

Biodistance

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Biodistance reconstructs evolutionary processes or patterns of relatedness in human populations on the basis of the analysis of heritable skeletal phenotypes. These phenotypes most often include metric variation of the cranium and dentition, minor discontinuous cranial and postcranial anatomical variants (see *CRANIAL MORPHOLOGY (HUMAN)*), and dental morphology (see *DENTAL MORPHOLOGY (HUMAN)*). Although the approach's development can be traced to early comparisons of cranial form in the context of race science (see *PHRENOLOGY*), biodistance now shares similar goals with the broader field of anthropological genetics. Both study human microevolution at different analytical scales. Although use of modern and ancient (see *ANCIENT DNA*) DNA to infer past evolutionary mechanisms continues to expand, biodistance provides a complementary perspective that has a number of attractive properties. For example, biodistance analysis is nondestructive, cost and time efficient, capable of producing statistically tractable datasets and sample sizes, applicable in most contexts even where the environment assures poor DNA preservation, and capable of direct sampling of the populations of interest rather than descendant proxies. The primary limitation of biodistance analysis is that the relationship between genotype and phenotype is unknown, imperfect, and confounded by environmental effects during development.

Despite this, analyses of phenotypic variation at multiple scales of analysis support the value of biodistance approaches. Heritability studies suggest moderate heritability for most cranial and dental metric dimensions. Although results for cranial nonmetric traits are mixed, dental morphological traits also show moderate to strong heritabilities. Concordance

studies that use genetic and phenotypic data from the same populations (and in some cases matched individuals) also support the validity of biodistance as an evolutionary proxy. This work has occurred at global, regional, and individual scales, with results indicating that the same general patterns of relationships are inferred by both genetic and phenotypic data. In addition, multiple studies indicate that cranial size and shape follows a neutral pattern at the global level (von Cramon-Taubadel and Weaver 2009). Finally, ongoing research on craniofacial development, plasticity, and integration, genome-wide association studies, and quantitative trait loci analyses using various model organisms support the evolutionary value of craniometric data. Similar work in the area of dental phenomics, evolutionary developmental biology, and allelic association studies are providing better linkages between dental variation and underlying genetic systems.

The choice of biodistance data type is often determined by local preservation, regionally defined research traditions, and investigator training. Of the four most widely recognized categories of data (craniometrics, dental metric, cranial nonmetric, dental morphology), craniometrics is the most well known, with the longest established history and greatest availability of comparative datasets. However, this history also links craniometry with typological and racist approaches of the nineteenth century (see *ANCESTRY (FORENSIC APPLICATIONS)* and *CRANIOLOGY*), leading some to discount all biodistance as typological. Doing so ignores the fact that dental anthropology (see *DENTAL BIOLOGY/ANTHROPOLOGY*) and cranial nonmetric anatomy (see *CRANIAL MORPHOLOGY (HUMAN)*) have distinct historical trajectories. Cranial data are age progressive and subject to plasticity and functional accommodation (see *CRANIOFACIAL MORPHOLOGY AND ADAPTATION*). This is less relevant for dental traits that form early in life and remain unchanged after enamel formation has

completed. Cranial data are also more susceptible to conditions of poor preservation, while dental data are severely limited by dental wear. A final consideration is data scale. Analyses of metric data are simpler because they are ratio scale variables, which makes them amenable to standard multivariate statistical analysis as well as the more theoretically grounded R matrix analysis (see *R-MATRIX ANALYSIS*) (Relethford 2007). Analyses of discontinuous data types (binary, ordinal, nominal) are more complicated and less supported by standard statistical analyses. As such, discontinuous traits are often dichotomized into binary variables for the purposes of frequency estimation. Dichotomization of traits also acknowledges the high levels of observer error associated with fine-graded ordinal variables.

A key feature of biodistance is its scalability, from global scale analyses to consideration of relatedness at the interindividual level (Buikstra, Frankenberg, and Konigsberg 1990). At the broadest scale, patterns of global phenotypic variation help identify processes of modern human emergence and migration throughout the Old and New Worlds. Remarkably similar patterns of variation have been identified using cranial and dental metric and nonmetric data types, suggesting the same serial bottlenecking effects as observed using genetic data. Biodistance has also contributed to our understanding of the timing and process of major human migration events, such as the peopling of North and South America (see *PEOPLING OF THE NEW WORLD*) and the peopling of Polynesia, and major transitions especially during the Holocene, such as the origins of agriculture in Europe, the repopulation of the Sahara, and the Bantu expansions. Differentiating in situ microevolutionary change and true population replacement events has been a long-standing challenge.

Regional scale inferences can be used to reconstruct patterns of migration and gene flow, ancestor–descendant relationships, population replacement events, population boundaries, and mortuary variability related to cemetery use practices, all of which are relevant to archaeology and bioarchaeology (see *BIOARCHAEOLOGY*) (Larsen 2015). Regional biodistance assumes that two populations that exchange mates are more similar to each other than two isolated populations (see *GENETIC DISTANCE*), which could reflect a more

recent shared evolutionary history, higher rates of migration or gene flow (see *ISOLATION BY DISTANCE*), or similar effective population sizes over time. More recently, biodistance studies have contributed to studies of social identity by linking the biology of mate exchange with the broader social world of humans. Intracemetery approaches also address a number of questions relevant to archaeology (Stojanowski and Schillaci 2006), such as site formation processes and cemetery organization practices. The identification of kin groups can inform fine-grained studies of health and status in the past, including heterogeneous frailty (see *OSTEOLOGICAL PARADOX*). Comparison of sex-specific phenotypic variation speaks to postmarital residence practices that inform our understanding of other aspects of prehistoric social organization.

While biodistance analysis will never replace direct access to genomic-level data, its use will continue to inform multiscalar analyses of evolution and relatedness. This is especially so in contexts with poor DNA preservation or for which destructive analyses are not possible. Future work must continue to refine our understanding of the relationship between phenotype and genotype, which may require a break with traditional methods of data collection and analysis.

SEE ALSO: Ancestry (forensic applications)

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FURTHER READING

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