RESEARCH ARTICLE

What Are We Really Estimating in Forensic Anthropological Practice, Population Affinity or Ancestry?

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ABSTRACT: While American forensic anthropologists often state that they estimate ancestry, is that what they are really estimating? Although typological terminology, the *oids,* was replaced with continental terminology, the change was linguistic rather than substantive. The American population is comprised largely of immigrants. Genetic data suggests a high degree of admixture within American population groups. Further, data from documented skeletal collections suggest that Americans have undergone secular changes. Our paper addresses the uniqueness of the American population as compared to ancestral continental and geographic origin groups to address what it is that forensic anthropologists are really estimating, ancestry or something else? We conclude, based on uniqueness of American population groups, that what forensic anthropologists are estimating is best described as affinity, a term that indicates similarity and is not exclusively attached to definitions of race and ethnicity.

KEYWORDS: forensic anthropology, population affinity, ancestry, craniometric, anthropological genetics, biological distance

"If we wish to get the greatest efficiency in forensic identification, we should stop trying to do it in a way in which the very real local variation becomes mere static to confuse the results, and try to do it in a way in which local variation makes a positive contribution to correct diagnosis." (Brues 1992:127)

Introduction

Though it has been stated that it is not possible to sort humans into more categories than continental origins (Williams et al. 2005), forensic anthropologists do this all the time, often working within a continent. Forensic anthropologists commonly refer to this practice as ancestry estimation. But is ancestry what we are really estimating? What we call ancestry and how we refer to it, harkens back to 19th-century racial typology—when skulls were observed and forced into one of three to five groups. Then along came the Modern Synthesis which shifted the focus from categorization to exploration of phenotypic diversity through an evolutionary lens (Huxley 1942). Inspired by Huxley, Sherwood Washburn proposed the

New Physical Anthropology (1951) which brought the tenants of the Modern Synthesis into biological anthropology. With this paradigm shift and to distance ourselves from the typology of the past, biological and forensic anthropologists changed the terms Caucasoid, Mongoloid, and Negroid, to European, Asian, and African. This was a small step to distance the discipline from the typology, as was the use of the term ancestry as a replacement for the word race. However, the change in terminology was a substitution of names while, at the time, maintaining the status quo with the often used three group model. New methods of estimation have been developed since the name change, along with data collection representing more diverse population groups. However, the term ancestry estimation is still used frequently in practice, what does it mean and is it what we are really estimating?

Ancestry refers to ancestral origins which could include continental origins or ethnic affiliation. Ancestral categories such as African, Asian, or European are broad and not informative for describing global or local population structure or for use in forensic case work. Although publications have highlighted the uniqueness of United States population groups with respect to migration, gene flow, genetic drift, and secular change, (Edgar 2009; Manthey et al. 2017; Ross et al. 2003; Spradley et al. 2008; Tise et al. 2014) the notion of continental ancestry persists. Ousley et al. (2009) among others, demonstrated that population groups can be accurately classified, using craniometric data, into social race categories within the United States (U.S.), by time period, ethnic affiliation, and geographic boundaries further demonstrating that ancestry (i.e., categorization into African, Asian, and

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European) is not what forensic anthropologists are estimating. Yet, despite evidence to the contrary, introductory textbooks frequently suggest that forensic anthropologists, in practice, are estimating continental ancestry (Bass & Trimble 2005; Black & Ferguson 2011; Byers 2016; Christensen et al. 2019; Gill & Rhine 1990; Klepinger 2006).

The term population affinity is an estimation of group membership indicating morphological or genetic similarity to a well-defined group and is based on some measure of statistical distance. Recent publications highlight an increase in the use of this term (Berg & Ta'ala 2014; Pilloud & Hefner 2016; Ross et al. 2004; Ross et al. 2011). Forensic anthropologists are good at estimating population affinity within the U.S. because assortative mating practices shaped by miscegenation laws, racism, and social class have shaped our current population structure (Gross & Edgar 2021). The ability of forensic anthropologists to estimate population affinity is an application of anthropological genetic studies, however this is rarely if ever discussed within forensic anthropology textbooks and neglected in the broad literature with the exception of a few (Algee-Hewitt & Goldberg 2016; Relethford 2009).

The purpose of this paper is to explore American population structure through comparison with ancestral groups to provide further insight to the estimation of population affinity and how it differs from ancestry.

Background

Forensic anthropologists in the U.S. can estimate population affinity because of population structure. Population structure refers to the genotype and phenotype frequencies that reflect mating structures. Population structure has long been studied by both population geneticists and anthropologists. Population geneticists study the genetic composition of populations, including changes in genotype and phenotype frequency resulting from the evolutionary processes of selection, genetic drift, mutation, and gene flow over time. Anthropological geneticists focus on biocultural processes relating to genetic and environmental interactions at the population level, most often studying the normal variation of complex traits (Crawford 2007), including craniometric data. Further, anthropological genetic analyses include theoretical models to test hypotheses focusing on microevolutionary processes related to population history (Relethford & Lees 1982:113). Anthropologists have long been at the forefront of studying the cultural and behavioral factors that impact population structure through the study of anthropological genetics (Algee-Hewitt & Goldberg 2016; Crawford 2001, 2007; Livingston 1958; Relethford & Lees 1982). Anthropological genetics uses model-bound methods to test hypotheses concerning human evolution, selection, and population differentiation (Algee-Hewitt & Goldberg 2016:558).

However, model-free methods explore population structure when testing explicit models of gene flow and drift are not central questions. Human behavior, influential on human history, is not static and as such, neither are populations. Population size, migration, and secular change all impact population structure.

The U.S. has a generally well-documented population history with an ever-changing population structure that has been the focus of much research (Algee-Hewitt 2017; Bryc et al. 2015; Go et al. 2019; Reich et al. 2012). Archaeological and historical documentation provides knowledge of the ancestral origins of the current population groups within the United States. The narrative of these origins is largely supported by early studies of classical genetic markers and elaborated on through more recent studies focusing on genome sequencing. Using SNP data with self-reported U.S. Census Bureau categories, Bryc et al. (2015) found that African Americans are genetically similar to Africans with variable amounts of European admixture and detectable, although low proportions of Native American admixture. Previous studies have specifically linked the African ancestry to West Africa (Baharian et al. 2016; Bryc et al. 2010) which is also consistent with historical narrative. Further, there is detectable structure in the variation of European admixture; African Americans in the Southeast have less European admixture than in the North and West (Baharian et al. 2016; Bryc et al. 2010).

The U.S. Hispanic[1] population is the second largest population group with the majority of the population having geographic origins in Mexico, Puerto Rico, El Salvador, and Cuba (Noe-Bustamante 2019). Further, foreign born individuals comprise a significant portion of these population groups, Mexican (31%), Salvadoran (57%), and Cuban (56%) (Noe-Bustamante 2019). Genetic studies highlight the complex population structure of Hispanic origin countries which influences further structure within the United States. Mexico exhibits clinal variation with higher amounts of European admixture in the north and less in the central and peninsular region (Ruiz-Linares et al. 2014), which has been documented with genetic and quantitative data (Rubi-Castellanos et al. 2009). Puerto Rico and Cuba also have documented complex genetic structures with differing levels of Native American, European, and African admixture resulting from unique population histories while more African admixture is found in Cuba and Puerto Rico (Cintado et al. 2009; Hanis et al. 1991). Thus, the U.S. Hispanic population is not genetically homogenous, rather it is complex with detectable structure evident

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1. The term Hispanic is used over Latinx for several reasons. According to the Pew Research Center *Hispanic Trends*, approximately 76% of individuals living in the U.S. with geographic origins/ancestral ties to Latin America have not heard of the term Latinx and only 3% use it (Noe-Bustamante et al. 2020). Additionally, at this time, it is the most common term utilized for reporting missing and unidentified persons.

across the country. European Americans have considerable admixture with other European groups and with African and Native Americans, although in relatively small amounts (Bryc et al. 2015).

In addition to the influences of population history and gene flow on population structure, skeletal secular changes have been documented in African and European Americans (Jantz 2001; Jantz & Meadows Jantz 2016). In particular, an increase in cranial base height has provided an increase in overall vault height for both groups (Jantz 2001; Wescott & Jantz 2005) along with vault width and cranial base length (Jantz & Meadows Jantz 2016). Investigating limb bone allometry in European Americans, Jantz and Meadows Jantz (2017) found that significant changes occurred in a short period of time suggesting that the unique American environment has disrupted developmental canalization. Although significant secular changes in skeletal morphology have occurred over the past century, such changes do not obscure underlying genetic structures (Relethford 2004) and support the use of skeletal morphology in exploration of population structure.

Given the complex population history, varying degrees of genetic admixture among all U.S. groups, and secular changes in skeletal phenotype due to a unique American environment, are American population groups similar to their ancestral populations? In the following analyses we use craniometric data and biological distance analysis to explore the pattern of quantitative variation among individuals who

self-identified into three U.S. Census Bureau racial and ethnic categories and geographically defined population groups in the U.S. (African American, Hispanic American, and European American) as compared to their ancestral geographic origin groups. The resulting structure from the biological distances will be discussed within the framework of the ancestry vs the affinity of local populations.

Materials and Methods

Craniometric data from U.S. and worldwide groups (Table 1) are used to generate biological distances. U.S. groups represent self-reported or next-of-kin-reported group labels that fit within the Office of Management and Budget's (OMB) Statistical Directive No. 15 that outlines race and ethnic categories for federal bureaucratic reporting purposes. These categories are also used by the National Missing and Unidentified Persons System or NamUs, which is a national missing and unidentified persons database used in medico-legal investigations. The OMB does not capture the range of variation or local group level for all U.S. citizens. However, it does capture the most often used terminology employed by forensic anthropologists when providing estimates of group membership for the biological profile. The data utilized in the subsequent analyses for American groups were based on availability and represent the three largest population groups

TABLE 1—*Sample Groups*

Group	Female	Male	Time Period	Curator /Reference
African				
Gold Coast	10	10	**19**th Century	American Museum of Natural History
Ashanti	13	17	19th Century	,,
Cameroon	10	31	19th Century	,,
Calabar	7	16	19th Century	,,
Dogon	52	47	17th–18th Centuries	https://web.utk.edu/~auerbach/HOWL.htm
Togo	7	28	19th Century	Berlin Society for Anthropology, Ethnology and Prehistory
South African	44	57	20th Century	20th Century
American				
African American	101	171	20th Century	Forensic Anthropology Data Bank
American/Hispanic	13	59	20th Century	,,
European American	169	343	20th Century	,,
Zuni	20	24	16th–17th Centuries	Smithsonian Institution
Asian				
Japan	55	64	20th Century	Dudzik, 2015
Hainan	38	45	18th–19th Centuries	https://web.utk.edu/~auerbach/HOWL.htm
European				
Croatian	0	31	20th Century	Vienna Natural History Museum
Czech	35	44	19th Century	Vienna Natural History Museum and Charles University Smithsonian
German	21	58	19th Century	Institution and Charite Anatomy
Italian	114	106	20th Century	Cattaneo et al. 2018
Portuguese	64	68	20th Century	Weisensee 2008
Latin American				
Mexican Migrant	15	156	20th Century	Mexican, Guatemalan, and Migrant Craniometric Dataset
Mexican Mayan	20	42	20th Century	,,
Guatemalan Migrant	15	25	20th Century	,,
Guatemalan Mayan	0	74	20th Century	Forensic Anthropology Foundation of Guatemala

in the U.S., African American, Hispanic American, and European American. There is currently a lack of skeletal data available for Asian Americans and contemporary Native Americans. However, with the development of New Mexico Decedent Image Database (https://nmdid.unm.edu/) and other large datasets derived from CT images (Colman 2019; Stull 2020), such data should increase in the future.

Population Groups and Data

Craniometric data (following definitions outlined in Howells 1973) from African American, European American, and Hispanic Americans come from the Forensic Anthropology Data Bank (https://fac.utk.edu/background/) and represent 20th-century birth years. These groups consist of positively identified individuals with self-reported or next of kin reported affinity. Although self-reported and next of kin reported mostly consist of the terms Black or White, in this paper we use the terminology African American and European American to convey the combination of ancestry and geographic birthplace/nationality. While the African and European Americans were born in the U.S., the Hispanic American sample consists of individual with ancestral ties to Mexico who were either born in the U.S. or born in Mexico and moved to the U.S. shortly after birth.

The West and Central African data were collected from the American Museum of Natural History and were part of the Felix von Luschan collection within the Royal Museum of Ethnology in Vienna, Austria (Smith 2002). The exact time period they represent is unknown, although likely 18th and 19th century (Smith 2002). The Dogon come from the (Howells 1973) craniometric data set and are published online. Togo are part of the von Luschan collection at the Berlin Society for Anthropology, Ethnology and Prehistory. These African data represent primary areas of origin for the enslaved Africans forced to immigrate to the New World. The South African data is from L'Abbé et al. (2013) and comes from the Pretoria Bone Collection.

Latin American data are represented by indigenous Guatemalan and Mexican Mayans and migrants from Mexico and Guatemala that died in U.S./Mexico border states, predominately Arizona and Texas and (Spradley 2020). All Latin American groups, Mexican and Guatemalan Mayan and migrants, have 20th century birth years and are well defined in the literature (Hughes et al. 2017; Spradley 2021). A Southwest Native American group, Zuni, was also included in the analysis in addition to two Asian groups, Hainan (Howells 1989) and Japanese (Dudzik 2015). Native Americans, including Indigenous groups in Mexico and Central America, have Asian ancestry from prehistoric migration (Hughes et al. 2019).

Data from Europe spans the West and East and includes a Czech sample that contains known individuals collected from the Vienna Natural History Museum in Austria and Charles University in the Czech Republic. The Croatian data are from the Vienna Museum of Natural History. Italian data were obtained from Manthey et al. (2018). The Portuguese data come from the New Lisbon Skeletal Collection (Weisensee & Jantz 2011).

Methods

Our research question addresses the pattern of variation among U.S. population groups as related to their ancestral, geographic origins, and as such the purpose is not classification. Rather we explore the pattern of population relationships through biological distance. The U.S. population groups are compared to ancestral and local groups based on historical narrative and supported by genetic studies. African Americans are compared to West and Central Africans, along with European Americans. European Americans are used in lieu of the European groups as the European American sample more closely approximates the population group with contributing gene flow to African Americans. The Hispanic American group is compared to all Latin American and European Americans. The Hispanic comparison also includes Asian and Native American groups due to shared ancestry. European Americans were compared to European groups as well as South Africans as the latter have a similar population history with European Americans.

Analyses were completed following procedures outlined in (Jantz & Spradley 2014) to produce Mahalanobis and Fst distances. Sexes were pooled to increase the overall sample size and sex differences were removed by centering on sex specific means. FORDISC 3.1 was used to generate the covariance matrices and means for each group which were centered and pooled. The eigenvalues and eigenvectors were extracted to obtain the principal component scores to compute Mahalanobis distances (D^2) and obtain the canonical variates to create two-dimensional plots. The plots are used to assess population structure and structure coefficients are used to interpret the craniometric variation.

Results

The CV plot featuring African Americans (Figure 1) shows the African American group intermediate to the West and Central Africans and European Americans on the first axis. The second axis highlights geographical patterns among the West and Central African groups with Nigeria (Gold Coast) most differentiated from Mali (Dogon) and situates African Americans with West Africans. Almost all variables contribute to CV1 as indicated by the structure coefficients (see Table 2). The pattern of loadings presents a clear pattern of morphometric variation. High scores on CV1 result from a wide cranial base, long cranial base length and vault height,
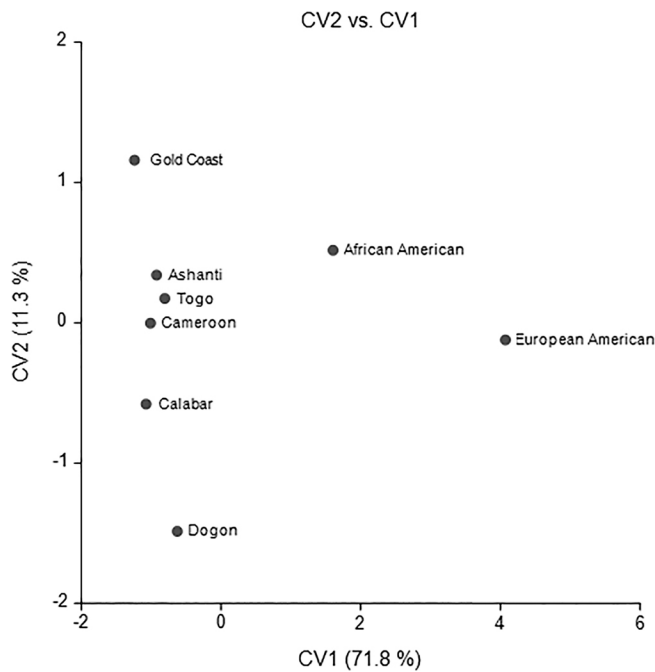
FIG. 1—*African American CV Plot.*

TABLE 2—*Structure Coefficients*

Variable	African American Can1	Can2	European American Can1	Can2	Hispanic Can1	Can2
AUB	0.947	0.036	−0.671	0.593	−0.316	−0.732
BBH	0.768	0.087	0.783	0.222	0.616	0.729
BNL	0.881	0.423	0.700	0.086	0.849	0.464
BPL	−0.723	0.608			0.300	0.242
DKB	−0.875	0.260	−0.507	0.672	−0.685	0.381
EKB	−0.658	0.228			−0.097	0.160
FOL	0.237	0.266	0.887	0.226	0.744	0.153
FRC	0.839	−0.202	0.868	−0.018	0.869	0.284
GOL	0.763	0.556	0.935	−0.249	0.938	0.104
MDH	0.700	0.468	0.611	0.770	0.765	0.080
NLB	−0.971	−0.088			−0.764	0.332
NLH	0.895	0.202			0.500	−0.451
OBB	0.942	−0.067	0.389	0.369	0.764	−0.413
OBH	0.156	0.093	0.229	−0.765	−0.385	−0.572
OCC	0.938	−0.147	0.952	0.189	0.753	0.335
PAC	0.006	0.910	0.738	−0.349	0.824	0.349
XCB	0.661	−0.581	−0.908	0.357	0.313	−0.496
ZYB	−0.269	0.001	−0.723	0.513	−0.766	0.147

high nasal height and narrow nasal aperture and interorbital distance. The reverse is the case for low scores on CV1. CV1 reflects a pattern of variation normally associated with African-European variation. High scores on CV2 mainly reflect longer basion-prosthion and basion-nasion lengths, and a longer, narrow cranial vault.

What is noteworthy in Figure 1 is that African Americans are about equidistant from West Africans and European Americans. This is shown quantitatively in the first column of Table 3. African Americans are slightly more similar to three African groups (Ashanti, Cameroon, and Togo) than to European Americans. But African Americans are slightly more similar to European Americans than they are to three other African groups (Calabar, Dogon, and Gold Coast). The distances show African Americans to occupy the approximate mid-point between Africans and European Americans. The Fst distances in the first row of Table 3 are all around 0.06, presenting the distances as a proportion of total variation attributable to between groups.

The CV plot for Hispanics (Figure 2) situates the U.S.-born group intermediate to European Americans and Latin American and Asian groups, with European Americans the most differentiated. CV1 mainly serves to separate Euro-Americans from the Indigenous Maya groups and Hainan. The second axis separates the Asian groups from all other groups. Considering Hispanic and Latin American groups, the Hispanic American group is most similar to the Mexican migrant group, followed by the Guatemalan migrants and most differentiated from the Mexican and Guatemalan Mayan groups (Table 4). Further, the Mexican and Guatemalan migrant groups are intermediate to Hispanic American and Guatemalan Mayan groups. High scores on CV1 mainly reflect long cranial bases (Table 2), generally long crania with narrow nasal apertures and narrow bizygomatics. CV2 reflects narrow cranial bases and high vaults, small orbits and wide interorbital breadth.

The European American CV plot (Figure 3) highlights that European Americans, South Africans, and Portuguese are distanced from all other European Groups on the first axis. The Croatians and Czechs are more similar to one another as are the Germans and Italians. The second axis emphasizes the intermediate nature of the European Americans as compared to the South African and Portuguese groups (Table 5). The

TABLE 3—*Mahalanobis distances (below diagonal) and Fst distances (above diagonal) for groups used in African analysis.*

|	Af_Am	Ash	Cal	Cam	Dog	Eu_Am	GoC	Togo
Af_Am	0.000	0.058	0.078	0.057	0.062	0.059	0.063	0.056
Ash	8.931	0.000	0.025	0.018	0.027	0.157	0.009	0.011
Cal	12.200	3.668	0.000	0.014	0.027	0.173	0.027	0.031
Cam	8.643	2.700	2.082	0.000	0.027	0.159	0.019	0.018
Dog	9.544	3.981	4.059	3.985	0.000	0.151	0.047	0.029
Eu_Am	9.102	26.727	30.075	27.285	25.522	0.000	0.175	0.155
GoC	9.682	1.381	4.019	2.836	7.176	30.635	0.000	0.022
Togo	8.481	1.605	4.572	2.676	4.344	26.325	3.304	0.000
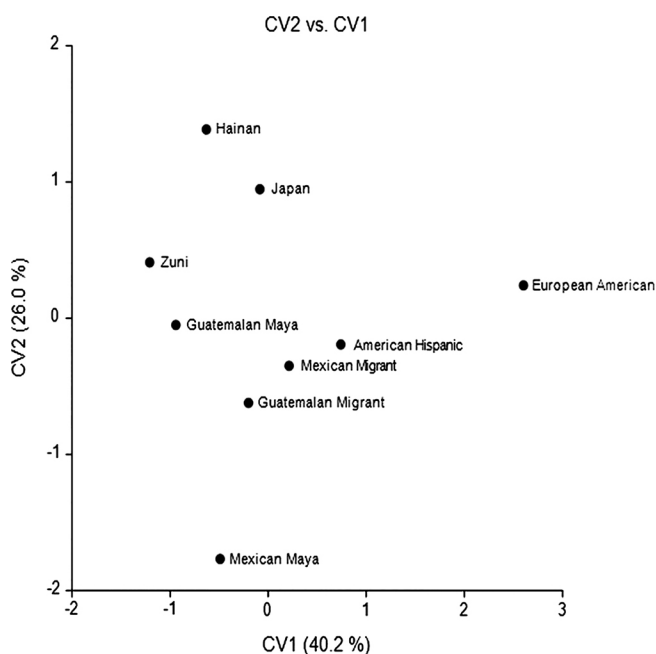
FIG. 2—*Hispanic American CV Plot.*
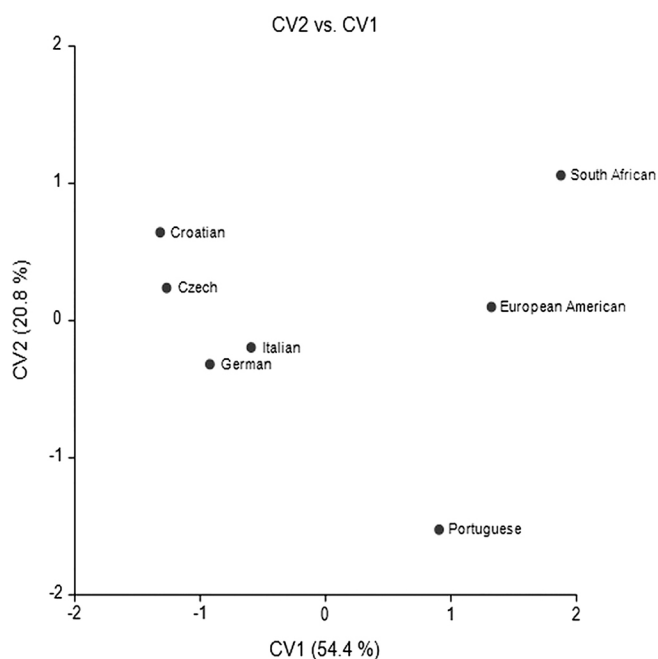
FIG. 3—*European American CV Plot.*

TABLE 4—*Mahalanobis distances (below diagonal) and Fst distances (above diagonal) for groups used in Hispanic analysis.*

	Eu_Am	Ghisp	Hai	Jap	Hisp Am	Mmaya	UShisp	Zuni	Gmaya
Eu_Am	0.000	0.064	0.085	0.058	0.048	0.095	0.031	0.098	0.089
Ghisp	9.801	0.000	0.046	0.032	0.007	0.035	0.020	0.029	0.019
Hai	13.359	7.015	0.000	0.019	0.042	0.069	0.050	0.039	0.045
Jap	8.847	4.713	2.734	0.000	0.026	0.058	0.025	0.031	0.027
Mhisp	7.288	1.012	6.353	3.822	0.000	0.040	0.012	0.031	0.023
Mmaya	15.034	5.210	10.597	8.862	5.964	0.000	0.046	0.061	0.051
UShisp	4.577	2.891	7.584	3.637	1.695	7.022	0.000	0.036	0.025
Zuni	15.585	4.324	5.821	4.623	4.626	9.340	5.443	0.000	0.018
Gmaya	14.080	2.820	6.733	3.974	3.368	7.670	3.753	2.688	0.000

TABLE 5—*Mahalanobis distances (below diagonal) and Fst distances (above diagonal) for groups used in European analysis.*

	Czech	Eu_Am	Ger	Por	Saf	Ita	Cro
Czech	0.000	0.078	0.018	0.071	0.091	0.018	0.023
Eu_Am	9.464	0.000	0.066	0.042	0.040	0.044	0.071
Ger	2.066	7.956	0.000	0.052	0.086	0.015	0.032
Por	8.543	4.954	6.203	0.000	0.067	0.043	0.085
Saf	11.227	4.674	10.501	8.064	0.000	0.074	0.100
Ita	2.047	5.176	1.696	5.002	8.896	0.000	0.024
Cro	2.669	8.543	3.698	10.395	12.502	2.699	0.000

structure coefficients show that high scores on CV1 are associated with long cranial bases, high vaults, generally longer vaults and narrow vaults and faces (Table 2). High scores on CV2 reflect greater vault and face breadth, low orbits, and greater mastoid height.

Discussion

Our results provide evidence of geographic structure in that American population groups are differentiated from their geographic, ancestral origin groups. Thus, these American groups represent local population groups and local variation found in the U.S.. These results are not surprising given the population histories of each group and the documented gene flow and secular changes that have taken place in the American population over the past 150+ years (Jantz 2001; Meadows Jantz & Jantz 1999; Spradley 2006; Wescott & Jantz 2005). It is possible that the dissimilarity of the American groups to their ancestral groups is due to a lack of directly comparable reference data, especially for the European Americans. However, the groups used in the present analysis

represent groups that are documented or have reliable contextual information along with available craniometric data.

The American population groups used in the current analyses have ancestry in Africa, Europe, and Mexico, all of which have documented population structure. Structure has been documented within Africa using genetic and craniometric data and is thought to be influenced by ethnicity, language, and geography (Keita 1990; Spradley 2006; Stull 2013; Tishkoff et al. 2009), although genetic distance and geography have varied strengths (Tishkoff et al. 2009) likely due to the Bantu migration. Europe is also highly structured based on geography. Relethford et al. (1980) found variation among local populations in Ireland using anthropometric data, but also found that as migration increased, among group variation decreased. Further, Novembre et al. (2008) demonstrated that across Europe, an individual's residence can be predicted geographically within a few hundred km based on SNP data. Mexico also demonstrates geographic structure on a clinal scale, with higher European admixture in the North and the least in the South and Peninsular regions with Central Mexico presenting intermediate (Algee-Hewitt et al. 2018; Hughes et al. 2013, 2017). The within group variation in Africa, Europe, and Mexico is not found within American population groups.

Using craniometric data and unsupervised clustering, Algee-Hewitt (2016) demonstrated that that the American population can be resolved into three basic clusters, African American, European Americans, and Native American/Hispanic. However, she found relatively little within group structure. Algee-Hewitt's results are also in line with genetic studies. Micheletti et al. (2020) found that over 90% of African Americans have genes from four major regions of West Africa suggesting that any initial structure resulting from the African Diaspora has been lost. Although the degree of admixture is patterned with higher percentages of African ancestry in the southeastern U.S. (Baharian et al. 2016). Although European immigrants came from many geographic areas within Europe, genome wide SNP data found relatively little structure in European Americans, identifying only NW Europeans, SE Europeans, and Ashkenazi Jews (Price et al. 2008). While structure has been found in Hispanic Americans, with more Hispanics of Mexican origin in the West and Caribbean in the East (Bertoni et al. 2003), Algee-Hewitt (2016) did not find structure in her Hispanic sample, most likely because her sample was predominantly of Mexican origin. Our results indicate similarity Hispanic Americans and

Mexican migrants; however, they are also differentiated. The Mexican migrants are less similar to the Mexican and Guatemalan Mayans as they are thought to exhibit more admixture (Spradley 2021), yet they are still differentiated from Hispanic Americans with Mexican ancestry.

Craniofacial secular change has been documented in historic to modern African and European Americans (Jantz 2001; Jantz & Jantz 2016; Jantz & Meadows Jantz 2000; Spradley 2006; Wescott & Jantz 2005) but less so in Hispanic Americans (Spradley et al. 2016). Studies focusing on African and European Americans find that both groups show changes in the same direction with a most notable increase in vault height, particularly in the cranial base (Wescott & Jantz 2005). Secular change can result from a variety of factors including gene flow, improvements in overall health conditions, and plasticity. Given that both African and European Americans have shared the same environment for over several hundred centuries, population structure is still apparent among these two groups. However, our analyses suggest that African Americans are more similar to European Americans than admixture proportions would predict, possibly due to the shared American environment. Although secular change has influenced the overall craniofacial morphology of American population groups, such changes do not obscure the underlying genetic structure (Relethford 2004). Therefore, secular change is not the sole driver of dissimilarity between American groups and ancestral groups.

Given the similarities between these two groups and their intermediate or dissimilar positions relative to their ancestral groups, an additional analysis, to highlight and contextualize our results within a forensic anthropological framework, was performed. A discriminant functional analysis (DFA) was performed to assess how well these American groups classify when compared to their ancestral groups. A cross-validated classification matrix is presented in Table 6. Only 29 African American misclassify into the African group, only 7 more than classify into the European American group. These results agree with the intermediate position of African American presented in our CV plot. Further, West Africans only misclassify into the African American group. A total of 61 European Americans classify into the European group and 20 as African American. Interestingly, Europeans misclassify into all other groups. Given that 75% of African Americans and 84% of European Americans are correctly classified into their own group, we suggest that the ability to predict group membership can be referred to as affinity.

TABLE 6—*Classification Matrix*

	N	Afr_Am	Eur_Am	European	W. African	% correct
Afr_Am	270	202	22	17	29	74.8
Eur_Am	509	20	427	61	1	83.8
European	406	56	61	279	10	68.7
W. Africa	242	27	0	0	215	88.8

Conclusions

Forensic anthropology has traditionally been a subdiscipline of skeletal biology. However, it should also be considered a subdiscipline of anthropological genetics. Brues (1992) understood population structure (and simulated it) before forensic anthropology crystallized as a discipline. Analyses of population structure through biodistance, including estimations made by forensic anthropologists, employ fundamentals of anthropological genetics and skeletal biology, and provide insights regarding mating structures, geography, and environment, and their impact on quantitative trait variation and local population structures. We suggest that the ability to predict group membership at the level of local variation rather than global variation can be referred to as affinity. All of which is to say that it is vitally important that forensic anthropologists understand the populations from which their cases are drawn.

Our three analyses suggest that when forensic anthropologists provide an estimation of group membership within the U.S., they are providing an estimation of population affinity rather than ancestry. The estimation of affinity is more specific than ancestry and considers local variation (e.g., Hispanic American, African American, European American). If we compare craniometric data from an unknown individual to African Americans, Hispanic Americans, European Americans, or other contemporary American groups, then we are estimating which group the unknown is most similar to, and therefore the estimation would be considered affinity. Is the suggested difference between ancestry and affinity trivial? On the surface, perhaps. However, Maier et al. (2021) recently pointed out confusion and inconsistencies with terminology in forensic literature concerning the terms ancestry and race and how they are perceived as interchangeable. They call for discussions of standardization to improve practice and public engagement. Affinity provides more flexible terminology that is dependent on the researcher to fully contextualize and describe the groups used in the analyses. Further, it is more flexible and can be used in areas where population structure exists but is influenced by geographic boundaries, isolation by distance, or cultural assortative mating practices rather than prescribed racial or ethnic variation.

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