

The Smithsonian Institution's Human Origins Program Database (HOP-DB) is a collaborative effort to make data from the published records of paleoanthropology and related disciplines web-accessible to interested students and researchers as well as the general public. This effort presents numerous issues and challenges, on both theoretical and practical levels. These include issues of compatibility of data collected by different researchers, the use of alternative methods or naming conventions, and the challenges of maintaining the most flexible database design to ensure maximum data reliability and usefulness into the future. Here we discuss these and other issues and challenges encountered during development of the HOP-DB, and we present the implemented solutions and discuss the problems that still remain. In particular, we emphasize the need to design a highly modular structure of back-end data relationships such that front-end interfaces and web-applications can easily evolve to meet the needs of current and future users while the continual refinements of scientific data are accommodated smoothly and efficiently. By following this approach, the HOP-DB contains artificial-like intelligence built into its internal structure, increasing the likelihood that this database and its many modular components will remain a reliable and useful source of scientific information for years to come. We highlight some specific examples of uses of the HOP-DB in both research and educational settings.

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Salivary measures of testosterone and functional innate immunity are directly associated in a sample of healthy young adults.

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Immune-endocrine interactions have been the subject of intense interest by evolutionary biologists due to the important life history trade-offs that are evident in the function of various hormones and immune factors. Testosterone has been considered the quintessential physiological moderator between the immune and endocrine systems. Testosterone may facilitate increased reproductive success but also compromise survivorship, particularly via immunosuppression. Because of its pleiotropic actions, testosterone levels may represent an honest signal of phenotypic quality. That is, because maintaining elevated testosterone levels

could handicap survivorship, characteristics dependent upon testosterone should be honest indications of quality. Therefore, we hypothesized that healthy adult men and women with excess energy availability (i.e., not constrained by trade-offs between immunity and other functions) should exhibit direct (positive) correlations between testosterone and a measure of innate immune function. Multiple saliva samples were obtained from each of 37 male and 57 female participants. Innate immunity (i.e., complement and lysozyme activity) was measured using a newly developed salivary assay for bactericidal properties against cultured *E. coli*. Testosterone levels were directly correlated with immune values in both the male (Spearman's rank order, $\rho = 0.45$, $p = 0.007$) and female ($\rho = 0.52$, $p = 0.000$) samples. Those individuals with higher salivary testosterone levels exhibited greater ability to kill pathogenic bacteria. These results suggest that, although testosterone levels may be inversely related to immune measures in some individuals (particularly during infection/injury), testosterone levels can also be directly associated with other immune measures in healthy individuals with excess energy availability. Funded by Indiana University-Bloomington.

Fossil water and marsh birds, as paleoenvironmental indicators, at Olduvai Gorge, Tanzania.

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Olduvai has received countless faunal community and environmental reconstructions, but none have adequately addressed the paleoecological implications of its avifauna. Birds may provide information on environments at a finer spatial scale than mammals, especially for Pliocene deposits where many extinct mammals, but primarily extant birds, occur. Here, taxonomic analysis of water and marsh birds excavated by the Olduvai Landscape Paleoanthropology Project (OLAPP) is used to help reconstruct Olduvai's Lowermost Bed II (1.75 Ma) landscape.

Water and marsh birds, which dominate the Olduvai avifaunal assemblage, exhibit especially narrow habitat tolerances related to vegetation structure, diet, water quality and depth. Their presence may therefore provide important paleoenvironmental and -ecological information necessary for interpreting hominin land usage.

Cormorants are most common, with 79 specimens (*Phalacrocorax* and *Microcarbo*). Anatids (ducks, geese, and swan) are less common but more diverse, with 25 specimens from 8 genera. Rail, grebe, flamingo, pelican, and

various ciconiiformes (storks, herons, and egrets) are also present in smaller numbers. Most specimens can be ascribed to extant taxa, increasing the fidelity of attributed life history traits.

Bird densities and distributions suggest a persistence of wetlands and deep swamps during Lowermost Bed II times, but also the occurrence of tall nesting trees and possible flooded grasslands. In terms of hominin land usage, these birds point to locations where potable water, water plants, safety trees, and bird nests may have occurred.

This study supports the inclusion of avifaunal assemblages, when recovered at other sites of paleoanthropological significance, in any paleo-environmental or -ecological assessments.

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New 3D automatic methods for the analysis of the endocranial shape and its relationship with ectocranial structures: assessment and preliminary experiments.

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Over these last years, new computerized methods have been proposed to build virtual endocasts based on 3D CT images of extant or fossil skulls. This allows analyzing large samples automatically and then obtaining significant statistical results about the shape of the endocast and its correlation relative to other anatomical structures.

We assessed two new algorithms to segment and process virtual endocasts. The first tool allows delineating the boundary of the 3D endocranial surface without any manual interaction, even in presence of large holes (such as the foramen magnum). We compared these virtual endocasts with the corresponding plaster endocasts manually casted by one the authors. The second algorithm allows the automated measurement of 3D asymmetry on the virtual endocasts, and the computation of a mean 3D endocranial shape over several individuals on which the mean population asymmetry can be assessed.

To show the potential of such automatic tools, we propose to study the relationship between the shape of the endocast

and the external shape of the skull. For this purpose, we selected about twenty dry skulls in the Morton collection. These skulls were selected from population samples which have been considered in the past to evince pronounced exo-cranial secondary-developing superstructures. These samples were CT-scanned and we automatically segmented both the external surface of the skull and the endocast.

We present the first results of our analysis by focusing on the exocranial versus endocranial differences at the level of the neurocranium of each individual. We also compare asymmetry patterns between individuals.

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A method for aging Scandinavian medieval sub-adults based on long bone length.

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The preferred method for aging archaeological sub-adult skeletons is by dental examination. In cases where no dental records are available age estimation may be performed according to epiphyseal union or diaphyseal lengths. Currently no data has been produced for aging Scandinavian sub-adults from the medieval period based on diaphyseal lengths. The problem with using data on Scandinavian samples which have been derived from a different population is the possibility of skewing the age estimates. In this study 58 sub-adult skeletons from three Danish medieval collections were examined, aged from approximately six years to twenty years. The samples were aged according to the dental method of Haavikko with Ubelaker acting as control. Regression formulae were then constructed for aging according to their diaphyseal lengths. This study indicated that with the regression formulae developed, estimation of age can be done with reasonable results on Scandinavian sub-adults. The Scandinavian data was then compared to data from a different archaeological sample and a modern sample. It showed that the growth pattern was comparable to that of another archaeological sample with a mean difference of nearly one year. However, there is a difference in growth pattern from the two archaeological samples to that of a modern population. The modern sample showed an underestimation that increased with age until reaching approximately 6 years. This study has showed the importance of using data for

age estimation for archaeological material which has been developed specifically for that population and have developed a possible solution for Scandinavian sub-adult material.

Shape analysis of the proximal MT 2 and MT 3 articular surfaces.

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The proximal MT 2 and MT 3 articular surfaces were analyzed using geometric morphometrics to test the hypotheses that the human articular surfaces are quantitatively different from those of apes, and that there is no difference in articular surface shape between shod and unshod humans. Shod and unshod humans are compared to *Pan*, *Gorilla*, and *Hylobates*. The MT 2 fossil specimens include OH 8, Stw 573 ("Little Foot"), Stw 377, Stw 595c, Stw 89, and SKX 247. The MT 3 fossil specimens include OH 8, Stw 387, Stw 388, Stw 435, Stw 477, and Stw 496. Shod and unshod humans are not significantly different from one another, but both human groups are significantly different from the ape groups. The human MT 2 and MT 3 surfaces are relatively narrower in the dorsal area compared to apes, but expanded in the plantar area. The human MT 2 surface tends to be slightly concave overall, whereas in apes the dorsal area is highly curved and has lateral torsion and the plantar area shows medial torsion. The human MT 3 surface is flat, while the ape surface is slightly convex. The MT 2 specimens SKX 247, Stw 89, and Stw 595c group with apes, while Stw 573 and Stw 377 group with humans. The specimen OH 8 (MT 2 and MT 3) groups with humans. The MT 3 specimens Stw 496 and Stw 387 group with humans, while Stw 388, Stw 435, and Stw 477 are intermediate in shape to humans and apes.

New Middle Pleistocene mandibles from the Sima de los Huesos (Sierra de Atapuerca, Spain).

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The sample of human fossils from the Sima de los Huesos (SH) includes a large number of mandibular remains. Previous studies of many of these specimens have highlighted numerous similarities between the Atapuerca (SH) mandibles and the later in time Neandertals and have revealed important insights into the evolutionary process in Europe. In particular, a number of derived Neandertal features in both the corpus and ramus are already present in the Atapuerca (SH) mandibles, confirming an early appearance of features related to midfacial prognathism in the Neandertal lineage. The present study provides an update on the inventory of the mandibular sample from the Sima de los Huesos. A number of mandibles are now more complete following recent discoveries and newly recognized associations between specimens. The more complete mandibles make it possible to confirm many of the details of previous studies made on more fragmentary remains. In addition, the enlarged sample has extended the known range of variation in some features and allows for a reassessment of the variation and stability proposed previously for a number of features. Finally, the recent dating of the site to >530 kya suggests a re-evaluation of the evolutionary significance of the Atapuerca (SH) collection is warranted. At this early age, it appears that features of the face and mandible are some of the first derived Neandertal features to appear in the fossil record and may even be associated with the origin of the Neandertal evolutionary lineage.

ASIP and PAX3 contribute to skin pigmentation differences between European and Native American populations.

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The variation in human skin pigmentation has long been a subject of anthropological interest and has been shown to be among the most rapidly evolving traits in many human populations. However, few studies have attempted to identify pigmentation genes that have undergone selection in Native American populations and contribute to variation in skin pigmentation between Native American and Old World populations. Four tests of selection – Locus-Specific Branch Length (LSBL), Tajima's D Difference, Cross Population Extended Haplotype Homozygosity (XP-EHH), and Log of the Ratio of Heterozygosities (lnRH) – were considered to identify signatures of selection. Of 76 pigmentation candidate genes, 14 showed compelling evidence for non-neutral patterns of