A43   How Large Is Too Large? The Effect of Assemblage Size in Reassociating Commingled Remains

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The goal of this study is to examine osteometric reassociation accuracy as assessed through correct classification rates on commingled assemblages of varying sizes.

This presentation will impact the forensic science community by addressing a largely unexamined aspect of resolving commingling — size of the commingled assemblage.

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. Osteometric sorting has been shown to be a reliable and relatively objective method for resolving commingling.[1] Two statistical and probabilistic osteometric reassociation approaches have been successfully applied to resolving commingling: frequentist and Bayesian.[1,2] This study focuses on the latter approach.

To accomplish the goal of this study, linear measurements of the femur from 435 individuals were analyzed from the William M. Bass donated skeletal collection. Individuals were randomly removed from the total sample, acting as a closed-population commingled assemblage. The smallest commingled assemblage examined in this study was two individuals. The next smallest assemblage was five individuals and assemblage size was increased by increments of five to a maximum of 50 individuals. One femur was chosen from the commingled assemblage as the independent variable, with the possible matching femora 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 possible matches were evaluated against this distribution to calculate predictive probabilities. The femur with the highest predictive probability was considered the best match. This process was repeated 100 times for each commingled assemblage size.

As expected, there is a general inverse relationship between correct classification rates and commingled assemblage size. Accuracy decreased as the commingled assemblage size increased, with the two-individual assemblage showing the highest correct classification at 98%, and the fifty-individual assemblage showing the lowest at 76%. Interestingly, accuracy did not decrease markedly as the commingled assemblage size increased. A 50-individual commingled assemblage represents a 2,400% increase compared to a two-individual assemblage, with only a 22% decrease in classification accuracy. These results show that a Bayesian approach to resolving commingling is powerful across a large range of commingled assemblage sizes.

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 Markov Chain Monte Carlo (MCMC). *Proceedings of the American Academy of Forensic Sciences*, 68th Annual Scientific Meeting, Las Vegas, NV. 121.

Commingling, Osteometric Reassociation, Bayesian Modeling