



### A136 Computerized Reconstruction of Fragmentary Skeletal Remains

Mohamed Mahfouz, PhD, University of Tennessee, Dept Mechanical, Aerospace, & Biomedical Engineer, 307 Perkins Hall, Knoxville, TN 37996; Emam E. Abdel Fatah, PhD\*, University of Tennessee, Dept Mechanical, Aerospace, & Biomedical Engineer, 307 Perkins Hall, Knoxville, TN 37996; Natalie R. Shirley, PhD, Lincoln Memorial University, DeBusk College Osteopathic Med, 6965 Cumberland Gap Parkway, Harrogate, TN 37752; Nicholas P. Herrmann, PhD, Mississippi State University, Cobb Inst Archaeology, Box AR, Dept of Anthro & Mid East Cultures, Mississippi State, MS 39762; and Ali Mustafa, BS, 206 Perkins Hall, Knoxville, TN 37996

After attending this presentation, attendees will have gained an understanding about 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 sharing results of the developed software program to enable the determination of the number of individuals present and make metric assessments of sex, ancestry, and stature based on statistically sound bone reconstructions.

Within the larger medicolegal system, forensic anthropologists perform the essential task of creating a biological profile to aid law enforcement in identifying unknown human remains — an important first step in the criminal apprehension and conviction process. In cases of mass disasters or commingled remains, the determination of individual biological profile parameters is complicated by the presence of multiple unassociated elements. The ability to make biological profile assessments on 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 2D methods developed in zooarchaeology and bioarchaeology.<sup>1-3</sup> 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 Minimum Number of Individuals (MNI) estimates.<sup>3</sup> These systems are time-consuming and are dependent on the observer to manually digitize each fragment into the OIS application. The resulting image provides an MNE estimate for the element under investigation.

**Methods:** 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 homologues points on the 3D surfaces. In order to generate such homologues points for all training sets, the 3D models had to be added to a statistical atlas that redistributes the points on the bone surface to ensure correspondence among landmarks.<sup>4</sup> Fragmentary remains are 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.

**Results:** During this study, 22,400 bones have been CT scanned — of those 17,700 have been sorted and coded, and 170 bone fragments have been 3D scanned. Using the developed software, the innominate reconstruction had a mean Root Mean Square (RMS) error of 0.6mm with a maximum of 3.29mm error, whereas the skull reconstruction had mean error of 1.1mm. The developed application allows all scanned skeletal remains from each scene to be reviewable within the user interface. An estimate of MNE of the scanned material is provided following osteological protocols developed in forensic anthropology and bioarchaeology.<sup>3</sup> 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<sup>®</sup> 3.0 or manually plugged into equations for the metric assessment of three elements of the biological profile: sex, ancestry, and stature.

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## References:

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## Fragmentary Remain, Computerized, Commingled