A62 Accuracy in Osteometric Reassociation: Comparing Geometric Morphometric Landmark Data and Linear Measurements

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The goal of this presentation is to inform attendees regarding accuracy rates for resolving small-scale, closed-population commingled assemblages using either geometric morphometric landmark data or linear measurements.

This presentation will impact the forensic science community by comparing the performance of two forms of bone size/shape quantification in resolving commingling.

Commingled assemblages present a common situation in osteological analysis in which discrete sets of remains are not readily apparent, thereby hindering biological profile construction and the identification process. Of the methods available for resolving commingling, osteometric sorting is reliable and relatively objective.[1] Traditional osteometric sorting methodology is a decision-making, error-mitigation approach, in which possible matches are eliminated if the accompanying *p*-value exceeds an analyst-defined threshold.[1] Elements are reassociated if all other possibilities are eliminated and the assumption of a closed-population is met; however, recent research has demonstrated that commingled remains can be accurately reassociated in small-scale assemblages using geometric morphometric landmark data in a predictive framework.[2]

The primary goals of the current study are twofold: (1) examine the accuracy (as assessed through correct classification rates) of a predictive framework for reassociation; and, (2) compare two forms of data for quantifying long bone morphology — geometric morphometric landmark data and linear measurements.

To accomplish these goals, landmark data from 208 individuals and linear measurements from 435 individuals were analyzed from the William M. Bass donated skeletal collection. Raw landmark data were fit using generalized Procrustes analysis to extract log-centroid size and Procrustes coordinates. Procrustes coordinates were subjected to partial least squares analysis to extract relevant components. Ten individuals were randomly removed from the total sample, acting as a small-scale, closed-population commingled assemblage. One element was chosen from the commingled assemblage as the independent variable, with the ten possible matching elements representing the dependent variable. Using the remaining total sample, Bayesian regression via Hamiltonian Markov chain Monte Carlo was used to estimate a range of possible dependent variable values. These values were smoothed into a probability density function using kernel density estimation and the ten possible matches were evaluated against this distribution to calculate predictive probabilities. The element with the highest predictive probability was considered the best match. This process was repeated 1,000 times for femur antimere comparisons for both linear measurements and landmark data.

Matches were correctly classified for 78.2% and 93.2% of the commingled assemblages, using landmark data and linear measurements, respectively. These results suggest that bones can be accurately reassociated using the predictive framework, without the need to eliminate all possible matches. Linear measurements performed markedly better than landmark data for resolving commingling, demonstrating that linear measurements contain ample information for predicting correct matches. Furthermore, the ease of data acquisition and analysis of linear measurements in comparison to landmark data make the former a better choice for resolving commingling.

Reference(s):

1. Byrd J.E., LeGarde C.B. 2014. Osteometric Sorting. In. *Commingled Human Remains: Methods in Recovery, Analysis and Identification.* B. Adams and J.E. Byrd, editors. 165-189.

2. McCormick K.A. 2016. Osteometric Reassociation Through Quantifying Long Bone Size and Shape and Prediction Using Bayesian Regression Via Hamiltonian Moarkov Chain Monte Carlo (MCMC). *Proceedings of the American Academy of Forensic Sciences*, 68th Annual Scientific Meeting, Las Vegas,NV. 2016.

Commingling, Osteometrics, Bayesian Modeling

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