## H14 The Use of Osteometric Sorting Techniques to Aid in the Resolution of Large-Scale Commingling

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After attending this presentation, attendees will understand how anthropological techniques can be used to aid in the resolution of large-scale commingling of human skeletal remains. The gross and metric sorting procedures can be beneficial in cases of large-scale commingling, particularly in situations when there are time and monetary constraints.

This presentation will impact the forensic science community by demonstrating the utility of gross and osteometric sorting techniques in the investigation of large-scale commingling such as in post-conflict and mass disasters.

The purpose of this study was to illustrate the practicality of utilizing gross and osteometric sorting techniques as a first approach in the sorting of commingled human remains. The Piggot archaeological ossuary site (31CR14), curated at the Forensic Analysis Laboratory at North Carolina State University was employed to represent a large-scale commingling. The Minimum Number of Individuals (MNI) was estimated at 78. The MNI was calculated using the right humerus, which was the skeletal element and side most represented in the assemblage.[1]

The sample used in this study consists of 114 skeletal elements. Each individual element was assigned an identification number. All bones were measured according to standard and non-standard measurements and recorded in a Microsoft® Excel® spreadsheet.[2-4] In cases of fragmentation, only available measurements were taken. All *t*-distributions were performed in Excel®; regression equations were derived in SPSS® Statistics 19.0.0.

Visual pair matching, the association of left and right elements based on parallels in morphology, was conducted on all complete or nearly complete elements.[5] Several elements were successfully pair matched and later confirmed with osteometric sorting.

The basic principle of osteometric sorting is that the two bones being considered are of a similar size and shape to have originated from the same individual. Osteometric sorting depends on the ability to distinguish anatomically normal size and shape relationships among skeletal elements. This is done by utilizing a reference sample to calculate means and standard deviations. The Forensic Anthropology Data Bank from the University of Tennessee, Knoxville was utilized because it consists of individuals of various age groups and ancestral origins. A database of non-standard measurements using the Osteology Skeletal Collection, curated at North Carolina State University, was created and utilized in this study.

Three models were used in the osteometric sorting process.[5] Model one compares left and right sides, which accounts for shape differences, similar to visual pair matching and, in many cases, performs equally as well. It takes the form $D = \Sigma(a_i - b_i)$. The standard deviation of the difference between left and right sides in the reference sample was compared against the summation of differences from each pair of right and left elements and evaluated against a two-tailed $t$-distribution. A significant value ($p$-value <0.10) indicates that the two elements are significantly different and could not have originated from one individual. Model two compares articulation surfaces of bone elements based on the size of articulating surfaces. It takes the form $D = c_i - d_j$. In this model, the reference sample mean is subtracted from the difference between measurements of articulating bone portions and the total is divided by the reference sample standard deviation. This value is compared to the two-tailed $t$-distribution ($\alpha = 0.10$). Model three compares bones of different sizes. The available measurements of a bone are summed and the natural logarithm of the sum is used in the regression model. The 90% prediction interval was used. If the sectioning point representing the two bones falls within the prediction interval, the null hypothesis that the bones were of a similar size to have originated from the same individual is rejected.

Using model one, comparing left and right humeri, out of 48 left and right pairs, 17 could be segregated. Using model two, comparing femora and os coxae, out of 42 left articulations, 8 could be segregated. Using model three, for the comparison of humeri and femora, the regression equation, HUM = -0.083(FEM)+6.281, 5 pairs were evaluated. No significant difference was found between any of the pairs; segregation based on osteometric sorting is not possible in this case and further testing would need to be performed. The use of gross and osteometric techniques could provide a first step in segregating commingled individuals, which could eliminate the need to perform DNA profile testing on each individual bone.

**References:**

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