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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 is 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 biiliac 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 were 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 underlie 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

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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.

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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 irretrievable, 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