A new 3D morphometric method based on a combinatorial encoding of 3D point configurations: application to skull anatomy for clinical research and physical anthropology.

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Three-dimensional (3D) shape analysis of anatomical structures is currently based either on the analysis of distances or angles between landmarks or on the computation of metric parameters which characterize the deformation of landmark configurations. However, significant differences which are not related to the normal inter-individual variation are not only metrical but also "structural". For example, in prognathism, it is a whole subset of landmarks which protrudes relative to another subset, in a correlated way. Such a deformation is not directly emphasized by the variation of the landmark coordinates and this suggests the need for additional 3D morphometric tools.
We propose to model the 3D landmark configurations by using the oriented matroid theory, a combinatorial mathematical structure which was developed over the past forty years. Oriented matroids allow one to model the relative positions of points in 3D without taking into account the distances between them. It is then possible to characterize some geometrical properties as the convexity or the alignment of subsets of landmarks and to detect structural changes as the crossing of a landmark through the plane defined by three others.
We applied this new method on sets of 133 3D cranial landmarks collected on 43 individuals presenting with varying types of coronal craniosynostosis. We computed the oriented matroid-based models and introduced a new discrete distance between two individuals. The matrix of all the distances allows differentiation among the craniosynostosis variant groups. We will also show how it could be used to compare extant and fossil skulls as STS5.
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New approaches to investigating ancient Maya diet: a three-isotope model for the reconstruction of dietary protein sources.

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The reconstruction of past dietary practices provides valuable information on the ethnicity, social relations, and subsistence strategies of archaeological populations. As one of the most extensively studied ancient societies, the Maya of Central America are ideal for region-wide investigations of synchronic and diachronic dietary practices. Here, by using previously-published isotope data, we apply a new dietary reconstruction model (Froehle et al., 2009, AJPA Suppl. 48:130) based on discriminant function analysis of three stable isotope variables (δ13Ccol, δ13Cap, and δ15Ncol) to generate hypothetical diet end-members representing different protein sources available to the ancient Maya. We model beans, squash seeds, C3 animal, C4 animal, and 100% maize as possible dietary end-members.
Using the model, we test for differential access to these sources between status groups, sexes and regions, as well as over time within groups. Our data demonstrate that there is no clear differential access to protein types between status groups or between sexes across the entire study population, but we find regional differences between the Southern Lowlands, Belize, and the Peten. Moreover, our data reveal significant within-site temporal changes in dietary practices. The residents of Laamani, for example, switched to a heavier reliance on C4-fed animal sources in the Post-classic Period, confirming the suppositions of earlier authors (Wright and White 1996:177), and possibly representing a greater reliance on domesticated animals, such as turkeys and dogs. This study provides a more nuanced understanding of the ancient Maya and highlights the utility of applying this dietary reconstruction model to archaeological populations.

Size and shape analysis of second deciduous molars in genus *Homo*.

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In the context of understanding human evolution, dental remains are a valuable subject to study: they represent the largest part of the human fossil record and allow comparisons between fragmentary individuals. Although juvenile hominin remains represent a large part of the fossil record, most studies in dental anthropology have focused on permanent teeth. The intraspecific variability in size and morphology is assumed to be high, which could challenge the use of deciduous teeth to assess taxonomic affinities of isolated dental remains. However, the use of geometric morphometric analysis can bring a new light on this issue.
The present study investigates second deciduous molar size and shape in the genus *Homo*, with a particular emphasis on Neandertals (n=20) and modern humans (n=218) . Dental crown shapes were analysed using two-dimensional outline analysis based on Radial Fourier transforms on photographs, that allow the inclusion of worn teeth to maximize sample size. Crown size has been estimated by measuring crown base area. Multivariate analysis and resampling methods were used to assess size and shape differences between taxa.
The results show that lower and upper second deciduous molars are useful for discriminating taxa, with a low rate of misclassified Neandertal and anatomically modern human specimens. Thus, we demonstrate the taxonomic utility of deciduous molars for identifying the taxonomic affinity of isolated or problematic specimens.
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Identifying differential patterns of activity: potentials and limits of tracing entheseal changes in archaeological populations.

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Bioarchaeological studies commonly and often too readily use musculoskeletal stress markers (MSM) to reconstruct past activities. Despite substantial progress in understanding the underlying factors of entheseal change, tracing past activities still suffers from largely subjective observation of trait formations, thus complicating inter-observer comparisons and interpretation of activity or stress impact.
The aim of this study was to apply a novel scoring method, based on clinical information and tested on documented collections (Villotte 2006), to archaeological populations as part of a research project on skeletal and archaeological indicators of identity in early medieval Alamannic populations. The skeletons of 304 adult individuals from the populations of Pleidelsheim (n=178) and Neresheim (n=126) were analysed for activity-related changes at 36 fibrocartilagenous and fibrous entheses.