

## A69 Osteometric Reassociation Through Quantifying Long Bone Size and Shape and Prediction Using Bayesian Regression Via Hamiltonian Markov Chain Monte Carlo (MCMC)

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After attending this presentation, attendees will be informed about methods for quantifying long bone morphology and using these data in a predictive framework for resolving small-scale, closed-population commingled assemblages.

This presentation will impact the forensic science community by integrating information on long bone shape into osteometric sorting models that largely rely on size as assessed through standard osteological measurements. Additionally, this presentation introduces a novel predictive framework for osteometric reassociation: Bayesian regression via Hamiltonian MCMC.

Commingled assemblages present a common situation in osteological analysis where discrete sets of remains are not readily apparent, thereby hindering biological profile construction and the identification process. Of the methods available for resolving commingling situations, osteometric sorting is reliable and relatively objective.<sup>1</sup> Current osteometric sorting methodology models long bone relationships by calculating a distance measure from standard osteological measurements, transforming that distance measure into a test statistic, and evaluating the value of that statistic against the appropriate distribution to arrive at a *p*-value.<sup>1</sup> This methodology is a decision-making, error-mitigation approach, where possible matches are eliminated if the accompanying *p*-value exceeds an analyst-defined threshold.<sup>1</sup> Elements are reassociated if all other possibilities are eliminated and the assumption of a closed-population is met (see reference 1 for a more nuanced consideration of this approach and its statistical foundation).

The primary goals of the current study are three-fold: (1) examine the reliability (as assessed through correct classification rates) of a predictive framework for reassociation; (2) study the utility of predictive probabilities and typicality values as metrics for reassociation; and, (3) incorporate information on long bone shape from geometric morphometric landmark data into osteometric reassociation models.

To accomplish these goals, landmark data were collected from the long bones of 208 subjects, males (*n*=103) and females (*n*=105), between 19 years and 62 years of age at death, 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 (PLS) analysis to extract relevant components. After the sample was transformed into log-centroid size (size variable) and PLS components (shape variables), 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 MCMC 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 and typicality values. The element with the highest predictive probability was considered the best match. Femur antimeres comparisons illustrate the utility of this approach.

Over the course of 1,000 simulations, matches were correctly classified for 77.6% of the commingled assemblages. When size and shape were analyzed separately, correct classification dropped to 51.1% and 60%, respectively. Despite the high classification rate, predictive probabilities for correctly classified matches were equivocal, with a mean value of 0.1755 and a range of 0.1164-0.2973. These values were similar to predictive probabilities of incorrect classification (mean: 0.1502, range: 0.1159-0.2649), suggesting predictive probabilities alone were a poor means of identifying classification error. Typicality values were minimally helpful in identifying classification error, with mean typicality values for correct and incorrect classifications of 0.8541 and 0.6919, respectively. Additionally, typicality values for both correct and incorrect classifications ranged all possible values.

These results suggest that bones can be reliably reassociated using the predictive framework detailed above. The osteometric reassociation model presented incorporates both shape and size information, providing a more complete representation of long bone form over standard osteological measurements. Additionally, Bayesian parameter modeling results in a distribution of possible values for the independent variable, directly modeling uncertainty in its estimation; however, practical applications of this model are currently limited by a means to detect classification error, as predictive probabilities and typicality values are similar for both correctly and incorrectly classified matches.



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### Reference(s):

1. Byrd J.E., LeGarde C.B. Osteometric sorting. In: Adams B.J., Byrd J.E., editors. *Commingled human remains: methods in recovery, analysis and identification*. Boca Raton, FL: CRC Press, 2014:165-189.

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### Commingling, Geometric Morphometrics, Bayesian Modeling