## H47 Osteometric Sorting of Commingled Human Remains

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After attending this presentation, attendees will gain knowledge of osteometric sorting methods that can be used to sort commingled remains.

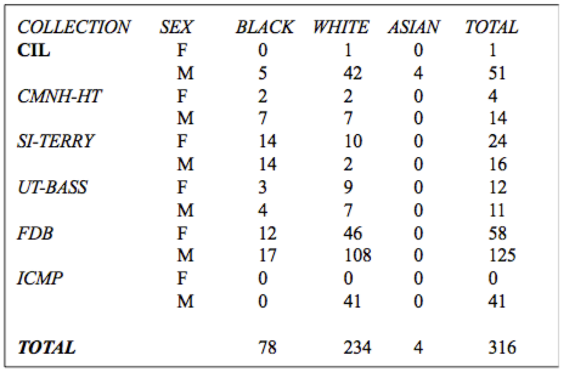
This presentation will impact the forensic community and/or humanity by introducing and describing methods that can be used to sort commingled human remains. Commingled human remains frequently result from mass disasters such as warfare, aircraft crashes, and terrorist attacks.

Assemblages of commingled human remains present special problems in the identification process. Biological profiles of individuals cannot be developed until the remains have been segregated into individuals. Though the presence of soft tissue can, in some cases, usefully inform the process (i.e., hair color and texture, skin tone, etc.), most of the information used to resolve commingling is obtained from the skeleton. The primary categories of information used to sort commingled remains are age, articulation, visual pair matching, size, build, taphonomy, and DNA sequence data. No one of these categories is sufficient as a sole basis for sorting most assemblages. The authors advocate the systematic use of these methods to sort commingled remains, so that each step in the sorting process is documented and can be replicated by other anthropologists (2, 4).

There are strong correlations among the sizes of the bones of the skeleton. Thus, a large humerus is associated with a large femur and a large metatarsal. This allometric reality can be exploited in the sorting process by formally comparing the sizes of two bones. Byrd and Adams (4) propose that a test of the null hypothesis that the two specimens are of a size to have originated in the same individual with the use of statistical tests. This approach requires the calculation of statistical models from a large reference data set appropriate to the population of interest. This method can be effectively applied to comparison of right with left paired bones, but has the advantage of being applicable to comparison between virtually any two elements in the skeleton. Naturally, some elements exhibit greater correlations in size with one another than with others. Recommend are three basic approaches to osteometric sorting: 1) comparison of left and right bones with models that key on shape, 2) comparison of adjoining bones with models recognizing that corresponding areas tightly covary (3), and comparison of the sizes of bones with the use of regression models. Each approach is described below following a brief description of the reference data.

The reference data used in this study (hereafter referred to simply as "the reference data") was developed at the JPAC CIL for broad applications in research and casework. The data is comprised primarily of postcranial measurements. The measurements include the standard measurements found in the Forensic Databank at the University of Tennessee, Knoxville(5) as well as new measurements designed by the authors to be taken on fragmented bones. The measurement numbering scheme was designed to integrate with the forensic databank. A considerable portion of the reference data consists of Forensic Databank data generously given to the authors by Dr. Richard Jantz. The individuals in the reference data set are as listed in Table 1.

**TABLE 2** ***Reference sample broken down by collection, race, and sex.***



| *COLLECTION* | *SEX* | *BLACK* | *WHITE* | *ASIAN* | *TOTAL* |
|---|---|---|---|---|---|
| **CIL** | F | 0 | 1 | 0 | 1 |
| | M | 5 | 42 | 4 | 51 |
| *CMNH-HT* | F | 2 | 2 | 0 | 4 |
| | M | 7 | 7 | 0 | 14 |
| *SI-TERRY* | F | 14 | 10 | 0 | 24 |
| | M | 14 | 2 | 0 | 16 |
| *UT-BASS* | F | 3 | 9 | 0 | 12 |
| | M | 4 | 7 | 0 | 11 |
| *FDB* | F | 12 | 46 | 0 | 58 |
| | M | 17 | 108 | 0 | 125 |
| *ICMP* | F | 0 | 0 | 0 | 0 |
| | M | 0 | 41 | 0 | 41 |
| ***TOTAL*** | | 78 | 234 | 4 | 316 |

*CIL*, JPAC Central Identification Laboratory

*CMNH-HT*, Cleveland Museum of Natural History Hamann-Todd collection

*SI-TERRY*, Smithsonian Institution Terry collection

** Presenting Author*

*UT-BASS*, University of Tennessee Bass collection
*FDB*, University of Tennessee Forensic Data Bank
*ICMP, International Commission on Missing Persons*

Models for comparison of right and left paired bones were developed that emphasize shape. These models respond to many of the same attributes that make visual pair matching(2) possible and in some cases perform equally well. Measurements of length and of girth at numerous positions along each bone are utilized. Where length measurements are not available (due to fragmentation), models utilizing only girth measurements are calculated. These models take the general form,

$$D = \Sigma (a_i - b_i) \qquad (1)$$

where $a$ is the right side bone measurement, $i$ and $b$ is the left side bone measurement, $i$ for each of the measurements included in the comparison. The null hypothesis of no difference is tested by way of a $t$ test comparing the value of $D$ against "0" (no difference) and using the reference data standard deviation for $D$. The authors recommend the 0.05 significance level for this test. This method has performed well in test applications, but would benefit from a larger reference sample.

Models for comparison of adjoining bones are calculated using the difference in size of adjoining areas as their basis. See Buikstra *et.al.*, 1984, for an example of this approach. For example, the innominate and femur are compared by subtracting the maximum diameter of the femur head (measurement #63 in Moore-Jansen et.al. 1994) from the maximum diameter of the acetabulum(1). The model takes the general form,

$$D = c_i - d_j \qquad (2)$$

where measurement $i$ of bone $c$ is subtracted from measurement $j$ of bone d. The null hypothesis that the two specimens are of an appropriate size to have originated in one individual is evaluated with a $t$ test comparing the $D$ value obtained from the case specimens to the mean $D$ value calculated from the reference data. The 0.05 significance level is recommended.

Models for comparison of different bone sizes are generally more complex in their derivation. After experimenting with numerous approaches, Byrd and Adams(4) settled on the following linear combination as an acceptable index for bone size. The available measurements on a bone are simply summed and the natural logarithm of this sum is the value used in regression models. Since length measurements typically show the highest correlations with one another, models including length measurements perform best. The addition of breadths and girth measurements into the indices offers a slight, but noticeable improvement in the statistical models. A surprising finding is that models utilizing several breadth and girth measurements, with no length measurements, perform nearly as well in some cases as those including length (4). This fact has great significance when working with highly fragmented assemblages. Error rate for the method as a whole, using the 90% prediction interval, has been found in one study to be approximately 5%. See Byrd and Adams(4) for a full account of this method.

The application of osteometric sorting in case work at the JPAC CIL
is currently done in an ad hoc manner, where the appropriate statistical models (utilizing measurements available in the case specimens) are calculated from the reference data as the need arises. Osteometric comparisons of paired bones and adjoining bones are most advantageous when sorting large assemblages where it is impractical to make visual comparisons of every possible match. Further, this method is superbly suited to computer automation. The authors hope to develop an approach whereby all available measurement values for the case specimens are entered in advance, and all relevant comparison results can be produced as the analysis proceeds, without having to generate the statistical models for each comparison as separate steps for the anthropologist. As specimens are sorted apart by the various methods described in this report, they can be eliminated from consideration within the software application.

**References:**

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**Osteometric Sorting, Commingled Remains, Forensic Identification**