Scott, GR, Pilloud, MA, Navega, D, d'Oliveira, J, Cunha, E and Irish, JD

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Abstract

The use of dental morphology to estimate ancestry has a long history within dental anthropology. Over the past two decades methods employing dental morphology within forensic anthropology have become more formalized with the incorporation of statistical models. We present here on a new application (rASUDAS) to estimate ancestry of unknown individuals using crown and root morphology of the dentition. The reference sample is composed of 21 traits based on the Arizona State University Dental Anthropology System and represents approximately 30,000 individuals from seven geographic regions. The statistical program was created in R and uses a naïve Bayes classifier algorithm to assign posterior probabilities for individual group assignment. A random sample of 150 individuals from the dataset was chosen and input into the program. In a seven-group analysis, the model was correct in group assignment 51.8% of the time. In a four-group analysis, classification improved to 66.7%, and with only three groups considered the accuracy improved to 72.7%. It is still necessary to validate the program using forensic cases and to augment the reference sample with modern skeletal data. However, we present these results as a proof of concept of the statistical application and the use of dental morphology in the estimation of ancestry.

Keywords: dental non-metrics, quantitative analysis, Arizona State University Dental Anthropology System, Bayesian statistics

In 1922, William King Gregory opined "Apart from a few striking cases, presently to be noted, racial characters in the teeth are at most not very conspicuous." The traits he considered variable enough to be noted included shovel-shaped incisors, upper molar cusp number, lower molar cusp number, "Dryopithecus" pattern, and Carabelli's cusp (Gregory 1922:476). This same sentiment was echoed 35 years later by Lasker and Lee (1957) who wrote that "the extravagant hopes for the use of dental features as 'hallmarks of race' have not been fulfilled" (pg. 401). Based on the literature of their day, these scholars were correct. Relative to developments in the field over the past century, they were far from correct. Dozens of human tooth crown and root traits have been defined since these statements that show patterned geographic variation.

Dental anthropologists have used morphology to address a broad range of historical issues, including the peopling of the Americas and the colonization of Pacific islands (cf. Scott and Turner 1997, for many examples). These biodistance studies are based on comparisons of sample frequencies between three or more groups and fall primarily within the realm of bioarchaeology. The use of dental morphology in forensic anthropology has fallen short of their application in bioarchaeological studies.

Forensic anthropologists often prefer bones to teeth in general and for ancestry estimation in particular (i.e., craniometrics, morphoscopic traits of crania and postcrania). In forensic labs, it is commonplace for individuals to follow methodological guides for finding cranial landmarks that are then used to obtain craniometric measurements. These measurements are input into the widely available Fordisc program that uses discriminant function analysis to assign an individual to one of 13 reference population samples (Jantz and Ousley 2005). By contrast, dental morphology receives relatively little attention, even when teeth are perfectly preserved and largely unworn. A brief review of major forensic anthropology manuals and texts illustrates this point.

In the edited volume on the *Skeletal Attribution of Race*, Rhine (1990) identifies six morphological variants of the teeth as being of forensic significance in the estimation of ancestry. These are Carabelli's cusps ("American Caucasoid"); shoveling of incisors, incisor rotation, enamel extensions, and buccal pits ("Southwestern Mongoloid"); and molar crenulations ("American Black"). Although, little data are provided on trait frequency in these groups. In the second edition of *Forensic Osteology*, Reichs (1998) does not include any papers on the role of dental morphology in forensic anthropology. In the *Forensic Anthropology Training Manual*, Burns (1999) notes two 'racial' traits in the dentition. In some ways harkening back to Gregory, the two traits noted are shovel-shaped incisors, characterizing Asian and American Indian groups, and Carabelli's cusp, characterizing European-derived populations. In *Introduction to Forensic Anthropology*, Byers (2002) only notes one trait for ancestry estimation, shovel-shaped incisors. In the associated laboratory manual, the exercise for 'attributing ancestry using cranial anthroposcopy' has only this trait for teeth: Upper incisors -- Spatulate (Whites), Spatulate (Blacks), Shoveled (Asians). In *Forensic Anthropology*, Komar and Buikstra (2008) do not mention dental morphology but note that for assessing ancestry "by far the most commonly used is the Fordisc computer program" (pg. 147). *A Companion to Forensic Anthropology* (Dirkmaat 2012) includes a chapter entitled "Morphoscopic Traits and the Assessment of Ancestry" by Hefner, Ousley, and Dirkmaat (2012). While the authors recognize the promise of dental morphology for ancestry assessment, they note these traits will only be useful when there is: (1) significant reference data from populations around the world; (2)

standardized protocols for scoring traits; and (3) rigorous statistics that can be used with categorical data. These recommendations are addressed in detail later.

The edited volume *Biological Affinity in Forensic Identification of Human Skeletal Remains* (Berg and Ta'ala 2015) includes two chapters by dental morphologists who address how dental traits can be used in ancestry estimation. Irish (2015) developed a method that assigns an individual to one of five groups (East Asian, American Indian, White, Polynesian, Black) based on ten crown traits. Although the method works well to determine which of the five group an individual most likely belongs, it does not involve the calculation of a probability. Edgar (2015) presents an overview of previous work (Edgar 2005; 2013), in which she uses ten crown traits and a logistic regression model to estimate ancestry for four groups (African American, European American, Hispanic from New Mexico, and Hispanic from South Florida). Relative to these four groups, a test sample yielded a correct assignment rate of over 70%. While errors and probabilities are presented in her work, the reference sample is somewhat limited for use in the United States. In contrast to all previous studies, this paper introduces a new application that uses an individual's suite of dental morphological traits that computes a posterior probability for group assignment, i.e. ancestry estimation.

1. Global variation in tooth crown and root morphology

1.1. What is tooth morphology?

Some researchers consider tooth size one aspect of tooth morphology. We do not. While tooth size, or odontometrics, provides a broad suite of useful variables (see Kieser 1990), our use of the term morphology relates primarily to traits that are present or absent, and when present, exhibit variable degrees of expression. Over three dozen such traits have been codified in the Arizona State University Dental Anthropology System (Turner et al. 1991). These traits have been described in books and articles (cf.., Edgar In Press; Scott 2008; Scott and Turner 1997; Scott and Pilloud In press; Scott et al. 2015), so there is no need to describe every variable in detail. To illustrate the general nature of these traits, we consider shovel-shaped incisors, the one morphological variable that receives attention in forensic anthropological circles (e.g., Birkby et al. 2008; Hinkes 1990; Hurst 2012; Rhine 1990).

Upper and lower incisors are typically spatulate in shape with straight incisal edges that serve for biting and cutting (e.g., check tooth impressions after biting an apple or block of cheese). Human incisors show a number of morphological variables, of which shoveling is the most useful and varied. Shoveling relates primarily to the development of distal and mesial marginal ridges on the lingual aspect of the crown. Hrdlička (1920) noted that Asians and American Indians often had well-developed marginal ridges while American Whites and Blacks showed ridges that were slight or absent altogether. To characterize geographic variation, he set up a ranked classification that included absence, trace-shovel, semi-shovel, and marked shovel. Dahlberg (1956) used this classification when he developed a set of standardized plaques for a dozen tooth crown traits.

Although the Hrdlička/Dahlberg scale was used extensively in dental anthropology, it did not capture the true nature of the shoveling distribution. In Pima Indians, for example, semi- and marked shoveling was over 80%. The distribution would be 1% absent, 9% trace, and 90% semi- and marked shovel, far removed from a normal distribution. When Scott (1973) set up a classification that included absence and seven degrees of trait presence, the distribution for shoveling expression assumed normality, evident even through the use of ranks (cf.., Scott 2008; Scott and Turner 1997).

Traditionally, when researchers observed marginal ridges in a forensic case, they would note the individual had shoveling. This general observation could lead to erroneous conclusions because the presence of shoveling is not the key observation. Many people around the globe exhibit lingual marginal ridges on their incisors. The key observation is *degree* of expression. For example, Europeans and Sub-Saharan Africans frequently exhibit shoveling but expression mostly takes the form of grades 1 and 2, and less often grade 3. Grades 4-7 are almost never observed in these two groups, but these pronounced grades are 30-40% in East Asians and American Indians. The point is that it is not the *presence* of the trait that distinguishes ancestry, but the *grade* of trait expression.

One question that dental morphologists contend with is which tooth or group of teeth to include in a characterization of shoveling. Shoveling is expressed on all upper and lower incisors. Some feel it is also manifest on the canines but the essential ridges of the upper and lower canines ameliorate the expression of the lingual marginal ridges. Shoveling is highly symmetrical between antimeres and also shows significant correlations between UI1[1], UI2, LI1, and LI2 (Scott 1977). The general practice is to use key teeth, or those that are defined as the most stable in each tooth class, to avoid the problem of interdependent variables. In describing human tooth districts, Dahlberg (1945) noted that, with few exceptions (i.e., LI1), the key tooth in a tooth district in terms of size, morphology, and number was the most mesial member (e.g., UI1 rather than UI2; UM1 rather than UM2 or UM3). For that reason, UI1 is used as the key tooth for scoring shoveling.

For most other variables, the key tooth in a district is the one employed in characterizing geographic variation (e.g., Carabelli's trait UM1, cusp 5 UM1; cusp 6 LM1, cusp 7 LM1). The

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[1] In this paper, and by convention, U=upper, L=lower, I=incisor, C=canine, P=premolar, M=molar, and number refers to tooth position. For example, UI1 refers to the upper first incisor.

exceptions to this rule are traits that show little variation on the key tooth (e.g., UM1 hypocone, LM1 groove pattern, UM1 root number). In such instances, trait frequencies for the second molar are used. Third molars are highly variable for crown and root structures, so these teeth are generally avoided for morphological comparisons. There is, however, one exception: pegged-reduced-missing UM3. Third molars are often reduced in size or lost altogether and this variable shows patterned geographic variation. It is more common in Asian and Asian-derived populations (15-35%) but is rare in Sub-Saharan Africans and Australo-Melanesians (ca. 5%).

1.2. Selection of variables for rASUDAS

The alpha version of rASUDAS was based on 17 variables listed in Appendix 1 of Scott and Turner (Scott and Turner 1997). In that appendix, all traits were broken down into two categories (e.g., absent and present, or presence frequencies at and above a certain breakpoint). For the beta version of the application, some traits on that list were considered too rare (e.g., premolar odontomes, Bushman canine) or were correlated with other variables on the list (e.g., double shoveling correlated with shoveling; 4-cusped LM1 correlated with 4-cusped LM2), and were therefore removed from the beta version. Other traits were added to the beta version (cusp 5 UM1; multiple lingual cusps LP2; UP1 root number), bringing the total number of traits to 21. In addition, four traits that show a wide range of variation were broken down into finer categories than 0 or +. These traits included UI1 shoveling (0-1, 2-3, 4+), UM2 hypocone (0-1, 2-3, 4+), UM1 Carabelli's trait (0-1, 2-4, 5+), and the LM1 protostylid (0, 1, 2+). Trait classifications and standards are described in Turner et al. (1991) and the forthcoming guidebook by Scott and Irish (2017).

1.3. Reference data and standards for scoring traits

Despite the fact that Hefner et al. (2012) had access to and reference Scott and Turner (1991), they nonetheless question the utility of dental morphology until there is sufficient reference data on world populations and standardized protocols for scoring crown and root traits. They also note the need for more rigorous statistics that can be used with categorical data, an issue that is addressed in the methods section.

As to the need for reference data and protocols for scoring traits, these have been around for two decades. The appendix from Scott and Turner (1997) has trait frequencies for 21 world populations based on over 30,000 individuals. Most of the data were collected by C.G. Turner II with African data provided by J.D. Irish (1993). The only significant geographic omission was South Asia (i.e., India, Pakistan). As for standardized protocol, the paper by Turner et al. (1991) provides descriptions associated with over two dozen standard plaques developed at Arizona State University across a two decade period (ca. 1970-1991). Over 400 sets of standard plaques distributed to researchers throughout the world have been used in countless theses and research papers.

Regarding the source of dental data, we grant that this can be improved with additional observations on recent populations throughout the world. For the time being, however, we can evaluate proof of concept using dental data from the extensive archaeologically-derived populations from throughout the world. Regarding standards for scoring crown and root traits, we strongly encourage the addition of new variables to the list already incorporated into ASUDAS. However, we currently have well-developed and widely used standards for the 21 crown and root traits used in rASUDAS, more than sufficient to evaluate the potential of dental morphology for ancestry estimation.

In the last paragraph of Scott and Turner (1997:317), the authors noted: “The geographic differences in dental trait frequency and expression are often pronounced. When these differences are assessed through advanced methods of classification (e.g., discriminant function analysis, Bayes’ theorem, neural networks), it will be possible to transcend educated guesses and calculate the probability that an individual belonged to a particular ethnic group.”

2. Application

2.1. Distance matrix and cluster analysis

For the alpha version of rASUDAS, 17 regional groups from the Scott and Turner (1997) appendix were used for individual assignment. Although it would be ideal for classifications to be that fine-tuned, it is not reasonable to distinguish Polynesians from Southeast Asians, Australians from Melanesians, etc. To arrive at a more manageable number of categories, Nei’s distance matrix was computed using each crown and root trait. From these distances, a hierarchical clustering tree was created using UPGMA algorithm with complete linkage. Based on a visual inspection of the clustering tree, seven biogeographic population clusters were defined: American Arctic & Northeast Siberia, North & South American Indian, East Asia, Southeast Asia & Polynesia, Australo-Melanesia & Micronesia, Sub-Saharan Africa., and Western Eurasia (Figure 1).

2.2. World variation in dental morphology for seven major groups

The crown and root trait frequencies for 21 variables in seven major geno-geographic groups are shown in Table 1. The pattern of variation exhibited by each is described briefly below.

2.2.1. UI1 winging

Bilateral winging is most common in American Indians (50%), followed by Asian and Asian-derived groups (20-25%). It is less common in Australo-Melanesians (14%) and is relatively rare in Western Eurasians and Sub-Saharan Africans (3-6%).

2.2.2. UI1 Shoveling

Broken down into three categories, shoveling is most common in American Indians. It is also common in East Asians and the American Arctic but expression is less pronounced in these groups. Southeast Asians and Australo-Melanesians show generally similar frequencies; for both, 4+ expressions are much lower than for American Indians and East Asians. Although 4+ grades are rare in Sub-Saharan Africans and Western Eurasians, the former have a lower frequency of 0+1 shoveling and more 2+3 shoveling. This trait remains one of the single most useful for discerning ancestry but grades must be taken into consideration.

2.2.3. UI2 Interruption grooves

These grooves are most common in East Asian and derived populations with frequencies between 40 and 60%. They are moderate in Western Eurasians and Southeast Asians (30-35%). They are less frequent in Australo-Melanesians (20%) and rarest in Africans (8%).

2.2.4. UM2 hypocone

The greatest amount of hypocone reduction (0+1 grades) is shown by Western Eurasians (25%). East Asian and derived populations are intermediate with frequencies of 10-15%. The least amount of hypocone reduction is shown by Australo-Melanesians, Southeast Asians, and Africans (2-8%). Pronounced hypocones (4+) are also in highest frequency in these three groups.

2.2.5. UM1 Carabelli's trait

For absent and trace expressions (0+1), Asian and Asian-derived populations have the highest frequencies, led by the American Arctic & Northeast Siberia (85%). For pronounced expressions (5+), Europeans have the highest frequency (26%) and Native Americans the lowest (3%). Other Asian and Pacific populations have frequencies for grades 5+ between 14 and 18%.

2.2.6. UM1 cusp 5

This trait shows similar frequencies throughout the world (15-30%), with one exception, Australo-Melanesia (60%). It is slightly less common in Europeans (15%) but not markedly so.

2.2.7. UM1 enamel extensions

One of the few traits noted by forensic anthropologists (e.g., Birkby et al. 2008; Hurst 2012; Rhine 1990) as useful for ancestry estimation, enamel extensions are rare in Western Eurasians and Africans (1-2%) and slightly more common in Australo-Melanesians (7%). The highest frequencies are in East Asian and derived American populations (40-45%), with slightly lower frequencies for Southeast Asia (27%).

2.2.8. LP2 multiple lingual cusps

Two or three lingual cusps is a common condition (65-80%) in most populations of the world. The exceptions are the two New World groups with frequencies around 40%.

2.2.9. LM2 groove pattern

Most world populations show the Y pattern on LM2 between 25 and 30% of the time. The exceptions are American Indians with the lowest frequency (10%) and Africans with the highest frequency (50+%).

2.2.10. 4-cusped LM2

The loss of the fifth cusp on the lower second molar is a hallmark of the Western Eurasian dentition (75%). A 4-cusped LM2 is rare in Native American populations (5-10%) and intermediate for all other world groups (25-35%).

2.2.11. LM1 cusp 6

Cusp 6 is relatively common in all Asian and Pacific populations (40-55%). The trait is relatively rare in Western Eurasian and African populations (5-15%).

2.2.12. LM1 cusp 7

This variable shows a distinct pattern of variation. It is rare (4-7%) in all world populations with one exception. Sub-Saharan Africans have the highest frequency of this trait in the world (33%). One in three Africans exhibit this trait while one of twenty exhibit the trait in all other populations.

2.2.13. LM1 protostylid

Positive (2+) expressions of the protostylid are uncommon in all world populations with the highest frequency in East Asians (11%). Buccal pits (score of 1) are most common in American Indians (32%), followed by Asian populations (15-25%). These pits are least common in Australo-Melanesians, Africans, and Western Eurasians (6-10%).

2.2.14. LM1 deflecting wrinkle

The highest frequencies of this trait are for Native American populations (55-65%), followed by all Asian and Pacific populations (25-35%). It is relatively infrequent in Africans and Western Eurasians (5-12%).

2.2.15. UP1 root number

Africans and Western Eurasians have the highest frequency of 2 and 3 rooted UP1 (50-65%). Asian and Pacific populations fall in the 25-35% range. Native Americans show the greatest amount of root fusion, as 2 and 3 rooted UP1 are relatively rare in these groups (5-15%).

2.2.16. UM2 root number

Africans have the highest frequency of 3-rooted UM2 (80%) while American Arctic & Northeast Siberia have the lowest frequency (38%). Other world groups fall in the middle at 55-65%.

2.2.17. LC root number

Although a relatively rare trait throughout the world, it is one of the few variables that sets Europeans apart from other populations. The frequency in table 1 is 6.1% but the trait occurs consistently in Europeans and can get up to 10%. This finding is noteworthy because Asian and Pacific populations rarely have a frequency above 1%. Africans assume an intermediate position with a frequency around 4%.

2.2.18. LP1 Tomes root

This accessory root is uncommon in all world populations. It is around 2% in American Arctic groups and 11% in Europeans. All other groups fall between 15-20%.

2.2.19. 3-rooted LM1

This accessory root is most common in East Asia and the American Arctic (20%) followed by Southeast Asia (10%). It is rare in Native Americans, Africans, and Australo-Melanesians (3-6%) and exceptionally rare in Europeans (<1%).

2.2.20. LM2 root number

Most world populations have 1-rooted LM2 frequencies of 25-30%. The exceptions are Australo-Melanesians (12%) and Africans (6%) who show the least amount of root fusion.

2.2.21. Pegged-reduced-missing UM3

The highest frequencies of reduced and lost UM3 are in East Asia and the American Arctic (25-35%). American Indians, Western Eurasians, and Southeast Asians are intermediate at 15-20%. The lowest frequencies of UM3 loss and reduction are Africans and Australo-Melanesians (5-6%).

2.3. Naïve Bayes classification algorithm

The naïve Bayes classification algorithm was used to calculate the probability that an individual exhibiting a certain suite of morphological traits would be assigned to a particular geographic group. The naïve Bayes classifier is a simple probabilistic model that uses Bayes theorem with the strong assumption of independence (Fielding 2007). That is, it assumes the presence or absence of a trait is not related to the presence or absence of any other trait. Such an assumption is called conditional independence. This modelling assumption offers a dramatic simplification: Individual class-conditional marginal density of features can be estimated separately using a one-dimensional kernel density estimator or any distribution model appropriate for continuous data. For discrete predictors, class-conditional probability tables can be obtained using a histogram estimator (Hastie et al. 2009). All analyses were conducted using the free statistical package R (R Core Team 2013).

For any given individual, the posterior probabilities for assignment to one of the seven groups always adds to 1.0. Although the probability for assigning an individual to one of seven groups would never be 1.0, there are some suites of characteristics that would produce a probability of 0.00 for geographic assignment. For example, if an individual had bilateral winging, grade 4 shoveling, and LM1 cusp 6, the probability that individual was African or European would be 0.000. To reverse that, if an individual had no winging, grade 0-1 shoveling, and no cusp 6, the posterior probabilities would be about 0.40 for both African and European, with the remaining 0.20 divided among the five Asian, Pacific, and New World populations. A trial case for an individual that exhibited no crown traits yields a probability of 0.926 Western Eurasian, 0.050 African, and less than 0.001 for the five Asian and Asian derived groups. If an individual exhibited all crown traits, the probabilities would be 0.589 for East Asians, 0.278 for American Indians, 0.128 for Southeast Asians-Polynesians, and 0.000 for Western Eurasians and Africans.

3. Test of application

3.1. Validation

To test the applicability of the model a random sample of 150 individuals from the Turner dataset were chosen and input into the program. Such a test was justified as the program is based on population frequency, not individual data. The goal of this test was to evaluate how an individual of known ancestry and group assignment would classify using these summary data. Based on the random sample, the overall accuracy of the model in predicting group assignment is 0.518 (95% confidence interval 0.432-0.603).The confusion matrix is presented in Table 2, which shows group classification. The summary results are in Table 3, outlining the sensitivity and the positive predictive value for each group. It is clear from these results that the Southeast

Asia and Polynesia group is consistently misclassifying, particularly with the East Asian and Western Eurasian groups.

Based on the results of this test, the seven-group model was re-evaluated and a second clustering analysis was conducted. Based on the results of the Nei's distance matrix and the hierarchical cluster analysis (Figure 2), the seven groups were further grouped into four groups: 1) Western Eurasia; 2)Sub-Saharan Africa; 3) Australo-Melanesia and Micronesia, Southeast Asia and Polynesia; and 4) American Arctic and Northeast Asia, East Asia, and American Indian. Model accuracy for four groups is 0.667 (95% confidence interval 0.582 – 0.744). Summary results are provided in Table 4. This clustering of groups provides better overall classifications and resolves the problem of misclassification with the Southeast Asia and Polynesia group.

A consideration was also given to the standard three-group model that is commonly employed by forensic anthropologists (i.e., Africa, Asia, and Europe). Therefore, a final test was run with only this three-group classification in which reference samples from East Asia, Sub-Saharan Africa, and Western Eurasia were used. The overall accuracy of this model was 0.727 (95% confidence interval 0.604 – 0.830). The summary results are listed in Table 5.

3.2. Discussion of Blind Test Results

The model is successful at predicting group assignment, and appears to perform better when there are fewer groups, which is to be expected. It is worth discussing here the misclassification of the Southeast Asia and Polynesian group in the seven-group analysis. This finding is likely related to the differences in Sinodonty and Sundadonty as described by

Turner(1990). The Sinodont dental complex is found in East Asia and represents a suite of specialized traits (e.g., shoveling, enamel extensions, deflecting wrinkle, 3-rooted lower molars, 4+ cusped lower molars, and missing-peg-reduced UM3). Whereas the Sundadont pattern is in Southeast Asia and is a conservative pattern with lower grades of these traits. Individuals from Southeast Asia and Polynesia are misclassifying as either other Asian groups (individuals who may tend towards a Sindont pattern) or as Western Eurasians (individuals with a more Sundadont pattern that lack many of the traits seen in other groups). Much of this is ameliorated when overall group number is reduced (from seven to four).

In these tests we did not differentiate between male and female individuals, as the rate of sexual dimorphism is reportedly low in dental morphology (e.g., Garn et al. 1966; Gašperšič 1994; Harris 2007; Scott 1980 ; Turner 1967). There is, however, one trait that does appear to consistently show sexual dimorphism: the distal accessory ridge of the canine (Kaul and Prakash 1981; Scott 1977). As this trait is not one of the main traits considered in this analysis, the reference sample was not further divided by sex.

4. Ramifications to forensic anthropology

4.1. rASUDAS in a forensic context

Within forensic anthropology, there are many methods to estimate ancestry. The more commonly used are based on craniometrics (Giles and Elliot 1962; Jantz and Ousley 2005) and cranial morphoscopics (Hefner 2009; Hefner and Ousley 2014; Rhine 1990). Many other skeletal elements have been studied as well, including the femur (Craig 1995; Gilbert 1976; Stewart 1962; Tallman and Winburn 2015; Wescott 2005), the metatarsals (Smith 1997), the hyoid (Kindschuh et al. 2012), the vertebrae (Duray et al. 1999; Marino 1997), the sagittal suture

(Mann et al. 2014), the mandible (Berg 2014), tooth size (Harris and Foster 2015; Kenyhercz et al. 2014; Pilloud et al. 2014), and postcranial measurements (Holliday and Falsetti 1999). While many of these methods have proven effective at differentiating ancestral groups – there is often little focus on biological development or the evolutionary reasons why various skeletal traits differentiate populations. That is, some of these traits do not have documented heritabilities and it is unclear what is driving population similarities or dissimilarities (e.g., genes, culture, environment).

As previously discussed, there are a few methods available to the practicing forensic anthropologist that utilize dental morphology (i.e., Edgar 2005; 2013; Irish 2015), although, they are somewhat limited in their application. We propose there are several advantages to incorporating dental morphology into the biological profile and that they are not subject to some of the shortcomings of other skeletal traits. First, there has been extensive work documenting the heritability and genetics of dental morphology (Berry 1978; Biggerstaff 1973; Harris 1977; Hughes et al. 2016; Kimura et al. 2009; Nichol 1990; Park et al. 2012; Saheki 1958; Scott 1973; Scott and Potter 1984; Sharma 1992; Škrinjarić et al. 1985; Townsend 1992; Townsend et al. 2009; Zhao et al. 2000; Zoubov and Nikityuk 1978). These traits show little influence from the environment and are therefore strong indicators of inherited population variation. Second, teeth are often well-preserved in forensic contexts, even in cases where remains are highly fragmentary, burned, or otherwise affected by trauma. Finally, the development of dental morphology is directed by distinct biological processes and genes from other parts of the skeleton that are used for ancestry estimation (e.g., craniometrics and cranial morphoscopics). Therefore, the incorporation of dental morphology as part of the biological profile provides a more robust view of human variation and population history.

While extensive work has been done to document secular change in craniometrics (e.g., Jantz 2001; Moore-Jansen 1989; Spradley 2006; Wescott and Jantz 2005), odontometrics (e.g., Ebeling et al. 1973; Garn et al. 1968; Harris et al. 2001; Kieser et al. 1987), and cranial morphoscopics (e.g., Vitek 2012), the role of time on population variation in dental morphology is less understood. The current version of rASUDAS has a reference sample that is primarily archaeological and spans several thousand years, which has the potential to limit the application in a medico-legal context. However, some research suggests that secular change is minimal in the expression of dental morphological population variation (Scott 1994). Our ultimate goal is to expand the reference sample to include data on a range of modern individuals throughout the United States and the world that would be more representative of modern forensic casework. The need to update the reference sample was illustrated in a recent paper by George and Scott (2016) employed rASUDAS to estimate the ancestry of Albuquerque Hispanics. These individuals overwhelmingly classified as Western Eurasians (69%), which illustrates the need for an increased reference sample with various population groups from the United States represented. As the modern reference sample grows, the Christy G. Turner, II sample could eventually be transitioned into an archaeological reference sample, much like the Howells database in Fordisc.

In its current form, rASUDAS can complement other methods in the estimation of ancestry. However, until more research is done on secular change in dental morphology and how this may affect interpretations, we do not recommend it be used as the *sole* method of ancestry estimation, at least not in a modern context. If the material appears to be archaeological in nature, rASUDAS can certainly be applied.

5. Conclusions

While we recognize the need to augment the reference sample, the current form of rASUDAS has illustrated the applicability of dental morphology in ancestry estimation. The incorporation of dental morphological analyses into forensic anthropological casework has several advantages: 1) there is a robust body of literature outlining the heritability, development, evolution, and population history of dental morphology, which allows for accurate interpretations of results, 2) teeth are not subject to plastic change over one's lifetime, and 3) teeth are often well-preserved when other parts of the skeleton may not be. Further, dental morphology represents a different aspect of the genotype and is the result of distinct evolutionary relationships that go beyond just the mid-face and the shape of the cranial vault. The ability to incorporate more information from the skeleton when assessing ancestry can prove to be critical in creating accurate ancestry estimates. We therefore argue that dental morphology couched in a statistical framework can become an integral part of the methods regularly used by forensic anthropologists in ancestry estimation. Ultimately, the incorporation of more aspects of the phenotype and genotype can lead to overall more accurate estimations of ancestry.

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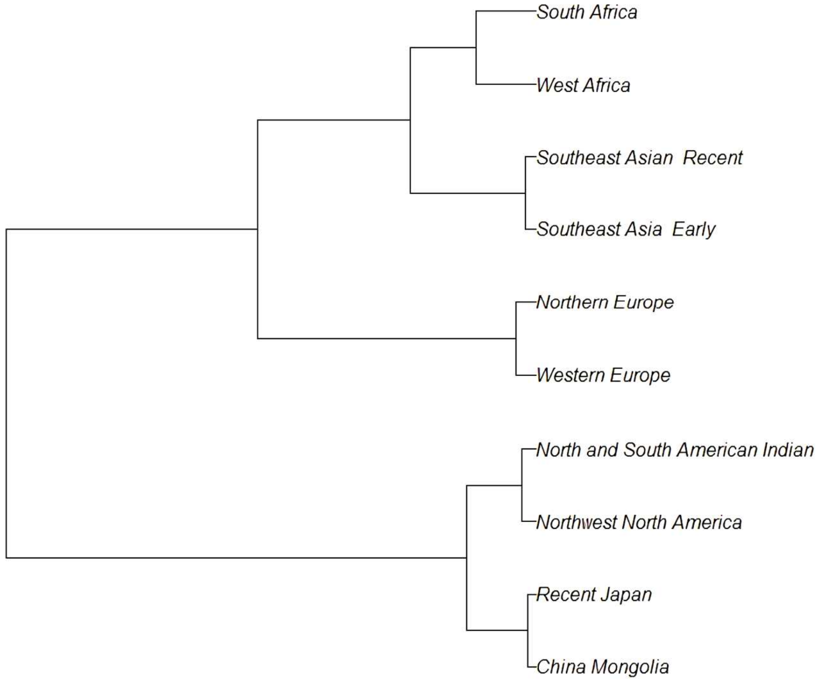

Figure 1. Results of Nei's distance matrix and hierarchical cluster analysis of original 17 groups that were further sub-divided into the following seven biogeographic groups.

601x551mm (72 x 72 DPI)

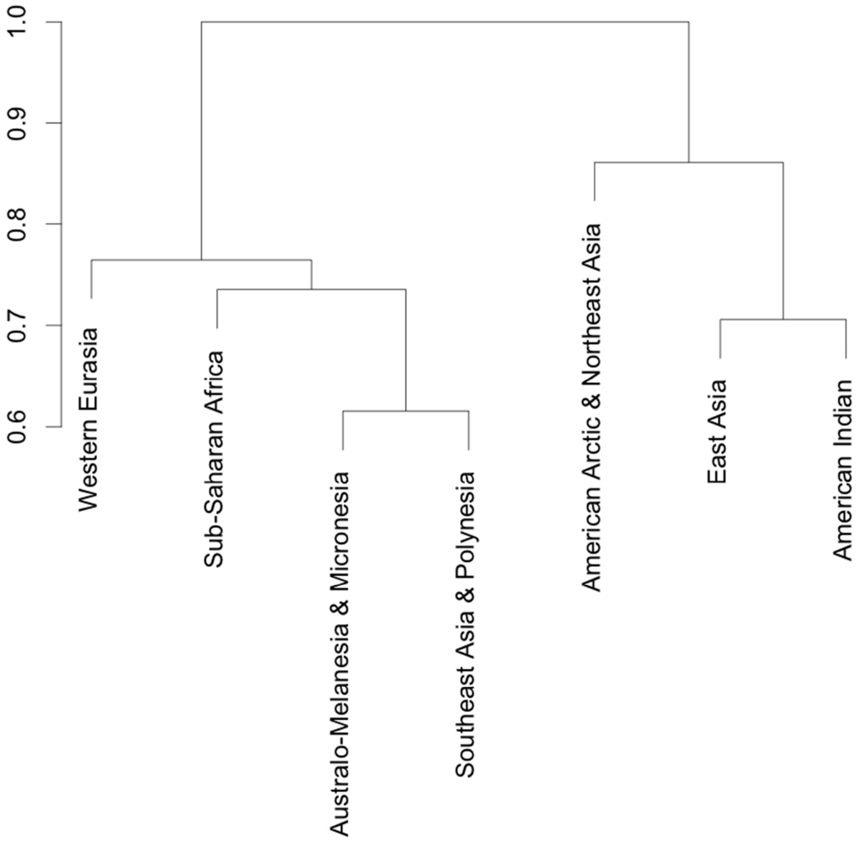

Figure 2. Results of Nei's distance matrix and hierarchical cluster analysis of original 7 groups that were further sub-divided into the following four biogeographic groups.

338x381mm (72 x 72 DPI)

Table 1. Trait frequencies used in rASUDAS application to compute posterior probabilities via naïve Bayes theorem.

Trait and tooth	Rank	American Arctic & NE Siberia	Australo-Melanesia & Micronesia	East Asia	American Indian	Southeast Asia & Polynesia	Sub-Saharan Africa	Western Eurasia
Winging UI1	0	0.773	0.860	0.746	0.500	0.773	0.967	0.938
	1+	0.227	0.140	0.254	0.500	0.227	0.033	0.062
Shoveling UI1	0 + 1	0.027	0.370	0.026	0.005	0.336	0.443	0.817
	2 + 3	0.811	0.606	0.654	0.542	0.589	0.558	0.181
	4+	0.162	0.024	0.319	0.453	0.074	0.000	0.002
Interruption	0	0.376	0.804	0.587	0.490	0.703	0.916	0.629
grooves UI2	1+	0.624	0.196	0.413	0.510	0.297	0.084	0.371
Hypocone UM2	0+1	0.145	0.059	0.097	0.115	0.018	0.086	0.253
	2+3	0.612	0.210	0.320	0.417	0.200	0.167	0.255
	4+	0.243	0.731	0.583	0.468	0.692	0.747	0.492
Carabelli's trait	0+1	0.845	0.606	0.690	0.620	0.647	0.460	0.450
UM1	2+3+4	0.134	0.213	0.165	0.325	0.168	0.426	0.288
	5+	0.021	0.182	0.145	0.055	0.185	0.144	0.262
Cusp 5 UM1	0	0.824	0.415	0.809	0.833	0.705	0.725	0.853
	1+	0.176	0.585	0.191	0.167	0.295	0.275	0.147
Enamel extensions	0+1	0.569	0.932	0.585	0.563	0.735	0.993	0.978
UM1	2+3	0.431	0.068	0.415	0.437	0.265	0.007	0.022
Multiple lingual	0+1	0.604	0.253	0.300	0.602	0.191	0.333	0.371
cusps LP2	2+3	0.396	0.747	0.700	0.398	0.809	0.667	0.629
Groove pattern	X and +	0.721	0.666	0.750	0.902	0.703	0.640	0.735
LM2	Y	0.279	0.334	0.250	0.098	0.297	0.460	0.265
4-cusped LM2	5	0.943	0.647	0.697	0.914	0.679	0.744	0.254
	4	0.057	0.363	0.303	0.086	0.321	0.256	0.746
Cusp 6 LM1	0	0.525	0.586	0.633	0.449	0.521	0.890	0.935
	1+	0.475	0.414	0.367	0.551	0.479	0.110	0.065
Cusp 7 LM1	0	0.962	0.931	0.945	0.939	0.945	0.674	0.956
	1+	0.038	0.069	0.055	0.061	0.055	0.326	0.044

Protostylid LM1	0	0.815	0.928	0.758	0.621	0.843	0.891	0.901
	1	0.169	0.061	0.137	0.321	0.231	0.100	0.091
	2+	0.016	0.011	0.106	0.060	0.012	0.009	0.008
Deflecting wrinkle	0+1+2	0.426	0.737	0.637	0.335	0.641	0.950	0.871
LM1	3	0.574	0.263	0.363	0.665	0.359	0.050	0.129
UP1 root number	1	0.942	0.612	0.744	0.857	0.644	0.359	0.501
	2+3	0.058	0.388	0.256	0.143	0.356	0.641	0.499
UM2 root number	1+2	0.624	0.301	0.355	0.441	0.386	0.189	0.391
	3	0.376	0.699	0.645	0.559	0.614	0.812	0.609
LC root number	1	1.000	0.999	0.988	0.993	0.993	0.957	0.939
	2	0.000	0.001	0.012	0.007	0.007	0.043	0.061
Tomes root LP1	1+2+3	0.985	0.815	0.842	0.801	0.809	0.823	0.885
	4+	0.015	0.185	0.158	0.199	0.191	0.177	0.115
3-rooted LM1	1+2	0.773	0.967	0.803	0.934	0.899	0.963	0.995
	3	0.227	0.033	0.197	0.066	0.101	0.037	0.005
LM2 root number	2	0.686	0.871	0.700	0.672	0.722	0.943	0.752
	1	0.314	0.129	0.300	0.328	0.278	0.057	0.248
Pegged-reduced-	0	0.786	0.936	0.641	0.842	0.792	0.950	0.835
missing UM3	1	0.232	0.064	0.359	0.158	0.208	0.050	0.165

Table 2. Confusion matrix of group assignment using archaeological reference sample in 7 groups.

	Reference							
Predicted	(1) American Arctic & Northeast Asia	(2) Australo-Melanesia & Micronesia	(3) East Asia	(4) American Indian	(5) Southeast Asia & Polynesia	(6) Sub-Saharan Africa	(7) Western Eurasia	TOTAL
(1) American Arctic & Northeast Asia	10	2	0	2	4	0	0	18
(2) Australo-Melanesia & Micronesia	1	11	0	4	2	0	0	18
(3) East Asia	2	1	12	1	6	4	5	31
(4) American Indian	3	2	2	9	0	0	1	17
(5) Southeast Asia & Polynesia	1	3	0	0	4	2	3	13
(6) Sub-Saharan Africa	0	0	4	0	2	11	4	21
(7) Western Eurasia	0	0	2	4	5	1	20	32
TOTAL	17	19	20	20	23	18	33	150

Table 3. Summary results of 7-group assignment using archaeological test sample indicating sensitivity and positive predictive value with a 95% confidence interval

Group	Sensitivity (95% CI)	PPV (95% CI)
(1) American Arctic & Northeast Asia	0.588 (0.329, 0.816)	0.556 (0.308, 0.785)
(2) Australo-Melanesia & Micronesia	0.625 (0.354, 0.848)	0.345 (0.179, 0.543)
(3) East Asia	0.467 (0.213, 0.734)	0.467 (0.213, 0.734)
(4) American Indian	0.579 (0.335, 0.797)	0.611 (0.357, 0.827)
(5) Southeast Asia & Polynesia	0.174 (0.050, 0.388)	0.308 (0.091, 0.614)
(6) Sub-Saharan Africa	0.611 (0.357, 0.827)	0.524 (0.298, 0.743)
(7) Western Eurasia	0.606 (0.421, 0.771)	0.714 (0.513, 0.868)

Table 4. Summary results of 4-group assignment using archaeological test sample indicating sensitivity and positive predictive value with a 95% confidence interval

Group	Sensitivity (95% CI)	PPV (95% CI)
(1) American Arctic & Northeast Asia | East Asia | American Indian	0.902 (0.786, 0.967)	0.821 (0.696, 0.911)
(2) Australo-Melanesia & Micronesia | Southeast Asia & Polynesia	0.487 (0.324, 0.652)	0.463 (0.307, 0.626)
(3) Sub-Saharan Africa	0.556 (0.308, 0.785)	0.588 (0.329, 0.816)
(4) Western Eurasia	0.576 (0.392, 0.745)	0.704 (0.498, 0.862)

Table 5. Summary results of 3-group assignment using archaeological test sample indicating sensitivity and positive predictive value with a 95% confidence interval

Group	Sensitivity (95% CI)	PPV (95% CI)
(1) East Asia	0.800 (0.519, 0.957)	0.800 (0.519, 0.957)
(2) Sub-Saharan Africa	0.778 (0.524, 0.936)	0.583 (0.366, 0.779)
(3) Western Eurasia	0.667 (0.482, 0.820)	0.815 (0.619, 0.937)