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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.

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.

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.

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.

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