H59 Computerized Reconstruction of Fragmentary Skeletal Remains

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After attending this presentation, attendees will gain an understanding of the process of fragmentary remains reconstruction using computerized methods and the use of Computed Tomography (CT) and 3D models to sort commingled fragmentary remains.

This presentation will impact the forensic science community by describing the development of a software program to facilitate the determination of the Minimum Number of Individuals (MNI) and make metric assessments of sex, ancestry, and stature from statistically sound bone reconstructions of fragmentary remains. Error rates in the form of a confidence score based on root mean square error will be established for the bone reconstructions, as well as for the computer-automated measurements generated by the software.

Within the medicolegal system, forensic anthropologists perform the essential task of creating a biological profile to aid law enforcement in identifying unknown human remains. The four primary components of the biological profile are age, sex, ancestry, and stature. The parameters of the biological profile are intricately interwoven in that, frequently, one component is necessary in order to make precise determinations about other components. In cases of mass disasters or commingled assemblages, the determination of individual biological profile parameters is complicated by the presence of multiple unassociated elements. The ability to make biological profile assessments using isolated bones or bone fragments is critical. Although developed independently, the 3D approach to the quantification of commingled remains is a logical extension of coding and two-dimensional methods developed in zooarchaeology and bioarchaeology.[1-3] Recent work quantified small fragmented remains into an Osteological Information System (OIS) using Geographic Information System (GIS) software to derive Minimum Number of Elements (MNE) values and MNI estimates.[3] These systems are time consuming and depend on the observer to manually digitize each fragment into the OIS application. The resulting image provides an MNE estimate for the element under investigation. The proposed application provides a system to perform such analyses and to manage complex mass disaster cases or commingled bone assemblages.

In order to enable the computerized reconstruction of fragmentary remains, a new method was developed to match fragmentary remains with 3D template bones for the pelvis, humerus, femur, and cranium. These template bones are average bones generated from a training set with homologous points on the 3D surfaces. In order to generate such homologous points, the 3D models had to be added to a statistical atlas[4] that redistributes the points on the bone surface to ensure correspondence among landmarks.[4] Fragmentary remains are then matched to each template bone using surface descriptors. Outputs of this process are fragmentary pieces that are registered together in space. The next step involves reconstruction of a full bone by interpolating missing data between registered pieces. This step is enabled by optimizing the principal components calculated from the training set. In order to develop and test the system, a highly fragmentary commingled sample was used as a proxy for a mass disaster: the Morton Shell Mound osteological collection. The Morton sample represents over 25,000 human bone fragments from approximately 125 individuals. At the time of submission, ninety catalog numbers containing 15,133 human bone fragments were sorted by element, of which 1,054 fragments have been CT scanned and isolated for analysis.

Upon completion of this study and finalization of the software, all scanned skeletal remains from each scene will be reviewable within the application. An estimate of MNE of the scanned material will be provided following osteological protocols developed in forensic anthropology and bioarchaeology.[3] MNE estimates will allow for the determination of MNI. Finally, the application calculates a combination of traditional anthropological measurements and frequently used biomedical measurements. The traditional measurements can be used in a program such as FORDISC 3.0 or manually entered into equations used for the metric assessment of the biological profile.

References:

1. Marean C, Abe Y, Nilssen P, Stone E. Estimating the minimum number of skeletal elements (MNE) in zooarchaeology: a review and a new image-analysis GIS approach. Am Antiquity 2001;66:333-48.
2. Buikstra JE, Ubelaker DH, editors. Standards for data collection from human skeletal remains. Proceedings of a Seminar at the Field Museum of Natural History; 1994; Fayetteville; Arkansas Archeological Survey Research Series No. 44.
3. Herrmann NP, Bennett DJ. Assessment of commingled human remains using a GIS based approach. In Adams B, Byrd J, editors. Recovery, analysis, and identification of commingled human remains. New York: Humana Press, 2008;257-69.
4. Mahfouz M, Merkl B, Fatah E, Booth RJ, Argenson J. Automatic methods for characterization of sexual dimorphism of adult femora: distal femur. Comput Methods Biomec 2007;10:477-56.

Fragmentary Remains, Commingled Remains, Computer Modeling

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