



A172 Population Structure, Population Heterogeneity, and Sources of Error in the Forensic Estimation of “Race”

Heather J.H. Edgar, PhD, Albuquerque, NM 87131*

Learning Overview: The goals of this presentation are to: (1) summarize the sources of error in race/ancestry estimation; (2) discuss the terminology used to describe such estimates; and (3) describe the underappreciated importance of intra-group variation within socially recognized groups traditionally treated as homogeneous.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by providing attendees with a deeper understanding of how evolutionary history and social forces have interacted to structure phenotypic variation in the United States.

Forensic anthropologists in the United States have traditionally tasked themselves with categorizing unknown human skeletal remains into socially recognized biocultural groups that have conventionally been referred to as “races.” Recognizing that this term carries harmful social connotations, scholars and practitioners are increasingly using alternative terms, such as ancestry or biogeographic ancestry. Regardless of the term used, forensic anthropologists use various probabilistic methods to assign individuals to these socially recognized biocultural groups. These probabilities result from at least two factors: (1) histories of population isolation, movement, and mixture occurring over the past 75,000 years; and (2) political and socioeconomic forces that determine how our society emphasizes or de-emphasizes groups. Though both of these factors shift over time, structured genetic and phenotypic variation exists today in the United States, permitting categorization, with attendant error, in social and forensic contexts.

In this presentation, the term “bioaffinity” is used to reference the socially recognized biocultural groups that derive from this structure. This study examines the sources of error present in estimation of bioaffinity generated from human skeletal remains. These sources include measurement error, mismatch between sample constitution and sample description, error associated with geographic and temporal population structure, and mismatch between the population an individual was ascribed to in life and that indicated by their phenotypic or genetic variants. Further, this presentation will reflect on the terminology used to describe bioaffinity, including the meaning forensic anthropologists hope to convey with each choice of terms and the ways non-forensic anthropologists may actually interpret that terminology.

Finally, this presentation will discuss intra-group variation. This variation has been well studied for bioaffinities that are recognized to derive from a mixture of parental populations, such as Hispanic Americans. However, intra-group variation often goes unexamined in other groups, such as African Americans, European Americans, and Native Americans. For example, using dental morphological characteristics, contemporary European Americans from New York can be discriminated from those from Tennessee with 88% accuracy. This structured intra-group variation means that the sample from which the categorizing discriminant function derives may or may not represent the group from which an unknown individual derives; the degree of the error associated with this mismatch is generally unknown. Similar traits and tests discriminate Hispanic Americans from New Mexico or Florida with at most 81% accuracy, yet the presence of this population structure is generally recognized among forensic and other biological anthropologists. There is to date a dearth of forensically relevant research considering effects of population structure on other markers of bioaffinity, such as craniometric variation, in African and European Americans. Failure to quantify this intra-group variation has important implications for the collection of reference samples and may lead to fewer positive identifications of unknown individuals.

Evolution, Ancestry Estimation, Intra-Group Variation