecinae subfamily are known to regularly hybridize and share an evolutionary history with modern humans. However, studies of baboons suffer from two major issues. First, baboons, up until recently, were not well genetically characterized, and second, the extent of hybridization has often been assessed based on field observations and phenotypic characteristics. Here we analyzed 881 olive (*P. anubis*) and yellow (*P. cynocephalus*) baboon genomes from the Southwest National Primate Research Center (SNPRC) in San Antonio, Texas. The SNPRC has a large, pedigreed baboon colony with active breeding programs. Using global and local ancestry estimates we were able to determine that many of the putatively unadmixed animals contained at least 10% admixture from a different baboon species. This also included estimates that some founding animals of the colony were also admixed, leading to errors in species labelling within the colony which potentially impacted breeding experiments. We generated over 1500 ancestry informative markers capable of differentiating olive and yellow baboons to a high degree of accuracy and identified more than 27,000 fixed markers between the two species. We also created updated genetic maps for the *Panubis1.0* genome build. In summary, our results show that genetic studies of baboons can highlight instances of cryptic admixture. Lastly, we helped increase the number of genomic resources available for baboons.

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Time-resolved histological and isotopic analysis of rachitic human teeth in an archaeological population: implications for paleopathology and paleodietary research

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The importance of understanding the health impacts of metabolic disease in past populations has driven rapid methodological advances and lively discussion in recent years. In particular, development of histological methods to assess interglobular dentine (IGD) in human teeth has shown significant promise as a means of identifying childhood micronutrient deficiencies in skeletal remains, especially vitamin D deficiency (VDD). Human teeth are also frequently sampled for isotopic paleodietary analyses, which may lend further insight to understanding the roots of childhood nutritional deficiencies in past populations. While the past decade has brought widespread awareness of the potential of macronutrient dietary deficiencies to create pathological alteration of isotopic values, metabolic impacts of nutritional microdeficiencies in analyzed human tissues are less commonly addressed. To investigate the potential of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) stable isotopes as biomarkers for VDD, we employed a method correlating histological evidence for IGD in human dentine with $\delta^{15}N$ and $\delta^{13}C$ analyses in incrementally-sampled dentine. Teeth (n=11) in 8 individuals with skeletal evidence of rickets from a postmedieval (18th-19th c.) Quaker cemetery at Coach Lane, North Shields, UK were selected and prepared for histological and isotopic analysis. Results suggest that relationships between anatomical and biogeochemical impacts of metabolic physiology are complex, and interpretation requires consideration of thresholds and potential comorbidities. Further isotopic analysis at the amino acid level may add specificity to interpretation. However, this method shows great promise as a means of accessing time-resolved multi-line data on metabolic health in childhood and adolescence.

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An evaluation of the patterning cascade model in the human lower diphyodont dentition

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The patterning cascade model (PCM) is a prominent evolutionary developmental framework outlining the evolvability of postcanine tooth form. According to the PCM, accessory cusp development with pronounced expression becomes more likely if: 1) the distance between early-developing primary cusps is reduced, 2) crown development is extended, and 3) cellular availability is higher to support the development of additional cusps. Previous research has focused on examining model expectations in upper permanent teeth, while the lower and deciduous dentitions have received less attention. The current study explores if lower molar accessory cusp expression (cusp 5, cusp 6, cusp 7) in human diphyodont metameres (dm_2, RM_1, LM_1) subscribes to model expectations.

Data on relative intercusp distance, morphological trait expression, and crown size were collected using 3D scans of mandibular casts from a contemporary Solomon Islands sample (n=126). Proportional odds logistic regression was utilized to determine whether reduced intercusp distance and larger crown size significantly influenced lower molar accessory cusp expression. In dm_2, an expanded cusp 4-5 distance increased the likelihood of developing a more pronounced cusp 6, while a reduced cusp 3-5 distance was an important predictor of greater cusp 7 expression. As a function of location within the permanent molar crown structure, the reduction and expansion of particular intercusp distances were highlighted as significant predictors of accessory cusp expression. Based on study results, competition for cellular resources exists among neighboring cusps, where the number of cells allocated toward cusp development will have direct and opposing consequences for surrounding cusp development and expression.

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Sleep architecture and nighttime vigilance in a rural agropastoral community in South Africa

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Stress is a primary cause of sleep disruption and poor-quality sleep. High levels of nighttime vigilance can reduce deep restorative sleep, as individuals maintain a low arousal threshold throughout the night to be alert for any threats. Here, we examined the sleep architecture (proportion of light, deep, and R.E.M. sleep) of an agropastoral community in the Eastern Cape, South Africa that commonly experiences livestock theft at night. We collected *Oura ring Gen2* sleep data from 30 participants (9 herders, 21 non-herders; overall 370 nights). We predicted that due to stock theft risk, herders would exhibit proportionally less N3 (deep) and R.E.M sleep throughout the night compared to non-herders, and that gender differences in sleep architecture would be found. Linear fixed effect models were run for each sleep stage, controlling for age and subject ID. Interestingly, no significant differences in sleep stages were found between herders and non-herders, or between genders. Findings indicate that both groups spent equal time in N3 sleep (herder: 22.5%, SD: 0.07; non-herder: 22.0% SD: 0.07), with minimal differences in R.E.M (14.6% and 19.3%, respectively). Our findings indicate that while there is large individual variation in sleep patterns, the community overall exhibited similar sleep staging. Thus, the effects of stress on sleep architecture are complex and multidimensional. As the community has a shared fear of stock theft, proportion of deep sleep may also be a protected trait in chronic stress situations. Our next steps will examine the effect of ecological variation on vigilance and sleep patterning.

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Balancing Act: Snout Length and Midfacial Function in Mammals

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In primates, the vision/olfaction tradeoff hypothesis stipulates that increased orbital convergence, especially in haplorhines, results in reduced snout length and less complexity of skeletal structures within the nasal chamber. To determine the degree to which internal nasal complexity relates to snout length alone, we examined bats, an order of mammals that also varies greatly in midfacial projection. We used microCT and iodine-enhanced computed tomographic (diceCT) scans of 59 adult bats from 12 families, to count the number of turbinals (scrolled or branched bones that are lined with olfactory or respiratory mucosa) in each species. Using Amira, we reconstructed skulls and measured palatal and cranial length, then computed a snout projection index (SPI = palatal length/cranial length). We also assessed rostrocaudal distribution of olfactory mucosa using a subset of specimens with matching histology. MicroCT samples revealed all specimens had between two and seven turbinals (excluding maxilloturbinal). Bats with elongated snouts (SPI 0.5 or higher) had five or more turbinals, while bats with foreshortened snouts SPI (< 0.4) have lost turbinal elements. Preliminary observations based on histology indicate that bats with the most foreshortened snouts also lacked olfactory mucosa in the most posterior end of the nasal cavity. Among bats with missing turbinals, all are echolocators, although other factors (e.g., dietary) are yet to be considered. Turbinal loss, as well as diminution of olfactory mucosa on the most posterior turbinals in echolocating bats presents an interesting parallel to primates, suggesting a possible trade-off in functions of the midface (i.e., echolocation and olfaction).

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Primate postorbital morphology and the question of omomyoid phylogenetic relationships

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The major clades of extant primates exhibit key differences in postorbital morphology. Strepsirrhines have a postorbital bar formed by the frontal and zygomatic, but have broadly confluent orbital and temporal fossae. By comparison, haplorhines have bony postorbital septa formed by the frontal, zygomatic, and alisphenoid that intervene between the orbital and temporal fossae. Tarsiers and anthropoids differ in the extent of the postorbital septum and the relative contribution of each bony element. These postorbital morphologies are generally described as representing three character states: a postorbital bar only in strepsirrhines, a "partial" postorbital septum in tarsiers, and a "complete" postorbital septum in anthropoids. Here we consider a fourth postorbital character state evident in a new omomyoid frontal bone from the Tornillo Basin of Texas. The new frontal resembles *Rooneyia viejaensis* in exhibiting a lateral process with a ventrally-directed flange separating the postero-superior orbit from the site of origin of the anterior temporalis. The inferior margin of the ventral flange is free and does not appear to have contacted the zygomatic or alisphenoid. Functionally, the ventral flange may have helped to prevent perturbations of the orbital contents by contractions of the temporalis during mastication. The evolutionary implications of these observations depends on the phylogenetic relationships of *Rooneyia* and the taxon represented by the new frontal (possibly *Mytonius*). The ventral flange may represent an intermediate character state between an unexpanded lateral process and more extensive postorbital septa. Alternatively, ventral expansion of the lateral process may have evolved in parallel in multiple primate clades.

Evolutionary Foundations of Privacy Perceptions

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Concerns over privacy are central to many high profile socio-political debates, yet relatively little empirical research has investigated privacy beyond the realm of digital communications. A dual-inheritance perspective posits i) there are universal psychological mechanisms which evolved via natural selection to regulate the dissemination or withholding of information, and ii) the process of cultural evolution has given rise to corresponding cultural institutions, including cultural models of privacy. Here, I test the influence of multiple distinct features of social interactions– the situation in which information was acquired, transmission of information to a third party, the identity of said third party, and the relevance of the information itself– on perceptions of privacy. Participants (n=280) were randomly assigned 4 of 24 possible vignettes, evaluating each along 5 dimensions. Each vignette portrayed a hypothetical information exchange between the participant and another individual (the "receiver"). Results support the notion that intentionality affects moral judgment, with participants rating situations in which the receiver actively sought to obtain information as significantly more wrong and a greater violation of privacy than those in which information was passively obtained. I additionally observed a main effect of information transmission, such that transmission to a third party beyond the receiver significantly raised participants' perception of privacy violation, with transmission to socially connected individuals rated as significantly more wrong, harmful, and a greater violation of privacy. Results suggest the concept of privacy overlies evolved psychological mechanisms which serve to regulate the transfer of fitness-relevant information towards adaptive ends.

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Pubertal timing during the late Avar period in Austria

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New methods to observe pubertal development on skeletons allow us to study the deep past of the life history stage of adolescence. Presently, there is a lack of studies from Central Europe and the Early Medieval Period. In order to address this research gap pubertal timing of 143 individuals (60 females, 81 males, 2 undetermined) from the Late Avar Period (7th-8th CE) sites Mödling (n = 96) and Leobersdorf (n=47) in Austria were analysed to allow evaluation of diachronic developmental changes in the European past. Individuals between the ages of 8 and 30 years were analysed for indicators that allow placing them in one of seven puberty stages. Reliable sex estimation for non-adult remains was achieved via genetic sex estimation. Additionally, the age-at-menarche was studied by observing the ages before and after menarche occurred. A comparison with previously published data from the Roman, Late Antique and High Medieval Period suggest that adolescents in general seem to mature later than in the comparison populations. This was statistically significant in the deceleration phase of the pubertal growth spurt (p=.019) (Roman – Late Avar). Sex-specific observations reveal that this seems to be especially true for males (p=.033). Similarly, the average age after menarche seems to have increased from the Roman to the Late Avar Period (p=.008). This could indicate a decrease in living conditions. This study provides new insights into adolescent development which has implications for health and life history development in the past.

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Late survivors: Traditional ecological knowledge and the timing of extinction of Madagascar's large-bodied Holocene vertebrates

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During the Late Holocene, Madagascar experienced the loss of ~50 vertebrate species including mammals, birds and reptiles. Many of these were relatively large-bodied (e.g., "giant" lemurs, hippopotamuses, flightless elephant birds, and horned crocodiles). Many are known to have survived into the past two millennia. Most extinction date estimates fall within a narrow window between ~800 to 1200 CE. There is broad skepticism regarding survival of any of these species into the second half of the last millennium – i.e., the period of European contact. Only one radiocarbon date (a *Palaeopropithecus* at 442.5 ± 122.5 cal BP from Ankilitelo cave in southwestern Madagascar) falls within this period. Ethnohistoric (lore and recorded eyewitness) accounts of large vertebrates abound within this period in Madagascar, but they are often fanciful and discounted as mythical. Simultaneously, many new species have been discovered even over the past decade, often spurred by the knowledge of local people. These are typically small species, but examples of the discovery of large vertebrates believed to be extinct exist outside of Madagascar, again aided by local people.

We synthesize data from traditional ecological knowledge of large vertebrate species in Madagascar, including apparent references to large-bodied lemurs (*Palaeopropithecus, Pachylemur*, and *Archaeolemur*), a large-bodied euplerid, horned crocodiles, hippopotamuses, giant tortoises and elephant birds. We map these findings and describe underlying patterns. We show how traditional ecological knowledge has been undervalued, and can help in our understanding of extinction processes, building research partnerships, and possibly, discovering remote populations of species believed to be extinct.

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Variation in Orangutan Development and Body Size: Implications for Assigning Sex and Age to Fossil Hominins

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Living great apes provide reference models for interpreting body size variation in fossil hominins and understanding how selection shapes development. Orangutans present a challenge to classifying fossils based off of sex and age given the wide range of body sizes in unflanged males, with some body size measurements overlapping with those of adult females. However, quantifying this variation has been challenging. Here, we highlight data obtained using three recent approaches to measuring body size in orangutans. We first present our work in Gunung Palung National Park, Indonesia, that uses a laser camera to non-invasively measure wild orangutan body size during development and across adult body sizes. Forearm lengths ranged between 113 mm in infants to 495 mm in flanged males. Second, we present our non-invasive methodology and data on forearm lengths of a similarly-aged unflanged male and flanged male housed at the Toronto

Zoo. Despite being different morphs, the males had similar forearm lengths (46.5 and 47cm, respectively). Third, we review data on orangutan limb lengths measured from museum collections that show a wide range in orangutan body proportions. We review the ecological and social conditions that have selected for slow growth in orangutans, variation in adult body forms, and facultative male development. Collectively, these approaches highlight that orangutan body size is highly variable, and strongly influenced by both ecology and social system. This variation in one of the three living great ape genera, introduces increased complexity to the task of identifying the maturity of individuals from fossil remains.

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Prevalence of cribia orbitalia and porotic hyperostosis in Dyrrachium (modern-day Durres, Albania) in the Roman and Late Antiquity periods

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Environmental conditions and socioeconomic organization influence general health status. Cribra orbitalia (CO) and porotic hyperostosis (PH) are skeletal lesions that may indicate malnutrition and infectious disease. Bioarchaeological data suggest that prevalence of CO and PH vary in different time periods and geographic locations. In the Mediterranean region, prevalence of PH and CO have also been linked to environmental factors, such as marshy areas with mosquitos carrying malaria. Dyrrachium (Albania) was an influential city during the Roman period (1st -3rd AD) and Late Antiquity (4th -7th AD) in the eastern Mediterranean. Although Late Antiquity was a transitory period associated with regression and political changes, Dyrrachium maintained its importance. We compare 25 individuals from the Roman period with 28 individuals from Late Antiquity to see the prevalence of CO and PH. Previously, we have compared the dental pathology of these individuals. We test the hypothesis that there is no difference between the individuals of the two periods for CO and/or PH since Dyrrachium did not experience an economic regression and dental pathology indicates no statistical difference between these time periods. The results show that 56% (14/25) of the Roman and 35% (10/28) of Late Antiquity samples have CO and/or PH, but they are not statistically different (Mann Whitney U, *p*-value=0.142). Environmental and economic factors are two potential influences on these pathologies, and this sample may provide information on how different conditions may influence the prevalence of CO and PH. We look at other Mediterranean areas to contextualize the results from Dyrrachium.

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Influence of environmental effects on fluctuating asymmetry of cranial nonmetric traits in rhesus macaques (*Macaca mulatta*) on Cayo Santiago

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Fluctuating asymmetry (FA), random fluctuations between right and left sides, is thought to be an indicator of developmental instability, with increased FA associated with factors interrupting development. In this study, patterns of FA of cranial nonmetric traits in rhesus macaques (*Macaca mulatta*) from Cayo Santiago, Puerto Rico were assessed to test whether increased FA occurs in response to identified environmental events during monkeys' development.

The history of the rhesus macaques on Cayo Santiago, Puerto Rico since 1960 is well documented, including dates of improved food provisioning, implementation of tetanus vaccinations, and dates of major hurricanes. Bilateral occurrence of eight cranial nonmetric traits were recorded in 466 individuals (263 females, 203 males) age 3 mo. - 31 years. Presence, absence, or number of each trait were recorded for right and left sides. We predicted that there was decreased FA with food provisioning and implementation of tetanus vaccination, and increased FA in individuals growing during a hurricane and its aftermath.

While there was a strong familial association for these cranial nonmetric traits, there was limited difference in FA across families. Similarly, FA is generally not significantly decreased with food provisioning or institution of tetanus vaccination or increased for individuals in development during hurricanes. This suggests that this population of rhesus macaques was generally buffered from large-scale environmental events. There were individuals that exhibit high levels of FA, suggesting that other factors may destabilize cranial development in certain individuals. More research is warranted to identify developmental insults leading to increased FA.

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Shape variation in the cuboid: cercopithecoids, hominoids, and a reappraisal of OH 8

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The cuboid is an element that contributes to lateral midfoot mobility in non-human apes and cercopithecoids, and to midfoot stability and a longitudinal arch in humans. Differences in cuboid morphology between genera are well understood, but less is known about differences between more closely related species and subspecies. Here we analyzed the cuboid shape of *Gorilla gorilla gorilla* (n=28), *Gorilla beringei beringei* (n=6), *Gorilla beringei graueri* (n=10), *Homo sapiens* (n=50), *Hylobates* sp. (n=44), *Pan paniscus* (n=19), *Pan troglodytes* ssp. (n=58), *Pongo abelii* (n=15), *Pongo pygmaeus* (n=26), *Mandrillus* sp. (n=5), and *Papio* sp. (n=23) to understand its correspondence with locomotor variation. We also included the OH 8 cuboid to investigate how it differs from these taxa. Cuboid shape was analyzed using three-dimensional geometric morphometrics. We used fixed landmarks, and sliding curve and surface semilandmarks to capture the entire morphology of the cuboid. Semilandmarks were slid to minimize bending energy and a generalized Procrustes analysis was used to align landmark configurations. Principal component analyses reveal that most shape variation occurs in the proximodistal length of the cuboid, with humans, OH 8, and gibbons exhibiting the longest cuboids, and great apes the shortest. Additionally, we observe differences in cuboid shape between gorilla species, between orangutan species, and between bonobos and chimpanzees. Notably, humans and OH 8 display an almost identical cuboid shape, with only slight differences near the cuboid beak. Our results emphasize shape diversity among closely related living taxa and suggest the presence of an essentially human cuboid by the Early Pleistocene.

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Maxillary Sinusitis in Ancient Xinjiang: Investigating Respiratory Health in Bronze Age to Early Iron Age Populations and its Environmental Determinants

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Chronic rhinosinusitis refers to chronic inflammation that occurs in the mucous membranes of the sinuses. Among the paranasal sinuses, the maxillary sinus stands as the largest. Due to its unique location and structure, it is more susceptible to infections and inflammatory reactions. Multiple bioarchaeological studies have indicated that maxillary sinusitis was a common health issue in ancient societies. In order to understand the respiratory health status of populations in the Turpan region of Xinjiang, China, this study conducted macroscopic and endoscopic examinations of the maxillary sinuses in individuals, who were buried in three cemeteries of Jiayi, Yanghai, and Shengjindian, from Bronze Age to the early Iron Age. Data related to chronic maxillary sinusitis and dental infections were collected. The results showed that approximately one-third of the individuals in these three populations exhibited osseous lesions of the maxillary sinuses. While the prevalence of maxillary sinusitis increased with age, there were no significant differences between gender, or between the right and left sides of the maxillary sinus. Moreover, the impact of oral diseases on maxillary sinusitis was relatively limited. Considering the archaeological context and literature materials, maxillary sinusitis in the Turpan region appears to be the result of various factors, including an extremely arid climate, the burning of animal dung, and air pollution, among others.

Food Insecurity in Childhood as an Indicator of Sleep Health Later in Life

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Research across disciplines identifies childhood food insecurity (CFI) as a social determinant of health. The current study among n=134 university students uses retrospective measures of CFI to test associations with current food insecurity, psychological distress, and poor sleep. We found that 1) psychological distress was the primary factor determining variation in sleep health, and 2) students reporting a higher incidence of CFI were more likely to experience extreme psychological distress (OR=4.61), food insecurity in college (OR=8.41), and lack access to very stable housing (OR=5.86). Therefore, those with higher CFI may be more likely to experience poor sleep through the mitigating factor of psychological distress. This study contributes to wider research that associates food insecurity and deleterious outcomes to health and wellbeing more broadly. We propose utilizing food insecurity as an easily obtained, gross measure of wellbeing that may signal a wide range of downstream effects important to human biology research.

Exploring the Association Between Biomarkers of Developmental Adversity and Adult Mortality in a Modern Greek Skeletal Sample

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Skeletal biomarkers of early life adversity are typically used to explore relationships among unequal developmental environments, later-life disease burdens, and death. These biomarkers manifest developmentally plastic responses to environmental cues. They also indicate divergence from "expected" environments, understood as environments in which non-adults could develop along their full potential growth trajectories. We evaluated the relationship between skeletal biomarkers of adversity—as representative of specific age ranges of development—and adult mortality through analyses of 20th century skeletal remains from Greece. These individuals experienced consecutive wars and government instability in Greece during their development in the first half of the century.

We collected basicranium landmarks for fluctuating asymmetry (FA) scoring and vertebral neural canal (VNC) anteroposterior and transverse measurements from 155 adult individuals representing three developmental windows: 0–7, 3–5, and 10–14+ years. Age-at-death, sex, and birthplace data were also recorded. We used hierarchical regression to evaluate the association of FA scores and VNC diameters on age-at-death.

Age-at-death was associated with smaller VNC diameters but not lower FA scores. Urban birthplaces were associated with smaller anteroposterior diameters while rural birthplaces were associated with lower transverse diameters, suggesting that early life adversity in Greece had differential long-term impacts on mortality risk based on where people were born. Rural differences in child-rearing potentially had protective effects in early development, but not in adolescence.

With this study we show that the application of a developmental window perspective to an underrepresented population in modern biocultural literature is important for considering spatiotemporal variations in developmental plasticity.

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Exploring the ethics of great ape skeletal remains research: historical perspectives and contemporary solutions

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While ample discourse considers the ethics of human skeletal research and curation, an absence persists regarding great ape skeletal remains, despite clear interest in ethical treatment of living apes. Here, we trace the history of great ape remains in natural history museums, contextualizing these ape bodies in a colonial era of collection and curation and the violence this entailed. We consider the enduring influence that this historical context has had on scholarly pursuits and offer a set of practices for research and curation of great ape remains. The proposed interventions involve the restoration of individual identity, narrative, and memory, coupled with an integration of contextual reflexivity and decolonial theory. Through these interventions, four resultant recommendations were developed to encompass a multifaceted approach. The recommendations include the imperative to 1) contextualize each individual great ape, 2) reassemble fragmented individuals, 3) scrutinize the captive-wild dichotomy, and 4) cultivate collaborative international conversations. It is critical to prioritize and amplify the perspectives of those from countries where apes originate and, in doing so, imagine what a reparative future for great ape research and curation could look like. Our foremost objective is to ignite a discourse to critically engage with the ethical and theoretical dimensions of research using great ape skeletal remains. Through this dialogue, we aspire to promote a more ethical and holistic approach to the study and curation of these invaluable specimens and build a deeper understanding of our relationship with our closest living relatives.

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Hip stabilization in an australopithecine hip: the influence of shape on muscle activation

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Hip stabilization through muscular activation of the gluteals is a key feature of hominin walking, but the role of pelvic shape on muscular activation remains uncertain. Coupled with this is uncertainty regarding whether or not the kinematics and kinetics of modern humans are appropriate proxies for the patterns in extinct hominins. In this work we treat modern human kinematics and kinetics as a hypothesis by applying them to musculoskeletal models with human-like and australopithecine-like hips and examine joint reaction and muscle forces. We hypothesize that the hip functional complex that includes biacetabular breadth, femoral neck length, and iliac blade flare produces hip abductor muscle activations and hip joint reactions that are similar in the modern human- and australopithecine-like forms.

Using previously developed musculoskeletal models that approximate gluteus maximus with twelve muscle elements, gluteus medius with twelve, and gluteus minimius with three, we calculated joint reaction and muscle forces using inverse dynamics analyses. We used data from ten individuals who walked at their normal velocity. We found that the shape of the australopithecine-like pelvis produces absolutely higher muscle activations in gluteus medius, but lower muscle activations across a long period of stance in gluteus maximus compared to the human-like pelvis when kinematics and size are held constant. Hip joint reaction forces are similarly heterogeneous: the australopithecine-like hip exhibits lower forces in the direction of travel but higher in the vertical. These results suggest that, while the australopithecine-like pelvis is compatible with human walking patterns, other influences on pelvic shape are present.

Occupational belonging and food insecurity: A cross sectional study among Haitian and Dominican tourism workers in the Dominican Republic

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Belonging is an important evolutionary trait of human sociality and is integral to socio-ecological adaptation within social structures, ultimately influencing access to resources. Social belonging in contemporary occupational settings may then be an important indicator of social and health inequities such as food insecurity. In the Dominican Republic's tourism sector, Haitian migrant workers invest substantial time laboring in environments characterized by unregulated employment, high local inflation, and disproportionate exposure to racialized police violence. Haitian laborers must also navigate social belonging while adapting to the Spanish-speaking host-country and an English-dominated globalized tourism market. Here, we used ethnographic data and exploratory factor analysis to formulate a novel 13 item scale of occupational belonging and tested associations with food insecurity in a 2019 cross-sectional study among Haitian (n=31) and Dominican (n=29) male tourism workers (ages 18-30) in Puerto Plata, Dominican Republic. We hypothesized differing levels of occupational belonging and food insecurity by nationality and a negative linear relationship between occupational belonging and food insecurity. Results demonstrate higher mean food insecurity (t(56)=-3.85, p=0.0003) and lower mean occupational belonging (t(51)=7.07, p<0.001) reported by Haitians compared to Dominicans. Multivariate regression, adjusting for nationality, age, and number of languages spoken, shows a negative association between occupational belonging and food insecurity (β= 0.16, p=0.017). Models stratified by nationality lacked power due to sample size. This research implicates occupational belonging as a potential biosocial indicator of population health inequities in increasingly globalized settings.

Co-occurrence of skeletal stress indicators: enamel hypoplasia and facial fluctuating asymmetry vs reduced vertebral dimensions

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Indicators of the skeletal response to early life growth disruptions are used to get insight into the level of stress experienced by past human populations. An array of skeletal stress markers has been studied, although the simultaneous occurrence of multiple indicators in the same individuals has been relatively rarely examined. The aim of this study was to analyze the co-occurrence of linear enamel hypoplasia and facial fluctuation asymmetry with reduced dimensions of the vertebral column. The analysis involved skeletal remains of adult individuals from a medieval cemetery in Cedynia, Poland. A set of 40 male and 41 female skeletons was selected, with both teeth and vertebrae from all sections of the spine available, and a set of 33 males and 41 females, for whom it was possible to perform both vertebral and facial measurements. Hypoplastic defects were recorded by presence or absence. Four 3D facial measurements were taken using Geomagic Studio 12, and then the fluctuation asymmetry index was calculated. The sagittal and transverse diameter of the vertebral foramen and the anterior and posterior height of the vertebral body were measured. ANOVA showed the association between enamel hypoplasia occurrence and reduced transverse diameter of the vertebral canal in the cervical spine of females. A correlation was found between higher level of fluctuation asymmetry in orbital height and width and lower vertebral dimensions. The co-occurrence of the examined skeletal stress indicators is related to partly overlapping development stages of the analyzed skeletal elements at the time of stress episodes.

Isotopic data from the Roman site of Scupi in Macedonia

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This paper presents isotopic results from a mass burial from the site of Scupi (0-300 CE), a Roman period site situated in the Balkans in the city of Skopje, Republic of Macedonia. Thirty young and middle adult males were analyzed, in detail, and here we present results from sampled paired rib and second or third molar teeth.

Bone collagen yields were very good, and light isotope results for carbon (-18.7‰, ±0.67) and nitrogen (9.5‰, ±0.85) broadly indicate a diet of C3 cereals (wheat, sorghum, rice) accompanied with fish and meat. Bone bioapatite results (relative to VPDB) for carbon (-10.2‰, ±0.99) and oxygen (-6.1‰, ±0.50) provide evidence for 'total' diet and perhaps climate, as do tooth enamel results for carbon (-11.1‰, ±1.02). and oxygen (-5.7‰, ±0.55). Heavy isotope results for strontium ^{87}Sr/^{86}Sr average 0.70975 (±0.001) with an observed range from 0.70808 to 0.71207. Lead (Pb) isotope averages for ^{208}Pb/^{204}Pb are 38.83 (±0.035), for ^{207}Pb/^{204}Pb are 15.66 (±0.004), and for ^{206}Pb/^{204}Pb are 18.70 (±0.025).

Intrasite discrimination indicates marked heterogeneity of results, including overall diet and mobility proxies. The data are compared against broadly contemporary sites in the circum-Mediterranean region for diet and climate. Additionally, the lead isotope ratios are discussed with respect to assessing variation in Pb values of local plumbing and regional baseline maps. Results underscore the importance of inter-regional trade and connections during the height of the Roman Empire.

Paleoproteomic analyses of Early–Middle Pleistocene hominids from the Sangiran Dome

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One of Southeast Asia's most extensive fossil records of hominids (Hominidae) originates from the Sangiran Dome (Java, Indonesia), where three genera dating to 1.3–0.5 Ma are identified: *Homo erectus*, *Pongo* sp., and the enigmatic species *Meganthropus palaeojavanicus*. This high diversity evokes questions regarding interspecific interactions and distribution of ecological niches among these taxa. Their phylogenetic placement within the Hominidae family is crucial for understanding processes of speciation, adaptation and demise of these extinct hominids in Southeast Asia, where only *Homo sapiens* and three species of orangutans exist today. We used high-resolution tandem mass spectrometry to sequence enamel peptides and recover biological and phylogenetically-informative information. Preliminary tests on faunal dental remains from the Sangiran Dome showed that enamel proteins are preserved and can be recovered. We then analyzed dental enamel of *Homo erectus*, *Meganthropus* and fossil *Pongo* from Sangiran using paleoproteomics. As a result, the *Pongo* specimen SMF-8864 can be confidently identified as a male, while only AMELX-specific peptides were identified in the *H. erectus* and *Meganthropus* teeth. While SMF-8864 clusters well with *Pongo*, the *H. erectus* and *Meganthropus* fossils group within the Homininae subfamily. Even though these results are still preliminary, and despite the various challenges related to protein preservation in dental remains from open-air sites in tropical areas like the Sangiran site, results demonstrate the potential of paleoproteomics to resolve phylogenetic relationships among Early to Middle Pleistocene hominids.

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Fertility and Stress in Colonial Peru: A Transition Analysis-Based Paleodemographic Reconstruction of Birthrates and Female Health in the Lambayeque Valley Complex

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Bioarchaeology has long sought paleodemographic insights on past populations but has been hindered by inherent limitations of traditional adult age estimation techniques. Continuing development of transition analysis helps transcend past issues in paleodemographic studies. Here, we apply transition analysis 3.0 (TA3) to adult human skeletal remains from the north coast of Peru in a paleodemographic reconstruction of crude fertility following Spanish colonization of the Lambayeque Valley Complex. We hypothesize that following conquest, the native Muchik communities of Mórrope and Eten (1535-1750 CE) experienced a shared decline in birthrate. Age estimations based on dental development were calculated for 401 nonadults and TA3 estimations generated for 176 adults. The well-established D30+/D5+ fertility estimation ratio demonstrates that the Mórrope community (D30+/D5+ = 0.8732) had lower fertility than Eten (D30+/D5+ = 0.5377), and that this difference is statistically significant ($z = 5.0156$; $p < 0.0001$). Also, D30+/D5+ values were calculated for Early/Middle and Middle/Late Colonial period subsamples at both sites. Birth rates in Eten seem to have increased over time while in Mórrope it declined slightly. Fertility is a function of female energetic status and biological stress. These findings parallel various independent lines of archaeological, skeletal, and contextual evidence indicating that Mórrope females endured significantly more stress compared to Eten. We reject the hypothesis. Colonization did not lead to uniformitarian outcomes, even locally. We also argue that paleodemographic fertility estimations reveal an embodiment of Indigenous female socioeconomic marginalization. This work further advocates for the wider use of transition analysis in bioarchaeological studies.

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Does oxytocin modulate cortisol in ring-tailed lemurs? A test of the social buffering effect

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Cortisol, the main stress hormone in primates, is a potent glucocorticoid (GC) released via the hypothalamic-pituitary-adrenal axis (HPA). Affiliative relationships counter its negative effects via social buffering (SB), whereby the amount of GC released in response to a stressor is reduced by the presence of group members. SB is believed to involve oxytocin, which modulates stress reactivity by inhibiting the HPA. We examine SB in 6 adult ring-tailed lemurs (*Lemur catta*) at the Duke Lemur Center.

We first obtained a blood sample to establish baseline GC and oxytocin concentrations. 2 weeks later we characterized the physiological outcomes of SB using an experimental stressor (netted capture) and two blood draws, to estimate peak and recovery concentrations (timed at 15-mins and 30-mins post-stressor). The stressor occurred under two conditions: a social condition (individuals could see and hear their group members), and a solitary condition (individuals were isolated).

We fit a mixed-effects model to the data with GC concentration set as a response variable and condition (social vs solitary), timepoint (baseline, 15-mins, and 30-mins), and OT concentrations as fixed effects, and a random intercept for ID. To evaluate the significance of the fixed effects, we conducted a Type II Wald chi-square test. Our results showed that only timepoint was significant ($x^2 = 17.28$, $p < 0.001$). The effects of condition ($x^2 = 1.18$, $p = 0.277$) or OT (x^2, $p = 0.347$) were not significant. Further testing is required to determine the conditions that produce SB in this species.

Femoral-pelvic interactions during growth in a cross-sectional sample of 4-23 year olds from England

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Though pelvic evolution is often touted to be under direct locomotor selection, a key aspect of locomotion depends upon the relationship between the pelvis and the lower limb, as mediated by femoral-pelvic interactions. As the pelvis and femur are under different developmental trajectories, the relationship between these structures may be dynamic: a relationship that should be better understood in order to fully interpret functional morphology and its evolution. Here we examine the relationships between femoral neck length and pelvic breadths (bi-iliac, biacetabular, bitrochanteric, and pelvic inlet) in a sample of 4-23 year olds from England included in a contemporary cross-sectional growth study (female n = 329, male n = 342). Measurements were extracted from dual-energy x-ray absorptiometry (DXA) scans. Piecewise regression was used to determine points of changes in the relationships between each measurement and age, and between neck lengths and pelvic breadths. Early growth is similar in both sexes, aside from accelerated bi-iliac breadth in females. Females slow growth in all measures at younger ages than males, with an accelerated inlet breadth increase between 10-14 years in females. Femoral neck length does not show consistent relationships with pelvic breadths. Instead, at certain points the slope declines substantially. This point occurs at smaller breadths in females than in males. Therefore, the pelvis shows variable growth trajectories across its constituent parts, and the functional biomechanics of the femur and pelvis together show further, diverse growth patterns that may differ between the sexes and with factors such as nutritional status or activity.

Brain Energetics and the Evolution of Hominin Growth and Development: Implications for Paleoanthropology

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The high energy needs of the human brain, which account for 20% of resting metabolism in adults, are widely assumed to have required trade-offs with competing functions within the body. However, the energy costs of the human brain are both absolutely and relatively highest during childhood, when costly synaptic processes related to learning are maximal. These high costs led to trade-offs that help explain a suite of co-evolved life history characteristics. Notably, age changes in the rate of weight gain are tightly inversely related to brain energetics, which led to deferring of rapid growth until after peak brain needs, thus helping explain the pronounced human pubertal growth spurt. Because the childhood peak in brain energetics occurs after weaning and when body fat reserves are at a nadir, the stable and buffered nutritional supply of food sharing/cooperative breeding was likely a prerequisite for human brain expansion. In this talk I will discuss our imaging work that quantifies these costs and the magnitude of trade-offs that they entailed. These findings show that cerebral blood flow follows a similar developmental pattern to glucose uptake, thus indicating that proxies of blood flow can be used to explore the costs and trade-offs related to human encephalization. In light of these findings, skeletal proxies of cerebral blood flow, which our collaborative work has shown track developmental changes in blood flow in humans, may provide an important tool to reconstruct developmental brain energetics, and the constellation of co-evolved modern human life history traits, in the fossil record.

Expanding investigations of cranial vault modification and social landscapes among ancient Andean communities using 3D imaging and geometric morphometrics

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The integration of 3D digital methods in bioarchaeology has allowed researchers to advance work on social identity, including new approaches to investigating cranial vault modification (CVM) that was practiced by ancient Andean communities to achieve a desired head shape during early childhood. Here, we expand on previous contextual work, examining the standardization of CVM using high resolution digital models from 11 coast and highland archaeological sites in the central and south Andes over 5,500 years of prehistory. Anatomical landmarks were recorded on the cranial vault of 120 individuals with tabular, annular, and unmodified types. Data were subjected to standard morphometric methods, principal components and discriminant analyses, followed by statistical pairwise tests to investigate CVM by type, time, and region. Results show clear distinctions between modification types, but weak separation between coast/highland regions when sites are plotted together. However, two of the chronologically earliest Peruvian sites (Chilca; coast/La Galgada; highlands), and a late-period site from La Real (Arequipa), all of whom have tabular types, show close morphological affinities to one another. Results also revealed low intrasite variability during the Archaic period in northern Chile (coast), but greater variation (e.g., less standardization) among late-period sites in the Peruvian Highlands and Patagonia, the latter of which could be explained by increased population movement in these regions during the late Holocene. Considering social context, we demonstrate that as early as 5,500 years ago, communities had standardized notions of head shape, which served as a powerful indicator of social identity throughout the entire Andean world.

Buried in iron shackles: A case study in how modern bioarchaeological method, theory, and terminology help us tell stories of the past

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Bioarchaeologists have a shared goal of trying to tell the story of the individuals and populations they study. In attempting to recreate the behavior of past peoples, we sometimes overstep and make assumptions about the people's lives that cannot be fully supported by the data. In some cases, bioarchaeologists use these gaps in current method and theory to build a story that is partly based on data and part extrapolation, such as with (fictive) osteobiography. In other cases, bioarchaeologists have attempted to build bridges between what we understand about health of the living and the lived experiences of the dead, such as with measures of allostatic load and stress indices. These efforts have resulted in methodological and theoretical improvements that allow us to better understand the lives of ancient peoples. Here we examine three individuals from the Greek colony of Himera who were buried in iron shackles. We use multiple bioarchaeological methods to try to tell their story. All three were interred in simple pit burials, and isotopically appear to have been local. Ancient DNA results suggest that genetically they were all biologically male and show Aegean and/or Italian ancestry. Phenotypically they likely had dark eyes and light skin. They died in late adolescence or as young adults, but show varying skeletal evidence for stress, and thus each individual has a unique story. We use this case study to unpack the many different terms we use in bioarchaeology in our attempt to elucidate the health experiences of ancient people.

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The Isotopic Ecology of a Serengeti Insectivore and Applications to Hominin Paleoecology

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Hominin paleoecological studies are increasingly incorporating stable isotopes as a dietary proxy. Understanding the finer dynamics of these isotope systems is imperative to their application to the terrestrial fossil record. Nitrogen (N) and zinc (Zn) isotope ratios correlate to trophic level and are used to estimate the frequency of meat consumption in prehistoric animals, including hominins. While results obtained from these isotope systems can demonstrate animal consumption, we are largely unable to specify with certainty what specific forms of carnivory were employed. Invertebrates may have been a major component of early hominin diets, but we presently lack the means to explicitly test for insectivory. To evaluate the contribution of insects to hominin diets, robust metrics for the insectivore isotopic niche space will be needed. The Serengeti ecosystem hosts one of the few obligate insectivores large enough to sample for N and Zn isotopes: the aardwolf (*Proteles cristata*), or termite-eating hyaena. We examine diet correlated isotopes, recovered from both tooth carbonate and collagen, in aardwolves and sympatric species of various dietary categories, including flesh-specialized carnivores, osteophagous carnivores, and omnivores. We compare $\delta^{15}N$ and $\delta^{66}Zn$ values for these taxa and evaluate differences in the trophic signal. We demonstrate that unequal fractionation of these isotope systems leads to observable differences in isotopic niche space, allowing for the differentiation of specialized carnivore diets. Future investigations will examine additional omnivorous taxa to evaluate the relationship between the frequency of insect consumption and the offset we observe in N and Zn isotopes.

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Until death do us part: A multidisciplinary study on joint human-animal burials from the Late Iron Age necropolis of Seminario Vescovile (Verona, Northern Italy)

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Animal remains are frequently uncovered at prehistoric and protohistoric burial sites. While immediate factors influencing the deposition of these remains can be determined through taphonomic and osteological analyses, the underlying cultural motivations remain unclear largely due to gaps in the archaeological record and the absence of contemporaneous written records. Here, we contribute to the discussion of these practices by focusing on Seminario Vescovile (Verona, Northern Italy: 3rd- 1st c. BCE), a necropolis culturally associated with the Cenomani group. Out of 161 excavated burials, only 16 feature the presence of animal remains, as complete skeletons, isolated parts, or as food offerings. Four inhumations are particularly interesting due to the presence of horses or dogs. This study addresses the possible factors influencing these practices by considering different variables. The archaeological, anthropological, and isotopic ($\delta^{13}C$ and $\delta^{15}N$ values) analyses of human (n= 92, 23 females, 32 males and 37 non-adults) skeletal remains, coupled with the zooarchaeological examination of all faunal finds aim at uncovering possible funerary, demographic, and dietary similarities among the individuals buried with animals. In addition, ancient DNA analyses test the possible presence of genetic relatedness between these individuals. Results fail to highlight specific demographic, dietary, and archaeological similarities, or genetic relatedness between individuals featuring this specific funerary treatment. Our finds underscore the intricacy of mortuary practices involving animals, resisting reductionist interpretations. Simultaneously, they establish a nexus between Seminario Vescovile and documented funerary evidences from transalpine regions, possibly also influenced by local customs and Roman cultural influences.

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Re-evaluation of morphometric variation among Plio-Pleistocene hominin distal humeri: 28 years later

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In tribute to the late William L. Jungers, this project re-examines his work (with the present author) regarding variation among early hominin elbow joints. In the 28 years since that work was published, the sample of available adult fossil humeri has doubled. It is unknown whether elbow joint variation in this expanded sample supports the taxonomic sorting recently suggested on the basis of cross-sectional shape of the distal humeral diaphysis. Along with the ten specimens originally used by Lague and Jungers, this study includes twelve additional fossils attributed to early *Homo*, *Paranthropus,* and *Australopithecus*. Using scale-free shape data based on new linear measurements, variation within various fossil subsamples is assessed using a bootstrapping procedure, with modern humans as a reference sample. Principal component analysis is used to visualize shape variation among specimens and to evaluate shape differences between groups. Based on statistical comparison of distance matrices, the pattern of overall shape differences among specimens observed by Lague and Jungers strongly resembles that observed in the present study. The results also lend support to the previous observation of at least two distinct morphological groups, one of which consists solely of fossils attributed to *P. boisei*. Among the non-*boisei* specimens, however, three additional morphological groups are now apparent: 1) *Homo*, 2) eastern australopiths, and 3) southern australopiths. This study expands upon the work of Lague and Jungers and demonstrates that variation in elbow joint morphology is consistent with recent taxonomic attributions to *Homo* and *Paranthropus* proposed on the basis of diaphyseal morphology.

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Experimental validation of simulated bite force-gape tradeoffs in *Eulemur* and *Varecia*

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Bite force is commonly used to assess dietary and social adaptations in primates and is a critical variable in models of fossil hominin feeding systems. Despite the importance of these performance variables for understanding form-function relationships in the feeding system, we lack *in vivo* bite force data in most primates, leading to bite force estimates based on *ex vivo* methods without validation. Here we quantify and compare *in vivo* bite forces and gapes with output from simulated Hill-type muscle models in two craniofacially distinct strepsirrhines—*Eulemur*, which has a shorter jaw and faster chewing cycle durations, compared to the *Varecia*.

A total of 1139 postcanine bites was collected across a range of gapes from 16 adults at the Duke Lemur Center in Durham, North Carolina: *Eulemur flavifrons* (n = 6; 3F, 3M), *Varecia variegata* (n = 5; 3F, 2M), and *Varecia rubra* (n = 5; 5F). One-way ANOVA tests indicate that maximum *in vivo* gapes were significantly higher for *Varecia* compared to *Eulemur* (p = 0.01). However, there were no significant differences in recorded maximum *in vivo* bite forces (p = 0.88). Simulated muscle models using architectural data for these taxa suggest this approach is an accurate method of estimating these performance variables. Our *in vivo* and modeling data suggest *Varecia* has reduced bite force capacities in favor of absolutely wider gapes compared to *Eulemur*, and our comparisons validate the simulated muscle approach for estimating bite force and gape in extant and fossil taxa.

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The influence of body size in estimating age-at-death from the auricular surface: An analysis of senescence of the features of the auricular surface

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Forensic anthropologists are commonly tasked with constructing a biological profile when attempting to identify an individual based on skeletal remains. During this process, age estimation is commonly accomplished by scoring the auricular surface of the os coxae. However, this process has encountered issues with accuracy due to biological variances such as height and weight. It has previously been determined that increased body mass index, or BMI, levels can result in an individual being 'over-aged' based on scoring of the auricular surface compared to their actual age at the time of death. However, less has been researched on estimating age-at-death from the auricular surface in low BMI individuals. In a sample of 150 individuals from the Bass Skeletal Collection at the University of Tennessee-Knoxville, three age groups (30-49, 50-64, and 65-80) were examined and their sacroiliac joints scored using the Buckberry & Chamberlain system. Using mean ages from the composite scoring system used in Buckberry & Chamberlain, each of the three groups were designated a lower bound and upper bound mean using a 95% Confidence Interval (30-49 age group: 34.66-39.11 CI; 50-64 age group: 46.72-50.28; 65-80 age group: 56.54-60.25). This data indicates individuals with low BMI are often 'under-aged' based on the scoring of the auricular surface. With these patterns in mind, age-at-death estimation methods can be improved in order to allow more accurate and complete biological profiles to be achieved.

The role of dentition in Aotus mandibular growth

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The Functional Matrix Hypothesis suggests that prenatal/early postnatal bone formation in the jaws is driven by the tissue of dental sacs, the soft tissue precursors of teeth. In a previous study on a growth series of *Aotus nancymaae* we found mediolateral expansion of the maxillary dental arcade is most pronounced during the newborn period, followed by rostrocaudal lengthening in subsequent months. Here, we continued this analysis to test whether mandibular growth follows similar patterns. We used conventional micro-CT and diffusible iodine contrast-enhanced computed tomography (dice-CT) scans from postnatal *Aotus nancymaae* at two days, five days, two weeks, 20 days, three months, and two years. We created 3D models of dental sacs, tooth crowns, and craniofacial skeleton using 3D Slicer, an open-source image analysis program. To assess spatial relationships of dental sacs and mandible we collected landmark coordinates capturing width and length of the dental arcade, in addition to points on the osseous mandible; interdentale inferior, the most lateral points on the first permanent molar, and the most distal point on the arcade were recorded. Our results demonstrated width in the mandibular dental arcade shows the greatest increase in the newborn period, followed by a dramatic increase in rostrocaudal length of the arcade. Intercondylar width and length of the mandibular rami increased primarily in the later period. Overall, the mandibular corpus grows at a higher rate than the ramus at a time when all developing teeth have reached the late bell stage, suggesting that dental sac development drives this growth perinatally.

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Utilizing *FORDISC 3.1* on Simulated Partial Crania and the Implications for Skeletal Analysis

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FORDISC 3.1 is a widely used statistical tool in forensic anthropology to estimate the sex and ancestry of human skeletal remains. It employs discriminant function analysis (DFA) based on cranial measurements to classify individuals into 13 sex and ancestry groups. However, viscerocranium bones (facial bones), which provide crucial measurements for classification, are more likely affected by taphonomic factors than neurocranial bones in forensic contexts. Therefore, classification often relies solely on vault dimensions from the neurocranium. A study by Lanfranchi and Pérez (2018) found that using only neurocranial measurements led to significant misclassifications among Dominicans of Hispanic ancestry. However, misclassification of Hispanic individuals is a known issue in *FORDISC 3.1* due to their diverse ancestry composition; thus, the misclassifications may not be due to the particular sample. This study expands on that previous study, assessing *FORDISC 3.1* with the same nine neurocranial measurements, but with a more diverse sample from the collections of Louisiana State University and Mercyhurst University. The results showed reduced accuracy in sex and ancestry estimation compared to previous research. Although some individuals were correctly classified, there was a decrease in posterior probability and F-Typicality. Thus, the trend of poorly classifying when only cranial vault measurements were used was not unique to the Hispanic population. Practitioners should be cautious when interpreting *FORDISC* results, especially when viscerocranial measurements are unavailable. The principal component analysis (PCA) and DFA analyses primarily categorized crania based on overall size and cranial shape, which may lead to less reliable classifications and potential misclassification.

Assessing childhood and adolescent lifeways through fracture patterns in four post-medieval Dutch communities (1650–1850 CE)

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Considerable research has been undertaken on traumatic injuries to assess past and present community health and activities. However, most bioarchaeological research has focused on individuals with completed growth and development. This research focused on childhood and adolescent lifeways. Fifty-five individuals (1–19 years) from four collections from the Netherlands were analyzed (Arnhem [1650–1829 CE] n=26; Eindhoven [1650–1850 CE] n=11; Alkmaar [1716–1830 CE] n=12; and Zwolle [1675–1828 CE] n=6). Fractures were assessed using detailed macroscopic analysis, microscopy, and micro-computed tomography. Socioeconomic status (SES) was inferred by burial location. Age is associated with the frequency, location, and type of fracture in modern communities. The analysis of fracture patterns in archaeological contexts may be used to recreate past behaviours and investigate social age. This research examines fracture patterns in children and adolescents to explore past lifeways and activities. Fracture prevalence for all four samples is 32.7% (18/55). Adolescents (10-19 years) presented with a high rate of vertebral stress fractures (61.1%, 11/18), including compression fractures and Schmorl's nodes. Clinically, compression fractures are associated with osteoporosis and advanced age. A Fischer Exact test found a significant correlation (p=0.0103) between middle- to low-SES and the presence of vertebral stress fractures. Explanations include malnutrition leading to decreased bone density, strenuous labor, or a combination of both as those with lower SES entered the workplace. Findings from this investigation indicate that detailed bioarchaeological assessments of fractures in children and adolescents are likely to contribute details on their social identities and lived experiences. Podium Presentation

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But some of us are brave: A Black feminist's work in bioarchaeology

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Black women were long excluded from institutions of higher learning and prevented from producing what has come to be viewed as "scholarly" work in the United States. But as Black feminist theorists point out, that did not stop us from other forms of knowledge production that should be given equal respect. Taking this into consideration, I inform my bioarchaeological practice with the scholarly and creative works of Black women to consider new ways of analyzing and interpreting human skeletal remains. In this talk, I illustrate how my practice contributes to and expands upon interpretations of bodies belonging to African descended Ancestors who are "owned" by universities and museums. Examples from my work at the Smithsonian's National Museum of Natural History, The Peabody Museum of Archaeology and Ethnology, and the Carnegie Museum of Natural History demonstrate that considering alter(ed)native perspectives expand options for repatriation and reconciliation between institutions and wider Black communities.

This research has been funded by the Wenner-Gren Foundation and the Smithsonian Institution.

Ash and Bone: Exploring skeletal biomarkers of chronic indoor air pollution via a rodent model

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Anthropology, University of Connecticut

Fire has long served as a trellis for hominin evolution. As pyrotechnology diversified and intensified over time and space, so too did exposure to biomass-produced air pollutants. In particular, the Neolithic Revolution introduced new cultural choices in architectural design, fuel consumption, and division of labor that exposed populations to high levels of indoor air pollution. The health ramifications of protracted smoke exposure in early agricultural societies have remained critically understudied. Here, we detail the preliminary results of a rodent model designed to address how exposure to indoor air pollution shapes bone isotope composition. 12 rats were exposed to two hours of wood smoke a day for 22 weeks. A control cohort of 12 rats was included alongside the exposure group. Bone collagen, apatite, oral swabs, serum, and fecal pellets were collected from both the control and exposure groups. Oxygen isotopes were used to assess how damaged lung alveoli shaped oxygen isotope fractionation in the lungs and overall body water pool. Carbon and nitrogen isotopes, alongside 16S rRNA data, were used to investigate how changes in the oral and gut microbiomes and host-associated immune response influenced the isotopic composition of host collagen in bone while cytokines in the serum were used to assess systemic inflammation. Results from this project provide insight into how signatures of indoor air pollution may be captured in bone and how chronic smoke inhalation affects the structure of the microbiome.

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Earlier Holocene diet and lifestyle shaped past and present global health and well-being

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The world began to change in fundamental ways beginning at the Late Pleistocene-Holocene boundary 10,000-12,000 years ago with the transition to and the later intensification of farmed resources, especially wheat in Western Asia and Europe, maize in North America, and rice in East Asia. The bioarchaeological record documents a global trend of challenges to health and wellbeing, lifestyle, behavior, conflict, and demographic outcomes of elevated and increasing birth rates over the course of the Holocene. These challenges include a continuous increase in human population from 10 million to the present-day 8 billion, mostly living in sedentary, densely crowded communities. These transitions provided the social and behavioral contexts for intercommunity competition, the appearance and rise of organized warfare, promotion of migration, and the presence, success, and expansion of older and newly emerging pathogens and the infectious diseases they cause (e.g., tuberculosis, coronavirus disease, leprosy, tuberculosis, treponematosis, plague, cholera) among other post-Pleistocene challenges that have shaped the world we live in today. This integrative analysis reveals ongoing trends documented in the records of paleopathology, stable isotopes, pathogen and human genomes, body mass and stature, interpersonal violence, demographic transitions, migration, and the behavioral contexts and consequences of the most impactful dietary and behavioral transitions in human evolution. The global dependence on dietary plant carbohydrates will continue to have profound implications for human health and well-being. The associated circumstances are rooted in the origins of foodways that fuel population growth, health, and behavioral outcomes now and into the foreseeable future.

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Cephalopelvic constraint in six monkey genera

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Birth in humans is said to be uniquely difficult, due in part to an exceptionally encephalized neonate and a peculiarly constrained birth canal. However, these claims have been based on comparisons between the dimensions of neonatal heads and the female pelvic inlet. This comparison is inappropriate for non-human hominoids, in which the narrowest part of the birth canal lies below the inlet. We have shown that the fit between fetal head and birth canal in gibbons is almost as tight as it is in humans. To determine whether this is true in other large-brained primates, we quantified cephalopelvic constraint in species of six monkey genera (*Ateles, Callithrix, Cebus, Lagothrix, Saimiri,* and *Papio*). Female pelves from these species were 3D-scanned, and the average minimum dimensions within each birth canal were measured and compared with fetal head dimensions. As with the non-human hominoids, the pelvic inlet was never the narrowest point in the birth canal. Fetal head dimensions drastically exceed the minimum cross-sectional area of the canal in *Callithrix, Cebus,* and *Saimiri,* producing an even tighter fit than that seen in humans. These monkeys must rely on sacral rotation, face-first presentation, and especially disarticulation of the pelvis, to achieve enough space for the fetal head to pass through the birth canal. Although human birth is not uniquely difficult, female hominin body mass and obligate bipedality preclude gross disarticulation of the mother's pelvis, thereby imposing unique constraints on the size of the neonate's head.

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Activity Levels and the Humeral Carrying Angle in a Recent Human Population

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Previous research indicates that the carrying angle of the human elbow differs between the right and left upper limbs, strongly suggesting that the underlying cause of variation in this feature may be partially functional. This analysis explores the relationship between the carrying angle and two measures of activity levels: self-reported history of strenuous activity and cross-sectional geometric properties of the humerus. Computed tomography scans of 40 individuals, 20 male and 20 female, aged 24-40, from the New Mexico Decedent Image Database were used. Recorded life histories of the individuals listed the activity pattern “strenuous lifting” and answers were self-reported as “yes” or “no.” Cross sectional geometric properties of the right and left humerii were taken at 35% of the bone from the distal end, and both asymmetry ratios and body size standardized values were evaluated. A moderate positive correlation between asymmetry in humeral diaphyseal strength and asymmetry in carrying angle was observed, indicating that individuals with greater bilateral asymmetry of humeral shaft strength tend to also demonstrate a higher degree of asymmetry in the carrying angle. Analysis of the body size standardized cross-sectional geometric properties indicates that there is a moderate correlation between left carrying angle and robusticity, but no significant relationship between right carrying angle and size-standardized right humeral strength. Further, no significant relationship between carrying angle and self-reported activity was found.

In vivo midfoot joint location estimation using external skin markers

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Musculoskeletal modeling (MSK) has gained popularity in biological anthropology to measure muscle forces during human gait. In MSK, the human body is modelled as a series of rigid segments connected by joints that are defined by their location relative to the segments they connect. Most MSKs represent complex segments like the foot as a single rigid segment because the internal joint locations can only be directly determined via invasive scanning. Thus, we propose a regression-based method to locate the *in vivo* position of the midfoot joint centers utilizing three-dimensional surface markers.

Simulated weight-bearing computed tomography (SWCT) scans of 20 randomly selected individuals from the database of a Level 1 trauma center were used for this study. Surface models of each foot were generated, and the following surface markers were collected in Avizo Lite: metatarsal heads 1,3 and 5, the dorsal navicular, navicular tuberosity, fifth metatarsal styloid process, lateral and medial malleoli, and the center of the heel. To represent the internal joint centers of the 13 midfoot joints, 26 additional landmarks (two for each joint) were placed within each foot. Stepwise regressions were employed to produce a best fit model for each joint center.

Three-dimensional surface markers can be used to predict the X (r^2=0.91-0.98; SEE:0.002-0.8mm), Y (r^2=0.93-0.99; SEE:0.004-0.6mm), and Z coordinates (r^2=0.70-0.95; SEE:0.02-0.5mm) for all midfoot joints. The predictive equations produced in this study have important implications for researchers seeking to create and validate a more detailed MSK of the foot.

A demographic analysis of transient dynamics in a wild population of white sifaka (*Propithecus verreauxi*) at Beza Mahafaly Special Reserve, southwest Madagascar

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From a given starting point, a population comprised of different aged individuals will typically fluctuate in number over time for a short-period before “settling down” to a given uniform rate of growth (the asymptotic growth rate) and the stable age distribution. These fluctuations are known as transient dynamics, and they have important implications for conservation. Most demographic analyses of populations structured by age/stage rely on long-term asymptotic estimates of population growth rate. Yet conservation interventions and anthropogenic perturbations operate over the short term (10’s of years, not 100’s), so analysis of the short-term dynamics of threatened primate populations provides a more realistic time-frame to anticipate threats and plan management strategies. In this study, I analyze the transient dynamics of wild white sifaka (*Propithecus verreauxi*) at Beza Mahafaly Special Reserve, southwest Madagascar. Using long-term census data of marked individuals and a five-stage matrix population model, I estimate, define, and analyze several indices of transient dynamics. Specifically, I look at two scenarios: the transient dynamics of low population growth rate due to drought (lambda = 0.93) and the transient dynamics of high population growth rate (lambda = 1.03). Under drought conditions, a change in stage structure to low reproductive value individuals results in a transient reduction in population density of 72% relative to asymptotic conditions. Under positive growth rate conditions, a change to this same stage structure results in a reduction of 81% population size relative to asymptotic conditions. I discuss these metrics, and others, in terms of their relevance for conservation.

Effects of hip joint orientation and skeletal torsion on human locomotor biomechanics: Implications for interpretations of hominin locomotor diversity

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Bipedal locomotion is a defining feature of the human lineage. However, the form of bipedality in different hominin taxa and the timing of emergence of a human-like striding bipedal gait have long been a subject of debate. Morphological features of the hip and pelvis have been used to argue for kinematically different gaits in *Australopithecus*, early *Homo*, Neanderthals, and modern humans. However, limited comparison of morphology and locomotor performance in living humans has left a weak base upon which to build hypotheses of locomotor diversity in fossil hominins. In this study, we address these problems by quantifying skeletal torsion features in the pelvis and lower limb and directly evaluating their relationships with transverse plane kinematics during walking in a sample of adult humans. Individually, femoral version, tibial torsion, acetabular version, and iliac blade orientation are not correlated with transverse plane walking kinematics in our sample. However, correlations between femoral version and tibial torsion and between femoral version and iliac blade orientation suggest that there may be anatomical compensatory mechanisms for lower limb skeletal torsion to maintain a forward-facing foot and relative lengths of hip abduction and internal rotation moment arms during walking. These results suggest that caution is warranted in interpretations of musculoskeletal function and performance based on features of skeletal morphology alone, especially in anatomical regions that are highly variable or functionally integrated. Future analyses will evaluate relationships of skeletal torsion features with moments acting about the hip and knee, which may better reflect functional differences in walking mechanics.

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Functional morphology of the human dental arcade

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Dental arcade morphology has altered dramatically across human evolution and the functional demands of mastication are regarded as the principal driver of these changes. This study contributes to our understanding of the form-function relationship in the masticatory apparatus which is crucial to the interpreting the fossil record and human dental health. We use geometric morphometric analysis, particle size distribution, and electromyography to examine the relationship between variation in dental arcade morphology, bite force production, and masticatory performance in 20 human subjects (10 males and 10 females with 28 permanent teeth who have had minimal orthodontic/dental treatment). Covariates include age, sex, weight, and craniofacial dimensions. We found significant sex differences in both dental arcade morphology (size and shape) and bite force, and some evidence for scaling of bite force with body weight that concurs with previous studies. However, our results highlight the independence of dental arcade morphology relative to craniofacial measurements, including jaw length, as well as relative to bite force production and masticatory efficiency. This work demonstrates the complexity of masticatory form and function within a morphologically constrained sample (complete permanent dentition) and suggests further measures that may help unpack the form-function relationship of the dental arcade.

The evolution of suid third molars and isotopic ecology over 10 million years of environmental change in eastern Africa

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In eastern Africa, the emergence of C_4 grassland ecosystems wielded significant influence over the evolution of the region's fauna. Many large herbivorous mammal lineages underwent morphological changes as they shifted from browsing to grazing diets. However, the timing and mode of these transitions varied among these animal groups. Our study delves into the fossil record of eastern African suids, exploring the connections between dental features, dietary habits, and environmental transformations spanning the past 10 million years. As C_4 vegetation proliferated, suid third molars progressively expanded, coinciding with carbon stable isotope data. Around 6-5 million years ago, there was a notable surge in C_4 resources in suid diets, culminated in the Plio-Pleistocene with the gradual abandonment of C_3 foods. Isotopic data from the Woranso-Mille research area in Ethiopia's Afar region, spanning approximately 3.8-3.2 million years ago, reveal a shift from more diverse to C_4-focused suid diets. Contrary to prior research, suines (the family of contemporary pigs) did not swiftly adopt C 4 resources when they migrated to Africa from Eurasia in the Early Pliocene. Their dietary transition was gradual, distinct from other suids, particularly the Tetraconodontinae subfamily, which had already become dedicated C_4 consumers during the same period. Unlike certain mammal lineages like proboscideans, where changes in stable isotopes preceded morphological adaptations, suids exhibited no noticeable time lag. Despite biogeographical disparities and potential samplingbiases, the ecological trends observed in eastern African suids offer some of the best documented cases of the intricate interplay between climatic shifts and evolutionary adaptations in mammals.

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Did preterm birth rates shift by nativity among Hispanic women in the United States during the COVID-19 pandemic?

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Despite chronic exposure to stressors, Hispanic women in the United States (U.S.) typically have lower than expected preterm birth (PTB) rates. This counterintuitive outcome is known as the Hispanic Paradox. The COVID-19 pandemic resulted in devastating hospitalization and unemployment rates, particularly among Hispanic communities. We hypothesized that foreign born Hispanic women (FBHW) experienced higher levels of pandemic induced stress resulting in an increase of PTB rates. We explored PTB data among Hispanics from the National Center for Health Statistics natality files containing all registered US births from 2016 to 2021. We compared singleton live preterm births to Hispanic women, restricted to the months of April-June to control for seasonal fluctuations, and plotted expected versus predicted PTB rates over time. We found PTB rates of FBHW have been increasing faster than for US-born Hispanic Women (USBW). During the early pandemic, PTB rates significantly decreased for all Hispanic women relative to 2019(OR=0.9607, p<0.001). However, only among FBHW was this decrease significantly below the predicted value (outside of the 95% confidence interval), adjusting for trends since 2016. In 2021, PTB rates increased again for all groups but remained below predicted rates for FBHW, indicating a lasting effect of the pandemic. Finally, we found that the PTB rates dropped significantly among spontaneous but less among induced births, implying a reduction of stress potentially resulting from an increase of time spent at home with extended family, and a loss of labor-intensive jobs, rather than changes in hospital policies or prenatal care.

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Optimizing Kraken2 Databases for Species Identification

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One of the challenges of conducting taxonomic identification on metagenomic samples is identifying and creating appropriate databases, with enough taxonomic resolution and appropriate parameters for particular dataset. Here, we explore database creation and optimization for species identification of fragmentary archaeological specimens. To test our database optimization, we conducted taxonomic identification on archaeological rockfish (*Sebastes* sp.), an extremely diverse genus of fishes. Rockfishes are nearly indistinguishable morphologically from one another in archaeological contexts due to the skeletal similarity amongst the species. In an effort to characterize ancient rockfish diversity in the North Pacific, we created and optimized a specialized Kraken2 database through testing of simulated ancient rockfish genomes. We tested the impact of four unique database compositions and several classification parameters (k-mer length and confidence interval) on simulated ancient metagenomic data for taxonomic identification with Kraken2. We compared the percentage of classified vs. unclassified reads, the taxonomic identifications vs. expected identification, and the breadth of coverage. We found that when our database was composed of all publicly available Perciforme genomes, there was a high rate of misclassification to the spiny red gurnard (*Chelidonichthys spinosus*) genome. This demonstrates the taxonomic identification bias based on database composition, even within specialized databases, as seemingly small issues with genome assembly can easily result in taxonomic misclassifications. This study highlights the importance of *in silica* optimization of databases for taxonomic identification and scrutiny of genome quality in publicly available databases.

Understanding the Influence of Colonial Contact on Asymmetry Trends in Cranial Morphology among Black South Africans over the late 19th and 20th Centuries

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The South African Bantu-speaking population represents a community with a long history of racial discrimination and Apartheid. The aim of this study was to perform an experimental analysis utilizing geometric morphometric techniques to understand the impact of colonial contact and the social determinants of health regarding Apartheid segregation policies on asymmetry changes of cranial morphology in this population. Adult cranium specimens (n=161) from the Raymond A. Dart Collection of Human Skeletons were examined. Procrustes Analysis of Variance was used to assess fluctuating asymmetry. Linear mixed models using age, sex and year of death as fixed effects were constructed using the Procrustes fluctuating asymmetry scores. Since this community experienced racism through social segregation polices even before the apartheid period, we expected no changes in fluctuating asymmetry between pre- and during apartheid groups however, fluctuating asymmetry was observed over the late 19th and 20th centuries ($p<0.0001$). Negligible differences were observed in regard to age ($p=0.850$) and sex ($p=0.068$), however, significant differences were observed when comparing pre- vs. during Apartheid groups ($p=0.006$). Notably, the pre- Apartheid group showed lower fluctuating asymmetry scores when compared to the during Apartheid group indicating increased developmental instability and stress during Apartheid. No differences were observed when examining the length of Apartheid experience within the during Apartheid group ($p=0.111$). Understanding how colonial contact specifically Apartheid segregation polices affect a marginalized community like the South African Bantu-speaking population provides insight on the potential lasting impact and outcomes of the health and well-being of similarly marginalized populations today.

Travel or Treat?: An Analysis of Spider and Howler Monkey Prehensile Tail Use

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Recent literature has hypothesized that all prehensile-tailed *Atelines* are inclined to feeding-based tail use. This study investigates prehensile tail use in the mantled howler monkey (*Alouatta palliata*) and black-handed spider monkey (*Ateles geoffroyi*) in order to examine differences between these taxa in weight-bearing prehensile tail use behaviors. Observational data on the two primate species' behaviors were collected at Camaquiri Conservation Initiative in Limón, Costa Rica, over the course of 7-days. A total of 14.4 hours of data were collected using focal sampling of 2-minute intervals across 20 minutes of observation time per subject. Results indicate that howler monkeys spent 23.91% of recorded movements engaging in weight-bearing tail postures and 34.88% of feeding engaged in weight-bearing postures of the tail. Spider monkeys spent 53.6% of their recorded weight-bearing tail postures for locomotor purposes and 28.78% for feeding purposes. Although the frequency of recorded general feeding or locomotor behaviors differed between the taxa, howler monkeys and spider monkeys displayed similar percentages of observed feeding behaviors in prehensile tail suspensory postures. This howler monkey data supports the assertions put forth by existing literature. However, the spider monkey data disagreed with this and instead supported a prehensile tail use preference for locomotion. The results of the current study demonstrate that similar habitat terrains and adaptations do not result in equal functional use. Future research should focus on investigating how seasonal nutritional resources influence prehensile tail use preferences.

Where the small things are: Modelling edge effects on mouse lemur population density and distribution in northwestern Madagascar

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Edge effects result from the penetration to varying depths and intensities, of abiotic and biotic conditions from the surrounding non-forest matrix into the forest interior. Although 70% of the world's forests are within 1 km of a forest edge, making edge effects a dominant feature of most forest habitats, there are few empirical data on inter-site differences in edge responses in primates. We used Spatially Explicit Capture-Recapture (SECR) models to determine spatial patterns of density for two species of mouse lemurs (*Microcebus murinus* and *Microcebus ravelobensis*) in two forest landscapes in NW Madagascar. The goal of our study was to determine if mouse lemurs displayed spatially variable responses to edge effects. We trapped animals using Sherman live traps in the Mariarano Classified Forest (MCF) and in the Ambanjabe Forest Fragment Site (AFFS) site within Ankarafantsika National Park (ANP), northwestern Madagascar. We trapped 126 *M. murinus* and 79 *M. ravelobensis* at MCF and 78 *M. murinus* and 308 *M. ravelobensis* at AFFS. For *M. murinus*, our top model predicted a positive edge response, where density increased towards edge habitats. In *M. ravelobensis*, our top model predicted a negative edge response, where density was low near the forest edges and increased towards the forest interior. Our results lend further support to the theory that some lemurs exhibit a form of ecological flexibility in their responses to edge effects.

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Trophic structure of the faunal assemblage at the Last Interglacial Middle Paleolithic Neanderthal occupation site Neumark-Nord, Germany using multi-isotope analyses of tooth enamel

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In this study we use stable isotope ratios of fossil tooth enamel (δ^{13}C and δ^{15}N) to investigate diet and evaluate the trophic structure of fossil fauna from the 120 ka site of Neumark-Nord, Germany. Neumark-Nord is a well-preserved Late Pleistocene interglacial site that offers a rare, high-resolution record for studying Neanderthal ecology. The site includes evidence for year-round occupation, landscape modification using controlled fire, and systematic exploitation of large mammals (including adult male straight-tusked forest elephants of up to 13 tons), all of which have major implications for the range of adaptive behaviors exhibited by Neanderthals.

We measured $\delta^{13}C_{enamel}$ and $\delta^{15}N_{enamel}$ values in the tooth enamel of all herbivores (n = 43), omnivores (n = 2), and carnivores (n = 6) in the assemblage. Herbivores have, on average, lower mean $\delta^{15}N_{enamel}$ values (x= 5.3 ± 1.3 ‰) than omnivores (x= 7.4 ± 1.5 ‰) and carnivores (x= 7.5 ± 1.9 ‰). $\delta^{13}C_{enamel}$ values suggest that Neumark-Nord fauna foraged predominantly in forested environments.

Our enamel-derived $\delta^{13}C$ and $\delta^{15}N$ values agree well both with published collagen-derived values for Neumark-Nord and with other Late Pleistocene European collagen data. Further, $\delta^{15}N_{enamel}$-based trophic reconstructions are in good agreement with reconstructions based on other isotopic proxies (i.e., $\delta^{44/42}Ca$) measured in the same specimens. These results highlight the potential for $\delta^{15}N_{enamel}$ for analyses of fossils from localities and time periods where collagen is not preserved. Moreover, our multi-isotopic approach allows us to glean new information about ancient food webs and the place of prehistoric humans within them.

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Generalized Additive Mixed Modeling of Primate Growth Spurts

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Body mass growth spurts are important features of primate ontogeny. We analyze body mass growth spurts in a previously-investigated sample of primates using new regression methods, comparing results between old and new regression methods to refine earlier estimates of growth spurts.

We use GAMM (Generalized Additive Mixed Models) with mixed-longitudinal samples of males and females of 13 catarrhine species (7 monkeys, 6 apes). GAMMs have some advantages over traditional methods: parameter estimates include confidence intervals, random effects can account for repeated measures, and regularization can reduce the risk of overfitting. Our overall expectation is that new methods will match earlier nonparametric regressions. Species selected for new analyses illustrate growth spurts for both sexes, males only, or no growth spurt for either sex.

Estimates of growth spurts from GAMMs generally agree with traditional estimates, with differences mostly in cercopithecoids. GAMMs do not show female spurts in *Chlorocebus aethiops, Macaca arctoides* and *M. fascicularis*. GAMMs indicate a higher likelihood of a female growth spurt for *Pan trogolodytes*. Finally, GAMM regressions and CIs reveal previously unappreciated distinctions by sex in early growth periods as well as fluctuations in size for adults.

GAMMs may be more conservative than traditional methods. In addition, GAMMs reveal details of growth by sex and species in early growth periods (aided by CIs) less evident with traditional methods. Similarly, GAMM plots clearly reveal the initiation of female-male size differences when present. Combining GAMMs with traditional approaches may be valuable, depending on data quality.

Integrating the evolution of placental birth with evidence from neonatal lines in mammal teeth

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While fossils do not typically preserve evidence of mammal birth such as milk production or parental care, some mammal teeth do record internal evidence of placental birth. The neonatal line (NNL) is well-documented in humans and non-human primates and is an incremental growth line that forms in certain teeth, as a marker of neonate birth stress. In humans, it is impacted by factors such as neonatal birth weight and mode of delivery. However, it isn't broadly identified across mammal taxa.

We present a literature review of mammalian genera which are reported as recording a dental neonatal line. These include 8 primates, 1 cervid, 1 phocid, 3 cetaceans, a fossil pantothere, *Pantolambda,* and a fossil notoungulate, *Toxodon*. We further examined M1/m1 dental histology from a selection of extant mammal taxa with molars known to develop pre-birth, aiming to visually identify the presence or absence of the NNL. We hypothesize that Marsupials will not have the NNL. The new Eutherian taxa (N=13) were selected to broaden the phylogenetic scope of mammals with known NNLs. Marsupials (N=3) and insectivorous Eutherians (N=4) were sampled as potential ecological analogues of mammalian ancestors. Preliminary histology and literature review results suggest the neonatal line is a shared trait in Carnivorans, Cetaceans, and Primates. Previously sampled marsupial teeth (*Monodelphis domestica*) do not appear to have the NNL. Future work will integrate dental neonatal lines into discussion of the timing of placental birth evolution, using staining, nanoCT, and laser ablation spectrometry identification techniques.

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Using stable isotope ecology of modern herbivores as a model to reconstruct palaeoenvironments

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This study explores the stable isotope ecology of 12 co-existing species of wild herbivores from Mmabolela, a game farm on the northern border of South Africa in the Limpopo Province. The aim is to investigate and interpret patterns in $\delta^{13}C$, $\delta^{15}N$ and $\delta^{18}O$ of different species of herbivores and to compare these results with previous studies. As expected in this summer-rainfall region, $\delta^{13}C_{bone\ collagen}$ values fall into two distinct groups: predominant browsers with mean $\delta^{13}C$ values ranging from -21.37‰ to -18.10‰, and grazing species with mean $\delta^{13}C$ values ranging from -13.25‰ to 10.49‰, the more negative values reflecting some supplementary feeding with lucerne during the dry season. There are no differences in $\delta^{13}C$ between the browsing species eland (*Taurotragus oryx*), bushbuck (*Tragelaphus scriptus*) and kudu (*Tragelaphus strepsiceros*). The $\delta^{15}N$ values for all species range from 7.73‰ to 11.20‰. $\delta^{15}N$ values of baboons fall within the range seen in bovids. Amongst bovids, there is no statistically significant difference between the $\delta^{15}N$ values of browsers and grazers. Zebras (*Equus quagga*) have lower $\delta^{15}N$ values. Seasonal changes were investigated by analysing serial samples of quills from three porcupines (*Hystrix africaeaustralis*), and tooth enamel from nine zebras. The porcupines show short-term, but not necessarily seasonal variations in their diets. $\delta^{13}C$ and $\delta^{18}O$ profiles of the second and third molars of nine *Equus quagga* individuals are highly variable. A better understanding of the isotopic ecology of communities such as this will help to interpret similar analyses of fossil faunal assemblages and assist in reconstructing palaeoenvironments.

This research was funded by the National Research Foundation and Professor Judith Sealy.

Importance of Reed's paleocommunity research for understanding carnivoran paleoecology

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Throughout her career, Kaye Reed has utilized a multifaceted approach to community paleoecology with an eye towards reconstructing fossil hominin habitats. Her research on Plio/Pleistocene African paleocommunities (and that of her students and colleagues) provides a framework within which individual taxa and ecological guilds can be studied. Reed herself demonstrated the importance of paleocommunity studies for understanding primate adaptations. In this study, carnivoran taxa from the Hadar research area (Ethiopia) are analyzed within the context of paleocommunity and habitat reconstructions made by Reed and colleagues. Pliocene African carnivorans include specialized forms (e.g., cursorial sabertooth *Homotherium*, bear-otter *Enhydriodon*) that often have no modern analogues, while others are more familiar (e.g., *Crocuta*). In some Hadar carnivorans, morphology may shift from member to member, while in others there is little change. For example, differences in postcranial morphology from the oldest to youngest Hadar *Homotherium* could represent size-related shape change, functional shifts, or both. The fragmentary nature of older specimens makes this difficult to assess. Reed's work supports the hypothesis that differences could relate to habitat shifts as younger material is from a time with more open grasslands (Denen Dora Submember 3) than older material (Basal Member). Thus, Reed's work provides a context for interpreting morphological change through time and lays the groundwork for determining why some taxa appear only in specific members or only at Hadar and not elsewhere in the African Pliocene. Reed's work has galvanized research into the ever-shifting paleocommunities surrounding sub-Saharan hominin evolution and our field is richer for it.

Portions of this project were supported by a Leakey grant to K.E. Reed and MEL and Stockton internal grants to MEL.

Patterns of Paternity in Verreaux's Sifaka (*Propithecus verreauxi*) at the Ankoatsifaka Research Station in Kirindy Mitea National Park, Madagascar

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Verreaux's sifaka live in groups with 1-3 females, and within-group estrous synchrony is low, despite breeding seasonally. Consequently, one male is expected to monopolize matings, even in multimale groups. We explored patterns of paternity in Verreaux's sifaka at the Ankoatsifaka Research Station, which differs from other populations by having a lower population density and female-biased sex ratio. Using 14 polymorphic STR loci, we genotyped 132 individuals and assigned maternity and paternity with high confidence for ~40 offspring born into 6 groups between 2006 and 2014 using a maximum likelihood approach and a candidate pool of 12-17 dams and 37-47 sires. Seventeen males from the candidate pool sired 1-7 offspring, while the remaining males sired none. Eighty-one percent of offspring were born to either the sole adult male resident in the group at the time of conception or the dominant of 2 to 3 resident adult males. Paternity by subadult males was rare (N=2 offspring). While dominant males sired two-thirds of offspring in multimale groups, this percentage was not significantly greater than expected by chance and was substantially lower than the percentage reported for another population. Extragroup paternity (N=3 offspring) occurred only in single-male groups and also was substantially lower than in other populations. Male sifaka at Ankoatsifaka may exhibit different reproductive strategies from other locations because low population density limits extragroup paternity and increases the importance of residency. Within groups, dominant males have difficulty monopolizing females due to female-biased intersexual power.

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Tests of morphological convergence in hindlimb bone cross-sectional properties in saltatory primates, rodents, and marsupials

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Previous work on hindlimb bone cross-sectional properties (CSP) in saltatory primates has suggested that adaptations to leaping locomotion are shared among saltatory taxa. Our recent work has demonstrated that these form-function associations are complex and that such hypotheses are not consistently supported. Here we build on this previous work by testing hypotheses of morphological convergence in CSP of hindlimb bones in a comparative mammalian sample (41 species of primates, rodents, and marsupials). We predict that taxa that share locomotor mode will exhibit convergence in CSP. Micro-CT scans of the femur and tibia were used to calculate estimates of CSP at diaphyseal midshaft: bending strength (*Zp*), torsional strength (*J*), compressive strength (cortical area), and maximum and minimum second moments of area (*Imax* & *Imin*). CSP were scaled by the geometric mean of all variables and multivariate phylogenetic tests of convergence were conducted in R. Relationships among body size, CSP, and locomotion were also explored using phylogenetic generalized linear models. Our results do not support a hypothesis of morphological convergence in CSP in this mammalian sample (i.e., both femoral and tibial multivariate convergence tests were not statistically significant). Furthermore, body size consistently has a significant effect on scaled CSP in phylogenetic linear models, while locomotor mode does not. Our results suggest caution when invoking adaptive explanations for perceived similarities in CSP across saltatory species.

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Ancient DNA Reveals the Genetic Connection of the Neolithic to Bronze Age Population in the Eastern Nihewan Basin

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The Jiangjialiang Site is located near Xishuidi Village, Dongcheng Town, Yangyuan County, Zhangjiakou City, Hebei Province. It is one of the largest Neolithic sites discovered and excavated in the Hebei region. The site is located in the eastern part of the famous Nihewan Basin, at the junction of northern Hebei, northern Shanxi, and Hequ regions. In history, this area was once a "three fork" in the contact between the ancient cultures of the Central Plains and the north. The discovery of the Jiangjialiang site is of great significance for studying the cultural exchange between the region and the Northeast and Northwest regions. Previous mitochondrial DNA studies have shown that the ancient population of Jiangjialiang should be an ancient indigenous population in northern China; The paternal genetic analysis of the Y chromosome suggests that this population may be closely related to the ancient population in the West Liaohe River Basin. In recent years, with the continuous innovation of ancient DNA research technology, using new methods to study and analyze human remains in the Jiangjialiang site will help us obtain more genetic information from it. This study conducted whole genome sequencing analysis on 49 ancient individuals obtained from the Jiangjialiang site. The results show that the Neolithic population in Jiangjialiang has a relatively complex genetic structure, with most ancient individuals having close genetic relationships with residents of the Neolithic period in northern China. In addition, some individuals have relatively more North or Northeast Asian components.

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Seasonal sleep variation among rural South African agropastoralists

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Communities experiencing seasonal differences in their sleep environment are assumed to exhibit seasonal differences in sleep since natural light, temperature, and humidity are known ecological modulators of sleep-wake patterns. Here, we examined drivers of seasonal sleep variation in a rural agropastoral community in the Eastern Cape, South Africa. We collected summer and winter actigraphy data from 114 participants (83 men, 31 women, 4767 nights). Based on discussions with the community, we expected sleep distinctions between seasons. Indeed, we found significant differences in all three sleep measures, after controlling for gender, age, and occupation. Total sleep time (TST) was higher in winter (7.26 h, SD = 1.0) compared to summer (6.40 h, SD = 0.88), but so were fragmentation index (FI) and wake after sleep onset (WASO). Longer sleep was accompanied by more disrupted sleep during the winter. Furthermore, sleep duration increased with scotophase (night length) and decreased with temperature while FI and WASO increased with scotophase. In addition, sleep was more fragmented and segmented during warm and humid nights, as summer weather conditions were generally linked to lower quality sleep. While ecological factors explained seasonal variation in sleep quantity, they did not sufficiently account for disparity in sleep quality. These findings suggest that extrinsic weather conditions (light, temperature, humidity) operate in tandem with socioeconomic pressures (stock theft) and labor demands (herding and farming) to drive seasonal sleep variation in this community. This understanding is crucial for future research, which should consider seasonal differences when reporting sleep characteristics in similar populations.

This project was funded by the Natural Sciences and Engineering Research Council of Canada, the University of Toronto School of the Environment and Department of Anthropology, and Sigma Xi.

Health impacts of agricultural intensification and urbanisation in Early China: A bioarchaeological analysis of disease patterns, subsistence economies, and lived environments in Shaanxi from 3000 BC to AD 220

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Today, half of the world's population live in cities, while one-third of the global gross-domestic-product comes from agricultural production. Yet agricultural production and urbanism are associated with many adverse health outcomes. Analysis of archaeological populations also suggests that agriculture and urbanism were two of the most important factors that caused past human health to deteriorate. Despite their profound health impacts, relevant bioarchaeological studies have rarely been conducted in China. To strengthen the knowledge base, this study explored temporal health trends and their associations with agricultural intensification and urbanisation in Early China. Adult stature and skeletal and dental lesions suggestive of malnutrition, infections, and respiratory illnesses were recorded from 249 skeletons excavated from Shaanxi (3000 BC-AD 220). The results showed that the intensification of millet agriculture and emergence of urbanism increased the frequencies of long bone periostosis, maxillary sinusitis, inflammatory rib lesions, cribra orbitalia, porotic hyperostosis, enamel hypoplasia, and dental caries. Yet such a health decline was soon reversed by cultural adaptations, and population health improved as indicated by increased adult stature over time. The frequency of tuberculosis also increased following the emergence of urbanism, although such a trend is based on a small number of affected individuals. In contrast, the frequencies of inflammatory endocranial lesions, scurvy, and vitamin D deficiency were influenced by biological, social, and climatic risk factors rather than changes in subsistence economies and lived environments. This study provides new knowledge from China to the health impacts of major societal challenges facing living populations.

Geographies of Otherness: Names, Narratives, and Images of Eurasian Nomads in Late Antique and Medieval Sources

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Greek, Roman, and Medieval authors used a variety of ethnic names and ethnographic categories to describe the peoples of the Eurasian steppe and interpret their migration towards the Mediterranean Basin. Nomads were one of the preferred targets of authors' othering strategies and nomadism was often judged as the first and most blatant distortion of civilization. Following the principle of environmental determinism, a multiplicity of writers often compared the characteristics of a given ethnic group with the features of the landscape that the same group inhabited. Thus, the solitary and wandering life of the nomads had to reflect the desolation and harshness of their environment and vice versa. Such attitudes were so widespread that expressions such as 'Scythian solitude' became proverbial and the only mentioning of nomads could prompt associations with historical or literary narratives, which in readers' minds substantiated claims of cultural superiority and political supremacy.

Names, narratives, and images of Eurasian nomads are particularly abundant in geographical texts and maps. In these sources, they serve to make sense of the ever-changing landscape and fill with meaning a part of the world that was only barely known by European authors and readers. By examining a large corpus of written and figurative evidence, dating from Antiquity to the High Middle Ages, this contribution will highlight the longevity of ethnic stereotypes, their adaptation to the developing political and military circumstances, and the coexistence of multiple literary traditions in the creation and conservation of such ethnic discourse.

This research was supported by the ERC Synergy Grant HistoGenes - Integrating genetic, archaeological and historical perspectives on Eastern Central Europe, 400-900 AD.

Sharing a tree, not behavior: Activity budgets and (moderate levels of) behavioral synchrony in white-handed gibbons

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Gibbons and siamang are often characterized as living in highly cohesive groups and as such, many researchers pool behavioral data and analyze by groups. However, given that females expend more energy on reproduction than males, it is possible that females and males exhibit different behavioral patterns even when in close proximity to one another, particularly in environments with high seasonal variation or low overall resource availability. We collected a total of 132 hours of behavioral data from both adults in three groups (n=6 individuals) of white-handed gibbons (*Hylobates lar*) in Huai Kha Khaeng Wildlife Sanctuary, Thailand. We then calculated individual and group activity budgets as well as the degree of synchronization between the adult female and male for each group. We hypothesized that activity budgets would not differ significantly between sexes but would differ between groups and that the female and male would be highly synchronized in their behaviors. Overall, individual activity budgets did exhibit significant variation when analyzed by individuals [$X2(25, 1579) = 152.020$, $p \le 0.001$], sex [$X2(5, 1579) = 27.693$, $p \le 0.001$] and groups [$X2(10, 1579) = 119.584$, $p \le 0.001$]. Percentages of synchronized paired behavior were also much lower than expected with only 55% of records behaviorally synchronized between the female and male (group B: 58.6%; group D: 58.5%; group L: 49.65%). We conclude that this considerable difference in behavior indicates a need for behavioral analyses that do not pool data from the female and male but instead analyze behavior as independent between group members.

Research in Thailand was supported by the Department of Anthropology at the University of North Carolina at Charlotte.

The role of genes and environment in human dental arch shape - a twin study

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Objective: To assess the contribution of genes to shape variation in permanent dental arches of individuals of Western European descent.

Methods: Subjects consisted of dental casts from 64 monozygotic and 38 dizygotic twins, housed in the Adelaide Dental School, Australia. Subjects were of Western European descent, with a mean age of 19.4 ± 5.4 years. Casts were scanned digitally, and landmarks placed cusp tips of teeth. Geometric morphometrics were applied to examine shape variation within arch. Two-block partial least squares analysis was used to assess shape covariation between arches. Structural equation modelling was utilised to decompose shape variation into genetic and environmental components.

Results: The first three principal components (PCs) of the maxillary and mandibular arch accounted for 53% and 50% of variation in shape space, respectively. PCs represented shape variability as follows: PC1 - arch depth-width ratio; PC2 - arch taper, canine position (and first premolar rotation for the mandibular arch); PC3 - incisor displacement and rotation. A model incorporating additive genetic and unique environmental factors optimally explained the observed variation for all PCs. Variation in maxillary and mandibular arch shapes exhibited moderate to high heritability (0.61-0.74). Upper and lower dental arches had strong and significant shape covariation, with high heritability in their reciprocal influences on shape (h^2= 0.72~0.74, r_{pls} coefficient= 0.87, p<0.05).

Conclusion: In this cohort, dental arch shape variation was predominantly influenced by genetic factors. This information may help underpin the shape of the dental arches as a useful measure of evolutionary change.

Cohort establishment was funded by the NIH, USA. Data collection was funded by the NHMRC, Australia. The 3D scanner was provided by the Kwok Paul Lee Bequest.

Stable isotope analysis of dietary protein in savanna chimpanzees (*Pan troglodytes*) from Sénégal: effects of tool-assisted hunting and anthropogenic disturbance

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Western chimpanzees (*Pan troglodytes verus*) at Fongoli in Sénégal are unusual in that females frequently hunt with tools. Assessing the impact of this hunting strategy on protein ingestion in females is challenging, however, due to ethical research practices to mitigate risk of infant poaching. To overcome this limitation, we used dietary stable isotope analysis of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) measured from non-invasively collected hair samples and contextualized these results with observations of hunting during focal follows of adult males. In addition, we compared values from Fongoli to chimpanzees from Assirik, a unit-group that ranges exclusively within Parc National du Niokolo Koba. Given that Fongoli females routinely hunt, we expected and observed that hair $\delta^{15}N$ was equivalent among the sexes (t(72) = -0.60, *p*= 0.550), however, we found an unexpected change between more recent (2020-2022) and older (2010-2011) hair samples, with higher $\delta^{15}N$ values from the earlier decade (2010-2011: = 3.52, sd = 0.388 n = 8; 2021: = 3.01, sd = 0.228, n = 30; 2022: = 3.03, sd = 0.245, n = 38; t(71) = -4.784, *p* < 0.001). At Assirik, the diet was higher in $\delta^{15}N$ (2019-2022: = 3.8, sd = 0.53 n = 34), indicating that these chimpanzees are consuming more animal tissues than Fongoli chimpanzees. We contextualize these results by discussing the overall male-bias in hunting and meat ingestion in chimpanzee societies, and exploring environmental hypotheses to explain temporal and spatial differences in animal prey consumption.

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Unraveling the impact of admixture and adaptation on patterns of genetic diversity at the TAS2R bitter taste receptor genes in distinct African populations from Cameroon

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Bitter taste perception is a highly variable trait in humans, and the ability to detect bitter compounds has been largely attributed to genetic variants in 25 bitter taste receptor (*TAS2R*) genes. Furthermore, bitter taste perception has been hypothesized to be a dietary adaptation in humans. However, few studies have characterized patterns of diversity and signatures of selection at the *TAS2R* genes in distinct African populations. Given the extensive genetic substructure and evidence for local adaptation in Africa, we hypothesized that Africans practicing diverse subsistence strategies could have distinct patterns of selection resulting from divergent diets. To test this hypothesis, we examined sequence variation at 22 bitter taste receptor genes in rainforest hunter-gatherers and Bantu-speaking agriculturalists from Cameroon. Here, we identified 353 single nucleotide polymorphisms (SNPs) across the *TAS2R* genes, 35 of which have never been previously described. We also observed striking signatures of positive selection, including unusually long haplotypes around alleles at the *TAS2R* genes. In addition, some of these signals of selection were shared between rainforest hunter-gatherers and Bantu-speaking agriculturalists. To better understand these results, we performed genomic genotyping in our African populations. Interestingly, we observed varying proportions of ancestry originating from Bantu-speakers in hunter-gatherers with the highest levels of admixture occurring in the Bakola population. These findings demonstrate that gene flow from neighboring agriculturalists has also shaped patterns of diversity in hunter-gatherers, including variation at the *TAS2R* genes. Overall, this research provides new insights into the evolution of biologically-relevant bitter taste genes in highly understudied African populations.

Age-related feeding behaviors in wild *Cebus imitator*

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Tufted capuchins (*Sapajus* spp.) are characterized by morphological adaptations for processing mechanically challenging foods. Previous research suggests juvenile tufted capuchins differ in feeding duration, frequency, and behavioral patterns compared to adults as they learn to navigate these foods. Untufted capuchins (*Cebus* spp.) consume less mechanically challenging foods than tufteds, but the extent to which juvenile untufted capuchins exhibit differences in feeding behaviors compared to adults is poorly known. Here, we examine how feeding behaviors differ with respect to age and sex classes for 14 species of fruit eaten by wild white-faced capuchin monkeys (*Cebus imitator*).

Videos of feeding were recorded for 50 individuals in Sector Santa Rosa (Costa Rica) over a six-month period spanning the dry season to the beginning of the wet season. Each video was viewed frame by frame, and over 3800 feeding behaviors were coded. Feeding behaviors were defined at the level of the feeding sequence as total sequence duration, frequencies of behaviors, and number of chews.

Our results suggest a significant relationship between feeding sequence duration and age class both within and between food types, such that older individuals had shorter feeding sequence durations ($p = 0.0298$). However, sex does not affect feeding sequence duration, behavioral frequency, or chew number (all $p > 0.05$). Feeding sequence duration varied across all fruits within each age class. These data suggest untufted capuchins display ontogenetic feeding behavior differences, and future analyses will directly compare tufted and untufted capuchin feeding behaviors.

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The Bioarchaeology of Prehistoric Agricultural/Metalworking Communities in Central Thailand

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The Thailand Archaeometallurgy Project (TAP) excavated three neighboring sites in the Khao Wong Prachan Valley (KWPV) in Central Thailand to investigate prehistoric metallurgy and its relationship to regional sociocultural changes. Non Pa Wai (NPW) includes evidence for early millet farming (ca. 2300–1800 BC) and evidence for substantial copper smelting in later components (ca. 1200–500 BC) and its neighboring sites. Here we explore human-landscape relationships in the intensively exploited KWPV using diet as a proxy. Nineteen tooth enamel and 20 bone samples representing 25 individuals from NPW are sampled for carbon, nitrogen, and oxygen stable isotope analysis. Sampling was based on representativeness in mortuary patterns, temporal sequence, and spatial distribution. For an ecological baseline, isotopic data from associated vertebrate fauna (6 teeth and 23 bones) are included representing 12 terrestrial and aquatic species recovered from NPW.

Results are integrated with Thai sites in regional context, and with a previously studied TAP site, Non Mak La (NML, ca. 1800-700 BC). Similar to contemporary sites, collagen yields are compromised and isotopic results are compared with bioapatite data from both teeth and bone. We hypothesize that NPW individuals will exhibit a tightly clustered mix of C_3-C_4, mid-trophic level diet, with no marked variability temporally or by sex. Such a dietary pattern would indicate that the NPW community maintained a long-term balance between the demands for subsistence and craft production on their immediate surroundings. This locale-specific, yet broad spectrum, dietary pattern is similar to NML, despite some differences in site characteristics and functions.

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The Resilience of Kin Networks under Market Integration in a Matrilineal Society

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Kinship is foundational to the social structures of pre-industrial societies. It is thought that the importance of kin declines as societies become more "modern" and individuals more economically autonomous. Social network theory provides a means of testing this idea by examining the size of cooperative social networks and their composition. In this talk, we test whether network size decreases and whether networks are composed more non-kin rather than kin under contexts of market integration. We do so in a matrilineal society, matrilineal ethnic Mosuo of Southwest China, where kinship has long been central to social, religious, and economic structures, but economic forces are rapidly changing the landscape of attendant costs and benefits. Preliminary analyses reveal that despite some decrease in kin density with market integration, a majority of respondents across a range of activities continue to prioritize kin interactions. This underscores the resilience and adaptability of kinship as a potent local cultural norm, shaping new transformations to align with ingrained traditions.

The research is funded by NSF DDRIG.

Evaluation of missing data imputation methods for human osteometric measurements

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USF Genomics, University of South Florida

Biological anthropologists often face the challenge of examining incomplete bioarchaeological or forensic skeletal samples. As a result, working with such incomplete data poses a significant challenge, especially since many quantitative multivariate analytical tools are not designed to handle missings in data.

To address this pervasive issue, imputing or estimating the missing data becomes an essential preprocessing step. Imputation isn't just about filling in gaps; it's about ensuring the integrity and accuracy of the data so that any subsequent analyses are meaningful and reliable.

Our study tapped into two human osteometric measurement data sets: the William W. Howells' Craniometric Data Set and the Goldman Osteometric Data Set. These served as our foundation to assess a range of widely used statistical techniques explicitly designed to impute absent metric values.

We discovered that methods involving multiple imputations, such as the Bayesian principal component analysis (BPCA), consistently outperformed their single imputation counterparts. Notably, the Bayesian linear regression available in the R package norm2, the Expectation-Maximization (EM) technique coupled with Bootstrapping found in Amelia, and the Predictive Mean Matching (PMM) method, along with several related linear regression models in the mice package, stood out. These methods were recognized for their precision, resilience to varied data scenarios, and computational efficiency.

In light of these findings, our research underscores the importance of careful imputation and offers professionals a guided, evidence-backed approach to selecting the most effective imputation strategies.

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Beyond battle scars: An analysis of injury patterns in the eastern Eurasian Steppe

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The eastern Eurasian Steppe is a region historically associated with organized military action, warrior elites, and advancements in weapons. This study investigates injury patterns there to assess the extent of violence. I analyse human remains from five archaeological sites: Bizili (206 BCE-605 CE) and Xiabandi (1550 BCE-550 CE) in north-western China, Neiyangyuan (2070-480 BCE), Fushanqiaobei (17th century BCE-220 CE), and Shuzhuanglou (1271-1368 CE) in north-central China.

This study hypothesizes a higher frequency of injuries in the north-central area for two reasons. First, the archaeological indicators suggest the presence of inequality (different burial practices) and specialized weapons (metal swords and dagger-axes). Secondly, this area was a conflict zone between nomadic and agricultural empires.

Results indicate significant differences in injury patterns. In north-western sites, more than 30% of injuries are direct-force cranial injuries. In Bizili, 22.9% of left and 12.5% of right nasal bones are involved, followed by parietal and occipital bones. In Xiabandi, the left parietal, temporal and both nasal bones are involved. Most victims are young adults, and no significant sex differences are observed. Conversely, in the north-central sites, only three mid-aged males exhibit nasal fractures.

To conclude, the observed injury patterns challenge archaeological findings and historical records. The north-central sites show few injuries related to either inter-group or intra-group conflicts. In contrast, the north-western sites primarily display blows to face, left side and back of head. Several individuals also show isolated ulna and indirect-force metacarpal shaft fractures, suggesting face-to-face and hand-to-hand combat in both sexes.

Resolution of commingled human remains using their elemental profile by Laser-Induced Breakdown Spectroscopy

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The resolution of commingled human remains continues to be a significant challenge in forensic anthropology and bioarcheology. This study provides the results of how portable laser-induced breakdown spectroscopy (pLIBS) can be used as a tool to group human skeletal remains into individuals, and thus resolve commingling, based on elemental profiles. LIBS is portable, minimally destructive and does not require sample preparation. It can detect low atomic weights such as carbon, nitrogen, and oxygen; thereby, making it a potentially useful tool for reassociating commingled remains beyond the capacity of other elemental methods such as the more popularly used portable X-ray fluorescence (XRF).

For this project, LIBS spectra were acquired from the remains of 45 human skeletons from the Western Carolina University's John A. Williams Human Skeletal Collection. The data from the 45 skeletons resulted in a dataset of 8388 profiles across 1284 bones. Variable selection was conducted to reduce the spectral profiles to the peaks exhibiting the highest variation between individuals. Emission lines corresponding to 8 elements (Ca, P, C, K, Mg, Na, Al, Ba, Sr) were found to be the most important for classification. Linear discriminant analysis (LDA) was subsequently used to classify each spectral profile. From the 45 individuals, each LIBS spectrum was successfully sorted to its corresponding skeleton with an average accuracy of 87.5%. These findings indicate that while there is variation between the LIBS spectra, this variation is relatively small and human skeletal remains can be sorted into individuals with the high rate of accuracy.

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Movement in the Miocene: A SPHARM analysis of fossil catarrhine tali to infer locomotor behavior

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Early Miocene catarrhines are known for their considerable taxonomic diversity and recent morphometric analyses within this group point to higher levels of postcranial adaptive diversity than previously recognized. Notably, the talus, a well-preserved element across fossil sites, remains underexplored in Miocene primates. Here we present a morphometric analysis of the talus among extant primates and nine complete early Miocene tali dated to ~19-17.5 Ma.

A total of 230 three-dimensional talar meshes representing major primate groups were obtained from MorphoSource or scanned by the authors. Talar shape was quantified using spherical harmonics, a method that describes each surface as a set of trigonometric functions with associated coefficients. These coefficients were subsequently used in a principal components (PC) analysis to evaluate shape variation among extant locomotor groups. The relationship of the fossils to the extant sample was examined to reconstruct their locomotor behavior.

The first three PCs explain 57.5% of the morphological variation in the sample and reveal discernible locomotor clusters. Average models and PC warps indicate that differences between groups arise from variations in neck length, talar head orientation, talar body height, and shape of the lateral and posterior processes. All fossils plot within the cluster defined by extant anthropoids, displaying a talar morphology that overlaps with African apes, suspensors, and arboreal quadrupeds depending on the fossil and morphological features examined. This study provides insight into the breadth of postcranial morphological variation observed in Miocene primates and the potential range of locomotor activities that comprised their locomotor repertoire.

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Revisiting the systematics of antilopin bovids from Makapansgat Limeworks

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Makapansgat Limeworks is a Pliocene paleocave site located in Limpopo Province, South Africa that has yielded a rich mammalian fauna, including *Australopithecucs africanus*. The site consists of a complex series of deposits traditionally subdivided into five members, with the most fossiliferous unit, Member 3, dated between 2.9 to 2.6 Ma based on biostratigraphy and paleomagnetism. Fossil Bovidae are abundant at Makapansgat, and their taxonomic diversity and inferred paleobiology have played a central role in reconstructing local paleoenvironments associated with *Au. africanus* and for understanding southern African biogeography and biochronology. Here, we revisit the systematics of two antilopin taxa from Member 3, *Gazella vanhoepeni* and *Gazella gracilior*.

Comparisons of horn core morphology between these two taxa affirm prior suggestions that they represent males and females of a single species, with *G. vanhoepeni* having priority. Basal horn core shape in females is similar to extant *Antidorcas* and *Nanger*, while males have more compressed horn cores than any extant antilopin. The combined hypodigms of *G. vanhoepeni* and *G. gracilior* reflect a single taxon with levels of sexual dimorphism in basal horn core dimensions similar to *Gazella gazella* and *Nanger soemmerringii*. Morphological features of the cranium in *G. vanhoepeni*, including large frontal sinuses extending into the pedicle, indicate greater affinity with *Antidorcas* than with *Gazella*. Preliminary phylogenetic analyses indicate that the Makapansgat antilopin is a sister taxon to *Antidorcas marsupialis*. We propose that the hypodigms of *Gazella gracilior* and *Gazella vanhoepeni* fossils represent a single antilopin species - *Antidorcas vanhoepeni* comb. nov.

The Maya are a People of Movement: An Isotopic Assessment at Chactemal (Santa Rita Corozal), Northern Belize

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Nestled between the Rio Hondo and New River in Corozal District of Belize and situated within the border zone between the Northern and Southern Lowlands, the coastal Maya archaeological site of Santa Rita Corozal, hereafter Chactemal, was continuously occupied from the Middle Preclassic (BCE 800–300) through the Late Postclassic (CE 1250–1531). While many sites in the Southern Lowlands experienced final abandonment in the Terminal Classic (CE 800–900), Chactemal reached its apex in the Late Postclassic when it rose to regional prominence to become the capital of the Chetumal Province. How people's movement influenced population growth at Chactemal is not well-understood. To gain answers, we measured stable oxygen isotopes of dental enamel (n=108 samples) and bone carbonate (n=96 samples) from 100 Ancestors recovered from Chactemal to diachronically assess movement. Approval for isotopic research was granted by the Belize Institute of Archaeology. Additionally, we co-developed this work with local Maya organizations and villages in Corozal District. δ^{18}O values (mean= – 4.0 ‰ VPDB, SD= 1.4, range= – 7.6 ‰ to – 0.8 ‰ VPDB) indicate non-local Ancestors are present within the burial population and suggest non-local Ancestors from the Preclassic came from different places than those in the Late Postclassic. We present evidence to suggest that Chactemal's geographic positioning on the coast, between two rivers, and within the border zone between the Northern and Southern Lowlands attracted people from other places throughout time.

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The revealing of past and present human remains in Swiss Alpine glaciers

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Retreating glaciers allow the recovery of ancient and modern human remains within Alpine areas. Given their cultural relevance and issues related to their identification and recovery, it is important to be able to provide forecasts about future finds. Here, we propose a joint analysis of the density of human remains found in Alpine areas and estimated rates of glaciers retreat.

We compiled a database including human remains found in Bernese and Upper Valais glaciers since the year 2000, considering a minimum postmortem interval (PMI) of 1 month. We classified individuals based on sex, age-at-death, PMI, skeletal elements, location and altitude of discovery. We then modelled the number of finds based on these variables and melting glacier areas.

Besides several archaeological remains, we identified a minimum of 16 cases with post-mortem interval ranges from 3 months to 53 years. All individuals were males and they were found at elevations from 1500 to 3300m a.s.l. The preservation of the remains varied greatly. Considering our sample and an estimated loss of glacier area of ca. 45% by 2050, we postulate around 20 finds of human remains until 2050 as a plausible estimate for the glaciers in our catchment area.

With glacier melt in the Swiss Alps proceeding rapidly, it is important to refine notions of the number of human remains preserved in ice and develop a legal and ethical framework for identification and recovery.

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Romans Were Local: Iron Age Ancestral Continuity in the Eastern Adriatic

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The Eastern Adriatic and hinterland were conquered by Rome (c. 200 BCE- 100 CE) and incorporated into the Empire as the Provinces of Dalmatia and Pannonia. The pre-Roman populations were long standing societies who fought Roman military advances but were defeated. Their cultural transformations are partially known through epigraphy and onomastics, but knowledge is limited by one-sided Roman records. As these populations' political and social structures were intertwined with kinship lineages, research was conducted to assess local biological continuity in the wake of Romanization.

Microevolutionary analyses of dental morphology were conducted between Iron Age peoples inhabiting the Eastern Adriatic and hinterland (Liburnians, Delmatae, Japodes, Pannonians), and subsequent local Romans. ASUDAS traits were scored for 313 individuals from 31 archaeological sites across Croatia associated with Iron Age (c. 600- 400 BCE) groups or local Romans during the Roman Republic and Empire (c. 200 BCE- 500 CE). Twenty-one traits were analyzed using the Mean Measure of Divergence. Results did not identify statistically significant differences among any of the populations: Iron Age Liburnians, Delmatae, and Pannonians compared to the Roman Liburnians and Roman Delmatae/Pannonians. The traits with the highest MDs were UM1Para, UM1EnExt, LM2C5, and LM1Prto; though all were less than .6, so variation among them was low.

In other words, "Romans" were descendants of the local populations who had previously rebelled. This finding suggests that ancestral relationships may persist even in the face of historical processes that are culturally transformative, contributing to discussions on the complexity of local identity and acculturation.

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Ultra-endurance sport as a model to study physiological and cognitive energetic trade-offs

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The use of sport as a conceptual framework offers unprecedented opportunities to improve our understanding of how the body functions, shedding new light on our evolutionary trajectory, our capacity for adaptation, and the underlying biological mechanisms. This approach has gained traction over recent years. To date, sport has facilitated exploration not only of the evolutionary history of our species as a whole, but also of human variation and adaptation at the interindividual and intraindividual levels. At the intraindividual level, evolutionary life history theory has a unique potential to increase understanding of human adaptive capabilities. Ultra-endurance challenges have emerged as a valuable experimental model in this context, allowing the direct testing of phenotypic plasticity via physiological trade-offs in resource allocation. This is enhancing our understanding of how the body prioritises different tissues or functions when energetically stressed.

Here, we analysed biomarkers relating to different life history traits in athletes before and after competing in 4 multiday ultramarathons ($n=111$; 78 male, 33 female). We demonstrate that during energetic stress, immune function (a proxy for survival) is prioritised at the expense of storage, maintenance and reproduction. These results were consistent with the predictions of life history theory, as the function with the greatest immediate survival value was prioritised. We discuss our findings with reference to the adaptive benefits conferred by phenotypic plasticity for a species with an evolutionary history characterised by repeated cycles of dispersal and colonisation.

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Age and sex differences in clinical signs of health in wild chimpanzees (*Pan troglodytes schweinfurthii*)

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Identifying sources of variation in health insults across the lifespan is critical for our understanding of the factors that influence survival and reproductive success in individuals. Here we examine patterns of clinical signs of health across age and sex classes in three communities of chimpanzees: the Mitumba and Kasekela communities of Gombe National Park, Tanzania and the Kanyawara community of Kibale National Park, Uganda. Clinical signs were recorded on a daily basis in all communities using comparable methods; for these analyses, we included 16 years of data from each community (2004 through 2019). We focus on two categories of signs that are frequent sources of morbidity and mortality: respiratory and injury. Using generalized linear mixed models, we analyzed data on respiratory clinical signs comprised of 16154 chimp months from 228 individuals. After controlling for seasonal patterns, we found no evidence of sex differences, but did find an increase in the likelihood of respiratory signs with age ($p<0.001$). Usings generalized additive mixed models, we analyzed data on injuries comprised of 15277 chimp months from 225 individuals. For both males and females the relationship between injuries and age was significantly non-linear ($p<0.001$). Males were more likely to exhibit injuries than females ($p<0.001$); in addition, the age smooth for males was significantly different from the age smooth for females ($p<0.001$), indicating that the shape of the relationship between age and injury is different for males and females. These findings illustrate the complexity of health impacts in wild long-lived primates.

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Hungarian Spina Bifida

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The cemetery of Kunszállás-Fülöpjakab is located in southern Hungary and is believed to have been in use from the second half of the 7th century until the end of the 8th century. It is believed that the individuals buried in the cemetery were part of the military court and their families, as the cemetery would have been located in the political center of the community. The cemetery was excavated during the mid to late 20th century, and 73 well-preserved skeletons were recovered. Of the 73 skeletons from Kunszállás-Fülöpjakab, eight of these skeletons had spina bifida occulta (SBO). SBO is the mildest type of spina bifida; most individuals are unaware of it or discover it in late childhood or adulthood. Occulta means "hidden," and this form of spina bifida is only visible on one or two vertebrae. SBO can be genetic and run in familial lines or environmental, such as a lack of folic acid in the mother's diet leading to a folate deficiency. Of the eight individuals with SBO in the cemetery studied, six were female but ranged in age from young to old. When compared to other pre-modern Hungarian populations, SBO is much more common but does not seem to lead to increased mortality.

Veterinary care and patterns of injuries and mortalities for a population of urban dwelling long-tailed macaques (*Macaca fascicularis*) at the Ubud Monkey Forest over a four-year period

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This study examines patterns of injury and mortality of long-tailed macaques (*Macaca fascicularis*) at the Ubud Monkey Forest in Bali, Indonesia from 2015 to 2018. The forest is situated in an urban landscape that is continuously developed to suit the needs of international tourism. There is an on-site veterinary clinic at the forest where sick and injured macaques are treated. The macaques face typical challenges of living in social groups, and novel challenges of negotiating an urban environment. We analyzed 275 recorded injuries and mortalities among six social groups of macaques brought to the veterinary clinic. Males sustained more injuries ($p < 0.0001$) and mortalities ($p < 0.01$). The frequency of injuries and mortalities changed over the study period, peaking in 2016, with significant differences amongst the six groups ($p < 0.0001$). The frequency of injuries was higher among macaques 5 to 9 years old, but mortalities were highest among 1- to 4-year-old macaques. We categorized injuries and mortalities as "natural" or "anthropogenic." Most injuries and mortalities were naturally occurring, but powerlines, motorized vehicles, and plastic present anthropogenic threats to macaque health. Most wounds and injuries were successfully treated, with healthy animals released to their group. This study demonstrates the importance of local stakeholders' knowledge of their environment to manage wildlife by synthesizing scientific methodologies with religious and philosophical approaches. We suggest other sites with high levels of human-alloprimate interplays consider the Ubud Monkey Forest veterinary office as a model of care, and potentially adopt their approaches for managing wildlife.

Establishing identity: Reconstructing the demographic profile of a human osteological teaching collection

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Recent critical research on anatomical collections has demonstrated through historical, archival, and skeletal evidence that demographic compositions of documented collections in the United States are further testimony of a colonial history of acquisition, exploitation, and structural violence. While these studies in structural violence focus on documented collections, a similar throughline can be observed in the development of human osteological and comparative anatomy teaching collections. In this paper, we present demographic results based on the analysis of skeletal remains from deceased individuals located recently in the Department of Biology's Comparative Anatomy Teaching Collection at the University of Louisville. We identified minimally 36 adult (over 18 years) individuals from 250 commingled identifiable bones or fragments. No juvenile remains were observed. Due to bone representation, only seven individuals could be confidently aged according to pubic symphyseal and auricular surfaces; ages-at-death ranged between 20 and 50 years. From postcranial metric data and pelvic and cranial morphologies, we estimated 16 individuals as probable males, 12 individuals as probable females, and three individuals as presenting intermediate biological variation. We calculated average stature for the sample based on lower limb bones: 163.7cm (overall), 171.7cm (males), and 156.5cm (females). Lastly, using referential collections from FORDISC and AncesTREES, we noted that craniometric data from five complete skulls were more consistent with African and Asian population variation. Collectively, these findings, alongside contextual and institutional information, suggest that these partial and partitive individuals were exploited, commodified, and sold within the broader global bodies trade of the 20th century.

Integration of the gut microbiome and immune system in response to habitat disturbance in white-faced capuchins (*Cebus imitator*) at the Taboga Forest Reserve

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The bacteria of the gastrointestinal tract, the gut microbiome (GM), play a direct role in immune system function by helping the host identify harmful pathogens and preventing pathogen colonization. To date, the gut-immune connection is primarily studied in a biomedical context with a focus on how dysfunction affects host health. While these studies highlight the cost of dysfunction, they do little to evaluate the evolutionary significance of the gut-immune connection. Studying the gut-immune connection in an ecological context can help evaluate if the integration between the GM and immune system helps the host respond to environmental change. We collected fecal GM samples (n= 607) and a noninvasive, nonspecific, immune biomarker, urinary neopterin (n = 576), from two groups (31 individuals) of white-face capuchins (*Cebus imitator*) living in the Taboga Forest Reserve in Guanacaste, Costa Rica. Taboga capuchins cope with extensive habitat disturbance which has been shown to affect both GM composition and infectious disease loads in wild primates. We found that exposure to disturbed habitat affects the GM composition and is associated with higher levels of neopterin, indicating higher immune activation in disturbed habitat. Further, exposure to disturbed habitat and increased levels of urinary neopterin affects the differential abundance of microbial families. These results are some of the first to suggest an integrated response between the GM and immune system in response to the host's environment and indicate the gut-immune connection may be an evolved mechanism that helps hosts respond to environmental change.

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Ancient Warriors: Inter- and Intra-population Variability of Dental Nonmetric Traits of Black Sea Scythians

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Scythians were nomadic people, who inhabited the Black Sea region in the Early Iron Age. Historical sources depict them as rulers of the steppes, warriors occupying vast areas of Eurasia. Our previous study revealed their low fertility and higher probability of dying in early adulthood, likely resulting from their engagement in warfare. This poses a question about maintaining their fighting strength. The present study aims to explore inter- and intra-population variability of dental morphology of Scythians from the Black Sea region. We assumed that this human group was not homogeneous, and embraced outsiders, who could have been recruited into their army from local people. Our analyses involved the permanent teeth of 245 individuals excavated in Glinoe (Moldova), dated to the 5th-2nd c. B.C. In total, 28 dental non-metic traits were recorded using the Arizona State University Dental Anthropology System. Inter-population data comparisons were performed using Principal Component Analysis (PCA), while the ancestry of particular individuals for intra-population analysis was assessed using rASUDAS2. The results indicate that the Scythians are most similar to the Eurasian population. In the study group, most likely ancestry of Western Eurasia was assigned to 59.4% of examined individuals, Southeast Asia & Polynesia to 20.9%, and East Asia to 19.7%. Individuals from the Classic and Late Scythian phases clustered similarly on the map of populations by origin. However, we noted a higher percentage of nobles and of older individuals categorized as most likely Western Eurasia ancestry. Our results may suggest that Scythians recruited soldiers from conquered areas.

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Wild-caught *Cebus-Sapajus* hybrid developmental trajectory, biometry and health

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Natural hybridization across primate genera has been documented for various catarrhine primates, such as *Papio* x *Rungwecebus*, *Papio* x *Theropithecus*, *Mandrillus* x *Cercocebus*, and *Chlorocebus* x *Cercopithecus*. However, there has been little if any evidence to date for recent natural cross-genera hybridization within Platyrrhini, even though within genus hybridization appears common in *Plecturocebus, Saimiri*, *Callithrix*, *Sapajus* and *Cebus*. Molecular evidence also suggests significant introgression across divergent taxa early on in platyrrhine evolution. In this case study we validate the genomic architecture of a wild-caught captive capuchin as representative of a *Cebus kaapori-Sapajus apella* first generation hybrid. We compare morphological and biometric data for this individual to that across the same developmental period for *Sapajus* and *Cebus* individuals of various species housed in captivity in Brazil. While our subject Jack as a young juvenile looked most like *Cebus kaapori*, by adulthood his pelage and jaw morphology converged upon a more *Sapajus apella*–like phenotype, but not completely. Jack also showed evidence for azoospermia throughout development, and was diagnosed with precocious aging as an adult. In our presentation we consider the scenario likely to have led to this hybridization event between a robust capuchin male and a gracile capuchin female, and compare the capuchin ecological and social systems to those for the catarrhines which produce natural intergeneric hybrids.

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Friends or Frenemies: Understanding the Quality of Male Bonds Among Wild Chimpanzees

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Among primates, affiliative behaviors such as grooming are often used to identify strong social bonds between individuals. While a focus on affiliation has successfully identified differentiated bonds and their fitness benefits, less focus has been given to what might constrain participation in bonds. For example, among wild chimpanzees, males must balance the benefit of having bond partners for cooperative coalitions with the need to compete against those same males for dominance. We examine this conflict of interest in male-male relationships by using 14 years of long-term data from the Kanyawara chimpanzees on grooming and aggressive interactions. We found that rate of aggression strongly predicted the rate of grooming among male dyads even when controlling for time spent together (F = 6.57s, p=0.01) suggesting that individuals who groom often are also the ones most likely to engage in aggression. Individuals who were identified as mutual friends from spatial proximity also exhibit this pattern but differed from non-friends in having higher grooming rates (F=26.335, p<0.005) and lower aggression rates (F=5.841, p=0.016). This supports previous work showing that males balance aggression for rank acquisition while repairing valuable relationships through grooming. However, some dyads, like mutual friends, consistently exhibited higher than average grooming and lower than average aggression across many years suggesting that high levels of aggression may constrain some kinds of mutual affiliation. These results contribute to the growing recognition of the diverse nature of social bonds.

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Porcelain gallbladder and other evidence of gallbladder disease and treatment at Asylum Hill

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Graves discovered during construction on the University of Mississippi Medical Center (UMMC) campus in 1992 and 2012 represent a burial ground established for patients who died in the Mississippi State Asylum in Jackson, MS, between 1855 and 1935. Systematic excavation of this cemetery, beginning in November 2022, has uncovered preserved evidence of cholecystitis (gallbladder disease) in the form of gallstones, as well as Penrose drain tubes whose placement is consistent with cholecystectomy procedures. Additionally, a middle to old adult female was found with a 46 mm-long ovoid calcification on the right side of the torso, an object that was initially believed to be a large gallstone, calcified hydatid cyst, or trichinosis cyst. Consultation with a surgeon from UMMC led to the tentative identification of the object as a “porcelain” (calcified) gallbladder. Conventional x-ray and computerized tomographic (CT) scanning confirmed the identification and revealed a single large gallstone within the gallbladder. Imaging of other likely gallstones demonstrated the efficacy of CT scanning for the identification of such objects, even when found out of context, such as within disturbed or commingled burials.

Epidemiologically, the expected rate of gallbladder disease in the primarily African American and Euroamerican population of the asylum would be 5.3-8.6% among men, 13.9-16.6% among women. Though the finding of nine individuals with evidence for cholecystitis among the first 210 excavated burials is unprecedented (based on a review of archaeological literature), the incidence rate of 4.3% is lower than expected for the living population of the institution.

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Adaptive responses in pelvic morphology during growth in forager populations

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This study sought to investigate pelvic morphology throughout growth and development using a geometric morphometrics approach, and to consider the ecological factors shaping this growth. In an ontogenetic sample of pelvic bones from four forager populations (Later Stone Age southern Africans, n=72; Indian Knoll, n=38; Sadlermiut, n=44; Point Hope, n=15), ilium and ischium morphological variation show distinct patterns from one another when plotted against age. Results of a principal components analysis show population-based patterning in ilium morphology from birth, but a similar pattern is not apparent in the ischium. This may imply a greater degree of adaptive response in the ilium to environmental stimuli or may reflect body shape differences. Age-related changes appear to be the most prominent source of variation in ischium morphology. Cross-sectional geometric (CSG) data of long bones, representing habitual activity patterns, were used to examine the impact of loading on pelvic morphology. Long bones are highly plastic and responsive to loading and environmental stimuli, and results from this study show that group differences in CSG are notable from approximately five years of age. Pelvic morphology, however, does not seem to show influences of habitual behaviours, as no relationship was found between pelvic shape and CSG data. As has been hypothesized for epiphyseal morphology, it may be that the functional significance of the pelvis has led to a form that is more canalized and less plastic than the cross-sectional parameters of long bones.

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Hominoid locomotion: Miocene and modern insights

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Matt Cartmill’s insights into links among anatomy, behavior and arboreality are foundational to primate locomotor ecology. A synthesis of hypotheses in this field posit that versatile positional behaviors involving orthograde and differential limb use evolved in hominoids to feed on fruit from terminal branches in forest canopies. However, *Morotopithecus*, a 21-million-year old ape from Uganda, and the oldest to possess indications of orthogrady, consumed leaves and lived in grassy woodlands. We used chimpanzees to test the association between feeding postures and food type in arboreal contexts. We defined versatile postures as involving orthogrady (excluding sit and squat), bridging and/or suspension. Focal follow data were collected from the Ngogo chimpanzees, Kibale Forest, Uganda and consisted of 8498 arboreal feeding observations of 103 chimpanzees over ten months. The proportion of arboreal feeding observations for each food type was 56.7% for ripe fruit, 14.3% for unripe fruit, 14.8% for young leaves and 0.2% for mature leaves. Chimpanzees sat while feeding most of the time. Versatile postures composed 7.6% of time spent feeding on ripe fruit, 7.6% for unripe fruit and 12.1 % for young leaves. There was a significant difference in the proportion of versatile modes used when feeding on leaves vs. fruit (chi-square = 27.37, df = 1, p-value = 0.1.6819e-07). These data show that for a large-bodied ape, postural versatility is at least as relevant when feeding on leaves as on fruit in arboreal settings, supporting paleontological evidence that leaves are important in the evolution of hominoid anatomy and positional behavior.

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One description does not fit all: Different interactions between MTHFR C677T genotypes and serum folate levels

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Introduction: The MTHFR C677T mutation alters one-carbon metabolism and is associated with increased incidence of recurrent pregnancy loss, neural tube defects, cancers, and cardiovascular events. Despite this, this allele is highly frequent in several populations. It is estimated that CT and TT individuals will experience a reduction of 17-75% of serum folate, where a folate-poor environment could decrease fertility (Kuroda et al., 2021). We investigate how serum folate values are altered amongst individuals in this cohort by genotype.

Methods: These data were compiled through a systematic review where N = 5616. Percent change of serum folate between CT and TT individuals was calculated compared to the wild type (CC). 2 of the study populations were taking folate supplements; 3 were not; 1 had participants both supplementing and not.

Results: The changes in serum folate between CC and CT individuals ranged from -5% to +151%, while those between CC and TT individuals ranged from -28% to +12%.

Discussion: Base values of folate for CC individuals varied greatly, reflecting diversity in diet and UVR amongst the cohort. Changes in serum folate also varied greatly, and supplementation showed little consequential change in CT and TT serum folate values. The only CT individuals who showed an increase in folate following supplementation were from Ankara. This indicates the relationship between genotype, serum folate values, and supplementation is complex. Recommendations for daily folate supplementation should be re-evaluated because even if CT and TT participants receive supplementation, their folate levels remain low (except in one case).

Bridging the lab bench to the field: assessing bone health and integrity in population-based field research in human biology

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Human biologists working in field-based settings are poised to contribute insight into health across diverse populations. Often, this includes understudied groups such as remote/rural and Indigenous peoples, whose health measures are typically and problematically compared to references derived from wealthy, affluent populations. Epidemiological insights across global settings therefore promote a more inclusive approach to understanding human biological variation. To this end, one area of burgeoning research focuses on skeletal health in non-clinical, subsistence-level populations. A few decades ago, skeletal health assessments across such settings were only possible via proxies like grip strength. A comprehensive understanding of mechanisms of bone gain and loss therefore remained unattainable. Yet, recent technological developments have expanded our understanding of factors influencing bone mineral density (BMD), one measure of skeletal health, across heterogenous settings. Ultrasound technology offers a means of estimating BMD in non-clinical environments revealing important contributors to bone loss often not observable in affluent regions. Additional developments in biomarker assays now permit a more nuanced view of bone turnover by measuring osteocalcin and TRAP-5b (markers of bone formation and resorption). This biological insight offers great value especially when coupled with ethnographic rich data, revealing complex relationships between sociocultural/behavioral factors and bone integrity. Apart from epidemiological value, continued work across diverse global populations also helps inform reconstructions of the fossil/archaeological record, where skeletons are comparatively decontextualized from their lived experiences. Here, I describe research that integrates these approaches while highlighting various evolutionary and epidemiological questions such measures can help address.

Initial results from the palaeoproteomic analysis of *Australopithecus africanus* dental enamel

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One hundred years ago, palaeoanthropology in South Africa was put on the map with the discovery of the Taung Child and subsequent naming of Africa's first truly ancient human ancestor, *Australopithecus africanus*. Since then, South Africa has produced a rich and taxonomically diverse collection of Plio-Pleistocene hominin fossils, including *A. africanus*, *Paranthropus robustus*, *Australopithecus sediba*, *Australopithecus prometheus*, *Homo erectus, Homo naledi* and *Homo sapiens*. Although there have been several proposals variously linking these taxa to each other and to other African hominins, phylogenetic relationships among many of the taxa remain uncertain. Additionally, for many hominin taxa, determining whether purported intra-taxon variation is due to sexual dimorphism versus taxonomic diversity is critical to understanding evolutionary relationships. A recent study on the palaeoproteomics of southern African *Paranthropus* demonstrated the feasibility of recovering ancient protein traces and determining the biological sex of Pleistocene hominin fossils in Africa. Here, we share the preliminary report of the proteins recovered from a dental specimen identified as belonging to *Australopithecus africanus* from Sterkfontein caves Member 4, dated 2.61-2.07 Ma, from the Cradle of Humankind. We demonstrate that the *A. africanus* specimen comes from a male individual and additionally identify single amino acid polymorphisms. Expanding this work to other hominins within and outside of South Africa will lead to a better understanding of the variation within and between early hominin taxa.

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From Ellis Island to Ellis County: Differential Mortalities among Descendants of Eastern European Immigrants in New York and Texas

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Franz Boas's classic 1912 study in New York City (NYC) described changes in cranial form and stature between European-born immigrants and their American-born descendants. Boas suggested that the transition from rural to urban life, not generalizable "American conditions", explained these morphological changes. Ellis Island is not the only port through which European immigrants entered the United States, enabling us to compare their experiences in different parts of the country. For example, many Bohemian immigrants, now known as Texas Czechs, also entered through the port of Galveston, and settled in central Texas (CTX) during the late 19th century. Texas Czechs therefore lived in a context that differed greatly from NYC in its colonial history, population density, and forms of racial governance. Here we compare mortalities among the descendants of Bohemian immigrants in NYC and CTX to assess how these different contexts influenced mortality. We compiled publicly available vital records data for 1324 individuals born in Ellis County, Texas between 1880-1900, including all 64 children born to Bohemian immigrants in this time period. We also compiled preliminary data in the same time interval for 100 people born to Bohemian immigrant parents and 100 people born to non-immigrant parents in NYC. We find that children of Bohemian immigrants in CTX outlive non-immigrants by an average of 8.84 years ($p=0.001$). Children of Bohemians in NYC live far shorter lives than those in CTX ($p<0.0000001$). However, we detect no significant difference in lifespan between the children of immigrant and non-immigrant families in NYC ($p=0.98$).

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Enamel growth of *Homo naledi*

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A modern pattern of dental development occurs relatively recently during human evolution. Given the temporal overlap of *Homo naledi* with the first appearance of fossil *Homo sapiens* in Africa, this small-bodied and small-brained hominin presents an opportunity to elucidate the evolution of enamel growth in the hominin clade. Here we use histological methods to reconstruct the development of two permanent mandibular canines and one permanent maxillary molar attributed to *H. naledi* recovered from the Rising Star cave system in South Africa.

Results reveal these *Homo naledi* teeth formed in a way that was most similar to recent humans. The fast rates of enamel secretion reported for *Paranthropus* and *Australopithecus* were not present in *Homo naledi*. Enamel extension rates, and the formation time of one canine, lay within the range of rates and formation times that are present in recent Europeans. Retzius periodicity values of 11-days for both canines and 9-days for the molar occur in recent humans but these values do not follow expectations for a small-brained fossil hominin.

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Quantifying Distal Phalanx Variation in Subfossil Lemurs

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"Subfossil" lemurs are recently extinct, large-bodied strepsirrhines from Madagascar. Cheiridial morphology has been related to locomotor behaviors, but their distal phalanges remain enigmatic. Shape of the distal extremity of the phalanges (apical tuft) varies with dorsal outlines ranging from circular and blunt (e.g., *Archaeolemur*) to triangular and sharply pointed (e.g., *Babakotia*). The significance of apical tuft morphology has been difficult to assess because it is not easily captured by traditional methods. A preliminary analysis was run to assess the feasibility of using a pseudolandmark approach to quantify it. Surface meshes were generated from a small sample of microCT scans of 15 subfossil (*Archaeolemur*, *Babakotia*, and *Megaladapis*) and 37 extant strepsirrhine distal phalanges. Meshes were landmarked and aligned using Auto3dgm in 3D Slicer. A relatively small number of pseudolandmarks (80) permitted successful alignment. A principal components analysis of Procrustes aligned coordinates derived from aligned pseudolandmarks was performed using the GPA module in SlicerMorph. The morphospace described by the first two components (explaining 35% of total variance) demonstrated success in clustering specimens with qualitatively similar tufts while also reflecting overall phalangeal morphology. Among extant taxa, *Propithecus* and *Loris* have rounded apical tufts on narrower phalanges, while cheirogaleids and lemurids tended to have more pointed tufts on wider phalanges. *Archaeolemur* and *Megaladapis* phalanges plotted nearest to those of *Propithecus* and *Loris*, but those of *Babakotia* plotted with extant lemurids. Neither locomotor behavior nor shared ancestry alone explains the observed pattern, which is likely influenced by a combination of factors.

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Inter-tissue isotopic variability in three sympatric primates (*Pan troglodytes schweinfurthii, Cercopithecus ascanius,* and *Piliocolobus rufomitratus*) from Kibale National Park, Uganda

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Stable isotopic analysis of fossil enamel provides insights into reconstructing the dietary paleoecology of extinct taxa. The utility of this method relies on establishing a comprehensive comparative framework of isotopic cycling in modern ecosystems. This includes documenting and quantitatively characterizing the physiological kinetic offsets associated with variable routing of dietary components to various tissues and the resulting isotopic variation within an individual. This is especially important when converting isotopic signatures between tissues and in extending patterns of variation into the past where enamel represents the only biogenically intact signal. In this study, we document isotopic variation in six tissues (bone apatite, bone collagen, tooth enamel, hair, dentine collagen and dentine apatite) from multiple individuals of three primate taxa in the Kibale Forest, for which foraging strategies are well known. δ^{13}C, δ^{15}N, and δ^{18}O values reveal significant and variable inter-tissue offsets with differences of up to 4.4‰ in δ^{18}O offsets (i.e., red-tailed monkey bone$_{ap}$ - enamel$_{ap}$ offset mean = 2.0 ± 1.4‰), at least 5.2‰ in δ^{13}C (i.e., the chimpanzee bone$_{ap}$ - dentine$_{ap}$ δ^{13}C offset mean = 1.0 ± 2.5‰), and more than 5.9‰ in δ^{15}N (i.e., red colobus monkey dentine$_{coll}$ – hair$_{keratin}$ offset mean = 0.8 ± 4.2‰). Patterns of δ^{13}C, δ^{15}N, and δ^{18}O covariation may relate to relative proportions of leaves/fruit in the diet, age, digestive physiology, body size, and vertical niche stratification. Inter-tissue offsets have implications for differentiating specific components of primate niches and ultimately for interpreting the δ^{13}C$_{enamel}$ and δ^{18}O$_{enamel}$ values of fossil primates, including hominins.

Faunal Analysis and the Stratigraphic Contiguity of the Black Mousterian Archaeological Level (> 45,000 BP) at Arma Veirana, Italy

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Palaeoecological reconstruction and taphonomy are critical for understanding and contextualizing archaeology sites. Arma Veirana is a cave site in northwestern Italy in the region of Liguria that preserves rich Mousterian archaeological deposits that extend beyond the range of radiocarbon dates and later strata that date to the Pleistocene/Holocene boundary. As of the most recent excavation season (2018), sediments belonging to the lowest excavated stratigraphic layer at the site [the Black Mousterian (BM)] was exposed in squares on either end of an east-west main trench. These squares are not currently contiguous in the excavation; thus, whether or not the sediments in the eastern exposure (provisionally labeled BM0) and western exposure (provisionally labeled BM3) represent the same archaeological horizon remains uncertain.

This study seeks to determine if BM0 and BM3 represent one horizon that was deposited together or alternatively, time-separated and distinct packets of sediment originating from under different depositional circumstances. To test this data was collected on variable that could reveal similar site use strategies, and ecological conditions: taxonomic ID, bone processing behaviors like heat alteration, and butchering behavior. Data collected on these measures from BM0 and BM3 will be used to test their similarities and differences via statistical analysis. Our null hypothesis is that there is no difference between BM0 and BM3; thus, supporting the stratigraphic model that they are similar enough to be consolidated as one Black Mousterian level.

Make no bones about it: Preliminary evidence that polycystic ovary syndrome (PCOS) is an evolutionary mismatch disease that may have benefitted bone health in ancestral populations

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Polycystic ovary syndrome (PCOS; a highly heritable globally distributed (4 – 20%) female endocrine disorder with ancient origins), is believed to be an evolutionary mismatch disease, which occurs when a heritable trait evolving in one environment becomes maladaptive in another. Previous mismatch arguments paint PCOS as a uniform ancestral ailment, despite significant variation in accepted phenotypes. Additionally, establishing a disease as a mismatch requires pinpointing a heritable trait. We suggest PCOS-related hyperandrogenism (i.e., heightened production of androgens) may have been beneficial to ancestral populations by reducing fracture occurrence and associated mortality and morbidity through increased bone mineral density (BMD), but now contributes to the pathogenesis of PCOS in post-industrial environments with an overabundance of food energy. This hypothesis is supported by PCOS treatments that control hypothalamic hormone feedback loops and insulin. Seventy-six females were surveyed (ongoing 2021 – present) as: high intensity interval training (HIIT; a proxy for metabolic and physical stress) athletes with hyperandrogenic PCOS (31.6%), HIIT athletes without PCOS (36.8%), or non-athletes with hyperandrogenic PCOS (31.6%). HIIT athletes without hyperandrogenic PCOS had significantly higher fracture occurrences throughout the lifetime (3.21 ± 3.794) compared to athletes with PCOS (1.21 ± 1.382) and non-athletes with PCOS (0.96 ± 1.551) ($p < 0.01$). There were no significant relationships between reproductive or lifestyle factors associated with bone health and fracture occurrence. This suggests females with hyperandrogenic PCOS may be less likely to experience bone fractures throughout the lifetime. These findings provide an initial step in establishing PCOS as an evolutionary mismatch disease.

Molecular evolution of X-specific immunity genes in primates

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Among humans and other mammals, there is distinct sexual dimorphism in immunity, or an ‘immunity gap,’ where females often have enhanced immunocompetence compared to males. This is likely a result of multiple interacting factors such as hormones, sociality, genetics, and life history differences. Primates are incredibly diverse ecologically, socially and genetically, making them an interesting order in which to study the evolution of this immunity gap. Genes involved in immunity are under strong selective pressure, and are generally either highly polymorphic or conserved. As the X chromosome has a high density of genes involved in immunity (~50 genes), it could be a primary proximate cause of the deficit between male and female immunocompetence. Using standard assessments of dN/dS ratio and protein evolution across primate phylogeny (e.g. branch and site variable models implemented in HyPhy), we explored patterns of selection across X-specific immunity genes that code for a multitude of aspects of immunity, such as pathogen recognition and immune regulation, using sequence data mined from reference genomes. Preliminary results show interesting clade and lineage-specific changes and signatures of episodic positive/diversifying selection (e.g., I826V substitution *TLR7* that seems to have evolved independently across independent primate lineages). There is also evidence of convergent evolution at specific sites, such as an A379G substitution in *MSL3* found in ring-tailed lemurs and orangutan species. This study reflects how the molecular evolution of the immune system is a particularly good study system for looking at local adaptation and convergent evolution.

Human fatigue resistance: from limitation to regulation

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Much of how we think about and interpret the basis of human physical performance is related to the notion of physiological limitation which when exceeded will fail and cellular catastrophe will ensue. The basis of this limitation underpins our understanding of how fatigue develops during physical performance. There are a number of factors proposed to limit human exercise performance but commonly referred to as a ‘cardinal exercise stopper’. These factors include muscle acidification, glycogen depletion, respiratory muscle fatigue, perception of effort, muscle pain and a maximally achieved heart rate. In contrast, a competing model of exercise *regulation* presents a departure from this classical view to one that posits that a system built to regulate muscular-metabolic rate by psycho-physiological feedback with ‘top-down’ effect allows for motor unit de-recruitment, or in some situations, overriding of signals to prolong motor output for optimal adjustment of performance during heavy exercise. There is now good evidence that during high intensity cycling and running, individuals adjust their skeletal muscle recruitment strategy to enable the successful completion of the exercise bout. Experimental evidence for this alternative model of physiological regulation shows that exercise regulation is perhaps an adaptation across multiple systems working together to enhance fatigue resistance.

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Running out of Space: Historic Mass Graves, Ossuaries, and Exhumations in Contemporary Urban San Juan, Puerto Rico

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In 1855, Puerto Rico was struck by the cholera epidemic, killing 20,000 to 50,000 individuals – 4-10% of the total population at the time. Due to the high volume of corpses piling up and fear of the disease's further spreading, a mass grave outside of the walls of San Juan's El Morro was established. Today, this area is in danger of being destroyed due to erosion and recent climate disasters on the island, as with urban use from tourists that share the space as part of a National Park trail. Our research is a rescue bioarchaeological investigation of the site, with the main objectives of collecting, analyzing, preserving, and repatriating the human remains buried here before erosion and intrusion destroy the site and its contents. Following initial geophysical surveys and excavations, a far more complex picture of the site has emerged. Here, we present survey, geophysical, and excavation data that shows the coexistence of a choleric mass grave, the dumping grounds of overflown ossuaries and exhumed plots, and a U.S. National Park Service public trail. These results provide us with a unique opportunity to study a complex palimpsest of violence and changes in the perceptions of the dead in this unique colonial and postcolonial Caribbean context.

Social drive explains rapid adaptation and eco-evolutionary feedback in small-scale human societies

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Social interactions play a crucial role in generating feedback between ecological and evolutionary dynamics. Developing generalizable, comparative models of eco-evolutionary feedback in social environments is, therefore, crucial for understanding convergent social evolution across the natural world, as well as for predicting population growth or decline in response to ongoing environmental change. In this talk, I will introduce and empirically test a novel eco-evolutionary feedback model that attempts to explain otherwise paradoxical patterns of rapid adaptation, both historic and contemporary, in small-scale human societies. This "social drive" model demonstrates how phenotypic plasticity among group members can generate and maintain feedback between the genetic causes and ecological effects of humans' social interactions in fluctuating environments. Using extensive long-term data on the indigenous Tsimane people of Bolivia (5823 births/1581 women/82 communities), we found strong support for key empirical predictions of this model. Results show that the heritability of fertility due to direct genetic effects is modest ($h^2 = 0.12$, 90% Bayesian CI [0.05,0.20]), but that indirect genetic effects due to interactions among neighbors accelerate adaptation in fertility by a factor of 6x (90% Bayesian CI [2.80,13.45]). Furthermore, we find that density- ($\beta_D = -0.07$, 90% Bayesian CI [-0.13,-0.01]) and frequency-dependent ($\beta_I = 1.93$, 90% Bayesian CI [0.52,3.12]) selection among neighbors maintain these accelerating effects across space and time. Overall, our study suggests that social drive is an important eco-evolutionary feedback process explaining unique features of human social evolution, while also unifying contemporary theoretical models of rapid adaptation across the biological and social sciences.

Monitoring the early Holocene Nile Valley biological diversity: a comparison of different 3D geometric morphometrics approaches on the enamel-dentine junction

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There is an ongoing debate regarding population dynamics along the Nile Valley from Egypt to Sudan at the beginning of the Holocene. Previous studies on outer dental morphology (i.e., non-metric traits, crown measurements), dental tissue proportions, and enamel thickness distribution patterns revealed marked morphological diversity among early to middle Holocene populations. To understand further this reported variation and its implications (i.e. *in-situ* evolution or biological discontinuity), we now explore enamel-dentine junction (EDJ) shape with two 3D geometric morphometric methods: a landmark-based analysis and surface deformation. Both were applied to samples of UM1s (*n*=40) and UM2s (*n*=42) from Late Paleolithic to Neolithic sites in the middle Nile Valley (Sudan). Principal component analyses show clear morphological variation among sites and periods. The landmark-based analysis highlights notable inter-sample diversity with variation in position of the dentine horns (especially the hypocone), and shape and position of the cervical line. The surface deformation method yields a similar signal, plus substantial variation in morphological complexity of the occlusal basin and lateral aspects of the EDJ surface. Surface deformation therefore appears to better identify EDJ variation that, in turn, provides improved estimates of affinities among samples. Altogether, these results suggest that a substantial morphological shift in the EDJ shape of both UM1s and UM2s occurred between the last foragers and the first food-producers from our sample. Considering the morphological stability and phylogenetic signal of the EDJ shape, we suggest that these results highlight significant biological discontinuity at the dawn of the Neolithic transition in the Nile Valley.

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The deciduous hominin molars from the Shungura and Usno Formations (Omo Valley, Ethiopia)

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The Lower Omo Valley is a region in eastern Africa significant for paleontological research. Some important sites in this area are Shungura and Usno Formations, where different hominin taxa have been discovered. The sediments from these sites date back to the Plio-Pleistocene, spanning a period of approximately 3-1 million years ago, providing a unique opportunity to understand the origin and evolution of the *Homo* genus.

The early childhood stage of development is essential in setting the course of life history. Because the deciduous dentition erupts during this life stage, it offers significant insight into dietary adaptation and behaviour. In this respect, the deciduous teeth found in the fossil record provide crucial insights into the evolutionary history of hominids. Their morphology and developmental patterns have allowed us to identify species, determine evolutionary relationships, and perhaps most critically, study how the juvenile stage of life has evolved.

The Shungura and Usno sample includes 16 upper and lower deciduous molars. The metric size and morphological traits of these teeth were analyzed against a comparative sample of 51 deciduous molars representing *Australopithecus*, *Paranthropus* and early *Homo* specimens. The preliminary results indicate that two of our Omo specimens can be clearly considered as *Paranthropus*, while the remaining ones show resemblances to other *Australopithecus* or early *Homo* used in the comparative sample. The ongoing excavations in the Omo Valley are yielding important discoveries that will undoubtedly shed light on the evolution of early hominids and the environment they inhabited, contributing to our understanding of human evolution.

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Estimates of Canine Sexual Dimorphism in Miocene Catarrhines using Six Different Methods

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Assessing sexual dimorphism in the fossil record is notoriously difficult as sex can rarely be assigned with certainty to any given specimen. This problem is exacerbated when examining Miocene catarrhines, as many specimens are isolated teeth and living primates display such a broad range of sexual dimorphism. Additionally, while several methods exist to investigate sexual dimorphism in extinct species, each has its own assumptions. These methods also perform differently depending on factors such as sample size, intrasexual variation, and sex ratio. As such, an investigation using a combination of methods for estimating sexual dimorphism may yield important insights. I analyzed several Miocene catarrhine fossil samples using six methods (Mean, Median, CV, BDI, MoM, and pdPeak) of estimating sexual dimorphism, focusing on the mandibular and maxillary canine teeth. The results indicate that for some species sexual dimorphism estimates are perhaps best considered as a range rather than a strict value, and that Miocene catarrhines are likely as diverse as extant catarrhines in their broad diversity of sex differences or lack thereof.

The Behavioral Ecology of Gender and wealth inequalities in Southwest China

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Contemporary inequality exists at an unprecedented scale. Social scientists have emphasized the role played by material wealth in driving its escalation. Evolutionary anthropologists understand the drive to accumulate material wealth as one that is coupled ultimately to increasing reproductive success. Wealth differentials are also thought to underlie the gender-biases in inheritance, suggesting gender and wealth inequalities are intimately connected. This talk reviews theoretical and empirical evidence linking wealth and gender inequalities to health among Mosuo people in Southwest China, who practice both son- and daughter-biased inheritance in different sub-populations. We describe differences in social networks (matrilineal women's are larger than men's (p=0.019)); and access to resources (men are less likely to report income in matriliny than patriliny; p=0.022)). These differences likely contribute to gender reversals in health, as evidenced by hypertension and inflammation (women's are elevated relative to men's in patriliny, but not matriliny). The series of results reveals nuances in how biology and cultural institutions affect gender disparities in wealth.

The work was funded by the National Science Foundation and the University of New Mexico.

A training-testing approach for the comparison of dominance rank reliability and its application to primate social systems

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Achieving a high dominance rank within a social unit can have proximate benefits (greater access to resources) for individuals that lead to ultimate consequences (e.g., longer survival, increased reproductive success). Thus, determining how to effectively operationalize rank is important for studying Darwinian fitness and the evolution of social systems. There are numerous potential rank metrics that can be used to estimate dominance hierarchies, and the choice of the 'best' metric for a target system is often ambiguous. Here, we analyze publicly accessible data on 44 years of agonistic interactions between female chimpanzees in Gombe National Park, Tanzania. We use a 'training-testing' approach developed by Vilette et al. (2020) and adapted from predictive modeling and machine learning to compare the reliability of four variants of the popular Elo rating method (traditional, randomized, maximum likelihood-based, and Bayesian). We found that applying a maximum likelihood approach to calculating Elo scores achieved greater reliability (predicting ~90% of dyadic interaction outcomes), while other variants produced meaningfully lower reliability estimates, ranging from 59 to 81%. Moreover, we found that metrics producing similar rank orders do not necessarily have similar reliability. We conclude that applying a training-testing approach to dominance hierarchy comparisons may be advantageous for identifying effective ranking metric(s) for one's target system. We discuss potential explanations for differences in reliability among metrics and the benefits of this comparative method to the identification of optimal metrics for calculating dominance hierarchies in primate social systems.

Cribra Femoralis in the Juvenile Skeletal Assemblage from Cueva de Sangre, Guatemala

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Cribra femoralis is a pathological condition that presents with localized porotic lesions on the anterior femoral neck, which are morphologically similar to the porous lesions seen in cribra orbitalia. The porotic lesions on the femur are essentially restricted to juveniles and may result from physiological periods of stress, dietary deficiency, and/or anemia making them useful as a proxy for the general health status of the population. This study investigates the prevalence of cribra femoralis in a sample of juveniles from Cueva de Sangre at the site of Dos Pilas, an important Late Classic (AD 600-900) political and economic center. The commingled and fragmentary skeletal assemblage contained eight juvenile femora with the proximal end preserved. None of the femora are matching pairs. Age-at-death was estimated using metaphyseal width. Femora were macroscopically examined for porotic lesions, and porotic lesions were microscopically examined, classified by grade, and scored according to degree of severity and stage of healing. Three out of eight femora presented with lesions consistent with cribra femoralis. These individuals, all aged to early childhood (1–5 years), each presented with lesions at different grades and stages of severity and healing. Two older juveniles may also have lesions consistent with cribra femoralis. Frequencies of cribra femoralis are compared with other Maya juvenile samples. Potential causes of cribra femoralis and the possible irrelevance of the osteological paradox in this assemblage are discussed. The generally well-preserved skeletal remains from subterranean contexts make these assemblages indispensable for understating the lives of the ancient Maya.

The Evolution of Primate Litter Size

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Litter size has been associated with the appearance of large brains, complex sociality, and long lifespans in mammals. Almost all extant primates give birth to singletons, but closely-related lineages Rodentia and Lagomorpha have much larger litter sizes. Despite its importance for understanding the evolution of human cognition, the timing and evolutionary history of primate litter size evolution remains contested. We compiled life history data and litter size for 955 boreoeutherian mammals, including 158 extant primate species. We find highly significant phylogenetic signal in litter size (Pagel's lambda=0.853, $p<0.001$; Blomberg's $K=0.057$, $p<0.005$) and other key life history traits. Smaller litter sizes are significantly associated with other traits typically linked to slow life histories: longer gestation lengths, older age at female and male maturity, and longer lifespans ($p<0.05$) across boreoeutherian mammals. Ancestral state reconstruction, using the most taxonomically comprehensive and speciose dataset to date, supports a mean litter size of 1.732 for the primate ancestor. The boreoeutherian last common ancestor also likely gave birth to twins (ASR litter size of 2.165). Twinning has thus likely played an important role in primate evolution and boreoeutherian evolution more broadly. In this talk, we discuss the implications of our finding that the last common ancestor of primates likely gave birth to twins. A better understanding of twinning in primates has important impacts for human health studies, particularly those focused on fetal growth rates, brain:body size relationships, and the evolution of human pregnancy.

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Ancient Human DNA from the Osmore River Valley, Peru: Demographics, Disease, and Adaptation

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Here we present preliminary ancient human DNA data from 85 individuals dating from 385 BCE to 1476 CE and spanning the Huaracane, Tiwanaku, Tumilaca, and Chiribaya cultures in the Osmore Drainage region of southern Peru with the goal of better understanding changes in population history and the spread of disease over time. Individuals with skeletal lesions specific to tuberculosis were sampled across multiple elements including teeth, vertebral elements, and ribs. We extracted 105 total subsamples, of which 81 were built into single stranded libraries that were shotgun sequenced on the Illumina NovaSeq X Plus to 4-50 million reads. The shotgun data was mapped to a human reference genome using NF-Core's Eager 2 pipeline. We recovered low coverage mitochondrial genomes from 18 samples (0.1X-3.7X) and low full genome coverage from 19 teeth (0.82X-8.31X), all of which could be candidates for further targeted enrichment. Using the recovered host DNA, we aim to explore regional demographic history, familial relationships, the spread of tuberculosis spatial-temporally, and possible evidence of adaptation.

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The Accessory Bone at the Bregma in the Skulls of Rhesus Macaques from Cayo Santiago

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In humans and nonhuman primates, accessory bone of the skull forms from extra ossification centers throughout utero. Accessory bones are expected to amalgamate after birth, though some are found to persist into childhood and adolescence with potential genetic predispositions or environmental disturbances as causes. In this study, the skulls of 2623 individuals from the Cayo Santiago population, with known age (0 to 31 years), sex, and matriline affiliation, were investigated for the presence of accessory bone at the bregma region. Results demonstrated that the accessory bone at the bregma was found in 2% of all individuals in the Cayo Santiago skeletal collection and limited to animals aged between 0 to 7.3 years. The distribution between males and females was comparable (males = 2.63%; females 1.84%). All individuals presenting with the bregmatic accessory bone derived from 20/99 known matrilines suggesting a genetic influence, though statistical comparisons between the largest 13 matrilines (N >20) did not support this (p = 0.097). The absence of accessory bone at the bregma after 7.3 years of age indicated that the total obliteration of this feature was achieved between age 7 and 8 years after birth in the Cayo Santiago Rhesus colony. Further investigation is warranted to understand the etiology of accessory bones, including non-metric variation, familial aggregation, or environmental exposures during growth and development.

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Analysis of Temporomandibular Joint Morphology and Dental Arch Shape on the Prevalence of Dysfunction

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Temporomandibular joint dysfunction has high clinical prevalence with treatment ranging from symptomatic management to corrective procedures. The morphology of the stomatognathic system, including mandibular teeth, mandibular condyle, and dental arch as well as variations in the muscles involved in mastication, has a significant impact on the prevalence of temporomandibular joint dysfunction. We analyze morphological variance in these structures primarily involved in the temporomandibular joint function and identify their relation to prevalence of dysfunction in a population of rhesus macaques (*Macaca mulatta*). We collected 3D scans of the mandibles and dental arches of *Macaca mulatta* specimens (N = 12) housed at the University of Oregon, and used 3D Slicer to outline mandibular dental arches and mandibular condyles. Generalized

Procrustes and principal components analyses were carried out on these landmark variables in the R geomorph package. Tooth wear was scored following a published system in the mandibular fourth premolars and second molars, the presence or absence of condylar remodeling was described as a marker of dysfunction within the joint. Proportional odds logistic regression was used to assess the relationship between morphological variables and condylar remodeling. Several dental arch and mandibular condyle shape variables were positively associated with condylar remodeling, but tooth wear and sex were not strongly associated with condylar remodeling. We conclude that narrow dental arches with angular, internally rotated condyles tend to co-occur with condylar remodeling in this population, and propose future research to understand which of these variables may be predictive of temporomandibular joint dysfunction in primates.

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Examination of the Relationship Between Linear Enamel Hypoplasia, Mortality, and Chronic Morbidity in a Modern Greek Sample

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Recently, McPherson (2021) has argued that skeletal biomarkers of stress should be evaluated in a developmental windows framework based on the ages at which skeletal elements start and end growth. With this framework, researchers can use a skeletal element (e.g., the mandibular canine) to evaluate adversity during a specific age window (i.e., 1.5-5 years) and that window's correlation with adult chronic disease and mortality. Measurement and demographic data were collected from 57 individuals from the National and Kapodistrian University of Athens Human Skeleton Reference Collection. Standard metric data were collected on first linear enamel hypoplasias (LEHs) of permanent mandibular canines to estimate age and duration of adversity. Mesial dental images were captured using a DinoLite digital microscope and midline profiles were plotted in ImageJ. Data were analyzed using multiple linear regression and multinomial regression. Age-at-death and cause-of-death were considered dependent variables, while age, duration of adversity, and sex were independent variables. We found no significant correlation between age or duration of first LEH expression, and age-at-death or cause-of-death, whether with the linear regression (P-Value=0.8031) or the multinomial regression (P-Value=0.9291). We conclude that developmentally plastic responses experienced during mandibular canine crown formation did not have significant effects on adult morbidity or mortality in this modern Greek population. Including additional skeletal elements in future analyses should help further elucidate later life outcomes in these individuals. These results aid in our understanding of the developmental timing of adversity and its potential life course effect across human populations.

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Archaeology of Black (M)othering: Somatic Legibility and Black Feminist Excavations of Dispossessed Lives in Historic Western Maryland

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Recent calls to action, community organizing, and legislative progress have turned increased attention toward the recovery of human remains from Black burial sites across the United States. As we continue to pursue their protection and repatriation, working collaboratively with community descendants in ways that honor the lives and stories of even the most marginalized within ancestral populations is of the utmost importance. This paper employs Black Feminist frameworks to trace the ways that the embodied labors of Black women in particular have become invisibilized both literally and figuratively. By situating established demographic, osteological, and biomechanical approaches to data analysis within the context of black feminist biopolitics, instances of disproportionate archival namelessness, evidence of reproductive violence, and labor disparity can be understood within the same racial-gendered continuum of dispossession. Focusing on the recovery of African-American burials from two sites: the Catoctin Iron Furnace in Frederick County, MD (MNI: 35) and the 3300 Block of Q Street NW in Washington, DC (MNI: 28), we mobilize practices of somatic legibility as a way of "reading" bodies across multiple contexts to excavate the absented presence of Black women that can be at times lapsed in bioarchaeological and osteobiographical analyses. Moreover, we argue that these practices work along strategies for community engagement, such as the Clientage Model, by broadening the range of non-destructive biocultural research that can be presented to community descendants.

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The cervical vertebrae of DIK 1-1

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Complete cervical spines are rare in the early hominin fossil record. Here we describe the nearly compete cervical vertebral column of DIK 1-1(~ 3.3 Ma), a juvenile attributed to *Australopithecus afarensis* from Dikika, Ethiopia. The vertebrae of DIK 1-1 were encased in matrix making it difficult to examine bony elements of the spine in isolation. The cervical vertebrae were partially exposed after extensive preparation and the thorax of DIK 1-1 was scanned at the European Synchrotron Radiation Facility to better visualize the cervical vertebral elements for description. All seven cervical vertebrae are present, with the atlas consisting of a partial lateral mass. Here we report on the morphology of the cervical vertebrae comparing them to those of *Homo sapiens* and *Pan troglodytes* individuals of similar dental developmental stage. Preliminary results suggest that for the axis, the inclination of the dens is more like what is observed in *Homo* than nonhuman apes. The upper cervical vertebrae of DIK 1-1 have dorsoventrally short spinous processes like *Homo*. In contrast, the length of the lower cervical spinous processes, mainly C7, are dorsoventrally long like *Pan*. Finally, the uncinate processes are craniocaudally taller than *Homo* and intermediate when compared to *Pan*. Our study shows the mosaic nature of the cervical vertebral morphology in *Australopithecus afarensis*. Future work will focus on interpreting the morphology of DIK 1-1 through the lens of function and ontogeny within the context of extant primates to better understand and reconstruct the locomotor repertoire of DIK 1-1 and its species.

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Piecing together the scavenged: Utilizing global information systems (GIS) to map and analyze locations of previous scavenging research within the United States

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When animals scavenge remains, the destruction they cause can alter valuable evidence, thus affecting both the recovery and forensic anthropological analysis of deceased individuals. Therefore, it is important for forensic anthropologists to understand which animals commonly exhibit scavenging behaviors within specific geographic areas. However, current scavenging research typically focuses on skeletal modifications resulting from animals within a few restricted geographic areas and is therefore limited in scope. The purpose of this project was to utilize GIS methods to provide a comprehensive overview of the current research that has been conducted on scavengers native to the United States. This project sought to answer three research questions: 1.) Where do the scavenging studies in the United States occur? 2.) Is there a distinction in spatial patterns between where scavenging case studies and where scavenging experimental studies occur? 3.) How much overlap is seen in different animal species recorded in each of the studies? For this project, information such as locational data and scavenging species were obtained from both experimental scavenging studies (n=27) and scavenging case studies (n=14). The data were uploaded to ArcGIS (version 10.8.2) and examined using GIS analyses (i.e., Thiessen polygons, kernel density plots, mean center, standard distance, nearest neighbor analysis). The results suggest geographic gaps are present, specifically regarding animals in Midwestern states. Therefore, further research utilizing scavenging studies that encompass a greater degree of locational documentation are necessary to fully expand forensic anthropological knowledge of animal scavenging in the United States.

Comparing dental stress markers in Sima de los Huesos hominins and classic Neandertals

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Stressful events like early life illness and injury create horizontal grooves on the surface of developing teeth. Previous research suggests that more severe and longer lasting stressors increase defect depth and width, respectively. However, enamel growth variation also influences dimensions with faster growth rates creating shallower defects and normal growth increments called perikymata. Here, we use confocal profilometry to create high-resolution 3D surface maps from the anterior teeth of the Sima de los Huesos (SH) hominins (N=24 teeth; 32 defects). We compare their defect depth to previously analyzed classic Neandertals (N=17 teeth; 36 defects). We find that Neandertals have more defects per tooth, in line with previous research suggesting low defect prevalence among SH hominins. However, defect depth is indistinguishable between the two samples (F(1,26)=0.07, p=0.79; mixed model used to control for individual effects due to multiple observations per tooth). This suggests similar stress severity among SH hominins and classic Neandertals, but more frequent stress events in classic Neandertals. There are few marked outliers or major plane-form defects in either sample. Perikymata are deeper in SH hominins than classic Neandertals within the canine subsample (F(1,9)=15.93; p=0.003), but larger sample sizes are needed to better compare dental growth patterns based on surface features. Ongoing research is also comparing defect width to assess whether there are discernable differences in the duration of stress events between groups. Together these results shed light on the evolutionary relationships and experiences of extinct hominins using nondestructive techniques.

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"Immigrants – We Get the Job Done:" Migration and Identity in an Emerging Urban Center during the American Revolution

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The Revolutionary War (1775-1783 CE) was a turning point in American history, as the thirteen colonies separated from England and established themselves as an independent nation. How did the dramatic changes during this period influence the origins and movement of populations living in Philadelphia, a growing urban center and the heart of young America? Were Philadelphians native to the Mid-Atlantic region, migrants from elsewhere in the thirteen colonies, or did they come from somewhere across the Atlantic? To explore population movement from infancy until the last three to five years before death, we undertook a life-course approach and present stable oxygen isotope analyses ($^{18}O/^{16}O$) on tooth (enamel and dentine), long bone, and rib samples from a subset (n=100) of a Revolutionary-era assemblage from the First Baptist Church of Philadelphia. While four individuals' phosphate oxygen isotope values are consistent with time spent in the mid-Atlantic region ($\delta^{18}O_{meteoric}$ -9.5 to -7.5 $^{0}/_{00}$), the remainder spent time outside of this region ($p \leq 0.013$), either in their infancy/childhood or adulthood. This data provides new context for the movement of individuals into the emerging urban center of Philadelphia, allowing specific distinction between northern versus southern regional migrants, and European immigrants. Radiogenic strontium ($^{87}Sr/^{86}Sr$) and lead ($^{206}Pb/^{204}Pb$, $^{207}Pb/^{204}Pb$, $^{208}Pb/^{204}Pb$, $^{206}Pb/^{207}Pb$, and $^{207}Pb/^{208}Pb$) isotope analyses were undertaken on the same samples; preliminary data add additional nuance to individuals' provenance and mobility. This project examines America's earliest history as a mosaic of diverse peoples and cultures who travelled to the United States' urban centers for new opportunities.

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Boiled vs. bottled: Analyzing oxygen isotope signatures from Taiwanese water to aid anthropological investigations

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Stable isotope analysis is used in bioarcheology for the reconstruction of mobility and migration patterns, and in forensic anthropology to predict region-of-origin to aid in the identification of unknown decedents. This research analyzes oxygen isotopic values to aid in forensic provenancing of unidentified human remains cases and to expand isotopic datasets from East Asia. Isotopic ratios in hair show a strong correlation with drinking water. However, no work has been conducted to establish baseline data for drinking water or hair samples in Taiwan. To fill this gap, this study collected samples of hair, tap water (both boiled and unboiled), and bottled water throughout Taiwan to establish baseline $\delta^{18}O$ values in hair and drinking water. In addition, this study examines how imbibing bottled and boiled water impacts drinking water $\delta^{18}O$ values in hair. Across eight regions of Taiwan, 207 water samples were collected from the tap or locally purchased bottled water, and 48 hair samples were collected from local hair salons. Oxygen isotopic values of tap water show regional patterns of variation based on unique geographic features, which reflect regional distinctions in the north/northeast compared to the rest of the island. This data set also explores how the consumption of bottled water creates variation in $\delta^{18}O$ values that can differ from local tap water. Additionally, the process of boiling water causes fractionation of oxygen isotopes leading to $\delta^{18}O$ values which differ from tap water. These data can assist in the provenancing of individuals to Taiwan in forensic investigations.

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Effects of Socioeconomic Status on Age at Death and Cause of Death

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This study investigates the relationship between socioeconomic status (SES), age-at-death, and natural causes of death (COD) as a way of examining the Developmental Origins of Health and Disease hypothesis (DOHaD). Recent studies show that SES is linked to health and COD due to differential access to resources. The aim of this study was to examine whether childhood SES was a better indicator of age-at-death and COD than adult SES.

Self-reported demographics, childhood and adult SES, COD, and age-at-death were collected from 92 individuals from the Texas State Donated Skeletal Collection. The CODs were grouped into ten broad categories for statistical testing. Fisher-Freeman-Halton Exact tests were conducted between COD, childhood SES, and adult SES. Spearman's Rho correlation tests were conducted to compare age-at-death, childhood SES, and adult SES.

No association was found between COD and either childhood or adult SES. There was no correlation between childhood SES and age-at-death. When adult SES was compared to age-at-death, there was a positive, significant correlation, r(90) = 0.309, p = 0.003, meaning as SES increases, age-at-death slightly increases.

These results indicate that adult SES is associated with age-at-death, possibly due to differential access to resources. This study illuminates the disparity in healthcare access and the effects of health and nutrition at a population level. Limitations could include sample size, available data, and varying interpretations of SES. In the future, we aim to reduce these limitations by incorporating other donated skeletal collections.

Short and healthy, tall and frail: disentangling height and health in skeletal samples

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In bioarchaeological studies, equifinality represents a significant interpretive problem. Different patterns of growth may incur different costs, with implications for frailty. Catch-up growth that facilitates late gains in stature may obscure evidence of costly trade-offs initiated in response to developmental stress. To explore this concept, we examined catch-up growth and its consequences in a forensic skeletal collection from New Mexico. In a sample of 177 individuals (male = 90, female = 86, age = 16.9-20.9 years), we assessed the relationship between developmental stress, adult stature, and bone mineral density (femoral, lumbar) and muscle density (quadriceps, psoas) standardized by age and sex. We organized our sample into four cohorts based on whether individuals experienced significant physiological stress in the first 12 years of life (stressed / not stressed) and their adult stature (short / normal), with short stature defined at the CDC 10th percentile for stature or below by sex. We then compared BMD and muscle density between these cohorts using a series of independent T-tests. Contrary to our expectations, no significant differences were found between the two normal stature cohorts. The short/stressed cohort exhibited significantly lower lumbar BMD (p=0.046) than its not stressed counterpart. Interestingly, the short/not stressed cohort exhibited significantly higher lumbar BMD (p =0.043) and quadriceps muscle density (p=0.05) than its normal stature counterpart. Differences between the short and normal stature cohorts may be attributable to the developmental lag between linear height and BMD and body mass observed in adolescents who undergo a typical growth-spurt.

Digging Deeper with a Biocultural Approach to Bone Biology

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Observations of rib bone remodeling is known to provide information about the lived experiences of people from the past. This research used a biocultural approach including rib bone histology, skeletal pathology, isotopic analysis, and historical records to contextualize the lives of adults (n=99) and children (n=87) who died at the Kilkenny Union Workhouse during the Great Irish Famine (1845-1852). The study examined bone remodeling patterns between four disease categories, identified through paleopathological analyses with support from historical documents, to determine if variation in bone microstructure exists between disease types. Additionally, $\delta^{13}C$ and $\delta^{15}N$ were compared to bone histological variables to determine if changes in diet, as documented in historical records, influenced cortical remodeling. The results show that rib bone porosity is highest in adults and children without lesions and lowest in adults with evidence of infectious disease. Comparisons of histomorphometry with stable isotope values showed a positive correlation between osteon size and $\delta^{15}N$ values in adults and a positive correlation between Haversian canal size and $\delta^{13}C$ values in children. The novelty of this presentation is that it showcases the advantage of incorporating historical records, first-hand narrative accounts, and other archival material with bone biology methods to conduct biocultural research that tells a more holistic story about the impact of resource restriction on the human skeleton.

Inner ear's sexual dimorphism in late Holocene humans from South America: an interdisciplinary assessment combining morphological, archaeological, and genetic data

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The use of the petrosal portion of the temporal bone has increased in the last decade within biological anthropology studies. Among the anatomical structures inside the petrosal, the inner ear stands out due to presenting good archaeological preservation and not being affected by bone remodeling or environmental factors during development. Likewise, it is the main focus in aDNA studies aiming at reconstructing population history, while it presents relevant morphological information for estimating the sex of the individuals. Regarding the latter, while some studies showed that there is strong sexual dimorphism in inner ear's morphological variation, others state the contrary. This discordance could be due to the differences in the methods used, as well as the sample composition, and the source from which the independent information on biological sex was obtained. The aim of the present study is to study the magnitude of sexual dimorphism in a sample of ancient South American individuals from Argentina and Brazil (N=80) for which information for the chromosomic sex is available. We conducted a preliminary evaluation by registering ~100 3D landmarks and conducting Principal Component and Discriminant Analyses to assess if individuals were mostly differentiated by biological sex. While most of the changes could be explained by population history, a large account could be interpreted as biological sex differences.

We expect that the results obtained in this study will be useful in forensic sciences, especially in cases where there is skeletal disarticulation or only small parts of the skeleton are preserved.

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Using geometric morphometrics to assess labor's impact on metacarpal morphology in ancient Mesoamerica

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Physical tasks performed during life have an enduring impact on skeletal morphology. Craft production such as weaving engages the hand muscles and causes subtle skeletal changes during life that are difficult to quantify and visualize. The goal of this project is to assess robusticity of Classic period burials from Río Viejo, Oaxaca, and late Classic period burials from San Pedro, Belize. Given that individuals from Río Viejo (PRV00 44-53, PRV00 47-56, and PRV12 81-90) participated in intensive craft production for a market economy, we would expect differences in shape between the groups reflecting different degrees of external bone robusticity (e.g., expression of entheses). Geometric morphometric shape analysis is utilized in this study to compare robusticity as landmarks and curve semilandmarks can be used to quantify subtle shape differences. The sample was comprised of 20 left second and third metacarpal bones of 12 individuals. Using an Artec Spider 3D scanner, three-dimensional digital surface models were generated, and 78 landmarks and curve semilandmarks were placed on the models. Results of the principal component analysis show that the metacarpal shape of individuals from Río Viejo, including individual PRV12 81-90, a known weaver, are distinct from individuals from San Pedro. This pattern may be explained by differing levels of intensive craft production at the respective sites, although factors such as sexual dimorphism and genetics must also be considered. The results of this study are significant as they reflect the first application of geometric morphometrics to the study of occupational stress in ancient Oaxaca.

Archaic Adaptive Introgression in Peruvian Populations

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Research into archaic introgression in Indigenous American populations have found higher rates of Denisovan introgression (Witt et al., 2023) within said populations compared to European genomes including regions responsible for facial variation (Bonfante et al., 2021). Our research focuses on Indigenous Peruvian populations and sites of archaic adaptive introgression. Using MalAdapt (Zhang et al., 2023), genomic regions were marked as potential candidates for archaic adaptive introgression. Of these, chromosomes 2 and 22 were chosen as regions of interest due to the lack of published literature. Genetic variation was calculated using FST among modern populations such as the Yoruban, Han Chinese, and Northern European. The Peruvian chromosome 2 shared striking similarities with the European chromosome while chromosome 22 was more similar to the Han Chinese chromosome. Testing for affinity with archaic genomes was also conducted. Overall, there was lower genetic divergence when compared to the Denisovan genome than the Neanderthal genome for chromosome 22 and the genomes contain protein coding segments most often found in brain tissue as well as whole blood. Chromosome 2 had incredibly similar genetic divergence between Neanderthals and Denisovans but the former was slightly lower, protein coding segments include brain and testis tissue. Further investigation regarding population history and time of selection is still being completed at this time.

Effects of social status on degenerative joint disease risk and severity in early medieval Thuringia, Germany

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In addition to biological factors, such as age and sex, aspects of lifestyle are important contributors to the risk of developing degenerative joint disease (DJD). Among these factors are the type and levels of activities, diet, injury risk, and somatic inflammation. Many of these factors are directly or indirectly affected by an individual's socioeconomic standing in a society. The Merovingian Period, marking the beginning of the early Middle Ages in Central Europe, is historically known to be characterized by strict social hierarchies related to personal or familial wealth, which is often reflected in burial goods.

This study investigates the relationship between DJD at different locations of the body and social status among Merovingian Period individuals from Thuringia (Germany). At the Merovingian cemetery of Großvargula (n=34 adults with observable joints), odds ratios indicate a varied pattern of differential risks for DJD with an overall tendency for greater risks of affliction for lower status individuals at younger ages and greater severities. For instance, low status adults under the age of 50 have 6.26 times greater odds to develop advanced DJD of the hip, compared to high status adults. Conversely, an odds ratio of 0.86 for knee DJD suggests a slightly greater likelihood for high status individuals to develop advanced stages of the disease when adults of all ages are included. These results highlight an overall greater burden of DJD for low status individuals, while also showing variation in the pattern of affected joints, suggesting differing risk factors associated with different joints.

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Manubriosternal variation in anthropoid primates: implications for thorax form in fossil taxa

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Reconstructing body form in extinct taxa is key for inferring positional and locomotor behavior, yet there are numerous challenges inherent in these reconstructions given the fragmentary nature of the fossil record. Carefully elucidating the relationships among individual skeletal elements across a wide variety of taxa helps address these challenges. Here, we investigated variation in manubriosternal morphology and its relationship to thorax shape across a large sample of extant anthropoids. We used calibrated photographs (n=244) and torso CT scans (n=52) to collect linear and angular metrics on the manubrium, sternal body, and ribcage as well as multiple body size proxies. We then compiled manubriosternal data for multiple fossil taxa, using the results of our extant sample to explore predictions about thorax form in these groups. Our results demonstrate that, as expected, hominoids have relatively broader sterna than do monkeys, although some of the more acrobatic arboreal monkey species overlap with hominoids in some metrics. Manubriosternal breadth is broadly correlated with thoracic breadth across anthropoids, which further supports reconstructing *Ekembo* and *Equatorius* as having had relatively narrow torsos, given their narrow sternebrae. Neandertals, however, have relatively narrower sternebrae than do modern humans, suggesting a different relationship of the sternum to thorax form. Humans differ from other extant hominoids in sternoclavicular joint orientation, and the MH2 manubrium suggests that *A. sediba* possessed a more horizontal clavicular posture than other hominoids. In sum, manubriosternal morphology varies across anthropoids and appears to track thoracic shape and thus positional behavior, providing useful information for fossil taxa.

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Territorial mobility in Switzerland during the La Tène period: the CELTUDALPS isotopic dataset

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The type and degree of territorial mobility in human communities has important biocultural consequences, with high degrees of long distance movements potentially influencing the genetic makeup and cultural variability of a population. Previous works have investigated mobility on a large series of Western European archaeological contexts. Conversely, patchy data are still available for the Swiss territory during the La Tène period (4th-1st c. BCE), despite the biocultural centrality of this region during for the European Iron Age. Here, we present a new isotopic dataset ($\delta^{34}S$, $\delta^{18}O$, $^{87}Sr/^{86}Sr$) covering good portion of the Central and Western Swiss plateau and alpine regions for the last centuries BCE. The set includes 320 human bone and dental enamel samples (131 females, 117 males, 28 unsexed adults, 46 nonadults). Local isotopic ranges are based on the analysis of faunal, plant and water samples (n: 65, 26, and 5 respectively). We evaluate context-specific territorial mobility patterns based on intrapopulation isotopic variance and relative deviation from local faunal and environmental ranges. Results highlight a dichotomy between the alpine regions and the Swiss plateau, with the latter showing a higher isotopic variance. Here, sites like Münsingen Rain, Cornaux/Les Sauges, and Engehalbinsel stand out for the higher frequency of nonlocals, mostly represented by male individuals. Our results offer a new angle from which to examine the biocultural processes characterising the Swiss territory between the 4th and the 1st c. BCE. Environmental, economic, and social factors emerge as the main triggers of mobility in the past, as nowadays.

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The role of the patterning cascade model in human premolar variation

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Human mandibular premolars represent a morphologically transitional tooth class, possessing a relatively caniniform third premolar (P_3) and more molariform fourth premolar (P_4). Variation in cusp height and lingual cusp number are characteristics unique to these teeth. The aim of this study is to determine if human premolar variation aligns with predictions of the patterning cascade model (PCM). The project sample is comprised of three-dimensional scans and two-dimensional images of mandibular casts representing contemporary Solomon Islanders (n=62). Three-dimensional intercusp distance (ICD) measurements were collected in Meshlab to account for differential cusp height, while crown area and two-dimensional ICDs were measured in ImageJ. To account for size variation, relative ICDs (RICD) were calculated by dividing ICDs by the square root of crown area. Analysis of variance and independent sample t-tests with a 1000 resample bootstrap procedure were performed to determine the relationships between lingual cusp number and RICDs. RICDs between the buccal and mesiolingual cusps did not differ significantly by lingual cusp number. The RICDs between the mesiolingual and distolingual cusps were significantly different as a function of lingual cusp number, with two lingual cusped premolars exhibiting greater RICDs on average than three lingual cusped premolars. These results were consistent for P_3s and P_4s. For P_3s only, individuals possessing two versus three lingual cusps significantly differ in buccal to distolingual cusp RICD, with two lingual cusped teeth exhibiting greater RICD, on average. These findings align with PCM expectations and demonstrate the potential use of RICD as a predictor for lingual cusp number.

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Mentorship beyond landing the dream job: guidelines for building and maintaining research laboratories in molecular anthropology

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Following the development of polymerase chain reaction and the first successful recovery of ancient DNA (aDNA) from museum specimens in the 1990s, the application of genetic techniques to address questions in a wide range of fields and species, including our own, has exploded (22,542 publications in 2022 referring to “DNA methods” or “DNA techniques” based on a Web of Science search, including 225 publications referencing ancient DNA). As research that applies molecular techniques continues to expand and fields of research become more specialized, the design, construction, and set-up of these more specialized laboratory facilities is now a skill that trainees and early-career scientists must learn. While mentorship has been shown to improve many aspects of job performance, including job searches, little attention has been given to what comes next: building and maintaining a lab as a new faculty member and principal investigator. Here, we provide an opportunity for further discussion and mentorship on this topic by presenting ten simple guidelines we learned and developed over the first three years (Fall 2021 - present) of designing, building, stocking, and running new ancient and modern DNA laboratories in the Anthropology Department at the University of Minnesota. In an effort to continue sharing, improving, and applying our guidelines, we will solicit feedback from attending biological anthropologists through an interactive survey. We aim to foster discussion and collaboration among researchers at various stages in their career to better support the expanding application of laboratory research techniques in anthropology, particularly among early career anthropologists.

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Analyzing variation in early hominin knee shape using a deformation-based approach

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The knee is a critical anatomy for assessing primate locomotion. This joint plays a crucial role in maintaining an efficient bipedal gait and thus can provide insight into the evolution of this locomotor behavior in the human lineage. While previous studies have analyzed aspects of the primate knee, none have conducted a full three-dimensional shape analysis of the early hominin knee joint, combining the distal femur and proximal tibia. Here, we investigate the relationship between knee anatomy and locomotion in a large sample of modern humans, non-human primates including *P. troglodytes*, *P. paniscus*, *G. gorilla*, *G. beringei*, *P. pygmaeus*, *Hylobates sp.*, *S. syndactylus*, *Papio sp.*, *M. fascicularis*, *N. larvatus*, *Ateles sp.*, and Plio-Pleistocene hominins *A. afarensis*, *A. africanus*, *A. sediba*, and *A. prometheus*. Analyses are performed using a landmark-free method of shape deformation called Diffeomorphic

Shape Matching (DSM). This approach has been successfully employed in previous studies of hominin craniofacial material and is used here, for the first time, on hominin postcranial fossils. Results from this study reveal that locomotor differences drive variation in the knee joint between modern primate taxa. Furthermore, this method provides more resolution than previous linear and angular-based analyses of the knee joint, particularly in differentiating between hominins and cercopithecoids. We find the australopith knee to be primarily human-like, indicating that extended-knee bipedal gait had evolved in early hominins.

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Integrating machine learning and artificial intelligence in understanding dental enamel development

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Deep learning is currently spurring revolutions in the acquisition and interpretation of data throughout the sciences. In this talk, we report on efforts to deploy physics-informed machine learning techniques to the quantitative analysis of amelogenesis. Our results illustrate that simple modelling assumptions, coupled with modern machine learning techniques, allow us to accurately interpolate local enamel secretion rates and other quantities of interest throughout a both simulated and real histological tooth section, using standard histological measurements like perikymata counts, crown height and crown formation time as inputs. These methods allow us to test various hypotheses about tooth morphogenesis in silico, and provide means for non-destructive inference of daily secretion rates, crown formation times and enamel extension rates. We highlight these results by presenting a novel dataset of ten thousand simulated premolar buccal cusps, from which we draw conclusions about how the integration of kinematic components of amelogenesis produce variation in enamel and tooth morphology.

Identifying Denisovan Fossils using ancient DNA Methylation

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Direct evidence of Denisovan anatomy is exceptionally limited due to the scarcity of confirmed fossils, including merely a finger, a lower jaw, a parietal bone and a few teeth. Consequently, studying their anatomical distinctiveness and adaptation to their environment poses a substantial challenge. We previously developed a method to reconstruct genome-wide premortem DNA methylation maps of ancient specimens. Using this method, we identified genes that were differentially methylated between modern humans, Neanderthals and Denisovans, many of which were informative on Denisovan skeletal morphology. Using these findings, we constructed an anatomical profile of the Denisovan, identifying traits that are likely shared with Neanderthals, such as an elongated face and a wide pelvis, alongside Denisovan-derived traits like a longer dental arch and lateral cranial expansion. A growing collection of middle Pleistocene East Asian crania, including specimens such as Harbin, Dali and Jinniushan, could have potentially belonged to Denisovans. However, these crania have yielded no biological material such as DNA or proteins, and thus could not have been associated with Denisovans. Here, we present a novel method that employs craniometric measurements of these skulls to quantify their resemblance to the predicted Denisovan anatomy. Our analysis revealed that the Xiahe and Harbin specimens closely match the predicted Denisovan morphology, whereas specimens like Jinniushan exhibit no significant similarity. In summary, our approach underscores the valuable role of ancient DNA methylation maps, combined with craniometric measurements, in identifying potential Denisovan specimens.

Artificial neural networks predict perikymata counts on worn teeth from two key paleoanthropological sites: Atapuerca (Spain) and Omo valley (Ethiopia)

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Long-growth markers on the enamel surface, perikymata, are key to assess enamel formation times of teeth. It is well known that crown formation times varied through evolutionary time, as *Australopithecus* and *Paranthropus* have significantly lower number of perikymata than *Homo* species, indicating faster rates of enamel growth. One hurdle in counting perikymata is that full crown height is not always available due to natural tooth wear. We developed a package in R, named *teethR*, to address this issue. First, there is a function enabling the reconstruction of the original position of the cusp tip of slightly worn teeth based on a reference microCT slice. With the reconstructed crown height, we calculate the percentage of missing enamel, and with that percentage we run a second function that predicts the number of missing perikymata. The prediction of perikymata is done by running trained artificial neural networks (ANN) that predict perfectly, or within 1 perikyma of difference in each of the first three deciles of the crown height in more than 90% of the cases for modern humans, no matter the tooth type. Using this ANN tool, we predict perikymata in slightly worn isolated teeth of different stratigraphic units of the Omo (Ethiopia), spanning approximately 3.5 Ma to 1.9 Ma (n = 13), and two sites at Atapuerca (Spain), spanning 0.86 Ma (Gran Dolina-TD6) and 0.43 Ma (Sima de los Huesos) (n = 43). Results indicate that ANNs can be used to accurately predict perikymata in fossil material and therefore.

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Growing a brain, growing a body: the evolution of hominid encephalization

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Biological anthropology has historically been consumed by the idea that larger brain size is linked to increased cognitive ability. This also applies to paleoanthropology, where encephalization is lauded as a defining feature of genus *Homo* and assumed to underlie advanced cognitive abilities relative to basal hominids. Almost 50 years ago, Pilbeam and Gould proposed that humans were simply a 'peculiar large primate' with large relative brain size that can be explained by interspecific positive allometry. Despite this, the anthropological community continues to rely on variation in encephalization metrics to explain perceived cognitive differences among hominids. We conducted the most comprehensive analysis of allometric scaling in primates to date using brain and body size data for 225 extant primate species and 18 fossil hominid taxa, including small-brained and small-bodied *Homo floresiensis* and *H. naledi*. All hominids after 3 Ma share derived, allometrically-scaled brain:body size proportions ($R^2 = 0.89$, $p<0.001$), with a significantly steeper allometric slope than other primates (slope F=5.26 (1, 236), $p=0.023$). Compared to this derived scaling relationship, humans are not more encephalized than other Pleistocene hominids ($p>0.05$). Perceived variation in encephalization, and differences in hominid brain sizes after 3 Ma, can be explained by positive allometry and selection on human body size diversification. Within the Pleistocene hominid lineage, encephalization has no value for explaining the evolution of human distinctiveness. We hypothesize that a fundamental biological shift ca. 3 Ma altered the trajectory of hominid encephalization and is directly implicated in the evolution of complex symbolic behavior in our lineage.

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Ancient DNA in Context: Port Cities and Mobility in the Iron Age and Roman Mediterranean

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The Iron Age saw the expansion of Phoenician and Greek colonies across the Mediterranean and later, the nascence of Roman Imperial expansion, facilitated by the ease of long-distance travel following major advances in seafaring. Ports were important sites of interaction between the maritime world and the hinterland beyond, between local and diasporic populations. We explore the relationship between these ports, the cities they serve and their hinterlands, as well as the limitations that may arise from differential burial practices across class and social-cultural groups, preservation conditions, and contemporary research attention across these contexts. For instance, the majority of people and goods coming into imperial Rome from the provinces arrived by boat, many of these would have docked at Rome's primary port complex of Portus Romae and Ostia. The inhabitants of these Portus and Ostia were buried at Isola Sacra necropolis, where inscriptions indicate that many were engaged in commerce and business. Ancient DNA analysis indicates the population at Isola Sacra was comprised of people with both local and non-local ancestries, spanning the empire. Isotopic analysis ($\delta^{18}O$) reveals that some of these individuals had isotope ratios compatible with having grown up locally (Prowse et al, 2007), suggesting the long-term, multi-generational settlement of families with diverse ancestries at Portus/Ostia. These biomolecular findings are supported by historical and archaeological evidence for established merchant guilds at the port, especially from the eastern Mediterranean.

Pelvic shape development and (no) menopause: a case of Japanese macaques

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It has been shown that the degree of pelvic sexual dimorphism decreases in humans in association with menopause, which is thought to represent developmental adjustment for obstetrical demands that change during ontogeny. It remains unknown whether such developmental adjustment, which is related to obstetrical constraints, is unique to humans. Here we track pelvic shape development from neonate to advanced ages in Japanese macaques using methods of three-dimensional geometric morphometrics based on medical-CT images. Japanese macaques have human-like cephalopelvic proportions but do not usually undergo menopause, and thus the obstetrical constraints are likely present throughout adulthood in females. It appears that the degree of pelvic sexual dimorphism does not remain constant during adulthood in Japanese macaques. The pelvic sexual dimorphism increases after primiparity, and it is most pronounced at the latest ontogenetic phase studied here due to continuous pelvic development in females. We hypothesize that this represents Japanese macaque's developmental adjustment to compensate for the increased obstetrical risks at advanced ages such as decreased flexibility of the pelvis due to fusion of pubic symphysis. Further studies are required to better understand the relationships between sexual and skeletal maturation, obstetrical constraints, and life history of primates.

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Molar form in grasshoppers correlates with diet, suggesting convergence between molar form and dietary physical properties in grasshoppers and mammals

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Molar form (shape and size) is correlated with dietary ecology in primates and other mammals. However, studies have shown both molar form and diet carry high phylogenetic signal, questioning whether the relationship between molar form and diet is a result of natural selection or phylogenetic inertia. Here, we use dental topographic analysis (DTA) – a landmark free method of quantifying molar form – to investigate convergence in dental form between grasshoppers and primates and other mammals. Grasshoppers (Acrididea) were chosen because the shape of their molars is correlated with diet, and there is no chance of convergence in dental form due to phylogenetic inertia. µCT scans were taken of grasshopper heads (30 species), representing all major extant subfamilies. Methods were developed to apply DTA to grasshoppers, and the sensitivity was tested. Relief index (RFI), Dirichlet normal energy (DNE), orientation patch count rotated (OPCR) and ambient occlusion (PCV) were used to quantify molar form. Grasshoppers were classified as graminivores, forbivores, or intermediate feeders, and differences in molar form between dietary categories were compared using Mann-Whitney U tests. Like mammals, graminivores (grazers) had lower RFI than forbivores (browsers) and intermediate (mixed) feeders (p = 1.29e-4 and 4.11e-5), and higher PCV (p = 4.76e-5 and 4.11e-5). DNE was lower in graminivores than forbivores and intermediates (p= 0.0278 and p= 0.0002) with OPCR higher in graminivores (p= 0.0007 and p= 0.0028). These results suggest grasshoppers and mammals have converged on similarly shaped molars for similar diets, presumably because of similarities in dietary physical properties.

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Assessing Perinatal Limb Bone Strength in Leaping and Quadrupedal Primates

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Prior studies have shown that primates specialized for leaping have more robust femora than quadrupedal taxa. This trend in femoral strength is observed in both adult and perinatal primates, suggesting a genetic component to robusticity independent of postnatal differences in limb loading. However, previous ontogenetic interlimb comparisons were made in a single primate clade – lemurid strepsirrhines (*Propithecus coquereli* and *Lemur catta*). Here we extend our sample to include perinatal samples of eight additional primate species *(Eulemur coronatus, Eulemur fulvus, Galago moholi, Galago senegalensis, Pithecia pithecia, Saimiri boliviensis, Trachypithecus francoisi,* and *Pan troglodytes*). Our sample included a total of 40 perinatal individuals (1-12 individuals per species). Species were grouped based on adult locomotor mechanics: hindlimb dominant (*Galago* and *Propithecus*) or quadrupedal (remaining taxa). We hypothesized that, even at birth, hindlimb dominant species should have relatively stronger hindlimb bones than quadrupedal species. Perinatal primate limb bones were µCT scanned to measure cross-sectional geometry then tested in three-point bending to determine material properties. As predicted, non-parametric Mann-Whitney U tests revealed that hindlimb dominant species were characterized by relatively greater values of femoral and tibial strength in bending (i.e., relatively higher values of polar section modulus; $p \leq 0.038$). Additionally, there was a trend (though not significant; $p=0.076$) for hindlimb dominant species to have relatively stiffer hindlimb bones (i.e., relatively greater femoral moduli of elasticity). Overall, our results suggest functionally important limb specializations can be detected at birth, well prior to functional variation in bone loading regimes.

Dental Wear Indicative of Spinning Found in the Midnight Terror Cave Assemblage

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The extra-masticatory use of teeth results in unique dental wear patterns. While several activities are associated with extra-masticatory incisal grooves, they are frequently linked to the habitual use of the anterior teeth for working materials to make yarn or thread. This study examines the incisal surface of isolated permanent teeth from a Late Classic (AD 600–900) dental assemblage from Midnight Terror Cave, Belize to assess the presence of extra-masticatory grooves which provides a glimpse into the lives of these individuals. Right and left maxillary and mandibular central incisors were macroscopically and microscopically examined. The morphology of the groove, frequency per tooth, and location on the incisal surface were recorded. The stage of attrition for each tooth was also scored. A total of 43 teeth were examined. Of these, 16 (37%) showed extra-masticatory grooves. Grooves were most frequent on left upper (3/6) and right lower (5/10) teeth. Frequencies of V- and U-shaped grooves were comparable across teeth. Most teeth (12/16) had one groove, and grooves were usually located centrally on the incisal surface (7/16) regardless of the frequency of grooves per tooth. All teeth with observed grooves showed low attrition. Based on ethnographic, ethnohistoric, and archaeological evidence, these findings suggest the presence of spinners in this assemblage. The sociocultural significance of ancient and modern Maya textile industries is discussed. When multiple lines of evidence are juxtaposed, interpretations of extra-masticatory dental wear can cautiously provide information about habitual behaviors at the individual level.

Unrealistic optimism during COVID: Evolutionary explanations for risky behaviors

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Despite potential costs associated with inaccurate risk assessment, one's perception of risk is often incongruent with actual risk. Unrealistic optimism (or optimism bias) occurs when one falsely believes (i.e., positive illusions) their personal outcomes will be more favorable than others' in a similar risk category, underestimating their own likelihood of experiencing negative outcomes. Accurately estimating risk is critical for avoiding negative outcomes while maximizing opportunities, and selection could favor overconfidence as long as the benefits of unrealistic optimism outweigh its costs. Positive illusions can yield psychological advantages, increasing motivation and promoting resilience in response to adversity. But in environments characterized by much uncertainty, such as during the early stages of a pandemic, these same positive illusions can lead to increased morbidity and mortality. We investigated relationships among perceived risk of infection and disease, compliance with shelter-in-place orders, travel restrictions, and public health recommendations, psychological distress, and other variables in a community cohort of 492 participants during early shelter-in-place orders in central Texas. Risk for severe COVID-19 disease was calculated using information about demographic characteristics (sex) and pre-existing conditions previously shown to increase the odds of experiencing severe disease. Higher clinical risk scores for severe COVID-19 disease were associated with lower perceived risk of becoming infected with SARS-CoV-2 virus, lower perceived stress, and feeling less depressed by and less helpless in response to the pandemic. Despite these psychological benefits, miscalibration of risk and overconfidence in one's outcomes during novel hazardous situations requires further study along with targeted public health messaging.

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Reproductive tactics in aging male chimpanzees

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Senescence impairs the ability of older males to compete for mates. Consequently, male reproductive strategies are expected to change with age. The terminal investment hypothesis proposes that older males should take greater risks to secure mating opportunities. Alternatively, older males might employ tactics such as increased affiliation with females or increased reliance on coalitions to compete with younger animals. We tested these hypotheses in wild chimpanzees of the Kanyawara community, Kibale National Park, Uganda, where old males are known to sire offspring at relatively high rates. Our dataset included >40,000 incidents of male aggression and >5800 copulations observed between 2005 and 2016. We found that, even as they declined in rank, old males maintained relatively high copulation rates, especially with parous females. There was no evidence for terminal investment in response to aging, as males became less aggressive with age. Nor did aging males form affiliative bonds with females, as male grooming decreased with age. Old males did, however, participate in coalitionary aggression at higher rates than young males, steadily increasing the proportion of their aggression that was coalitionary. Coalitions were positively associated with mating success, particularly for low- and middle-ranking males. These results support the hypothesis that aging male chimpanzees used coalitions as an alternative reproductive tactic. The lack of evidence for terminal investment in response to aging appears to reflect a broader mammalian pattern in which males who rely on fighting to secure mating opportunities avoid excessive risk-taking as their formidability wanes.

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Epigenetic signatures of intergenerational exposure to violence

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Maternal trauma is known to impact fetal and adult health outcomes, possibly through epigenetic modifications such as DNA methylation (DNAm). In contrast to model organisms, research in humans on the intergenerational epigenetic transmission of maternal trauma effects is much more limited. In this study, we hypothesize that exposure to violence leaves intergenerational epigenetic marks. Thus, we assessed DNAm signatures of war-related violence, comparing germline, prenatal, and direct exposure to violence across three generations of Syrian refugees. We compared families in which the pregnant grandmother vs the pregnant mother was exposed to war violence and included a control group of Syrian refugees unexposed to war violence. We collected buccal swab samples and survey data from mothers and two children in each family (n=131 participants). Based on an epigenome-wide association study, we identified multiple DNAm marks that were associated with germline and direct exposure to violence. Identification of a germline epigenetic signature of violence in humans supports our hypothesis and highlights DNAm as a mechanism to preserve information about trauma exposures across generations. Most sites showed the same directionality in DNAm change across germline, prenatal, and direct exposures, suggesting a common epigenetic response to violence. Furthermore, in children, we identified epigenetic age acceleration in association with prenatal exposure to violence highlighting the critical period of *in utero* development. These results have profound implications for understanding how lived experiences become embedded in the genome and ongoing efforts to ameliorate multigenerational cycles of violence, abuse, and poverty.

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Trends in NAGPRA Literature

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Biological anthropology greatly contributed to the presence of Native American ancestral remains held in museum and university collections, and recently has been engaged in discussions about the ethical engagement with these collections. An important step in this discussion is to consider how the NAGPRA law, which has been in effect for over 30 years, has been incorporated in the discipline's primary literature. This study aims to understand the trends in the literature regarding mentions of NAGPRA. Keyword searches were conducted using Web of Science to generate a database of articles that referenced the law in any way. The search was restricted to journal articles published between 1990 and 2023, and returned only 103 articles with direct mention to NAGPRA. Title, authors, date of publication, publication title, and abstracts were collected. Journal descriptions were used to assign disciplines for each publication.

Results show that few journal articles discussed NAGPRA in the 1990s (N=15) and 2000s (N=22), and publications become more common in the 2010s (N=56). Museum Anthropology is the journal with the most articles (N=13), while the American Journal of Biological Anthropology only has 5 articles mentioning NAGPRA. The journals aimed at general anthropology disciplines contained 21 articles, archaeology journals had 14 articles, biological anthropology journals had 9 articles, and museum studies journals had 22 articles. This initial result demonstrates that, despite its importance, NAGPRA has not been significantly incorporated in bioanthropological literature, and that conversation is occurring primarily in museum and archaeology literature.

Semi-prehensile tail use in wild cercopithecid monkeys

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Prehensile tails are found across the globe as an adaptation for stability in arboreal environments. Among primates, only some platyrrhines have prehensile tails, but evidence of some caudal prehensile ability has been documented in cercopithecids. To document wild primate locomotion, we collected videos of eight species of cercopithecid monkeys from Kibale National Park, Uganda. Preliminary review of the sample has identified 31 videos with tail behavior classified as "semi-prehensile", e.g. the tail is partially or fully wrapped around a substrate. This behavior was identified in adult *Papio anubis*, *Cercopithecus mitis*, *Cercopithecus ascanius*, *Colobus guereza*, *Lophocebus albigena*, and *Chlorocebus aethiops* (N videos=18). Juvenile and infant *P. anubis*, *C. mitis*, *C. ascanius*, and *C. aethiops* also displayed semi-prehensile tail behavior (N=13). In adults, this behavior was typically associated with foraging for leaves or tree gums (N=17), and/or utilizing an "unstable" stance, defined by support of three or fewer limbs (N=16). Juvenile *P. anubis* used its tail in a semi-prehensile way to stabilize locomotion on a precarious substrate (N=3). Infant *C. mitis*, *C. ascanius*, and *C. aethiops* wrapped their tail around their mother's tail or hindlimb while clinging ventrally (N=10). This is the first time semi-prehensile tail behavior has been described in detail in wild cercopithecid monkeys. Quantification of semi-prehensile tail use in non-platyrrhine primates will provide a better understanding of the evolution of platyrrhine tail prehensility. It will also increase our understanding of the ways in which the tail facilitates stability in an arboreal environment.

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Longevity is a special kind of endurance

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Endurance can refer to an organism's capacity for physiological resilience in the face of environmental stressors. Research on the molecular basis of aging has elucidated ancient regulatory pathways that act as longevity circuits when properly stimulated including short periods of moderate physiological stress (a concept called hormesis).

Such stressors include moderate hyperthermia, exercise, or calorie restriction. In addition to the considerable energy females transfer to their offspring during gestation and breastfeeding, in many groups they must also effectively carry children, water, food, and fuel.

We believe the ability of females to cooperatively share energy likely allowed females across a wide age span to operate in a hormetic stress zone, enhancing their lifespans, although potentially at the cost of a slower preferred speed of walking due to habitual load carrying.

To learn whether older women had the physiological resiliency to walk faster again, in 27 women 55-88 years old we tested whether a novel mobility trainer – a 4-wheel, spring-loaded, upright pivoting frame designed to cue each step through timely proprioceptive feedback – could improve their preferred walking speed. After only nine 30-minute training sessions over three weeks, we found that the women who walked using the mobility trainer had increased their walking speed compared to their baseline values (p=0.03) and against a comparable group who walked the

same amount without any device and who did not improve their speed. We suggest that females throughout history have engaged in the moderate endurance activities that enhance their resiliency for the long haul.

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Cranial patterns of fluctuating asymmetry in hybrid canids (*Canis latrans* var.): implications for the hominin fossil record

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Fluctuating asymmetry (FA) refers to random deviations from symmetry and is often used as a measure of developmental instability or noise. The influence of hybridization on FA remains unclear. However, it has been hypothesized that developmental instability caused by the combination of divergent genomes during hybridization would result in greater FA. If supported, this hypothesis may be applied to the hominin fossil record to help identify events of hybridization throughout human evolution.

This study explores the influence of hybridization on FA using a canid model. Cranial landmarks were collected from 3D surface scans of canid crania, specifically the eastern coyote (n=87), a hybrid between wolves and coyotes, and its parental taxa (*Canis lupus*, n=40; *Canis latrans*, n=40). Geometric morphometrics was used to assess directional asymmetry, FA, and individual variation in each group. Measurement error was accounted for by repeated landmark collection on two individuals from each canid group. The results were similar across groups with variation among individuals accounting for the greatest amount of variation (89.92 – 92.34%) followed by FA (6.75 – 8.46%), and finally directional symmetry and replication error accounting for less than 1% of variation each. Although patterns were similar, the eastern coyote showed greater similarity with wolves. Overall, the eastern coyote did not show elevated FA, which may indicate similar resistance to genetic and environmental stressors. These results indicate that high FA may not characterize all hybrid groups. However, more research including other hybrid species and across other anatomical regions will help to clarify this relationship.

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Inflammation Mediates the Relationship Between Moderate to Vigorous Physical Activity and Telomere Length in Middle to Older Age Adults

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Recent work suggests a physically active hunting and gathering lifestyle may have played a role in the evolution of long human lifespans. However, the mechanisms linking physical activity (PA) with longevity remain unclear. Moderate PA is associated with longer telomere length (TL), while shorter TL has been associated with increased cellular senescence and functional decline with age. Some research also suggests increased levels of bioinflammatory markers, such as C-reactive protein (CRP), are associated with telomere dysfunction. Here, we tested the hypothesis that CRP levels mediate the association between moderate to vigorous physical activity (MVPA) and TL, providing a potential mechanistic pathway linking PA and longevity. To evaluate this mechanism, we used the UK Biobank, a large-scale biomedical database, and analyzed adjusted T/S ratio (relative telomere to single gene copy), serum CRP, and MVPA measured via device-measured actigraphy data (n=79,839). To examine these relationships we used general linear models controlling for a range of covariates (age, ABSI [body shape index], smoking status, sex, ethnicity, time between data collection, and socioeconomic status). In this sample, MVPA was positively associated with TL ($p=0.007$). CRP was found inversely associated with TL ($p<2.6e-16$). Mediation analysis suggests CRP mediates the relationship between MVPA and TL (mediation total effect = 0.001; $p=0.004$). Our analysis supports the hypothesis that CRP acts as a mediator between MVPA and TL. These results suggest inflammatory markers play a role in cellular aging and may provide insight into how the evolution of high PA levels may have influenced cellular aging in humans.

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Colonization and inequities in child development: What can Biological Anthropologists contribute, and how should we do it?

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Colonization is a key contributor to inequities. This ongoing process affects approximately 5,000 Indigenous Nations around the world. It involves marginalization, stigmatization and the loss of land, resources and ancestral knowledge, including language and traditions. This process affects all individuals, but it is particularly pernicious for children because their health, wellbeing and opportunities in life depend on the characteristics of the social and physical environments in which they are conceived, born and raised. Indigenous peoples have, thus, centered their efforts on optimizing child development as paramount to achieving their main goal: Nation Rebuilding.

Many non-Indigenous scientists are eager to work as allies of Indigenous Nations; to be of service in decolonization efforts. A number of Western scientific disciplines have focused on the study of child development which can produce valuable information to reduce inequities including those resulting from colonization processes. Contributions range from theoretical models that focus on social determinants to the study of biological mechanisms by which social and physical environmental factors "get under the skin". Yet, many scientific endeavors that involve Indigenous peoples have been tainted by colonial practices and biases. Thus, understandably, Indigenous peoples are often wary of Western scientists and are demanding a change in the way we work together. In this presentation we will identify colonial biases to be avoided, share lessons we are learning from our Indigenous partners and use that knowledge to review current theoretical models of child development and protocols that foster healthy and productive research collaborations.

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Skeletal muscle gene expression is associated with differences in mobility and signatures of osteopenia

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Within the skeletomuscular system, bone and skeletal muscle (hereafter, 'muscle') constitute a tight functional unit with bidirectional communication through mechanical and biochemical signals. As individuals age, components of the skeletomuscular system deteriorate leading to reduced physical mobility and declines in bone volume and mass - traits that are associated with osteopenia. Few studies have investigated transcriptional changes in the muscle associated with reduced mobility and osteopenia. Here, we combine morphological measurements of hip extension (n=224), as a proxy of mobility, and proximal femur bone volume fraction (BV/TV; n=62), as a measure of osteopenia, with transcriptomic data from muscle biopsies in a free-ranging population of rhesus macaques. We characterized gene expression differences associated with reduced mobility and BV/TV after analytically removing the effect of age. We found that individuals with lower hip extension had higher expression of genes associated with inflammation and muscular atrophy as well as genes associated with cellular regeneration and proliferation. After adjusting for age, expression of genes that were associated with an individual's hip extension recapitulated expression of age-related gene profiles. In addition, we identified 13 muscle genes that were significantly associated with BV/TV. Overall, these findings reveal novel associations between muscle gene expression and both mobility and osteopenia, and identify potential molecular targets for mitigating musculoskeletal disorders.

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A geometric morphometric study of scapular ontogeny in modern humans

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The scapula is an important part of the human shoulder complex, and its development in children has been understudied. Human adult scapular morphology differs from nonhuman apes in many ways, and some previous research has suggested that the contrast is greater for subadult humans than for adults. This study investigates the role of allometry in influencing the shape of the scapula to determine if the human developmental pattern is attributable simply to size differences between developmental stages. CT scans of 70 modern human juveniles were collected from The Cancer Imaging Archives (TCIA) database. Landmarks were placed for the geometric morphometric analysis and linear measurements were taken to determine relative size in 3D Slicer. Developmental stage was determined by the degree of fusion at the acetabulum, and a proxy for body size was taken by measuring femoral head diameter. A principal components analysis was performed to determine shape variation, and PC scores were analyzed against the relative size of the scapula compared to body size and trunk size to account for allometry. An adult sample (n = 60) was also collected from TCIA and the same measurements were taken to determine if smaller adult scapulae resemble small (and younger) juvenile scapulae.

The results of this study suggest that while size differences account for some variation in scapular morphology during ontogeny, the pattern of extreme features in smaller/younger individuals is present only before adolescence and is absent in smaller adults.

Old solutions for colonial problems: queering biological anthropology

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Same-sex sexual behavior (SSB) is common among primate species, but our understanding of this behavior has been molded by the scientists conducting this research, their identities, experiences, and cultures. In evolutionary anthropology, the study of SSB has historically been shaped by the hetero-patriarchal norms of Christian colonial Western culture. For example, some of the first studies on SSB characterized SSB as an abnormal behavior, a product of captivity, or a behavior that needed to be "cured". It is imperative to address how such biases impact scientific findings on this topic because these results can be weaponized against marginalized LGBTQIA2S+ individuals around the world today. Here, through a queer lens, we aim to question and reframe some of the traditional research practices on this topic. We present an overview of terminologies and hypotheses commonly used to describe and explain SSB behavior in primatology. Further, we describe potential implications and impacts of these traditional frameworks, propose ways to reframe paradigms to mitigate negative impacts on marginalized communities, and provide guidance for best practices going forward. Although we focus on SSB in primates, these biases and their negative consequences are applicable to many species and research areas. We hope that anthropologists and biologists continue to study primate SSB while incorporating perspectives of diverse authorships and consulting with relevant community members and advocacy groups to ensure best practices and mitigate unintended harm.

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Parasite Richness in Wild Lemur Populations

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Parasite species richness within primate populations may be influenced by intrinsic and environmental forces, reflecting the complex host-parasite relationship. We examined the effects of lemur host phylogenetic relatedness, host conservation status, population density, and host extent of occurrence on parasite species richness. Using published literature, we compiled data on the helminths and protozoa found in wild lemurs, host population density, host conservation status, and host estimated extent of occurrence. Parasite hosts encompassed five families, 13 genera, and 30 species of lemurs, among which one species was non-threatened and 29 species were threatened. In wild lemur populations, helminth parasites predominated, comprising 23 species (95.8% of the recorded parasites), including 15 nematode species (55.5%), three cestode species (11.1%), and five trematode species (18.5%). Additionally, four protozoan species (14.8%) were documented. Jaccard indexes were very low at the family level, whether for closely related ($0.12 < J < 0.36$) or distantly-related ($0.11 < J < 0.33$) lemurs. Distantly related host genera had weak parasite sharing ($0.13 < J < 0.33$). Parasite species richness was positively correlated with the estimated extent of occurrence ($r = 0.47$) and population density ($r = 0.44$). Threatened hosts (3± 2.61 parasites/host) had significantly lower parasite species richness than non-threatened hosts (14 ± 0.0 parasites/host). Parasite sharing in wild lemur populations was not driven by phylogeny. Due to their small and restricted habitats, parasite transmission was limited, resulting in low parasite species richness. Threatened species hosted fewer parasites, indicating that host extinction likely leads to parasite loss.

Changing Mammal Communities across Southern Africa in the Terminal Pleistocene

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Southern African environments during the Last Glacial Maximum (LGM, ~ 26-19 ka) supported diverse communities of terrestrial mammals, with high proportions of large-bodied grazing specialists. Our understanding of the ways that global and regional climate events locally impact environments in Southern Africa's three distinct rainfall zones across this time interval can be improved by examining mammal community composition and turnover. Here, we analyze a dataset of South African fossil-bearing sequences dating to the last 40 kyr to test for differential responses of mammal communities in the winter- (WRZ), summer- (SRZ), year-round (YRZ) rainfall zones to LGM environments. Our dataset consisted of a species by site presence-absence matrix for faunal sequences in the WRZ (e.g., Elands Bay Cave), SRZ (e.g., Bushman Rock Shelter), and YRZ (e.g., Boomplaas). Functional trait data (diet, body mass) were collected for each species and our final analyses were restricted to large-bodied (> 1 kg) taxa to mitigate sampling/taphonomic biases. We found a variety of mammal community change patterns leading up to, during, and following the LGM across the South African fossil sequences—for some sequences, taxonomic turnover was high but functional turnover was low, whereas in others taxonomic and functional turnover were strongly coupled. Intra- rainfall zone variation through time was greater than inter-zone variation, suggesting that faunal sequences are more sensitive to local climate-environment relationships than to regional patterns.

Bacteria Killing Assay; Novel *ex vivo* method for immunocompetence in human

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Bacteria Killing Assay (BKA) is an ecoimmunology assay to measure fresh whole blood's capacity to kill bacteria *ex vivo* in vertebrates. This assay allows the assessment of functionally relevant immune responses instead of relying on assays that measure the concentration of single analytes (e.g., sIgA, Il-6). However, traditional BKA requires fresh whole blood to be used in the lab; thus, it can be unfeasible for some scientists. We introduce a salivary BKA for humans that doesn't require fresh sample. Human salivary BKA involves mixing saliva with a known number of live bacteria, incubating samples on agar plates, quantifying the remaining colonies, and comparing them to reference plates (positive and negative control). We run several tests to determine the most reliable protocol for human saliva. We determined that inappropriate storage conditions, but not multiple (up to 5) freeze/thaw cycles, can alter the assay results. Results also show that the ability to kill bacteria is relatively stable across consecutive days, morning vs evening, and men vs women samples. Samples are often contaminated with other microorganisms that can grow on agar plates. We tested a heat-inactivation protocol that showed strong correlation (r = 0.86) with samples that have not been inactivated. This assay can be utilized in other species, but it usually requires running several dilutions to calibrate bacteria killing. In our experience, saliva dilution of 1:2 is correct for humans. The BKA measures functionally relevant ability to eliminate pathogens and, therefore, an appropriate, noninvasive assay for ecoimmunology.

Herbivore migration during the Last Glacial Period of Kenya

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Eastern Africa is home to the largest terrestrial migrations on Earth. Though these migratory systems have been well-studied for decades, little is known of their antiquity and evolutionary history. We analyze the strontium stable isotopes (^{87}Sr/^{86}Sr) of 18 fossil bovid and equid species from four localities in Kenya to characterize prehistoric migratory systems during the Last Glacial Period (115-11.7 ka). Of the species analyzed, 16 lack evidence for migration, including blue wildebeest (*Connochaetes taurinus*), Thomson's gazelle (*Eudorcas thomsonii*), and plains zebra (*Equus quagga*), which are long-distance migrants today in the Greater Serengeti Ecosystem and historically in the Athi-Kapiti Plains, and all other extant species. In contrast, the extinct wildebeests *Rusingoryx atopocranion* and *Megalotragus* sp., were migratory. These findings suggest a possible alternative narrative about ecosystem dynamics during the Last Glacial Period and shed light on the behavior of both extant and extinct species at this time. In particular, these results suggest that migratory behavior in extant species either emerged during the Holocene or was more spatially limited in the past. These findings alter our interpretation of the ecosystems in which key phases of human evolution are thought to have occurred, and the extent to which we can rely on modern analogs to interpret them. Additionally, our findings have implications for mammal paleoecology and ecosystem dynamics in a period prior to large-scale extinctions in Africa coincident with environmental shifts.

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What's stress got to do with it? Quantifying measures of physiological stress and their relationship to inequality in a contemporary pediatric decedent sample

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Skeletal and dental alterations are thought to reveal aspects of an individual's lived experience, including experiences of stress in early life. Assumptions as to cause are often made, for example cribra orbitalia (CO) porotic hyperostosis (PH) are often assumed to represent nutrient deficiency and anemia. This can shape interpretations of porous cranial lesions (PCLs) as indicators of inequality, poor resource access, high disease-load, and poor population-level health, among others. However, stress indicators, like PCLs, may poorly correspond to lived experience. We investigate PCLs, bone mineral density (BMD), and adipose tissue (AT), alongside social race/ethnicity, proxy measures of SES, and rurality.

Methods. 803 (478 males, 325 females) individuals 6 months to 20.9 years.

Analysis. Logistic/linear regression assesses relationships between AT, PCLs, BMD, muscle density and demographic variables: sex, age, race/ethnicity, familial SES, and manner of death.

Results. Non-Hispanic White (NHW) individuals have lower odds of CO and lower subcutaneous-AT; those with PCLs have higher visceral-AT; CO is associated with lower BMD. Rural life is associated with increased subcutaneous-AT.

Discussion & Conclusions. PCLs are differentially associated with other stress measures. Likewise, physiological stress indicators are differentially associated with social race. Interpretations vary and could include: 1) NHW experience lower social stress [no lesions]; 2) NHW are frailer in the face of illness [no lesions]; 3) non-NHW groups experienced greater stress in early life [higher visceral-AT/lesions]; 4) non-NHW groups show resilience and adaptability in the event of stress [lesions]; 5) rural individuals face stressors that are not visible in the skeleton, among others.

Assessing the Impacts of a Genetics Education Partnership with High School Teachers

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Educators recognize the need to engage with historical, ethical, legal, and social dimensions of genetics with their students. However, high school teachers may feel they lack expertise, confidence, and institutional support to do so effectively. The Building Awareness, Respect, and Confidence through Genetics (ARC) Project (2016-2021) empowered teachers to facilitate dialogue about genetics and its societal impacts within classrooms and in communities. The project provided a) professional development workshops, b) curricula resources iteratively refined with instructor input, c) opportunities to participate in a community of practice, and d) opportunities for sharing and learning within schools and communities. The five-year project supported 17 in-person and two virtual workshops, reaching 396 teachers, who collectively taught an average of 5,100 students annually. Seven (7) full lesson plans and 19 distance learning resources were created, the latter in response to educators' needs during the COVID-19 pandemic. Pre- and post-workshop surveys as well as annual follow-ups found that a) teachers' interest in teaching genetics is high; b) teachers' confidence in conversations about genetics topics increased after workshop participation; c) teachers' knowledge increased in all measured topic areas; and d) according to teachers, course topics were interesting and engaging for students. Anecdotal evidence indicates that course content was shared beyond the classroom through conversations with peers and family members. The most prevalent barrier to implementation was time. Future studies would benefit from evaluating impacts on students themselves in addition to teacher perceptions. The free project resource library is regularly updated and continues to grow.

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Evaluating the Accuracy of External Limb Measurements for Predicting Skeletal Lengths from CT Scans

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Biomechanical and energetics studies of living humans frequently utilize external landmarks as substitutes for skeletal measurements, given that assessing the internal skeletal structure of living individuals necessitates invasive and costly radiographic or CT imaging. These procedures also expose participants to harmful radiation. Nevertheless, the accuracy of employing external proxies remains unverified.

This study evaluates the precision of using external anatomical landmarks to estimate internal skeletal measurements by analyzing cadaveric CT scans from the New Mexico Decedent Image Database (NMDID). A total of 112 individuals (62 males and 50 females aged 20-40 years with no lower limb trauma) were examined using 28 landmarks (16 skeletal, 12 external). Skeletal lengths of the femur and tibia and skeletal crural index were determined, along with external thigh and shank measurements and external crural index (all ICCs >0.90). Linear regression was employed to assess how well external lower limb measurements predicted skeletal lengths.

We found a strong correlation between skeletal femoral and external thigh length ($p<0.01$, $r^2=0.96$) and between skeletal tibial and external shank length ($p<0.01$, $r^2=0.98$). External crural index, however, explained less than 65% of the variation in skeletal crural index ($p<0.01$, $r^2=0.62$). Further investigation is needed to understand this phenomenon. Our study emphasizes the importance of caution when using external crural index as a proxy for skeletal crural index, even though external measurements can effectively predict skeletal lengths in lower limb segments.

The 9+ -month Marathon: How pregnancy may have shaped human endurance capacities

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A key understanding of the human evolutionary trajectory is the link between human endurance capacity and persistence hunting. Theoretically, the reliance on persistence hunting would have driven selection for increased endurance abilities particularly among males who are purported to have done most of the persistence hunting. However, females, and more specifically the physiological changes observed during pregnancy in a highly mobile species, may be at the core of the high human endurance capacity. Our evolutionary ancestors were highly mobile as they had to contend with harsh, seasonal environments, long daily travel distances, predator avoidance, hunting, gathering, tool making, etc. These activities could not have been halted when a female became pregnant and then delivered offspring. Pregnant and childrearing females would have had to maintain their contributions while also incurring the additional metabolic "burden" of gestating and feeding a fetus and newborn, respectively. Pregnancy, subsequent lactation, and childcare exert numerous challenges on the body including increased metabolic rate, altered substrate utilization, increased cardiac output, and major endocrinological shifts. Here I review the anatomical and physiological features of pregnancy which resemble changes accompanying endurance training, with a particular focus on metabolism and the cardiovascular system. These changes likely improved endurance capacities of females and males across our evolutionary lineage. Instead of persistence hunting as the sole driving force in human evolution, it could well be that pregnancy-associated metabolic physiology triggered our ancestral endurance once bipedalism appeared and thus enabled the success of persistence hunting.

N/A

Turnover of Mio-Pliocene large mammal communities at Lothagam (West Turkana, Kenya)

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The late Miocene was a dynamic period of major climatic and environmental changes globally, including cooling and the rise of open ecosystems dominated by C4 biomass (tropical grasses). Understanding the degree to which eastern Africa's diverse terrestrial mammal communities responded to these global-scale changes has been hampered by the scarcity of late Miocene fossil-rich sites in this region. An important exception to this pattern is the site of Lothagam (West Turkana, Kenya), which preserves a relatively continuous Mio-Pliocene sedimentary sequence with abundant vertebrate fossils. Here, we analyzed taxonomic and functional turnover patterns in fossil mammal communities from four of Lothagam's sedimentary units (Lower Nawata, ~9.1-6.6 Ma; Upper Nawata, ~6.6-5 Ma; Apak, ~5-4.3; Kaiyumung ~3.5 Ma). Our dataset consisted of >2000 fossil occurrence datapoints derived from newly georeferenced aerial photos from earlier expeditions to Lothagam (e.g., the Koobi Fora Research Project in 1990-1993) and 2022-2023 collections by the Lothagam Research Project. We find that, despite >85% of taxa being replaced moving from the lowermost to the uppermost part of Lothagam's sequence, the functional trait structure of communities is remarkably consistent through time, with only modest declines in frugivores/browsers and increases in grazers. We propose that functional stability in Lothagam's mammal communities can be explained by 1) community resilience due to broad ecological niche breadths/environmental tolerances in large-bodied mammals and/or 2) that the Turkana Basin exhibited a muted response to global-scale changes due to overprinting and/or modulation by local processes (e.g., basin tectonics and hydrology), favoring functionally similar faunas.

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Genomic diversity and demographic history of the non-anthropoid primates

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The non-anthropoid primates–lemurs, lorises, galagos, and tarsiers–constitute roughly one-third of the primate order, yet despite this diversity, they have long been understudied. The underrepresentation of strepsirrhine research in the genomics community is particularly alarming given that most strepsirrhines and almost all lemurs are threatened with extinction. To explore the genomic diversity and demographic history of these primates, we analyzed high-coverage whole genomes from 239 individuals comprising 74 species, including multiple individuals from most species. With this dataset we demonstrate that genomic diversity varies widely across the infraorder yet is broadly consistent among individuals within species. Among the Lemuriformes, we reveal a pattern of widespread introgression in multiple genera. Their generally high levels of genomic diversity likely result in part from allele sharing that occurred during periods of connectivity and fragmentation during climatic shifts. Our results show distinct patterns of demographic history in lemurs across the ecogeographic regions of Madagascar within the last million years. Within the past 2000 years lemurs have undergone major declines in effective population size that correspond to the timing of human expansion in Madagascar. Furthermore, in multiple regions of the island we identified chronological trajectories of inbreeding that are consistent across genera and species, suggesting localized effects of human activity. Our results provide a major advance in our understanding of how primate genomic diversity has been influenced by ecological and anthropogenic factors, while revealing the extraordinary diversity of these long-neglected, endangered primates.

Terrestrial positional behavior of wild *Pongo pygmaeus*

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Pongo pygmaeus is the world's largest arboreal mammal, yet little is understood about their terrestrial behavior in the wild. There are many outstanding questions concerning how their natural locomotor and postural behavior on the ground compares to that of the African apes. Do orangutans heel strike when quadrupedal walking? Do they engage in terrestrial bipedality? Positional behavioral studies of orangutans have been largely limited to arboreal contexts and captive settings; terrestrialism in the wild is understudied as descents to the ground are rare. However, camera trap footage allows for remote capturing of their natural terrestrial behavior. Video footage of Bornean orangutan terrestriality in the wild was collected over a five year period in the Gunung Palung National Park, Indonesia. 120 videos containing footage of orangutans were analyzed for positional behavioral modes as well as for hand and foot positions, with adult males (both flanged and un-flanged) and females and subadults represented. Results indicate that, when locomoting terrestrially, *Pongo pygmaeus* is primarily quadrupedal, practicing fist-walking and heel strike, with flexion of extremely long toes seemingly forcing lateral heel contact. Bipedal locomotion constituted 9% of locomotor bouts. For posture, individuals stood upright more often than not, on one or two legs, with monopedal stands occurring more than bipedal (59% of orthograde stands). When standing erect, individuals almost always fully extended hips and knees, as they do when arboreal, indicating consistency in the performance of this behavior regardless of support type. This camera trap data thus provides new insights into orangutan positional behavior.

Testing Distal Tibia Shape Convergence in Mammals with Hindfoot Reversal

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The relationship between arboreal locomotion and postcranial morphology is well-studied in primates, but the degree to which arboreal primate-like morphologies are present in other mammals is poorly known. Arboreal locomotion often involves complex adaptations, including specialized behaviors like headfirst descent, allowing mammals to navigate the canopy with precision. Headfirst descent is closely associated with hindfoot reversal, a maneuver allowing the hindfoot to medially rotate 180 degrees, that has been observed in various primates and non-primates in the mammalian orders Carnivora and Marsupialia. Here, I present a geometric morphometric analysis comparing distal tibia morphology among primates and non-primates to test for morphological convergence in adaptations related to hindlimb reversal. Seven landmarks were used to characterize the shape of the articular surface of the distal tibia, which facilitates multiaxial movement on the dorsal talus. Ordination of the landmark data using principal components analysis reveals mediolateral compression of the distal tibia in arboreal primates and marsupials, lacking well-defined distal articular grooves. Arboreal carnivorans have mediolaterally elongated distal tibiae and exhibit deep articular grooves. Nonarboreal primates, those without hindfoot reversal, share similar morphology with arboreal carnivorans. Nonarboreal carnivorans and marsupials have an anterolaterally elongated distal tibia with deeply pronounced distal articular grooves. Overall, there appears to be distinct morphological pathways through which hindfoot reversal has evolved within primates, carnivorans, and marsupials. Furthermore, these results suggest that the mechanism behind hindfoot reversal could be linked more closely to the talocalcaneal or talonavicular joints rather than the distal tibia, indicating promising directions for future research.

Hominin postcranial remains from Drimolen Main Quarry in the Cradle of Humankind, South Africa

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Drimolen Main Quarry (the primary focus of excavation within the Drimolen paleocave system in Gauteng Province, South Africa) dates to between ~2.04 and 1.95 Ma and has yielded numerous hominin remains. Most craniodental specimens are attributed to *Paranthropus robustus* but the collection also includes a cranial vault of *Homo* aff. *erectus* and teeth with early *Homo* affinities. Among the assemblage are 65 postcranial fossils including isolated pieces and associated specimens belonging to two juvenile individuals. Only a partial ulna (DNH 109) and partial pelvis (DNH 43) have been formally described. Consequently, the Drimolen postcrania have seen only limited incorporation into comparative studies. Here we present an overview of the postcranial assemblage to assess its potential for informing our understanding of early hominin biology.

Hand and foot elements compose the largest single proportion of the assemblage with most of that consisting of middle phalanges. Apart from the partial DNH 43 pelvis and two juvenile tibiae, rib fragments (from a single individual), forearm, arm, and vertebral elements together compose the remainder. Approximately 75% of the specimens are juvenile/subadult in developmental stage providing some opportunity to study growth and development, but also complicating taxonomic and functional studies. Phalangeal morphology suggests moderately strong grasping (possibly involving climbing behaviors), but functional inferences remain conservative given the preserved anatomy. Though most specimens likely belong to *P. robustus*, taxonomic attribution is challenging given the known mixed assemblage at Drimolen and the currently poor understanding of *Paranthropus* and early *Homo* postcranial anatomy and variation.

Comparative relationship reconstruction from external and internal molar crown shape in a sample of pedigreed macaques

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Biological anthropologists use tooth crown size and shape to reconstruct relationships at various scales. Most of this work involves data collected from the outer enamel surface (OES), which is easily accessed in living or skeletal/fossil specimens. Microcomputed tomography (microCT) now provides non-destructive access to internal dental structures, including the enamel-dentin junction (EDJ). This tissue surface is established earlier in ontogeny and is thought to be more evolutionarily conserved. However, little work has systematically compared variation and phenetic affinities among individuals as reconstructed from these separate tissue layers. Here, we present a 3D geometric morphometric analysis of maxillary second and third molars (M^2 and M^3) using microCT images of pedigreed macaques from the free-ranging Cayo Santiago colony. Fourteen homologous landmarks were digitized at both the OES and EDJ. Generalized least-square Procrustes superimposition yielded coordinates that were subjected to principal component and cluster analyses. While PC1 appears to primarily capture size variation, preliminary results based on PCs 2 and 3 (n=12 molars) indicate greater sample dispersion at the OES, which may reflect a protracted period of development during which environment can influence enamel form. While we expected greater shape variation in M^3 given its comparatively later development, morphospace dispersion was greater for M^2. Of note, the two tissue surfaces did not provide identical signals of phenetic affinity, nor was clustering of individuals stable across molars. Future research will examine the mechanisms (e.g., genes, health/stress events) driving these patterns and harness this information to refine applications of dental data to bioanthropological inquiry.

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Anthrozoology, travel health, and conservation medicine in the Galápagos islands

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Education on risks of potential zoonotic/anthropozoonotic pathogen transmission and appropriate human-animal contact is critical, particularly at ecotourism destinations where tourists and residents can impact fragile ecosystems with endangered species. Biophilia, loss of inhibition and situational awareness, relaxed attitudes toward safety, and other factors may contribute to disease transmission between humans and nonhuman animal species. To understand these issues better, an anonymous survey was distributed to tourists and residents in both English and Spanish (67% of respondents) in San Cristobal and Santa Cruz, Galápagos islands, Ecuador, across ten days in July and August 2023. Data were collected on signs of infection, environmental attitudes, propensity for risk taking, and interactions with wildlife, among other variables. 846 surveys included 559 tourists (53% female) and 287 residents (38% female). Among tourists, only 69% reported traveling with an updated immunization certificate and 4% reported at least one current respiratory symptom. Proportionately more resident respondents (22%) had at least one current respiratory symptom. 9% of tourists and 7% of residents reported that they would touch a wild animal, with reported examples including sea lions which are common in some of the islands. Most surprising was that only 68% of tourist and 53% of resident respondents agreed with the statement that humans can GET diseases from wild animals. 68% of tourist but only 29% of resident respondents agreed with the statement that humans can GIVE diseases to wild animals. Despite the recent pandemic of zoonotic origins, education on appropriate contact between humans and wildlife remains needed.

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Proximal Tibia Morphology and the Evolutionary History of Locomotor Shifts in Primates

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Primate knee anatomy reflects locomotor differences due to the different forces and loads placed upon the knee by distinct locomotor modes used by individuals, along with inherited morphology associated with ancestral locomotion for a given species. A locomotor shift occurs when ancestral locomotion differs from present-day locomotion, which may lead external shape morphology to more strongly reflect ancestral rather than present-day locomotion. This study aims to determine whether external morphology of the proximal tibia changes similarly across primate species in response to specific locomotor shifts. The sample consists of wild-caught adult males and females for 200 specimens across 50 species, with at least one male and female per species. Landmarks, curved semilandmarks, and surface semilandmarks were placed on articular surfaces using Checkpoint from Stratovan. Principal components (PCA) and linear discriminant function with leave-one-out cross-validation (DFA) analyses were run on the complete landmark dataset. A marginal ancestral state reconstruction was generated for all extant haplorhines in 10k Trees for ancestral locomotion. Three locomotor mode (arboreal, semi-arboreal, terrestrial) and locomotor shift (arboreal, terrestrial, unchanged) categories were used as the grouping variables for the DFA. PCA and DFA results are as expected with group separations/misclassifications primarily driven by arboreal/semi-arboreal and arboreal/unchanged groups (77% locomotor mode correct classification; 76% locomotor shift correct classification). These results suggest that both present-day locomotor mode and locomotor shifts can be identified using external morphology. Higher misclassification rates in arboreal/semi-arboreal and arboreal/unchanged groups are most likely due to higher similarity in locomotion among those groups compared to terrestrial locomotion.

Environmental enrichment for laboratory primates: current practices and research trends

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Environmental enrichment is crucial for ensuring the physical, physiological, and behavioral needs of laboratory-housed primates, and understanding current practices and research trends can inform environmental enrichment programs at research institutions by encouraging new, innovative forms of enrichment and thus improving animal welfare. Here, I report findings from a systematic literature review to assess past and present research efforts on environmental enrichment for laboratory-housed primates. The results from this study demonstrate a steady increase of publication and citation rates over the past four decades. Occupational enrichment was the most frequently referenced form of environmental enrichment, followed by sensory and physical enrichment. This is likely a result of recent advancements in technology such as virtual reality devices, which double as enrichment and tools for studying cognition in laboratory-housed primates. For 30.5% of publications, the enrichment type could not be determined. Detailing types of enrichment used in publications should be prioritized in future research, as doing so can provide invaluable information on the effects of enrichment at the individual, group, and species level. The findings from this study underscore the growing importance of environmental enrichment in laboratory-housed primate research and highlight the continued need for exploring and documenting the diverse range of enrichment techniques and their implications for animal wellbeing.

Archaeogenomic insights into Anatolia-Caucasus interactions since Neolithic

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Archaeological evidence indicates that the Neolithization in the Caucasus commenced 3-4 thousand years after its onset in the Fertile Crescent. Material culture data proposes southern regions, specifically Anatolia or Mesopotamia as the origins of Neolithization in the Caucasus rather than the local Mesolithic hunter-gatherers transitioning to farming. Archaeological findings also hint at two-way population interactions between Anatolia and the southern Caucasus from the Neolithic onward. While archaeogenomics studies, albeit based on a limited number of genomes, support these archaeological views, the precise dynamics of populations within the Caucasus and its neighboring regions remain inadequately understood. Here, we present analyses of 18 new genomes (0.01-0.26X genome coverages) from the Neolithic (N=9) and Bronze Age (N=9) periods in Azerbaijan along with previously published data. Our results corroborate earlier studies indicating the genetic proximity of southern Caucasus Neolithic genomes to Neolithic populations in Southwest Asia, rather than Caucasus Mesolithic hunter-gatherers. This suggests a population replacement during the Caucasus Neolithization. Furthermore, our findings affirm genetic discontinuity between Neolithic and Bronze Age populations in the southern Caucasus, a reflection of the shift in population structure due to significant human mobility. Lastly, our analyses reveal the clustering of Caucasus Neolithic genomes with Anatolian Bronze Age genomes refining the direct source of increasing Caucasian ancestry observed in Anatolia after the Chalcolithic period as southern Caucasus rather than Upper Mesopotamia.

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Deconstructing the monolith: integrating biogeochemistry and biodistance to better understand the migrant experience

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Biogeochemical analyses of residential history rely on the isotopically defined categories of "local" and "non-local" to identify potential migrants. Such monolithic distinctions, however, are limited to the identification of first-generation migrants and may not always provide a culturally salient indicator of social difference. Ethnographic research indicates that the social category of "migrant" is not merely limited to those who migrated themselves; subsequent generations are often still culturally identified as migrants. I integrate biogeochemical ^{87}Sr/^{86}Sr data with intrasite biodistance analysis of cervicometric dimensions to access a diversity of migration experiences within both "local" and "non-local" individuals (n=73) at Non-Grid 4, a shrine site in Epiclassic (600-900 CE) central Mexico where a minimum of 180 individuals were sacrificed and interred. I generate 2,628 unique pairwise estimated phenotypic distances (Mahalanobis distances, d^2) among individuals interred at Non-Grid 4 to identify 12 individuals who appeared biogeochemically "local" but shared a small estimated phenotypic distance (top 1% of all generated estimated phenotypic distances) with a "non-local" individual. I posit that these individuals may represent *n*th generation migrants who would have been considered culturally distinct from populations living in Epiclassic central Mexico. Moreover, eight individuals in the top 1% of all estimated pairwise phenotypic distances shared similar first molar ^{87}Sr/^{86}Sr values, suggesting they originated from a similar region, allowing for the reconstruction of migration networks. The integration of biogeochemical and cervicometric data thus adds a time depth to our analyses of paleomobility in ancient Mexico beyond first-generation migrants identified by biogeochemical methods alone.

Maternal aye-aye (Daubentonia madagascariensis) anxiety peripartum

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Mothers are anxious peripartum. Our previous pilot study of three hours per day for three days peripartum demonstrated that a mother aye-aye (Daubentonia madagascariensis) displayed anxiety behaviors such as repetitive, non-purposeful movements (stereotypies) (unpub). In this study, a mother aye-aye's anxiety behavior peripartum was assessed 24 hours before, the day of, and 24 hours after birthing an infant. It was hypothesized that anxiety behaviors would change over the three days. With IACUC approval, Pelco IMM12027-1S cameras were placed in a Duke Lemur Center (DLC) aye-aye mother's enclosure and nest to record her activity the three days peripartum. The resulting videos were watched and continuous focal animal sampling was used to note the time, duration, and type of repetitive behavior such as scratching or grooming. Data were analyzed using a Kruskal-Wallis Test and Chi squared test. Results showed that the day before birth, the mother repeatedly constructed and deconstructed nests significantly more than the other two days (n=162x), while on the birth day, the mother auto-scratched and examined her genitalia significantly more (n=37x, n=27x, respectively). The day after birth, the mother was hyper-alert significantly more times (n=19x). Therefore, the hypothesis was supported as the mother exhibited signs of behavioral anxiety and her behaviors changed over the three-day period. Limitations included the small sample size (n=1). This study is the first to examine maternal anxiety in aye-ayes over three complete days peripartum. The results yield insight into maternal behaviors exhibited by the rare and difficult-to-see aye-ayes.

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Developing a macro-archaeological infrastructure to help assess the relationship between hominin technological and biological change

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The causal role technology played in the evolution of hominin brain size, life history, and other important traits is unclear. Hominin technological evolution is a driver of biological evolution in some explanatory models, while in other models technological evolution plays a peripheral role. There are many reasons for this disagreement, but one issue is a lack of comparative studies that measure technological change at the theoretically appropriate spatio-temporal scales. Current measurements of technological change tend to focus on particular periods, or contrasts between adjacent periods, which is a temporal scale too narrow to fully address the relationship between technology and biology. Macro-scale studies that include millions of years of change, however, tend to focus on global scale patterning, which may mask meaningful variability within hominin lineages. Building rich datasets describing technological change over time within particular geographic regions, and within particular hominin lineages, is a likely prerequisite for assessing models describing relationships between biological, and technological change. We report on an analysis of technological change across the Pleistocene in East Africa, South Africa, the Levant, and Western Europe (N = 885 assemblages). We found similarities in technological trajectories over time between each region, suggesting that disparate sets of hominin populations shared similar histories of technological change, each of which is broadly similar to the global pattern of technological change. We discuss these results, other important issues they highlight, and future directions that could help clarify the relationships between technological, and biological change in the hominin lineage.

Maternal placentophagy: exploring practitioner satisfaction following consumption of the placenta postpartum

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Due to its purported therapeutic benefits for postpartum individuals, maternal consumption of the placenta postpartum is an emerging 'alternative' health-seeking practice in some high-income countries. Surveys have shown that the vast majority of mothers who engage in placentophagy do so in the hopes of preventing postpartum depression, the most commonly cited purported benefit of the practice, along with improved lactation, and reduced fatigue, among other reported benefits. To date, however, no clinical scientific studies have identified any objectively measured health benefits resulting from the practice compared to matched controls. Given the persistence of the practice, especially among mothers in the home-birth and birth-center community, we wondered how placentophagic women evaluated the practice in terms of satisfaction. For the present study, we reviewed a number of published surveys, and analyses of web-based discussion groups and parenting forums regarding practitioner satisfaction. Our analysis revealed an overwhelmingly positive experience with the practice; as measured by stated satisfaction, as a practice they would recommend to others, or would engage in again after a subsequent pregnancy. These results provide insight into the discussion of postpartum maternal care and what may be lacking in the modern biomedical system that leads women to seek out complementary and alternative health practices.

A comparison of the gut microbiota of two ateline species with variable diets and altitudinal ranges, the common woolly monkey (*Lagothrix lagotricha poeppigii*) and the yellow-tailed woolly monkey (*Lagothrix flavicauda*)

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Living at high elevations presents a number of evolutionary challenges, including a lack of high-energy foods in an energetically stressful environment. The gastrointestinal microbiome is crucial to host metabolism and may be part of how animals adapt to such environments, by allowing a host to extract energy from otherwise inaccessible sources, such as complex plant polysaccharides. We compared preliminary data on the gut microbiome of the high-elevation yellow-tailed woolly monkey (*Lagothrix flavicauda*), which is restricted to cloud forest between 1,400 and 2,700 m.a.s.l, in Andean Perú, to that of the red woolly monkey (*Lagothrix lagotricha poeppigii*), which can also reach up to 2,200 m.a.s.l, but is widely distributed across the western Amazonian lowlands. Compared to *L.l. poeppigii*, *L. flavicauda*'s diet includes a higher proportion of leaves and insects and a lower proportion of fruit. We used the Oxford Nanopore 16S rRNA Kit and a MinION Mk1B using a Kit 9 flow cell to amplify and sequence the entire 16S gene from 24 fecal samples (20 *L. flavicauda* and 4 *L.l. poeppigii*) and analyzed the data using the Epi2Me wf-16S workflow. The microbiomes of both taxa were dominated by *Firmicutes* (88.9% for *L. flavicauda* and 82.9% for *L.l. poeppigii* respectively) with *Proteobacteria* (4.8% and 7.9% respectively) and *Candidatus melainabacteria* (4.3% and 5.1% respectively) being the next most abundant phyla. Overall microbiome composition was similar between the two species, though samples from *L. flavicauda* had significantly more *Lachnospiraceae* than samples from *L.l. poeppigii*, perhaps reflecting *L. flavicauda*'s increased reliance on leaves.

Evaluating efficacy of single- vs double-stranded DNA library preparation strategies for ancient microbiome research

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Advances in next-generation sequencing have improved our ability to recover genomic information from degraded DNA. However, factors such as DNA preservation, post-mortem damage, and loss of DNA during purification impact the successful conversion of DNA molecules into sequencing libraries. Thus, the choice of library preparation protocol is pivotal in ancient DNA research. Furthermore, the neotropics, characterized by their unique biodiversity, pose distinct challenges in ancient metagenomic studies. Here, we compare the performance of two library preparation methods: double-stranded Blunt-End Single Tube (BEST) and single-stranded Santa Cruz Reaction (SCR), on ancient dental calculus samples from 1200-1500 year-old humans from neotropical sites in Southern Belize (N = 12). DNA extracts were built into paired BEST and SCR libraries and shotgun-sequenced using Illumina technology. SourceTracker analysis confirmed that we recovered ancient oral microbiomes. Taxonomic profiling was performed using MetaPhlAn4. We detected a significantly higher number of species in the SCR than BEST libraries (two-tailed t-test p-value 0.0014). Preliminary analyses suggest that relative abundances of common opportunistic oral pathogens were not significantly different between the two protocols. However, in several cases, we detected opportunistic periodontal pathogens such as *Porphyromonas gingivalis*, *Tannerella forsythia*, and *Treponema denticola*, as well as *Haemophilus parainfluenzae*, a bacterium implicated in infective endocarditis, in SCR libraries but not in the corresponding BEST libraries. These results underscore that the SCR method may have implications for interpreting community composition and downstream diversity analyses. Our findings highlight the efficacy of single-stranded DNA library preparation methods in ancient microbiome research.

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Beyond Continental Groups: shifting from Static Clusters to Dynamic Communities in Genetic Networks

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Traditional clustering and visualization approaches in human genetics often operate under statistical and conceptual frameworks that assume inherent, discrete groupings. These methods can inadvertently simplify the multifaceted relationships among individuals, functioning to unveil assumed underlying differences between static groups. To challenge this limitation and offer a more nuanced understanding, we introduce a network-based computational pipeline and visualization tool grounded in relational thinking.

Our pipeline constructs networks using a range of genetic metrics—such as genetic relationship matrices (GRM), principal components, and identical-by-descent (IBD) segments. Through the application of Louvain's algorithm for community detection, we dynamically identify emerging communities at multiple resolutions. This is a departure from typological models of analysis and interpretation that strive to categorize individuals into a predefined number of sets.

We applied our pipeline to a dataset merged from the 1000 Genomes and Human Genome Diversity Project. Our analysis not only reveals the limitations of traditional groupings but also captures the complexities introduced by recent and distant demographic events and evolutionary processes. For example, spanning a resolution range, 6 to 31 communities are revealed in an IBD network, compared to 2 to 6 in a rare-variant GRM network. This underscores a fluid spectrum of genetic relationships that challenges the notion of universal categorization.

To enable broader engagement with these intricate genetic landscapes, we provide a user-friendly web application (sohail-lab.shinyapps.io/GG-NC) for interactive visualization, for both researchers and the general public.

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Grip Force and the Role of the Digits in Human Throwing

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Anatomical evidence suggests that humans possess adaptations to the trunk and shoulder that enable exceptionally forceful throwing. However, little is known about adaptations that could enable humans to throw with high accuracy. Sports science research suggests grip force may be a critical factor in throwing accuracy. Humans may differ from other apes in their ability to control grip due to their relatively long and strong pollices. We quantified digit forces during throwing to investigate the role of the human pollex in enabling accurate throws.

Eight participants (25.6 ± 3.2 years, 65.8 ± 26.7 kg) threw three differently weighted baseballs (85 g, 170 g, 340 g) 15 times each at a target eight meters away. Digit forces were recorded using a manual pressure sensor system consisting of small flexible pads attached to digit segments that measure normal forces at 200Hz. Pollex force peaked before digits II and III, and digits II and III reached their maxima nearly simultaneously just before ball release. Force increased significantly with throw velocity for all digits ($p < 0.01$), and heavier baseballs resulted in higher digit forces ($p < 0.001$). The rate of force increase was greater for digits II and III compared to the pollex, and digits II and III always experienced higher peak forces than the pollex. Contrary to expectations, these results suggest the pollex is less important in throwing than digits II and II, although further research is needed to understand the full role of the pollex in the complex mechanics of throwing.

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The Typical Body Segment Approach to Getting a Job

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Gross anatomy (i.e., 'gross') has a reputation for being both an incredibly challenging course to take as well as a daunting responsibility for instructors. The subject is a sprawling, complex, and intricate web of facts and information, which also collides with emotional, spiritual, and ethical intrigues as students explore the human form through cadaveric dissection. Constructing and executing a successful gross course comes in many forms but one approach in particular hits on several proven pedagogical strategies and is frequently praised by students and instructors alike. Matt Cartmill, partly through the writing of his influential text *Human Structure*, showed anthropologists and biologists how they could leverage their skills and knowledge of evolutionary anatomy. Cartmill created a template for importing the concept of the Typical Body Segment—a schema based instructing model which helps reduce the cognitive load for students, giving them a 'foothold'—into teaching gross. He artfully combined this heuristic model with storytelling drawn from the evolution, development, and function of the human organism to produce a course design which has proven incredibly successful at transforming novices into competent anatomists. *Human Structure* and his approach to teaching gross has spread to many other institutions beyond Duke University where it was originally conceived, providing numerous opportunities for young anthropologists and biologists to find research-sustaining careers teaching this crucial subject. Here we explore what has made this approach so successful, highlight some of its many disciples, and describe the pervasive influence it has had on teaching gross anatomy throughout North America.

Complete Phylogeography of Mitochondrial Haplogroups P and Q

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The first peopling of the paleocontinent of Sahul – modern-day Australia and New Guinea- has been long debated by anthropologists. Anatomically Modern Humans (AMH) first settled Sahul approximately 50,000 years ago. However, the exact modes of the earliest human migrations into Sahul, the routes they followed, and the number of original migratory waves remain unclear. We took a phylogeographic perspective to these questions by utilizing all publicly available mitogenome sequences (n= 898) representing the “Papuan” haplogroups P, Q, and M29. Our findings indicate that haplogroup P emerged around 51kya, just before the time of the initial settling of Sahul as suggested by the oldest known archeological site in New Guinea – Ivané Valley (45–49 kya). On the other hand, haplogroups Q (38.4 kya) and M29 (14.6 kya) are likely indigenous to New Guinea. Our analysis of P and Q subclades also confirm the long separation of New Guinean and Australian mitochondrial lineages. Our study improves the current understanding of the phylogenetic structure of mitochondrial haplogroups P and Q by suggesting minor corrections to their existing phylogenetic trees.

Ontogenetic Variation and Evolutionary insights from the Suprainiac area in the Middle Pleistocene Population of Sima de los huesos

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The Sima de los Huesos site (SH) has yielded a huge collection of Middle Pleistocene hominin remains, including multiple cranial fragments. The SH cranial collection currently comprises 20 nearly complete crania, spanning juvenile to adult specimens. The SH paleodeme is phylogenetically related to Neandertals, yet its cranial anatomy features a unique blend of primitive and derived Neanderthal traits. One of the most documented cranial apomorphies in the Neandertal lineage is the suprainiac fossa, a depressed oval region located above the occipital torus. This feature is present in all Neandertals and emerges early in their development. In SH crania, an irregular area above the occipital torus has been considered as resembling the Neanderthal fossa. Here we present the characterization of the internal and external structure of the SH suprainiac region using microscopic and computed tomography images. Our results reveal that this region lacks the characteristic depression associated with Neanderthal diploe reduction. Additionally, the development of external bone texture reflects ontogenetic variation in SH. In the youngest specimens, these areas exhibit a cratered surface, progressing to a densely pitted porous surface in young adult specimens. Finally, in the oldest specimens such as Cranium 4, a secondary bone deposition can be observed covering the porous surface. This ontogenetic variation in the suprainiac fossa offers a valuable tool for age estimation in Middle Pleistocene occipital bones, particularly when conventional criteria like dentition are unavailable.

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Extensive pedigree analyses reveal young women’s mobility in early medieval Europe

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The unique integrative approach of anthropology, genetics, archaeology and history can shed new light on the social reality of ancient people’s ways of life as exemplified by the ERC SyG HistoGenes project. Detailed anthropological data combined with genetic analyses of the two, so far largest, entirely sampled Austrian Avar period cemeteries Leobersdorf and Mödling Goldene Stiege (in total n>600 skeletons) allowed reconstructions of reproductive unions and pedigrees. Our studies revealed: a) two main pedigrees, b) six to seven generations each, c) about 70 % of individuals in the core pedigrees, d) up to 30 % distantly related (3rd to 6th degree) and unrelated individuals, e) mainly patrilinearity in the core pedigrees, especially in Leobersdorf (c. 90 %), f) similar proportions of multiple reproductive unions in both (10–20 %). Strikingly, our analyses also show significantly less females than males in both core pedigrees (ratio women to men: c. 1:1,6 and boys to girls c. 1:1,7, $p<0,05$). In contrast, in the unrelated as well as the distantly related groups of both sites we found: a) significantly more women ($p<0,01$) as in the pedigrees where all age classes are represented, b) who mostly died during reproductive age. Our main interpretations are that especially young women were mobile, most came from outside these communities (80 % do not have parents buried on site) with the intention to engage in reproductive relationships in the sites, however, died there before reproducing.

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Differential Identification of Juvenile Grey Seal and Subadult Human Remains at Sable Island NPR, Mi'kma'ki (Nova Scotia, Canada)

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In the fall of 2023, an archaeological site became naturally exposed by erosion at the East Light location of Sable Island National Park Reserve off the southeast coast of Nova Scotia, Canada. Upon an initial ground survey and investigation of the emerging site, the archaeological context suggested the remnants of a possible burned structure, likely a house. Small bones were also recovered from the surface. The bones were sent for laboratory gross examination and shown to contain a mix of possible juvenile faunal and possible subadult human remains. Following a protocol of excavation that was informed by the possibility of encountering further possible human remains, the remainder of an almost intact subadult grey seal skeleton was found, but no human remains were recovered. This poster conveys the archaeological context of the site, the recovery of the faunal remains, and ultimately the differential identification process that is recommended for sites that likely contain juvenile seal remains that can be easily misidentified as subadult human.

Exploring placenta evolution: Insights into placenta morphology, life history traits, and cancer

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Placenta morphology varies greatly across mammals, ranging from highly invasive and integrated maternal and fetal tissue to shallow connections between the maternal-fetal dyad. Further, life history traits such as gestation length and body weight can influence placenta's phenotypes.

Cancer is ubiquitous across the tree of life, and humans seem to be particularly subjected to it. It shares many hallmarks with placenta invasion in the maternal body, and this led to the hypothesis that the degree of placenta invasiveness is positively correlated with cancer prevalence. However, previous studies reported contradictory data on this relationship. Here we retest this relationship, and further take into consideration another divergent feature of placental morphology: the degree of interconnection of tissue at the maternal-fetal interface, or interdigitation. To do so, we leverage comparative oncology data gathered from 99 North American Zoos and aquariums. Our dataset results in 83 mammalian species (n = >20 individuals) and a total of 3,206 necropsies.

We use Phylogenetic Least Squares (PGLS) models to test the association of placenta invasiveness with neoplasia prevalence (p=0.335, t=0.0363, R2=0.300), malignancy prevalence (p=0.611, t=0.014, R2=0.300), and malignant transformation (p=0.138, t=0.151, R2=0.340). Additionally, we also test the association of placental interdigitation with neoplasia prevalence (p=0.458, t=0.026, R2=0.260), malignancy prevalence (p=0.371, t=0.023, R2=0.260) and malignant transformation (p=0.111, t=0.153, R2=0.290). In analyzing all our outcome variables, we controlled for the life history traits of gestation length and body mass.

Our results provide evidence against the existence of a statistically significant relationship between placenta morphology and cancer overall.

PrimateFace: Large-scale resource for cross-species primate facial analysis

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Faces are central to primate social communication, encapsulating emotions, social cues, and individual identities. The advent of deep learning has heralded a new era for robust, high-throughput video-based facial analysis; however, non-human primates present unique challenges due to morphological variability and environmental complexities. To overcome these challenges, we need a dataset devoted to cross-species primate faces to train deep learning models for accurate face tracking and quantification. Here, we introduce PrimateFace, a novel large-scale, cross-species dataset of primate images, annotated with face bounding boxes and facial landmarks, capturing a diverse array of settings, facial expressions, developmental stages, and social interactions. Of the 500,000 images, 10,000 of these images are further annotated for face recognition and facial action units. Using a self-supervised approach, we first pretrained models on unlabeled PrimateFace images, then fine-tuned the representations on smaller annotated subsets for supervised facial analysis tasks. We contribute trained notebook tutorials with fine-tuned transformer and light-weight architectures, including the self-supervised DINO and efficient MobileViT architectures, demonstrating competitive performance and generalizability across primate species and tasks. PrimateFace opens new avenues for cross-species facial analysis and opportunities to study primate social cognition.

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Spider monkey social dynamics, habitat, and behaviors

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Spider monkeys exhibit a highly flexible fission-fusion social system. Here we report preliminary results on the demography and activity budgets of the Black-handed spider monkey, *Ateles geoffroyi,* in the Osa Peninsula, Costa Rica. We recorded the subgroup size, composition, individual sex and age, primary behavior of each individual (feeding, moving, resting), proximity of group members, and group location of 57 subgroups in July of 2023. Results show that subgroup size was significant in predicting the moving behavior of groups. Groups of 2-5 are significantly less likely to be moving than solo monkeys, groups of 6-10, and 11 or more. Group size was also significant for feeding behavior, particularly groups of 2-5 are more likely to be feeding than groups of 6-10. No significant difference was found regarding sex ratio. An additional analysis showed that proximity of groups to human-made open space is not currently significant for predicting behavior. However the data is trending towards significance when collapsed into groups near open space and groups removed from open space. This is a preliminary study that aims to establish a foundation for later examining spider monkey social group functions with regard to forest fragmentation and habitat changes to advance conservation efforts. Understanding that group size is a predictor of both moving and feeding behaviors provides insight into social dynamics of fission-fusion societies.

Beyond Enamel: Stable Isotope Values and Radiocarbon Dating of Dental Calculus from a Medieval Icelandic Sample

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Until recently, dental calculus was viewed as an impediment to making observations on tooth crown size, morphology, and oral health variables. However, research over the past two decades shows calculus is a critical medium for reconstructing past lifeways. Like a sponge, dental calculus absorbs food particles, oral bacteria, and sometimes cloth fibers. It can also be used to estimate stable carbon and nitrogen isotopes. This study evaluated stable isotopes from the dental calculus of fourteen burials from the Keldudalur site in northern Iceland. Calculus δ15N values (x = 11.60) are almost identical to collagen δ15N values (x = 11.55). Calculus δ13C values exhibit a comparable range to collagen δ13C, but the values are shifted approximately -4‰ (x = -23.33 for calculus; -19.26 for collagen). These results parallel those for the Greenlandic Norse, where δ15N values are almost identical to collagen values, but δ13C differs by -4‰. In addition to stable isotopes, three calculus samples were used to estimate radiocarbon dates. Mean dates based on collagen ranged from 970-1075 BP, while mean dates from calculus were higher at 1178-1253 BP. Although the sample of three is limited, there is a high correlation between calculus and collagen-based dates (r = 0.81 - 1.00). The disparity in calculus and collagen C14 dates of about 200 years may be related to the lighter δ13C values for calculus.

Metacarpophalangeal joint orientation and function in extant anthropoids and fossil hominoids

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Both arboreal and terrestrial quadrupedal monkeys dorsiflex their metacarpophalangeal joints (MCPJ) extensively during the stance phase prior to toe-off. In contrast, living hominoids that are facultatively or habitually suspensory, and/or bipedal, tend to exhibit reduced capacity for MCPJ dorsiflexion. The MCPJ function in Miocene hominoids and Plio-Pleistocene hominins remains unclear and highly controversial. Thus, accurate inferences about hand functional morphology of the last common ancestor of African apes and humans are incomplete. In this study, orientation angle (OA) of the proximal articular facet of proximal phalanges, a proxy for MCPJ range of dorsiflexion, was quantified using 3D landmarks collected from extant (n=650) hominoids, cercopithecoids, platyrrhines, and 23 fossil specimens from the Miocene and Plio-Pleistocene. Quadrupedal monkeys exhibit the highest OAs (more dorsal canting) with extensive overlap among palmigrade and digitigrade taxa, and the most suspensory (Asian) apes have the lowest OAs. Variation among African apes (which use knuckle-walking digitigrady in their positional repertoire) and suspensory/quadrupedal atelines overlap and is between generalized quadrupeds and forelimb suspensors. Living and fossil hominins, including those from the Pliocene, are within the lower ranges of monkeys and upper ranges of African apes/atelines. Miocene apes, including *Ekembo*, *Equatorius*, *Sivapithecus*, *Pierolapithecus,* and *Hispanopithecus*, have OAs like most non-ateline monkeys, but do overlap with most hominins except those from the earliest Pliocene. These results highlight that functional interpretations of MCPJs based on OA alone are complicated within a diverse anthropoid sample. But at least for Miocene apes, the documented variation reveals that their MCPJs differed from living apes.

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Relationships among testosterone, age, and coronavirus-19 disease risk in men

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Testosterone exhibits complex relationships with morbidity and mortality in men. Variation in testosterone levels in response to different stressors, including infectious diseases, likely represents an adaptive response to modulate energetic investment in different life history functions. While testosterone levels may predict clinical outcomes in some cases, they also naturally change with age and respond to different disease states (for example, with transient decreases following the onset of acute infectious diseases). Low testosterone may therefore be both a cause and consequence of illness, including COVID-19 disease. While SARS-CoV-2 infection is associated with a decrease in serum testosterone, testosterone levels also tend to be lower in men who progress to severe or fatal disease. To understand this better, we investigated relationships among age, comorbidities, and testosterone in a group of 142 men (ages 19-82). A clinical risk score for severe COVID-19 disease was calculated from previous studies, utilizing the following chronic conditions: high body mass index, smoking, diagnosis of diabetes, cardiovascular disease, chronic obstructive pulmonary disease, kidney disease, liver disease, and cancer. As predicted, serum free testosterone levels decreased with age. A higher clinical risk score, indicative of more pre-existing conditions for severe COVID-19 disease, was associated with lower testosterone levels, but only in men younger than 40. Older men already had lower testosterone as a result of age, limiting the statistical effects of clinical risk score on testosterone levels. Pre-existing conditions as well as age may therefore confound relationships between testosterone and COVID-19 disease outcomes in men.

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Imprecise female fertility signals facilitate extended mating effort in the Kinda baboon

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Unlike other large terrestrial mammals, female anthropoid primates exhibit extended receptivity beyond the fertile period. However, in many species most mating still occurs during fertile phases, particularly with high-ranking males. Male timing of mating to female fertility is thought to be facilitated through female sexual signals, but the relationships among signal expression, fertility, and mating behavior varies across species. We studied a wild population of Kinda baboons (*Papio kindae*) where female sexual signal expression is not precisely timed to intracycle fertility, to determine: 1) how consortships and copulations with males vary in relation to sexual swelling size and/or intracycle fertility; and 2) if male dominance rank mediates this relationship. The frequency of consortships and copulations with all males and the alpha male was predicted by the size of the sexual swelling. While consortships and copulations with all males were less frequent in the post-fertile phase, there was no difference in mating frequency between the pre-fertile and fertile phases, a time when females sexually solicit more often. Further, females mated with the alpha male equally across the cycle. Our results suggest that Kinda baboons have evolved imprecise fertility signals that may function to increase mating opportunities with multiple males across the cycle, and which may contribute to low mating skew observed in this species. In species characterized by reduced male contest competition, female signals may evolve to facilitate greater female control over reproduction.

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Global variation in childhood intestinal absorptive capacity: An overlooked factor influencing energetics, phenotype, and health

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Evolutionary and environmental constraints shape the ability to extract energy and nutrients from food. Among humans, acquired conditions that impact children's intestinal absorptive capacity under unsanitary living conditions (e.g., environmental enteric dysfunction) are increasingly recognized to impact energy availability and growth. Documenting and understanding variation in childhood absorptive capacity is thus a critical need for understanding the drivers of human phenotype and health. Here, we analyze the existing literature from LMICs to characterize the variation in childhood gut absorption across different environments. The lactulose to mannitol test (L:M) is the gold-standard non-invasive approach to measure intestinal permeability and absorption. It compromises the administration of the two sugars, followed by a continuous urine collection of 2-5 hours. 27 L:M studies in children aged 0-9 and published between 2000 and 2023 were reviewed. Mean L:M was 0.24 (SD= 0.1), with all but one study exceeding the reference L:M value (0.12) for healthy UK children. This indicates an impaired permeability and gut absorptive ability among children from LMICs compared to their healthy counterparts in industrialized countries. Three studies reported associations between L:M and unsanitary conditions, and seven reported associations with deficits in linear growth. Notably, a high degree of variation is observed in L:M values among children from LMICs (CV=41%, min=0.1, max=0.41). Additional analyses were performed to identify factors of local environments driving absorption variation. Absorptive efficiency likely generates variation in daily energy requirements. Limitations in energy availability will ultimately drive childhood phenotypic plasticity with short- and long-term health consequences.

The when, why and how of employing machine learning and mathematical modeling for behavioral data analysis: examples from marmosets

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Artificial Intelligence (AI) has become a pivotal force in animal behavior research, excelling in data analysis and pattern recognition. However, its interpretability diminishes as models become more biologically realistic. We explore AI's interpretability challenges for animal behavior studies, offering solutions using marmoset vocal and social behaviors as examples. For vocal behaviors, we developed a hierarchical machine-learning classifier that accurately determines the caller-identity, surpassing traditional non-hierarchical methods. While it streamlines caller-identity determination and captures inter-individual differences and temporal changes in calls, it falls short in elucidating the mechanisms underlying such changes. To resolve this, inspired by dynamical systems theory, we mathematically modeled the temporal changes in marmoset calls. Our model suggests that marmosets learn certain aspects of calls from their partners, leading to vocal convergence with time, and they do so dynamically while accounting for any changes in their partners' calls. For social behaviors, we used DeepLabCut, a machine-learning-based animal pose estimator, to track points on the body of each marmoset before, during, and after prosocial tasks with another marmoset. While DeepLabCut's utility was limited to the quantification of pose synchrony and coordination, mechanisms underlying coordination could be uncovered by mathematically modeling pairs of marmosets coordinating anti-predator vigilance as coupled oscillators. The model suggested that marmosets estimate the current degree of asynchrony and adjust coordination accordingly. In summary, while AI excels at classification and pattern recognition, mathematical modeling aids in understanding the mechanisms underlying animal behaviors. We offer guidelines for animal behavior researchers on when and how to apply these approaches.

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Mushrooms in a Mosaic: The Importance of Fungi for a Primate Community in the Issa valley, western Tanzania

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Human have consumed mushrooms for centuries, with well-known culinary and nutrition (selenium, vitamin D, and vitamin B6) benefits. Mushrooms have been described as a key forest food for Neanderthals based on dental calculus remains and their presence in contemporary African grasslands suggests that mushrooms may have been available for early hominins (e.g., *Australopithecus*) and played a role in the evolution of cognition and language as far back as two mya. Situating this key resource in a broader (savanna mosaic) context of primate dietary ecology may provide new hypotheses for how hominins exploited similar landscapes during the Plio-Plesticocene. For 20 months (2022-2023), we assessed mushroom availability and consumption by sympatric chimpanzees, baboons, and red-tailed monkeys living in a mosaic habitat in the Issa valley, western Tanzania, and found that across three primate species, at least 180 mushroom morphotypes were consumed, only 93 of which we could obtain species identifications. Primate mushroom consumption tracked its availability (wet-season restricted). As a function of overall diet composition, it peaked similarly for each primate species at the very end of the rains in April (*Pan* 29% vs. *Papio* 45% vs. *Cercopithecus* 19%), when overall fruit availability was lowest. We show that mushrooms are a key, if insufficiently studied resource for primates, with availability and consumption revealing dietary flexibility and micro-niche partitioning at Issa. We conclude by examining the role of savanna mosaics in mushroom exploitation for extant primates and extinct hominins.

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Maintenance and Mobility of Neolithic Communities in Anatolia

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Recent research in Western Asia has begun to focus on how the process of adopting the general changes associated with the Neolithic (i.e., *Neolithization*) occurred in a non-linear fashion, thus marking a shift away from the notion of the "Neolithic Revolution." Neolithization has mainly been studied to date by analyses of material culture, and we know little about how social structures changed during this period. This project aims to analyze the phenotypic and genetic structures of several sites in Anatolia to address the process of Neolithization though consideration of the structure and mobility of human populations in this key area for the development of the Neolithic package.

Dental morphometric and genetic data were explored from several Neolithic Anatolian sites that span the early aceramic to the later Pottery Neolithic (Boncuklu, Aşıklı Höyük, Musular, Çatalhöyük, and Barcın Höyük). To understand social structure, biological relationships within interments were explored. The data reveal that biological relationships were more frequent between individuals buried within the same building early in the Neolithic, but, over time, such relationships appear to become less important, as the number of biologically related co-burials decreases. Variation in phenotypic data between sites and males and females was explored to understand migration patterns. The data demonstrate increased variation over time suggesting increased migration to larger sites. Data also indicate slightly higher female variation, indicating females as the more migrant sex; however, this trend decreases over time. This research highlights socio-cultural variation during the Neolithic and the importance of Anatolia in understanding Neolithization.

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"Eight mummies, eight stories". Imaging the Radziwiłł family and their fellow citizens of Kėdainiai, Lithuania (17th-18th centuries AD)

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The eight individuals discussed in this paper were recovered during a project aimed at investigating the mortal remains of members of the Radziwiłł family, a powerful dynasty in the former Polish-Lithuanian Commonwealth. They had been contained in a crypt at the evangelical reformed church of Kėdainiai, a historic town in central Lithuania, where an additional subterranean chamber was utilized as a resting place for dignitaries unrelated to the family. Both rooms had been desecrated, resulting in disturbance and possible mixing of their contents over time, which also led to the loss of identity of those deceased. Therefore, in July 2019, we were involved in recovering the remains from both burial contexts, attempting to identify some of the bodies, and eventually providing them with new coffins. Out of the 37 individuals investigated, eight mummified persons equally represented by four males and four females were submitted to computed tomographic (CT) scanning due to their remarkable preservation status. The goal of this presentation is to provide the results of that investigation, including the estimation of age, sex, and the recording of other distinguishing features, as well as the interpretation of the pathological changes seen on the hard and soft tissues during medical image examination. These comprise two cases of cardiovascular conditions, four examples of lung calcifications, two notable cases of neoplastic disease, and a number of different skeletal abnormalities. Lastly, ethical issues encountered during the study will also be discussed in light of the current recommendations available for the study of mummified remains.

Evaluating the relationship between brown adipose tissue thermogenesis and bone mineral density in young adults in New York City

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Objectives: Chronic cold exposure is associated with lower bone mineral density (BMD) because of the effect of the sympathetic nervous system on bone turnover (e.g., increase in bone resorption, decrease in bone formation). Brown adipose tissue (BAT) has been shown to be associated with higher BMD and may have protective effects against this relationship; however, support for this relationship is mixed. We report on the relationship between cold exposure, BAT, and BMD among a sample of 57 young adults in New York City.

Methods: Participants were exposed to a mild colling condition to activate BAT. We used indirect calorimetry to measure energy expenditure and created thermal images of areas where BAT is present to measure BAT activity. BMD was measured at the radius using a non-invasive MiniOmni bone sonometer. Anthropocentric data was collected to control for body fat percentage and fat free mass. Linear regression analysis was performed to determine the relationship between BMD and BAT activity.

Results: The analysis showed a negative association between BMD and BAT activity (p=0.02) after controlling for covariates. When analyzing these relationships by sex, a similar relationship was demonstrated in the female subsample, but not for males.

Conclusion: These results did not provide conclusive support that BAT has protective effects on BMD. Larger sample size, repeat measures of BMD across multiple skeletal sites, and adding a more nuanced view of bone health including biomarkers of bone turnover may shed more light onto the proposed relationship between BAT and BMD.

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A reality-based understanding of human intergroup relations, past and present, undermines racist tropes

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Despite popular depictions of human nature as marked by intergroup conflict, often fueling racist tropes, intergroup relations in Homo sapiens are remarkably flexible. How have humans past and present relied on members of other groups to manage the risks we face as a generalist species living all over the globe? Here, I review work done by my teams and others that highlights the diversity of strategies humans have used to manage environmental risk, often in collaboration with individuals living at a distance and from different identity groups. One key take-home is that despite emphasis on ethnic groups in the evolutionary anthropological literature, interethnic conflict is not inevitable. I conclude by underscoring that humans wouldn't be where we are today without connections spanning distance and identity boundaries.

Craniofacial length and breadth dimorphism in primates

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Several studies suggest that sexual selection targets the development of craniofacial breadth dimorphism as a function of female choice for broad faces or male threat displays, including in hominins. Evidence for excessive circumorbital dimorphism in red colobus monkeys is compelling, but comparative evidence for this across primates is less certain. This analysis evaluates the relationship between craniofacial breadth and length dimorphism across primates. Data for 8 craniofacial breadth and 10 craniofacial length dimensions were measured for 191 primate samples. Size dimorphism was estimated using body mass data from the literature (or the museum specimens themselves where available), and the geometric mean of 40 craniofacial dimensions. Dimorphism was estimated as the ln-transformed ratio of the male mean divided by the female mean for each species. Data were evaluated using standard regression as well as PGLS, with the latter yielding slightly smaller sample sizes depending on phylogenetic information from the 10K trees web site. Results show that craniofacial length dimorphism is generally more strongly correlated with size dimorphism than breadth dimorphism. Interestingly breadth dimorphism tends to be negatively allometric by comparison to length dimorphism. However, breadth dimorphism tends to be nearly isometric with size dimorphism, while length dimorphism tends to be positively allometric. This is most consistent with the hypothesis that craniofacial length dimorphism is impacted by the expression of canine tooth size dimorphism, and offers no support for the hypothesis that facial breadths generally are an independent target of sexual selection.

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Climatic influences on space use and activity in a nocturnal primate

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It is suggested that nocturnal primates share physical and behavioral traits that resemble those of early primates. By studying extant nocturnal primate species, we can reconstruct how early primates may have solved various ecological problems through behavioral adaptations. Short- and long-term environmental changes are one influential ecological problem that is purported to have contributed to our own evolution and is exceedingly relevant today. Here, we used the Bengal slow loris (*Nycticebus bengalensis*) as a model for how responsive smaller-bodied nocturnal primates may be to changes in temperature and humidity patterns throughout the night, as well as what behavioral changes they may exhibit. We collected data at the Sakaerat Slow Loris Project, based in Northeastern Thailand, at the Sakaerat Biosphere Reserve in Nakhon Ratchasima between June and October 2023. Between 18:00 and 06:00, we recorded animal height, behavior, posture, temperature, and humidity concurrently. Our analysis included 3000 data points across 17 Bengal slow lorises. We found that, on average, they were 8.67+3.17 m high and tended to occupy the upper third of the tree they were using. Regarding climatic variables within a single observation period, the nightly temperature changed as much as 4.1 degrees, and humidity changed as much as 12%. We saw a trend where temperature difference peaks corresponded with nights with a higher height difference. These results offer a rare insight into temporal changes Thai Bengal slow lorises experience and how they may use vertical movement to mitigate these changes on a nightly basis.

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Ontogeny of masticatory muscle architecture in tufted and untufted capuchins

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Behavioral work has shown that tufted capuchins (*Sapajus* spp.) consume a more mechanically challenging diet than untufteds (*Cebus* spp.). These behavioral differences have been linked to morphological differences in mandibular cross-section, craniofacial shape, and masticatory muscle leverage across ontogeny, as well as in architectural features of the jaw adductors in adults.

We analyzed muscle architecture in an ontogenetic sample of tufted and untufted capuchins (20 captive *Cebus*; 20 captive *Sapajus*; 20 free-ranging/semi-provisioned *Sapajus*). Superficial masseter and temporalis muscles were weighed before digestion in 30-40% nitric acid. Fiber lengths were then measured and physiological cross-sectional area (PCSA) calculated. One-way ANOVAs and regressions were used to examine differences among age classes/samples and scaling relationships, respectively. Fiber lengths did not differ significantly across ontogeny or among samples. However, *Sapajus* showed larger muscle masses and PCSAs relative to *Cebus* ($p<0.05$), even early in ontogeny; free-ranging *Sapajus* had the largest muscles and PCSAs of all groups. While fiber lengths generally scaled with isometry relative to mandible length in all samples, *Sapajus* and *Cebus* show different scaling relationships for PCSA and muscle mass, with *Sapajus* exhibiting marked positive allometry.

Results are consistent with prior work showing that adult tufted capuchins have similar fiber lengths but larger PCSAs than untufteds driven by increased muscle mass. Increasing muscle mass/PCSA while maintaining relatively long fibers could facilitate *Sapajus* generating relatively larger bite forces at wider gapes, allowing them to process relatively large, tough foods throughout ontogeny.

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Preliminary study: A total-evidence approach to hominin phylogenetics using 3DGM data

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In phylogenetic analyses, the accuracy of reconstructed trees generally depends on employing a sufficient quantity of character data. Fossil studies may be particularly prone to weak results due to the paucity of available material. The use of multiple data types in phylogenetic total-evidence analyses may, therefore, provide an additional source of information that can be utilized to strengthen analyses. Hence, the high dimensionality offered by 3D geometric morphometric data (3DGM) could represent a good solution to the study of complex morphological information, especially that of fragmentary fossil species. However, 3DGM data in phylogenetic analyses has been the subject of considerable debate, and because of this, many previous GM-based phylogenetic studies have used the principal component scores derived from landmark data as continuous character data, rather than the Procrustes-aligned landmark coordinates. Here, we iteratively test the ability of Procrustes data to recover the phylogenetic relationships of fourteen extant anthropoids and four fossil hominins (*Paranthropus boisei, Homo habilis, H. erectus, H. heidelbergensis*) both independently and in total-evidence analyses with traditional discrete characters. Craniodental landmarks were collected on high-resolution 3D models and analyzed using parsimony. A previously published traditional character matrix was employed for total-evidence analyses. Results indicate that more accurate trees are recovered when 3DGM data are combined with traditional data in total evidence analyses. This approach allows for the inference of ancestral landmark configurations (i.e., shape) that can be used to evaluate the fossil record, demonstrating the utility of GM data in their ability to add information to phylogenetic analyses.

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The genetic differentiation of early South Americans

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The early genetic diversification of Native American populations has for long remained poorly understood because of the scarcity of ancient DNA data from the Americas. In the last few years several studies reported genome-wide data from almost a thousand ancient individuals spanning from Alaska to Patagonia. Co-analysing these data revealed that ancient South Americans derived their ancestry from one of the two early lineages that contributed to non-arctic Native Americans. This ancestry resulted from an early dispersal and rapid star-like radiation, followed by genetic continuity in different regions for at least ~9,000 years. Moreover, at least two additional gene flow events between North and South America were identified such as the one that provided new ancestry to the Andes by ~4,000 years ago and one that contributed to individuals older than 9,000 years from Chile and Brazil. However, only a limited number of genomes is available from early to middle Holocene individuals. This presentation discusses recent efforts to fill critical gaps in the geographic and temporal distribution of ancient genomic data from South America. These enlarged datasets reveal a lack of shared genetic drift among early Holocene hunter-gatherers and confirm a common South American radiation. Moreover, they allow a better understanding of the timing of previously described gene flow events between North and South American populations. Genomic findings are evaluated in comparison to cranial morphological studies to investigate the biological transformations that took place when groups ancestral to present-day populations became established in different regions of South America.

Ancient DNA Reveals Diverse Mitogenomic Lineages in an Afro-diasporic Peruvian Population

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Latin American populations have a long history of voluntary and forced migration from Europe, Asia, and Africa, which has created highly complex patterns of admixture. However, Afro-descendant populations such as those living at the 18th-century *Hacienda La Quebrada* sugar plantation in coastal Peru remain understudied. As part of a community-engaged research project, we use ancient DNA to investigate patterns of genetic diversity among individuals buried in the plantation's cemetery by assessing their maternal mitogenomic lineages. We isolated ancient DNA and prepared single-stranded and double-stranded libraries for 30 individuals, followed by shotgun sequencing. Using Haplogrep 3, we successfully obtained mitochondrial haplogroup assignments with ≥70% quality for 15 individuals based on 5 single- and 15 double-stranded libraries. Mitochondrial coverage in these libraries ranged from 1.14 - 47.26X (mean of 7.86X). 60% of these individuals carried haplogroups L1, L2, or L3 (associated with African populations), and 40% carried haplogroups A2, B2, C1, and D1 (associated with populations indigenous to the Americas). These diverse maternal ancestries from Africa and the Americas suggest that contemporary admixture patterns in Afro-Peruvians have been present since at least the 18th century. Mitogenomic target enrichment is ongoing to improve the quality and quantity of haplogroup classifications, as well as whole genome enrichment to identify genome-wide admixture patterns based on genetic similarity to contemporary reference populations. As the first ancient DNA study of an Afro-diasporic population in Peru, this work contributes to better characterizing the demographic history of African and Afro-descendant communities in Latin America.

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Not one, but multiple radiations underlie the biodiversity of Madagascar's endangered lemurs

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Lemurs are a well-known example of adaptive radiation. Since colonizing Madagascar, more than 100 extant lemur species have evolved to fill the variety of ecological niches on the island. However, recent work suggests that lemurs do not exhibit one of the hallmarks of adaptive radiations: explosive speciation rates that decline over time. We test this idea using a phylogenomic dataset with broad taxonomic sampling of lemurs and their sister group, the lorisiforms of Asia and continental Africa. We find higher rates of speciation in Madagascar's lemurs compared to lorisiforms and we confirm that lemurs did not experience an "early burst" of speciation after colonizing Madagascar. Instead, we identify three independent bursts of speciation approximately 15 million years ago that underly much of today's lemur diversity. We demonstrate that the lemur clades with exceptionally high diversification rates have higher rates of introgression. This suggests that hybridization in these primates is not an evolutionary dead-end, but a driving force for diversification. Considering the conservation crisis affecting strepsirrhine primates, with approximately 95% of species being threatened with extinction, this phylogenomic study offers a new perspective for explaining Madagascar's exceptional primate diversity and reveals patterns of speciation, extinction, and gene flow that will help inform future 60 conservation decisions.

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Symphyseal biomechanics of extant hominids during simulated chewing

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Biomechanics of the mandibular symphyseal region feature prominently in discussions of hominid mandibular mechanics. During the power stroke of mastication the symphysis is hypothesized to be subjected to: lateral transverse bending (bending in transverse plane); anteroposterior transverse shear; positive frontal bending associated with twisting of the mandibular corpora about their long axes; dorsoventral frontal shear; and transverse twisting (about the transverse axis of the symphysis). We used finite element modeling (FEM) to test hypotheses about symphyseal loading and strain regimes during mastication in *Pongo, Homo, Gorilla* and *Pan* (female and male) during first molar chewing. Three-dimensional FEMs were made from CT scans and assigned material properties of *Macaca*. To simulate chewing, species-specific muscle forces were scaled using EMG activity in *Macaca*, and boundary conditions set to those used in our macaque modeling. The results confirm similar deformation and strain regimes across models but with subtle differences in strains in the lingual symphysis, possibly related to differences in symphyseal morphology. The mandibles of *Pongo* (female), *Homo* (male), *Pan* (male) experience higher principal strain magnitudes in the lingual symphysis, whereas *Pongo* (female), *Gorilla* (female), and *Pan* (male) experience higher strains in the basal area. Our FEM research reveals that the mandibular symphyses of *Pongo, Homo and Pan* share similar loading, deformation and strain regimes during mastication, and that the strain regimes are associated with lateral transverse bending, or "wishboning" in the mandibles of the extant hominids.

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A three-dimensional virtual assessment of hominoid hallucal divergence

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The evolution of human bipedalism is associated with the loss of hallucal grasping facilitated by substantial modifications to the hallucal tarsometatarsal joint. This study tests the hypothesis that the hallucal divergence angle (HDA) reflects frequencies of arboreality and terrestriality among hominoids. A total of 920 3D scans of hominoid first metatarsals, second metatarsals, medial cuneiforms, and intermediate cuneiforms were virtually articulated, representing 230 individuals and 10 taxa. The HDA was computed as the inverse cosine of the dot product between vectors fit to the diaphysis of each metatarsal. ANOVA was used to test the null hypothesis that HDA values are random with respect to locomotor groups (F = 605.54, p = < 2.2^{-16}). Overall, the results show that, among the non-human taxa, orangutans tend to have the largest, and eastern gorillas have the smallest, HDA values. Chimpanzees, bonobos, and western gorillas tend to have reduced hallucal divergence angles compared to orangutans and hylobatids on average, but the magnitude of the difference is small, and there is substantial overlap across species. This result implies that a large-bodied, forest-living ecological niche may select for hallucal grasping features in taxa that otherwise spend a large proportion of their locomotor budget on the ground, as in most African ape species. These data provide a comparative context for inferring foot grasping adaptations in extinct taxa.

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Reassessing the taxonomy of Pleistocene papionins from Sterkfontein, Makapansgat and Swartkrans using a nonmetric analysis of mesio-lingual maxillary molar morphology

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The phylogeny of fossil papionins from southern Africa has been heavily contested. Previous studies have utilized molar dimensions and the morphology of the cranium and mandible to differentiate taxa. However, considerable variation within each taxon and between taxa have limited the degree to which a phylogenetic signal can be distinguished. This study uses a nonmetric approach to differentiating fossil papionin taxa by scoring the absence or degree of expression of an accessory feature analogous to Carabelli's trait of the mesio-lingual cusp (protocone) of the maxillary molars, which shows considerable variation in both extant *Papio* and fossil papionin taxa. A pairwise comparison of the comparative samples which includes four extant *Papio* taxa (n = 134) shows *P. anubis* is significantly different from all other extant papionins whereas *P. kindae, P. ursinus,* and *P. cynacephalus* do not show significant differences in the expression of this trait. Analysis of the extinct papionins (n = 49) demonstrate *Papio robinsoni* to be significantly different from all other fossil taxa. *Parapapio jonesi, Pp. whiteii, and Pp. broomi* are not significantly different in the expression of the mesio-lingual accessory and show a higher instance of absence, much like extant *Papio ursinus*. A Kruskal-Wallis test shows no significant difference exists among the three *Parapapio* species (p = 0.410) whereas the extant *Papio* taxa are significantly different (p < 0.001). To the degree to which the mesiolingual accessory is taxonomically informative, these results call into question the existence of three separate *Parapapio* species within Makapansgat and Sterkfontein caves.

Improving the non-human ape model outgroup in hominin evolution: a review of available data on growth and development

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Identifying derived versus ancestral traits and conditions, accounting for variation at multiple levels, and making predictions in the face of crucial gaps in the fossil record are all challenging tasks for paleoanthropologists. Better understanding ancestral traits and conditions in living hominoids across their varied environmental and behavioral ranges is as crucial since they most often serve as an outgroup in studies of early hominins. Given the increase in subadults in the fossil hominin record, here we focus on maturity variables of the skeleton and dentition—direct evidence available to compare in the fossil record—and their reproductive correlates. It is well documented that wild and captive primates mature at different paces. Forest-living *Pan troglodytes* females from long-term field sites enter adulthood between 13.7-14.9 years, when they achieve full dentition, skeletal maturity and first reproduction. In captivity, *P. troglodytes* females mature earlier, between 10.5-11.2 years; captive data has historically relied on biomedical research animals kept in stressful environments. The contrast in maturity timing among forest-living and captive populations highlight how environmental quality and conditions affect somatic development, a well-established pattern in human growth studies. The current study adds additional data from savanna-living chimpanzees of Fongoli in Senegal, the only wild chimpanzees habituated in a semi-arid biome. The savanna mosaic environment analogues the selective pressures facing early hominins. Fongoli females exhibit faster reproductive rates than chimpanzees elsewhere. Incorporating data from chimpanzees in various habitats improves our model for identifying how selective pressures have shaped life history variables over the course of human evolution.

Employing local ecological knowledge to understand slow loris ecology in anthropogenic landscapes

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Deforestation is increasingly forcing primates into proximity with people. It is important, that we understand how species navigate human-dominated environments and if these interactions threaten their populations. Local knowledge is a valuable source of information on underrepresented and cryptic species, and studies relating to nocturnal species are limited in Thailand, including those of the Endangered slow lorises (*Nycticebus bengalensis* and *N. coucang*). Here, we analyze data regarding the knowledge, beliefs, and experiences of local people from Khao Lak, in southern Thailand, an area that is composed of rural and urban areas. We conducted 36 interviews using photo cards to determine (1) where and how often people see slow lorises, (2) what they see them doing, and (3) what they know about them. We analyzed meaningful common words and how they clustered together, as well as, identified key concepts that define the local beliefs about slow lorises. We found that people reported that slow lorises ate fruit, were not aggressive, but were 'bad omens', and they reported that there used to be more lorises, but interviewees did not specify how recently this change occurred. We also determined that slow lorises were often seen in anthropogenic landscapes like rubber plantations and the people of Khao Lak live in passive coexistence with lorises with minimal conflict and exploitation. Our findings indicate that lorises can persist in and around human-altered habitats and we discuss how private lands could contribute to slow loris conservation in this area in the future.

Unraveling the genetic basis of skeletal muscle endurance to understand hominin locomotor evolution

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Research suggests that the high proportion of fatigue-resistant slow myofibers within human lower limb muscles is due to human-specific variation within the spatiotemporal regulators of myofiber gene expression (e.g., *cis*-regulatory elements, CREs). To identify these CREs, we used a mouse model to characterize the regulatory landscape of fast- and slow-biased muscles at two timepoints using RNA-seq and ATAC-seq. We identified thousands of potential CREs unique to each myofiber bias and timepoint, as well as those shared across categories.

To narrow our candidates to active CREs, we filtered our data using publicly available mouse muscle ATAC-seq and ChIP-seq datasets. We then identified 12 candidates near genes associated with myofiber phenotypes: 3 associated with slow myofiber genes (e.g., *Atp2a2* and *Bdnf*), and 9 associated with fast myofiber genes (e.g., *Mybpc2* and *Myh4*). To test the activity of these CREs in muscle cells (HSMM and C2C12), we are currently testing the function of candidate sequences using reporter assays.

To identify candidates important to human biology and evolution, we intersected our data with human muscle (DNAseI-HS) and evolutionary datasets (HARs, HAQERs, and hCONDELs). We then targeted conserved regions near myofiber genes and identified 6 additional CREs for functional validation: 4 universally accessible across all muscles and timepoints, one adult slow-specific, and one fetal slow-specific. We are currently testing the function of human- and chimpanzee-specific sequences in muscle cells. We hypothesize that the human-specific sequences will drive higher gene expression *in vitro*, leading to more slow-biased, fatigue-resistant muscles compared to those of chimpanzees and mice.

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How do clinicians define and use race and genetic ancestry?

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Race is commonly used in clinical decision-making as a proxy for genetic and environmental risk factors, despite lack of consensus on how to define and classify race and confusion around how it contributes to disease. Little empirical research has explored the way clinicians define and use race and genetic ancestry when making clinical decisions. We interviewed 21 clinicians to analyze how they define race, classify a patient's race, use ancestry data, and what racial cues they prioritize. Clinicians were presented with a mock hypertensive patient with conflicting cues about ancestry data, phenotype, and self-identity. Our findings indicated no clear consensus on how to define race in general or for the specific patient cases presented, suggesting that clinicians hold a variety of non-standardized, overlapping, and often conflicting definitions of race. Of the 21 clinicians, five defined race as sociocultural, one as self-report, four as biological, and nine as varying combinations of these categories. Interestingly, clinicians classified patients' race in non-convergent ways that sometimes contradicted their own definitions of race. When asked about the relevance of ancestry data to treating hypertension, twelve clinicians considered it to be irrelevant, and most thought it was only relevant for screening but not for treating other diseases. Based on our findings, the clinical utility of race and ancestry data should be reconsidered given the inconsistent processes through which race is determined, the difficulty of classifying individuals into discrete racial groups, and the lack of evidence for the role of race and ancestry in complex diseases.

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Later pubic symphyseal fusion in female primates and the accuracy of virtual reconstructions of the adult primate pelvis

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Pelvic form, often linked to obstetrics, is variable in primates, but it is unclear at present a) how well reconstructions of the pelvis from osteological material that is unfused at the pubic symphysis reflect *in vivo* form, and b) which factors influence the fusion the pubic symphysis (where this occurs). To determine pelvis rearticulation accuracy, 3D complete pelvis visualizations for one male and one female adult were created from CT scans of cadaveric specimens of *Homo sapiens, Pan troglodytes, Macaca mulatta, Lepilemur mustelinus, Galago senegalensis* and *Nycticebus pygmaeus* and compared to the same bones segmented individually and rearticulated virtually. The presence/degree of pubic symphyseal fusion was determined via a cross-sectional sample of adults of known sex/age for *P. troglodytes* and *M. mulatta*. The rearticulation results suggest that most virtual reconstructions from separated pelvic elements closely resemble the living condition of the complete pelvis; the only notable differences are in smaller taxa with more widely open symphyses. When divided into age categories (four equal stages from age at first female reproduction to age of female reproductive senescence, plus one post-reproductive stage), the proportion of fused symphyses in *Pan* and *Macaca* increases with age and occurs earlier in males, despite males reaching skeletal maturity later in other (including pelvic) regions. The results suggest that virtual rearticulation is a viable method of evaluating osteological/fossil pelvic material, particularly for larger taxa, even when the three bones are separated, and that pubic symphyseal fusion is dependent on age and sex in non-human primates.

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Effects of age on trabecular bone morphology in the rhesus macaque upper limb

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Although age-related skeletal deterioration diminishes quality of life, the role of trabecular change during aging is not well understood. This study explored trabecular volume change during senescence in rhesus macaques (*Macaca mulatta*), a non-human primate model for human aging. High-resolution microCT scans of the humerus, ulna, and radius were obtained from the Caribbean Primate Research Center - New York University Rhesus Macaque Skeletal Collection. Bone volume fraction (BV/TV), degree of anisotropy (DA), and trabecular thickness (Tb.Th) were compared in the distal humerus, proximal ulna, and proximal radius of prime and post-prime aged rhesus macaques, across sex and age. Point clouds of BV/TV, DA, and Tb.Th were generated for 3D visualization and point-to-point Bayesian statistical analysis and whole bone means were compared using t-tests. Patterns of BV/TV, DA, and Tb.Th across the elbow were similar in prime and post-prime groups, reflecting a habitually semi-flexed elbow in terrestrial quadrupeds. Cohen's D effect size demonstrated regional variation in BV/TV, DA, and Tb.Th across all three bones, specifically higher thickness in the post-prime humerus and radius but decreased in the ulna. This study used a novel, fine-tuned approach to analyze the impact of age on trabecular structural variation on a region-to-region basis across a load-bearing joint, allowing the visualization of regions of increased density in addition to expected regions of decreased density. Our results underscore the complexities of trabecular structural variation. Future research will focus on the impact of other social and physical factors on skeletal tissue.

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Reconstructing the Demographic History of South Asia: Insights into Ancient to Modern Genome

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Reconstructions of the effective population size from the past firmly point out that South Asia has been inhabited since the Early Upper Palaeolithic period. This hypothesis can be explained by the fact that South Asia was among the first regions in the world to be inhabited by modern human beings after the Out of Africa migration. South Asia represents a rich assemblage of tribes, castes, and populations identifying themselves by different religions. Most of these populations are highly endogamous and hence reveal the complex, multilayer genetic differentiation in the region. This complex nature of the South Asian proximity has raised multiple questions for our and other research groups' interests. These questions were unanswerable just a few years back but the advances in new technology and resolution have made the analysis easier. The new applications rely on the extensive high-coverage sequencing of specifically targeted modern and ancient samples, autosomal SNP genotyping of specific populations, extensive Y chromosome resequencing of selected population groups (Tribal and caste populations from different geographical regions) and statistical analysis of the results in the context of human genomic variation worldwide. I will be discussing and presenting data from the complex population structure of the Indian Sub-continent and future research directions to understand the deep ancestral components of South Asians at the Eurasian and global scales, patterns of admixture and migrations derived from studying ancient and modern genomes.

"Bolinao Skull": male or female? Morphological traits of a human cranium, mandible, and dentition with goldworks retrieved from a 14th-15th century site in northern Philippines

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I-1964-F-57 ("Bolinao Skull") is a human cranium and mandible retrieved from a 14th-15th century archaeological site in northern Philippines in 1960's. Studies on early aesthetics in the Philippines often associated with female practices briefly introduced I-1964-F-57's ornate dental goldworks in literatures; however, biological information about Bolinao Skull is lacking and presents challenges on generalized view about dental ornamentation practices during pre-Spanish Philippines and individual characteristics.

Physical examination of cranial, mandibular, and dental traits based on standard protocols in determining sex, ancestry, and age was conducted; assessment of non-metric traits of the anatomical tooth crowns follows the ASUDAS. I-1964-F-57 have protuberant supraorbital tori and nuchal crests, sloping frontal, round-edged supraorbital margin, large mastoid process, and prominently angular mandible. All teeth are present with fully erupted third molars and incisors exhibiting strong expressions of shoveling and dental tubercle; moderate to large metacone and hypocone of the maxillary molars as well as cusp 5 of mandibular molars were observed. Other dental traits with minimal expressions, palatine torus, tooth wear, and caries were also noted. Tooth crown dimensions were measured thrice with a digital caliper; both non-metric and metric dental characteristics exhibit potential trend in growth and development.

Morphological characteristics investigated herein indicate that Bolinao Skull was an adult Asian male, showing that dental ornamentation practices during the pre-colonial period was not uncommon among men. The results provided a different insight on early dental practices in the Philippines.

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A comparison of stature estimation methods for contemporary American Indians

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Data from contemporary American Indians (AI) are rare in reference samples used in forensic anthropology. The absence of these data is not surprising given the history of exploitation by anthropologists. These data are necessary in contexts where AI comprise a large part of the population and can become part of the forensic record, like New Mexico. Currently, analytical methods used for AI are created from archaeological samples or other Indigenous populations and may not be appropriate for forensic use.

To investigate accuracy, precision, and secular change in allometry, we compared three stature estimation equations derived from different data sources: Auerbach and Ruff (A&R; 2004), calculated from archaeological material; Genovés (1967), derived from an Indigenous Mexican sample; and newly created equations from a contemporary forensic sample, the New Mexico Decedent Image Database (NMDID), For this research, long bone lengths and cadaveric height were collected from computed tomography (CT) scans (n=222) and linear regression equations were determined. Results show point estimates from A&R underestimate stature by ~2-5cm, with the greatest discrepancy seen among females. Genovês' equations are more precise for female stature (> 1 cm); however, they underestimate male stature by ~3 cm. Stature estimates from NMDID equations differ from cadaveric height by less than 1 cm across both sexes. Additionally, we note an increase in limb length and stature compared to samples used in the A&R and Genovés studies. We demonstrate the benefit of using modern datasets to assess the biological profile in forensic contexts.

Lower limb prosthetic use in northern Sri Lanka: a biomechanical and prosthetic wear study

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Lower limb prosthetics aim to mimic the function of an intact limb, improving mobility and providing independence. International standards that regulate the design and testing of lower-limb prosthetics focus on prosthetic use in high income countries and do not take into account biocultural variation or perspectives from the global south. To better understand biocultural variation in lower-limb amputees and its implications for prosthetic foot design, we investigated the failure mechanisms on 294 prosthetic feet replaced due to failure by a local prosthetic and orthotic centre in northern Sri Lanka, the Jaffna Jaipur Centre for Disability Rehabilitation (JJCDR). Unlike in high income countries, most feet failed due to excessive wear due to a high level of barefoot walking and not wearing shoes indoors. Foot wear patterns were quantified on 66 prosthetic feet using techniques derived from dental microwear studies. The largest areas of observable wear were located at the end of the keel, the heel, and the perimeter of the foot, where dynamic plantar pressures and bending stresses would have been the highest. 19 lower limb prosthesis users then underwent static and dynamic tests using a plantar pressure mat and confirmed the relationship between plantar pressure during standing/walking and the magnitude of prosthetic foot wear. Variations in wear and pressure patterns were observed during ethnographic observations that related to how the prosthetic users moved about their environment, including their kitchens and stores. Our results show that international design standards are Eurocentric, and need to incorporate biocultural variation.

The project has been funded by the Global Challenges Research Fund (GCRF), London South Bank University, and the British Council.

Moving great ape osteobiographies forward: Digitally linking macro and micro data and media at the individual level

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Efforts to move our discipline in a more ethical direction include new recommendations for great ape skeletal research and collections management (Kralick et al., *in press*). Examining and measuring microscopic features on skeletal materials is time-intensive and requires specialized equipment and training, limiting opportunities for access. Simultaneously, the copious amount of generated data could aid in examining the lives and biology of individuals through a more holistic lens.

For a dental anthropology project, we recorded 3D scans and photographs of adult great ape skulls (seven orangutans, five chimpanzees, one bonobo, and nine gorillas) from the Field Museum, to be made available through MorphoSource. Those media capture scale, macrowear, calculus, and damage. High-resolution casts of permanent teeth (N=262) exhibit wear on the buccal and lingual enamel surfaces, enamel defects (e.g., linear enamel hypoplasia), and 83.59% exhibit perikymata. In at least five cases, damage to the enamel exposes daily cross-striations and underlying striae of Retzius. As this collection has been extensively studied, data that further capture these apes' cranial and postcranial morphology likely exist in the literature. Thirteen individuals lived some of their lives in captivity: one is identified by name and 11 are likely identifiable. Integrating data and media capturing micro- and macro-level processes would facilitate research connecting somatic growth processes and embodied outcomes across different systems. Linking the individuals' historical and museum records, data, and media in a digital database would promote greater participation in science from researchers around the world and at different career stages.

Subfossil birds at Vintany Cave: a key to understanding the past ecology and recent history of Tsimanampesotse National Park

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The end of the Holocene is marked by a significant turnover of the vertebrate fauna of southwestern Madagascar which was shaped first by a pronounced drought and later by human activities. A number of published works have examined the paleoenvironment and climate of southwestern Madagascar prior to this turnover event. Here, we use subfossil birds to reconstruct the ecological history of this region, specifically from the Tsimanampesotse area. We examined ~890 bones belonging to 35 bird species excavated from Vintany Cave and reconstruct ecological envelopes. There is no evidence of human presence at Tsimanampesotse until after the period that certain birds species went extinct or locally extirpated. These birdsbelonged to a community that occurred locally before ~2,000 years BP and that also included large-bodied (now-extinct) lemurs and carnivorans. The park, specifically at the foot of the Mahafaly Plateau, was during this period predominantly open-canopy forest and on the plateau bush thicket similar to that currently present in the region, and an open area. The current saline lake was a vast, clear, freshwater wetland harboring a diverse aquatic fauna and was bordered by stands of trees or scattered trees. Our paleoclimatic inferences from the site based on the bird material are similar to the conclusions drawn from stalagmite studies and suggest that Tsimanampesotse was influenced by a subarid climate during the late Holocene prior to human disturbance. Our approach demonstrates the value of avian skeletal remains as a source of paleoecological information.

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The man who searched for Madagascar's hidden past treasures, and who was himself a living treasure – Dr William L. Jungers

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In the early 1970s, a young and enthusiastic American graduate student left his home in Michigan to travel 12,000 miles to the 4th largest island in the world, Madagascar, in search of the island's hidden treasures. This experience – studying the fascinating bones of subfossil lemurs, discovering the culture of Malagasy people and seeing some of the island's endangered fauna – made a huge impression on him. Bill Jungers completed his doctoral degree in 1976 and began conducting fieldwork in Madagascar in the 1980s with Elwyn Simons, David Burney, Laurie Godfrey, and Malagasy scholars. He explored caves and open-air sites from the northern to the southern tips of Madagascar over several decades, including Ankarana, Anjohibe, Amparihingidro, Ampasambazimba, Taolambiby, and Andrahomana! He worked on subfossils from these and other sites, most recently Beanka in western Madagascar. As faculty in the Anatomy Department and the IDPAS program at Stony Brook University, he mentored many Malagasy students, whether or not he was their primary advisor. With Steve Goodman, Bill co-authored two books on Madagascar's hidden treasures ("Extinct Madagascar: Picturing the Island's Past"), and contributed dozens of more specialized articles, including a half dozen review articles on this topic. Towards the end of his life, he was one of 19 subject editors reviewing contributions from more than 600 experts on various aspects of Goodman's "The New Natural History of Madagascar". Bill Jungers was born to search the hidden treasures of Madagascar and to help save the lemurs. His career made a difference.

Back to basics: Cartmill and the analysis of cranial integration, allometry and adaptation

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For over five decades, Matt Cartmill has generated a highly diverse body of theoretical and comparative research on determinants of phenotypic variation in primates and other mammals. Indeed, his approach to unraveling the complex network of influences on the primate skeleton has inspired multiple generations of bioanthropologists. As part of a symposium honoring Cartmill's scientific legacy, I will focus on several fundamental aspects of his research program regarding primate cranial function and evolution. In presenting personal empirical data, I will make a broader argument that Cartmill's myriad contributions continue to generate significant interest as well as provide an analytical template still relevant for examining morphological diversity in primates.

Cartmill's contributions to our understanding of the origin of early primates and anthropoids have emphasized the need for an explicitly multifarious approach to circumorbital evolution in both such clades. Such research was novel in recognizing the need to incorporate the central role of allometric variation in the brain and eyes into models concerning the function and evolution of the primate postorbital bar and anthropoid postorbital septum. Arguably, this is fundamental for evaluating size-related variation in determinants of cranial integration, a perspective that necessarily includes a consideration of both structural and adaptive factors. Given the unique importance and challenges of the fossil record for informing our understanding of evolutionary transformations, Cartmill's work with Kay on developing an explicit framework for adaptive inference in skeletal materials has proven to be requisite for articulating the benefits and limits of morphological inference in primate comparative research.

Humans as reservoirs: Historical microbiomes uncover hidden zoonotic pathways

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Marine biome modifications and ecosystem alterations due to significant human activity extends deep into antiquity. Historical exploitation of California sea lion (CSL) (*Zalophus californianus*) fur, meat and oil during the 18th and 19th centuries have consequently fostered a modern population heavily shaped by anthropogenic disruptions. Our study assesses the scale of human impacts by examining the oral microbiomes of CSL over the last ~130 years. Using dental calculus subsampled from CSL held at the Santa Barbara Museum of Natural History and the Smithsonian National Museum of Natural History (n=75), we reconstruct the oral microbiomes of CSL and link microbial diversity within the oral microbiome to anthropogenic alterations to CSL. Metagenomic analysis revealed that CSL have maintained a stable and unique oral microbiome signature that is different from other mammalian species; suggesting that the oral microbiome may be less prone to alterations than observed with the gut microbiome due to diet and environmental impacts. We also identified reads classified to human associated pathogens including *Tannerella forsythia, Desulfomicrobium orale, Neisseria* and *Enterobacteriaceae* species. Investigating antibiotic resistance genes commonly associated with these pathogens in humans will elucidate how anthropogenic disruptions may be impacting the CSL oral microbial diversity over composition. Finally, we regularly recovered CSL host DNA and highlight the importance of studying animal microbiomes for human-animal interactions. Our project provides the first historic study of CSL oral microbiomes and offers a novel approach to use dental calculus as a sentinel for documenting transitioning environmental health and microbial dynamics among humans and animals.

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Evaluating Body Donation Procedures by Comparing Observed and Reported Antemortem Alterations in a Donated Skeletal Collection

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Donated skeletal collections (DSCs) are vital for research in biological anthropology, but the question of whether or not DSCs are representative of local populations or their lived experiences has not been fully explored. The discrete categories on donor background forms may or may not capture the multifactorial and cumulative biological effects of an individual's behavior. In contemporary DSCs, the associated biographical information of a donor represents an individual's life history for the purposes of future research. During next of kin (NOK) donation, narrator reliability regarding the biographical information may vary, i.e., perception, memory, and significance of life events, may differ from what the individual themselves or a skeletal analyst recognizes. This pilot study examines the consistency between observed and reported antemortem alterations of ten individuals donated to the Louisiana State University Forensic Anthropology and Computer Enhancement Services (LSU FACES) Laboratory. The purpose of this comparison is to determine how the lived history of the donor can be captured most accurately when communicating with the NOK. When assessing the donation documentation for degree of completion (i.e., any acknowledgement of a category, even "unknown"), the NOK completed an average of 94% of the categories. However, preliminary results indicate that antemortem fractures were underreported for 90% of the donors, while surgeries were underreported for only 30%. Oral pathologies were not fully characterized for 80% of donors. Consequently, nascent changes to the donation process should expand these sections of the donation documentation to more thoroughly prompt the next of kin during accession.

Kaye Reed's impact on paleoanthropology: a network analysis

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Kaye Reed is a leading expert in hominin paleoecology. She has contributed extensively to reconstructing the environmental parameters of African Plio-Pleistocene hominin localities, and is one of the few women in our field to build a major research project from the ground up. Here, we use citation network analyses to both assess and visualize the widespread influence and impact of Kaye's work on our field.

Citation network analyses can be used to analyze and visualize the impact of specific authors or themes on a discipline. In this study, we use both CitNetExplorer and Gephi to analyze publication lists derived from Web of Science and Google Scholar. We explore themes of research most associated with Kaye's work, and illustrate the impact of her major scholarly contributions through visualizations of the citation networks created as scientists in our field cited her expertise.

Results suggest that the primary themes associated with Kaye's research include multivariate approaches to primate and mammalian communities, her work at Ledi-Geraru, and dietary adaptations of fossil species. Her most-cited works include analyses of major paleoecological patterns across the African Plio-Pleistocene as well as critical evidence for the environmental contexts of the evolution of bipedality. The impact of Kaye's work is deeper, however: she often publishes with women scholars and has been a key collaborator with her students since she began her career. Our field is more diverse because of Kaye's mentorship and collaborator networks, and our network analysis illustrates her profound impact on the study of our ancestors.

New Theropithecus fossils from Woranso-Mille (3.5–3.33 Ma): their implications for the evolution of the lineage

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The 3.5–3.3 Ma Woranso-Mille horizons have provided diverse hominin species and abundant cercopithecid materials. We focused on the 178 craniodental specimens allocated to*Theropithecus*, which comprises nearly 80% of cercopithecids identifiable below the family level, and includes a well-preserved partial cranium, maxillae, mandibles, and isolated teeth. We compared these to *T. o. serengetensis* (Woranso-Mille, Galili, Laetoli),*T. o. darti* (Hadar, Dikika, Maka, Koobi Fora, Makapansgat), and *T. o. oswaldi* (several sites). Qualitative and quantitative comparisons were employed. While generally similar in size and morphology to crania from Hadar and Dikika, the Wornaso-Mille cranium has six features previously identified as specific to Makapansgat. The mandibles are similar to those from Hadar and Dikika in the absence of mental protuberance and symphyseal slope, and variable presence of mandibular fossae and mental ridges. They are distinct from Hadar, Dikika and Makapansgat in having a flat curve of Spee. Molars from 3.5–3.3 Ma Woranso-Mille horizons are more derived and larger than those of *T. o. serengetensis*, but comparable to those from Hadar, Dikika, Maka, and Koobi Fora. On the other hand, the 3.5–3.3 Ma Woranso-Mille *Theropithecus* mandibles are not significantly different from *T. o. serengetensis* in breadth and depth at M_2/M_3 contacts. Overall, the Woranso-Mille *T. o. darti* fits the pattern in molar morphology, size and relative breadth observed in the *T. oswaldi* lineage given its age. Furthermore, cranial material from Woranso-Mille shares features with both the Hadar and Makapansgat, suggesting more variation in these features within populations of the subspecies.

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East African bovids show specialized molars to feed on a wear-inducing diet during the late Pliocene

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In many herbivore ungulates, increased molar crown height is among the major functional dental adaptations geared towards increasing the durability of teeth against wear-inducing diets and grits that are more abundant in open habitats. Here, we employed the Hypsodonty Indices (HI) of bovid molars to interpret paleoenvironments of hominin-bearing sites in eastern Africa. Although our result shows a positive isometric scaling between molar width and length, we used the ratio of height to width for comparability with published data. HI score of bovid tribes from the Hadar and Shungura Formations is compared with published HI data from Kanapoi and extant bovids. The result shows that most of the modern grazing bovid tribes fed on wear-inducing diets starting from the late Pliocene. Bovids from Kanapoi were browse-dominated mixed feeders, whereas most of the Shungura bovid tribes were mainly grazers like their extant representatives, save for Tragelaphini, which was consistently mixed feeder. Most of the Hadar bovid tribes are slightly less hypsodont than the Shungura bovids, and hence, were grass-dominated mixed feeders. For example, the tribes Bovini and Reduncini, at least in our sample, became hypsodont after the late Pliocene. Moreover, our result suggests that caution must be exercised for tooth-wear stages when using HI and when employing actualistic approaches to interpret past environments. We speculate that, in addition to many other adaptations, similar dental specializations in Plio-Pleistocene hominins may have been used as strategies to cope with the adaptive challenge of venturing into wear-inducing open habitats.

Prestige in chimpanzees: learning through social relationships across the lifespan

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Henrich and Gil-White (2001) proposed that humans possess a form of status, termed prestige, that evolved alongside dominance status under selection pressures generated by opportunities for selective cultural learning. Here, dominance is based on the control of force and coercive threat, while prestige arises from informational asymmetries based on differences in knowledge, skill and expertise. Recent studies suggest other animals who rely on social learning during their long, slow lives may have evolved forms of prestige status. Drawing on 60 years of published chimpanzee research and our own observations at Ngogo, in Kibale National Park, Uganda, we demonstrate how chimpanzees' investment in certain relationships appear to reflect a dynamic of prestige instead of dominance or two other alternatives, reciprocal exchange and caregiving. We present supporting evidence from published work on chimpanzees, and propose future investigations into each of Henrich & Gil-White's (2001) predictions that: 1) distinguish the dynamics of prestige in dyadic interactions from those of dominance, exchange, and caregiving, and 2) indicate prestigious individuals in these dyads are more knowledgeable than those who defer to them. We then empirically test a subset of these predictions using an available dataset of adolescent and young adult males (n = 30, age 9-20 years) who form social relationships with other mature males at Ngogo (n = 58, age 9-55 years). We show that adolescent and young adult males' relationships with relatively old, past-prime males, sometimes referred to in the literature as "mentors," reflect prestige rather than dominance, exchange, or caregiving dynamics.

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Solutions to the Nomenclatural Muddle of the Middle Pleistocene

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Recently, the taxon *Homo bodoensis* Roksandic et al., 2022 was proposed for Chibanian hominins from Africa with the Bodo specimen as the type and including Kabwe and Saldanha in the hypodigm. The proposal provides an alternative to *H. rhodesiensis*, a toponym burdened by colonialist history. The *bodoensis* proposal met criticism on two fronts. First, the International Code on Zoological Nomenclature (ICZN) does not have a mechanism for suppressing taxonomic names that are politically or culturally inappropriate. Secondly, the Saldanha skull is also a type specimen bearing the name *Homo saldanensis* Brennan 1955, and this name also has priority over *H. bodoensis* if *H. rhodesiensis* is bypassed.

This paper evaluates solutions to these nomenclatural challenges. A comprehensive list of over 200 hominin nomina was compiled from the Origins online database, and 32 nomina were identified as relevant to the *Homo heidelbergensis* debate. A review of each name based on the original literature indicates that 6 are nomina nuda or otherwise unavailable, 5 are available but objectively invalid and 21 are potentially valid. Furthermore, Africa is found to be the region where priority of names is most sensitive to the specific composition of the hypodigm because there are many type specimens. I argue that *H. rhodesiensis*, should be avoided on ethical grounds, and depending how the hypodigm is construed other names have priority over *H. saldanensis*. Finally, I suggest a mechanism, under the rules of the ICZN, whereby a List of Available names can be established to ensure nomenclatural stability going forward.

Comparison of the trabecular development within the juvenile human distal tibia and talus

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There is an increasing understanding of ontogenetic changes in trabecular bone, nevertheless, gaps in our knowledge remain. By comparing two anatomically different bones that share similar locomotive demands, we aim to investigate how developmental and biomechanical factors interact. We hypothesise that the talus and distal tibia will share a developmental trajectory until the acquisition of the bipedal gait, after which the trabecular architecture will diverge to adapt to forces.

Thirty-three pairs of articulating distal tibia and tali from the Scheuer Collection, ranging from 28 intrauterine weeks to 8 postnatal years, were microcomputed tomography scanned. Scaled volumes of interest (VOIs) were placed within the distal tibia and talus. Within each VOI, anisotropy, bone volume fraction, trabecular thickness, trabecular separation, trabecular number, and structural model index were quantified. Mann Whitney-U tests and Independent T-tests were used to compare trabecular parameters between the distal tibia and talus. Additionally, bone volume fraction and anisotropy vector fields were mapped.

Our hypothesis was rejected. All trabecular parameters, except anisotropy, share a developmental trajectory within the distal tibia and talus. Tibial anisotropy was statistically significantly higher than talus anisotropy. Prior to the onset of the bipedal gait, it is postulated the talus is more isotropic due to differences in ossification patterns. Once the bipedal gait has developed, the transmission of weight-bearing forces likely results in the differences in anisotropy.

Overall, this research provides insight into how different trabecular parameters respond to developmental and biomechanical factors during development, adding to our growing knowledge of trabecular ontogeny.

Variation in body composition in relation to evolutionary models of human thermoregulation

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Anthropologists widely attribute climate adaptation in human shape to Bergmann's and Allen's rules, which state that differences in skin surface area relative to body volume (SA/V ratio) will affect the body's thermoregulatory abilities. However, the volume of the human body is heterogeneous, with various tissues (e.g., bone, muscle, fat) having disparate thermoregulatory properties. Furthermore, human body composition is sexually dimorphic, with females consistently exhibiting higher adiposity across populations. Therefore, differences in body composition may have played an underappreciated role in human thermoregulatory evolution. Accordingly, this project tested the hypothesis that body composition varies independently from SA/V ratio. Eight participants (4M, 4F) were imaged using whole-body computed tomography (CT). Then, body surface area, total body volume, and body composition (i.e., fat, lean, and bone volumes) measurements were extracted from each scan using Avizo 3D software. Total volume was significantly correlated with lean (R^2=0.581, p=0.027) and bone volumes (R^2=0.580, p=0.027) but not fat volume (R^2=0.074, p=0.512). Additionally, fat represented a substantially larger percentage of total volume in females ($\bar{x}$=42.4%) compared to males ($\bar{x}$=28.8%). These results indicate that increases in total body volume involve disproportionate increases in bone and lean volumes compared to fat, and support sex-based differences in body composition. Consequently, the findings of the current study do not support the assumption that body composition is uniform. Given the differential thermoregulatory properties of various body tissues, failing to account for such variability in internal body composition may contribute to overly simplistic interpretations of thermoregulation within evolutionary contexts.

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Exploring the preservation and etiology of ossified thyroid cartilage in the bioarchaeological record: A case study of four individuals buried at the Roman necropolis of Histria, Romania

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The ossification of thyroid cartilage is a documented medical phenomenon, but medical and archaeological sources disagree about its prevalence in human populations. Medical literature presents it as a natural part of the aging process, and in modern forensics research, the degree of ossification of the cartilage surrounding the larynx has been used to assess chronological age of human bodies, though with low precision.

Despite the claim in medical studies that ossification of thyroid cartilage is common, it is rarely discussed in bioarchaeological literature. It is infrequently included in the identification of bones in Human Osteology courses and when ossified cartilage is identified in the archaeological record, it is categorized as abnormal or unusual. The disagreement between medical and archaeological sources may be due to the fragility of ossified cartilage and its poor preservation in bioarchaeological contexts or an imperfect understanding of the prevalence and etiology of this phenomenon in living populations.

This study presents an osteological case study from the Roman necropolis at Histria, Romania (1st-6th centuries CE). Of the 10 adult articulated skeletons excavated from 2018 to 2023, four individuals had well-preserved ossified thyroid cartilage. Three of these individuals were interred in a monumental stone cist tomb containing the remains of at least 18 people, perhaps representing a family group. This study will explore different expressions of ossified thyroid cartilage in the bioarchaeological record, investigate contributing factors such as genetics, disease, and age, and provide criteria for future identification and application of the presence of ossified thyroid cartilage.

Sleep habits and their drivers: a cross-cultural ethnographic survey across small-scale societies

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Human sleep patterns are influenced by a complex interplay of biological, social, and environmental factors. However, our understanding of sleep has been primarily derived from controlled clinical settings, often lacking cultural context. To address this gap and gain insights into the cultural dimensions of sleep, we conducted a comprehensive cross-cultural ethnographic survey using the Human Relations Area Files and related sources, examining sleep behaviors across small-scale societies. Our search identified 1,191 ethnographic paragraphs related to sleep from 143 different cultures across nine geographic regions. These paragraphs were coded for evidence related to ecological factors (both physical and social), cultural perspectives, and sleep habits. Our findings revealed widespread evidence of co-sleeping within small-scale societies, with nuclear family co-sleeping observed in 70% of cultures and extended family co-sleeping in 92%. Additionally, we observed a diverse range of mixed-age and gender sleeping arrangements. Daytime napping was a common practice, with 92% of paragraphs supporting its occurrence (<1-h in duration). The timing of sleep was influenced by various ecological factors, such as safety against predation (81%), sunrise (69.5%), sunset (51%), and work-related activities. This cross-cultural survey highlights the profound influence of social, ecological, and economic factors on sleep habits. These findings underscore the importance of integrating cultural perspectives into the study of sleep behaviors, with sleep presenting as a dynamic and multifaceted aspect of human life.

The Human Extended Lifespan – an Endocrine Hypothesis

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The modern human lifespan is 25-35 years longer than those of the longest-living great apes, our nearest primate relatives. Humans have an approximately 33 year plateau of near-constant low mortality upon entering the reproductive phase and we contemplated that consistent somatotrophic hormones and growth factors may be responsible. We propose that the low rates of mortality plateau is due to the larger volume of the hypothalamus which dictates activity of the endocrine system. We used published data to compare the relative volumes of hypothalamus and, as controls, whole brain and cerebellum of humans (Hs), chimpanzee (Pt), and gorillas (Gg). Hypothalamus: Hs to Pt x2.1; Hs to Gg x1.6. Cerebellum: Hs to Pt x3.15; Hs to Gg x1.99. Brain: Hs to Pt x3.28; Hs to Gg x2.66. Doubling the number of hypothalamic neural stem cells could maintain the activity of the hypothalamus-pituitary axis, ensuring long-term health of the other endocrine organs and soma. We plotted published cranial volumes from over 60 hominin fossils using whole brain volume as a proxy for hypothalamus volume; we performed linear regression analysis ($r^2 > 0.83$) to identify the evolutionary trend in increased brain volume over time. A simple model of the predicted size of the hypothalamus since 3.3 million years ago (Mya) (australopithecines: mean 457 ml) suggested that that region of the brain was approximately doubled by around 1.3 Mya (predicted cranial capacity about 914 ml) at the *Homo erectus/heidelbergensis* transition and we speculate that the plateau of extended lifespan to have begun by then.

Mysterious drops in preterm birth and overmedicalization of childbirth: Reflections on the COVID-19 pandemic

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Preterm birth rates in the United States (U.S.) have steadily increased over the past few decades; however, there was an unexpected decrease in the first few months of the COVID-19 pandemic. Compared to other developed countries, the U.S. has poor metrics of maternal care, including high rates of maternal mortality, and majority-centered care that often disadvantages marginalized communities. This study incorporated both quantitative and qualitative methods to analyze if any hospital policies, behaviors, or care changes may have contributed to this decrease in preterm birth. Our analyses of nationwide birth outcomes showed the largest decrease among induced preterm births (OR=0.917, p<0.0001) in April through June of 2020 relative to the same period in 2019, but no significant change among spontaneous preterm births (OR=1.01, p=0.3908) during this time. To contextualize these trends, we interviewed obstetricians and midwives who were practicing in various urban and rural locations during the pandemic, across the East and West Coast. We found that the most commonly mentioned explanation for the decrease in preterm inductions was reduced access to in-person prenatal care. While the pandemic lockdown may have led to missed indicators for preterm birth, it also may have prevented over-prescription of preterm inductions for lower-risk pregnancies. This study leveraged the natural experiment of the pandemic to explore larger issues around over-medicalization of childbirth and how convenience and fear of litigation are potentially prioritized over long-term outcomes for the mother and child in the American medical system.

Assessing the concordance between IUCN species distributions for *Nycticebus* and community science sightings: A comparative analysis

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Community science is a collaborative approach to scientific research in which members of the public, often individuals without formal scientific training, actively participate in various stages of the scientific process. Data collection could include sightings, species identification, and habitat quality. The aim of this study is to conduct a comparative analysis to assess the association between International Union for Conservation of Nature (IUCN) species distribution data and community science sightings (using the iNaturalist platform) for *Nycticebus*, a genus of slow lorises that is a primate of conservation concern. Here, we compare IUCN species distribution ranges for eight *Nycticebus* species to 429 crowd-sourced community science species sightings taken from iNaturalist. We found that the percentage of community science sightings falling outside the IUCN species ranges varied from 0% to 33% with a mean value of 9.83% ± 12.67% SD. However, five species of the total eight species had 100% agreement between sources. The study results emphasize the valuable contribution of community science to scientific data collection efforts. However, they also raise questions about its reliability, especially when considering species-specific factors. Different loris species exhibit distinct behaviors, occupy specific ecological niches, and inhabit various habitats. Therefore, when integrating community science data into research, researchers should consider combining community science with other methods, selecting a reputable community science source, and thoroughly evaluating their data collection protocols. Findings from this analysis will enhance our understanding of the distribution of these elusive primates and contribute to more effective conservation strategies.

Surveying and Genotyping an Insular Population of Dwarf Lemur (*Cheirogaleus*) from Northwestern Madagascar

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In the summer of 2022, we surveyed a cryptic population of dwarf lemurs on the uninhabited island of Nosy Hara, located off the northwestern coast of Madagascar. This population came to the attention of scientists in 2015, when two naturalists on a pleasure trip photographed the animals and published a physical description. Our survey of the island confirmed the presence of these animals with additional photographic evidence and collected fecal and hair samples for DNA extraction and sequencing. This genetic material will be compared to other dwarf lemur populations on the mainland to determine the taxonomic status of the Nosy Hara population. Observation of these animals *in situ* confirmed the earlier report that they are considerably smaller than other surveyed dwarf lemur species and may therefore be under the effect of insular dwarfism. We also observed limited dietary behavior, with a notable preference for trees in the genus *Delonix*. Dwarf lemurs at Montagne d'Ambre National Park (*Cheirolgaleus andysabini*) are the closest identified population to these animals geographically, although previously closer populations extirpated by ecological changes or other factors cannot be discounted. The notable observed size variation between island and mainland populations indicates a likelihood of significant time isolated on Nosy Hara. While not ruling out a human introduction at some point in the past, this phenotypic variation makes that scenario less likely than other means of distribution such as over-water dispersal or isolation by rising seas at the end of the last glacial maximum.

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Exploring the Ecological Context of Female Drug Use in the Ethnographic Record: Roles of Gender Inequality, Fertility, and Famine

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Cross-national data indicate a near-universal male bias for drug use, but the extent to which this holds cross-culturally is unknown. Conventional explanations for low female use highlight gender inequality, whereas evolutionary perspectives highlight the neurotoxic effects of drugs on the developing central nervous system. Evolutionary theories also highlight pathogen and/or food stress, but how these relate to female drug use is undetermined. We examined the ethnographic record for patterns of female drug use to inform evolutionary and cross-cultural debates. Using the electronic Human Relations Area Files, ethnographic descriptions of drug use were recorded and scored on 96 uniquely created demographic and cultural variables for each of the 186 Standard Cross-Cultural Sample populations, resulting in 1,396 cases of drug use across 176 cultures. Bivariate tests of association and logistic multilevel mixed-effects models were used to examine associations between female drug use and cultural, political-economic, and environmental variables. Results support a male bias in evidence for drug use in that the proportion of documents containing evidence for female drug use was significantly lower than that for males. Controlling for male drug use, the odds of female drug use decreased as male dominance and female empowerment increased, and the odds increased when the drug was shared, used in courtship or sex, and/or used medicinally. Famine threat also emerged as a potential risk factor for female drug use, whereas fertility and pathogen stress had no effects. These results provide important ecological context to cross-cultural patterns of female drug use.

Neanderthal Teenagers: Puberty, Growth Spurts and Adolescence?

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Adolescence is a complex phase of the current human life cycle, where major biological and social transitions occur, leading to adulthood. It is the only life stage whose human uniqueness is still discussed in the paleoanthropological literature, with research focused on two defining features, the growth spurt in skeletal tissue and its late occurrence. A comprehensive study of adolescence would include dental, skeletal and somatic maturation, as well as size measurements, recorded in a longitudinal sample, a scenario beyond the hominin fossil record. However, advances can be made in this direction. As an example, we present here the Neanderthal remains from El Sidrón site (northern Spain), whose individual maturation stages would place them in the adolescent stage by modern human standards. These remains include dental, cranial and postcranial remains (vertebrae, scapula, humerus, ulna, metacarpals, femur, metatarsals and hand and feet phalanxes). The combinations of dental and skeletal maturation stages observed with the measured size and percentage of adult size, would indicate that we could not differentiate between modern human adolescents and these Neanderthals. The inferences and limitations that can be drawn from these findings are discussed considering the biological and social complexities of adolescence and the paleobiology of Neanderthals.

Neanderthal pelvis: implication of different reconstructions

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The pelvis is a key structure for understanding human locomotion, posture, thermoregulation, and obstetrics. In Neanderthals, the only nearly complete pelvis comes from the Kebara 2 individual (Israel). However, the pelvis is taphonomically distorted and shows signs of asymmetry. Therefore, multiple attempts of reconstruction have been performed, but none of them has sufficiently addressed the taphonomic defects of the sacrum and the left hipbone. Here, we present a new reconstruction attempting to correct for the taphonomic distortion of the sacrum and accounting for pelvic asymmetry. Simultaneously, we analyze all the reconstructions in comparison with a large dataset of extant and fossil samples using geometric morphometric methods. In general, all Kebara 2 pelvic reconstructions converge to a very similar morphology except for their differences in the longitudinal curvature of the sacrum and sacral position within the pelvis. Our analysis mostly confirms the proportional differences in the Neanderthal pelvic morphology that have first been described by Yoel Rak, such as laterally flared ilia, long superior pubic ramus, laterally oriented acetabulum, short ischium, and a more anteriorly positioned sacrum. The overall shape of the Kebara 2 pelvis falls within modern male variation. However, focusing solely on the pelvic inlet/canal shape, the specimen clusters closer to the modern female variation due to the relatively long pubic segment. To better understand the biological aspects related to pelvic morphology, our results call for further analysis of sexual dimorphism of Neanderthal pelvic remains.

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An analysis of the mandible of *Troglodytes kooloo-kamba*; a purported chimpanzee-gorilla hybrid

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Hybridization in primates has long been a topic of interest. While on an expedition in the Ashankolo mountains, Gabon, in 1861, Paul Du Chaillu shot and killed a male adult ape which was known to the local Goumbi as "Kooloo" because of its distinctive call. Du Chaillu collected the skin and skeleton of specimen and declared it a new species, largely due to its distinctive call. Craniofacially, the specimen was described as having a large supraorbital ridge, high zygomatic ridges, decreased prognathism, 'unique' incisors, and a larger cranial capacity compared to common chimpanzees. While Du Chaillu described the specimen as a new species of chimpanzee he named *Troglodytes kooloo-kamba*, other researchers in the late 1800s and early 1900s purported that kooloo-kamba was a hybrid between a chimpanzee and gorilla.

Subsequently, many “questionable” specimens in zoos and museum collections were suggested to be examples of chimp-gorilla hybrids and were referred to as Du Chaillu’s kooloo kamba.

Here, we present microCT scans of the *T. koolookamba* specimen hunted by Du Chaillu, and show that while the specimen is pathological, geometric morphometric analyses on the mandible clearly group it with chimpanzees. Through the 1990s, *Pan troglodytes koolokamba* was suggested to be a rare subspecies of chimpanzees that lived in the mountains of Gabon and surrounding countries. Our results suggest that the mandible of the Du Chaillu’s specimen is most similar to *P. t. troglodytes* and *P. t. verus*, although larger samples are needed to determine which subspecies it groups best with.

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Paleoecology of the Hadar carnivore guild: New insights from enamel stable isotopes

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The Pliocene Hadar Formation at Hadar (Awash Valley, Ethiopia), spanning approximately a half-million years (~3.45-2.9 Ma), has yielded a rich paleontological record, including many fossils of the hominin species *Australopithecus afarensis*. The paleoecology of the Hadar Formation has been approached from community ecology, paleosol analysis, and herbivore and primate enamel stable isotopes. Less attention in these reconstructions, however, has been paid to the interaction of carnivorans with potential prey in the Hadar Formation fauna. Here we investigate predator-prey dynamics based on stable carbon and oxygen values that allow reconstruction of the paleoecology of the carnivore guild at Hadar. Overall, the members of the Hadar carnivore guild have relatively high carbon values (-4.6 ± 1.4‰), with the highest values indicated in the middle part of the sequence of the Denen Dora Member. These values are similar, but slightly higher than the carbon values of carnivores from penecontemporaneous sediments in the Turkana Basin (-5.5 ± 0.4‰; southern Ethiopia and northern Kenya). Oxygen values are variable though the Hadar Formation, but reconstruction of estimated meteoric water oxygen values indicate a wetter and more pluvial climate than the present. Understanding the paleoecology of the carnivore guild at Hadar allows us to predict which taxa may have been in direct or indirect competition with hominins, offering insights to the selection pressures and evolutionary patterns of Plio-Pleistocene hominin evolution in eastern Africa that cannot be inferred from paleoenvironmental reconstructions alone. Moreover, our analyses provide a valuable insight into the little-known isotopic ecology of extinct African carnivores.

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Toddler gestural accommodation in Portuguese nursery schools

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Adult humans accommodate their speech and gestures when communicating with young children (aka: ‘motherese’, ‘child-directed communication’) by using simpler vocabulary, a slower tempo, and more prominent communication. A species-typical phenomenon, it nevertheless shows flexibility and cross-cultural variation in its expression. Research to-date has focused on accommodation in spoken languages and in adult-infant interaction. Some evidence suggests young children can adapt their speech in similar ways to the patterns described in adult child-directed speech. However, before the predominance of speech, young children employ diverse sets of gestures – including those that overlap with the gesturing of other apes. To what extent toddlers adjust their early gestural communication remains unknown. We investigated whether toddlers accommodate their vocabulary complexity, tempo, and the prominence of their gestures to their partner’s age. We compared toddlers’ adult-directed and peer-directed gestures, then examined fine-grained adjustment to younger and older peers. Video data from 53 toddlers (410-1080days, 27boys) were collected during free play time in three Portuguese nursery schools. Toddlers adjusted vocabulary complexity and the temporal patterns of their gestures to the recipient’s age but did not change their prominence. Toddlers communicated with younger peers at a slower pace and using simpler vocabulary, following child-directed communication patterns. However, contrary to predictions from speech, toddlers used more diverse and shorter gestures to peers, as compared to adults. Our findings show our ability to accommodate communication emerges before language fully develops, and the ability to accommodate flexibly, in consequence of their social partners intersecting features, may have deep evolutionary roots.

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Bonobo bromances, bonobo frenemies: How do sociosexual behaviors vary in male-male bonobo relationships?

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Bonobo (*Pan paniscus*) sociosexual behavior gets a lot of attention. However, despite this attention, there is far more research on the function of these behaviors among female-female dyads compared to male-male dyads. Here, I present data on patterns of male-male sociosexual behaviors in a captive group of bonobos, and consider why these relationships have been overlooked. Data was collected at the Columbus Zoo on bonobos living in a managed fission-fusion social structure. Using Multiple Regression Quadratic Assignment Procedure (MQRAP), which controls for covariation of behavioral matrices, I compared patterns of male-male sociosexual behaviors compared to overall group patterns. Sociosexual behavior was treated as the dependent variable, while agonism, grooming, and huddling were set as predictor variables. Among the full group, huddling significantly predicted sociosexual behavior (r=0.8106, p=0.002, N=11, 1,000 permutations). However, among males, only agonism (r= 0.6191, p=0.012, N=6, 1,000 permutations) significantly predicted sociosexual behavior. I consider why these findings differ, particularly in the context of triadic interactions and reconciliation, and what they mean for understanding male-male social relationships. I further consider the cultural biases that shape our research on bonobo sociosexual behavior, and how this may lead to male-male sexuality being overlooked.

Body mass estimation based on bi-iliac breadth and femoral head diameter

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Body mass is an important biological parameter for understanding the evolution and life history of humans and has the potential to aid in positive identification in medicolegal death investigations. This study investigates the accuracy of the stature-bi-iliac breadth (ST-BIB) method by Schaffer and the femur head diameter (FHD) equations by Ruff and colleagues. Skeletal remains with documented stature and body weight from the Texas

State University Donated Skeletal Collection were used and include 333 individuals (135 female and 197 male) ranging in weight from 32.6 to 219.0 kg (with n=165 "high" BMI [pre-obese/obese]).

As expected, both methods underestimated the body mass of high-BMI individuals by 45.1 kg and 42.5 kg for the FHD and ST-BIB, respectively. Individuals with a moderate BMI between 18.5 and 24.9 were also underestimated by both methods by an average of 4.94 kg for FHD and 5.8 kg for ST-BIB. Both methods overestimated the body mass of low (>18.5) BMI individuals by 19.89 and 20.36 kg for FHD and ST-BIB, respectively. Interestingly, the differences in the estimates for all BMI categories are not statistically different between the methods. Both methods are relatively accurate for individuals with a moderate BMI, but significant deviations occur for higher and lower BMI category individuals. Because FHD requires a single measurement and ST-BIB requires measuring pelvic breadth and estimating stature, FHD equations are preferred. Methods of determining BMI status from the human skeleton are needed in order to improve the accuracy of body mass estimates in a modern U.S. population.

First known cervical vertebrae of *Shoshonius cooperi*: implications for omomyoid relationships

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Shoshonius cooperi is the only known species of fossil primate with orbital hypertrophy relative to cranial size similar to extant tarsiers. *Shoshonius* and tarsiers also share a shortened rostrum, ventrolaterally located posterior carotid foramen, and basioccipital flange overlapping the bulla. These features have been interpreted as evidence that *Shoshonius* is a stem tarsiiform. Conversely, extant tarsiers and anthropoids share derived cranial features that are not present in *Shoshonius*: a postorbital septum, an anterior accessory cavity, a perbullar course for the promontory artery, reduction or loss of the stapedial artery, and loss of an olfactory recess and numerous olfactory turbinals. Postcranially, *Shoshonius* lacks derived features of tarsiers associated with vertical clinging and leaping. Here we describe the first known cervical vertebrae of *Shoshonius*: the axis and two lower cervical vertebrae. These elements provide evidence that *Shoshonius* lacks derived morphology associated with high neck mobility seen in tarsier cervical vertebrae. The spinous process of the axis of *Shoshonius* is mediolaterally compressed and craniocaudally expanded, closely resembling cheirogaleid lemuriform morphology, and unlike the mediolaterally expanded and craniocaudally compressed spinous process of a tarsier axis. The lower cervical vertebrae of *Shoshonius* have zygapophyses oriented intermediate to the transverse and coronal planes, more comparable to cheirogaleids and other lemuriforms, and unlike tarsier zygapophyses that are oriented subparallel to the transverse plane. The gross similarity between the cervical vertebrae of *Shoshonius* and quadrupedal lemuriforms adds further support to the hypothesis that *Shoshonius* is more likely a stem haplorhine than a stem tarsiiform.

Effective Primate Conservation Requires a Focus on Human Well-being: The Importance of Evaluating the Consequence of Protected Areas on Human Happiness

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Effective primate conservation is inextricably linked to the happiness and well-being of people living in and around conservation areas. Historically, conservationists have focused on a narrow range of externally defined socio-economic proxies for human well-being, failing to provide the affected population with the opportunity to assess their own life and connection to conservation interventions. If conservation area assessments do not faithfully detect the complex nature of human well-being, conservation practices may be misaligned with the core objectives of conservation and detrimental to human livelihoods. To address this concern, we performed a human-impact assessment of Kirindy Mitea National Park, Madagascar, home to multiple endangered lemur species, and documented an alarmingly high incidence and intensity of poverty (n = 594 households). Human well-being was low, but the link between poverty and human well-being was not as strong as anticipated, indicating that human well-being is not solely determined by socio-economic factors, even among the most impoverished communities. Notably, most people did not connect their socio-economic standing or overall well-being to the park. While our findings provide reassurance that conservation areas may not be the primary cause of poverty and reduced well-being locally, our study highlights substantial human costs associated with stringent environmental protections, and illustrates the importance of integrating assessments of human well-being together with socio-economic evaluations of conservation areas. Our approach not only safeguards the interests of local communities, but also helps to ensure that the goals of primate conservationists are met without compromising the happiness and well-being of the people involved.

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Genomic Insights from Buca del Corno: Exploring Copper Age Burials in Central Italy

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Buca del Corno (BDC, Lucca, Italy) is a karst cavity used as a collective burial. The site returned the remains of six adults and four children, along with several artifacts, in a chaotic assemblage due to natural displacement by water. The radiocarbon dating allows us to consider the burials restricted to the Copper Age (3576-3461 calBP, int cal20). The ornaments and metal artifacts are generally comparable to coeval and similar findings in the Italian peninsula. However, some necklace elements represent a rare example of processing raw aragonite in Italian coeval communities. The sampling on the teeth allowed us to generate whole-genome data for all samples, reaching a coverage ranging from 0.0001X to 0.0145X. Despite the diagenesis impacting the DNA preservation, strict quality control allowed us to obtain over 10,000 SNPs shared with the 1240k variant panel for two individuals. Principal Component Analysis and Admixture models allow for comparing BDC and the Southern Europe Copper Age communities, focusing on the few Copper Age genomic data for the Italian Peninsula. In that perspective, our findings underline the significance of this site in the evaluation of the regional demographic history, focusing on a genomically under-explored time transect of Italian Prehistory. Our results pave the way for the deeper evaluation of putative long-haul people movements occurring in the geographical area in that prehistoric period.

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Dental shape complexity in Eastern chimpanzees and bonobos

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Chimpanzees occupy a wide range of habitats across sub-Saharan Africa. Previous studies have used molar morphometrics to infer phylogenetic distances in chimpanzee subspecies. However, little is known about ecogeographic factors influencing molar complexity among closely related *Pan* species. Here, three-dimensional (3D) topographic metrics were used to compare occlusal surface shape patterns of the first lower permanent molars between wild-caught eastern chimpanzees (*Pan troglodytes schweinfurthii*, *n*=39) and bonobos (*Pan paniscus*, *n*=38) of known geospatial origin from Democratic Republic of Congo. Analyses were limited to infant individuals with no dentine exposure. Tooth meshes were generated from high-resolution polyurethane replicas with a Shining 3D® structured-light scanner and post-processed (Geomagic®) for smoothing and cropping using the basin cutoff method. The R package 'doolkit' was used to calculate the relative crown height (occlusal relief), surface curvature (area-relative curvature) to estimate tooth sharpness and inclination to collect the flat/steep variation of the tooth surface. Variance and regression analyses were used to determine the between-species differences in metrics and covariations with specimen location. Results show significant different occlusal topographic features between species. *Pan t. schweinfurthii* showed lower crowned molars with sharper and more complex crenulated occlusal surfaces, despite geographical variation. Instead, *Pan paniscus* exhibited steeper surfaces and taller rounded cusps, showing a larger amount of dental-shape variation with less complex smoother surfaces as geographical longitude decreases. Our findings denote relevant aspects of occlusal morphological variability across geography in eastern chimpanzees and bonobos, raising questions about phenetics and diet-related functional shape significance in great ape molars.

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Antemortem tooth loss and craniofacial fluctuating asymmetry in captive olive baboons (*Papio anubis*)

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Fluctuating asymmetry (FA), or random deviations from symmetry arising from disruptions to development, has long been considered a nonspecific indicator of stress across the animal kingdom. However, there are many influences on cranial shape apart from fluctuations that develop throughout ontogeny. Antemortem tooth loss (AMTL) is associated with bone remodeling of the alveolus, potentially causing shape changes to the bone and changes to mechanical strains that can influence other areas of the cranium. Olive baboons (*Papio anubis*) are known to have high rates of dental pathologies and AMTL when compared with other cercopithecoid primates. Therefore, this study aims to detect influences of AMTL on the magnitude of fluctuating asymmetry in a sample of captive olive baboons (n=154). Using 3D geometric morphometrics, FA and AMTL presence/absence by tooth position were quantified and two-way ANOVAs were performed to assess the relationship of FA to sex and AMTL. The results of these analyses suggest FA is present in the sample (p<0.001), and higher in males than females (p<0.001). Further, FA does change with AMTL, especially in the anterior teeth (p=0.02). There is also a steady increase in average FA value with the number of tooth types missing (e.g., incisor, canine, premolar, molar; p=0.02). These results suggest that changes in bone deposition due to AMTL influence levels of FA, and researchers should exercise caution when investigating FA in samples with high frequency of AMTL.

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Can we use iliac flare to infer gut size in humans?

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Pelvic morphology has been used to infer gut size in hominins. However, recent research on modern humans suggests that the relationship between the gut and the pelvis is not straightforward, especially when considering the effects of sex variation. We explored the sex differences in the variation of the iliac flare and its relationship with gut size in humans. The ratio of the lower ilium width to upper ilium width was used to capture iliac flare; this method was adopted and modified from Boyle and Almecija (2018). Intestinal volume was used as a measure of gut size and was obtained using CT volumetry. There is a mild positive correlation (R2=0.25, *p*<0.05) between iliac flare and gut volume in male individuals. There was no correlation between gut volume and iliac flare in female individuals. It seems that the pelvis is responsible for about 25% of the gut volume variation in male individuals but not in female individuals. Differences in the relationship of gut size with the pelvis is more complicated than originally thought, with iliac flare in female pelves seemingly having no relationship with gut size at all.

N/A

Trends in Bioarchaeology: Marginalization studies from 1970 to 2023

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Marginalization is a process of othering impacted by economic, political, or social institutions or environmental conditions (Mant and Holland, 2019). Structural violence is one example of the culmination or interaction of such forces on an individual or group of individuals. Evaluating how bioarchaeologists methodologically and theoretically explore marginalization is crucial to improve our ability in interpreting the embodiment of structural inequalities and our understanding of this process in the past and present. This project seeks to identify trends in bioarchaeological research regarding marginalization to evaluate the current state of such work and directions for future research.

Eleven journals (e.g., *Bioarchaeology International, American Journal of Biological Anthropology*) were selected based on their likelihood to include publications relevant to bioarchaeology. To capture broad temporal trends in marginalization research, articles from 1970 onward were selected. Eighty-nine articles were identified as specifically studying marginalization within a bioarchaeological context. These articles were coded for relevant key words (e.g., marginalization, inequality, discrimination), methodology, theoretical approach, regional focus, and time period.

Results reveal that terminology employed in discussions of 'marginalization' is variable, with terms like 'marginalization,' 'inequality,' and 'structural violence' used interchangeably, for example. Paleopathological observations of stress markers (especially cribra orbitalia and linear enamel hypoplasia) are used most often. Regionally, areas of focus are concentrated in Europe (44%) and North America (21%) with the fewest (0.01%) in the Middle East. While a range of time periods are represented, 66% of studies utilize archaeological samples from periods with written records.

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Using stable carbon and nitrogen isotope values to estimate exposure to agricultural chemicals among green monkeys (*Chlorocebus sabaeus*) in St. Kitts

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This study examines the relationship between stable carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) isotope values and exposure to pesticides among green monkeys (Chlorocebus sabaeus) on St. Kitts. Specifically, of concern is the risk of toxic exposure to pesticides among crop feeding monkeys. Accordingly, we analyzed hair samples from 20 individuals across 10 social groups for $\delta^{13}C$ and $\delta^{15}N$ values and the presence of the insecticides, acetamiprid and methomyl, which are associated negative health outcomes. Given habitat and human interaction types, we placed the groups into three broad categories: "agricultural," "forest," and "settlement." Specifically, those in the agricultural category were predicted to test positive for both insecticides and exhibit high $\delta^{13}C$ values and low $\delta^{15}N$ values due to crop consumption. Of the 9 monkeys in the agricultural category, we detected methomyl in 4 and acetamiprid in 1. Four monkeys in the settlement category were also positive for methomyl, indicating exposure through market foods rather than crop consumption. While $\delta^{13}C$ ($P<0.01$) and $\delta^{15}N$ values ($P<0.05$) were significantly different among categories, $\delta^{13}C$ values were lowest within the agricultural category (contrary to expectations); however, $\delta^{15}N$ values were lowest in this group as predicted. In sum, we found support for predictions regarding agricultural chemical exposure (e.g., methomyl) and stable isotope values (e.g., low $\delta^{15}N$). The application of analytical chemistry for understanding green monkey ecology has promise, but a fuller understanding requires primate observations and ethnographic data. Moreover, this work has implications for human health given similarities in physiology, diet, and exposure to the same agricultural chemicals.

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Do the math or someone will do it to you: Re-strategizing approaches to combating race science

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Race science – a school of thought that claims humans are organized into biological races and that differences among putative races in cognition and behavior are insensitive to environmental intervention – has been subject to a standard critique by mainstream scientists for many decades. The conceptual core of the standard critique has remained unchanged for decades and critics of race science have failed to take aggressive steps to undermine the theoretical foundation of race science. As such, race science has become immune to the standard critique. I argue that countering race science requires going on the offensive and ceasing the production of work that supports race science. I model an offensive posture by undermining one of the key theoretical pillars of race science that has not been subject to formal scrutiny for decades: The within- and between- group heritability framework. Using analytical and numerical models in conjunction with data on secular trends in traits of varying heritability, I demonstrate this framework is theoretically unsound and invalid on its own terms. I also show that it makes plainly absurd claims about the possibility of environmentally induced change in phenotypic traits. I also critically evaluate the data and models used in the standard critique of race science and find that, more often than not, they support the race scientific view of the world. Undermining the production of race science will involve fighting it more aggressively and reforming our own sciences so that we no longer give it support.

Taking a broad view of the evolution of the human pelvis

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Yoel Rak is probably best known among paleoanthropologists for his meticulous descriptions and functional analyses of the cranial morphology of early hominins. However, his contributions to research on human evolution extend far below the skull. Thirty years ago, Rak made an important insight about the pelvic anatomy of australopithecines when he observed that their wider pelvis (compared to extant apes) gave these short bipeds a long stride during hip rotation without requiring much vertical displacement of the center of mass. The fragmentary Nariokotome specimen from Kenya was interpreted as having narrow hips suggesting that pelvic breadth decreased in *Homo erectus*. However, later more complete discoveries (such as the Gona specimen from Ethiopia and Jinniushan from China) tell a different story, as they are also broad, like australopithecines and the later Neandertals. We can now see that throughout evolution, all humans have a relatively broad pelvis. Thus for much of human evolution, this pelvic form probably provided the advantages proposed by Rak as well as reduced energy expenditure during carrying, especially by females (Wall-Scheffler). Evolutionary changes in the pelvis since the origin of obligate bipedalism have been primarily in the anterior–posterior dimension rather than the transverse one. As Ruff has argued, these changes may have enabled the birth of more encephalized neonates through the evolution of rotational birth. As Rak recognized, moderate narrowing of the pelvis only took place in modern humans.

Why all the variation in primate hyoid chain morphology?

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Hyolingual function underlies performance of important behaviors in primates, including feeding and vocalization, but we lack information on variation in the form and function of the hyoid chain in primates and their relatives. We used micro-CT scans to assess evolutionary variation in resting hyoid position, hyoid morphology, and head-neck posture among therian mammals. We ask whether the expanded basihyals, which can be shield-shaped or plate-like, are associated with more incomplete hyoid chains, and if expanded basihyals tend to have more anterior resting positions than more rod-shaped basihyals. Preliminary results suggest covariation between basihyal morphology and hyoid chain completeness evolved convergently among marsupials, chiropterans, and euarchontans, but the resting position of hyoids is clade-specific. Shield-shaped basihyals combined with incomplete hyoid chains is associated with an anterior resting position in euarchontans. On the other hand, marsupials have convergently evolved the expanded basihyal and incomplete hyoid chain, yet their basihyal resting position is posterior the mandible, as in some mammals with rod-shaped basihyals and full hyoid chains. Rhinolophoid bats have shield-shaped basihyals and a full hyoid chain, and their basihyal is anteriorly placed. Manipulation of static head posture in opossums, ferrets, rabbits and macaques also suggests hyoid position is highly sensitive to head-neck posture, although patterns of interspecific variation in hyoid position are still evident despite intra-individual variation associated with head posture differences. Our results demonstrate a nuanced relationship between hyolingual anatomy and resting hyoid position in mammals; multiple lines of evidence are required for inference of hyo-laryngeal anatomy in fossil hominins.

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Consider the Teeth: Assessing the Viability of Dentinal Collagen Preservation for Isotopic Analysis at Phaleron Cemetery (700-480 BCE)

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Carbon and nitrogen stable isotopes from bone collagen and tooth dentin provide an essential window into archaeological population subsistence patterns and can clarify the impact of diet on health outcomes. However, attempts to assess diet from bone collagen at the Archaic Athenian cemetery of Phaleron (ca. 700-480 BCE) have not proved productive due to insufficient collagen preservation and diagenetic change. Teeth, with their higher inorganic component, are much less prone to diagenetic change and preserve better than bone in the same environment. To assess dentin preservation at Phaleron, we measured $\delta^{15}N_{collagen}$ and $\delta^{13}C_{collagen}$ from serial dentin samples of first and third molars from 6 males and 4 females interred in Phaleron Cemetery. Previous study of bone collagen at Phaleron has only yielded six viable results out of 98 bone collagen samples. In contrast, 20 teeth in this study provided sufficient sample for the IRMS - 10 with sufficient preservation to produce serial samples of sufficient quantity and 10 with sufficient preservation for bulk sampling of tooth dentin. From these teeth we have captured longitudinal dietary data spanning from birth through early adulthood that suggest a high degree of variability between individuals. Although tooth dentin only captures part of the life course, we have demonstrated that dentin does have better preservation than bone collagen at Phaleron and is more reliable to sample. Thus, further study of tooth dentin with greater sample sizes is warranted.

Biogeographic evolution of eastern African mammal faunas over the last 6 Myr

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Mammals comprise the bulk of eastern Africa's late Cenozoic fossil record and their diversity and ecological sensitivity provide a key comparative and contextual framework for understanding the evolution of hominins. Here, we provide a quantitative synthesis of eastern Africa's biogeographic evolution over the last 6 Myr through an analysis of fossil mammal communities from three subregions: the Afar of northeastern Ethiopia, the Turkana Basin of northern Kenya and southern Ethiopia, and the Southern Rift of southern Kenya and northern Tanzania. We calculated the Simpson-based multisite dissimilarity index—a beta diversity metric that quantifies species replacement across space (i.e., spatial turnover)—using 500-kyr time bins to measure biogeographic change. We then partitioned the overall regional trend into its functional group components (here, diet and body size classes) to understand the intersection of species ecology and biogeography. We identify a long-term decline in beta diversity over the last 6 Myr, indicating decreasing faunal provincialism. This shift was primarily driven by the loss of endemic species across many functional groups and a growing number of shared grazing species, which closely track the regional expansion of grass-dominated ecosystems. Although grazers exhibit low beta diversity in open environments of the Early Pleistocene, high beta diversity in late Miocene to Pliocene browsers and frugivores occurred in the context of extensive woody vegetation. Through our analyses, we identify several other key aspects of eastern Africa's late Cenozoic biogeographic evolution, providing a new framework for understanding links between environmental change and hominin evolution.

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DNA metabarcoding reveals fine-resolution partitioning of arthropods in a community of cheirogaleid lemurs in Southwestern Madagascar

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Investigating species interactions and coexistence at the community scale is essential to understanding primate communities' ecological and evolutionary histories. However, meta-analyses have found that the data needed to understand community-level interactions are insufficient, with existing studies relying on low-resolution data that do not match the scale in which the organism experiences the environment. This is particularly true for understanding arthropods as a dietary resource in primates, as traditional methods of feeding observations and morphological identification of arthropod fragments in fecal samples have produced coarse-resolution data, preventing investigations of arthropod consumption as a mechanism driving species interactions. We employed molecular techniques of DNA metabarcoding to understand competition for arthropods in a community of lemurs of the family Cheirogaleidae (*Cheirogaleus medius*, *Microcebus murinus*, *Mirza coquereli*, *Phaner pallescens)* located in Zombitse-Vohibasia National Park, Madagascar. We analyzed a subset of 374 fecal samples opportunistically collected from live captured individuals between November 2021 and June 2022. We found arthropod DNA in 99% of our samples across all four species. In total, we recovered 723 unique sequences (barcode index numbers, BINs). These sequences comprised three classes, 17 orders, and 91 identified arthropod families. We found that differences in arthropod dietary niches were primarily driven by vertical space, with an association between vertical space and arthropod dietary niches. The classification of arthropods using BINs provided detailed insight into niche characteristics that investigation at higher taxonomic levels cannot provide, supporting the need for finer resolution data to better understand species interactions in primate communities.

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Exploring the limits of energy expenditure and water turnover in modern, free-range humans

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Humans have unique physiological capabilities to sustain extended bouts of work/exercise in a wide range of environmental conditions. It is hypothesized that the expectant ceiling for human energy and water budgets are dependent on duration, available resources, strategic intake, pacing and environmental conditions. Total energy and water budgets were calculated from the elimination rates of ^{2}H and ^{18}O for ultra-endurance events and other occupational models (N=60, n=21 F, n=39 M). For ultra-endurance events (12-24 h), energy demands were 35±6, 41 and 68±12 MJ/race for Ironman (10.8±1.1 h), Mudslinger 24 (24 h), and the Western States 100 (25.9 h). Total water budgets were 10.8±2.5, 17.2 and 26.8±3.1 L, respectively. In contrast, energy budgets (MJ/24 h) for longer (3-7 days) events/tasks were 18.2±4 (wildland fire management), 18.1±1.6 (Alaska backcountry hunting), 24.7±4.2 (Race Across America, RAAM), 25.6±5.5 (Arctic ski). Total water budgets were 8.1±2.1, 3.6±1.6, 10.2±0.8 and 4.4±1 L/24 hours, respectively. The water budget relative to the total energy demands varied during warm weather scenarios (0.31, 0.39, 0.41, 0.42, 0.46 L/MJ for Ironman, WS 100, Mudslinger 24, RAAM, and wildland fire, respectively). Values were lower in colder environments (0.20 and 0.17 L/MJ for Alaska backcountry hunting and Arctic ski, respectively). These results demonstrate unique variations in the human water:energy budget ratio across different ambient conditions and work intensity/duration and may reflect reliance on evaporative or environment driven thermoregulation, fluid availability and intake behaviors.

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Radial to ulnar strength is an arboreal signal in extant hominids and early hominins

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Reconstructing behavior from fossil postcrania can be challenging because of possible retention of primitive traits of little contemporaneous adaptive value. Long bone diaphyseal structure responds to functional use of the limbs during life, with variation in lower/hindlimb to upper/forelimb strength accurately reflecting changes in locomotor behavior. A.L. 288-1 (*A. afarensis*), StW 573 (*A. prometheus*), and StW 431 (*A. africanus*) have been shown to have humeral strength proportions more similar to those of nonhuman apes than humans, implying significant use of the upper limb for weight-bearing. Here we show that examination of forearm strength proportions can provide more detailed information on locomotor behavior in fossil taxa. Paired radial and ulnar diaphyseal strengths were determined in 94 chimpanzees, 132 gorillas, and 100 modern humans. Based on experimental, anatomical, and behavioral observations, we predicted that climbing would produce particularly large anteroposterior (A-P) loadings of the radius, while the ulna would be subjected to relatively higher loads during quadrupedal knuckle-walking. In accordance with expectations, radial A-P bending/ulnar overall strength is strongly correlated with frequency of arboreal behavior across ecological/behavioral groups of modern African apes. Humans are intermediate in proportions, since neither forearm bone is weight-bearing. StW 431 and 573 show radial/ulnar strength proportions most similar to those of *Pan* and above those of *Gorilla*, and above (StW 431) or within the uppermost range (StW 573) of humans. Since other comparisons strongly support the weight-bearing role of the upper limb in both fossil specimens, this indicates a high frequency of arboreal climbing in these taxa.

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Robusticity and articular shape variation within *Alouatta*

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Skeletal variables and ponderal indices for *Alouatta* samples were compared. Differences were not expected because field studies suggest considerable behavioral variability within taxa. Nonetheless, notable and consistent morphological distinctions were identified.

Data consist of humeral and femoral midshaft cross-sectional properties and articular dimensions from radiographed museum specimens, supplemented by masses and head-body lengths from additional sources. Skeletal data were compared using Mann-Whitney test p-values. Ponderal index was calculated using mass and length.

Results show *palliata*, *pigra*, and *insulanus* are the most robust, while eastern *macconnelli* are the least. Male *palliata* average the greatest femoral relative cortical area and percent cortical area, while eastern *macconnelli* have the lowest values. For ponderal indices, *palliata, pigra,* and *insulanus* have the highest values. *Caraya* are next, followed by *seniculus*, *arctoidea*, and southern *macconnelli*. Eastern *macconnelli* have the lowest values.

Another major finding is that *palliata* have narrow humeral heads compared to other taxa for which skeletal data are available. The ratios of humeral head superior-inferior diameter to mediolateral diameter, and mediolateral diameter to body mass, indicate that *palliata* have narrower humeral heads than other taxa.

More behavioral data are needed to interpret robusticity results. Theoretically, greater values may stem from ancestral isolation and reduced resources for *palliata, pigra,* and *insulanus*, some of which are also low in mass. The gracility of eastern *macconnelli* likewise awaits more field information. Narrower humeral heads may reflect more quadrupedalism for *palliata,* as supported by some behavioral studies.

Macroevolution of the hominin basicranium

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The morphology of the basicranium in modern humans is distinct from that of our closest living relatives—the great apes—and has thus been a key region of interest in comparative and functional paleoanthropological studies. Here, we test the utility of previously-established measures of basicranial morphology for distinguishing modern humans and extinct hominins from other anthropoids using a broad comparative sample of >100 extant and fossil primate species. Three-dimensional basicranial landmark data from >800 individuals were aligned using Generalized Procrustes Analysis and explored using a phylomorphospace. Four angular measurements were evaluated using univariate multi-optima Ornstein-Uhlenbeck (OU) evolutionary models and visualized using heat maps of optimal trait values in self-organizing maps. The allometries of six linear measurements were also evaluated using multi-optima OU evolutionary models, as well as pANCOVAs and phylogenetic generalized least squares regressions. Tympanic morphology drove much of the basicranial shape variation among anthropoids in the sample. However, when tympanic landmarks were removed, patterns of inter-taxon variation were primarily influenced by the location and orientation of hormion and the carotid canals, the location of inion, and the orientation of the petrous apices. Significant shifts in external cranial base angle were observed for cercopithecids, hominins, and modern humans. Hominins form a regime, separating them from other anthropoids, with respect to foramen magnum position, basicranial length, and basicranial width, but not foramen magnum angle. Results confirm that several basicranial features form a synapomorphic suite that distinguishes hominins from extant anthropoids.

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Evaluating morphological change in the maxillary dentition of an anaptomorphine (Omomyidae) lineage from the Willwood Formation (early Eocene) in the Bighorn Basin of Wyoming, USA

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The Willwood Formation in the Bighorn Basin of Wyoming offers a virtually continuous fossil record documenting evolutionary changes at high resolution. Previous studies found that the *Tetonius* – *Pseudotetonius* lineage exhibits a pattern of gradual morphological change in lower dentition spanning 1.5 million years, resulting in progressive compaction of antemolar teeth and loss of P_2 in later taxa. Initially, insufficient samples of fossil maxillae prevented formal analysis of similar changes in the upper dentition. Additional fossil maxillae from this lineage have been recovered and are studied here.

We present results of morphological analyses designed to test whether coordinated changes in the upper dentition match modifications previously documented in the lower dentition. While our analyses document morphological changes in the upper dentition through time, these transformations do not evolve in tandem with those in the lower dentition. While dentaries of *Tetonius* from higher meter levels demonstrate evolutionary loss of P_2, several partial *Tetonius* fossil maxillae from the same strata maintain P^2. Additionally, while crown size and roots of P_3 are reduced and fused at higher meter levels, crown size and roots of P^3 at these meter levels are widely splayed and unfused.

Our findings suggest that the morphological changes occurring in the dentition of this lineage conform to a pattern of mosaic evolution. The presence of P^2 in later meter levels may indicate retention of a vestigial structure while selective pressures acted on increasing the crown height of the upper and lower fourth premolars to perform or enhance specific masticatory functions.

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Do biomarkers associated with placentation hold potential for early risk detection of postpartum hemorrhage?

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Nearly 1 in 3 maternal deaths worldwide is attributed to postpartum hemorrhage (PPH). In the U.S. rates of PPH are higher for Black, Native American, and Native Hawaiian/Pacific Islander and Asian people than for non-Hispanic White people, with associated disparities in mortality/morbidity. Approximately 40% of PPH cases have no identified risk factors, and current clinical approaches focus on management of bleeding in the third stage of labor, not earlier risk assessment and prevention. PPH is a consequence of the dysregulated shearing off of the placenta during labor, leaving maternal blood vessels unconstricted and blood loss unrestricted. We were the first to propose that since hemorrhage is relatively rare in other mammals including other primates, the deep engagement of the human placenta with maternal vessels may play a fundamental role (Abrams and Rutherford, 2012). This case study in evolutionary medicine has two objectives: 1) we expand our earlier theoretical work proposing that PPH may be a function of overly invasive placentation and discuss the potential mechanistic role of invasive trophoblast antigen (ITA), matrix metalloproteinase-9 (MMP9), and placental growth factor (PlGF) as biomarkers of first-trimester placental invasion and vascular remodeling; and 2) we report the initial findings of associations among these biomarkers measured in serum across gestation and blood loss and hematological status in 349 women from a clinical site in Columbus, Ohio. Identifying mechanisms of action for PPH is critical for early risk assessment of excessive blood loss, especially in areas with high rates of loss and low availability of resources.

This research is funded by the University of Arizona College of Nursing.

Advancing the Quantification of Bone Surface Morphology and Texture through 3D Scans and 2D Images

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Analyses of bone surface morphology and texture hold critical significance across both clinical and anthropological research. Such investigations offer insights into conditions such as pathology presence, health status, and musculoskeletal development, which can then provide information about daily life and behavior. However, prevailing methods rely heavily on qualitative observations, introducing issues of reliability, repeatability, and limited data analytics.

This study addresses these challenges by exploring advanced quantification techniques based on 3D surface scans and 2D photographs of bone. By incorporating established methods from other fields, for example material science and engineering, we apply and compare the outputs obtained from five open source programs for the quantification and analysis of bone surface morphology and texture: 1) Gwyddion for the leveraging of 2D photographs to obtain fractal analyses, 2D FFT, and roughness parameters; 2) R for Procrustes shape analyses and elevation analyses from 3D scanning data; 3) R and Python for heightmap analyses; 4) ImageJ/FIJI for performing gray-level co-occurrence matrix analyses; and 5) the VERA method for quantifying surfaces in Meshlab.

These techniques yield multiple values capable of characterizing surface morphology (e.g. R-values, surface area and volume, shape descriptors). This work defines protocols for each application and initial findings reveal that each method offers objective quantitative data output that is more easily applicable to broader and more encompassing data analytics. These preliminary results suggest the suitability of the tested methods for advancing data collection and treatment, promising new rigorous investigations into the functional, developmental, and pathological aspects of skeletal remains.

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A meta-analysis of ancient and present-day Central Eurasian genome data to revise ancestries from archaic hominins

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Central Eurasia is a region which experienced extensive migration from both Western and Eastern Eurasia throughout history and has been home to modern humans and the archaic hominins since at least the Late Pleistocene. Introgression from Neandertals and Denisovans has shaped the evolutionary history of Eurasian populations with selection and phenotypic traits. While European populations have been extensively studied, archaic introgression has not been addressed in previous studies on Central Eurasia. However, as East Asian populations carry introgressed variation from possibly several Denisovan-like lineages, Central Eurasian populations also carry ancestries from various sources and might expose a unique set of archaic variation.

Archaic ancestry represents a minor fraction of modern human genomes, hence reconstruction of the temporal landscape of archaic introgression in Central Eurasia requires multiple genomes sampled at different points in time. We used whole-genome sequencing data from present-day and ancient individuals from Central Eurasia to assess the variation in the individual genomes using a local ancestry inference tool, admixfrog, and inferred genomic regions in a "human-typical", "Neandertal-typical" or "Denisovan-typical" state. This allowed us to estimate the proportion of introgressed material from each archaic source along with genes and genetic variants inherited from archaic hominins during Bronze and Iron Age as well as in the present.

Inferring introgressed regions in Central Eurasians, and connecting the variation within these regions to potential phenotypic and disease outcomes is valuable to understand the impact and importance of such admixture in comparison to other populations from different parts of Eurasia.

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Gaze following in wild chimpanzees (*Pan troglodytes schweinfurthii)*

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The ability to follow another's gaze direction is a foundational skill in human cognition that underpins more complex social abilities. Although basic gaze-following responses have been documented in many primate species, previous experimental work has focused on captive populations. Studying cognition in the wild is crucial to understand psychological processes in the context in which they evolved, and to relate cognitive skills to aspects of natural behavior. We conducted field experiments to assess patterns of gaze-following in 53 chimpanzees (23 females, 28 males) ranging from infancy to adulthood in Kibale National Park, Uganda. Across up to four trials on different days, individuals saw a human experimenter either look up (test trials) or down (control trials, as a metric of baseline looking). We then coded from video whether chimpanzees looked up across these conditions. Wild chimpanzees followed the actor's gaze, looking up more often on test trials (x^2=15.85, df=4, p=0.003); additional tests of latency to look up show that these responses were quicker in test trials (x^2=9.62, df=4, p=0.05). We further characterized the development of this skill, and whereas juveniles (Least-squares means, p=0.03) and adults (p=0.05) consistently followed gaze, infants under 5 years did not (p = 0.49). This parallels previous work from captivity suggesting that chimpanzee gaze following develops more slowly than in humans. This work establishes a new method for assessing individual variation and development of social cognition in wild chimpanzees in natural contexts.

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Locomotor development and climbing in *Homo naledi*

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Locomotor development is an important life history characteristic. All non-human apes are partially arboreal, especially as infants and juveniles. The role of climbing in hominin evolution has been debated for decades. However, based on locomotor development in non-human apes, if hominins climbed regularly, then subadults likely did so most frequently. The evolution of hominin locomotor development is poorly documented due to the dearth of subadult postcrania. A large number of recently described subadult fossils attributed to *Homo naledi* provides a unique opportunity to study locomotor ontogeny in this small brained hominin. The aim of this work is to reconstruct age-related variation in locomotor loading in *Homo naledi* by comparing diaphyseal robusticity and trabecular bone structure throughout the postcranium of juvenile and adult *Homo naledi* to age-matched great apes.

The humerus, femur, tibia, talus, and calcaneus of adult and juvenile *H. naledi*, *H. sapiens, P. troglodytes, G. gorilla,* and *P. pygmaeus* were micro-CT scanned. Scans were segmented using a deep learning model and classified into cortical, trabecular and non-bone. Standard diaphyseal cross-sectional properties calculated in long bones and 3D distributions of trabecular properties were mapped throughout whole bones.

A more ape-like pattern of upper/lower limb diaphyseal robusticity and trabecular bone degree of anisotropy were observed in *H. naledi* compared to age-matched *H. sapiens.* Juvenile *H. naledi* has a greater ratio of upper/lower limb diaphyses compared to adults. These results indicate that, mirroring trends in extant apes, juvenile *H. naledi* may have climbed more frequently than adults.

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Alouatta caraya femoral bone density and cortical thickness with respect to sex and age

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Several studies have shown an increase in bone density and cortical thickness with maturity in humans, especially in males. It was predicted that similar patterns would be seen in nonhuman primates such as *Alouatta caraya*. The femoral head and shaft were selected as skeletal features comparable to those of humans.

Materials include radiographs of museum specimens. The sample consists of eight adult males, six adult females, four juvenile male and two juvenile females. Variables are femoral head transect density, femoral neck transect density, and midshaft cortical thickness. Additionally, Ward's triangle was examined within the neck for density. This is an area of low density associated with osteoporosis evaluation. T-test p-values were used to compare the means. Trends were observed using box and whisker plots.

Comparing adults, males have greater femoral neck, head, and triangle density when compared to females. There was no difference in the percent of the cortical area in the shaft. All the adults had a triangle present. Comparing adults and juveniles, adult males have greater femoral head and neck density, as well as greater midshaft relative cortical thickness. Only one juvenile has a triangle, preventing comparison. Female adults and juveniles show no clear difference in densities and cortical thickness. Both juvenile females have a triangle.

Greater density in males is probably a result of increased testosterone during development. This may be why age differences are more noticeable in the *Alouatta* males, while they are not distinguishable within the small sample of females.

Life and death in the Middle Paleolithic of Qafzeh, Israel through comprehensive taphonomic study of hominin remains

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The Qafzeh Cave (Wadi el-Hajj, Israel) houses one of the most comprehensive assemblages of early *Homo sapiens* in the Euroasiatic fossil record. Since the first excavations in 1937, at least 25 individuals, with an age of death ranging from perinatal stage to adulthood, have been recovered from Mousterian levels dating around 100 -90 ka. The Qafzeh individuals are renowned as one of the leading examples of Paleolithic funerary practices, since the archaeological context is consistent with intentional burials. However, no direct taphonomic analysis of the bones has been conducted.

This research presents the first comprehensive taphonomic analysis of the bone surface modifications, fracture patterns, as well as some anomalies arising from trauma and other pathologies. Microscopic analysis has revealed a prevalence of postmortem modification patterns in almost all individuals, including dry bone fractures, concretions, mineral precipitations, among other modifications. Additionally, the use of mCT allowed us to analyze antemortem skeletal modifications (in individuals Q-25 and Q-11) and perimortem modifications (Q-11). The analysis not only provides insights into the post-burial processes, but also enhances our understanding of the lifestyles of the population, revealing evidence of violent behavior including blunt and sharp force traumas, care of the sick and funerary practices. This sheds light on Paleolithic culture of death during a significant period in human evolution.

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Factors Influencing Patient Satisfaction During PCOS Diagnosis

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Polycystic Ovary Syndrome (PCOS) is a common reproductive health condition, affecting approximately 8-13% of reproductive-aged women. Despite the frequency of PCOS, it is understudied in both etiology and patient experience. PCOS diagnosis is often delayed or initially misdiagnosed, with implications for quality of life, mental health, and trust in healthcare. However, few studies have examined the PCOS diagnosis experience, especially to identify gaps between patient expectations and provider behavior. Here, we surveyed 149 PCOS patients diagnosed in the US to understand factors associated with positive and negative diagnosis experiences. In our sample, 24% reported no interest from their provider in the description of their PCOS experience, and 57% did not feel their treatment plan at diagnosis was suited to their personal needs. Linear regression analysis found that receiving sufficient information about the diagnosis and whether the provider discussed symptoms considered important by the patient significantly predicted if the treatment plan was suited to personal needs ($F(3,145) = 67.5$, $p<.001$). Similarly, patient satisfaction was significantly predicted by discussion of personally important symptoms, sufficient information, and if the provider appeared interested in the patient's description ($F(7,141) = 33.4$, $p<.001$). While the significance of sufficient information has been previously reported, our results emphasize the importance of patient narrative in healthcare encounters. Notably, the inappropriate treatments that may result from dismissal of the patient narrative can harm reproductive health or increase risk for complications, like endometrial cancer. Addressing the factors driving negative diagnosis experiences will improve PCOS patient health in the long-term.

Bonobo and chimpanzee metacarpal bone density: Implications for understanding theorigin of gracile morphology

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Domesticated animals, following the commensal pathway, undergo morphological,physiological, and developmental changes compared to their wild counterparts. In dogs,this results in juvenile cranial features, including shorter faces, mandibles, roundercrania, and reduced cranial capacity, akin to other domesticated species, althoughdebate persists on this subject. Similarly, bonobos, believed to have undergone 'self-domestication', exhibit a reduced cranial capacity and depigmentation of lips and tailtufts in comparison to chimpanzees. Recent research also suggests that Holocenemodern humans may have experienced self-domestication, evident in traits like reducedcranial capacity, a globular cranium, and postcranial gracilization. This gracilization isoften linked to reduced physical activity with the advent of agriculture. An alternativehypothesis suggests that self-domestication, due to increased selection for prosocialityas humans settled in communities, led to the evolution of a gracile skeleton in havinglow trabecular bone density (bone volume/total volume). To test this, we examined bonevolume fraction (BV/TV) in 3D images of the third metacarpal heads of bonobos andchimpanzees (n=10). Our prediction was that bonobos, due to self-domestication, wouldexhibit lower BV/TV, indicating greater gracility. Preliminary results showed a slightlyhigher mean BV/TV in chimpanzees but Wilcoxon rank sum tests did not showstatistical significance. This suggests the need for a larger dataset to confirm ourprediction. In summary, additional data will help elucidate the differences in gracility ifany, between bonobos and chimpanzees which may have implications forunderstanding human self-domestication, and the various pathways through whichgracile traits emerged in recent Holocene humans.

How to answer the big questions in biological anthropology

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What are humans and how did we evolve? We have made little progress toward an answer to the guiding question of biological anthropology. This is because humans are distinct from many other animals and evolutionary processes are difficult to infer. Given these challenges, biological anthropologists often resort to just-so stories (and just so-so stories) about human evolution rather than testable hypotheses or we avoid big, interesting, and theoretical questions in favor of more manageable and at times myopic ones. But biological anthropology has the wherewithal to overcome these limitations if we embrace our holistic and multi-disciplinary foundation. I outline five recommendations drawing from the work of Matt Cartmill. Biological anthropology needs

(1) more comparative studies of extant species linking behavior to anatomy; (2) those comparisons should extend across mammals (and beyond) for cases of convergence; (3) we need to acknowledge the possibility of parallelisms rather than homology in closely-related species; (4) research should be theoretically motivated, and test hypotheses that can be generalized across taxa; in this regard, we should focus on what traits "makes us human," and what evolutionary processes shape such traits; (5) but we also need critical reflection on these guiding questions, and an appreciation that the animal-human boundary and our definitions of humanness are based on historical fictions that are often destructive rather than productive. I illustrate this approach with a phylogenetic comparative analysis of hair density in mammals and a study of the psychophysiology of social relationships in wild chimpanzees.

Physical activity patterns and age-related bone loss in Ancient Nubia

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This study compares entheseal changes and trabecular microarchitecture characteristics in individuals from two Ancient Nubian sites, Kerma and Tombos, to better understand the connection between physical activity and age-related decline in trabecular bone quality. For each individual, microCT scans of 4th lumbar vertebrae were analyzed to calculate standard measures of trabecular microarchitecture (e.g., trabecular number, connectivity density, etc.), and entheseal scores were averaged to generate an Upper, Lower, and Overall Body score. An entheseal score of three indicates a transition to more robust muscle markers reflecting higher levels of physical activity, which in turn are associated with higher measures of bone quantity and quality. Individuals were placed into groups defined by an average score of below three or above three. Since entheseal scores are positively correlated with age, only individuals under 50 years were included. Independent Samples *t*-Tests were used to compare differences in trabecular microarchitecture between groups. In both samples, individuals with entheseal scores below three interestingly displayed higher markers of microarchitecture quality and lower markers of microarchitecture decline. In the Tombos sample, significant differences in microarchitecture measures were found between groups, most notably in comparisons using Lower Body scores. In the Kerma sample, statistically significant differences were only found between groups based on Upper Body scores, though similar patterns were seen based on Overall and Lower Body scores. These results suggest that biocultural factors other than physical activity may be contributing to trabecular bone health in these populations, such as reduced nutritional status due to resource access.

Niche partitioning in fossil bovids near the Mio-Pliocene boundary at Lothagam, Turkana Basin, Kenya

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The spread of C_4-dominated environments constituted a major shift in eastern African terrestrial ecosystems during the late Miocene to Pliocene periods. While previous work has shown that many families of eastern African herbivores adopted C_4 diets during this time, we know little about how dietary resource partitioning was structured at finer, taxonomic scales, such as within the speciose and diverse bovid tribes. The Lothagam sequence (Turkana Basin, Kenya) spans the late Miocene to Pliocene (~7.5 to 3.5 Ma) and has produced an abundant mammal fauna that is ideal for investigating how increasing abundance of C_4 grasses influenced niche partitioning within the large herbivore guild. Here, we report new $\delta^{13}C$ and $\delta^{18}O$ isotope data from tooth enamel (n = 120) and body mass estimates from tooth measurements (n = 93) for nine bovid tribes from Lothagam. Linear models predicting $\delta^{13}C$ and $\delta^{18}O$ values and estimated body mass by time revealed no significant shifts, which implies that most tribes were characterized by static dietary and body mass niches. Alcelaphins and bovins were both C_4 specialists but differed in average mass (~ 65 versus > 100 kg, respectively). Tragelaphins were relatively large-bodied (~ 80 kg on average) and had the lowest average $\delta^{13}C$ values (-6.6‰), suggesting mixed-feeding with a preference for browse. Other taxa seem to have been mixed feeders varying only by mass. We concluded that Lothagam bovids may have differentiated their niches in other ways (e.g., microhabitat use and migratory behavior) that are common among extant taxa today.

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Adulthood longevity of males and females during a Japanese prehistoric period, Jomon, estimated from reduction of dental pulp cavity, with additional information from clavicles

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The Jomon period is a Holocene prehistoric period of Japan before introduction of wet-rice agriculture. Sasaki and Kondo (2016) estimated the adulthood longevity based on 234 tooth remains from Jomon sites around the archipelago. Using teeth was expected to alleviate age biases due to differential preservations. They focused on the reduction of dental pulp volumes in mandibular canine roots, and estimated the age profile of the Jomon to have been within the variation of modern hunter-gatherer populations. In their study, since reduction rate of referenced population, as it is, had rendered implausibly long longevity, they assumed that the rate was variable among populations, and estimated it simultaneously with the age profile by maximizing likelihood. In this study, based on the same approach as Sasaki and Kondo (2016), the age profile was estimated separately for males and females. The sex information was obtained from the volume of canine root in form of posterior probability, and incorporated into the likelihood calculations. Since the tooth sample alone was not enough for detection of significant differences between the sexes, information from the state of clavicle sternal end was additionally incorporated to narrow down possible range, utilizing timing of the fusion reported by Langley-Sirley and Jantz (2010). As the result, it was observed that the number of deaths was greater in females than in males during the life stages of adolescent–early adulthood. The greater mortality was suggested for early stages of female lives compared to the male during the Jomon period.

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Investigating risk avoidance during arboreal locomotion in wild primates

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Existing research on the arboreal origins of primate locomotor evolution often seeks to connect variation in postcranial morphology with locomotor performance, ignoring cognition and behavior per se. This study aims to integrate the cognitive processes that may also determine performance outcomes of primate arboreal locomotion. One way to characterize how primates may assess risks in their environment is to understand latency – the time spent pausing between sequential bouts of locomotion. Periods of latency can be used to gather and process information before making the next move. We recorded high-speed videos of free-ranging cercopithecid monkeys (3 species, Kibale National Park, Uganda) and lemurs (4 species, Ranomafana National Park and Anja Community Reserve, Madagascar) as they engaged in spontaneous arboreal locomotion. For preliminary analysis, we distinguished between bouts of generalized quadrupedal locomotion, leaping, dropping, and other types of movements, using the behavioral coding software Datavyu. Initial results show that primates are capable of transitioning between different locomotor modes as well as between gaps in substrates without pause. These results affirm the previous understanding that primates are adept at arboreal locomotion. Nevertheless, latent periods do occasionally occur before crossing gaps. In ongoing analyses, we are investigating whether such pauses happen more frequently, for example, in large-bodied primates – for whom arboreal locomotion in particularly precarious. We are also investigating what happens during these pauses, such as exploratory touching of a substrate before locomotion resumes.

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A potentially adaptive increase in *AMY1* copy number in Peruvian populations

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The gene duplications and deletions in the amylase locus are of particular interest regarding their influence on human evolution and health. Prior work has associated the copy number variation of the starch digesting enzyme, salivary amylase (*AMY1*), with an increase in starch consumption during the agricultural revolution. While many earlier studies have attempted to describe the landscape of this copy number variation across populations, the sequencing of new genomes every year renders this an ongoing task. Utilizing a copy-number caller, mrCaNaVaR, on samples from the 1000 genomes project along with the Human Genome Diversity Project, we have demonstrated that the Peruvian in Lima and Pima in Mexico populations have the highest known copy numbers. Using digital droplet PCR on samples from the PEL population, we have confirmed this finding for Peruvians. As a secondary measure, we also calculated the gene copy number from unadmixed Quechua and Mayan samples that yielded the same results. Genome-wide Vst analyses between Peruvian and other American populations determine this region to be an outlier. Furthermore, low copy numbers in Tibetan samples indicate that high-altitude is not driving this observation. Instead, we hypothesize this variation in Peruvians is influenced by the heavy dietary reliance on starchy potatoes domesticated in the Andes around 6000-10000 BP. Our results shed light on the ongoing investigation regarding the evolution and adaptive potential of the amylase locus and how this history may impact modern day human variation in metabolic responses to starch-rich food.

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How much variation can we expect in subadult growth due to geographic and environmental variation? Evidence from *H. sapiens*

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To aid interpretation of sub-adult fossil hominin skeletal material, knowledge of variation in skeletal dimensions during the growth-span is needed. This analysis will provide measures of variation in specific skeletal dimensions at specific ages. Data were drawn Eveleth and Tanner's compendium of studies of growth from around the world limited to samples with the most complete reports on size and variation across the 2-18 year age range for sitting height, biacromial and billiac breadth. Only boys were included owing to their greater size variability compared to girls. Samples from Europe and of European descent, Africa and African descent, Asia, New Guinea were compared in terms of coefficients of variation (CV) to remove effects of differences in dimension sizes. CVs of sitting heights, ages 2-10 years ranged from 1.74 to 5.56, and for ages 11-17, from 0.71 to 2.05. CVs for biacromial breadth, for ages 3-10 years of age ranged from 0.71 to 0.14 and for ages and from 11-17, ranged from 4.83 to 9.73. CVs for biiliac breadth, ages 3-10 years of age, ranged from 25.62 to 38.43 and for ages 11-16 from 19.73 to 22.44. CVs of biacromial breadth increased in the pubertal years while CVs for biiliac breadth and sitting height weere lower. Compared to the mean CV of sitting height, the mean CV for biacromial breadth was 3.6 times and that biiliac breadth was 13 times greater. Expectations of skeletal variation among hominin subadult samples are informed by knowledge of normal geographic variation during the growth span.

Sex-based differences in dental microwear texture among the adults from Herculaneum

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The people of Herculaneum died via a pyroclastic event caused by the eruption of Mt. Vesuvius in AD 79. This study employs dental microwear texture analysis (DMTA) to address age and sex-based differences in the diets of 58 Herculaneum adults, 31 males and 27 females, aged 16 to 58. The DMTA followed standard procedures and the DMTA variables were complexity, anisotropy, scale of maximum complexity, and textural fill volume. Statistical testing used Bayesian linear regression and a binary logistic regression (BLR). This study considered Bayes Factors (BF_{10}) greater than 3 in favor of the alternative model compared to the null model significant. The BLR used all DMTA variables. Female anisotropy increased significantly with age ($P(M) = 0.50$; $P(M|data) = 0.85$; $BF_M = 5.72$; $BF_{10} = 5.72$; $R^2 = 0.25$). The BLR results indicate about half of the young adult males (16-29 year-old) had diets like the females. For the middle adults (30-49 years-old), only 17% and none of the old adult (over 50 years old) males had diets like the females. Compared to females, older male diets did not change as they aged, and males of all ages tended to eat harder foods compared to females. Older females ate a greater variety of foods compared to younger females and preferred soft or tough/fibrous foods. All told, differences in male and female diets increased as they aged, which gave middle and old adult females a distinct microwear signature compared to males and young females.

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Total number of neurons is not necessarily a better measure of cognitive ability than overall brain size

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What is the best measure of brain anatomy for predicting cognitive and behavioral ability across species? Absolute brain size in Primates is known to be associated with interesting behavioral dimensions, including social group size. Estimates of total neuron number, from the pioneering work of Herculano-Houzel and colleagues, have been suggested to be a better measure. However, neuron number by itself ignores the degrees and kinds of interconnections between neurons. Abnormal connectivity is specifically thought to underly some cognitive disorders in humans. By contrast, brain volume potentially indexes neuron number plus the complexity of neuronal interconnections and other support cells. Brains with lower neuron densities likely harbor correspondingly greater axonal and dendritic interconnection complexities. Using a small sample (n=10) of Primate species for which estimates of cerebral cortex neuron number (NN), absolute brain size (BR), general cognitive ability (GC), and social group size (GS) have been published, it is shown that BR rather than NN is actually a slightly better predictor (though not significantly) of both GC and GS. For GC the correlation with BR is $r=0.76$ ($p<0.01$), but with NN $r=0.64$ ($p<0.03$). For GS, the correlation with BR is r=0.75 ($p<0.01$), but with NN r=0.72 ($p<0.01$). Although a small sample, this suggests natural selection has worked to optimize both neuron number and complexity of interconnections, making BR at least as good an estimate of cognitive/behavioral abilities as NN. Implications for interpreting the evolution of human cognition from the fossil record will be addressed.

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Recent Advances in LC-MS/MS Analysis of Ancient Hormones

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Archaeological interest in the quantification and analysis of ancient hormones, particularly cortisol, has increased in the past decade. Prior studies have employed enzyme-linked immunosorbent assay (ELISA) methodologies; however, there are inherent limitations to ELISA-based analyses of ancient hormones. In this presentation we discuss these limitations, but also present recent results using liquid chromatography-tandem mass spectrometry (LC-MS/MS). The high sensitivity and selectivity of LC-MS/MS has the ability to produce data that are more accurate and reliable, although costly.

Here we present new paleohormone data from the Netherlands (post-medieval period, *ca.* 1600-1850), illustrating LC-MS/MS capability. Initial testing of human bone suggests progesterone, testosterone, and estradiol can be quantified using LC-MS/MS within acceptable ranges of precision and accuracy. However, cortisol could not be reliably detected. We propose a new method for paleohormone analysis of human bone, moving beyond previous studies of archaeological hair and dentine. These findings have the potential to revolutionize the study of paleohormones in the past, given that LC-MS/MS is arguably more reliable than former ELISA-based analyses and present an opportunity for a lifecourse approach. Furthermore, the examination of additional hormones beyond cortisol could have profound impacts on what we know about the past.

This research is part of the project The Evolution of Stress (project number 406.XS.01.118 of the research programme Open Competition which is financed by the Dutch Research Council (NWO).

Sex, death, and disability: Intersections of identity at Carrier Mills, IL (6000 – 3000 BC)

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Fourth Wave bioarchaeology uses intersectionality as a tool for creating more nuanced interpretations of the past. I explore the intersections of sex, age, impairment, and identity by analyzing atypical burials of individuals with mobility impairments from the Archaic period (6000 – 3000 BC) site of Carrier Mills, IL. The people of Carrier Mills were semi-mobile foragers who congregated at the site during the fall and winter. Burials were flexed or extended with the head oriented to the West and the body facing the Southwest. Middle aged males were buried with larger quantity and variety of grave goods, while females were buried with tools associated with household tasks. SA1187-4 is a 50-59-year-old female with tuberculosis placed in a flexed position with her head oriented south, facing the southeast, and buried with a modified deer bone tube. SA1187-7 is an old adult female with chronic illness placed in a flexed position with her head oriented east and facing the north. SA1187-38 is a 60+ year old male with tuberculosis placed in a flexed position with his head oriented east, facing southeast, and buried with several grave goods. SA1188-94A is a 30-34 year old male with leg asymmetry placed in a flexed position with his head oriented north, facing east southeast, and buried with several grave goods. Each of these individuals suffered mobility impairments from their pathologies. The atypical nature of the burials facing east combined with their mobility impairments suggests they were singled out for special status within the Carrier Mills community.

Using evolutionary quantitative genetics in taxonomy: a case study from the African Middle Pleistocene

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The Middle Pleistocene hominin fossil record is taxonomically diverse, with *Homo sapiens*, *Homo neanderthalensis*, *Homo naledi*, and *Homo erectus*, all existing at various times during this period. These species are generally recognized as valid, but there is also an ambiguous group consisting of individuals that are difficult to categorize. This 'Muddle in the Middle' has been central to many debates in the palaeoanthropological literature, with the main disagreement centered on how many species this group consists of. This disagreement has been further exacerbated by the difficulty of defining species in the fossil record. Challenging as this is, some species concepts do include predictions that can be tested. One of these is Van Valen's Ecological Species Concept (ESC), which describes a species as a group that occupies an adaptive zone, with stabilizing selection acting to maintain its morphological stability. As a proof of concept, an established quantitative genetics approach was used to test whether the pattern of variation among the crania of eight African Middle Pleistocene hominin individuals is more consistent with diversifying selection, stabilizing selection, or genetic drift. The vast majority of results indicate a pattern of stabilizing selection, which aligns with the definition of a species according to the ESC. Four comparisons involving the Bodo 1 cranium show possible evidence of diversifying selection, which may allude to taxic diversity. In conclusion, most of the individuals in this study follow the expectation of a single ecological species lineage. This is the first study to use this approach for taxonomic purposes.

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Redefining the treponemal history through pre-Columbian genomes from Brazil

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Treponemal infections and their current emergence are considered a global threat to human health. Their origins, still unresolved, have instigated many conflicting hypotheses, especially surrounding the sudden onset of the first syphilis epidemic, and its possible arrival to Europe from the Americas with Columbus' expeditions in late 15th century. Novel studies on ancient treponemal DNA, long presumed inretrievable, have recently confirmed the presence of treponemal diseases in the pathological human remains from both early modern period Europe and colonial-era Mexico. However, genomes reliably predating the first transatlantic contact have so far not been retrieved from either side of the Atlantic.

Here, we report the first four treponemal genomes from nearly 2,000-year-old human remains from Brazil. These genomes, deemed most closely related to the bejel-causing agent, *Treponema pallidum* ssp. *endemicum*, contradict the geographical niche of modern bejel strains in the arid regions of the world and showcase the adaptive abilities of treponemal subspecies, extending the plausible range of their dispersals in the past. Furthermore, one of the genomes exhibits particularly high coverage (33.8-fold average coverage), allowing improved molecular clock dating estimations that place the divergence of all modern *T. pallidum* subspecies firmly in pre-Columbian times.

Overall, our findings demonstrate the ancient genomes' potential in uncovering the evolutionary history of *T. pallidum,* and their value in forging unprecedented hypotheses on the spread of treponematoses across time.

Ecological and social pressures shape chimpanzee nest site selection

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Hominins are unique among great apes in displaying central place foraging, a pattern of behavior linked to mate provisioning, bipedality, and tool use. However, the factors leading to this behavior remain unclear. Given that all extant great apes build nests and early hominins display both similar body sizes to chimpanzees and morphological adaptations for arboreality, it follows that the earliest hominins likely built nests prior to the evolution of central place foraging. Chimpanzees provide an important proxy for understanding the potential drivers of nest site selection in early hominins and examining their nesting behavior will shed light on the pressures shaping the location of central place foraging sites in later Pleistocene hominins. However, the influence of sociality and foraging on chimpanzee nesting behavior remain unexplored. Using 43 years of long-term data from Gombe National Park, Tanzania, we investigated the effects of community territory boundaries and proximity to food sources on nest site selection. Preliminary results suggest that chimpanzees select nest sites that minimize morning travel distance to fruit sources and that the role of intergroup avoidance in nest site selection is sensitive to population demographics. Together these preliminary results provide evidence that chimpanzees are intentional in their nest site selection, suggesting that central place foraging likely emerged from intentional, rather than random, nesting sites. Overall, this work improves on our current understanding of the factors influencing chimpanzee nest site selection, a necessary step required to make inferences about the transition to central place foraging in hominins.

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The evolution of dental development and life history in extinct and extant Malagasy lemurs

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Alongside his major contributions to size and scaling in primate biology, much of our current understanding about the paleobiology (anatomy, functional morphology, diet, growth, and development, etc.) of extinct, giant subfossil lemurs is due to the diligent, insightful work of a giant in our field: Bill Jungers. From the early 2000s onwards, Bill was an integral member of our team research focused on reconstructing the 'growth biology' of subfossil lemurs. Collectively, our team has now reconstructed aspects of life history for six extinct species of Malagasy lemurs across four major families (Megaladapidae, Archaeolemuridae, Palaeopropithecidae, and Lemuridae) of Malagasy lemurs and ranging in size from 11-88 kg. Here we review our findings about growth, development, and life history in extinct subfossil lemurs and interpret them within the context of comparative data on living prosimians and extant anthropoids. We found remarkable diversity in patterns of growth and development among extinct lemurs, with some resembling extant members of the family Indriidae, others more closely resembling extant lemurids, and still others resembling neither of the above. Despite the very large size of some extinct lemurs, none resembled anthropoids of similar body mass, and body mass fails to predict growth pattern variation even within the lemurs. We explore how variation in aspects of growth biology relates to phylogeny, diet and other niche characteristics, encephalization, and mtDNA substitution rates.

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Review of *Eurygnathohippus* from Ledi-Geraru, Afar Depression, Ethiopia

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The Ledi-Geraru Research Site is located between the Awash and Ledi River basins in northeastern Ethiopia, east and north of the famed Hadar hominin site. Fluvio-lacustrine sedimentary deposits at Ledi-Geraru date between 2.84 and 2.58 Ma, and have yielded the earliest record of the genus *Homo* along with an abundant vertebrate fauna. Fossils from the site are plentiful if often fragmentary, and include numerous remains of hipparionine horses belonging to the endemic African genus *Eurygnathohippus*. Equid craniodental remains consist largely of maxillary and mandibular fragments and isolated teeth, while postcrania are primarily distal limb elements. Two species, the larger *Eurygnathohippus hasumense* and the smaller *E. afarense*, have been reported to be represented in the assemblage.

Previous studies of hipparionine horses from the older Hadar site proposed a possible reduction in body size near the top of the available stratigraphic section, based upon a small metacarpal III from the Kada Hadar 3 member of the Hadar Formation (c. 3.0 Ma). Fossils of *Eurygnathohippus* from Ledi-Geraru demonstrate that both large and small forms were present in these younger sediments. Although the overall vertebrate fossil record from the region suggests faunal turnover related to the spread of more open and probably arid habitats, *Eurygnathohippus* does not appear to have uniformly responded to these environmental shifts with significant body size reduction.

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From Iberia to Chukotka: assessing dental morphological variation across Eurasia

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Across the vast expanse of Eurasia, there are no major barriers to population movement -- Western Eurasians have traveled east, and East Asians have traveled west. How has the constantly churning to-and-fro movement impacted Central Asians and Siberians? Rather than assessing clines and biodistance, we use the application rASUDAS2 to estimate the most likely ancestry of Central Asian/Siberian individuals based on tooth crown and root morphology. A naïve Bayesian algorithm estimates the probability that an individual will exhibit a suite of traits consistent with seven biogeographic groups: (East Asia [EA]; Southeast Asia [SEA]; Australo-Melanesia [AM]; American Arctic [AA]; North and South America [NSA]; Western Eurasia [WE]; and Sub-Saharan Africa [SSA]. Tungusic groups are primarily assigned to AA (0.442) and secondarily to NSA (0.209) and EA (0.163). Mongolic groups are more commonly affiliated with AA (0.286) and NSA (0.286) than with EA (0.114). Turkic individuals show a high WE (0.276) component followed by SEA (0.172) and EA (0.155). An Ugric group, the Khanty, have the highest assignments with EA (0.320) and AA (0.200) but there is a notable WE (.240) component. Although Western Eurasians reached Lake

Baikal in the Upper Paleolithic, Neolithic Baikal individuals are assigned to EA (0.368) and AA (0.237). We have documented Eurasian clines in dental traits (Heim et al., 2016), but individual assessment highlights the within-group heterogeneity of samples and linguistic groups. For these Asian groups, there are only rare assignments to AM and SSA. This is also true of WE except for Turkic and Ugric groups.

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Annual Rainfall and Mammal Species Diversity in a Costa Rican Rainforest

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Understanding drivers of biodiversity is a crucial goal of ecological studies. Prior research of tropical ecosystems reports that annual rainfall and species diversity are positively correlated, likely because rainfall is a primary driver of plant productivity, which, in turn drives species diversity. Based on these studies, we predict that annual rainfall and species diversity at La Selva Biological Station (LSBS), Costa Rica will be positively correlated. The dataset included rainfall and annual census data for 21 diurnal mammal species, including *Alouatta palliata, Ateles geoffroyi,* and *Cebus imitator,* collected between 1994 and 2017. Simple linear regression was used to test if rainfall significantly predicted biodiversity measures ($p<0.05$). Regression results were non-significant for any of the predicted biodiversity measures for diurnal mammal species: biodiversity ($r^2=0.0001$, $p=0.9771$), relative abundance ($r^2=0.008$, $p=0.9138$), Shannon Weiner Index H ($r^2=0.0242$, $p=0.5514$). Results were also non-significant for any of the predicted biodiversity measures for primate species: biodiversity ($r^2=0.024$, $p=0.8531$), relative abundance ($r^2=0.0019$, $p=0.8672$), Shannon Weiner Index H ($r^2=0.017$, $p=6175$). Our hypothesis predicting a positive correlation between annual rainfall and species diversity at LSBS was not supported, and the amount of rain at LSBS might offer an explanation. Average annual precipitation at LSBS exceeds 4300 mm/year, and reported correlations between annual rainfall and species diversity indicate the correlation weakens as rainfall increases beyond 2500 mm/year. Instead, when rainfall exceeds 2500 mm/year, tree species richness, a factor in plant productivity, plateaus, possibly due to poor soil nutrients or declining energy availability.

If science is broken, how do we fix it? An analysis of how race science spreads through the mainstream academic literature

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Race science claims to provide scientific evidence that racial hierarchies exist and are inevitable. Research produced by race science often falls short of agreed standards for scientific rigour yet succeeds in being published in the mainstream academic literature. This paper will provide an analysis of how race science spreads through the scientific literature, using the example of Lynn's 'national IQ' dataset. An evaluation of the dataset will be presented first, demonstrating that it does not meet scientific standards of rigour; for example, a methodology for its construction has never been provided. Then an analysis of the publications which have used the dataset will show how >80 publications have appeared in mainstream academic journals, mostly published with the for-profit publishers Elsevier and Springer. Evidence will be provided that, once papers using the dataset are published, they are difficult to remove from the scientific literature: editors, authors and publishers are reluctant to act on concerns raised about the dataset. The paper will end by discussing the role of the academic community in allowing this example of race science to achieve 'mainstream acceptance', and what changes need to be made to the publishing process to counter the spread of race science in mainstream journals.

Genomic signatures of male reproductive skew in chimpanzees and bonobos (genus *Pan*)

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Though bonobos (*Pan paniscus*) and chimpanzees (*Pan troglodytes*) share many aspects of their behavioral ecology, they differ in some key reproductive traits. Male chimpanzees compete aggressively, mate-guard, and coerce females for mating opportunities—behavior that is rare in bonobos. Additionally, female bonobos display longer maximum sexual swelling phases with greater variability in the timing of ovulation than female chimpanzees. Such differences should result in chimpanzees exhibiting greater variance in male reproductive success. However, recent paternity analyses have revealed greater male reproductive skew in some bonobo communities. To investigate whether these results are due to stochastic demographic variation or true behavioral differences between bonobos and chimpanzees, we used whole genome data from the five extant *Pan* lineages (46 individuals) to explore the historic sex-biased demography of the genus. We compared neutral genetic variation on the X chromosomes and autosomes (X/A ratio) to assess the extent of male reproductive skew in each lineage. Using an approximate Bayesian computation framework, we inferred male reproductive skew at different timescales using multiple population genomic measures. As expected, we found more variance in male than female reproductive success across all *Pan* lineages (X/A diversity ratios ranging from 0.74-0.95). However, in contrast to paternity analyses, we found evidence for greater male reproductive skew in chimpanzees than bonobos (chimpanzee/bonobo X/A ratios > 1, ranging from 1.06-1.32). These results emphasize the insights gained from genomic data and reveal the evolution of male and female mating strategies in *Pan*.

MoTChA: A point-cloud registration and measurement package for automatically collecting morphological data

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Collecting morphological data can be time-intensive, especially when performing large comparative analyses or addressing questions involving variation and integration. To address this challenge, we developed MoTChA (morphological transformation and character automation), a software package that automatically collects linear distances, angles, and fiducials from 3D scans. The user initially takes measurements on one scan designated as the reference scan and a few additional scans used for model training. By registering a subject scan to a reference scan, any measurements taken on the reference can be transferred to the subject. Point-cloud registration or scan matching involves aligning two or more 3D scans such that corresponding points on each scan have the same coordinates. MoTChA partitions registered training scans with K-means clustering and learns to identify the same partitions on new scans. By identifying corresponding partitions on new scans, MoTChA infers the optimal transformation to register the scans. Our software will then transfer measurements collected in the training dataset onto the subject scans. To validate MoTChA's performance, we collected 12 measurements from 55 femora of gorillas, chimpanzees, humans, and orangutans. For training, we used 13 gorilla femurs, and for validation, we used the rest of the dataset. Compared to those obtained manually, MoTChA generated measurements with mean percentage error of 4.2% and standard deviation of 1.8%, demonstrating MoTChA's reliability and high accuracy. The results suggest that MoTChA offers evolutionary morphologists a powerful way to take many measurements in an efficient and accurate manner which could significantly impact the field of evolutionary morphology.

Tooth wear has a greater effect on molar pulp volume reduction than aging in *Macaca fascicularis*

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Odontoblasts lining the dental pulp cavity deposit dentine throughout life, meaning pulp cavity volume decreases with age. Primate species with more abrasive diets have relatively higher molar pulp volume (PV) in the unworn state than those with less abrasive diets. Therefore, species with more abrasive diets may deposit more dentine across their lifespans to resist wear. While both age and wear affect dentine deposition, it is unknown which of these variables has a greater impact. We measured PV in micro-CT scans of lower first molars of *Macaca fascicularis* (n=13) of known age and calculated wear on these specimens as the ratio of exposed dentine to occlusal surface area. We used ordinary least squares regression (alpha=0.05) to test if age or wear was a better predictor of PV. Both variables have a significant negative relationship with PV (age: p=0.008, r^2=0.439; wear: p=<0.001, r^2=0.772). A mixed linear model of PV against wear as main effect and age as covariant had a non-significant interaction effect (p=0.078), and confirmed that both age (p=0.030) and wear (p=0.004) are significantly negatively correlated with PV. Our results suggest that while PV decreases with age (unsurprisingly), enamel loss is more strongly correlated with, and a better predictor of, PV decrease. These findings have implications for interpreting odontoblast activity in response to sensory feedback and the relationship between PV and diet over long primate lifespans. Future work will compare these results with how PV changes in response to wear and age in primate species with more abrasive diets.

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The relationships between skull shape, muscle morphology, and muscle force vector orientation during chewing in hominids

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Hominid evolution has been characterized by profound changes to craniomandibular morphology which are thought to reflect trophic adaptions. Many of these changes have unclear effects on feeding biomechanics, obscuring our understanding of the evolution of the feeding system in hominids. Here, we investigate relationships between craniomandibular anatomy, muscle physiological cross-sectional area (PCSA) and orientation, and feeding biomechanics. We used Strand7 to map muscle attachments and calculate muscle vectors. We calculated muscle forces as species-specific measures of PCSA scaled using previously published electromyographic muscle recruitment and mandibular boundary conditions in *Macaca*.

Although jaw muscle configurations were comparable across the sample, we identified key differences between resultant force vectors during chewing. We found that a higher proportion of jaw muscle force was converted to resultant force in *Pan* and *Gorilla* relative to *Pongo* and *Homo*; there were no sex differences. The jaw muscle resultant in *Homo* was oriented closest to superoinferiorly, whereas the resultant of other taxa angles anteriorly by 2°—10°. This is associated with the narrower mandibular ramus of *Homo*, which reduces the size of the anteriorly directed masseter. Although *Homo* lacks a sagittal crest, relatively larger braincases provided a sufficiently large temporal fossa to make temporalis the strongest jaw muscle in this taxon. Although differences in mandibular morphology are often invoked to explain variation in mandibular stress and strain, our results show that muscle variation may make substantial contributions. These preliminary results will facilitate future studies investigating the coevolution of craniomandibular morphology and feeding biomechanics in hominids.

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Emerging resilience and patterns of stress: Microscopic evaluations of LEH defects among individuals from colonial Mórrope and Eten

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Dental enamel microstructures are an underutilized but indispensable tool for analyzing linear enamel hypoplasia (LEH) to provide a higher resolution of past patterns of stress. Previous research has demonstrated that individuals from neighboring colonial-era sites of Mórrope and Eten, Peru, exhibited clear differences in patterns of biological stress and disease with significantly higher prevalence of nearly every skeletal pathological condition in Mórrope. Eten shows evidence of varying degrees of buffering against negative impacts of stress. This study compares microscopic LEH patterns from the Early/Middle Colonial (ca. AD 1535-1620) Chapel of the Niño Serranito (CNS), Middle/Late Colonial (ca. AD 1620-1750) Church of Santa Maria de Magdalena de Eten (CSMME), and from both temporal periods in Mórrope. We analyzed anterior dentitions from every individual available from these sites, successfully identifying matched stress events for 10 individuals from CNS, 11 individuals from CSMME, and four individuals from Mórrope. This study tests the hypothesis that microscopic defect patterning will reflect similar patterns of stress to previous macroscopic analyses, but with higher resolution. Results of this work identified more LEH defects than previous macroscopic studies, particularly defects at earlier ages. CNS and Mórrope had the most similar patterns in distributions of age-at-defect and risk of defect by developmental stage. A significant difference in mean age-at-defect was observed between CNS and CSMME, with CNS individuals exhibiting more defects at younger ages. Results are consistent with biocultural buffering systems against the systemic oppression of colonialism which developed over time and were unique to specific communities.

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Comparisons of the skeletal preservation between the owners and sacrificial victims in ancient burials (A.D. 5th-6th centuries), South Korea

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Skeletal preservation from archaeological sites can differ by various factors including biological, natural-environmental, and sociocultural features. The purpose of this study is to explore the causes of differential skeletal preservation between the owners and sacrificial victims from the ancient Korean burials (A.D. 5th–6th centuries). We tested the hypothesis that the owners and sacrificial victims would be differently treated based on ancient burial customs by the individual's social class. To test the hypothesis, we calculated the preservation score for the 46 individuals (11 owners and 35 sacrificial victims) from Joyeong site, Gyeongsan. The preservation score was calculated for the 80 skeletal landmarks, consisting of 35 paired and 10 unpaired cranial and postcranial features, following the method of Stojanowski et al. (2002). The difference of preservation score by the individual's social class was compared using nonparametric Mann-Whitney test.

The results show that the average preservation score for the entire Joyeong population was 0.144 ($n=46$, $SD=0.157$). The average score for the owners was 0.069 ($n=11$, $SD=0.09$), while sacrificial victims had a score of 0.168 ($n=35$, $SD=0.167$). There was a statistically significant difference between two groups ($p<0.05$). These findings suggest the possibility that the skeletal preservation between two groups may be related to ancient Korean burial customs of placing the owners in a specific place during funeral preparation. It can be considered that the owners are even more poorly preserved because of their longer exposure to natural environment than the sacrificial victims, who would have been sacrificed just before the burial was covered.

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Biological relationships at pre-colonial Tlatelolco as reconstructed fom adult tooth size

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The ancient site of Tlatelolco was a high traffic market center, boasting tens of thousands of visitors daily. Despite its dense population and political influence as the sister city to Tenochtitlan—the Aztec capital—few bioarchaeological studies have focused on within-site patterns of relatedness to reconstruct microevolutionary processes at Tlatelolco. A recent analysis of subadult dentitions revealed limited biological structure and potentially high levels of gene flow at the site. Here, we present a biodistance study aimed at reconstructing relationships using permanent dental remains recovered from the ceremonial center and residential barrios of Tlatelolco. After preliminary data treatment, 22 tooth measurements representing 135 individuals were subjected to principal components analysis, hierarchical clustering, and multidimensional scaling (MDS) of resulting Euclidean distances. UPGA agglomeration resulted in two primary clusters: Cluster 1 containing 23% of the sample, and Cluster 2 containing 77% of the sample. Cluster 2 is also comprised of three distinct sub-clusters. While MDS plots reveal little visual structure, the presence of outliers suggests the sample includes individuals of distant bioregional origin. Paleopathology assessment indicated skeletal manifestation of stress and/or illness in approximately 16% of Cluster 1 individuals and 18% of Cluster 2 individuals. Evidence of antemortem trauma was observed for approximately 6% of Cluster 1 individuals and 3% of Cluster 2 individuals. Based on these patterns, it appears biological relatedness did not appreciably structure experience of stress or illness at the site, but individuals in Cluster 1 experienced violence and skeletal injury at slightly elevated rates.

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The diversity of postmarital residence patterns during the Holocene

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The history and diversity of human postmarital residence patterns and how these were shaped by social, economic and ecological conditions have long been debated. Recently, isotope and ancient genome analyses have emerged as new and potent sources for discovering matrilocal or patrilocal residence patterns. Here we used a world-wide dataset of more than 5000 ancient human genomes covering the last 12,000 years, where we studied diversity patterns compatible with matrilocal or patrilocal residence using multiple approaches. In Europe post-5000 BCE, which comprises the bulk of our data, patrilocal residence appears as the main trend, consistent with recently published site-based studies. However, the data overall mark the diversity of residence patterns among human groups across the globe, in line with ethnographic and historical evidence.

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Renewed research in the Kibish Formation with revised chronology

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The Kibish research site, which yielded some of the earliest members of *Homo sapiens,* previously dated to ca. 200,000 years ago (Brown and Fuller, 2008), exposes fossil bearing fluvio-lacustrine sediments representing a critical age interval between Middle Pleistocene and Upper Pleistocene when anatomically modern humans are believed to have emerged. The Kibish Formation is one of the few key sites for investigating the evolution of early members of *H. sapiens.* We have reinitiated field research in the Kibish Formation in 2021. During the fieldwork our team has reappraised the geological setting of the area and collected paleontological data. Recent resampling and geochemical fingerprinting of tephra layers (Vidal et al., 2022) has suggested a minimum age of 233,000 +/- 22,000 year for the Kamoya's Hominid Site (KHS) Tuff situated towards the bottom of Kibish Member II, which overlies Kibish Member I, where Omo I and II hominins were recovered in the late 1960s. This new date raises many questions about the stratigraphy and chronology of the Kibish Formation and its paleontological record. The new age for KHS Tuff implies the age of Omo I and II hominins will be older than 233,000 years. Some key questions pertaining to the current debate on the emergence of *H. sapiens* can be addressed by detailed reconstruction of the stratigraphy, geochemical fingerprinting, and dating of tephra layers particularly within Member I. Increasing the sample size for early *H. sapiens* and evidence of their behavior is a key component of our research in the area.

This research has been funded by the Leakey Foundation and the University of Arizona.

The effects of selective mortality on stature on the north coast of Peru

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Settler colonialism was a violent experience for the indigenous peoples of the Lambayeque Valley region of Peru. However, past work showed no impact upon either terminal adult stature or body mass. In particular, stature has remained remarkably consistent in both the late pre-Hispanic and Colonial periods. This study tests the hypothesis that selective mortality shaped stature, in that shorter individuals would not survive into adulthood. Stature was then estimated in 343 pre-adults and in 133 adults from archaeological sites spanning 900 CE (Middle Sicán) to 1750 CE (Colonial era). Summary ages were estimated using pre-adult dental development and adult ages were based on pubic symphysis, auricular surface, and cranial suture estimations. Sex estimations were based on cranial and os coxae morphology in adults. Using forward selection modeling, growth patterns of pre-adults were compared to the terminal stature of their adult counterparts. This indicated shorter pre-adult statures than the statures of both adult male and females. Additionally, the pre-adult stature estimates were compared to current World Health Organization fifth and 95th percentiles for body size which were larger, on average, than both late pre-Hispanic and post-colonial subadult sample populations. This model suggested that both smaller-bodied late pre-Hispanic and Colonial pre-adults were dying at greater rates relative to their adult counterparts. As a result, invariant stature before and after Spanish conquest appears related to selective mortality. These results are consistent with higher mortality for pre-adults who experienced growth disruptions and a lower mortality for taller individuals who survived into adulthood.

Diverse thinking in biological anthropology and data science: methods and mentoring

AMY E. SHAPIRO

Data Science, Nana Technologies

Diversity in thinking leads to novel approaches to solving problems; to cultivate diverse thinking, it's important to cultivate a diverse community. Dr. Kaye Reed contributed significantly to the field of paleoanthropology by applying novel approaches to analyze fossil assemblages, but also through mentoring students focusing on a wide range of disciplines. Here I share examples of how my training under Kaye's guidance has been used in my current field of data science, both through using novel approaches and being a role model and mentor.

While working as a data scientist at Yelp, I used diversity indices, a method commonly used in ecological analysis, to examine cuisine diversity among U.S. cities. I recreate this analysis by sampling over 18,000 restaurants from 10 U.S. cities in the publicly available Yelp dataset, classifying each restaurant as a single cuisine, and calculating richness and evenness indices for each city. These methods mirror how we think about the presence and abundance of species at a site and allow us to compare species diversity among sites. The number of restaurants in each city correlates positively with the diversity indices, but Tucson and New Orleans show significant deviations from expectations; I explain this by the dominance of Mexican cuisine in Tucson and more abundant "rare" cuisines in New Orleans.

I also discuss ways we can promote diversity in thinking such as through public data access, mentoring, and having diverse leadership, all aspects of Kaye's diverse legacy.

Introduction to the symposium: The contributions and legacy of Bill Jungers to the field of biological anthropology

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With this symposium, we honor the legacy of Bill Jungers and his immense impact on the field of biological anthropology. For nearly 50 years, Bill produced an extensive body of highly acclaimed research. Like many others in our field, the symposium participants have been influenced and inspired by Bill Jungers, and their research reflects his broad areas of expertise, including the evolutionary history of Madagascar, primate evolution and functional morphology, morphometrics, size and scaling, and human evolution. To provide a deeper view of Bill's research contributions, we conducted a citation analysis of his publications using Web of Science and Google Scholar. Since 1976, when he received his PhD, Bill published 193 journal articles and book chapters, co-authored two, and edited/co-edited four books. Bill's journal articles have been cited over 8,000 times, across approximately 5000 citing articles. His top-cited contributions (205-888 citations each) span not just one, but all of his myriad research interests, demonstrating his breadth of influence. Bill's research has had an impact on many fields and many scholars, both nationally and internationally - according to Web of Science, the ~5000 articles citing his work were published predominantly in anthropology, evolutionary biology and zoology, but they extend across a total of 157 related disciplines. Obviously, a citation analysis is only one small measure of a scholar's contribution and barely scratches the surface of Bill Jungers' incredible legacy to our field. This symposium aims to show that Bill's work will live on in the research of those he inspired.

Symposium supported in part by AABA

Exploring the Interplay of Diet and Shoulder Morphology in Primate Adaptations

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Geographically scattered throughout the world, non-human primates are characterized by a diverse array of locomotor adaptations. Previous studies show that variation in the morphology of the forelimb bones in Cercopithecidae reflects substrate use (Rector & Vergamini, 2018). Non-human primates' shoulder joint anatomy can similarly provide crucial details regarding their ecological adaptations and locomotor activity (Scott, 2011). The current study aimed to further explore the intersection of diet, substrate patterns, environment, and the diversity in shoulder shape to better understand how primates evolved in diverse ecological niches.

Using a 3D MicroScribe, landmarks were collected from 300 individual specimens across the Primate order. Each species was assigned to categories reflecting primary diet, primary locomotion, and environment. The primary hypothesis tested the relationship between scapular shape and locomotor strategy across the Primate order. The secondary hypothesis tested how diet and environment can also be identified through shape variation of the shoulder joint.

Non-human primates have adapted to several significant terrestrial ecoregions, including boreal tundra woods and tropical rainforests (Galán-Acedo et al., 2019). Adaptive radiation of species are linked to seasonal and changing climatic circumstances as well as forest structure in a variety of large geographic areas. These adaptations are also a reflection of primate diets. Results of this study suggest that shoulder variation in the Primate order can reflect ecological markers, such as locomotion and diet. These analyses can be used to replicate the behaviors of primate paleocommunities and their paleoenvironments by studying the relationship between forelimb anatomy and behaviors in extant primates.

Does Endocranial Shape Change Occur After the Majority of Brain Growth is Complete?

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Modern subadults complete 95% of brain growth by ~6.0 years-of-age. Given the close relationship between neurocranial shape and brain growth, it might be suggested that endocranial shape changes little after 6.0 years-of-age. Here, we test the hypothesis that endocranial shape in subadults having completed the majority of brain growth does not differ significantly from adult endocranial shape.

We collected 85 endocranial landmarks from CT scans of 5.0-8.9-year-olds (N=76) and adults (N=34: dry skulls or ammonized CT). Developmental age and sex are either known or were assessed from the dentition (crown/root only) and skeleton, respectively. Endocranial shape variation was assessed via Principal Components Analysis, on Procrustes-aligned shape variables, in Morphologika and R.

PC1 and PC2 explain 13.4% and 8.8% of the variance, respectively. Subadult-adult endocranial shapes are separated along PC1, less so on PC2, and not separated on PC3-6. PC1 defines a dolichocephalic-brachycephalic transition. Adults cluster along -PC1 (dolichocephaly), even though their shape ranges from brachycephaly-to-dolichocephaly. There is a general tendency for individuals to distribute along -PC1 in accordance with their assessed adult shape. Further, males tend to be more dolichocephalic than females. +PC2 is characterized by width expansion and cranial base angular change in adults, relative to the subadult condition.

We could not validate our null hypothesis; endocranial shape is not stable in later juvenile-to adult ages. Endocranial shape appears to become more dolichocephalic in adults as they develop. These data are consistent with newly recognized changes in brain anatomy in later juvenile-to-adult ages.

UC Berkeley Student Opportunity Fund

New postcranial fossils of *Proconsul major* from Napak, Uganda

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Proconsul major is a female gorilla-sized hominoid from the Early Miocene of eastern Africa. Few postcrania are attributed to this taxon, so little is known about its ability to navigate arboreal versus terrestrial substrates at such a large size. An associated proximal radius and distal humerus (UMP NAPCC 06'1431/1432) were recovered from the 20 Ma Napak fossil complex, Uganda. This radiohumeral joint possesses a highly spherical humeral capitulum and a well-developed lateral lip on the radius that may have facilitated pronation and supination while maintaining joint stability in a partially flexed, pronated position. A distance matrix was used to calculate the degree of dissimilarity in 3D space (Euclidean distance) between the *P. major* radiohumeral joint and those of 19 genera (424 specimens) of anthropoid primates using indices calculated from linear measurements. The morphology of the distal humerus was closest in 3D space to *Lagothrix*, *Hylobates*, and *Nasalis*, while the radial head was closest to *Colobus*, *Hylobates*, *Nomascus*, and *Papio*. Results demonstrate that the elbow of *P. major* shares affinities with taxa practicing varying locomotor modes, including suspension and both arboreal and terrestrial quadrupedalism. *P. major*'s radiohumeral joint morphology lacks any analogs among extant anthropoid primates. However, the combination of traits indicating both a fluid range of pronation and supination along with particular stability during pronation, as well as its overall similarity to arboreal taxa, suggest it could have navigated arboreal contexts despite its large size. It is not possible to infer from these fossils whether it used below-branch behaviors.

A geometric morphometric study on sexual dimorphism in human juvenile facial morphology

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Sex determination of unknown individuals is one of the primary goals of biological anthropologists. The adult skull is often used in sex estimation, due to its marked traits of sexual dimorphism. However, estimating skeletal sex from juvenile remains is controversial due to the uncertainty surrounding the presence of sexual dimorphism prior to sexual maturity. The aim of this study is to apply geometric morphometric shape analysis to juvenile skulls to explore patterns of sexual dimorphism during ontogeny and to identify the most dimorphic region(s) of the skull. Three-dimensional surface models were created from computed tomographic scans from the New Mexico Decedent Image Database of 101 male and 99 female juvenile and young adult skulls of known age and sex, between birth and twenty-one years of age. Three-dimensional coordinates of 42 landmarks and 290 curve semilandmarks were digitized. Four configurations were constructed from the skull: the viscerocranium, mandible, frontal bone, and mastoids. Generalized Procrustes superimposition, principal component analysis, and discriminant function analysis were applied to all four configurations independently. In line with previous studies, results demonstrated a low degree of sexual dimorphism and poor cross-validated classification accuracy in individuals less than 13 years of age, with the highest accuracy in the mandible and the viscerocranium. The shape similarities found between the sexes prior to 13 years of age prevent consideration of the craniofacial bones as a sex indicator in the early stages of development but support its use in adolescent individuals, especially when using multiple regions of the face.

The movement ecology of orangutan male bimaturism: alternative male tactics impact the sinuosity, total displacement, length, and speed of path trajectories

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Orangutans (*Pongo spp.*) demonstrate a unique phenomenon among primates of male bimaturism, where there are alternative morphs of "flanged" males with secondary sexual characteristics and "unflanged" males with no secondary sexual characteristics. Previous research has suggested these morphs may reflect differences in alternative reproductive tactics, with flanged males exhibiting a "sit-and-wait" approach and unflanged males performing a "go-and-find" sexual strategy. However, we lack a clear understanding of the underlying movement behaviors involved in this phenomenon. GPS data from focal animal follows (n = 379) conducted at the Tuanan Orangutan Research Station (*Pongo pygmaeus wurmbii*) and follows (n = 158) at Suaq Balimbing (*Pongo abelii*) were used to estimate the path trajectory metrics of day journey length (DJL), total displacement distance (TDD), daily path speed, path sinuosity index, and path straightness index. Data were analyzed using generalized additive mixed models (GAMMs) with the fruit availability index (FAI) included as a smoothed predictor. Unflanged males travel farther, faster, and with less sinuous path trajectories, exercising more efficient mate searching behavior. Flanged males display less linear paths, possibly to avoid male competitive interactions, but they travel farther and more linearly when long calling. Both morphs were found to travel farther during periods of higher fruit availability and adapt to low food abundance by adopting more meandering paths, possibly to better forage randomly distributed fallback foods. Our findings demonstrate the utility of the tools of movement ecology for investigating questions relating to sexual selection and reproductive tactics.

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The effect of developmental stress on survival in the Hamann-Todd Collection

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Physiological stress during growth and development often correlates with decreased likelihood of survival and increased mortality in adulthood. Physiological stress during key developmental stages is associated with long-term health consequences such as suppressed immune function and increased allostatic load. This study analyzes two indicators of developmental stress— adult stature and linear enamel hypoplasia (LEH) prevalence—in a sample of 296 individuals with known ages-at-death from the Hamann-Todd Osteological Collection and explores their association with differential survivorship. Kaplan-Meier survival analysis and log rank tests were used to test for differences in survival between groups analyzed. Here, we test the hypothesis that shorter statures and LEH presence are associated with reduced survival. Overall, there are significant differences in survival, regardless of LEH occurrence or stature, between males and females and between Black and White Americans. Contrary to the expectation, shorter statures are associated with a higher probability of survival for females (x^2=13.450, p=0.001), and there were no significant differences in survival for males (x^2=3.776, p=0.151). There were no significant differences in survival by LEH status for all groups analyzed in this sample (Females: x^2=0.373, p=0.541; Males: x^2<0.001, p=0.992; Black Americans: x^2=0.299, p=0.585; White Americans: x^2=0.009, p=0.923). Thus, differences in survival within this sample are likely influenced by factors related to adult environmental quality, as opposed to early developmental stress. Nevertheless, shorter females show lower mortality rates, which is probably the result of complex interactions between their social environment and vulnerabilities at all ages.

The Neolithic Reorganization: A Preliminary Synthesis of Paleodemography from Neolithic Age to Iron Age in Northern China

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Referred to as the "Neolithic Decline" (circa 3000–2200 BCE), the changes detected in human populations globally during this period were previously attributed unilaterally to global climatological shifts. However, modern ecological and anthropological frameworks are being developed through interdisciplinary and multiscalar analyses in attempts to better describe the human-environment interaction and *reorganization* during the Neolithic Age and proceeding Bronze and Iron Ages. Through a survey of 92 archaeological sites from Northern China dated from 6000 BCE to 0 CE containing 22,726 human remains, preliminary results demonstrated that there was no significant difference in the minimum number of individuals (MNI) or the ratio of females to males between intervals measured every 250 years (Kruskal-Wallis ANOVA: *p*=0.2165 and *p*=0.08191, respectively). Additionally, estimated x^2-values indicated no differences in estimated age groups between 250-year intervals (Children *p*=0.8999, Adolescents *p*=0.3942, Young Adults *p*=0.2029, Middle Adults *p*=0.9848, Old Adults *p*=0.1423). Nonetheless, there was a marked inflection point of MNI at archaeological sites at 3500-3000 BCE that aligned with Holocene Event 3, which marked the beginning of the Neoglacial, suggesting the negative effects of the new environmental regime. The well-studied Quaternary geologic records, ecotone diversity, and archaeological richness of China make it an ideal location to develop dynamic models of human behavior and environmental change through time and space. These models will be of importance during the current period of climate change and hold potential for guiding policymaking and informing both positive and negative changes in human, animal, and environmental health in the present and future.

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Ecological and phylogenetic signals in catarrhine root morphology

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Reconstructing primate behavior through the analysis of morphological variation is an essential part of studying primate evolution. Much of what we know about the evolutionary relationships and dietary adaptations of extinct and extant primates comes from the dental crown, as such, root system remains a relatively understudied site. This work seeks to understand differences in catarrhine molar root shape through the quantification of ecological and phylogenetic signals.

Cross-sectional slices from lower molars (*n*=191) were taken at the root cervix using micro-CT scans. 2D landmark curves were applied to the inner and outer margins of the cross-section following the cervix and pulp chamber. Semilandmarks were used to fully capture the cervical morphology. Analyses were performed on individual tooth positions (M_1, M_2, M_3) using diet to indicate group. Statistical significance was set at (*P*= < 0.05).

Allometric regressions (log-transformed centroid size) were significant for all tooth positions. Regression residuals were used as size-corrected variables for ANOVAs with randomized residual permutation procedure (RRPP). All models were significant and pairwise comparisons revealed differences between most categories except mixed folivores. Multivariate *K*-statistic (*K*-mult) indicated less phylogenetic signal in the data than would be expected under Brownian motion (M_1= 0.75; M_2= 0.69; M_3= 0.75). PCAs were used to examine data structure independent of, or aligned to, phylogeny. First and second PCs from both models were tested using the ANOVA with RRPP. Most models did not return significant results when the phylogenetic signal was redistributed. However, in significant models, folivores retained a strong ecological signal.

Funding for this research was provided by the L.S.B. Leakey Foundation.

Is the cortical-robusticity-threshold hypothesis necessary for discerning the applicability of collagen fiber orientation (CFO) analysis in understanding load history of hominin and chimpanzee femoral necks?

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Regional variations in predominant collagen fiber orientation (CFO), as seen in thin bone sections when using birefringence(brightness) analysis in circularly polarized light (CPL), are highly sensitive in detecting strain-mode-related (tension vs. compression) adaptation of habitual bending. Thus, CFO/CPL analysis should help discern load history of femoral neck (FN) regions of primates. We analyzed CFO patterns in 29 modern human femoral necks (hFN;18-95yrs) and nine adult chimpanzees (cFN). We expected CFO patterns indicative of bending (dark CFO/CPL=tension; bright CFO/CPL=compression). While regional

CFO/CPL cFN data detected adaptation for habitual bending, in the hFN the consistently bright CFO/CPL in the superior and dark in the inferior cortex across the age range ($p<0.05$) suggests net tension-to-compression (inferior-to-superior) bending (biomechanically implausible). Perhaps a 'cortical robusticity threshold' (CRT) exists below which histomorphology no longer exhibits 'conventionally expected' adaptations, explaining paradoxical histomorphology of the thin hFN. In this context, greater cancellous bone load-sharing is likely at play in the thin-walled hFN compared to the thick-walled cFN. But finite element studies show that the hFN experiences shear/torsion in addition to bending and axial compression. Animal studies have shown that bone cortices subject to prevalent/predominant shear might exhibit the brightest birefringence (shear adaptation). Shear stresses might also significantly influence the histomorphology of the hFN in ways that have evaded detection. Although conventional wisdom teaches that bright CPL/CFO is associated with adaptation for compression, high shear might be at play in mediating histomorphology of the superior hFN, which might explain its paradoxical CFO, negating strong consideration of the CRT hypothesis.

None

A comparative morphometric analysis of hominin lower third molars from Woranso-Mille, Afar State, Ethiopia

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Since the start of fieldwork almost twenty years ago, the Woranso-Mille (WORMIL) field site has yielded numerous hominin fossils that have supplemented the Pliocene record, particularly from the period between 3.8-3.2 Ma. However, the naming of *Australopithecus deyiremeda* from 3.5-3.3 Ma, the mosaic morphology of *Australopithecus anamensis* and *Australopithecus afarensis* traits present in many of the specimens from 3.7-3.6 Ma, and the overlap in dental metrics between these different species has since confounded the taxonomic assignment of hominin specimens, particularly isolated teeth, from this site.

To begin to address this issue, a more fine-grained analysis of dental variation in these samples is necessary to identify the most taxonomically informative qualitative and quantitative traits. 2D geometric morphometric (GM) analyses of tooth crown shape and analyses of cusp area and proportions have been successfully used to distinguish other hominin taxa. This study conducted GM analysis on lower third molars from WORMIL (n=11) based on 8 fixed and 30 semisliding landmarks and investigated differences in crown anatomy. It also measured cusp areas of main and accessory cusps to investigate differences in cusp proportions among the different taxa. The comparative sample included lower third molars of *A. anamensis* (n=3) and *A. afarensis* (n=11). Preliminary results of the 2D GM analyses indicate that the WORMIL specimens generally overlap with *A. afarensis* and *A. anamensis* specimens. Analyses of cusp proportions indicate that the relative cusp areas of the WORMIL sample are broadly comparable to *A. afarensis*.

Woranso-Mille project fieldwork and laboratory research was supported by the National Science Foundation (BCS-1124705), The Leakey Foundation, and the Cleveland Museum of Natural History.

What, if anything, is a primate community?

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Modern mammal communities are integral to understanding trends in evolution, biogeography, and paleoecology. Community ecological studies can focus on all species found together at a site or on subgroups defined by features like shared resource use or phylogenetic proximity. Here I review the concept and application of the primate community in comparison to other ecological groupings.

As a test case of African mammals, correspondence analyses were performed on four datasets drawn from 205 species lists and published ecological trait data: 1) all macromammals (293 species), 2) primates and potential mammalian competitors (138 species), 3) fruit-eating taxa (103 species), and 4) primates only (84 species). Sites were compared based on proportions of species traits and exhibited a similar distribution across all four subsets corresponding to habitat types and general regions within Africa. However, the distributions of species traits underlying these site-level patterns differed between the primate-only dataset and the three mixed mammalian datasets. The former differentiates sites with relatively more terrestriality, insectivory, and larger body sizes against omnivorous diets and semiterrestrial locomotion, while the latter separate sites according to arboreality and frugivory, carnivory, and large body sizes and grazing.

This confirms that studying co-occurring primates can provide valuable information about these species and their broader environmental contexts but also indicates caution is needed when defining and interpreting ecological studies based on different community subgroupings. I recommend that researchers consider using more precise terminology to facilitate extant comparisons as well as application to the fossil record.

Variation and uniformity in the linguistic expression of mindreading across four languages

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The ability to impute others' mental states, or mindreading, is a cognitive capacity expressed widely across animal genera. Despite variation in the relative complexity of its expression, mindreading exhibits structural similarities across species, pointing toward positive selection constraining the targets and function of this capacity. While some components of human mindreading may be so constrained, studies in developmental psychology suggest that the development of mindreading may be shaped by variable social phenomena, like caregiver mental state talk. Given ethnographic research indicating that there exist language communities wherein third-party mental state talk is prohibited, it is possible that human mindreading may vary more than that of other species in ways related to linguistic and cultural variation. The present research explores this outstanding conflict by comparing talk about others' mental states across L1 speakers of English, Korean, Mandarin Chinese, and Moroccan Arabic (N=224). Participants observed video stimuli and were recorded describing what they had seen. Speech samples were transcribed and coded for lexical references to third-party mental states. Rates of such references were determined by scaling the count of lexical third-party mental state references by the total number of words produced in each speech sample. Rates were then modeled as a function of language, stimulus, and participant using hierarchical logistic regression. Speech content (e.g., stimulus) was found to be the strongest predictor of the rate of mental state talk. A main effect of language was also observed, suggesting there may exist cross-linguistic differences in the frequency of third-party mental state talk.

Tracing human-animal-environment interactions using isotopic analyses in Bahrain

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Recent calls for the integration of bio- and zooarchaeological analyses, including isotopic analyses, have demonstrated the importance of multispecies approaches to understanding human-animal interactions in the past. In Bahrain, an archipelago in the Arabian Gulf, pastoralism and date palm agriculture were key strategies used by humans to procure food on an arid island. An approach analyzing humans and non-human animals is therefore necessary for understanding subsistence, and the ways in which humans transformed the landscape and the species that inhabited it over thousands of years. We demonstrate how the use of spatial statistical approaches to isotopic data (e.g., isotopic niche) offer a unique way to consider multispecies relationships and can contribute to understanding human niche construction.

Our analysis included carbon and nitrogen isotope data from humans plus 11 other taxon (n=126) spanning 4,000 years. The results showed that humans managed domesticated species in Bahrain differently, with some animals kept in the gardens sharing a dietary niche in part with humans and others more marginalized. Even within the ovicaprines, there was variability in the isotopic data suggesting seasonal or breed-specific management by humans, who needed to use specialized strategies to raise animals in this environment. Chickens had diets similar to humans, showing that their dietary isotopic niches had 100% overlap with humans (KUD 90). These results from Bahrain showcase why multispecies analyses are not simply providing a baseline for human dietary studies, but should consider the perspectives of these species and what they can reveal about human-animal-environment interactions in the past.

First insights into the inner ear otolith system of *Australopithecus* and *Paranthropus*

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The bony labyrinth of the inner ear houses the sensory end-organs responsible for balance (otolith system-utricle and saccule, and semicircular canals [SCCs]) and hearing (cochlea). The study of bony labyrinth form revealed considerable morphological diversity in the hominin lineage (SCCs and cochleae), and aided in reconstructing essential aspects of primate evolution, including positional behavior, audition, and phylogenic affinities. However, evidence of evolutionary change in the otolith system remains elusive. Such morphological variation in these gravito-inertial sensory end-organs may suggest functional differences, as their geometry is linked with positional behavior.

We approach the question of evolutionary morphological change in the hominin otolith system by first examining bony vestibule morphology in two South African hominin taxa *Paranthropus robustus* (n=8) and *Australopithecus africanus* (n=6), compared to that of *Pongo pygmaeus*, *Gorilla gorilla*, *Pan troglodytes*, and modern *Homo sapiens*. We use landmark-based shape analyses of 100 inner ears by means of virtual 3D models derived from micro-CT scans. Thirty bony landmarks were chosen to approximate otolith organ form and relative configuration.

Results show a distinctive morphology present in *P. robustus* compared to *A. africanus* and extant hominids. Specifically, *P. robustus* exhibits anteroposterior compression in bony otolith organ structure, reducing the size of the saccule and vestibular aqueduct. In contrast, *A. africanus* exhibits a modern human-like otolith system. This newfound morphological diversity: 1) aids in the taxonomic attribution of fragmentary temporal bone remains, and 2) suggests functional differences related to gravito-inertial sensation, reinforcing hypotheses on differential positional behavior in *P. robustus* and *A. africanus.*

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A closer look at the perinatal and infantile environment: A case study of deciduous microdental structures

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The microstructures in the enamel forming around the time of birth include a defect termed the neonatal line (NNL). This defect is an indicator of the birthing event where amelogenesis is interrupted creating a darkened band. Additional microdefects, or accentuated striae, are the atypical formation of enamel as a result of nonspecific stress indicators. Current research focuses on the relationship between NNL thickness and the environment during gestation and the birth event as well as correlating accentuated striae to stress events. However, additional research is required to understand how and why the NNL and accentuated striae develop.

Two individuals from the United States with known medical histories, sex, and gestational age had their deciduous dentition thin sectioned for histological analysis. The teeth viable for analysis included anterior and posterior dentition of the maxilla and mandible. The NNL and accentuated striae were identified, measured, and timing of defect was calculated.

Results indicated that all teeth analyzed possessed a NNL. However, the thickness of NNL between the individuals differed, which may be associated with differences in the birth event. Further findings include an accentuated stria found in an individual one month after birth that did not match known history of illness. This defect is potentially related to known hypoplastic enamel defects due to environmental factors during dental development. Future research will aim to gather more data from more samples to continue to explore correlations of accentuated striae to known stress events and explore the utility of dental microstructures in understanding lived experiences.

Vindija Cave (Croatia) and the Nature of Neandertal-Early Modern European Introgression

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Vindija Cave in northern Croatia is one of the most significant later Neandertal sites in Eurasia. It has yielded a large series of Neandertal fossil, Paleolithic archaeological and Pleistocene faunal remains that span the period of the arrival of early modern humans in Europe and the disappearance of the Neandertals. To date some 86 definite Neandertal skeletal specimens have been recognized at Vindija, some based only on genetics. While fragmentary, the hominin fossils exhibit a clear pattern of morphology commensurate with their placement in Neandertals. Since 2010, the biological focus on Vindija has been genetics and genomics, because the first draft Neandertal genome and later a “full coverage” genome has been extracted from specimens from the site. These data show that Neandertals contributed small, but significant genetic material to modern humans. Here we present analysis of Vindija Neandertal morphology demonstrating that Vindija’s facial morphology, anterior brain case, and scapular morphology consistently approaches that of early modern Europeans. After excluding other explanations, we argue that gene flow from early modern Europeans is reflected in the Vindija morphology despite lack of current genetic support for this interpretation. In addition, new dating results and other contextual factors that bear on this interpretation are discussed, particularly the indication that the main

Neandertal levels at Vindija (G1 and G3) are likely the same age and the chronological evidence of overlap between these Vindija levels and the earliest modern Europeans.

Vindija dating is supported by the "Last Neandertals at the Crossroads of Central Europe and the Mediterranean" project of the Croatian Science Foundation (HRZZ-IP-2019-04-6649).

Digital facial imaging as restorative action? Methodological and ethical considerations for applying virtual forensic facial imaging techniques to heritage and restitution contexts

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The depiction of modern past persons in heritage and museum contexts is a well-established practice in the United States, Europe, and the United Kingdom, but less so elsewhere. This is especially true for South Africa, where even fewer examples exist which explicitly address aspects of colonial history.

This paper offers a self-reflexive analysis of the creation, reception and impact of facial depictions produced in the context of two collaborative interdisciplinary processes directed at historical restitution. The Sutherland Restitution Initiative included facial reconstructions by Smith/Face Lab, and 'Fugitive', commissioned for the digital humanities project *Biography of an Uncharted People* produced composites by Smith and Mamathuba from slavery archives.

We consider how, in both cases, visual strategies of redaction and remediation restage the forensic facial reconstruction and facial composite – methods originating in the forensic identification of the missing and unidentified and producing images that are simultaneously products of scientific analysis and artistic interpretation – into forms of visual repatriation.

Visual methodologies, technical processes and modes of presentation operate here as metaphors of restorative action where the recreation of likely facial appearance and retrieval of names may offer forms of (attempted, provisional) repair of colonial wounds through restoring individual personhood. Scholarship which reflects on the reconstruction and presentation of human remains is considered in the context of the demands of historical restitution in post-apartheid South Africa, alongside the impact of involving 'source communities' as participants in creating and circulating these forms of visual and public communication of science.

The Sutherland Restitution Initiative was supported by National Geographic Society, Face Lab LJMU, and the University of Cape Town. 'Fugitive' has been supported by Stellenbosch University and the Dutch Consulate.

Paleogenomic and Isotopic Evidence of Maya Persistence at Late Postclassic and Early Colonial Chactemal (Santa Rita Corozal), Belize

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Santa Rita Corozal, hereafter known as Chactemal, is a Maya city located in what is now northern Belize on the coast of Chetumal Bay. Chactemal is significant because it was home to some of the earliest known Maya peoples in northern Belize during the Middle Preclassic (~800-300 BCE), was continuously occupied throughout all subsequent phases of Maya chronology, grew to become an influential Postclassic Maya capital, and was the site of the earliest Spanish colonization and Maya resistance in Belize (1531 CE). Ethnohistoric records indicate that Maya peoples strategically left Chactemal just prior to Spanish invasion and launched Guerilla-style attacks from the surrounding countryside that prevented permanent Spanish settlement in the region. By the 19th century, northern Belize became home to Yucatec Maya people who moved south across the Rio Hondo following the Caste War of Yucatán. However, there is no prior archaeological or ethnohistoric evidence that Maya people returned to Chactemal in the 16th century. With approval from the Belizean Institute of Archaeology and in close collaboration with Maya partners in northern Belize, we generated radiocarbon, stable isotopic, and paleogenomic data from 17 Maya Ancestors at Late Postclassic Chactemal to refine the settlement chronology, migratory history, and genetic relationships of the final interments at the site. We present $\delta^{18}O$, AMS dates, and genomic data indicating that some Maya people returned to Chactemal in the decades after Spanish occupation and argue that their return was shaped by memories of their ceremonial and kinship ties to the ancient city.

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A Biocultural Analysis of a Roman Tomb from Ancient Hierapytna, Crete, Greece

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The early Roman period on Crete has not received much archaeological attention, and even more sparse is published research on the inhabitants of early Roman Crete. This study of a tomb from ancient Hierapytna, one of the largest Roman cities on the island, seeks to fill this void. Rescue excavations revealed a large necropolis of over 60 tombs. One of these, Tomb 8, was a well-built stone-brick constructed tomb. Among the impressive finds are coins from the 1st and 2nd c. CE, a lead mirror frame of the 3rd c. CE, lamps dated from the 1st to 3rd c. CE, and gold jewelry.

A MNI of 12 individuals was recovered from the tomb, including adults and children with an age range of under 3 years to over 50 years. Pathologies present include arthritis, healed periosteal new bone formation, and a healed displaced fracture of the tibia and fibula. The dentition has significantly more examples of LEH than other Byzantine dentition on Crete indicating that these adults had childhoods marked by periods of stress.

The analysis of this tomb's contents provides us with a look at the lives of relatively wealthy individuals from early Roman Crete. Results show that even though the grave goods indicated wealth and the tomb was more substantial than other tombs in the necropolis, the individuals buried in the grave endured nutritional or other health stresses as children, as evidenced from their teeth, and suffered from infections and broken bones.

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A new method for measurement of nitrogen isotopes in tooth dentine at high temporal resolution

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Nitrogen isotopes ($d^{15}N$) are widely used to study nursing patterns and weaning ages. Conventional methods involve sampling dentine from sequential 1 mm thick sections— producing an averaging effect where values of each section integrate months of dentine formation. Here, we detail a protocol for $d^{15}N$ measurement of dentine with a Sensitive High Resolution Ion Microbe (SHRIMP). We sampled $d^{15}N$ on a weekly- to monthly-basis along the enamel-dentine junction in the first molar of a healthy Australian child. By relating spot position to enamel formation, we identified prenatal dentine, as well as the ages of postnatal positions over more than four years. Results show a rapid postnatal isotopic increase of 2 per mil, during which time the child was exclusively breastfed, followed by a gradual decline of 6 per mil from ~ 7 - 23 months of age as the frequency of breastfeeding decreased. The d^{15}N values varied cyclically by 1 - 2 per mil starting at ~2 years of age; a largely milk- and meat-free diet was consumed from ages 2 - 3, after which chicken and soy milk were consumed. The overall isotopic difference between complete maternal dependence and nutritional independence is consistent with trophic-level differences amongst mammals. Comparison with SHRIMP measurements of oxygen isotopes in the child's enamel do not show a similar isotopic enrichment due to nursing, instead mirroring local precipitation trends. The high spatial resolution of our measurements minimizes time averaging and can thus be precisely related to an individual's early life history and environmental variation.

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The role of tooth germ follicles in jaw osteogenesis in primates

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Rodent based studies show that cells of the dental follicle, a cellular and loosely fibrous layer encapsulating a developing tooth, form periodontal tissues. Some follicular cells express osteoblast differentiation markers and ultimately migrate to sites of alveolar bone. Whether these processes occur in primates is unstudied. Here, we studied histologically sectioned fetal and perinatal primates (n=8, including strepsirrhines, anthropoids, tarsiers) that died in captivity. We examined the tooth germs and described the degree of cellularity of the follicular lining as densely cellular (multiple layers of cells within the follicular lining) or sparsely cellular (fewer scattered cells). Next, an immunohistochemical study of selected specimens tested if follicular cells express Osterix, a marker of late differentiation stage in osteoblast precursors. All tooth germs preceding the late bell (LB) stage possess sparsely cellular follicles. In newborns, LB stage teeth varied from sparsely to densely cellular. In most fetal specimens, follicles of LB stage teeth are sparsely cellular; but in *Tarsius syrichta*, tooth germs of most LB stage permanent teeth are densely cellular. In neonates, cells within and immediately peripheral to the follicle are of varied diameter and shape (ranging from small, spindle shaped to large, oval cells). Preliminary results indicate that some follicular or perifollicular cells express Osterix, as do fully differentiated osteoblasts observed lining alveolar bone. We speculate that Osterix-reactive follicular/perifollicular cells are osteoblast precursors, implying that developing deciduous and successional teeth play a role in alveolar bone formation in primates, as demonstrated previously in mice.

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Region Dependent Patterns of Trabecular Bone Growth in the Human Proximal Tibia

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Trabecular bone is a highly responsive tissue found within the marrow cavities of the human skeleton, and it is crucial to maintaining skeletal integrity and supporting bodily functions. Bone functional morphology studies assume a direct adaptive relationship between skeletal development and mechanical function with age, and a simultaneous increase in body mass produces ontogenetic changes in the microstructure of trabeculae. However, analyses of the trabecular bone structure have revealed heterogeneous patterning of trabecular development with loading and region. Besides age and mechanical loading, factors that have the potential to influence the development and adaptation of trabecular bone include nutritional status, differing kinematics, hormonal regulation, and genetic variability, producing heterogeneous ontogenetic patterning in trabeculae development. This study utilized high-resolution 3D micro-CT scans of 31 tibiae from the Norris Farms #36 cemetery site from individuals ranging from 8 to 37.5 years old to investigate the variability of ontogenetic changes in the microstructure of trabecular bone in the proximal tibia. Dragonfly V4.1 was used to isolate trabecular bone volumes of interest (VOIs) in the metaphyseal and epiphyseal regions. Results indicated that the epiphyseal trabecular architecture was more directly influenced by loading than in the metaphyseal region with age. A morphometric analysis of metaphyseal and epiphyseal trabeculae of these tibiae will allow for a better understanding of ontogenetic changes in the bone development of different age groups and anatomical regions.

The Woman of Drybread: One person's life on the goldfields of Otago, New Zealand

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The discovery of gold in Otago in the 1860s drew tens of thousands of people to Aortearoa/New Zealand. Initially, most were younger men. In popular media, goldfields women are usually depicted as sly groggers or prostitutes, there to serve the more "animal needs" of the male prospectors. Archival research tells a more nuanced story: women also owned claims, managed hotels, worked as servants, and ran shops. In 2020 the Southern Settlers Archaeology Project, a joint endeavour between the University of Otago and Southern Archaeology, excavated unmarked graves at the Drybread Cemetery which served several regional goldmining sites in the mid-late 1800s. An older adult female, buried in a grave next to a middle-aged male, is the only woman in a sample of 12 individuals. We employed macroscopic and microscopic analyses to reconstruct some of her biological history and learn about how she lived and died on the Otago goldfields. Macroscopic analysis revealed evidence of antemortem trauma and tertiary stage treponemal disease in the form of carries sicca and gummatous periostitis in some of her limb bones. The male buried next to her exhibits evidence of a long-standing infection in the form of mixed active and remodelled periostitis in his lower limbs. Histological analysis of her teeth shows that she experienced developmental stress between one and five years-of-age and may have had a difficult childhood. We integrate our findings with the historical record to explore the female experience of frontier life and disease in 19th century Aotearoa/New Zealand.

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Paleoecological implications of the late glacial hyena den from Besaansklip (southwestern Cape, South Africa)

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South Africa's Cape Floristic Region (CFR) has long been a focus of research aiming to integrate relationships between Quaternary climate dynamics, terrestrial ecosystem change, and modern human origins. Pleistocene mammal assemblages play a key role in this research, but a lack of securely dated sites, especially from the west coast of the CFR, has posed a challenge for understanding faunal transitions and their connection to Pleistocene climate dynamics. Here, we present a paleoecological analysis of the large mammals from Besaansklip, a well-dated Lateglacial (~16 ka) hyena den from the west coast of the CFR. We identified > 400 mammalian faunal specimens from Besaansklip, which we use to infer past climate and terrestrial environmental change. Furthermore, we conducted triple oxygen isotope analysis ($\Delta'^{17}O$) on 10 ostrich eggshells (OES) from the site to estimate pCO2 during the Lateglacial in the region. Besaansklip has a high abundance and richness of water-dependent grazing herbivores, many of which are extinct (e.g., *Equus capensis* and *Syncerus antiquus*) or extirpated (e.g., *Connochaetes gnou*). This is similar to nearby sites such as Sea Harvest and Hoedjiespunt, suggesting the presence of well-watered grassy habitats. Additionally, $\Delta'^{17}O$ of OES are systematically higher than modern OES, which is consistent with expectations of low pCO$_2$. These findings reinforce previous models suggesting links between low pCO$_2$, expansion of grassy vegetation, and increased moisture availability during glacial Pleistocene.

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Isotopic evidence of subsistence patterns in Lebanon during the 5th/6th century CE

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During the 5th and 6th century CE, a series of crises strongly affected the economy of human populations living in the Mediterranean. To assess the fragmentation of subsistence models in that time in a small regional scale, we measured $\delta^{13}C$ and $\delta^{15}N$ values in human collagen from three contemporary archaeological sites in central Lebanon: Jiyeh located on the seashore (N=11), Barja laying in the hilly land c. 2km away from Jiyeh (N=24) and Chhim, further c. 5km inlands (N=30). Additionally, animal collagen was available from local ovicaprids (N=11), pigs (N=10) and cattle (N=6). Observed positive correlation between $\delta^{13}C$ and $\delta^{15}N$ values in humans (Spearman Rank Order Correlation, r_s=0.57, N=65, p<0.000001) indicates variable share of marine resources as the source of protein in diet. At Chhim most individuals have relatively low $\delta^{13}C$ and $\delta^{15}N$ values (median -19.4‰ and 7.0‰, respectively, N=26), but there is a distinct small cluster of outliers (median -18.8‰ and 10.6‰, respectively, N=4). Comparison of the four subsets indicated significant differences between Barja (median -19.6‰ and 7.3‰, respectively) together with the major Chhim cluster and Jiyeh (median -19.1‰ and 9.0‰) together with the smaller Chhim cluster. Distribution of the $\delta^{13}C$ and $\delta^{15}N$ values in animal samples suggests that pigs were more important source of proteins than ovicaprids and cattle. The results show that marine resources were consumed mainly on the seashore, and even a few kilometers away they were much less available, leaving pork and some quantities of dairy products as the major source of protein.

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Perimortem trauma in children reveals Neolithic conflict in northwestern Italy (Liguria)

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Neolithic Europe has been often depicted as relatively peaceful, perhaps due to the lack of funerary/iconographic emphasis on the armed male that would develop only later, during the Metal Ages. However, recent discoveries in Central Europe of burials resulting from massacres demonstrate that intergroup conflict was present among early farmers. Indeed, compared to earlier periods, the scale of organized collective violence increased, aiming sometimes towards the annihilation of entire groups, including children. This topic has been little researched in Italy, resulting in this region being often absent from reviews about Neolithic conflict in Europe.

We surveyed the skeletal remains from cave burial sites in the Finalese area (western Liguria) belonging to the Square Mouthed Pottery Neolithic (SMP; ca. 5000-4400 BCE), including Arene Candide Cave. Adults and adolescents showed a 9% (5/54) frequency of healed/perimortem trauma, including stabbing wounds. Surprisingly, children below 12 years of age displayed frequent (ca. 17%; 9/54) perimortem trauma attributable to interpersonal violence, such as combinations of cranial fractures, stabbing wounds, and projectile impact marks/perforations. Although frequencies were based on MNI estimates, due to taphonomic disturbance of several burials, even the absolute number of perimortem injuries due to interpersonal violence in children is remarkable, especially considering the published record for Neolithic Europe. Results suggest that SMP communities experienced warfare, which, according to some scholars, can be distinguished from feuding and other forms of conflict based on the principle of "social substitutability", i.e. considering all members of the rival group as legitimate targets, including the helpless.

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An investigation of the understudied skeletal elements of the Brazilian subfossil platyrrhines: The talus

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The nearly complete skeletons of the "giant" subfossil platyrrhines *Cartelles* and *Caipora* provide a unique opportunity for investigating the evolution of the distinctive locomotion of atelids. While the cranium and long bones of these fossils have been the focus of systematic 3DGM analyses, other parts of the skeleton like the foot have yet to be used to answer questions about the functional or phylogenetic affinities of the taxon. The talus is known to vary across extant platyrrhines based on both locomotor pattern and phylogenetic affinity; previous 3DGM analyses have recovered good separation between leaping, quadrupedal climbing, and suspensory taxa. Here we use a high dimensionality landmarking approach that includes sliding and surface semilandmarks to more thoroughly capture the complicated shape of the articular facets of the talus that have been shown to be important indicators of locomotion in previous studies. A comparative sample of extant platyrrhines (representing all three families) were included as well as the nearly complete tali of both *Cartelles* and *Caipora*. Principle Components Analysis shows strong separation between atelids and cebids, and, to a lesser extent, pithecids.

There is also separation between *Ateles* and other atelids, and partial separation between *Lagothrix* and *Alouatta*. *Cartelles* falls out with the *Ateles* distribution, in agreement with previous studies of its long bones. Contrary to prior comparative work on long bones that suggested *Caipora* resembles a giant spider monkey, the talus of *Caipora* most closely resembles *Lagothrix*.

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Best Practices for DNA Extraction from Burned Human Remains Using Rapid DNA Technology

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In 2018, the Camp Fire became the deadliest wildfire in California history, resulting in 85 fire-related fatalities, and in 2023, the Lahaina Fire became the deadliest U.S. fire of the century, resulting in a minimum of 97 fire-related fatalities. These high fatality events often cannot rely on conventional means of identification (odontology, fingerprints, etc.), necessitating a reliance on DNA technology. The ANDE Rapid DNA analysis unit allows for expedient DNA analysis, but while extensive testing in recent fires have demonstrated its efficacy as a disaster victim identification (DVI) tool, no formalized recommendations for sampling exist.

This project seeks to develop best practices for tissue and region-based sampling using the ANDE unit. Following a simulated wildfire using a human donor, 29 osseous and 30 non-osseous samples were tested using the ANDE unit, and STR amplification was assessed through both the ANDE Expert System software and manual analysis of electropherograms. While the majority of the samples yielded results consistent with predictions based on tissue conditions, multiple samples initially assessed to be too calcined did in fact exhibit positive DNA amplification. When the Expert System yielded results, median yields were 26/27 alleles. Regionally, the distal portions of the extremities most consistently amplified DNA, with 85.71% of samples being successful. Cranial and pelvic elements additionally yielded well. This preliminary testing demonstrates the efficacy of the ANDE unit for DVI work, and highlights the need for further research.

Funding for the donor was provided by the CA Office of Emergency Services for SAR Wildfire Response Training. ANDE gifted analysis chips and some associated lab materials.

Forensic taphonomy: The impact of carrion biomass load on experimental outcomes

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Forensic taphonomic research assists with time-since-death estimation in medicolegal casework, often involving simultaneous deployments of several human or animal remains, a study design that improves statistical reliability. However, this does not simulate common forensic scenarios and may affect the behaviour and abundance of local vertebrate scavengers and subsequently, the decay rate. This study, validating and expanding upon pilot research presented in 2022, examined the seasonal effect of carrion biomass load on decomposition and scavenging for a forensically relevant habitat in Cape Town, South Africa. Baseline data were compared for single and multiple clothed, 60kg porcine carcasses in summer and winter. Weight loss rate was used to track the progression of decomposition whilst motion-activated cameras recorded scavenging activity. Single carcasses decomposed rapidly, especially in the cooler, wetter winter, and experienced more scavenging activity by the Cape grey mongoose (*Galerella pulverulenta*). Across seasons, the single carcasses lost 68% of their mass by day 32 on average (567 accumulated degree days [ADD]), compared to an average of 80 days (1477 ADD) for the multi-carcass deployments. Single carcasses were scavenged substantially more, with an average of 53 hours over 384 individual visits, compared with 20 hours in 320 visits for multi-carcass deployments. Although further corroboration of these results is required, the stark differences in decomposition and scavenging activity between single and multiple carcasses suggest that carrion biomass load impacts results. In future taphonomic research where vertebrate scavengers are present, longitudinal examination of multiple single carcass deployments may produce more accurate and forensically realistic outcomes.

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From Paucity to Plenitude: Linking Hominin Diet, Habitat, and Nutrition

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Climate and environmental change have been posited as drivers of hominin evolution. Indeed, there can be little doubt that the African Plio-Pleistocene witnessed changes in vegetational physiognomy, and that these changes were sometimes broadly coincident with speciation and/or extinction events in the hominin fossil record. However, the linkages between environmental change and the challenges faced by early hominins are unclear. We know a retreat of forest environments would impact *Papio* and *Pan* very differently given decades of neoecological research on their diets, habitat tolerances, and more. For early hominins, however, our ecological knowledge, while not inconsiderable, is derived from a handful of dietary and environmental proxies which are applied at millions of years remove. Thus, even where Plio-Pleistocene environmental change and heterogeneity are evident, the consequences of each on early hominins are not straightforward.

In this poster, we begin to address this gap by revisiting hominin dietary data in the context of modeled nutritionally explicit landscapes. We take as inspiration three issues raised by Reed & Rector (2006): 1) many early hominin environments appear to have no true modern analogs, 2) hominin taxa, such as *Australopithecus afarensis*, experienced highly diverse habitats, and 3) *Paranthropus* in eastern and southern Africa were associated with open, but different environments.

A Central Asian perspective into the history and evolution of plague

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Over the last decade, the fast-growing field of ancient pathogen genomics has generated temporal transects of microbial diversity and has provided key insights into the evolutionary histories of several clinically-relevant infectious diseases. To date, the best studied pathogen using ancient genomics is the zoonotic bacterium *Yersinia pestis*, the causative agent of plague. The history and evolution of *Y. pestis* is tightly linked to its long presence and activity among sylvatic rodent populations across Central Asia, an area which today harbors the highest concentration of active plague reservoirs worldwide. This presentation offers a synthesis of archaeological, historical, ecological and genomic data from Central Asia that reveal key stages of the evolution and history of plague, focusing both on its prehistoric occurrences and historically-recorded pandemic eruptions. Ancient DNA research has uncovered the oldest lineages of *Y. pestis* between ~5,000-2,500 years ago, across regions of Europe and Central Asia, shedding light on its widespread impact on prehistoric populations and on key genetic changes that led to its emergence as a highly virulent, flea-adapted, pathogen. Furthermore, the diverse corpus of data from historical periods has revealed Central Asia's role in the emergence of historical pandemic lineages, including the Plague of Justinian (6th century CE) and the Black Death (14th century CE), and has provided insights into the formation of disease reservoirs within this region and across other areas of the world. The example of plague shows how continuing interdisciplinary research can help elucidate the processes that shaped the landscape of contemporary infectious diseases.

Unveiling the Identities of the Juvenile Mummies from the Capuchin Catacombs of Palermo, Sicily

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Two kilometers west of the historic city of Palermo (Sicily) lie the Capuchin Catacombs. This site is home to 1,284 mummified individuals, including the mummified and skeletal remains of at least 163 children. The individuals within the Catacombs provide a window into historical funerary rites, beliefs, and traditions. Until recently, anthropological research has focused on the adults; this study aims to rectify this imbalance. Using a portable direct digital (DR) radiography unit and anthropological methods, forty-three individuals, the majority of whom were housed in the "Children's Room", were examined. This methodological approach provided an insight into demography, pathology, funerary attire and artifacts, and mummification methods associated with the children of nineteenth-century Palermo.

In total, 35/43 (81.4%) individuals were between two and eight years of age. The high concentration of young children in the "Children's Room" may have been an attempt to appeal to visitors' preferences over the course of the twentieth century. Despite the high social standing of these children, some individuals exhibited Harris Lines, which suggest physiological growth disruption or disturbance. Most individuals (35/43) were spontaneously mummified, while evidence suggests the remaining juveniles were likely offered anthropogenic mummification. This may indicate a difference in social identity and/or status, which was possibly associated with family wealth. The overall findings have revealed new evidence for the age profile, health status, and funerary rites associated with the children who inhabited and died in late modern Palermo, allowing researchers to form a fuller understanding of the city and its inhabitants during this period.

This research was funded by the Arts and Humanities Research Council (AH/V014331/1).

Temporal trends and geographical variation in dentition of *Macaca sylvanus*

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The fossils of European macaques are generally considered to belong to a single lineage of *Macaca sylvanus*, which is represented by the extant nominotypical subspecies *Macaca sylvanus sylvanus* in northern Africa and Gibraltar. During the Plio-Pleistocene this lineage was much more widespread than at present, with three extinct subspecies (*M. s. prisca, M. s. florentina,* and *M. s., pliocena*) being described on the basis of bio-chronological criteria. However, no prior work has examined metric variation in this lineage across its entire geographic and temporal range. This study aims to test the hypothesis of dental reduction and geographical variation in the *sylvanus* lineage.

We collated published dental measurements of fossil macaque upper and lower teeth, specifically from P4 to M3. We utilized one-way ANOVAs and linear regressions to analyze the relationship between dental variables and temporal factors as well as geography (e.g., longitude, latitude, and country). We found significant ($p<0.05$) temporal variation in length/breadth measures and observed that samples from different geographic regions vary consistently from one another. However, different teeth and measurements (mediodistal length vs. buccolingual breadth) show different patterns, such that there is no clear support for a hypothesis of dental reduction across time. We do find partial support for a relationship between buccolingual breadth and longitude, perhaps suggesting that populations vary on an east/west gradient. As a whole, these data suggest that the current subspecies framework for the *Macaca sylvanus* is questionable and requires further investigation.

Research funded by University of Arkansas, Department of Anthropology.

Composting together: A systematic review embracing the Chthulucene

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Donna Haraway's concept of the Chthulucene captures the forces and powers in which our shared futures are at stake. The Chthulucene calls for reshaping both who is telling the stories, and the stories that are told, in order to embrace a future based on connectedness and kinship. Historically, biological anthropology has failed to follow through on calls for feminist research, defaulting to the white male gaze. Here, we provide a systematic review of the last 50 years of biological anthropology literature, focusing on research with the keywords feminist theory, gender, and women. Our review centers upon prominent anthropology and biological anthropology journals, edited volumes marking critical shifts in biological anthropological thought, as well as other works by feminist biological anthropologists. Through this review, we will consider how the repeated calls for feminist research have been accepted across the discipline without inducing a fundamental shift, demonstrating how deeply rooted patriarchal structures are within the foundations of biological anthropology. At the heart of this problem are the ways in which women's lived experiences are continuously viewed as an antipodal to the masculine. Through the lens of the Chthulucene, we reflect on the need to enact these widespread shifts reframing the discipline. Consequently, by embracing the Chthulucene, biological anthropologists can center feminist research to create spaces of refuge as praxis. Through this process of "composting" our disciplinary past, we can get both elsewhere and somewhere; we can create a biological anthropology of the Chthulucene.

Evaluating Sampling Design Effects in Isotope-Based Geolocation Assignments

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Isotopic geolocation methods, whether for forensic, archaeological, or paleoanthropological studies, rely on reference data documenting geographic isotopic variation in human tissues. As more studies provide reference data, the value of these data depends strongly on good research design principles, including the inclusion/exclusion criteria. For geolocation using oxygen stable isotope δ-values of carbonate in human tooth enamel ($\delta^{18}O$), donors who moved residences during their childhood may be inappropriate for the creation of reference datasets.

Teeth collected by Laura Regan for her dissertation research comprise one of the largest collections of isotopically analyzed teeth from living donors with known residence information. In this study, we compare spatial models of isotope distribution (isoscapes) generated when all individuals of American birth from this collection are included (n=281) with those created using only teeth that were mineralized while the donor lived in a single geographic location (n=120).

We compared both versions of the dataset against $\delta^{18}O$ values of tap water modeled at the reported locations of residence for each donor. The smaller dataset with more selective residence criteria produced higher adjusted R^2 (0.40, $p<0.001$), although the larger cohort still demonstrated significant correlation with the water δ-values ($R^2=0.31$, $p<0.001$). Split-sample iterative quality assessment reveals that use of the more rigorous exclusion criteria improves the geographic specificity of isotope-based assignments for unknown-origin samples by 20%, despite having less than half the sample size. This study showcases the importance of research design and sample selection in isoscape outcomes.

This work was supported by a grant (#4666) from the US Department of Defense and the Henry M Jackson Foundation for the Advancement of Military Medicine.

Cortical bone reflects signals of intrinsic hand muscles in *Homo sapiens* and *Pan troglodytes* across the metacarpus

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Humans and chimpanzees have distinct hand muscle configurations, reflecting different functional capacities. As muscles do not preserve in the fossil record, muscle strength and insertion anatomy must be inferred from bones. Differential patterns of cortical bone thickness are hypothesized to reflect direct attachment of muscle to bone and be related to muscle strength.

This study applied a novel approach using whole bone cortical thickness mapping and cross-sectional properties, to compare muscle functional capacities. One *Pan troglodytes* and one *Homo sapiens* hand were fixed, stained with Lugol's iodine, and µCT scanned at ~61 µm. Muscles, tendons and bones were then segmented to delineate muscle volumes and attachments within the same individual. Avizo Xfiber software visualized individual muscle fascicles, from which internal architecture and 3D force-generating capacity were estimated. Cortical bone thickness was calculated from meshes created in Stradview, and cross-sectional properties and cortical thickness quantified, and maps generated with Morphomap.

Results show force generating capacities of muscles in the human hand are greater than the chimpanzee, especially in the thenar and hypothenar regions. Absolute metacarpal cortical bone thickness values were higher in the chimpanzee, perhaps reflecting overall muscle strength and relatively long metacarpals. Cross-sectional properties were higher in the human indicating greater resistance to bending and torsion, likely reflecting stronger thenar musculature and thumb use.

Overall, these results support that muscle force generating capacity and muscle attachment geometry are reflected in differential cortical bone thickness in the metacarpals, suggesting potential for using cortical bone mapping for functional inferences in fossil hominids.

The role Kaye Reed's seminal Makapansgat research played in understanding Plio-Pleistocene paleoecology and biogeography

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Kaye Reed's research stands as a cornerstone in unravelling the complexities of paleoecology and biogeography within the hominin sites across South Africa and East Africa. Through her work at Makagansgat and other Plio-Pleistocene hominin localities using ecovariables to define vegetation habitats for various mammalian species, Reed's research has significantly advanced our understanding of the past habitats that once hosted *Australopithecus africanus*. Her work on the fauna at Makapansgat and other fossil sites in the Cradle of Humankind led her to conclude that habitats over time became more open with longer dry periods, leading to the extinction of *A. africanus*. This research has not only shed light on the biodiversity of Makapansgat and other early hominin sites but also improved our understanding of the ecological dynamics of the region.

In addition, Reed's biogeographical research incorporating large data sets of modern mammals across various habitats was used to interpret community structures to unravel the distribution patterns of fossil mammals, particularly primates and their responses to environmental changes over geological time scales. This understanding has not only provided insights into the behaviours and adaptations of mammals but also discerning how environmental changes influenced distribution and diversity.

Reed's body of work has provided a crucial foundation for comprehending the intricate interplay between hominins and their environment. Her work continues to be instrumental in shaping the narrative of human evolution.

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Gibbons as seed dispersers in a mosaic forest in Huai Kha Khaeng Wildlife Sanctuary

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Gibbons are frugivorous primates and known seed dispersers in Southeast Asian forests. Through consumption and defecation, they can disperse seeds away from the parent plant while providing additional nutrients for growth. The mutually beneficial act of seed dispersal is predicated on the fact that the seeds are not damaged after consumption. The white-handed gibbons (*Hylobates lar*) living in Huai Kha Khaeng Wildlife Sanctuary inhabit a low-fruit-producing mosaic forest. Here we sought to identify the dimensions and species of the seeds that can be passed through the gibbon digestive tract intact to understand the seed-dispersing role of gibbons in this unusual habitat. From July to September 2023, we collected fecal samples from gibbon groups, recording the seed's weight, size, state, and species. Our analysis of over 700 seeds of eight identified species found that the seed length had a mean of 9.46 ± 3.66 mm, while the mean width was 7.69 ± 3.09 mm. Most of the digested seeds passed through intact, with no visible damage (>90%). These gibbons are safely passing consumed seeds of several species, likely providing benefits to all species with seeds smaller than the upper limit of our data's length and width. This information benefits conservation efforts in Thailand by demonstrating the utility of gibbons in forest regeneration for many fruiting trees, even for species found in an atypical gibbon environment.

This research was supported by the American Society of Primatologists with the Small Research Grant.

Reuse revisited: Sleeping tree reuse by white-handed gibbons (*Hylobates lar*)

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Previous studies across gibbon species have recorded little reuse of sleeping trees and long intervals between reuse events. Gibbon sleeping tree selection is thought to be influenced by predator avoidance and proximity to morning feeding trees. White-handed gibbons living in savannah habitats in western Thailand are thus an intriguing community for sleeping studies since they cope with both an intact predator community and a resource-poor environment. We followed a single social group over a three-month period from June-August 2023 (study days = 34). Since reuse typically occurs on average after 77 days, we predicted sleeping tree reuse would be a rare event. Following Reichard et al. (1998), tree reuse was defined as repeated selection of a sleeping tree by the same individual or another group member. We observed 79 individual entries into 40 different sleeping trees. Individual reuse varied and was highest for the adult female (78.1%), followed by the adult male (70.4%), then the subadult (45.0%). We found higher rates of sleeping tree reuse, shorter intervals between reuse, and more frequent consecutive reuse than has previously been observed. Despite the presence of predators, increased sleeping tree fidelity at this site might reflect a scarcity of suitable sleeping trees in relative proximity to available food resources.

Research in Thailand was supported by the Graduate School at the University of North Carolina at Charlotte.

The effect of ambient temperature on ultramarathon performance in males and females

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Running speed decreases with increasing ambient temperature in both males and females. However, the decrease in running performance was shown to be lower in females than males at marathon distance (42.2 km) and 161 km ultramarathons. Nevertheless, the effect of ambient temperature on performance across shorter ultramarathon distances is unknown. Furthermore, except for morphological and physiological differences between males and females, it was suggested that the average speed of finishing females in higher ambient temperatures might be increased by slower females dropping out of the race. We aim to analyze the relationship between ambient temperature and average speed of males and females during shorter ultramarathon distances (50–100 km). We also aim to test the relationship between ambient temperature and the ratio of finishing females relative to males.

We obtained results of 1,545,448 participants of ultramarathons from the publicly available Deutsche Ultramarathon-Vereinigung database. The weather data for ultramarathons were obtained from the Weather Underground website. Data were analyzed using linear regression with distance as a covariate. There was a decrease in average speed with increasing ambient temperature for both males and females, but the decrease was significantly steeper in males than females (p-value < 0.0001). There was no effect of ambient temperature on the female/male ratio of finishers. Our results therefore show that the decrease of running speed with increasing ambient temperature is lower in females than males across distances from 50 to 100 km and that this difference cannot be attributed to the increased dropout rate of females.

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Exploring covariation in epiphyseal fusion in extant and extinct hominins

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Subadult remains comprise the paleoanthropological record but are difficult to interpret. One way to potentially re-evaluate immature fossilized skeletal remains is to explore the covariation patterns in skeletal data. This study quantifies the multivariate relationships among epiphyseal fusion data in contemporary *Homo sapiens* (n=1,316) and then uses data from hominin species (*Homo neanderthalensis*, *Homo naledi, Homo erectus,* and *Australopithecus sediba*) to calculate the probability of observed fusion patterns at any point during human development. Eleven appendicular epiphyseal fusion scores from the contemporary United State sample were fit to a multivariate Bayesian model in the Stan programming language to measure covariation and correlation. The results were compared against published epiphyseal fusion scores and reveal that *H. neanderthalensis* and *H. naledi* have a high likelihood of their sequences occurring in modern children under 10 years old. *H. ergaster* and *A. sediba* show higher likelihoods at certain ages, but in general, the probability of observing a comparable epiphyseal fusion pattern is quite low across all of ontogeny. Overall, the higher probabilities in *H. naledi* and *H. neanderthalensis* suggest a possible concordance with extant human populations in the multivariate sequence of epiphyseal fusion. The decreased probabilities of *A. sediba* and *H. ergaster* may be expected because the species date further in the evolutionary history. Future studies should strive for greater precision in epiphyseal fusion scores and increased diversity in the comparative hominin assemblage for future ontogenetic comparisons.

Paleoenvironments of *Australopithecus afarensis* and implications for early hominin habitat preferences

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Since its naming in 1979, *Australopithecus afarensis* has been recovered from numerous sites spanning ~800,000 years and over 1700 km. This allows us to compare the local environmental conditions that *A. afarensis* populations at each site might have experienced and formulate hypotheses regarding its habitat preferences. We examined the faunal community structures of *Au. afarensis*-bearing sediments in Woranso-Mille, Hadar, Dikika, Laetoli, Kantis, and Turkana Basin to make inferences about their seasonality patterns, rainfall, and presence of surface water. We compared their bovid abundances as an indicator of general vegetation cover. Our results suggest that *Au. afarensis* sites experienced relatively high seasonality and lower levels of annual rainfall, but that the presence of permanent rivers and/or lakes allowed for more mesic and vegetated conditions than might otherwise be possible based on the inferred seasonality and rainfall. The local hydrological systems in combination with different rainfall patterns would have been important factors for determining vegetation structures. Laetoli did not have a perennial river or lake and bushlands and shrublands were common. Woranso-Mille, Kantis, Dikika, and Hadar had perennial lakes and/or rivers, but with varying proportions of wooded and open habitats, with Kantis likely being the most open. Turkana Basin localities were all more wooded than these other sites. Relative abundance of *Au. afarensis* at Kantis, Laetoli, and the Turkana Basin were much lower than those at the other sites, suggesting that both more open and more closed conditions may have been less optimal for *Au. afarensis*.

Geometry of ranging behavior in the African apes

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Bonobos differ strikingly from chimpanzees in several aspects of their social behavior. In contrast to chimpanzees, bonobos have not been reported to kill members of neighboring groups; intergroup interactions can be tolerant and cooperative rather than uniformly hostile; and males cooperate less within groups. Pusey (2022) proposed that these differences arise from the economics of territorial defense: data showing large home range sizes in bonobos suggest that it might be uneconomical for them to defend group territories. Here we test this hypothesis using geographic information on daily travel routes of individuals in sites with at least two neighboring communities over the course of two years in bonobos (Kokolopori: N=3 communities, 2020-2022) and chimpanzees (Gombe: N=2 communities, 1973-74). We limited Gombe data to the 1970s, because previous analyses revealed a decline in competition for space with the collapse of Gombe's Kalande community. To broaden the scope of the comparison, we also included comparable data from eastern gorillas (Bwindi: 12 groups, 2012-2013) and western gorillas (Loango; 2 groups, 2020-2022). As predicted, the index of defendability was higher for chimpanzees (median = 1.12, range = 0.75-1.20, N=4 group-years) than bonobos (median = 0.63, range = 0.50-1.38, N=14 group-years), western gorillas (median=0.88, range = 0.46-1.11, N=3 group-years), and eastern gorillas (median=0.21, range = 0.11-0.49, N=24 group-years). These results support the view that economics of territoriality shape species differences in social behavior in African apes.

Are sacralization of a lumbar vertebra and lumbarization of a sacral vertebra a paired duality, with opposite expressions but with the same domains of homeotic transformation in humans?

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Are human vertebrae (V) 24 and 25 a paired duality, with opposite expressions of sacralization and lumbarization, and are these opposite expressions part of the same or different domain of homeotic transformation? This study evaluates associations among modern humans with 23 presacral vertebrae (PSV), 24 PSV, and 25 PSV with other costal-vertebral transformations. Study sample is 431 females and 1,406 males, all skeletonized, who were 20-49 years of age-at-death and who died in the United States in the 20th and 21st centuries. Data collected are numbers of PSV and sacral vertebrae, presence of rib of V7, and measurements of transverse processes of V5-V9 and V21-V22, and ribs of V8-V9 and V18-V19. Comparison of individuals with 23 PSV, 24 PSV, and 25 PSV show these significant results in both females and males: (1) individuals with 23 PSV have the shortest ribs, and individuals with 25 PSV have the longest ribs, of V18 and V19; and (2) individuals with 23 PSV have the highest frequency of six sacral vertebrae, whereas individuals with 25 PSV have the highest frequency of five sacral vertebrae. Interpretations are as follows. Individuals with 23 PSV and 25 PSV show posterior and anterior homeotic transformation, respectively, of the thoracic-lumbar and lumbar-sacral boundaries, but only individuals with 25 PSV show homeotic transformation of the sacral-coccygeal boundary. As the set of costal-vertebral transformations differs between sacralization of V24 and lumbarization of V25, inferentially the set of vertebral patterning genes that influences these vertebrae also differs.

Temporal Trends in Pacific Coast Athapaskan Stature: A Comparison of Archaeological and Early Reservation Period Data

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Physical stature is widely used as an indicator of overall nutritional status and stress. In the present study, stature estimates derived from the examination of skeletal remains of Late Pre-contact/Early Contact (ca. 500 to 1800 CE) adult Pacific Coast Athapaskans (PCA) are compared to anthropometric data from the early reservation period (ca. 1890 to 1907) to see how stature has changed over time. Applying formulae developed by Auerbach and Ruff (2010) for calculating stature from Indigenous North American remains, Precontact/Early Contact average heights of PCA adults were estimated to be 157.2 ± 2.3 cm and 149.1 ± 3.3 cm for males and females, respectively. Comparison of these data to PCA reservation period adult statures, collected by Boas and associates and by Gifford (1926) from four different reservations, indicate a sharp and statistically significant positive secular trend in stature for both biological sexes. The results are further analyzed with respect to differing developmental histories, differing historic-era reservation experiences, and other potential factors to understand the possible causes for the shift. This analysis suggests that changing diets and stress during the reservation period likely played significant roles in the secular change in stature.

Exploring the relationship between hyoid position and basihyal shape in an ontogenetic sample of tufted capuchins

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Mastication and swallowing have been proposed to be important behavioral factors in shaping the hyoid apparatus of primates. During swallowing, the hyoid is pulled cranioventrally via the suprahyoid muscles, which piston the hyoid toward the oral cavity, thus displacing the lingual base and forcing food toward the esophagus. Repositioning of the hyoid would require differences in suprahyoid muscle forces to accomplish this displacement. As variation in suprahyoid musculature would affect hyoid morphology, we hypothesize that basihyal shape reflects hyoid position relative to the mandible.

We use 3D geometric morphometrics to investigate the relationship between basihyal shape and hyoid position in an ontogenetic sample of tufted capuchins. Hyoid position was collected as linear distances from the basihyal to gnathion, gonion, posterior nasal spine, foramen magnum, and C1, and as 3D configurations using these as landmarks. Multivariate multiple regressions reveal significant relationships ($p<0.001$) between basihyal shape and all linear dimensions of hyoid position across ontogeny when size is included. However, when these distances are scaled by basihyal centroid size, only basihyal-gnathion remains significant ($p=0.052$). Principal component analyses of basihyal shape and position landmarks suggests basihyal to gnathion distances increase throughout ontogeny, while basihyals become dorsoventrally deeper, particularly around the attachment of the geniohyoid. Additionally, two-block partial least squares analyses reveal significant relationships ($p<0.001$) between basihyal shape and position, where basihyals deepen as they move posteriorly from gnathion. These results suggest that as individuals grow, the basihyal is effectively stretched by increasingly powerful suprahyoid muscles needed to displace an ever-distant hyoid during swallowing.

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From Birth to Maturity: A Phylogenetic Investigation of Sexual Dimorphism in Primates

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Hair patterning serves as a mechanism for complex visual and social signaling in primates. Our study offers a comprehensive analysis, focusing on two primary aspects: 1) Natal Coats and 2) Adult Sexual Dimorphism. Adult Sexual Dimorphism is divided into two sub-aspects: 2a) Sexual Dichromatism and 2b) Hair Morphology Dimorphism (beards, capes, etc). We analyzed data from 244 primate species to investigate these traits and their interrelationships in a phylogenetic context. Natal coats were observed in 50% of the species. Using phylogenetic logistic regression, we found that 82% of species with hair morphology dimorphism and 84% of species with sexual dichromatism exhibited natal coats. In other words, species with some form of adult hair sexual dimorphism were more likely to have natal coats. Sexual dichromatism was present in 33% of species (partial and complete), with females lighter than males in 58% of these species. Among the 15 species with complete (full-body) dichromatism, only one had darker females. For partial dichromatism, no single body part was consistently affected across species. Hair morphology dimorphism was observed in 23% of species. In a focused analysis of 55 species with dimorphism, 23 displayed dimorphism exclusively on the head and face, 6 solely on the pubis, and dimorphism varied across affected body parts in the remaining species. Our research delivers a detailed trait-wise analysis across primate species, providing key insights that pave the way for future studies on both social signaling mechanisms and biological underpinnings of sexual dimorphism in primates.

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Inequality Emerging: Habitual Activity in Relation to Diet and Mortuary Practices at Zvejnieki, Lake Burtnieks, Latvia

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The emergence of inequality among hunter-gatherers is associated with patterns of mobility, resource intensification, and ideological practices related to the appropriation of memory. The Zvejnieki site along Lake Burtnieks in Latvia is a persistently occupied landscape that dates from 7000 to 2500 cal BC. Approximately 25 percent of burials at the site include tooth pendants affixed to the body. Individuals buried with pendants consumed more terrestrial resources. Individuals without pendants consumed more aquatic resources. These differences begin in the post-weaning environment. This work predicts that variation in burial practices and diet will be further embodied in habitual activity. Cross-sectional properties and shape ratios were estimated for adult humeral and femoral diaphyses using PQCT scanning methods, and these properties were standardized by relevant size variables. Cross-sectional properties and shape ratios were then compared between individuals buried with and without pendants to understand if differences in intensity and pattern of habitual activity could be identified. Significantly greater femoral polar second moments of area were recorded in males with animal tooth pendants, though no differences in femoral strength ratios were found. In addition, significantly greater anteroposterior relative to mediolateral humeral strengthening was found among individuals without tooth pendants, while those with tooth pendants had more equivalent ratios. No differences in humeral strength/rigidity or asymmetry were observed. These results suggest that inequality is tethered to behavioral practices that reverberate across multiple spheres of the life cycle. Bioarchaeological studies of inequality will benefit from a life history approach that captures these interactions.

Social Science and Humanities Research Council of Canada (944066): "Individual life histories in long-term culture change: Holocene hunter-gatherers in Northern Eurasia"

Maternal Connections: The Circulation of Support During Pregnancy Among Shodagor Women

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Human reproduction has evolved to be a social process through the appearance of cooperation between individuals to increase the survival and well-being of both mother and infant. Previous research has illustrated the importance of support systems for the mother during the postnatal period. Specifically, the presence of support is associated with positive maternal and infant health outcomes while a lack of support is associated with negative outcomes. Less research, however, has been done regarding social support during the prenatal period, another critical time in the health and well-being of both mother and fetus. Within this exploratory study, the prenatal period is studied for the purposes of both filling in the research gap regarding support provided to mothers prior to giving birth and understanding the extent of social support networks within a Shodagor community. Data was collected retrospectively via thirty in-depth interviews with Shodagor women living in Matlab, Bangladesh who had previously given birth. Interviews were translated, transcribed, and analyzed for themes regarding the forms of support given to mothers during pregnancy. Data analysis concluded the prominence of several different themes within support provided during pregnancy, including giving advice about the processes of birth and breastfeeding, as well as reassurances about the normality of pregnancy. The results conclude the importance of others providing support to women prior to giving birth and how this support can circulate throughout these various networks of support.

This exploratory study was funded by a NSF REG Grant.

The use of macromorphoscopic analysis to examine nonmetric skull variation within a gorilla subspecies: *Gorilla gorilla gorilla*

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Macromorphoscopic analysis (MMA) was used to assess variation of ten skull features in 20 western lowland gorilla (*Gorilla gorilla gorilla*) specimens. Non-metric analysis has been used to document human variation in skulls to track ancestry. MMA has yet to be used in the study of population variation among non-human primates; rather, most studies have been focused on metric variation of dentition and limb bones. Here, western lowland gorilla specimens were chosen based on the availability of digitized skulls, the number of complete skulls of adult individuals, and documented geographical origin of specimens. Twenty adult individuals (14 males and six females) were online collected from the Smithsonian 3D digitalization catalog. After specimens were selected for analysis, a methodology was developed based on previous MMA studies conducted with human specimens. Eight traits common to hominoids were analyzed, as well as two non-human primate traits included to link macromorphoscopic analysis to heritability in non-human traits. Ten traits were scored on each of the 20 individuals using MMA. The data was then analyzed using correspondence analysis in RStudio. Results were interpreted based on male versus female expression of traits, geographical expression of traits and the expression of traits on each specimen. The results showed that while there were no significant differences among males and females, nor differences in geographical location, there were four traits that showed significant differences in the expression of traits in the overall sample.

Identification of ecological, locomotor, and morphological indicators of semi-terrestriality in anthropoid primates

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Semi-terrestriality, the utilization of both arboreal and terrestrial environments, is commonly discussed in the primatological literature but inconsistently defined, limiting its study in fossil taxa. This project aims to fill that gap by investigating the ecological, morphological and locomotor variables that characterize semi-terrestrial taxa.

18 semi-terrestrial and 17 arboreal anthropoid taxa were identified from the literature. Ecological data were collected from mammalian demographic and environmental databases; postcranial measurements and locomotor data were collected from the literature. Three stepwise canonical variate analyses (CVA) were run (ecological, locomotor, and morphological) to identify factors that discriminate between semi-terrestrial and arboreal primates.

The ecological CVA retained population size, social group size, and percentage of leaves in the diet as variables. CV1 (55.8%) differentiated semi-terrestrial platyrrhines from arboreal and semi-terrestrial catarrhines. CV2 (26.9%) distinguished semi-terrestrial platyrrhines and catarrhines cluster away from their arboreal counterparts. The behavioral CVA retained bridging, leaping, quadrupedal walking, climbing, scrambling/clambering and bimanual suspension as variables. CV1 (62.3%) separated semi-terrestrial platyrrhines from semi-terrestrial catarrhines, while CV2 (31.5%) distinguished both semi-terrestrial taxa from arboreal taxa. The morphological CVA did not retain any size-corrected variables, with no iteration of relative long bone lengths differentiating between any of the groups.

These results indicate select ecological and locomotor variables can reliably identify semi-terrestrial taxa, helping to improve our understanding of this enigmatic behavior. Future studies should likely include measures of specific bony features to more fully investigate potential morphological indicators of semi-terrestrial behaviors.

The influence of evolutionarily significant human facial characteristics on perceived attractiveness: An experimental approach

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Mate choice systems in animals often involve evolutionarily-selected honest signaling mechanisms assessing mate quality, including direct selection for higher parental investment and indirect selection for higher genetic quality of potential offspring. Secondary sexual characteristics often act as signals of mate quality, and hormone-dependent features can evolve due to either type of sexual selection. In humans, secondary sexual characteristics include larger chins and more prominent brows in male faces, which evolved in tandem with changes to forehead height and midfacial length in response to brain growth. The aim of the present study was to identify the independent and relative influence of each of these four distinctively human traits on perceived attractiveness, where a tall forehead, smooth brow, small face, and prominent chin were considered the facial dimensions more recently evolved through sexual selection. 503 participants in an online survey ranked both attractiveness of incremental alterations within single traits, and attractiveness of large alterations across multiple traits in a series of silhouetted facial profiles. Results suggest stabilizing preferences for forehead height and chin prominence, and directional selection against brow prominence and midfacial length. Overall, preferences were strongest for a prominent chin and smooth brow. Relative preferences were sex-dependent—brows were the most influential trait for male preferences, and chins were the most influential for female preferences. These findings suggest that smooth brows may signal high parental investment and remain under direct sexual selection, while prominent chins may signal genetic quality and heterozygosity and remain under indirect sexual selection.

Heterogeneous intergroup encounters in a single population of blue monkeys

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Relations between conspecific primate groups are variable, ranging from intolerant (antagonistic or avoidant) to neutral to affiliative. In some cases, this variation is evident in a single population, whose groups interact in multiple ways. We examined one such taxon, the blue monkey (*Cercopithecus mitis stuhlmanni*), whose intergroup interactions in an equatorial rainforest may be intolerant (64%) or neutral (36%). We evaluated ecological and social factors that might predict different types of encounters, using data from 9 groups over 24 months. We first investigated monthly encounter rates, finding that fruit availability related positively to the rate of intolerant encounters, but not to rates of neutral or total encounters. We next examined variables that might predict whether *individual* encounters were intolerant versus neutral. Ecological factors (fruit availability, time of day) did not influence the odds that an individual encounter was intolerant versus neutral. We examined social variables in a subset of the data including encounters between two study groups with well-known histories. The odds of intolerant (versus neutral) encounters were lower when opponent groups were of more dissimilar sizes and when they had fissioned more recently, but appeared unrelated to the proportion of females with dependent infants or the location of an intergroup encounter on an edge-center axis in opposing groups' ranges. Overall, social factors appeared more important than ecological factors in explaining variable encounter types within this population. More generally, these results suggest that it is important to consider social factors to understand variable inter-group relations.

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Proportional Mortality During the 1918 Influenza Pandemic in Alaska

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Background: During the 1918 influenza pandemic, social and biological factors combined to create a marked heterogeneity of disease burden within populations. Alaska, then a territory of the United States, shows particularly striking mortality diversity, and Alaska Natives (AN) have a higher baseline mortality than their non-Indigenous counterparts. This study expands on baseline knowledge of mortality within Alaska territory during the pandemic and introduces mortality rates by indigenous status and sex.

Methods: All available death certificates recorded in Alaska from 1915-1921 (n=7,147) were analyzed. Mortality rates were calculated using population estimates from United States census reports (1910 & 1920). A multilinear regression analysis was used to determine the impact of Indigenous status and sex on pneumonia and influenza (P&I) death.

Findings: Raw mortality numbers show that AN P&I deaths were 4.4 times higher than non-Alaska Natives (NAN). Correcting for population size, proportional deaths were 6 times higher among Alaska Natives during the height of the pandemic. This is an increase over the baseline disparity in mortality. There were no sex-based differences in either group.

Conclusions & Implications: Calculations of proportional mortality allow for deeper investigation into the 1918 pandemic, especially when comparing mortality distributions by Indigenous status. These findings reinforce the importance of incorporating various sociocultural analyses into pandemic mortality studies, and highlight the need for increased understanding of pandemic impact on Indigenous populations.

Human mitochondrial DNA informs about early wheat cultivation and its introduction routes from the Levant to Central Europe

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Legend suggests that pasta first arrived in Europe when Marco Polo introduced noodles to Italy during his historical exploration of the Far East in the late 13th century. However, newer research provides evidence that pasta can be traced to Europe back to the 4th century BCE. when an Etruscan tomb carving shows a group of natives making flat pasta. Furthermore, by 800 BCE, the Greeks mention the existence of laganon, a flat pasta sheet sliced into irregular strips. The ancient Romans later adopted this practice after they occupied Greece and renamed it Lasagne platina.

Tracing domestication and cultivation of wheat, and its evolution into different kinds of pasta and wheat products, provides a possible migration route from the Levant to central Europe. The accumulation of human mitochondrial DNA mutations and phylogenies can also be used as tools to trace haplogroup migration over time. By considering both ancient and modern mtDNA lineages, and using Network phylogenetic software, we determined that several mtDNA haplogroups, including X2f, U8, X2m2, T1c1a, and W6c, reveal evidence of movement possibly paralleling the introduction of wheat and evolution of pasta across two possible westward migration routes: maritime and land routes.

Of those mtDNA haplogroups, X2f and X2m2 show an age, structure and spread pattern that makes them viable candidates to model this westward historical migration. The co-examination of wheat evolution and mtDNA haplogroup tracking helps show the migration pattern of central Europe innovatively and interestingly, and can provide new insights in the field of food Anthropology.

DNAm of stress-related genes in persons living with HIV

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Persons living with HIV are likely to have experienced high levels of lifetime trauma and are vulnerable to mental health disorders. Lifetime trauma and PTSD have both been associated with DNA methylation (DNAm) at various stress-related genes, but have not yet been studied in people living with HIV. In a sample of 70 participants with HIV (mean age = 50 yrs, SD = 12.6) recruited from an urban HIV program at baseline, and 51 of these participants after 2 year follow-up, we investigated DNAm in whole blood of two sites in intron 7 of *FKBP5*, a glucocorticoid feedback regulator, and six sites in the promoter of *SLC6A4*, the serotonin transporter gene. We performed multiple linear regressions to evaluate whether DNAm was associated with trauma exposure and mental health symptoms, adjusting for age, sex, and race. Despite high levels of lifetime trauma (mean = 4.6 traumatic events, SD = 3.9), DNAm at neither gene region associated with trauma exposure. However, DNAm was consistently associated with various mental health outcomes at both genes. Specifically, *SLC6A4* methylation negatively associated with PTSD symptoms at baseline (B = -0.03, SD = 0.01, $p = 0.0135$). *FKBP5* was negatively associated with anxiety (B = -0.30, SD = 0.07, $p = 0.0002$) and depression (B = -0.23, SD = 0.10, $p = 0.0251$) at follow-up. This is the first study of DNAm of stress-genes in persons living with HIV, and generates hypotheses to be replicated with larger samples.

This study was funded by the Feinstein Institutes for Medical Research Advancing Women in Science and Medicine Award, provided by Concerned Parents for AIDS Research.

Fluctuating Cranial Asymmetry among Housed and Unhoused Individuals in Los Angeles County

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Fluctuating asymmetry (FA) is defined as a random deviation from perfect symmetry in bilateral elements and a comprehensive body of literature supports the use of fluctuating cranial asymmetry (FCA) as a biomarker for interpreting socioeconomic status in both modern and archaeological populations. In the present study, we test whether higher degrees of FCA may be seen among a sample of unhoused Los Angeles residents. Documenting markers of physiological stress amongst the unhoused in this post-COVID pandemic world can also establish a baseline from which we can compare the health inequities that will be exacerbated as a part of the multitude of consequences of the pandemic. To determine FCA, an asymmetry metric can be calculated as the arithmetic difference between left and right inter-landmark linear distances. We obtained craniofacial metric measurements, which captured facial and neurocranial shape, from 2-dimensional photographs of Los Angeles County Medical Examiner forensic anthropology cases using ImageJ and craniometric measurements used in Fordisc analysis (n=33). Housing status was estimated from contextual information provided in investigators' reports as well as scene photographs. When comparing asymmetry of the housed and unhoused individuals, the greatest differences in absolute asymmetry were found in opisthion to most posterior point of the occipital condyles, mastoid height, malar maximum height, and orbital breadth. This pilot project will help guide future research in FCA in Los Angeles and beyond.

The Turkana boy turns 40: a new reconstruction of the pelvis of KNM-WT 15000 and its projected adult morphology

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The year 2024 marks the 40th anniversary of the discovery of the remarkably complete male *Homo erectus* juvenile skeleton KNM-WT 15000. However, his pelvic shape remains enigmatic owing to its fragmentary and subadult condition. Specifically, the lack of associated craniodental and pelvic remains for *H. erectus*, coupled with the inability to estimate adult pelvic morphology in this particular specimen, complicate confident taxonomic assignations of other isolated early hominin pelves that are not associated with craniodental specimens, such as KNM-ER 3228. Here, we used 3D geometric morphometrics to predict adult hipbone morphology of KNM-WT 15000 by applying the growth trajectory of modern humans to our pelvic reconstruction. Our comparative sample included 103 CT scan-generated 3D models of hipbones from boys aged 8 to 19 with about 10 individuals per year cohort, 100 adult hipbones ≥20 years and other fossil hominin pelves. Due to the discrepancy in previous age-at-death estimates of KNM-WT 15000 based on dental microanatomy, tooth development, epiphyseal closure of the elbow joint, and the shape of the distal femoral epiphysis, we calculated mean growth form vectors from all possible ages of individuals aged 8–15 years to individuals aged 20 years and older, and we applied these vectors to our KNM-WT 15000 hipbone reconstruction. The projected adult KNM-WT 15000 hipbone shapes showed phenetic affinities with that of KNM-ER 3228 in the main axes of morphological variation (i.e., PC1 and PC2), but exceeded the intraspecific variation in other aspects. Hence, the implications for taxonomic attribution of KNM-ER 3228 are discussed.

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Exploring pitting enamel defects as a potential new tool for phylogenetic connections in fossil hominins

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Pitting enamel hypoplasia (PEH) is common in *Paranthropus robustus*, but has rarely been described in other primates. This study investigates PEH occurrence in 83 hominin dental remains with intact crowns from Omo, Ethiopia, comparing the findings to taxa in other locations. Tooth size and 2D enamel thickness were also quantified in both eastern and southern African samples to examine potential associations with PEH occurrence. PEH was not observed in Omo anterior teeth, enabling a comparison of frequencies in posterior teeth only. The PEH observed in Omo specimens, both robust and non-robust, closely resembles that in *P. robustus*. A high prevalence of PEH was found in *Paranthropus* (*P. boisei* and *P. aethiopicus*) specimens, with eight of 29 permanent teeth, and a minimum of three deciduous molars, exhibiting PEH, spanning a broad range of Omo stratigraphic units (approximately 2.9 Ma to 1.9 Ma; Omo stratigraphic levels C to G). For non-robust material, only the earliest deposits (Omo stratigraphic level B, around 3.0 Ma) showed PEH (5 of 15 permanent posterior teeth; likely *Australopithecus afarensis*). Later non-robust hominin specimens (including early *Homo*) did not exhibit PEH (Omo stratigraphic levels C to L: 2.9 Ma – 1.1 Ma; N = 32 permanent posterior teeth). No support was found for a reduction in tooth size or enamel thickness being associated with PEH. These consistent defects across early hominin taxa in eastern and southern Africa suggest a shared etiology. We hypothesize a common genetic cause, therefore potentially offering novel phylogenetic insights into the hominin family tree.

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Asymmetrical heat and moisture exchange during the nasal cycle: Investigating the influence of mucosal congestion on human nasal form and function

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It has been hypothesized that the nasal cycle—the periodic alternation of mucosal congestion and decongestion between the two nasal passages—allows the congested side to "rest" while the decongested passage handles the majority of respiratory air-conditioning. However, decongestion inherently reduces a passage's surface-area-to-volume (SA/V) ratio, which diminishes its capacity for respiratory heat and moisture exchange—counter to expectations for an increased role in respiratory air-conditioning. Accordingly, this study employed Computational Fluid Dynamics (CFD) analysis to directly compare heat and moisture transfers between the nasal passage in 3 models of the same human nose with varying mucosal congestion levels: asymmetrical (left/right = 90/10%), mid-cycle (left/right = 50/50%), and fully decongested (left/right = 0/0%). Consistent with expectations, the SA/V ratios of both passages were higher in the asymmetrical (left=1.06, right=0.56) and mid-cycle (left=0.84, right=0.64) models compared to the fully decongested model (left=0.60, right=0.48), which also corresponded to higher choanal air temperature and moisture values. For the asymmetrical model, the highly congested left passage exhibited substantially higher air temperature and moisture values (32.6°C, 75.3% of pulmonary humidity) at the choana compared to the more decongested right side (23.2°C, 54.7% PH). These results suggest the possibility that the decongested side may primarily facilitate volumetric intake of oxygen, leaving the congested side to contribute enough heat and moisture to adequately condition the entire inspiratory volume once the two airstreams coalesce in the nasopharynx. Additional testing of this hypothesis is needed to better understand the role of soft tissues during human nasal evolution.

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Testing the application of *seda*DNA techniques for potential recovery of leached DNA during decomposition

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As genetic research continues evolving and the value of genetic information is increasingly recognized, interest in ancient and forensic DNA is growing rapidly. In bioarchaeological and forensic contexts, DNA is typically recovered from bone or other biological sources; however, bone is not always preserved and destructive techniques can raise ethical or cultural concerns for communities. These concerns may be addressed by indirectly targeting human DNA using secondary sources, such as DNA that has leached into surrounding sediments during the decomposition process. This alternative approach allows for genetic information to be produced without any destructive analysis of human remains.

In this study, we explore how human DNA *might* be recovered from sediments by testing multiple *seda*DNA extraction methods using proxy samples of homogenized mammalian DNA and sediments. The quality and quantity of DNA recovered from each method were compared to assess the effectiveness of existing *seda*DNA techniques in extracting mammalian DNA from sediments. This study serves as a preliminary exploration into the possibility of recovering human DNA from sediments. In this early stage of development, proxy samples were used to allow for extensive testing, optimization, and replication without causing harm to human remains. These test results will guide the development of an optimized DNA extraction protocol that maximizes the recovery of authentic mammalian DNA from sediments, which will subsequently be tested with sedimentary samples containing human DNA.

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Dental mapping: A potential GIS application for identifying congenitally missing teeth

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Differentiating between antemortem tooth loss and congenital absence can be challenging in archaeological human remains. This distinction is often made through analyses of dental attrition, and the size of the remaining diastema. In cases of dental agenesis, it is common for the teeth to shift mesially to fill the gap left by missing teeth. However, this is complicated by clinical literature that highlights both the variable degree of shifting, and the possibility for shifting in cases of AMTL at a young age.

Dental radiographs of 598 individuals were assessed from the open-access Panoramic Radiography Dataset from the Universidad Nacional de Asunción, Paraguay. Individuals with fully erupted second molars exhibiting missing premolars, canines, and/or incisors, either due to agenesis or AMTL, were included in this study (n=46). GIS methods were used to standardize radiographs for tooth size and position through georectification. Teeth were then converted into polygon shapefiles and investigated statistically using nearest neighbor analysis and cartesian coordinate values.

A Mann Whitney test was used to compare the nearest neighbor ratio as a proxy for dental spacing between individuals with agenesis and AMTL ($p = 0.045$). Coordinates for tooth position when adjacent teeth were missing were compared to a control group using both Mann Whitney and Kruskal Wallis tests. These revealed significant shifting in most cases ($p < 0.05$), but only occasionally separated agenesis from AMTL.

This study represents a preliminary investigation into the application of GIS methods for problems facing dental anthropology and highlights the potential impact of continued research.

According to Matt Cartmill, using the word "unique" to describe humans is complicated, but it may be a good term for describing Matt

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The quest to define humans as unique has a long history with claims for particular features frequently challenged. Matt Cartmill, is a contributor to these debates and has noted that we can call anything unique because we have the power to define what unique is (see Cartmill and Brown "Being Human Means that "Being Human" Means Whatever We Say it Means"). A classic example is the proposal that language is unique to humans because that's how language is defined. Candidates for human uniqueness that Cartmill and Brown have explored are prosociality, preverbal imitation in infants, theory of mind, and ability to destroy the world in which we live. We ourselves have fallen victim to the need to define our species as "special" in our research on human birth. We have referred to several aspects of the process as unique or, at least, unusual, including rotational birth, emergence facing away from the mother, and the presence of birth attendants. All of these assertions have been challenged with data from the fossil record and observations of primate birth. We suspect that calling these characteristics unique or special sparked research to debunk our claims. Cartmill and Brown have turned the question of human uniqueness around to ask "Which of our peculiarities give humanity its unique importance and significance?" This may be a better way to consider human characteristics. In the end, it may be true that only the individual human can be called unique. In that case, Matt Cartmill certainly fits the description.

Collective movement behavior of sulawesi moor macaques in an anthropogenic environment

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How group-living primates come to a consensus about navigating their environment is a result of their decision-making processes, where overall decisions can be made by one or many individuals. Although decision-making has been examined in several primate taxa, it remains underexplored for primates living in anthropogenic landscapes. To shed light on consensus decision-making and flexibility in this process, we examined collective movement behavior in a group of wild moor macaques (Macaca maura) experiencing roadside provisioning within Bantimurung Bulusaraung National Park in South Sulawesi, Indonesia. Our goal was to determine whether individual characteristics (i.e., sex, dominance rank, and/or social network centrality) predict the likelihood of initiating collective movements and if the opportunity to receive food provisions along the road would alter these patterns. Using the all-occurrences method, we recorded the location, time, and identity of initiators and followers of each collective movement observed from March - June 2023. We observed a total of 61 successful collective movements. Initiation was distributed amongst most of the group, indicating partially shared decision-making. While dominance rank was found to be a predictor of initiation overall, sex and social network centrality were not, diverging from our predictions. However, initiation may also be context-specific, as initiation in forest-directed collective movements was better predicted by sex (males), while road-directed collective movements were better predicted by dominance rank. Examining the decision-making processes in this species through collective movements can provide insight into how primates come to a consensus and the extent to which anthropogenic factors shape these processes.

Faith and medieval mouths: dental pathological lesions in a multi-faith Portuguese skeletal assemblage

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We present here the analyses and results of dental pathological lesions (caries, antemortem tooth loss, periodontitis, periapical inflammation, dental wear, and calculus) from skeletal remains recovered from municipal excavations in central Portugal. These assemblages comprise multiple faith communities from the medieval period (Muslims and Christians), as based on their distinct funerary treatment. As such, the presence of distinct faith communities buried in adjacent graves offers us the opportunity to furnish a comparative approach to see how health and disease (in this case, of the oral cavity) vary by faith community. Based on previous dietary, ethnohistoric, and textual evidence, we hypothesized that Islamic dental remains would exhibit significantly lower frequencies of dental pathological lesions (especially caries and calculus) compared to their Christian counterparts. A total of n = 1,945 dental septa (925 female, 1,020 male) and n = 1,560 (723 female, 837 male) teeth from Islamic individuals were compared with n = 1,160 Christian dental septa (488 female, 672 male) and n = 866 (343 female, 523 male) teeth from Christian individuals to examine inter- and intra-faith variability in dental pathological lesions. Results from likelihood ratio tests exhibited significant differences once corrected for antemortem tooth loss, with Christian males in particular exhibiting higher frequency of caries ($G = 21.40$, $p < 0.01$) and calculus ($G = 5.42$, $p = 0.04$) compared to their Islamic counterparts. Results and patterns of dental pathological lesions are discussed in terms of religious and temporal differences in diet, hygienic regimens, and reproductive ecology.

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Stature Comparison Between 18th Century Blacks in the Western Hemisphere

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Adult stature is achieved through a combination of genetic potential, climate, nutrition, development history, environmental quality, and social and economic stressors. Previous research has shown that the compounded contributions of all these factors cause significant variations between and within human populations. Exposure to systemic stress has a significant impact in the stature of individuals, and as such support the use of stature as a measurement of accumulated stress during early life. This study examines regional variation in stature outcomes between contemporary populations of free and enslaved Africans, to help quantify the lived experiences of enslaved people in the U.S. Adult stature was estimated from Newton Plantation cemetery (n=10) using regression formulae for black males and females. Comparative stature estimates were obtained from four other collections: Paul Remely and Belleview Plantations (n=19), which represent the lives of Africans enslaved on two estates in South Carolina between 1738 and 1870, and three samples (N=225) of free blacks in the United States during the late 18th and early 19th centuries. The results of an ANOVA indicate significant differences ($p<0.05$) in the variation between populations for both males and females. Pairwise comparisons show variance among females of the Newton, Belleview, and Remly Plantations. These results demonstrate regional variations in stature, and highlights the differential exposure to stressors and resources. A comparison of population statures adds important details to the growing literature dedicated to better understanding the lived experiences of enslaved and free African people.

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Erasing identity: Presenting postmortem skeletal alterations as evidence of structural apathy in a human osteological teaching collection

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Human skeletal teaching collections provide integral sources of data and resources for education in biological anthropology. With increased emphases on ethical considerations, instructors are reevaluating the use of purchased skeletons and unprovenanced deceased individuals in their teaching collections, as there is always a risk of unintentionally damaging remains with repetitive handling. In this study, we analyzed postmortem damage on human skeletal remains recovered from the Department of Biology's Comparative Anatomy Collection at the University of Louisville. For cranial, postcranial, and dental elements we categorized postmortem alterations broadly, noting 1) cortical bone damage/trabecular bone exposure, 2) cracks/fractures, 3) discoloration/ink/staining, 4) adhesive inclusions, and 5) hardware/discoloration associated with hardware. All cranial bones (n=12) retained some adhesive material; eight bones exhibited postmortem cracks; eight were discolored from ink marks or staining; and four bones showed evidence of hardware. Among dentition, 16% (8 of 51) anterior teeth and 13% (10 of 79) posterior teeth were damaged postmortem. Of 81 appendicular bones (scapulae, clavicles, humeri, ulnae, radii, os coxae, femora, patellae, tibiae, and fibula), we observed high rates of cortical damage/trabecular exposure (79%), discoloration (26%), evidence of hardware (17%), and adhesive (4%). Lastly, 87% of ribs and 91% of vertebrae showed trabecular exposure. These postmortem alterations, however, are consistent with amateur restorations, long-term skeletal deterioration, and damage from handling. While the acquisition history of this teaching collection represents a narrative of structural violence, we maintain that the postmortem treatment reflects structural apathy, unfortunately, embedded in the classroom.

Seeing Stress in Small Spines: A Biomechanical Approach to Spinal Lesion Distribution in Children from a Post-Medieval Industrial Dutch Community

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Activity-related pathological lesions such as osteoarthritis and Schmorl's nodes have been used as proxies for interpreting the influence of manual labor on the human skeleton for decades. However, biomechanical approaches to osteoarcheological analysis have yet to be applied to certain activity-related lesions, specifically those related to excessive strain and heavy loading in the human spine throughout ontogeny. The three-column spinal theory is the ideal biomechanical framework for this study because it assesses the influence of normal and abnormal weight distribution throughout the spinal column and how variations in flexion, extension, and torsion impact spinal health. This study will combine paleopathological analysis with the three-column spinal theory to map the distribution of activity-related paleopathological lesions in children from a post-medieval Dutch community (1650-1850 CE) with historically documented child labor practices.

Preliminary analysis of this collection suggests that all 39 individuals assessed between the ages of 4 and 20 years at death exhibited signs of activity-related stress on at least one of their vertebrae. In total, 44% of analyzed vertebrae showed signs of activity-related pathological lesions (contour changes, pitting and porosity, osteophytic growths, and/or Schmorl's nodes), with lesions occurring most frequently in the upper thoracic region across all age categories (49.8%; x2 = 9.412, p = 0.024). Applying the three-column spinal theory to paleopathological analysis on both an individual and populational level has shown abnormal weight distribution patterns in all age groups, ultimately allowing for a better understanding of the types of activity these children were participating in during life.

Machine learning and discriminant function analysis in the formulation of models for sex estimation using skull measurements of contemporary Black South Africans

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Sex estimation from bone measurements is one of the most critical steps in human identification. Skull measurements have been shown to be sexually dimorphic and previous studies based on skeletal collection–derived data showed that the average accuracies of formulated population-specific standards are reasonable. However, no previous studies have investigated the reliability of these equations on the contemporary population. In this study, data were collected from three–dimensional computed tomography (3DCT) scans of the skull of contemporary Black South Africans (BSA). Eight variables were measured from 350 skulls of BSA housed in the Radiology Department of Johannesburg Academic Hospital. Xiris and IntelliSpace softwares were used to reconstruct the images into three–dimensional (3D) forms. Previously derived equations from skull measurements of BSA were evaluated using data from the current study. The average classification rates were low (50-72%) which necessitated the formulation of new standards Eight classical machine learning (ML) techniques along with feature ranking techniques were used to identify the best feature combinations for sex prediction. A stacking machine learning technique was trained and validated to classify sex. We used the top–performing three ML classifiers as base learners and the predictions of these models were used as inputs to different ML classifiers as meta learners to make the final decision. The average classification accuracies obtained from the use of ML techniques (82-84%) are similar to those from multivariate discriminant function analysis (78-83%). The models proposed in this study are useful for sex estimation in forensic cases involving contemporary BSAs.

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Pre-sympatric Niche Divergence in Early *Homo* and *Paranthropus*

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Previous studies on the effects of possible competition between early *Homo* and *Paranthropus boisei* have focused on traditional post-sympatric character displacement. In this study, we use *Paranthropus* and early *Homo* cranio-dental specimens from the National Museums of Kenya (94 *Paranthropus* and 37 early *Homo*) to test for evidence of post-sympatric character displacement versus pre-sympatric ecological incumbency. We used the Transcan C (resolution 0.035 mm) to generate textured 3D surface-scans of the specimens, and analyzed 2D and 3D geometric morphometric data for any evidence of character displacement through time, or any evidence of asymmetrical morphological change in either of the species, as would be predicted if pre-sympatric niche divergence was operating. Preliminary results suggest there is evidence of cranio-dental change through time in *Homo*, but not in *Paranthropus*. Instead of seeing diverging traits through time in both genera, only the non-incumbent, early *Homo*, shows significant trait change. This evidence, together with the currently older first appearance dates of *Paranthropus* in eastern Africa, is consistent with *Paranthropus* being the ecological incumbent, resulting in pre-sympatric niche divergence between these genera. Instead of assuming early *Homo* had a competitive advantage, an alternative competition-based hypothesis is that a non-ancestral lineage (e.g., *Paranthropus*) influenced the evolution of a surviving lineage (e.g., *Homo*) through pre-sympatric niche divergence.

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Genetic histories of the Adivasi and Sinhalese populations in Sri Lanka

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Mobility and genetic admixture have been pervasive in human history. The island nation of Sri Lanka is home to several populations, resulting from multiple historic migrations. Consequently, the rich socio-cultural tapestry of the country is mirrored by its complex population genetic structure, supported by studies on uniparental and limited autosomal markers. To investigate the population history of Sri Lanka on a finer scale, we conducted a whole-genome study of two present-day Sri Lankan populations with long settlement histories in the country: Adivasi (N = 23) and Sinhalese (N = 34). Adivasi are believed to be descendants of the early inhabitants of Sri Lanka (~0.1% of the total population). Sinhalese are the most prevalent contemporary group in Sri Lanka (~75% of the total population), while oral and written records as well as linguistic evidence suggest that the Indo-European-speaking Sinhalese migrated from India in the first millennium BCE.

We evaluated the genome-wide affinities and population structure of the study populations, finding that they are genetically more similar to each other and to present-day South Indians. Moreover, while both populations were modeled with genetic sources previously used to model other South Asians, our analyses suggest that the Adivasi have maintained a small effective population size for a longer time than the Sinhalese. Overall, although the study populations are part of the broader South Asian genetic cline, they have unique demographic histories that motivate further anthropological genetic and paleogenetic studies on the complex population structure in Sri Lanka.

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Can gut size be inferred from ribcage form?

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Ribcage "flare" has been used to infer gut size in fossil hominins. This study examines the relationship between gut size and the ribcage form in anthropoids. Differences in the ribcage form across genera and across gut size categories (small, medium, large, extra large) were used to test if (1) ribcage form distinguishes groups from each other and (2) if ribcage breadth can predict gut size in humans. Ribcage form was quantified using an osteological sample from *Homo sapiens* (N=40), *Hylobates lar* (N=70), *Gorilla gorilla* (N=12), *Pan troglodytes* (N=20), *Pongo pygmaeus* (N=13), *Macaca mulatta* (N=25), and *Cebus apella* (N=16), a total of 196 individuals across seven genera. Gut sizes for each species were obtained from published sources. Results confirm that ribcage form is distinct in *Homo* and that ribcage form can distinguish the small gut size category from all others. Abdominal CT scans of living humans (N=89) were used to directly measure gut volume and lower ribcage breadth to test for a correlation. The results show that gut volume correlates with ribcage breadth and body weight ($R^2=0.48$, $p<0.001$). These findings suggest that we might be able to infer a small gut size from a human-like ribcage form; all other forms cannot distinguish between medium, large, or extra-large gut sizes. Hominins with mediolaterally wider lower ribcages may have larger gut sizes than hominins with narrower lower ribcages, if they possessed the human condition.

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Errors in Translation: Bioanthropology, The Public Sphere, and the Rise of Race Logics

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Mainstream scholarship in biological anthropology has argued against racial taxonomies as an organizing principle for understanding human biological variation for more than half a century, with roots that can be traced even earlier. Nevertheless, race logics applied to understanding human evolutionary history and biological diversity remain readily available in the public sphere. Previous scholarship has shown the myriad ways a racist public actively aligns research on human biological variation with a racial worldview (e.g. Panofsky, Dasgupta & Iturriaga, 2021). Building off of our own scholarship on the ways in which biological anthropologists fail to consistently identify and demarcate basic units for understanding human biological diversity (Van Arsdale & Nelson, 2022), we demonstrate in this paper how that failing opens up the door for racialized interpretations of biological variation. We apply a thematic analysis to case studies of public discussions of anthropological research in both informal and mainstream online settings. Analyses reveal a consistent pattern in which inconsistent use of populational categories in primary research is repeated in mainstream writeups, lending these categories a scientifically established "naturalness," while failing to specify constraints on associated evolutionary forces. When this research is then re-presented in other outlets, evolutionary forces are invoked across widely differing scales to support racialized views of human biodiversity, shielded by a veneer of plausible evolution/scientific credibility. Even if a uniform definition for populations is not possible in biological anthropology, researchers should be attentive to openly identifying the constraints on their own research samples and the resulting research conclusions.

Opening the Can of Worms: exploring porotic hyperostosis, endemic parasites, human ecology, and nutrition in pre-contact Eastern North American populations

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Porotic hyperostosis in North America has historically been linked to iron-deficiency anemia resulting from substantial maize consumption. Recent scholarly investigations suggest that cobalamin- and folate-deficiency anemias are more likely contributors. This study delves into a dataset of over 5,000 individual skeletons from eastern North America, spanning from 6000 BCE to 1550 CE, and is substantiated by a thorough literature review encompassing the realms of ecology, paleoparasitology, and bioarcheology.

This research employs stable isotopes $\delta^{13}C$ and $\delta^{15}N$ to trace dietary variations across diverse temporal and spatial contexts. In addition, enamel hypoplasia frequencies serve as a comparative metric for evaluating early childhood stress alongside the prevalence of porotic hyperostosis. The analysis reveals statistically significant disparities in these parameters, defining a clear distinction between coastal and inland populations and variations across different time periods. Notably, a moderate positive correlation is found between $\delta^{13}C$ values and porotic hyperostosis, although with an unexpected low degree of covariation. These findings do not substantiate a direct link between maize consumption and porotic hyperostosis, suggesting a peripheral cause potentially associated with urbanization. Urbanization, often linked to maize horticulture, promotes the transmission and concentration of endemic gastrointestinal parasites like *Ancylostoma* and *Ascaris*. These parasites function as reservoirs for cobalamin and folate, consequently affecting the nutritional status of the host. This research thus posits that multi-generational factors, driven by a feedback loop interweaving nutrition and early childhood infections within a complex ecological matrix, constitute a pivotal element in the intricate narrative surrounding porotic hyperostosis.

The association between body size and risk of death during the 1918 influenza pandemic in Alaska

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The 1918 influenza pandemic was severe in Alaska, especially in the Seward Peninsula on the Bering Strait and among Alaska Native people. There is little data available worldwide on body size in historical populations and how body size may have been an additional factor in pandemic flu disease severity, and ultimately death. Alaskan death records from the Alaska Bureau of Vital Statistics with recorded height and weight at death ($n = 2{,}480$) were analyzed to illuminate the relationship between body mass index (BMI) and risk of death from influenza and pneumonia (P&I) during the 1918 influenza pandemic (1918-20) and a comparative non-pandemic period (1917, 1921-24). Logistic regression models were fit to predict the likelihood of a P&I death against four other major causes of death, first using only BMI as a predictor, then additionally controlling for district, age, sex, and race category. No significant relationship was observed between BMI alone and the probability of a P&I death during or outside the pandemic. When controlling for all variables, BMI (OR=1.07, $p<0.001$), district (Seward Peninsula region: OR=6.12, $p<0.001$), age (OR=0.99, $p<0.003$), sex (male: OR=0.66, $p<0.001$), and race category (non-Alaska Native: OR=0.39, $p<0.001$) significantly predicted the likelihood of a P&I death. In the non-pandemic period, only age, sex, and race category were significant predictors. This research contributes novel data on historical population biology and insights into whether body size, in combination with other demographic characteristics, is related to probability of death during the 1918 influenza pandemic.

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Automated detection of red titi monkey (*Plecturocebus discolor*) duets in the Ecuadorian Amazon

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Passive acoustic monitoring (PAM) via autonomous acoustic recording units is a valuable tool to monitor vocally active primates. However, extracting useful information from PAM data often requires substantial human effort. We evaluated the efficacy of an automated and open-source template-based detection algorithm to automatically detect duets of pair-living red titi monkeys (*Plecturocebus discolor*) in audio data collected using PAM at the Tiputini Biodiversity Station in the Ecuadorian Amazon. We initially tested the algorithm with a set of seven titi duet templates. The algorithm achieved a precision (accuracy of positive detections) of 39% and recall (completeness of positive detections) of 21%, mainly due to a large number of howler monkey (*Alouatta seniculus*) roars being registered as positive detections. We then used the seven titi templates in combination with a set of "off-target" howler monkey roar templates to define a new detection function aimed at reducing the number of false positives. This increased performance considerably (recall = 71%, precision = 75%), and titi duets with a signal-to-noise ratio (SNR) > 10 dB were always correctly detected. An important next step will be to evaluate the efficacy of deep neural networks (DNNs) for automated detection of duets as several recent studies suggest that DNNs consistently outperform traditional techniques like template-based detection. Studies of other vocally active species that use PAM would benefit from following similar analytic procedures as described in this study.

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Isotopic insights into dietary shifts and life history changes in Southern Europe during the Metal Ages (3600-400 cal. BCE)

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The substantial demographic growth recorded during the Metal Ages (3600-400 cal. BCE) in Southern Europe was undoubtedly linked to socioeconomic and technological advancements, but was probably underpinned by changes in parental care that influenced life history parameters such as the duration of weaning and breastfeeding, and therefore fertility. The reconstruction of these practices is possible through biomolecular analyses of human skeletal remains, providing direct data on dietary changes from birth to adulthood. The remarkably well-preserved assemblages from caves in western Liguria (northwestern Italian coast) allow for diachronic investigations from the Copper to the end of the Iron Age, in an area where scarcity of archaeological traces of settlements renders difficult the reconstruction of late Prehistory socio-economic and demographic dynamics.

We analyzed CNS isotopes from 250 individuals, and incremental dentine from nine, spanning the Copper to Iron Ages. Results reveal significant diachronic changes in adult diets, which primarily relied on C_3 foodstuffs until the Bronze Age. Subsequently, an increase in both $\delta^{15}N$ and $\delta^{13}C$ values suggests higher animal protein intake and consumption of C_4 plants such as millet, as also suggested by archaeobotanical records. In parallel, incremental dentin analysis indicates a gradual decrease in weaning and breastfeeding duration over time, and suggests a transition from animal protein-based weaning foods to plant-based gruels, probably thanks to the availability of a wider variety of vegetal resources. This study offers new insights on the timing of life history changes in Liguria, and on the dietary factors that may have contributed to demographic growth.

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Homo floresiensis and Komodo Dragons consumed *Stegodon* at Liang Bua

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Liang Bua is well known as the type locality for *Homo floresiensis*. Initial studies and descriptions of the faunal remains from the site suggested that *H. floresiensis* hunted, butchered, and possibly cooked proboscideans (*Stegodon florensis insularis*) for food based on stegodont remains found in association with stone artifacts and the presence of cutmarks on three of these bones. To test these early and influential interpretations of *H. floresiensis* behavior, we sampled 3,155 stegodont elements from Liang Bua for more detailed zooarchaeological and taphonomic analyses, including skeletal part profiles, breakage and fragmentation patterns, post-depositional processes, and bone surface modifications. Traces indicative of predation were molded and scanned using a 3D non-contact profilometer and compared to collections of marks with known origin. Our results indicate that both Komodo dragons (*Varanus komodoensis*) and *H. floresiensis* had access to and almost certainly consumed *Stegodon* at Liang Bua based on the presence of both varanid tooth scores and hominin tool marks, respectively, on stegodont elements. Only a single stegodont rib showed signs of exposure to fire but as it was recovered in sediments unconformably overlain by much younger deposits, the burning was likely not due to *H. floresiensis* behavior. Stegodont age profiles indicate a dominance of subadult individuals but both adult and subadult elements exhibit high rates of post-depositional fragmentation, which makes it challenging to determine whether *H. floresiensis* or Komodo dragons obtained primary access to these stegodont carcasses. Thus, whether *H. floresiensis* hunted stegodonts on Flores remains an open question.

Comparison of medical vs. micro-computed tomography in the assessment of cortical bone thickness distribution in the primate femoral diaphysis

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Recent advances in computed tomography (CT) have led to an increase of medical CT and micro-CT data being utilized in conjunction in biological anthropology research, particularly with new virtual tools to extract data from internal structures. To ascertain if data extracted from these differing resolutions are capturing comparable signals, we compared the cortical bone thickness distribution data continuously through the femoral diaphysis of 30 specimens selected across *Pan, Gorilla, Pongo, Hylobates, Ateles, Lagothrix, Mandrillus*, and *Pithecia*. Each individual femur was scanned using both modalities. A landmark-based automatic orientation was applied to align all femora in the same way and all diaphyses were automatically segmented to extract cortical bone. In the R package *morphomap* 180 cortical thicknesses were measured on 61 cross-sections extracted from proximal (80%) to distal (20%) of the femoral biomechanical length. The data extraction protocol was tested for inter-observer error. Intraclass correlation coefficients measured for each individual show good to excellent reliability with high correlation values (>0.75) between medical and microCT modalities. This result is supported by the mapping of the error measurements between medical vs. microCT dataset for each individual. We obtained a very high correlation of the distance of the principal component (PC) scores of the two PC analyses of the two sets of our primate data. These results demonstrate that either medical or microCT scans of fossil primate femora can be used interchangeably for the analysis of the cortical bone thickness distribution using *morphomap*.

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Title: Navicular height changes due to added burden and increasing velocity

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The human foot functions as a pivotal component in bipedal gait, serving a key role in both propulsion and load bearing. The medial longitudinal arch helps to stabilize the foot. The navicular plays a crucial role in maintaining the height of the medial longitudinal and acts as a keystone between the hind and forefoot. As load on the foot increases, the arch height decreases, but little work has examined this phenomenon during walking. This pilot study assesses if navicular height changes while walking at varying velocities and burden conditions.

Six females and five males with no history of recent foot trauma or pathology walked at three self-selected walking velocities (slow, normal, and fast). For each velocity, five trials were collected in unburdened and burdened (10kg) conditions. Optical markers were placed on the navicular tuberosity of each foot. For this study, navicular height (NH) was measured as the distance from the ground to this optical marker. We calculated the lowest point of the navicular tuberosity for each stance foot in the capture volume (three or four steps for each trial). Controlling for mass and stature, linear regression analyses were used to determine if there is any difference in the lowest point of NH among burden or velocity conditions.

Burden is not a statistically significant predictor of the lowest NH (all p's>0.05). Velocity demonstrated a potential statistically significant interaction (p=0.07). Future research is required to fully understand the effect of burden and velocity on NH and overall foot arch structure.

The Cart Before the Horse: Disentangling narratives of domestication and transport along the Great Steppe Routes

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Recent evidence from genomics, proteomics, and archaeology have challenged longstanding narratives of domestication and transport in North-Central Asia. I outline the conceptual and methodological problems with previous narratives of domestic species in the region, as well as the processes by which traction and riding began. Then, I counter these hypotheses with new proteomic data alongside published results to reconceptualize how we understand the Great Steppe Route (GSR) and its use through time. This study includes the compilation of bioarchaeological data across this vast zone of interaction. Among the most significant impacts on human societies is the transition to the use of transport. This is especially true for the Great Steppe, a vast grassland located primarily in northern Kazakhstan, where there is early evidence for carts and wagons. I provide evidence that indicates that cattle, then horses, were introduced into the GSR primarily from the west. Further, humans first cooperated with domesticated cattle for transport by wagon, while collaboration with horses occurred later in time. Similarly, before horse-riding began there is strong evidence from other regions of humans riding cattle or other bovines. A persistent process occurs where bovines preceded horses in the process of domestication, traction, and riding. Thus, human-cattle interactions provided a framework for how collaborations would transpire between humans and horses.

What's baby eating? An Isotopic Characterization of Baby Foods and Formulas in the US

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There is currently no reference dataset for the isotopic characterization of baby foods and infant formula, a dataset which could aid in dietary studies, forensic applications, and– beyond anthropological applications– food origin verification. To address this gap, we isotopically analyzed δ2H, δ18O, δ13C and δ15N values from baby foods and formulas to create a reference dataset. Samples were purchased across the United States. Powdered and ready-to-eat formulas were also analyzed. Beyond characterization of these values, we present initial findings evaluating if food types or formulas could assist in identification efforts of sub-adults in the United States.

We found clear isotopic distinctions between baby foods labeled "organic" and other labeling designations, and between foods with and without added water. The δ15N values of foods labeled "organic" were significantly higher than those of foods not labeled (F(3, 11)=[7.45], p<0.001), consistent with the expected use of natural fertilizers. For sweet potato and banana-based baby foods, those containing added water had higher average deuterium-excess values than samples without (sweet potato, F(1, 36) = [5.24], p = 0.028; banana, F(1, 39)= [4.99] p=0.031)), as expected for the dilution of natural water sourced from fruits and vegetables. We found no differences between purchase locations or brands, lending support to the supermarket diet concept. Our current formula sample set is small, but the relative δ13C-enrichment restricted δ15N range relative to baby foods may be of forensic utility.

Hand use during food retrieval on arboreal substrates in northern tree shrews (*Tupaia belangeri*)

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Grasping, nail-tipped extremities are a defining primate feature and grasping behaviors are invoked in various adaptive scenarios for primate origins. Strepsirrhine primates use manual grasping when pursuing dynamically mobile foods, such as insects, and predominantly oral grasping for static foods like fruits. Additionally, *Microcebus murinus* increase their manual grasp frequency when retrieving mobile but not static foods on relatively narrow diameter substrates, suggesting that a fine branch niche context may have contributed to shaping the use of manual grasping adaptations in early primate evolution. To provide comparative context for these behavioral patterns in primates, this study evaluates the effect of substrate diameter on hand use during food retrieval in the northern tree shrew (*Tupaia belangeri*), a close relative of primates that lacks primate-like manual adaptations. Modified GoPro cameras recorded five captive individuals crossing simulated arboreal substrates of varied diameters (3, 8.5 and 20mm) to retrieve static foods (n= 619 trials). Animals made first contact with the foods orally in 98.7% of trials and used their hands during any phase of food retrieval in only 4% of trials. Manual repositioning of the food during ingestion was observed in 22% of trials. Mixed-effects logistic regressions showed no significant effect of substrate diameter on hand use patterns. The oral retrieval of static foods regardless of substrate diameter observed in *T. belangeri* is consistent with previous results in *M. murinus*. Future work will evaluate the effect of substrate diameter on hand use during retrieval of dynamically mobile insect prey in this species.

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Assessing research practices and perspectives in anthropological genomics

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This study analyzes current anthropological non-GWAS genomics and genetics research literature that utilizes primary data collected by the authors in order to grasp how research has been practiced in anthropological genomics since 2020. While many genomic studies in anthropology have continued questionable practices by employing colonial ideologies and methodologies, there is a push for better practices and more inclusive genomic research. Many scientists conducting anthropological genomic research tend to study populations in the countries they are currently in; however, researchers in the United States and England are more likely to also conduct research on populations outside of the country. While research on modern DNA almost always discloses ethical practices such as IRB approval, few articles discuss community engagement efforts and even less have discussions on ethical considerations of ancient populations. Though it is difficult to say whether the researcher(s) conducting studies on present-day populations have maintained contact and discussions on research findings to communities, it is rarely mentioned within the articles. Few researchers from Argentina, Italy, and the United States studying ancient DNA have followed guidelines to collaborate with descendants of ancient populations they study. Additionally, it is essential to understand the perspectives of researchers in these studies and how they conduct research to determine the direction of ethical research practices. Future directions for this project are to understand how these researchers identify themselves in a socio-cultural context, which could disclose how many researchers from communities historically excluded and harmed by science are responsible for the push to better practices.

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Investigating size effects on heritability: a case study using the primate vertebral column

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Body size plays an important role in organismal adaptation. However, size is often assumed to confound results when investigating form-function relationships, even though size itself is under selection. Here, we assess the effects of size on estimates of heritability in the vertebral column, to better understand its role in vertebral evolution. We assessed heritability on typical cervical (C3, N =186), thoracic (T3, N =182), and lumbar (L2, N =183) vertebrae from a sample of pedigreed *Macaca mulatta* from the Caribbean Primate Research Center. We collected 3D coordinate data and extracted 24 linear measurements from each vertebra using raw data and both symmetric and asymmetric size-corrected components of shape variation. We then performed heritability estimates using generic priors in the MCMCglmm package on R and assessed our results using paired t-Tests. We find that heritability estimates from raw linear data are significantly higher than those from all size-corrected data (*p* <0.01). The magnitude of differences varies and heritability estimates from raw data are more variable (S.D. 0.124-0.149 versus ~0.050). Differences are not equally distributed among traits, and heritability of neural arch components increases substantially when size is included (*p* <0.01, *h2* =0.253-0.465 versus 0.178-0.245) while the vertebral canal, pedicle, and body are more similar across estimates (p <0.05 to p =0.133, $h2$ =0.243-0.301 versus 0.231-0.248). This may suggest the presence of particular size-linked constraints in the neural arch, particularly among complex articular regions, while other areas of the vertebra are more responsive to environmental cues related to body size.

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Archaic introgression into modern humans: can it be co-opted into race science?

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Humans carry a small fraction of archaic ancestry across the genome, the legacy of admixture with Neanderthals, Denisovans, and other hominids. The geographic distribution of Neanderthal archaeological sites, which are largely located in Europe, has created a strong impression that individuals of European descent uniquely carry Neanderthal genomic elements. This impression was exacerbated by early archaic ancestry genome maps published in 2014, which were only available for one Central European and two Han Chinese populations. This confluence of incomplete understanding has been co-opted by white supremacist groups, who seek evidence of European ancestry as “unique” or “special”, to promote the idea of genetic differences between the races—a concept that has been debunked by geneticists for decades. Here, I survey how the impression of Neanderthals by the larger public is constantly revised from negative to positive, as it fits ideas of European superiority. I find that historical impressions of Neanderthals were negative, as they functioned as an example of inferior human relatives to prop up modern European self-reflection. Impressions shifted toward the positive in 2007, when aDNA evidence of Neanderthal light skin, blue eyes, and red hair was published, and towards the positive once again post 2010 when the Neanderthal draft genome revealed admixture with modern humans. Finally, I present revised archaic ancestry genome maps, which identified Europeans as carrying the lowest amount of unique Neanderthal ancestry relative to all other Eurasian populations. I then posit how societal impressions will shift once again, as understanding of this data becomes widespread.

Temporal trends in *Aepyceros* horn cores: Interpreting the ecology of hominin landscapes

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Globally, the Pliocene was warmer and wetter than today but, on a regional scale, some African environments became more arid through time. One example is recorded in the Hadar Formation, Ethiopia, where increasing aridity is documented between 3.44–2.95 million years ago (Ma). This climatic trend is associated with an increase in the mandibular size of the hominin *Australopithecus afarensis*. Here, we show that an extinct impala, *Aepyceros*, also records size change in the youngest sediments of the Hadar Formation, with the KH-2 submember (2.95 Ma) specimens having larger basal horn cores compared to older Hadar sediments (n=32 specimens from all submembers).

We use the extant impala, *Aepyceros melampus*, to investigate how horn size might be related to aridity. We measured basal horn size from impalas representing nine countries in eastern and southern Africa (n=81 individuals). Results show a geographic trend for extant impalas; larger horns are found where rainfall is greater and less seasonal (i.e., reduced aridity). Basal horn size in *Aepyceros* may thus be a good proxy for environmental signals. However, large horn size in the late Pliocene may indicate a different driver than aridity. Both *Australopithecus afarensis* and *Aepyceros* are sexually dimorphic taxa, and our results suggest a potentially complex relationship between sexual selection and environmental change. Further research using bovid taxa in which females possess horns, such as Alcelephini, could tease apart the relationship between climate change and sexual selection as drivers of size change in the evolution of large African mammals

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First Report of Proline-Rich Proteins, a Counter Adaptation Against Dietary Tannins, in the Saliva of Diademed Sifakas (*Propithecus diadema*)

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Protein is a crucial component of animal nutrition and growth. However, many foods consumed by herbivores, including primates, are deficient in protein. Even leaves, which are typically higher in protein than fruits, often have defensive chemicals that constrain protein absorption. These plant secondary metabolites (PSMs) include tannins, which bind with proteins, making them inaccessible to the animal. Herbivores have evolved counteradaptations such as proline-rich tannin-binding salivary proteins (TBSPs) and specialized digestive tracts to absorb more protein that defend against PSMs. Thus, when a primate eats tannin-rich foods, estimates of protein intakes and requirements based on traditional lab tests may be too high unless we somehow account for these PSMs, and further, may be too low if we do not account for counteradaptations. This issue is poorly understood across primates, leaving a significant gap in understanding protein intake and its impact on health in the wild, and may also create mismatches between wild and captive diets. I studied the presence of TBSPs in five wild diademed sifakas *(Propithecus diadema)*. PRPs was determined by gel electrophoresis. I identified one protein band at 50 kDa that has tannin-binding capacity. I suggest that the TBSPs is an evolutionary dietary strategy that allows *P. diadema* to consume a tannin-rich and diverse diet. This research will provide valuable first steps for understanding true protein intakes improving our toolkit for the assessment of lemur populations, especially in degraded and changing habitat.

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The evolution and development of the bicondylar angle

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The bicondylar angle of the femur is a characteristic trait of the hominin lineage and is associated with the adaptation to bipedalism. The femoral bicondylar angle in hominins limits lateral center of mass displacements during bipedal locomotion by placing the center of mass directly over the knee and ankle joints.

Within modern human populations, some studies have found sexually dimorphic patterns for the angle, with females having as much as 1.5 degrees greater obliquity than males. Here we investigate potential functional influences on the bicondylar angle, with an eye to factors such as dimorphism in pelvic dimensions, femur length, and body mass. We predict that males and females will exhibit different relationships between bicondylar angle and body size measures due to differential pelvic morphology.

Using data from museum skeletal populations we investigated the relationship between bicondylar angle and an array of lower limb variables and indices, including femoral length, femoral head diameter, femoral neck length, femoral neck angle, bi-acetabular breadth, and bi-iliac breadth. Our results confirm the pattern of sexual dimorphism, with females having roughly a 1 degree (~14%) greater angle. Surprisingly, we found no relationships between bicondylar angle and any of the variables we studied.

Bicondylar angle is known to be affected by developmental processes, so further investigation into potential differences due to exercise regimes is warranted, especially in the aesculapian context, given anecdotal data on high rates of knee pain and injury in female athletes.

Intra-tooth variation of stable carbon, nitrogen, and oxygen isotopes in fossilized equid tooth enamel from Neumark-Nord 2, Germany

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Stable carbon, nitrogen, and oxygen isotope measurements provide important geochemical data, serving as valuable tools for reconstructing ancient diets and paleoclimates. Carbon and oxygen isotope ratios are routinely measured in tooth enamel bioapatite, which is resistant to chemical alteration. In contrast, nitrogen isotopes are traditionally measured in collagen, which rarely preserves in bone or dentin older than 120,000 years. A recently developed method enables us to measure nitrogen isotope composition of tooth enamel, and allows measurement of carbon, nitrogen and oxygen isotopes on the same aliquot of fossil enamel.

This study aims to investigate the detection and preservation of potential seasonal patterns in nitrogen isotopes of (fossilized) tooth enamel. We present combined isotope data from serial-sampled equid third molars from the Last Interglacial Middle Palaeolithic site Neumark-Nord 2, Germany. Carbon and oxygen isotopes were measured using a cryofocussing method, while nitrogen isotopes was measured using an oxidation-denitrification method. This study expands the geochemical dataset at Neumark-Nord 2, providing first serial-sampled isotopic data of hypsodont teeth.

Oxygen isotope values exhibit distinct seasonal patterns, whereas both the carbon and nitrogen datasets lack such signal. This suggests that it is unnecessary that, in temperate environments, bulk samples of equid tooth enamel – and potentially of other large herbivores – cover an entire year of growth to obtain an accurate average nitrogen isotope value. We also observe a strong positive correlation between carbon and nitrogen isotopes, which can be attributed to variations in feeding habits between individuals.

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On f*ckability: Fitness, reproductive success, and the role of non-reproductive individuals in evolutionary theory

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Our society places immense value on women's reproductive potential, often emphasizing its importance to the exclusion of other factors and distilling women's worth to their value as sexual objects. Within cis-heterosexual socialscapes, however, attaining worth through reproduction relies on not only women's sexual desirability and attainability by men, but their ability to confer status to those who have sex with them - that is, their "fuckability". Cultural definitions of "fuckability" capture the interplay between sexual worth and identity politics, particularly regarding axes of sexuality, race, disability, and age. Here I examine how cultural assignations of female worth are reflected in primatology, using female reproduction in callitrichine primates - where reproductive success is skewed toward a single female - as a case study. In evolutionary theory, reproductive success is commonly upheld as the primary indicator of fitness, where individuals with higher reproductive output are considered to have higher relative fitness and are thus able to pass on traits to future generations. In primatology, the value assigned to reproductive success has led to hundreds of studies detailing the intricacies of reproductive patterns. Yet while studies of reproduction in males focus on characteristics mediating reproductive success, studies of reproduction in females focus on characteristics explaining reproductive failure. I demonstrate how these disparities in the treatment of female versus male reproduction in primatology have negatively impacted our understanding of fitness and evolution, highlighting the obfuscating impact that desire, objectification, and cultural constructs of "fuckability" have on evolutionary paradigms within primatology and biological anthropology overall.

From the late Roman period to the Early Middle Ages in modern Slovenia: Population changes on the crossroads

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We analyzed archaeological, genomic, and isotopic data from cemeteries from three regions in present-day Slovenia, Celje, Ljubljana, and Vipavska dolina. Altogether, we generated genomic and isotopic (C, N, Sr) data from over 300 individuals dated between the 4th and 10th centuries CE. These regions are situated along the main road that connected Italy to Pannonia and to the eastern half of the Roman Empire. A crossroads for most of its history, this area served as an important route for multiple historically documented migrations, as such it offers a great opportunity to study their impact.

We found that during the post Roman period there was a substantial contraction in genetic diversity relative to the late Roman period, notably with the loss of non-European ancestry in the region. Furthermore, we found that there was limited genetic evidence of migration into the region. Similarly, we find a contraction in strontium isotope ranges during the post-Roman period, which suggests possible differences in mobility patterns and/or sustenance practices During the 9th-10th centuries, we found a strong shift in genetic ancestry towards northeastern Europe, as well as significant differences in strontium isotope ranges possibly as the result of newly arriving groups forming communities in the territory. Between all three time periods, we also see considerable shifts in biological kinship. We found relatively few individuals in pedigrees during the Roman period, whereas during the post-Roman period we found a few medium/large pedigrees and during the 9th-10th century non-pedigree individuals were fairly uncommon.

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When the youngsters teach the old timers: Inferring turbinal identification in adult primates based on ontogenetic stages

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Primates exhibit a simplified turbinal skeleton compared to many other mammals. The plasticity of morphological (shape) and topological (structure) characteristics can make it challenging to identify homologous phenotypes in adults. Since turbinal development resembles the placental *bauplan*, inferring homology from developmental series represents the most reliable approach in comparative anatomy. We studied histological serial sections and µCT data from a comprehensive age series of three strepsirrhine, two catarrhine, and four platyrrhine genera. We reconstructed the cartilaginous precursors in prenatal specimens and followed their growth patterns until adulthood. The cartilaginous nasal capsule of the fetal strepsirrhines exhibits a species-specific number of turbinals. Only postnatal *Lemur* specimens vary between three and four ethmoturbinals (ETs). Results on catarrhines reveal two ETs across the age stages, except one subadult *Papio* (third osseous ET). Platyrrhines have more varied patterns of turbinal development. Some have up to three ETs in the cartilaginous template, but only two postnatally (*Saguinus*). Others have fewer ETs at birth than in adults (*Aotus, Pithecia*); because these turbinals are partially cartilaginous at birth, we surmise that the third ET develops without a cartilaginous precursor, i.e., via appositional bone growth. We conclude primates have great variability in the cartilaginous template, which presents questions regarding the plesiomorphic state of the order. The observed phenomena of developing turbinals without a cartilaginous precursor suggests that fossil haplorhines (e.g., *Rooneyia*) may have more turbinals than extant species for the same reason. Turbinals lost in the cartilaginous template may be acquired by other developmental mechanisms.

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From part to whole: A novel approach to holistic welfare assessment in wild olive baboons (*Papio anubis*)

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An animal's well-being is known to influence its physiology and behavior, but welfare has typically only been assessed in captive animals. Only recently have these methods begun to be applied to populations of wild animals, and welfare considered a potentially important factor when studying their behavior. Here, we present an exploratory approach to the holistic assessment of welfare in wild olive baboons (*Papio anubis*) at the Uaso Ngiro Baboon Project. Using data collected from January-December 2022 on adult females, we apply a Five Domains model (i.e. health, behavior, nutrition, and environment, with the fifth domain represented by the composite of the other four domains) combined with an Animal Welfare Assessment Grid (AWAG) score, to determine if this can reveal individual variation in overall welfare. For this initial proof of concept, we only included direct measures of health (i.e. body condition) and behavior (i.e. quality of grooming relationships) as these are highly variable across individuals, and set the other two domains at a hypothetical constant since these are less variable across individuals. Measures of health and grooming quality did not significantly correlate (n=37, τb=.069, p=.547), indicating they are independent and merit separate inclusion in the holistic measure. The individual AWAG scores ranged from 6-27 (mean=15.41±5.20, with a lower number indicating higher overall welfare). This interindividual variation suggests that this method produces a useful variable: future analyses will further expand our scoring system to include additional validated variables and test if overall welfare is predictive of fitness measures such as offspring survivorship.

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Marasmus and Morality: Infant Deaths at a Catholic Infant Asylum in Buffalo, New York in 1880

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The St. Mary's Asylum for Widows, Foundlings, and Infants in Buffalo, New York was a wing of the Sister's of Charity Hospital founded by Catholic nuns in 1848. The institution served as a maternity hospital but also a home for abandoned infants and those of unwed mothers. The present study examined deaths of children under the age of two at the St. Mary's Asylum (n=99) vs. those from the general population in Buffalo (n=491) reported in the 1880 Federal Census Mortality Schedules. Mean age at death (0.27 vs. 0.57 years) was significantly lower in the St. Mary's cohort (p<.00001). Chi-square tests of demonstrated that marasmus associated mortality was higher at St. Mary's (p<.00001), with Buffalo having significantly more deaths due to acute digestive (p=.01) and respiratory diseases (p<.00001), and infectious diseases (p=.01). There were no significant differences in frequencies of death due to infantile convulsions, congenital conditions, or other causes. It is concluded that the disparity of deaths due to marasmus at St. Mary's resulted from nineteenth century social policy; unwed mothers were seen as a moral stain on their children who were relegated to foundling homes because of this social stigma. A central theme in deaths in infant care homes in nineteenth century America was chronic malnourishment due to lack of breast feeding in addition to infectious disease.

Women carry loads longer: Morphological adaptations to long distance loaded transport

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Endurance activity is allowed by a series of crucial interactions between morphology and physiology that prevent hyperthermia. Human females have advantages in preventing hyperthermia directly related to common reproductive strategies across cultures. In addition to the loading females undergo while pregnant, females are also in charge of load carrying cross-culturally. These two forms of loading offer distinct pressures to long distance walking. Here we compare the speed of two samples, one of pregnant women (N=5) and one of indigenous pack-basket-carrying (PBC) women (N=14). All women walked at four, self-selected speeds, with temperature data collected on PBC women. The pregnant women walked at the same four speeds across pregnancy, and the PBC women walked at self-selected speeds under both unloaded and loaded (20kg loads, approximately 30% of body mass) conditions. PBC women show a highly correlated decrease in self-selected walking speeds (7%, p<0.05) as body temperature increased with loading (p<0.05, R^2=0.96) suggesting that load, low sweat rate, and the loss of back surface area may impact speed choices. Conversely pregnancy increases both mass and surface area, with an associated increase in sweating. These changes allow pregnant women to walk faster (3%, p=0.07) through the second trimester even though they are carrying a 7% load. By the third trimester, women do slow down 1.5% (not significant), though by this point the load is 24% of their initial mass. Therefore, women show the ability to maintain speed at extreme loads throughout life, with further advantages during pregnancy specifically.

Effects of aging on excess post-exercise oxygen consumption

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Following intense physical activity, people continue to breathe heavier than normal after the activity has been completed. This sustained heavy breathing is called excess post-exercise oxygen consumption (EPOC) and reflects an elevation in metabolic rate that restores the body to its resting metabolism and adapts the body to the activity just performed, including by repairing and adapting muscle, bone, and other tissues stressed during the activity. The duration and magnitude of EPOC are known to be affected by intrinsic factors such as sex and physical fitness level, but the effects of aging on EPOC are not well studied. Here, we experimentally compare EPOC in younger versus older people for a given activity intensity and duration. Specifically, we measured oxygen uptake in mixed-sex samples of younger (aged 18-35 years; n=15) and older individuals (aged 60-75 years; n=5) before, 4 hours after, and 20 hours after 120 minutes of treadmill walking at a speed corresponding to 50% of their maximal oxygen consumption. We found that treadmill walking caused elevated oxygen uptake at 4 and 20 hours post exercise among both younger and older individuals. EPOC magnitude was higher at 4 than 20 hours among both age groups. At neither time point was EPOC magnitude significantly different between age groups. These results appear consistent with a key assumption of the recently proposed "Active Grandparent Hypothesis," that even into older age, physical activity promotes the repair and maintenance of human bodily tissues and thus may contribute to the long lifespans characteristic of our species.

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Iron deficiency, anemia, and risk for COVID-19 among healthcare workers

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Immune defense against infectious disease (ID) requires the micronutrient iron, however, iron that is available to support immune defense may also be exploited by infectious agents. This results in a tradeoff in iron nutrition, such that risk for ID may be lowest when iron nutrition is inadequate to meet overall iron needs. This tradeoff may be more relevant for ID with a history of evolutionary arms race dynamics with human immune defenses, compared to emerging infectious diseases. We assessed the impact of iron deficiency and anemia on risk for coronavirus disease 2019 (COVID-19) among healthcare workers (HCW) in Nigeria in 2021-22. 300 HCW across two sites provided blood specimens for characterization of iron deficiency (via zinc protoporphyrin:heme, ZPPH) and anemia (via hemoglobin) and saliva specimens for SARS-CoV-2 PCR testing. For a follow-up period of 3 months, participants provided additional saliva specimens at 2-week intervals for SARS-CoV-2 PCR testing and reported symptoms weekly. Complete information was available for 199 participants, of these, 20 had at least one positive PCR test. COVID-19 was positively associated with older age (age > 35 years, among our working age sample, OR: 2.63, 95%CI: 0.95, 7.89) and anemia (OR: 2.27, 95%CI: 0.80, 6.72), and was unassociated with iron deficiency. Symptoms of respiratory infection (reported by 78 participants) were positively associated with anemia (OR: 1.76, 95%CI: 0.86, 3.63) and inversely associated with age (OR: 0.46 95%CI: 0.24, 0.87). Anemia seems to increase risk for new and established infectious agents among HCW in Nigeria, likely via compromised immunity.

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Reevaluating the taxonomy of a lumbar vertebra (Omo 105-7) from lower Omo basin (Plio-Pleistocene) using 3D geometric morphometrics

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Since the 1970s, numerous hominin fossils have been excavated from the Shungura Formation dated to the Pliocene-Pleistocene boundary of the lower Omo basin, Ethiopia. A lumbar vertebra (Omo 105-7) from locality 105 was considered a hominin by Howell and Coppens (1974). However, Omo 105-7 possesses anatomical features that are shared by cercopithecoids but distinct from hominins. For example, the vertebral body of Omo 105-7 is heart-shaped with a pronounced ventral kneel, which are reduced or absent in hominins; the base of the transverse process arises from the vertebral body instead of the pedicles as in hominins; and the spinous process is relatively long compared to that in hominins.

Here, we reassess the taxonomic affinity of Omo 105-7 using the aforementioned features along with 3D geometric morphometrics. The robust base of the right transverse process suggests Omo 105-7 as the ultimate lumbar vertebrae, and the fused apophyseal ring shows its adult status. We apply 40 landmarks to quantify the morphological variation of the ultimate lumbar vertebrae of a broad taxonomic range of living adult anthropoid, and that of two fossil hominins, Sts14a (*Australopithecus africanus*) and the Shanidar 3 Neanderthal.

The results of principal components analysis and canonical variate analysis show that Omo 105-7 separates from hominins and falls close to cercopithecoids, in particular *Papio*, in the morphospace. Additionally, a linear discriminate analysis classifies Omo 105-7 as *Papio*. Thus, our result supports the affinity of Omo 105-7 not with hominins but with cercopithecoids, and we suggest this vertebra represents an extinct cercopithecoid.

Preliminary study of the feasibility of extracting ancient proteins from Plio-Pleistocene eastern African contexts

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Palaeoproteomics refers to the study of protein traces retrieved from ancient specimens. This field is still in its early stages in the African context, as there have been very few works published utilising palaeoproteomics on African samples. Recent work by Madupe *et al.* (2023) analysing tooth samples of *Paranthropus robustus* from Swartkrans, South Africa, has shown the feasibility of sex identification of Plio-Pleistocene hominins based on their dental enamel proteomes. This research has raised the question of whether or not palaeoproteomic investigation of Plio-Pleistocene hominins is feasible in an eastern African open-air context, an important region for human evolution during this time period. As an initial pilot study, here we present the preliminary data obtained analysing the dental enamel of four bovid samples from the pre-1970 Omo collections, dated to 2.31 Ma, using nano-liquid chromatography coupled to tandem mass spectrometry (nanoLC-MS/MS). We compare the results we obtain with those previously obtained analysing roughly contemporaneous bovid material from the closed cave system context of Swartkrans (as reported in Madupe *et al.* 2023). The relatively low recovery of proteins suggests that the open-air context the analysed fossil specimens originate from may be unfavourable to ancient protein preservation, at least with the methodologies currently available. There are multiple factors that may contribute to this, and we suggest a number of strategies going forward for potentially improving protein recovery.

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Deconstructing human nasal adaptation: An iterative assessment of morphological influences on intranasal air conditioning in two and three dimensions

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Previous research has established that tall/narrow nasal geometries are strongly correlated with cold-dry climates, while short/broad geometries are associated with hot-humid climates. It is thus widely postulated that taller/narrower nasal airways functionally enhance intranasal air-conditioning (i.e., heat and moisture transfers) but this hypothesis has not been empirically demonstrated.

This study employs 3D models of decongested nasal passages generated from cranial CT scans of individuals of predominantly European (5 males, 6 females) and African (5 males, 5 females) ancestry to directly investigate proposed form-function relationships. Morphological measurements of nasal passage area, perimeter, and circularity (i.e., shape) were subsequently collected from cross-sectional planes spanning the length of the passage. Corresponding planar measures of intranasal air temperature and humidity were then derived from computational fluid dynamics analyses of airflow through each model. Multivariate regressions were then performed to assess relationships between morphological and physiological variables at each 2D plane and cumulatively across the entire 3D passage.

Regression results indicate that nasal passage morphology and intranasal air-conditioning are significantly associated ($R^2 = 0.54$, $p=0.029$). Consistent with proposed hypotheses, individuals with taller/narrower (i.e., less circular) turbinate chamber cross-sectional shapes were found to be associated with higher total inspiratory heat and moisture transfers.

This study supports assertions that climatic pressures for intranasal air conditioning promoted adaptive changes in nasal morphology during human evolution, likely accounting for the appearance of taller/narrower nasal passages in Pleistocene and Holocene *Homo sapiens* following migrations into colder and/or drier environments.

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Investigating growth and stress of Merovingian children and adolescents from Großvargula and Sondershausen-Bebra

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Adaptive developmental responses protect organisms during nutritional deprivation that shift energy production from growth towards the current stressor. Growth is particularly sensitive to environmental insults, making the analyses of children and adolescents vital in understanding the adaptation and plasticity of past communities. The Merovingian period (401CE to 800CE) represents a transformative era with political, cultural, and societal impacts. This research examines the relationship between growth and stress amongst 29 children and adolescents interred in two cemeteries, Großvargula and Sondershausen-Bebra, in Germany. Body mass, stature, and BMI of nonadults were contrasted to the nutritional variables, cribra orbitalia and stable nitrogen isotope ($\delta^{15}N$) values, to understand stress impacts on Merovingian children and adolescents. Long bone diaphyseal lengths, midshaft diameters, femoral head and distal metaphyseal breadths were used to predict stature and body mass from established formulae. $\delta^{15}N$ values of bone range from 7.9‰ to 11.8‰ with the highest value from a breastfeeding infant. Sixty-nine percent of the nonadults interred at Großvargula with preserved crania had observable cribra orbitalia. There are no relationships between statue, body mass, or BMI and $\delta^{15}N$ values. Significantly, late children (7 to 12 years old) are taller at Sondershausen-Bebra than Großvargula ($p = 0.015$) by 13.6 cm on average. Our preliminary research demonstrates that children interred at the "elite" Sondershausen-Bebra cemetery were less impacted by stress. Since $\delta^{15}N$ values represent dietary protein quality, quantity, trophic level, or nutritional status, compound-specific analysis of amino acids is needed as additional supporting evidence for nutritional stress.

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Exploring childhood and adulthood diet in late medieval-early modern Romania using stable isotope analysis of enamel and bone collagen

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Romania's late medieval-early modern period was characterized by Ottoman rule and a rural agricultural society with a feudal social system of landed nobility and peasants, resulting in differential access to food resources. However, how an individual's diet changed over time is not fully understood. Stable carbon isotope analysis of skeletal remains from three late medieval-early modern (14th–18th C.) cemetery sites in northeast Romania was conducted to explore childhood and adulthood diet, as indicated by tooth enamel and bone collagen, respectively. Additionally, enamel represents bulk diet while collagen represents protein sources, making it possible to explore different components of the diet and contributes to our understanding of dietary composition over the life course.

Stable carbon isotope analysis of enamel and bone collagen was conducted for 77 individuals from Suceava Fortress and Cnejilor Palace, fortresses for Romanian rulers, and Schitișor, a small village. The $\delta^{13}C$ values for enamel and collagen indicate that individuals consuming a C_4 diet during childhood were also consuming C_4 protein in adulthood. Most of these individuals were males from Cnejilor Palace and Schitișor. At Suceava, individuals were consuming C_3 protein in adulthood and a mixed C_3/C_4 diet in childhood. The collagen $\delta^{13}C$ values for Cnejilor Palace and Schitișor are consistent with previous analyses that showed most individuals from these sites were consuming C_4 protein in adulthood. The addition of enamel $\delta^{13}C$ values suggests a C_4 diet was also consumed during childhood, further elucidating dietary composition over the life course at these sites.

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Age and sex-related changes along the length of the human clavicle in an elderly Scottish sample using Pore Extractor 2D

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Intracortical porosity can be defined as the percentage of pores in cortical bone, being affected by intrinsic and extrinsic factors such as age, sex, and pathology. The aim of this study is to investigate intracortical porosity in relation to intra-skeletal variation, sex, and age on the clavicle in an elderly sample.

Thirty Scottish individuals were included (15 males and 15 females; age range: 67-97 years). Ninety thin sections were produced from the medial, midshaft and lateral clavicular segments. Photomicrographs were analysed using Pore Extractor 2D assessing cortical area (CA), total pore number (TPN), mean pore area (MPA), mean pore circularity (MPC) and cortical porosity (CP). Comparisons were made between anatomical segments, sexes, and age groups (70s, 80s and 90s) using different statistical tests.

TPN and MPA in males, and CA and MPA in females, produced statistically significant differences between clavicular segments. No statistically significant difference between anatomical segments was found for CP, suggesting that intra-skeletal variation is minimal for this parameter. CA was significantly different between sexes in all clavicular segments, with the remaining parameters providing varying results depending on the segment under consideration. Age group differences were not reported.

This study provides further information about intracortical porosity in the clavicle for advanced age individuals. The effect of age-related pathologies such as osteoporosis might explain the sex differences observed, and considerations of bone biomechanics could justify the reported intra-skeletal variability. Moreover, age does not seem to alter intracortical porosity suggesting no significant change in the last three decades of life.

Relevance of Chimpanzee Predation on Non-Cercopithecoid Mammals for Human Evolution

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Chimpanzees hunt more often and eat more meat than any other nonhuman primates. Nevertheless, some have discounted the relevance of chimpanzees to understanding the importance of hunting and meat eating in human evolution because diurnal cercopithecoids, which early hominins presumably could not easily have captured, comprise most chimpanzee prey, and the relevant literature overwhelmingly focuses on red colobus monkeys, the main prey where they are sympatric. However, chimpanzees prey on at least 71 vertebrate species, including at least 23 non-primates. Hunting of prey other than arboreal cercopithecoids has been under-incorporated into debates about chimpanzee models for human evolution. Here, I use a literature review plus observations at Ngogo, Kibale National Park, Uganda, to show (1) non-primate mammals contribute 12% of prey captures at research sites for which long-term data exist; (2) including sessile primate prey increases this to 13%; (3) non-primate prey are mostly immatures of bovid and suid taxa that hide infants, which were presumably included among early hominin prey; (4) the density of infant-hiding small bovids is higher in African humid forests than in drier habitats approximating those of early hominins; but (5) overall density of infant-hiding ungulates is much lower in chimpanzee forest habitats, so prey availability would have been higher for hominins. Moreover, methods chimpanzees use to capture prey other than arboreal cercopithecoids were available to bipedal hominins. Finally, rare chimpanzee hunting of bushbuck at Ngogo exemplifies how hominin prey choice could have expanded in response to habitat change.

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Remote Measurement of Morphological Traits on Wild Critically Endangered Yellow-Tailed Woolly Monkeys (Lagothrix flavicauda) in Perú

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Morphological data can provide powerful insights into primate health and life history. Measuring these traits in wild primates is challenging, as it typically involves invasive techniques which local ecology and conservation strictures may prohibit. Advances in photogrammetry allow for non-invasive collection of morphological traits on wild animals. Although validated as a viable technique to obtain accurate morphological measurements for several primate species, the use of parallel-lasers has not been widely implemented for arboreal species or smaller-bodied juvenile primates.

The Critically Endangered yellow-tailed woolly monkey (*Lagothrix flavicauda)* is endemic to the cloud forests of Andean Perú. Despite its conservation status, *L. flavicauda* is among the least studied non-human primates, and extremely limited morphological data is available on this species. We used parallel-laser photogrammetry to collect morphological data on a group of wild yellow-tailed woolly monkeys residing in montane cloud forests near the community of Beirut. We found this methodology to be viable for *L. flavicauda,* including juveniles and infants. Average CVs for repeated measurements collected on individuals ranged from 0.19-4.37%. The indices of sexual dimorphism in measured characteristics ranged from 1.01-1.28. Additionally, in comparing adult male body measurements of *L. flavicauda* to comparably collected measurements of wild male lowland woolly monkeys (*L. lagotricha poeppigii*), we found size for *L. flavicauda* to be within the range of *L. l. poeppigii,* contradicting previous claims that body size, on average, is larger in *L. flavicauda.* The validation of this methodology will allow for the future study of the growth and development of this species.

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Reconstructing the evolutionary processes that produced cranial differences between Neandertals and humans

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Understanding why Neandertals and humans differ in cranial form has been an enduring question in paleoanthropology, arguably dating back to the discovery of Neandertal fossils more than 150 years ago. Many of the explanations have been adaptive, proposing that the reason there are cranial differences is because natural selection acted differently in the two groups. For example, in a key contribution, Rak (1986) argued that the Neandertal face is adapted to resist the rotation of the anterior part of the face from heavy loads generated by powerful biting with the anterior teeth. Alternatively, the cranial differences might not be adaptive, instead being produced by neutral evolutionary processes (genetic drift and mutation) in groups that had been isolated from each other for many generations.

Here, we address this question using methods introduced by Weaver and Gunz (2018), which combine theory from evolutionary quantitative genetics with geometric morphometric visualizations and comparisons. Our analyses are based on a cranial dataset comprised of 246 Neandertals and humans. The data are hundreds of landmarks and semilandmarks, after the semilandmarks have been slid on curves and surfaces. Patterns are consistent with neutrality in the dimensions of form space that reflect the largest amounts of variation among individuals but deviate from neutral expectations in certain dimensions reflecting less variation. Natural selection appears to have acted most strongly on the occipital, parietals, and mid-face. Overall, both adaptive and neutral evolutionary processes appear to have played a role in producing cranial differences between Neandertals and humans.

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Variation in vitamin D levels (serum 25-hydroxyvitamin D) in NHANES 2015-2016

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Vitamin D is an important micronutrient for maintaining optimal health. Most individuals synthesize vitamin D in their skin via exposure to UVB rays from sunlight and from fortified industrialized food products and nutritional supplements. Yet the National Center for Health Statistics estimates that 25% of the US population risks deficiency in vitamin D as determined by serum 25-hydroxyvitamin D (25OHD) levels. This study investigates factors that might influence population variation in serum 25OHD in the 2015-2016 NHANES (N=8040). Multivariate regression models indicate that serum 25OHD levels are positively, yet weakly, influenced by sunlight exposure across the seasons, daily multivitamin intake, age, and the race/ethnicity categories reported in NHANES. Serum 25OHD levels are significantly higher in individuals tested in May through October than in those whose levels were drawn from November through April. Serum 25OHD levels are also positively correlated with daily consumption of a multivitamin supplement. People who identify as white tend to have higher serum 25OHD values than other groups. Dietary intake as indicated by dietary recall data shows no correlation with serum 25OHD levels. These patterns suggest that social and environmental factors that reflect variations in daily lifestyle influence serum 25OHD levels.

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geoFOR: Comparative trends between medicolegal death investigation and human decomposition facility cases using a large forensic taphonomy database

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This research presents an ongoing collaborative forensic taphonomy database called geoFOR to better understand factors that impact the rate of decomposition. GeoFOR utilizes ArcGIS to automate the collection of environmental data and a machine learning model to deliver data-driven PMI estimations. In addition to the PMI estimation calculator, this database allows us to examine trends across a large sample of anonymized medicolegal death investigation (n=1850) cases from across the U.S. and two decomposition research facilities (n=750). Documenting variation in presence of clothing, deposition site, and skin penetrating trauma, among others, provides a comprehensive understanding of decomposition and allows more informative models for estimating PMI. Among our sample (n=2600), all donors at facilities were located on the ground surface and unclothed while less than 20% of forensic cases involved the unclothed and the vast majority were found indoors. Donors also exhibited more skin penetrating trauma (70%) than those in medicolegal settings (<10%). Skin penetrating trauma in donors involved antemortem medical intervention devices, while trauma in forensic cases had medicolegal significance. Although the context of research facilities does not reflect the complexities of medicolegal cases, they provide longitudinal data regarding the decomposition process with more exact and longer time frames. By combining the data sources from controlled, longitudinal studies at decomposition research facilities and forensic cases encountered within the medicolegal sphere, a more comprehensive understanding of forensic taphonomy is possible. GeoFOR's informative capacity is novel due to its comprehensive sample size, geographic representation, and melding of cases from forensic settings and facilities.

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Interpreting Childhood Growth Disruption: Findings from a Medieval Toulousian Cemetery (10th-13th Century, France)

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The skeleton embodies an individual's environment and lived experiences. Studying childhood growth disruption can, therefore, provide insight into the experiences of children in the past. Using femoral length, total subperiosteal area, cortical area, relative cortical area, and Harris line (HL) assessment, this study evaluates femoral growth disruption in n=76 subadults (fetal-12.49yrs) from the 10th-13th century St. Étienne cemetery of Toulouse, France. Our research aims to explore factors that may have influenced childhood growth and mortality at this site and assess the utility of Harris line interpretations in bioarchaeology. To determine the prevalence of growth disruption, femoral length z-scores were calculated using data from the Denver growth study.

The majority of subadults (~59%) in this sample suffered from femoral growth stunting. Children aged 2.0-3.99yrs were the most affected, with ~95% of children in this age group experiencing growth stunting at time-of-death. The high prevalence of disrupted growth in the youngest individuals of this sample suggests that many children were likely born to malnourished mothers and provided nutritionally inadequate complementary foods during early development. Additionally, while many individuals presented with observable HLs (~41%), femoral growth did not significantly differ between individuals with and without HLs. However, since growth resumption is an essential component of HL formation, using statistical tests alone may not provide meaningful interpretations of past childhood growth. Through assessing multiple aspects of growth and development it became evident that interpretations regarding the presence and, especially, the absence of HLs, may require a more nuanced and individualistic approach in bioarchaeological research.

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Exploring Relationships Between Entheseal Changes and Historically Documented Life Histories

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Musculoskeletal attachment sites evolve throughout life, resulting in bony modifications called "entheseal changes" that are visible after death. Although mechanisms for their appearance and intensity remain unclear, studies have found a possible relationship between early life experiences and later bony development, suggesting they represent embodied lived experiences on bone. This study examined 237 individuals of differing age, sex, ethnicity, and occupational role from two documented historic skeletal collections representing the years 1850-1950 to further explore how entheseal changes are distributed between individuals with diverse life histories. Entheseal changes at both the *m. subscapularis* and common extensor tendon attachment sites were scored using the Coimbra method, and resulting scores and documented background information for each individual were analyzed using generalized estimating equations and Pearson's chi square tests to test for overall significance. Results indicated that significance within occupational risk factors and related movements are more likely tied to differences between the sexes as opposed to assumed activity levels. For both depositional and resorptive entheseal changes, their number and developmental stage significantly increased with age ($p=<0.05$), but noted bilateral asymmetry suggests some level of significance with activity. Finally, disproportionate numbers between the two skeletal collections suggest a potential underlying relationship between entheseal changes and historic socioeconomic disparities, the latter even displayed in the archival documentation for individuals in this study. More research is needed to understand how the musculoskeletal system reflects individual lived experiences, or if there are other causes yet to be explored.

Monkeys and Microbes: Examining gut and oral microbiota in SIV-infected sooty mangabeys

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The microbiome plays a critical role in primate health and is shaped by many environmental factors. In Human Immunodeficiency Virus (HIV) and Simian Immunodeficiency Virus (SIV), gut epithelial damage, and microbial translocation from the gut to systemic circulation are key determinants of disease progression, and are also associated with increased viral loads and CD4+ T-cell depletion. However, in natural SIV host species such as sooty mangabeys (*Cercocebus atys*), the gut barrier remains intact, and microbial translocation does not occur despite high levels of viral replication. Moreover, disease progression to AIDS is not commonly observed. This phenomenon has promoted interest in the microbial communities that play a role in maintaining gut homeostasis in SIV. Here we examine gut and oral microbiota of sooty mangabeys from Emory National Primate Research Center (NPRC) and their free-ranging counterparts living in Ivory Coast's Taï Forest – completing the first characterization of SIV in the saliva of wild sooty mangabeys. Our results indicate that saliva sampling is more accurate than fecal sampling for noninvasively detecting SIV in sooty mangabeys. SIV viral load in saliva was found to be significantly higher in mangabeys housed at Emory NPRC than those living in the Tai Forest. We observed differences in alpha and beta diversity metrics of the salivary microbiota based on SIV status. We establish correlations between the gut and oral microbiota, viral load, immune markers, and several social and ecological variables. These results highlight the importance of a wholistic approach in examining microbiome-disease interactions in wild primate populations.

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Widening the recoverable skeletal proteome with a sequential enzyme approach

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The exploration of the proteome of human skeletal remains has been hampered by the overabundance of collagen, as it makes up approximately 90% of the proteins found in bone and dentine. As shotgun proteomics (DDA) works by identifying the most abundant peptides per 2-3 milliseconds, those that are at low abundance can be "swamped out" by the dominance of collagenous proteins in the sample. We have developed a novel workflow that incorporates a second digestion enzyme, ProAlanase following the traditional trypsin digestion. Through this new method, we have been able to reduce collagen recovery by an order of magnitude while exposing a larger range of the non-collagenous proteome. Our aim was to uncover mycobacterial proteins from M. leprae as well as those related to human immune function to see if there are recoverable biomarkers that could be indicative of active infections in the past. We began by extracting proteins from archaeological individuals from a Medieval leprosarium as well as others from a non-leprosy associated contemporaneous cemetery in Barcelona. We found that two individuals from the leprosarium had immune proteins present that are linked to modern patients with leprosy, we must take inherent biases (sampling, preservation, etc) into account. While we have not been able to unequivocally determine specific ancient biomarkers for leprosy, our methodological work will open new avenues for the study of palaeoimmunology through the application of proteomics.

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Variation in the diet of Neandertals from El Sidrón, Spain

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El Sidrón, Spain, dated to 49 ka before present, preserves at least 13 Neandertals. Among these, Adult 2 exhibits right-handedness from incisal striations, heavy dental chipping and dental calculus containing wood fragments, evidence of wood smoke inhalation, bitumen and numerous plant starches. To ascertain the dietary profile of Adult 2, a male, complexity (Asfc) and anisotropy (epLsar) values from dental microwear texture analysis are compared to other individuals from El Sidrón, specifically female Adult 3, and male Adolescent 1, as well as Neandertals from Hortus (n = 5), Krapina (n = 19), Kůlna 1, La Quina 5, Malarnaud and Spy I and recent human foragers, farmers and herders (n = 182). Although taphonomic agents affected the preservation of microwear, we confirm Adult 2 is similar to other Neandertals whereas Adult 3 and Adolescent 1 both exhibit much higher complexity values. For anisotropy, Adult 2 and Adult 3 resemble Spy 1. Adolescent 1 exhibits higher anisotropy than Adults 2 and 3 and is most similar to subadult Kůlna 1 as well as foragers from the Americas. Adult 3 and Adolescent 1 present elevated complexity from a diet heavily predicated on plants containing hard, brittle and gritty particles, whereas Adult 2 exhibits a plant-poor diet typical of Neandertals from cold and dry habitats such as Hortus. Differences between Adult 2 and Adult 3 in complexity and between the adults and Adolescent 1 in anisotropy demonstrate considerable dietary variation at El Sidrón, perhaps stemming from seasonal availability, food preferences or social/sex-based groups.

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Interspecific variation in numbers of presacral vertebrae in amniotes: where do mammals stand?

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Mammals are known to vary remarkably little in numbers of cervical vertebrae, with seven represented in >99% of known species (range 6-9). In contrast, larger ranges of variation are reported in many other groups of amniotes. In mammals, presacral numbers of vertebrae vary more widely, although constraint is still sometimes invoked to explain relatively low levels of variation compared to other amniotes. We compile data on extant and fossil mammals (N=822 species) with modal numbers of vertebrae of other amniotes (N=388 taxa) reported in the literature. We compare the ranges of variation and quantify interspecific variation within major clades. Our results demonstrate that, while mammals are highly stable in numbers of cervical vertebrae, several other major groups are also relatively stable interspecifically: non-mammalian synapsids (5-8), crocodylomorphs and their fossil relatives (8-10), and pterosauromorphs (7-9) have comparable ranges to mammals, and turtles and their fossil relatives are invariable at 8 cervical vertebrae. Regarding presacral numbers, mammals are fairly variable, comparable to non-mammalian synapsids, crocodylomorphs and their fossil relatives, and saurischian dinosaurs. Turtles and their fossil relatives are nearly invariable. Marine reptiles and legless squamates are highly variable in both cervical and presacral counts, with vast increases in numbers common. Among mammals, cetaceans are invariable in cervical numbers, whereas their presacral numbers are highly variable. We interpret these results as evidence for strong constraint on mammal cervical numbers and lack thereof on presacral numbers. Rather, selection on presacral numbers of vertebrae operates similarly in mammals and most other amniote clades.

Understanding ageing in the elderly: a combined histomorphometric approach to cortical and trabecular bone in the clavicle

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Bone can be assessed microscopically to further understand changes in material and mechanical tissue properties occurring with advanced age. This study investigates age-related histomorphometric changes in the cortical and trabecular bone of the clavicle in later life.

Thirty sternal end left clavicles were collected (mean age = 83 years, 15 males, 15 females, Scottish population). Five trabecular variables were collected through microcomputed tomography considering two volumes of interest (VOIs: superior and inferior). Fourteen cortical bone parameters were evaluated using traditional histology, with eight periosteal locations considered for osteonal parameters. Intra-observer error was assessed using intra-class correlation coefficient. Correlations between age and parameters were calculated, and comparisons between age groups (by decades and under/over 85 years of age) and the sexes were conducted. Linear regression assessed the relationship between the parameters and age.

Repeatability was overall attained. Only trabecular bone volume fraction did not differ between VOIs. Significant correlations to age were found for cortical area parameters, intact osteons, and connectivity density. Trabecular thickness and bone volume fraction differed between the 70s and 80s groups. Differences were found for under/over 85-year-old individuals for relative cortical area and between the sexes for cortical area. Relative cortical area and trabecular inferior connectivity explained 30% of the variation in age.

As the global population gets older, it is crucial to further explore bone age-related changes in the elderly. This study reports age patterns for both cortical and trabecular bone potentially explained by age-related pathologies, biomechanical changes, and physiological alterations accumulating with age.

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Bioarchaeology in the time of climate change: a case study from Turkana, northern Kenya

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The wide-ranging and increasingly severe impacts of climate change require rethinking how we approach bioarchaeological research. In regions such as Kenya's Turkana Basin, global warming is causing widespread erosion of archaeological sites, and in many cases, exposure and fragmentation of ancient human remains. We present one such case study from Nakwaperit 2, a new Holocene-age locality located on the west side of Lake Turkana. The site was first identified in 2016, in part because of dense material culture and human remains on the deflating surface. Initial bioarchaeological excavations in 2018 targeted these surface remains as well as partly exposed burials in danger of being washed away. Only five years later, in 2023, community reports of additional exposed remains necessitated further mitigation. Spatial analysis of the >2000 fragments of human bone on the site's surface suggest most are from disturbed primary burials in the process of being fragmented and dispersed by water moving through erosional channels. Osteological analyses indicate at least 8 individuals, with more likely present among the generally small (<2g) and unidentifiable to element surface remains. By contrast, burials found soon after initial exposure were well-preserved and highly informative, establishing a narrow window for recovery. Combined spatial and bioarchaeological analysis resulted in identifying burials in the earliest stages of exposure, preserving important mortuary and osteobiographical data. This work raises questions about how we might adapt bioarchaeological research agendas to a changing global climate and shifting ethical responsibilities, particularly in the context of community-engaged research.

Leveraging biology and culture in forensic anthropology: An analysis of the factors that contribute to the identification of long-term unidentified persons

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While forensic anthropology has historically been tasked with assisting in the identification, there is an increasing focus within the field on identifying long-term unidentified persons. Within the changing landscape of forensic anthropology, it is possible to leverage the multidisciplinary aspects of anthropology in new ways.

The Louisiana Repository for Unidentified and Missing Persons has been the central location in Louisiana since 2007 for gathering biometric, biological profile, and cultural information about long-term unidentified persons. Between 2007 and 2022, there were 457 unidentified persons cases entered into the Louisiana Repository that date back as far as 1978. Of these 457 cases, 273 (59.7%) have been resolved and the remaining 184 (40.3%) unidentified persons are cases considered "cold" or long-term.

Looking to the resolved cases for insights into how cold cases are identified, it becomes clear that biometric data, completeness or skeletal representation, and cultural identifiers are the most significant influences on identification. The identification methods for the 273 resolved cases included 164 DNA comparisons (60.1%), 71 dental identifications (26%), 24 circumstantial identifications (8.8%), 8 medical record comparisons (2.9%), and 6 fingerprint comparisons (2.2%). It is important to note that some of these identification methods require a putative identity for comparison and cultural identifiers (e.g., clothing, hair, recovery location, etc.) must be considered.

Although not the complete story of how forensic anthropologists can facilitate difficult identifications, an emphasis on collecting biometric and cultural/personal information alongside the traditional biological profile can boost the odds of resolving long-term unidentified persons cases.

Living and Dying in Modern New Mexico: Structural Vulnerability and the Embodiment of Social Inequity in a US Forensic CT Sample

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Structural vulnerability theory highlights an individual's positionality and experiences of hierarchical social processes rooted in inequity. The conditions under which people live and labor, and the sociopolitical and economic processes undergirding them, produce population-level patterns of suffering and ill health that are embodied in skeletal and dental tissues. Here, we present preliminary findings from the application of 41 dental/skeletal biomarkers constituting our Structural Vulnerability Profile (SVP) to 350 anonymized, kin-consented CT datasets from the New Mexico Decedent Identification Database (NMDID).

Following Margaret Lock's theory of local and situated biologies, we explore how regional context complements our dataset, enabling population-level analyses of structural marginalization. According to the CDC (2021), New Mexico ranks first in the nation for chronic liver disease/cirrhosis mortality, third for firearm injury deaths, and fourth for both homicides and suicides—statistics that illuminate axes of social marginalization among NMDID decedents.

A productive terminological framing of the SVP is important. We chose the term SVP to reference—and contrast—the oft-biologized and hereditarian focus of the traditional *biological* profile. Yet, "profile" has many meanings, not all innocuous. We discuss constructive dialogues surrounding this and other terms emerging from our work.

We close by recognizing multi-subdisciplinary approaches. Medical anthropology's original structural vulnerability theory has been integrated with bioarchaeological theories of frailty and resiliency and forensic anthropological calls to leverage skeletal interpretations of vulnerability toward policy change. Multi-scalar, collaborative approaches to health and disease allow us to access the full spectrum of vulnerability embodied in the individuals and populations we serve.

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The sound of conspecific laughter induces positive affect in bonobos: a cognitive bias experiment

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Emotions influence many aspects of cognition, including judgements about the likelihood of future positive events (i.e., optimism). Recent research highlighted the need to investigate positive affect, which is much less studied than negative affect. Laughter presents a unique opportunity for cross-species comparisons of positive affect in hominidae, as all great apes display homologous laughter-like vocalizations during play, a behavior characterized by positive affect. Our study asked whether hearing conspecific laughter would elicit positive affective states in bonobos (*Pan paniscus*). Four adult bonobos at the Ape Initiative in Iowa were trained on a go/no-go task with positive and neutral stimuli. Then, after hearing recordings of laughter from unfamiliar infant bonobos, their approach responses towards ambiguous stimuli were measured. Bonobos were more likely to treat ambiguous stimuli as positive after hearing laughter than after hearing a control sound. Despite the small sample size, a binomial GLM found a borderline significant association between laughter and positive stimulus interpretation after controlling for subject, date, session number, and stimulus type ($p = 0.05$). This suggests that simply hearing laughter triggered a positive affective state in bonobos. These results add bonobos to a growing number of species (including humans) that show positive emotional contagion in response to hearing playful vocalizations. Our study highlights the interconnected nature of emotional and cognitive processes across species and paves the way for additional research into the evolutionary implications of laughter and the evolution of human prosociality.

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The Geographic Spread of the 1918 Influenza Pandemic in Alaska

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During the 1918 influenza pandemic, Indigenous people in New Zealand, the United States, and Norway suffered disproportionate mortality compared to non-indigenous groups. This phenomenon is particularly evident in Alaska, in which some Alaska Native villages suffered up to 90% mortality in 1918. Why Indigenous people experienced such high mortality is not entirely clear. While lack of exposure to prior pathogens is a likely contributor, the influence of other cultural and geographic factors on pandemic outcomes is uncertain. This study continues this discussion by investigating the spatial distribution and spread of deaths from the 1918 influenza pandemic in Alaska. Specific research objectives include examining whether the spatial distribution of pneumonia and influenza deaths in 1918 differed from the distribution in non-pandemic times, and investigating how differences in the spread and spatial distribution of influenza deaths was driven by the high proportion of deaths among Alaska Natives. Data on indigeneity, cause of death, and place of death were collected from over 7,000 death certificates from Alaska dating between 1915 and 1921. Results show major differences in the spatial distribution of pneumonia and influenza deaths between pandemic and non-pandemic times. Furthermore, the magnitude of the pandemic in Alaska was largely driven by high mortality among Alaska Natives in the Seward Peninsula. These results lay the foundation for future work investigating the social and ecological causes for the disparity in mortality between Alaska Natives and non-Alaska Natives.

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Ancient DNA Analyses of Mongolian Aurochs Shows Connections to Ancient East Asian Cattle

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Taurine cattle were domesticated in the Fertile Crescent and introduced to East Asia over 5000 years ago. Wild aurochs, the ancestor of domesticated cattle, were also present in East Asia both before and after the introduction of domesticated cattle. It has been suggested that East Asian aurochs show some evidence of human management and may have interbred with taurine cattle, but genome-wide data from East Asian aurochs has thus far been limited. Here, we sequence low-coverage genomes of 23 ancient Mongolian cattle to assess whether wild aurochs admixed with ancient taurine cattle and determine whether ancestry from Mongolian aurochs can be found today in living cattle. Our work suggests that Mongolian aurochs are part of the same population of aurochs that was domesticated into taurine cattle. Mongolian individuals postdating the arrival of taurine cattle to East Asia also show evidence of admixture, with taurine cattle mitochondrial genomes. We also observe genetic relatedness between Mongolian aurochs and early domesticated cattle from China. However, there is very little East Asian aurochs ancestry in modern East Asian cattle, suggesting that this ancestry was lost over time. Future work in additional cattle populations in Mongolia and elsewhere in East Asia will further clarify the demographic history of East Asian cattle.

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Exploring Covariation in Dental Development across Modern Humans, Non-Human Primates, and Homo naledi

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The timing of tooth mineralization in the adult permanent dentition provides evidence to reconstruct the life history of extinct hominins. To accurately infer life history from fossilized dental remains, a better understanding of the normal range of (co)variation in human and African ape dental developmental sequences is necessary. This study quantifies the multivariate relationships among the adult mandibular dentition of contemporary *Homo sapiens* (n=1,316), *Pan troglodytes* (n=34), *Pan paniscus* (n=80), and *Papio anubis* (n=50). The scores for developing mandibular teeth are fit to a multivariate Bayesian model in the Stan programming language to quantify covariation and correlation. The results are compared against published dental scores from *Homo naledi* (n=2). Correlation in tooth mineralization among the mandibular dentition is variable across all species. *Pan* demonstrates strong correlation patterns among all developing teeth (highest posterior density – $\rho > 0.5$). *P. anubis* displays relatively weak correlation patterns (highest posterior density – $\rho < 0.4$). *H. sapiens* pattern is intermediate, with evidence of modularity among disparate teeth. Specifically, teeth developing during similar periods of ontogeny are more strongly correlated versus teeth developing at other times. The multivariate sequence of tooth mineralization from *H. naledi* is probabilistically unlikely for any of the explored species and, instead, expose a unique pattern. The results suggest that life history reconstruction of extinct hominins based on tooth mineralization from modern extant primates may be less straightforward than initially understood. Future studies should incorporate a greater diversity of hominin specimens to clarify the exposed relationships in the current study.

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Variation in the rotational profile of the lower limb as it relates to activity

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The rotational profile of the lower limb includes femoral and tibial torsion, which combine to affect the mobility of the hips, rotation of the knees, and angle of the feet. Both torsions are likely developmentally plastic. Femoral torsion likely decreases while tibial torsion likely increases with higher muscular activity. Despite this general understanding, little research has explored how specific activities affect these measurements, or how the rotational profile might relate to more common lines of evidence for inferring behaviours, like cross-sectional properties (CSP).

We examine how the rotational profile varies between Avar horseback riders (n=42), Early Bronze Age (n=36) and Early Middle Age (n=22) agriculturalists from eastern Austria, and industrial era individuals (n=45) from Canada. Lower femoral and higher tibial torsion was expected in Avar horseback riders due to increased activity in the hip abductors and greater external rotation at the hip and ankle. All variables in the rotational profile and CSPs were derived from whole-bone 3D models. Differences between groups were assessed using ANOVA and *post hoc* Tukey's pairwise tests. Relationships between femoral and tibial torsion and CSPs were evaluated with Pearson's correlations.

There were significant differences in femoral and tibial torsion between the groups, which was driven by higher average torsion in both the femur and tibia in the Early Bronze Age compared to all other groups. There were some correlations between femoral torsion and CSP, but none in the tibia. Future studies will explore these relationships in living elite athletes with known patterns of loading.

Yoel Rak: Architect of Understanding

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Yoel Rak's prolific career has included some of the most important contributions to paleoanthropology in diverse areas, encompassing, among other things, field work in the Levant and East Africa, the anatomy and functional morphology of australopithecines and Homo, and issues of systematics in human evolution. Yoel's unusual attention to detail has had a profound influence on our discipline and us. It has been a great asset to his field work (would AL 444-2 have been discovered without it?) and has provided the basis for Yoel's view of hominid systematics. For us, most importantly, it has provided a foundation for many of his most innovative insights into the adaptations of fossil humans.

Here, we focus on the evolutionary insights derived from Yoel's deep knowledge of anatomical structure and function in the tradition of D'arcy Thompson. The idea that form follows function, a principle of design in architecture, underlies much of Yoel's work explicating the biomechanics of australopithecine and Neandertal crania and the function of the Neandertal pelvis. We know from experience that Yoel derived many of his structural models for anatomy from architectural forms. Just walking down the streets of Chicago with Yoel is an education. We share some of his insights and their applications here.

Face-to-face encounter with the Taung child: facial ontogeny in southern African early hominins

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Raymond Dart interpreted the Taung child, the holotype of *Australopithecus africanus,* as "a creature well advanced beyond modern anthropoids in just those characters, facial and cerebral, which are to be anticipated in an extinct link between man and his simian ancestor" (Dart, 1925, p. 198). The utilization of high-resolution computed tomography (micro-CT) to examine the craniofacial structure of the expanding sample of juvenile australopiths from southern Africa, offers a novel way of investigating their facial development, as well as the ontogeny of the key distinctions that set them apart from contemporary chimpanzees, bonobos and modern humans. We explore how recently-discovered juvenile hominin fossils recovered from Kromdraai and Drimolen help provide insights into facial morphogenesis and developmental modularity in southern African early hominins in general, and in the Taung child, in particular. We use the principles of evolutionary developmental biology ("evo-devo") to investigate differences in the ontogenetic programs among contemporary apes, modern humans, *Australopithecus africanus* and *Paranthropus robustus.* We explore the implications of these differences for efforts to generate hypotheses about the relationships between *Au africanus* and *P. robustus*, and between the latter and *Paranthropus boisei* from eastern Africa. Our focus on the face recognizes, and pays homage to, Yoel Rak's singular and seminal monograph *The Australopithecine Face* (1983). Its insights and wisdom continue to inspire us.

Culturally-determined Interspecies communication and cooperation between humans and honeyguides

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Species interactions that vary across environments can create geographical mosaics of genetic coevolution. However, traits mediating species interactions are sometimes culturally inherited, providing additional possibilities for behavioral variation, local adaptation, and coevolution. In this study, we show that traditions of interspecies communication between people and wild birds vary in a culturally-determined geographical mosaic. Honey-hunters in different parts of Africa use different vocal calls to communicate with greater honeyguides (*Indicator indicator*) that lead them to bees' nests and wild honey. We conducted acoustic playback experiments in Tanzania and Mozambique to measure whether honeyguides are more likely to initiate cooperation in response to signals of their local human culture than to those of a foreign culture, or to arbitrary human sounds that serve merely as a cue of human presence. Results indicate that honeyguides in Tanzania more readily respond to the calls of the local Hadza honey-hunting community, and honeyguides in Mozambique more readily respond to the local calls of Yao honey-hunters. These results were not explained by variation in sound transmission, and instead suggests that honeyguides learn local human signals. We discuss the forces stabilizing and diversifying interspecies communication traditions, and the potential for cultural coevolution between species.

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Endocranial volume in eastern chimpanzees (*Pan troglodytes schweinfurthii*) and western chimpanzees (*P. t. verus*)

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Although endocranial volume (ECV) of chimpanzees (*Pan troglodytes*) has been studied repeatedly, the possibility that it varies by subspecies has never been directly investigated. This is surprising because the eastern (*schweinfurthii*) and western (*verus*) subspecies have been separated for ~0.5 my, similar to the separation times of species of *Homo* and *Pongo* that have evolved significant within-genus differences in ECV. Furthermore the few published data that allocate ECVs by subspecies have suggested that *verus* has smaller ECV than *schweinfurthii*; and self-domestication theory also suggests that ECV could be smaller in *verus*. I used 3 mm diameter glass beads to measure adult ECVs in *schweinfurthii* (n = 53 females, 77 males, mostly from Uganda and Democratic Republic of Congo) and *verus* (42 females, 36 males, from Liberia and Ivory Coast). ECV was consistently higher in males than females (Mann-Whitney $p < 0.005$ in all comparisons). Within subspecies there was no evidence of between-country differences in ECV ($p > 0.4$ for all comparisons). Differences were also undetectable between subspecies (mean ± standard deviation, females: *verus*, 373.1 ± 29.6 cc; *schweinfurthii*, 367.9 ± 30.2 cc; males: *verus*, 403.1 ± 33.4 cc; *schweinfurthii*, 403.3 ± 34.6 cc). ECV therefore appears to be a stable average feature of chimpanzees despite varying widely among individuals (e.g. *schweinfurthii*, Uganda: females 318.3 – 406.3 cc; males 329.5 – 477.7 cc; *verus*, Liberia: females 313.3 – 464.2 cc; males: 332.2 – 459.7 cc). How chimpanzee ECV is related to variation in body size remains to be determined.

Body Size and Scaling in Indriid Biology

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Bill Jungers' legacy in the field of size and scaling is particularly evident in his contributions to our understanding of extant and extinct lemur biology. While interspecific studies provide insights into evolutionary morphology and ecology, intraspecific studies afford opportunities to examine patterns of growth and selection at different stages of the life cycle. Extinct and extant indriids have been studied extensively in terms of their unusual life history strategies, rapid early dental development, and slow somatic growth. Extant indriids face the challenge of a dynamic locomotor style dominated by leaping despite slow somatic growth. We examined intraspecific scaling of limb segment lengths, cross-sections, and intrinsic hand and foot elements in a wild sifaka population from Beza Mahafaly Special Reserve. Morphometrics were collected on over 850 animals (1-34 years, 0.85-3.73 kg). Scaling parameters are compared with other studies of captive sifakas age 0-2 years, as well as interspecific studies of strepsirrhine skeletal proportions conducted by Jungers and colleagues. Limb segments, especially thigh length, grow disproportionately fast in infant sifakas and are characterized by negative allometry for the rest of the life cycle. Cross-sections exhibit strong positive allometry as expected by the need for relatively more muscle recruitment during leaping in heavier animals. While cheiridia exhibit negative allometry, the lateral digits are relatively long and the sole/palm relatively short in larger animals. Unique scaling patterns found in sifakas are associated with a need for relatively short juveniles and heavy adults to leap long distances and maintain functional equivalence throughout the life cycle.

Variation in faunal composition among phases of fossil collection in the Lemudong'o Formation, SW Kenya

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Paleontological fieldwork at the late Miocene localities of the Lemudong'o Formation (~6 Ma) in southern Kenya, can contribute to understanding of ape/early hominin paleoecology and evolution. The primary fossiliferous localities are Lemudong'o 1 (LEM1) and Enamankeon (ENK), which are ~5 km apart. Fossil collecting efforts can be grouped into three phases over 28 years, each associated with its own constraints on resources and methodology. We investigated whether taxonomic compositions changed among phases and between localities, as indicators of any shift in collecting efforts.

Specimens of the Lemudong'o Formation (N = 2123) were counted at the family (e.g., bovids and hippos) or the order level (e.g., primates and carnivores). Specimen counts and relative abundance of the taxonomic groups were summarized for each phase, and the two localities.

Faunal composition at both localities is dominated by bovids (~35%). ENK differs from LEM1 by having more large-bodied taxa (e.g., hippos and perissodactyls) and fewer small-bodied taxa (e.g, primates and hyraxes). Within LEM1 (N = 1895), there is little change in faunal composition among the phases (except for suids), indicating relatively consistent collecting efforts through time. We found higher percentages of specimens collected at ENK (from <5% to ~25%) for Phase II and III, which suggests increased collecting efforts after Phase I. The later collecting phases now document the presence of *Cainochoerus* (Suidae) and a more diverse primate fauna, including a galago.

Analyses of tuff, biomarker, paleosol, phytolith and enamel samples in progress will provide more comprehensive paleoenvironmental reconstructions of the Lemudong'o Formation.

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Behavioral Patterns of the Western Rong Population during the Eastern Zhou Period⍰2300-2100 BP⍰in the Dunping Cemetery, Northwestern China

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Located in Northwestern China and dated to the Bronze Age (2300-2100BP), the archaeological culture of Western Rong showed a combination of nomadic and agricultural elements. However, historical records of people in this area were so limited that whether they relied more on animal husbandry or agriculture remained unknown. In this study, stoutness indexes, cross-sectional geometry, and entheses of the limb bones, as well as the prevalence rates of Poirier's facet, were collected from 123 skeletal individuals from the Dunping Cemetery, to address this question.

Results show that the Dunping people had a low stoutness of humeri, a high stoutness of femora, and flattened proximal tibiae. The middle tibiae of males were more robust when compared with females; marked sex difference was also noticed in the robustness, stiffness, and bending resistance of the femora, as indicated by biomechanical measurements. In addition, the ratio of maximum to minimum cross-section moments of the middle femora suggests that Dunping males had moderately more robust lower limbs than males in other Neolithic and contemporary populations.

Overall, the behavioral pattern of the Dunping people is much different from the agricultural populations. They seemed to have had a long-term riding habit, and animal husbandry might have been their major ecological pattern, which was also supported by archaeological evidence collected from the cemetery. Due to the lack of literature records on the patterns of human occupation during the Bronze Age, it is an inevitable trend to use human skeletal data to explore how humans adapted to early environments.

The intersections matter: Sex, site, and survivorship in Ottoman-era Hungary

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Differences in the health of women and other marginalized groups in the past can be obfuscated by research designs that fail to consider how subgroups within a larger population may differ in their risks of death, exposure to hazards, or probability of survival. An intersectional perspective encourages researchers to explicitly address the existence of multiple identities and experiences in the past by examining additional intersections in their analyses. In this study, Kaplan-Meier survival analysis is used to compare survivorship among estimated males and females in two different communities from Ottoman-era Hungary (16th-17th centuries). A log rank test was run to determine if there were differences in survival between males and females within each site. The survival distributions for males and females were significantly different in the Fonyód-Bézsenypuszta (FB) sample (p=0.034) but not the József Nádor Tér (JNT) sample (p=0.499). The results echo previous analyses that found differences in the risks of mortality between estimated males and females at FB but not JNT, and they suggest that considering sex or site separately is not sufficient to understand survival or risk in this context; rather, these two aspects of identity and experience should be considered in concert with one-another to better understand how experiences varied by sex or gender in the past. In this context, decreased survivorship among males in the FB sample may have been because males in this community were more likely to be involved in violent border skirmishes compared to females and individuals living in Budapest.

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Endocranial Shape Variation and its Impact on Neural, Dural, and Cranial Base Structure

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In a preliminary 2D study of adult endocrania, we demonstrated a relationship between the angle of the straight sinus/tentorium cerebelli and cranial base. This linkage results in neural rotational events and relocation of brain structures, consequent on changes in endocranial shape. To better delineate endocranial changes in soft/hard tissues in the presence of normal shape variation, we expanded our analysis to include a 3D geometric morphometric assessment.

We collected 85 endocranial landmarks from anonymized CT scans (N=90; GE LightScribe VCT scanner, helical mode, standard convolution kernel). Shape variation was assessed via Principal Components Analysis, on Procrustes-aligned shape variables, in Morphologika. To visualize soft tissue change, we employed sagittally sectioned cadaver heads (N=10). On sagittal CT slices, we measured linear dimensions and angles of the cranial base and the angle of the straight sinus.

We confirmed the relationship between the orientation of the straight sinus and cranial base (r=0.47) and the resultant reconfiguration of the brain. A brachycephaly-dolichocephaly transition with cranial base flattening occurs along PC1 (17.3%). Superoinferior endocranial flattening occurs on PC2, with cranial base flexion at extreme PC2 (11.3%). Change in the sellar region dominates PC4, with anterior base elongation and posterior sellar rotation. Sphenoethmoidal bowing occurs as an isolated event along PC6.

Our 3D analysis both confirms and expands earlier results of the impact of normal shape variation on adult endocranial contents. Further, we are now able to assign morphological variations in the cranial base to discrete events and link them to positional variation in brain structures.

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Energetic trade-offs: Urinary C-peptide in the Zanzibar red colobus (*Piliocolobus kirkii*) across a habitat-disturbance gradient

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The ability to mobilize energy is critical in facing environmental challenges, however different strategies may be pursued according to physiological tipping points. Where habitat fragmentation due to anthropogenic disturbance is degrading resources for animal populations, energetic biomarkers can be measured to determine activity trade-offs. We evaluated the influence of activity budgets on urinary C-peptide (uCP) in seven groups of Zanzibar red colobus (*Piliocolobus kirkii*), an endangered primate, across sites of increasing disturbance categorized by food availability: forest (high), agriculture (moderate/low), urban (low). We found uCP strongly related to activity, negatively associated with foraging effort and was significantly higher in groups that spent more time resting. Consistent with seasonal variation, uCP increased in all groups during periods of abundance. Whilst poorly-resourced agricultural groups rested most and maintained the highest uCP levels, moderately-resourced agricultural groups travelled most and recorded the lowest levels. Forest and urban group measures fell between these extremes. Previous studies show colobines adjust energy expenditure to endure nutritional deficit and it appears disturbed *P. kirkii* exhibit divergent responses to habitat degradation. Highly disturbed groups pursue an energy-minimizing behavioral shift to resting, whilst moderately disturbed groups pursue a resource-maximizing shift to travelling. Forest groups represent a more balanced energetic state, with urban groups unable to pursue either strategy. Our results capture the tipping point for an adaptive trade-off in *P. kirkii*, however resource abundance is not the only determinant of activity and uCP. Remaining discrepancies indicate other anthropogenic effects play a role, as well as differences in social dynamics.

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Applying Cartmill's Test for Adaptation to Human Internal Nasal Anatomy

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In a series of critiques of the common paleoanthropological practice of proposing causal explanations for unique human features, Cartmill postulated that evolutionary events can only be explained if they conform to regularly recurring patterns. This theoretical perspective forms the basis for a relatively straightforward test for adaptation: if an anatomical structure evolved multiple times in different organisms under similar circumstances, this recurrence provides evidence for the adaptation of that structure. Human internal nasal variation follows a clinal pattern (short/broad passages in warm, humid environments and tall/narrow passages in cold/dry environments) and has been suggested to be the result of climatic adaptation, but a Cartmillian test of this hypothesis has proven difficult due to the reduced anatomical complexity of human internal nasal structures compared to those of other mammals. However, assessing the pattern of human nasal variation with respect to the anatomical parameters that affect intranasal heat and moisture exchange and then comparing the human pattern to that of other mammals with a wide climatic range should provide the basis for a sufficient test for adaptation following the Cartmillian method. Here I present the results of a comparative analysis of internal nasal variation in humans and bears (polar, brown, sun, and sloth bears) as a test of climatic adaptation. The patterns of variation in both groups show anatomical changes in individuals from cold/dry regions that would enhance intranasal heat and moisture exchange efficiency, thus supporting the conclusion that the nasal regions of both humans and bears show evidence of adaptation.

The interplay of sociability and head-load carrying on energy expenditure: implications for efficient mobility strategies

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Head-load carrying is an ancient, energy-efficient way to transport heavy, awkwardly shaped cargo, i.e., water and firewood. These head-supported loads are often carried in various social settings, with women and children walking together as they collect necessary materials throughout the day. This social aspect of head-load carrying may be the root cause of a potential energetic predicament for individuals transporting loads. Here we assess the relationship between mobility and sociability, comparing speed and energetic cost during load carrying and when walking with a friend. Speed and Cost of Transport (CoT) were measured in individuals (N=11) who walked in four conditions: loaded alone, unloaded alone, loaded with a friend, and unloaded with a friend. Our findings show that people walked significantly slower with a load (p=0.015) and considerably slower with a friend (p=0.116). Load continued to have strong significance in relation to CoT (p<0.001) while sociability had no effect (p=0.972). However, there is a complex relationship between sociability and CoT, as the presence of a friend decreased CoT in unloaded conditions, but increased CoT in loaded conditions. These findings have implications for mobility strategies of individuals who often carry head-loads. Due to the complex relationship between CoT and walking with a friend, it may be favorable for individuals to transport cargo alone, particularly in energetically demanding environments.

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eQTL analysis of cold adaptation regulation in Peruvian Quechua populations

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Andeans have thrived in the extreme hypobaric conditions and drastic winter temperatures (50 to -40 during austral winter) of the Altiplano for the last ~10,000 years. While frequently the focus of hypoxia adaptation research, there has been little investigation on cold climate adaptions. Using a large-scale sweep for positively selected genes among 514 Peruvian Andean Quechua speakers, we identified evidence of selection in genes related

to cold-induced thermogenesis (*ESRRG*, *IL18R1*, *ABHD6*, *AARDC3*, *RB1*, *DYNC1H1*, *NR1D1*, *PCTP*); differentiation of thermoregulatory brown fat cells (*EBF2*, *METRNL*, *ZNF516*); and thyroid function (*DUOX* family). However, it is important to differentiate the effects of natural selection from drift and other demographic events. In particular, SNP-only data shows how variation occurs along known sites in the genome, but can obfuscate pleiotropic heritability data. In order to accurately measure regulatory variation at all sites, we performed eQTL and allele-specific expression (ASE) analysis on the data set to provide functional validation for candidate SNPs. This analysis identified departures between Quechua populations and a Maya control group. Our findings help to detangle the complex web of cold adaptation regulation in humans, and highlight how ecological/climatological stress shapes human metabolism, adiposity, and thyroid functioning.

It seems they glide: aerodynamics of vertical descent in *Galago moholi*

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Lesser galagos (*Galago*) are superlative leapers, capable of vertical jumps of >2m (i.e., >15 body lengths) and horizontal leaps of >4m (i.e., >30 body lengths). Though morphological and biomechanical studies have investigated how galagos produce the take-off forces required for high-performance leaps, few have considered how the animals modulate their trajectory once airborne. Nevertheless, both observational and theoretical studies suggest that galagos use aerodynamic forces during the floating phase of a leap to adjust their trajectory and mitigate landing speed. Here, we quantify the aerodynamic force production (i.e., drag forces) of Mohol galagos (*Galago moholi*) during airborne descent. Two zoo-housed *G. moholi* (body mass: 174-200g) were filmed with two cameras operating at 240Hz and calibrated to a common volume as they dropped between perches (fall distances: 1-1.4m). We digitized the 3D position of the animal's nose, shoulder, hip, and base of tail, calculating their instantaneous angular position with respect to gravity (i.e., angle of attack), instantaneous velocity, and instantaneous acceleration. Net aerodynamic force was quantified as the difference between instantaneous acceleration and gravity (i.e., -9.81ms^{-2}), multiplied by body mass. Angle of attack was maintained at ~49º (range: 48.6-49.5%), suggesting a compromise between parachuting and positioning the body for landing feet-first. Drag forces during descent averaged 52.4% of body weight, permitting the galagos to decrease landing speeds to an average of 88.5% of what they would have been under freefall. These data constitute the first quantitative evidence that leaping primates can use aerodynamic forces to modulate their movement dynamics while airborne.

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Pelvic incidence and pelvic tilt impact greater sciatic notch shape

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The greater sciatic notch (GSN) of the pelvis varies within and between sexes. J-shaped GSNs are associated with individuals assigned male at birth; U-shaped GSNs are associated with individuals assigned female at birth. The latter relationship is attributed to obstetric requirements, but more work is needed to understand the processes impacting GSN variation. GSN shape likely relates to pelvic incidence (PI) and pelvic tilt (PT), angles that show how the sacral plateau is positioned over the hip joints. The posterior ray of PI is formed from a line perpendicular to the center of the sacral plateau. The anterior ray is the sacro-acetabular distance from the plateau center to the bi-acetabular midpoint. PT is the angle between the sacro-acetabular distance and a coronal plane through the hip joint centers.

Here, I use three-dimensional landmark coordinate data and geometric morphometrics to analyze a sample of re-articulated pelves from the Bass, Terry, and Hamann-Todd collections and from medieval Kulubnarti, Nubia representing 76 assigned females and 81 assigned males, aged 19-100 years. I performed ordinary least squares regressions to separately test the impact of PI and PT on GSN shape. Greater PI is significantly associated with more U-shaped GSNs. Greater PT is significantly associated with a more pronounced piriform tubercle region. Results support a connection between factors relating to sagittal balance, PI and PT, and GSN shape. This study underscores the importance of considering proximal processes rather than simply obstetric selection to explain GSN variation.

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How to identify early *Homo*? Geometric morphometric approach based on multiple craniodental structures

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There is a general view that the first members of our genus evolved c. 3–2 million years ago in Africa. However, there is considerable debate about which features can be used to identify a fossil as belonging to *Homo* and whether some 'early *Homo*' material would be more appropriately reassigned to an australopith taxon. Here we use geometric morphometrics to test whether 'early *Homo*' fossils are most similar in key aspects of craniodental morphology to unambiguous *Homo* species (*Homo erectus* s.l. and successive species)*, Australopithecus,* or *Paranthropus*. The study sample consists of published craniodental specimens belonging to 'early *Homo*' (e.g., LD 350-1, A.L. 666-1, UR 501, OH 7, 13, KNM-ER 1802, 1813, 5431, StW 80, SK 27, 847). Geometric morphometric analyses of cranial vault (2D lateral and posterior profiles), mandible (2D dental arcade and symphysis cross-section shape), and molar enamel-dentine junction shape were conducted. To assess within and between group variation and the classification of particular specimens we computed principal components analyses, between-group principal component analyses, canonical variate analyses and typicality probabilities. Results suggest that a number of 'early *Homo*' specimens consistently show greater morphological resemblance to *Australopithecus* and/or *Paranthropus* than to *Homo erectus* s.l. and successive *Homo*. This is particularly the case for pre-2.2 million year old specimens, while more recent fossils show an intermediate morphology between *Australopithecus* and *Homo erectus* s.l. The implications of these results for the taxonomy of particular specimens and the morphological features used to define and diagnose 'early *Homo*' species will be discussed.

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A Reference Mitogenome for *Lagothrix lagotricha poeppigii* using Portable Oxford Nanopore Sequencing

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Portable sequencing technology enhances the efficiency and feasibility of primate genomic research in remote areas. We constructed a reference mitogenome for the silvery woolly monkey (*Lagothrix lagotricha poeppigii*) from DNA sequencing reads generated by an Oxford Nanopore MinION Mk1C using Kit 9 chemistry – one run in the field and one in a molecular genetics lab in the US – and compared them to an established *Lagothrix lagotricha* reference. Tissue samples were collected during necropsy from a wild individual that died of natural causes at the Tiputini Biodiversity Station in Amazonian Ecuador, where field-based sequencing was also conducted. We re-basecalled ONT reads at high-quality using Dorado, and mapped reads to a high-quality spider monkey reference mitogenome (*Ateles belzebuth*; NC_019800.1) using minimap2. Sufficient reads from both the lab (355 reads, 0.13% of total) and field (1,235 reads, 0.39% of total) aligned to the *A. belzebuth* reference to generate 55X and 58X coverage, respectively. Assemblies constructed using Flye and polished with Medaka generated shorter total mitogenome lengths (16,593 bp, 98.4% identity; and 16,590 bp, 98.6% identity) than a published reference for *L. lagotricha* (16,595 bp; NC_021951.1); base count discrepancies appear to be in single nucleotide tandem repeats missing in the ONT assemblies (a common ONT basecalling error). The differences between the field-based and lab-based assemblies appear to be more reliant on flow cell health (i.e., initial pore number, pore-clogging) than lab conditions *per se*. This work demonstrates that portable third-generation technologies can create high-quality and accurate reference mitogenomes in field-based lab conditions.

Genetic Insight into the Paternal Genealogy of the Kazakh population through Y-chromosome analysis

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Kazakhs, a Turkic-speaking indigenous population of Central Asia, have retained the paternal genealogical memory of clans within their gene pool structure. The Y-chromosome is an effective tool for studying the gene pool structure and genetic genealogy of clans.

To study Y-chromosome variability within the Kazakh population's gene pool and its relationship with clan structure, a study covered 17 geographical subpopulations in Kazakhstan encompassing approximately 20 major tribes and 50 clans. The research analyzed 37 Y-STRs and 62 SNP markers on the Y-chromosome, involving around 4,000 Kazakh males, with deep sequencing of approximately 200 Y-chromosomes (22.5 Mbp).

The AMOVA method revealed that clan group differences are 1.5 times greater than geographic population differences. The Mantel test showed a strong correlation between genetic and quasi-genetic (clan frequency) distances, and a weaker correlation between genetic and geographic distances. These findings are further supported by geneogeographical maps, where the distribution area of 50 Kazakh clans exhibits similar patterns to maps of genetic distances and frequency distributions of Y-chromosome haplogroups in the regions of Kazakhstan.

Phylogenetic analysis identifies founder effects in numerous clans with distinct Y-chromosome haplogroups. Deep sequencing revealed clan-specific haplogroups, for example Argyn (G1a-L1323), Alshin (C2a-Y15552), and Konyrat (C2b-ZQ402). This has enabled the verification of genealogical legends about clan origins and the assessment of their genetic connections to Eurasian populations.

New genetic insights into the paternal gene pool of Central Asian populations are being used by experts in fields like anthropology, archaeology, ethnography, linguistics, demography, and history to investigate interdisciplinary questions about ethnogenesis.

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Trophy or Vessel? Skull artifact from Liangzhu Culture site in Neolithic China

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Human bone artifacts are important cultural phenomenon found worldwide dating back to the Palaeolithic. Among them, skull artifact is generally interpreted as victory tokens from dead enemies, a commemoration of their venerated ancestors, or as sacrifices to their gods for rituals. The archaeological ruin of Liangzhu is one of the most developed ancient cultures in Late Neolithic China (about 3,300-2,300 BCE). The Bianjiashan Site is located on the south side of the archaeological ruins of Liangzhu in Hangzhou, integrating cemeteries, residential sites, and wharf. The cranial artifact was found in the ditch during the archaeological excavation in 2005, and the concomitant charcoal dated back to 4410±37 BP (laboratory code: ZK▯8230▯1).The calathiform showed diagnostic anatomical features indicating that it came from a human skull. It was horizontally cut above the temporal bone with part of the frontal bone, parietal bone, and occipital bone preserved. The cut marks around the horizontal cutting lines were obvious with diploë exposed. Two artificial circular holes could be seen on the frontal and occipital bones, respectively. The horizontal parallel swirls could be seen on the inner wall, which were perpendicular to the inner and outer walls of the bone. All the macroscopic and microscopic observations showed that only holes on the posterior side were artificially worn by long-term use. During the late Neolithic society of the Liangzhu Culture, the skull artifact was thought not to be a vessel for containing things but a hanging trophy.

Social Group Interactions and Mating Patterns of the Cayo Santiago Rhesus Macaque Colony: A Retrospective Approach

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The rich records of Rhesus macaques at Cayo Santiago (CS) with detailed information of individual and family relationships enables extended genetic analyses of the reproductive history of the colony. As a part of a collaborative effort to build a Knowledge Model of the history of health of the CS Rhesus colony, this study further delves into the intricate social group interactions and reproduction dynamics to provide an integrated perspective for a deeper understanding of familial connections and genetic aggregations. Leveraging matrilineal lineage developed from previous work and patrilineal tracing made available since mid-1970's, as well as inter-group transfer data, this study attempted to provide retrospective views of group evolution history, with an emphasis on dyad interactions regarding their natal and transferred groups. Employing tools and techniques popular in social community analysis, including graph database and Gephi, this study conducted a comparative analysis focused on animals born between 2005 and 2014. Preliminary results indicated that communities identified by using Gephi matched well with census records, while deviations from historical sketches of group evolution summaries existed as well. Upcoming results from using Neo4j, a graph database system, will be compared with these findings, which can be integrated more smoothly with CSViewer for Analysts, the graphical user interfaces for the CS

Knowledge Model to be introduced in a workshop at AABA 2024 annual meeting. Findings of this research can help add one more perspective to pathological studies seeking correlations with environmental factors such as food provision and natural disasters like hurricanes.

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Investigating cell-type specific shifts in metabolic gene expression between human and chimpanzees

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The human brain is more energetically costly than that of other primates, utilizing approximatly 20% of all of the body's metabolic resources, while chimpanzee brains use less than 10%. Previous work on whole brain tissue have consistently determined significant differences in metabolism between species. A cell-type specific comparison is necessary to understand distinct cellular contributions to interspecific differences in neurological function. Here, we conducted a cell-type specific investigation of neural differences between humans and chimpanzee by conducting RNA-Seq on neural progenitor cells (NPCs), neurons, and astrocytes generated from induced pluripotent stem cells (iPSCs) from both species. Differential expression (DE) analyses demonstrate that the greatest proportion of genes exhibiting DE are between species' astrocytes (12.2% of all expressed genes), followed by NPCs (8.57%), and neurons (5.8%). Categorial enrichment analyses of genes exhibiting DE show that all three neural cell types display interspecies gene expression enriched for metabolic processes, driven primarily by higher expression of metabolic genes in human cells. Gene set enrichment analyses reveal that human neurons and astrocytes are enriched for greater glucose transport while chimpanzee neurons and astrocytes exhibit greater lactate transmembrane transport. Cell-type specific gene expression evolution in primates can provide exciting insight into the cell type specific metabolic changes that were necessary to support evolution of the human brain.

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Exploring the Origins and Cultural Significance of Cranial Deformation in Northeast Asia: Evidence from a 10,800-Year-Old Case Study

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Cranial deformation, referring to the intentional modification of the skull, is a cultural practice observed worldwide, although its origins remain unclear. Increasing evidence suggests that the Northeast Asia region is one of the significant origins of cranial deformation. Here, we report a case of cranial deformation in a male individual discovered in Baicheng City, Jilin Province, China, with a radiocarbon dating of 10800-10170BP. This individual exhibits pronounced parallel-fronto-occipital deformation, heavy dental attrition, and severe periodontal disease, along with evident signs of tumor erosion on the cranial vault. Stable isotope analysis indicates a diet primarily composed of aquatic animals and C3 plants. Combining the findings from previous discoveries of cranial deformation in sites such as Songhuajiang I and II, as well as Houtaomuga site, distinct cranial deformation customs are evident in the Northeast Asia region. These variations existed during the early Holocene and may reflect the emergence of social complexity and hierarchical systems.