

appearance of adult Neandertal characteristics in this Pleistocene population. The remains from the uppermost levels correspond to OIS 3, and offer further evidence of a late persistence of Neandertal anatomy and Mousterian tools on the Iberian Peninsula.

If I only had a...: missing element estimation accuracy using the Fully technique for estimating statures.

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Fully's (1956) technique for estimating statures relies on the rare completeness of skeletal remains. Few studies have systematically investigated how to account for missing elements, or how the accuracy of total skeletal height reconstruction is affected by estimating missing elements. We investigated these issues using 160 skeletons from four population samples: 111 Terry Collection whites and blacks, and two populations of Native Americans (total n=59), all measured using a revised protocol for Fully's method.

Contributions of individual vertebrae to total vertebral column length, though statistically different between populations in some cases, do not significantly affect the estimation of missing vertebral elements. Sex differences in vertebral element contributions to total column length, however, are significant, with females having relatively taller lumbar vertebrae in all populations; thus, sex-specific equations are necessary to estimate missing vertebral heights. All populations differ in limb to trunk length proportions, as expected from ecogeographic principles. Therefore, both sex and population affinity must be considered in reconstructing missing skeletal elements.

The Terry sample, because it includes individuals of known stature, was used for further tests of the accuracy of proposed missing element reconstruction techniques. The complete Fully method (no missing elements) yields non-significantly different estimates compared with living statures in this sample. Fully and Pineau's (1960) stature equations based on lumbar and one lower limb long bone do not differ significantly from true statures for white males, but do for the tibia-based equation for black males ($p < 0.05$) and for both equations for both populations of females ($p < 0.05$).

A new method for assessing endocranial morphology: calculating local curva-

ture from 3D CT images.

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Assessment of endocranial morphology is central to research on brain evolution. Unfortunately, endocranial surfaces frequently do not unequivocally and clearly indicate surface features of the brain. Controversies over the existence and/or placement of subtle features on particular fossil endocranials have thus been relatively common and difficult to adjudicate. A method of objectively identifying and marking surface features evident on a particular specimen, in such a way that accurate measurements could be made between and among features, would therefore be particularly useful. Methods for highlighting surface features date back to Le Gros Clark et al. (1936), who rubbed soot-blackened plaster endocranials with cloth, thereby revealing ridges and bumps as white areas. We describe an analogous, but mathematically rigorous method of evaluating endocranial surfaces, in which the curvature of each point of the surface of CT-derived virtual endocranials is calculated. By determining both the mean and Gaussian curvature at each point, it is possible to objectively classify areas of the surface as either pits, peaks, ridges, troughs, planes or one of three saddle-type shapes. These areas can then be color-coded and rendered in 3D, aiding in the objective assessment of endocranial features. Specific locations can be easily identified in 3D space, allowing measurements between features of interest. These methods are demonstrated on CT-derived virtual endocranials of Taung, SK 1585, and several modern *Homo sapiens* and *Pan troglodytes* specimens. The usefulness of these methods in illuminating debates on features such as the lunette sulcus in early hominid brain endocranials will be discussed.

A review of the putative Paleolithic human remains from Japanese Archipelago.

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Since 1931 nearly twenty Paleolithic sites in Japan were reported to have yielded human remains. Our recent re-

evaluation of these remains indicate that about a half of them belong to Neolithic and later ages (e.g. Akashi, Mikkabi, Hijiridaki, and part of Kuzuu), and that some of them are not human but animal remains (e.g. Ushikawa and part of Kuzuu).

Morphological characters of definitive human remains with secure Paleolithic ages are reviewed. Except the Hamakita remains from Central Japan, relatively well preserved and well-dated Paleolithic human remains are found in the Okinawa Islands, southwestern Japan, where limestone deposits are abundant. For example, the Minatogawa remains consist of at least four skeletons, dated around 17,000 BP. They possess short and gracile limbs and a primitive and robust skull. This may indicate adaptation for a probable nomadic gathering and hunting life in the small islands of Okinawa. The Pinza-abu remains, consist of skull and other fragments, dated around 25,000 BP. They show similar features to those of the Minatogawa remains. Yamashitacho remains, consist of a femur and a tibia of a seven year old child, they are dated around 32,000 BP, which is the oldest chronological date for human remains from Japanese Archipelago.

Mitochondrial DNA sequence evidence for a deep phylogenetic split in chacma baboons (*Papio hamadryas ursinus*) and the phylogeographic implications for *Papio* systematics.

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In a recent publication, Newman, Jolly and Rogers (2004) proposed a phylogenetic hypothesis for *Papio* based on sequence variation in the Brown region of the mitochondrial genome. Their analysis revealed 4 major lineages and identified chacma haplotypes as the oldest (1.8mya) and most divergent, being the sister clade to other *Papio* allotaxa. While paleontological and morphometric data support this conclusion, their sampling scheme did not encompass the spectrum of morphologically distinct populations that fall under the taxonomic umbrella of "Chacma baboon" (*P.h. ursinus*). We collected 44 samples representing 7 distinct, well provenienced locations throughout South Africa (Western Cape - two locations, Eastern Cape, central South Africa, Gauteng province, Limpopo province). We sequenced the samples and aligned them with published sequences used in the