A comparison of spherical harmonic and sliding semilandmark analyses as methods for three-dimensional shape evaluation

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The ability to quantify morphological variation is integral to biological research. The use of sliding semilandmarks in geometric morphometric (GM) analyses allows for the evaluation of whole bone morphology in three dimensions. A sliding semilandmark analysis, however, is difficult to complete when structures lack obvious homologous features for landmark placement. Spherical harmonics (SPHARM) offers an alternative method for shape analysis in such cases. Here we evaluate the SPHARM method by comparing results to those from a sliding semilandmark analysis of the calcaneus in African apes and modern humans.

Modern human (n=20), chimpanzee (n=20), and gorilla (n=20) calcanei were surface scanned. For the GM analysis, 1007 sliding semilandmarks were evenly distributed across the external surface of each calcaneus. Semilandmarks were slid to minimize the bending energy of the thin plate spline interpolation function relative to an updated Procrustes average. Final landmark configurations were then aligned using Generalized Procrustes Analysis. For the SPHARM analysis, surface models were mapped onto the surface of a sphere (parameterization), and then decomposed into a weighted sum of spherical harmonic functions. Because the spherical harmonics provide a standardized basis for quantifying shape, coefficients of the harmonic functions can be used as shape descriptors. Calcaneal shape variation was summarized using a principal components (PC) analysis of the Procrustes coordinates and SPHARM coefficients. Analyses were compared through calculation of the root mean square (RMS) and maximum distance between surface models of the average specimen from each species, as well as surface models of PC warps created two standard deviations from the average along PCs 1–3.

Both sliding semilandmark and SPHARM analyses separate species along the first two PCs. For both analyses, African apes and modern humans separate along PC1. Average RMS between species averages was 0.25 mm. Maximum surface distances between average surface models from the two analyses were all less than 0.23 mm. Average RMS between all respective PC warps was 0.82 mm. Maximum surface distances between PC warps were all less than 1 mm. Although there were minor differences between PC plots produced from the two analyses, the same general morphological distinctions between species were identified. The primary differences between SPHARM and sliding semilandmark-based surface models of PC warps and species averages occur around sharp edges, which are less defined using the SPHARM analysis, although these differences are small. Overall, SPHARM provides the same shape representation as a sliding semilandmark analysis, making it a comparable method for the evaluation of shape in three dimensions.

Support or Funding Information

This project was supported by NSF grant # BCS - 1824630.