H60 Performance of FORDISC 2.0 Using Inaccurate Measurements

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The goal of this presentation is to present to the forensic anthropological community the necessity of proper training in the collection of metric data for use in discriminant function analysis.

This presentation will impact the forensic community and/or humanity by showing the sensitivity of discriminant function analysis to measurement errors. These results demonstrate the necessity of receiving proper training in the collection of metric data as well as the need to check instrumentation used to collect metric data. It is suggested that only individuals who have received a substantial amount of training should be using FORDISC 2.0 in a professional arena.

Once decomposition has progressed beyond the point of recognizing the soft tissue indicators of an individual's sex and ancestry ("racial" affiliation), it becomes the job of the forensic anthropologist to make these determinations. The determination of sex and ancestry are part of the biological profile that the anthropologist constructs during a skeletal analysis. The anthropologist uses both non-metric and metric analyses to determine these characteristics. However, the determination of ancestry is not always a clear or simple task. In recent years the use of metric analysis has become more prominent due to the advancement of computers and use of statistical software. FORDISC 2.0, distributed by the University of Tennessee at Knoxville, is a program that facilitates the collection and use of metric data in discriminant function analysis to determine sex and ancestry from the skeleton. The program was developed using the Forensic Data Bank, which is an electronic accumulation of data from modern forensic cases from around North America. The use of FORDISC 2.0 is prevalent in the field of forensic anthropology and at times it may be used by individuals having only a cursory knowledge of measurement techniques and morphometrics. This poster will examine the outcome of poor data input into FORDISC 2.0 to determine how well the program performs with inaccurate data.

The 24 standard FORDISC 2.0 cranial measurements were taken on four carefully-selected crania that had been positively identified or had enough soft tissues at autopsy to make a determination of sex and ancestry. The measurements were entered into the program to classify each specimen using the "White" male, "White" female, "Black" male, and "Black" female reference groups. Two of the specimens were chosen because they were classified as strongly belonging to one of the reference groups, while the others were weakly classified. The measurements with the highest relative weights in the discriminant functions were then selected and manipulated by the addition and subtraction of 1 to 5 mm from the original measurement, and the changes in probabilities and classification were recorded. Measurements were changed all at once and in isolation. Results demonstrate that individuals who are classified strongly into a reference group remain strongly classified in that same group even with significantly altered measurements. Individuals with a weak classification into a reference group can be subject to a significant change by the addition or subtraction of even as little as 1 mm to a single measurement. It is generally accepted that interobserver error among trained individuals can reach 2 to 3 mm. Depending on the measurement and the morphology of the subject, errors of this magnitude can have a significant influence on the discriminant function analysis. These results demonstrate the necessity of receiving proper training in the collection of metric data as well as the need to check instrumentation used to collect metric data. These findings in no way suggest the abandonment of the use of FORDISC 2.0 or other forms of discriminant function analysis, however, the authors suggest that only individuals who have received a substantial amount of training should be using FORDISC 2.0 in a professional arena.

Ancestry Determination, FORDISC 2.0, Discriminant Function Analysis

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