

Estimating hominoid reciprocal joint congruence: A comparison of two morphometric techniques.

W.E.H. Harcourt-Smith^{1,3}, J. Kim^{3,4}, E. Delson^{1,2,3,5,6}, ¹Vertebrate Paleontology, American Museum of Natural History; ²New York Consortium in Evolutionary Primatology (NYCEP); ³NYCEP Morphometrics Group; ⁴Institute of Anthropology, University of Vienna; ⁵Anthropology, City University of New York Graduate School; ⁶Anthropology, Lehman College/CUNY.

One of the central issues surrounding the analysis of hominin fossil assemblages is the allocation of skeletal elements to the correct taxon, and, in some cases, to the correct individual. One little studied approach to this issue is the statistical estimation of congruence between reciprocal joint surfaces – that is, the closeness of fit between articulating elements of a joint complex. Aiello et al. conducted a preliminary analysis of talo-crural joint congruence in extant hominoids, but limited statistical techniques and computing power made it difficult to address the complex 3D relationships between the joint surfaces. In this study we compare and contrast two recently developed techniques of estimating joint congruence and test the effectiveness of each technique in correctly assigning reciprocal elements at the individual and species levels.

Both techniques use three dimensional landmark and semi-landmark data collected from high resolution Laser Surface Scans of the reciprocal surfaces of the humero-ulnar component of the elbow joint. The sample consists of adult specimens representing *H. sapiens*, *P. troglodytes*, *G. gorilla* and *P. pygmaeus*. The first technique is indirect, and uses Partial Least Squares (Bookstein, 2003) and matching by discriminant analysis to assess to what degree two surfaces covary. The second technique is a direct measure of congruence, and is based on the overlap ratio between the two surfaces throughout the range of the joint's motion.

Results show that both techniques confidently assign reciprocal elements at the taxonomic level, and that further refinement will provide a useful tool in matching unassociated skeletal elements. Funding: NSF ACI 9982351.

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