

2) Pore Modifier: This is a new toolkit for modifying pore ROI sets through superimposition on the histological image. Tools include one-click selection of missed pores by modulating wand tolerance, quick toggling for ROI labels, and easy savepoints.

3) Pore Analyzer: This new, fully automated routine includes a) Classification of individual pore type as cortical or "trabecularized", b) Regional subdivision of rib cross-sections into cutaneous / pleural halves and limb cross-sections into anatomical quadrants, and c) Summary statistics for percent porosity and pore area and shape descriptors, subdivided by anatomical region and pore type.

Testing new trait definitions and scoring procedures for subadult sex estimation

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This presentation will inform attendees about a new method for estimating subadult sex that utilizes the most commonly relied upon adult morphological sex traits of the skull and pelvis, but with reworked trait definitions and scoring procedures that are more appropriate for use with immature remains. The skull traits include: mastoid process, glabella, supraorbital margin, nuchal crest, and mental eminence. The pelvic traits include: ventral arc, pubis shape, subpubic contour, medial aspect of the ischiopubic ramus, obturator foramen, greater sciatic notch, and pre-auricular sulcus. Intra- and inter-observer agreement between one and two observers with high and moderate levels of sex estimation experience, respectively, were evaluated using Cohen's quadratic weighted kappa and a sample of 10 individuals from the Subadult Virtual Anthropology Database. Results indicate substantial to perfect agreement ($k = 0.65-1.00$) for intra-observer analyses for all traits. Inter-observer analyses were more variable, with agreement for most traits ($n = 7/12$) being substantial ($k = 0.66-0.722$). Inter-observer agreement was highest for glabella ($k = 1.00$) and lowest for ventral arc ($k = 0.27$), which is a likely consequence of this trait being underdeveloped in subadults and difficult to discern on CT images. Despite modest agreement for some traits, discrepancies never exceeded more than a 2-stage difference between observers and account for only 8.3% of all observations. Trait modifications are currently underway and will be tested by additional observers. New classification formulae will then be developed for inclusion in the freely available databases, MorphoPASSE and KidStats.

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A pilot study of qualitative and quantitative methodologies for commingled remains

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There are numerous methods employed to assist forensic anthropologists and bioarchaeologists in determining the minimum number of individuals (MNI) and sorting commingled remains. This study seeks to compare three methods: visual pair matching, osteometric sorting, and X-ray Fluorescence (XRF) Spectrometry analysis. The authors aim to compare methodology and accuracy. Individuals with varying levels of expertise participated in a blind study. The sample was a known, modern collection of 56 skeletal elements, which was selected from the Mercyhurst University's Osteological Collection by a third party. It is hypothesized that visual pair matching will have the greatest error rate due to its subjectivity and dependency on experience. The quantitative methods will have lower error rates due to the objectivity of metric data. XRF sample results will be processed at a later date, but its use is hypothesized to be highly dependent on the variability of the sample. Participants correctly analyzed that the MNI of the sample was 4. Preliminary results show that the majority of the participant's measurements in the osteometric sorting method were within the accepted 2mm range, resulting in nearly identical groupings of the remains. Visual pair sorting showed a significant difference in results. The 56 elements were from 8 individuals, element grouping ranged from 1 to 12 elements. One participant organized the sample into 22 groups, 12 of those groups contained only one element, producing a statistically significant error rate. The second participant had 7 groups with grouping accuracy ranging from 57%-100%. Preliminary results support the hypothesis.

Morphological integration of the human lower appendicular skeleton with respect to locomotion and biomechanics

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The extent to which morphological integration is driven by functional constraints is as-yet unverified. Here we explore the integration of the human lower limb from a functional perspective. Landmark data were collected from 3D surface scans of 60 adult human and chimpanzee os coxae, femora, tibiae, fibulae, scapulae, and humeri as well as adult crab-eating macaques (*Macaca fascicularis*) as an outgroup. Integration of homologous elements, as well as functionally-defined *a priori* modules of the lower limb

were quantified in two ways. First, the Integration Coefficient of Variation (ICV) was calculated using interlandmark distances and distributions of values generated using a resampling protocol. Additionally, integration was calculated using a Partial Least Squares (PLS) analysis. Comparison of ICV distributions was performed via pairwise Mann-Whitney U tests with Bonferroni correction. Comparison of rPLS values was carried out via comparison of effect sizes.

The hominoid taxa included here presented lower integration among developmental homologs, when compared to the macaque outgroup, which is consistent with previous research. Further, the human sample returned significantly higher integration values for functional modules of the lower limb when compared to the macaques, as well as *Pan*. Additionally, the human knee and hip were found to be highly integrated. These results provide further evidence for the evolutionary "de-coupling" of the hominoid appendicular skeleton. Results also suggest that the integration in the human leg is, at least partially, a result of constraints imposed due to the evolution of bipedalism. However, further research with specific biomechanical variables is necessary to confirm this.

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Evaluating the craniofacial feeding biomechanics in *Homo floresiensis* using the finite element method

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Homo floresiensis is a small-bodied hominin from Flores, Indonesia that exhibits primitive craniofacial features, such as a robust mandibular corpus, thick mandibular symphysis, and presence of superior and inferior transverse tori. These features are shared with "buttressed" australopithecines and are suggested to be adaptations to high masticatory stresses. However, *H. floresiensis* also exhibits marked craniofacial gracilization and short first molars more similar to that of later *Homo*, indicating a reduction in high magnitude occlusal loading relative to more robust hominin species. This discrepancy makes it difficult to infer feeding behavior in this species. This study uses finite element analysis