

Automatic Crest Lines Extraction for 3D Morphometry of Fossil Structures

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«Geometry morphometrics» methods (Bookstein 1991) use configurations of landmarks to define the shape of an anatomical structure. Coordinates of these landmarks are then processed to compute an «average» shape, to quantify the variability or to emphasize the differences between data. In general, the considered landmarks are 3D anatomical points which are located either on the real surface of the fossil or on a digital representation. Then it becomes possible to extrapolate «semi-landmarks» in order to define more precisely the shape. Nevertheless, some researchers have proposed to use 3D feature curves directly (Dean 1993) which gives much more information than sparse points. But it can be difficult to define these curves manually and the result remains user-dependent. So, some researchers in computer science have developed methods to extract such kinds of curves automatically (often called «crest» or «ridge» lines) from a 3D image and they have used them to analyse the shape of a fossil skull (Subsol et al. 2002). They also have shown that crest lines are very close to anatomical lines which are extracted under the supervision of an expert. We present the latest algorithms to compute fully automatically crest lines and we apply them on several anatomical structures (tooth, skull, endocranium) of a database of CT-Scan and microCT-Scan images of primates and hominid fossils. We show how these lines emphasize the bony structures of the skull such as the zygomatic process. We find also that crest lines on endocranium data may help to define the different lobes in a reproducible way. Lastly, we use crest lines to characterize the geometry of the grooves in the Enamel Dentine Junction. Based on these preliminary results, we aim to develop new computerized tools to study the morphological variability of anatomical structures and to compare the fossils found on the Sterkfontein site (Braga et al. 2008).

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Comparative Ecological Settings of *Homo* in Plio-Pleistocene East Asia and East Africa

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Homo dispersed to continental East Asia by 1.7 Ma, with early evidence found at Yuanmou and at Majuangou (Nihewan Basin), China. Many early Pleistocene East Asian mammalian species differ taxonomically from East African species of this time period, but it is unclear whether hominins colonized places that differed from East Africa in their ecological properties. Evidence from large mammals is used to determine whether hominin populations dispersed into areas where the fauna was similar ecologically to Africa, or whether hominins colonized substantially different environments during their initial dispersal. Large mammal specimen data were collected from East Asian early Pleistocene hominin sites. Specimens from non-hominin early Pleistocene and late Pliocene sites from Asia and from Olduvai Gorge and Lake Turkana were included for comparison. Modern faunal data drawn from Asian and African nature reserves also were analyzed. Body mass and hypsodonty were estimated from craniodental measurements. Each species was then classified into an ecological category combining body mass, diet, and substrate (terrestrial, arboreal, or aquatic). The number of species in each category at each site was used in a correspondence analysis. Results show that East Asian early Pleistocene sites had different ecological structures compared with East African sites, and that ancient sites differed ecologically from modern faunas. A greater number of grazing species tends to differentiate East African from East Asian Plio-Pleistocene sites. Browsers and carnivores were common in the East Asian fossil sites. By contrast, modern sites show a different pattern; African sites have many grazing and browsing species, while the East Asian sites have more species of omnivores and small predators. Differences in ecological structure between the Plio-Pleistocene African and Asian sites indicate that as hominins spread into East Asia, they encountered faunal communities that differed in their ecological characteristics and resource availability as well as taxonomically.

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