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characterization have aided in the identification of the pathocenosis affecting ancient Romans and several susceptibility loci revealed specific variation in pathological individuals.

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Greater Male Variability in Chimpanzee (*Pan troglodytes*) Brain Structure

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Across taxa, sexually selected traits are more variable in the target sex than 1) the same trait in the opposite sex or 2) non-sexually selected traits, likely due to their condition-dependent expression. In humans, males show greater variability in certain cognitive abilities and brain structures that 1) may facilitate intra- or intersexual competition and 2) are greater/larger in males on average, suggesting these traits may also have been subject to sexual selection. This study investigates sex differences in brain structure variability in chimpanzees. Although male chimpanzees exhibit strong intrasexual competition, reproductive skew is reduced by female mate choice and male coercion. In vivo MRI scans were collected from 226 (135F/91M) individuals and surface areas were calculated for 25 cortical sulci. Outliers for each sex and sulcus were removed prior to analysis. We measured sex differences in variability by calculating the ratio of male-to-female standard deviations of MCMCglmm residuals, controlling for age, rearing condition, scanner type, and kinship. We tested for significant sex differences through permutation. We find that males are significantly more variable at the cingulate (ratio=1.18;p=0.043), middle-frontal (ratio=1.36;p=0.001), occipital-lateral (ratio=1.20;p=0.029), occipital-temporal-marginal (ratio=1.8;p=0.006), superior-temporal (ratio=1.36;p<0.001), subcentral-posterior (ratio=1.62;p=0.033), and superior-parietal (ratio=1.21;p=0.028) sulci. These regions are associated with social perception, face recognition, and motion prediction. Females are more variable at the medio-parietal-occipital sulcus (ratio=0.78;p=0.009), a region associated with planning. This is the first study to demonstrate greater male variability in brain structure in a nonhuman primate species, and suggests sexual selection may lead to greater variability in male cognition across taxa.

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Understanding human craniofacial bone properties and biomechanics - a perspective on macaques, baboons, and beyond

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Studies of the crania of macaques from Cayo Santiago Island have led to insights especially concerning craniofacial growth, suture biology, functional anatomy, and heritability. An understanding of these areas can be enhanced by knowledge of the material properties of the craniofacial skeleton, which are especially important for building models of the function of craniofacial bone. This investigation compares results from separate studies in our laboratory of the material properties of cortical bone of the macaque cranium and mandible. Comparisons of these results to other studies in primates and other vertebrates, including baboons, chimpanzees, gorillas, capuchins, humans, alligators, bats, and pigs, suggest that while there are similarities among species, the details of regional variation are important for understanding patterns of growth and functional anatomy. Material properties including density, cortical thickness, and elastic properties (elastic and shear moduli, and Poisson's ratio) were measured using standard and ultrasonic techniques in 10 adult macaque skulls. Comparisons between mandibular and cranial measurements showed that mandibular cortical bone is overall thicker, denser, and stiffer than cranial bone in most regions. Directional differences in elastic moduli (anisotropy) were similar in many regions of the mandible and cranium, although the mandible did show a tendency toward more consistent orientations of the direction of maximum stiffness. Overall, these regional differences between the mandible and cranium are also found in humans and baboons and are important to consider when modeling bone function in the skull. Bone structure and presumably adaptation presents functionally significant differences between the cranium and mandible.

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Girl, you'll be a woman soon: Examining associations between pelvic dimensions and body composition in growing girls living in London

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The relationship between body composition and pelvic dimensions in women is unclear, principally with regards to preparing the body for reproduction. Previous work has demonstrated that pelvic

breadth increases more slowly overall than linear growth and that girls reach their mother's height before they reach their mother's pelvic breadth. Fat mass increases as girls enter puberty; however precocious development as a result of increased adiposity in girls is unconfirmed. This study examines the interaction between pelvic breadth and changing adiposity that could impact pelvic dimensions as girls grow into women.

Body composition data and pelvic dimensions were collected from dual energy x-ray absorptiometry (DXA) scans from 286 girls and women living in London today between the ages of 4 and 22 years. Body composition data collected were four-component model lean mass and fat mass. Measures of adiposity collected were subscapular, suprailiac, tricep and bicep skinfolds and waist circumference. Tanner development stages and age at first menses were also collected. Outcome pelvic dimensions collected from DXA scans were bi-iliac breadth, mediolateral inlet breadth and biacetabular breadth. Variables were converted to age-adjusted z-scores to enable accurate body composition comparison between women and growing girls.

Multiple regression analyses demonstrate that only biacetabular breadth and mediolateral inlet breadth were associated significantly with both fat and lean mass. Tanner development stage and waist circumference associated significantly with mediolateral inlet breadth. These results suggest that bony pelvic dimensions vary in association with body composition and adiposity, potentially as part of preparing the female body for reproduction.

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Sulcal pattern variation in extant human endocasts

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Our knowledge of human brain evolution primarily relies on interpretation of paleoneurological evidence. In this context, the endocast (i.e., replica of the internal table of the bony brain case) constitutes a proxy for reconstructing a timeline and mode of cerebral changes in human evolution. The identification of cerebral imprints, with specific focus on cortical sulci, is critical for assessing the topographic extension and structural organization of cortical areas. However, the description of these crucial landmarks in fossil

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endocasts is challenging. The recent introduction of high-resolution imaging techniques in (paleo) neurology offers new opportunities for tracking detailed endocranial neural characteristics. This study aims at providing an atlas documenting the variation in the extant human endocranial sulcal pattern for subsequent use as a comparative platform for the study of the fossil record. Overall, more than 90 extant human crania from the Pretoria Bone Collection (University of Pretoria, South Africa) were detailed by X-ray microtomography at a spatial resolution ranging from 94 to 123 μm at MIXRAD, located at the South African Nuclear Corporation, Pelindaba. Based on our preliminary analyses, sulci are nearly consistently identifiable on the frontal (i.e., superior, intermediate and inferior sulci) and temporal (i.e., superior and inferior sulci) lobes. Interestingly, sulci bordering critical functional areas (e.g., Broca's cap) could be labelled as well. The construction of an atlas is a prerequisite for developing protocols involving automatic sulci recognition in endocasts. In this regard, our study introduces a promising perspective for discussing long outstanding questions in paleoneurology.

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Making Silenced Voices Speak: Restoring neglected and ignored identities in anatomical collections

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The Hamann-Todd, Robert J. Terry, and William Montague Cobb anatomical collections have played important roles in the history and development of bioarchaeology. However, little is known about the individuals that comprise these collections as their voices have been silenced. It is important to know who these persons were as our human identification and standardized methods are based on their skeletons. Most were poor, relied on charity hospitals, or were institutionalized. This presentation will utilize cross-disciplinary approaches that push beyond the biocultural synthesis to restore the ignored identities of individuals in anatomical collections. Key to this is the role structural violence played (and continues to play) in targeting the poor and socially marginalized for dissection and skeletal curation. Life history and embodiment theory are also applied, in addition to structural violence, to argue how the socioeconomic status, ancestry, and the mental health of these individuals resulted in their pathologies, institutionalization, and dissection. Restoring the voices and identities of persons in our historic anatomical collections

is ultimately important to the discipline, both from an ethical and social justice perspective.

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Genomic insights into early maritime adaptations in Western Patagonia

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Several studies have contributed to our understanding of the initial human occupation and diversification in the Americas. However, fewer have concentrated their efforts in geographically restricted areas such as Patagonia. With this work, we aim to contribute to the genomic characterization of local populations from Western Patagonia through the analysis of two ancient individuals from the region. These individuals are associated to the earliest maritime tradition identified in Patagonia, which according to archaeological evidence, developed locally around 6,000 years ago. Given that the connection between early and late maritime populations as well as the geographical origin of this tradition has not yet been fully understood; the analysis of these two early genomes is very valuable to shed light into its origin and later diversification. Low coverage genomes were generated for two individuals dated at 6,290 \pm 50 BP and 4,520 \pm 60 BP. These data was compared with modern and ancient individuals from America. Using f3 statistics and a Principal Component Analysis, we found a close proximity between the ancient genomes and populations from America, in particular South America. Historical individuals from Patagonia are the closest to both early maritime individuals, reflecting a long-term genetic continuity. Using a D-statistic analysis we saw that among the historical individuals, neither terrestrial nor maritime groups are genetically closer to the early genomes, reflecting their ancestral position before the differentiation of maritime populations. This evidence suggests a single origin for two of the main maritime

populations (Kawéskar and Yámana), strongly supporting a deep genetic history in the region.

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My, what big teeth you have! A structural model for relative snout length in primates

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Primates exhibit a range of variation in midfacial length. Strepsirrhines tend to have relatively elongated snouts, and most haplorhines are characterized by facial reduction. In our study of growth in neonate primates, we have developed an ontogenetic structural model of primate cranial diversity. Here, we ask whether the size of developing tooth germs predicts the relative length of the midface in primates at or around the time of birth.

We used virtual reconstructions of the cranium from microCT data for neonate primates (late fetal to 6-days-old) representing tarsiers and multiple genera of anthropoids and strepsirrhines. Shape of the cranium was quantified using Procrustes superimposition of landmark coordinate data ($k=40$). Dental volumes were estimated as the cube root of summed areas of postcanine dentition from serial histology. Distances representing nasal, dental arcade, and cranial base lengths were calculated. Data were scaled by regressing against cranial base length.

Morphometric analyses indicated that the greatest amount of shape variation, including relative length of the midface, was explained by clade. Dental arcade length was significantly greater in strepsirrhines than anthropoids. For the pooled sample of primates, relative dental volume explains almost all the variation in dental arcade length independent of phylogenetic group ($r = 0.94$, $p < .0001$), and these values scale isometrically. There was no corresponding relationship of dental volume to relative nasal length. These data suggest that some but not all midfacial differences across major groups of primates are significantly influenced by difference in size and timing of tooth development.

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Population differences in aging-related inflammation are associated with change of central adiposity

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