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# Estimation of Ancestry Using Dental Morphological Characteristics*

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## Abstract

The use of dental morphological characteristics to estimate the ancestry of skeletal remains commonly includes few traits, combines dental traits with other skeletal characteristics, and is non-statistical. Here, discriminant function equations for estimating whether an unknown person was African American, European American, or Hispanic American are reported. Equations were developed from observations of 29 dental traits in 509 individuals. These equations were then applied to the original sample and a test sample (n=40). Correct assignment rates for estimating African or European American vs. Hispanic American range from 66.7% to 89.3%. Correct assignment of African Americans vs. European Americans is 71.4% to 100%. Correct geographic assignment of Hispanics from South Florida or New Mexico ranged from 46.2% to 72.7%. Various discriminant equations using combinations of characteristics are provided. Coupled with the error estimates, these equations offer an important step in the use of dental morphology in contemporary, post-*Daubert* forensic science.

### Keywords

forensic science; forensic anthropology; ancestry estimation; dental morphology; discriminant function; African Americans; European Americans; Hispanic Americans

The purpose of this paper is to provide logistic regression formulae for using dental morphological data to estimate whether an unknown person would have been considered African American (AA), European American (EA), Hispanic from New Mexico (NMH), or Hispanic from Southern Florida (SFH) during their lifetime. Additionally, equations are provided that can be used to estimate whether skeletal remains represent a person who would have been considered Hispanic American (HA), without specifying their geographic origin within the United States.

Dental morphology, as the term is generally used in anthropology, considers observations of minor structures of the tooth crown and root, including grooves, ridges, and cusps (1). Most practitioners of forensic anthropology are aware that shovel-shaped incisors are more often seen in persons of Asian or Native American heritage. Many may believe, perhaps erroneously (2), that the presence of Carabelli's trait indicates European ancestry. Often, the use of dental morphology in forensics has been non-statistical, with one or two characters included among cranial morphology and overall skull shape descriptors (3). This kind of

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qualitative use of dental morphology has been shown to be ineffective (4), and similar results have been shown for morphoscopic characteristics of the skull (5).

The use of dental morphological characteristics to quantitatively estimate the biological ancestry of a skeleton, in much the same way cranial metrics are currently used, has been rarely encountered (6, but see 7). Dental anthropologists usually utilize many characteristics of the tooth and relatively complex statistics to describe how much variation exists within and between populations in order to learn how the populations may be related, especially ancestor-descendant relationships. As data, observations of dental characteristics are good for this purpose, because they are highly heritable and do not change (except through wear or caries) after a tooth is developed (1, 8). These same features make the use of a wider variety of dental traits, coupled with a statistical approach, a good potential tool for use in forensic contexts.

The material, methods, and results presented here provide a quantitative method for the assessment of ancestry when the potential group affiliations are AA, EA, SFH, NMH and HA. Any practitioner of forensic anthropology familiar with the adult human dentition can use the equations that are developed and described below.

## Material

Due to secular changes in populations, methods developed for medico-legal applications should be tested on contemporary or very recent samples. Therefore, all of the materials used in this study date to the twentieth and twenty-first centuries. The materials used in this research are dental models (casts) taken from living persons, and include materials representing contemporary AA, EA, NMH, and SFH. The sample numbers listed below represent the number from each collection used in developing the logistic regression formulae. Additionally, there was a test sample of 10 individuals of each of the four groups. The entire study included data from 549 individuals.

Composition of each of the groups discussed here is expected to approximate those described by the United States Census (9). How each individual was assigned to a group is described within the sample descriptions, below. In most cases a subject’s orthodontist, who had personal interactions with the individual, and knew their name, made group assignment. Previous research has estimated the accuracy of medical practitioners’ knowledge of their patients’ race and ethnicity by examining the frequency with which two observers agree about an individual’s group assignment. Such work has shown that medical records created by practitioners much less familiar with patients than these orthodontists are in good agreement for EA and AA (~90%), and are less reliable for HA (35–75%) [10–16].

For this paper, AA refers to people who are thought to have at least part of their ancestry traceable to individuals who were most often forcibly moved from West Africa to the United States since 1492. EA are people who are thought to have European ancestry exclusively. HA refers to people who are thought to have at least some part of their ancestry from Spanish-speaking regions, including Cuba, Mexico, Puerto Rico, and or South America. The term “Hispanic” is used in this paper because the United States government recognizes it, and because it is in more common use than “Latino” or other terms in the author’s home state, New Mexico.

Hispanics in different areas of the United States have different patterns of continental ancestry. Hispanics in Florida are predominantly from Cuba, Puerto Rico, and the Caribbean, and have been shown to have ancestry primarily from Africa and Europe, much like AA. Hispanics in the American Southwest, however, are chiefly from Mexico or have long family histories in the territory of the United States (17). Their ancestry is Native

American and European, with only small contributions from Africa. For this reason, the samples from South Florida and New Mexico were initially treated independently in this research. As only samples from New Mexico and Florida were included in this work, application to other regions of the county may be limited.

### Case Western Reserve University (n=44 EA)

Observations were made on dental casts taken from individuals born in Cuyahoga County, Ohio, from 1920 to 1945 (18). The casts are part of the large collection of the Bolton-Brush Longitudinal Growth Study. Subjects had been chosen to represent the growth of healthy children with good access to nutrition and health care (19). The Bolton-Brush study only included persons considered “White” by the original researchers.

### University of Tennessee, Memphis, Health Science Center (n=90 AA, 101 EA)

Orthodontic students took these casts in association with treatment being performed at a dental school. Most of the individuals were adolescents or young adults during the last two decades of the 20th century (Edward Harris, personal communication, 2002). The treating orthodontist determined group affiliation for each patient.

### Nova Southeastern University (n=191 SFH)

Orthodontic students took these casts in association with treatment being performed at a dental school near Ft. Lauderdale, Florida. All individuals were current patients at the time of data collection (2009), and most were adolescents or young adults. The treating orthodontist determined group affiliation for each patient.

### Economides Orthodontic Collection (n=83 NMH)

These casts are part of a large collection (n~5,650) held at the Maxwell Museum of Anthropology, University of New Mexico, and available in part at http://hsc.unm.edu/programs/ocfs. An orthodontist in private practice collected the casts from 1972 to 1999 and donated them to the Museum in 2005. Most patients were adolescents or young adults at the time of their treatment. Graduate and undergraduate students working in the Laboratory of Human Osteology determined group affiliation through examination of patient records, which include full facial photographs and patient names. This study only includes individuals for whom at least two students agreed on group affiliation. Overall agreement between two observers that a subject was Hispanic was 84% (20).

## Methods

### Observational Methods

Observations were documented for a total of 29 dental characteristics, all on permanent teeth. Traits were scored according to the Arizona State University Dental Anthropology System described by Turner et al. (21). This system utilizes plaques that illustrate expression levels for various traits. The plaques are inexpensive and available from Arizona State University’s School of Evolution and Social Change. Scoring followed the expression count method, meaning that both antimeres are scored when present, with the higher or more complex of the two scores representing the expression of the trait in that individual (22, 23). At most, 136 observations could be made per dentition. Because observations were made on dental models, only occlusal, buccal, or lingual surface morphological characteristics were observed. Other limiting factors included cast quality, dental reconstructions, breakage, and dental wear. However, teeth with wear, caries, or calculus were observed to the extent possible. Permanent teeth in mixed dentitions were included to allow for a larger sample. This is a commonly used method of gathering the most observations per each individual (1).

### Statistical Analysis

Trait frequencies were computed for each group (AA, EA, NMH, and SFH) and between-group comparisons were made. Originally, the intent was to only consider in analyses traits with frequencies that varied more than 30% among groups and had more than 350 total observations. However, only two traits that could be used to discriminate between NMH and SFH fit this description. Therefore, in this comparison only, discriminant function development included traits with frequencies that varied by as little as 25% between the two groups.

Using SAS 9.2 (24), logistic regression was used to develop discriminant function equations for the estimation of ancestry in unknown individuals. Logistic determination is similar to commonly used discriminant function analysis, but allows the prediction of discrete outcomes, such as group membership, from a dichotomous, discrete, continuous, or mixed set of measures (25). Additionally, logistic discrimination does not assume that variables are normally distributed, linearly related, or of equal variances (26, 27). By considering the difference between frequencies in the groups being compared, a series of equations were developed for each intergroup comparison. The equation with the most terms includes all traits for which there was a greater than 30% difference in frequency between the groups being compared (except for NMH and SFH, where the similarity between these groups required that 25% be used as a cutoff point). Each successive equation removed the characteristic with the least amount of frequency difference between the groups.

These logistic discrimination equations were then applied to both the samples used in their development and test samples. These test samples included dentitions that were pulled from the same subject populations as the samples from which the discriminant equations were created. However, the individuals in the test samples were not used in the creation of the equations.

## Results

Table 1 lists the traits that met the criteria of more than 350 total observations and at least 30% variation in frequency among the groups (25% variation between NMH an SFH), along with the abbreviations for these traits that are used throughout this paper.

Table 2 provides the coefficients and intercepts for each of the nine equations developed for determining whether an individual is closest to the group AA/EA or the group NMH/SFH, along with the standard error of each equation. When applying the equations, a result greater than zero indicates affiliation with the group AA/EA. A modification of the terms had to be made for equations one through eight, concerning the observations of two traits, UI1DS and UI2DS. UI1DS is absent in the AA/EA group, and UI2DS is virtually absent in the same group. These zero frequencies confounded development of the regression equations, resulting in overestimation of their coefficients and extremely high associated errors (2.5 to three orders of magnitude of all other standard errors). Therefore, the data were modified so that each of these characteristics had a five percent frequency in AA/EA. However, this lowered the difference in frequency of UI1DS between AA/EA and NMH/SFH to less than the 30% cutoff, so it was removed from further analyses.

Table 2 also provides the accuracy of each equation for the sample group and the test group, for AA/EA, NMH/SFH, and combined groups. Because of the modification to the UI2DS frequency in AA/EA, the expected accuracy of the equations that utilize that trait is slightly underestimated. Accurate combined group assignment frequencies range from 79.6% to 91.7% for within sample assignment, and 66.7% to 89.3% for group assignments in the test sample. Of course, there is a trade-off between applicability and accuracy among the equations. The fewer the traits included, the more individuals to which it can be applied. However, in general, accuracy declines when fewer traits are available. This is true for all three sets of equations presented.

Table 3 provides coefficients and intercepts for nine equations for estimating whether an individual is AA or EA, along with associated success rates in sample and test group estimations. Accurate combined group assignment frequencies range from 89.8% to 94.1% for within sample assignment, and 71.4% to 100% for group assignments in the test sample, which are better results than for the AA/EA versus NMH/SFH functions. Application of an equation with a result greater than zero indicates an individual is affiliated with AA. Table 4 provides the same information for five equations for estimating whether an individual is NMH or SFH. A greater than zero result of these equations indicates NMH affiliation. Accurate combined group assignment frequencies range from 70.7% to 81.5% for within sample assignment, and 46.2% to 72.7% for group assignments in the test sample. These accuracy rates are significantly below that of the other two function sets, and are likely of little practical value in forensic contexts.

## Discussion

The equation sets presented here discriminate quite well between the groups AA/EA and NMH/SFH, and even better between AA and EA. The functions intended for use in discriminating between NMH and SFH are not as accurate. This is not surprising, given the two groups' shared ancestry. NMH descend primarily from European immigrants and Native Americans, including Native Mexicans. SFH descend from Europeans, Africans, and Native Americans (17). Clearly, the Native American component of ancestry has an important effect on the pattern of dental morphology in both groups. Whether it is possible to determine if someone is NMH or SFH is interesting from a biocultural and biohistorical perspective, but may not be of use in a forensic investigation, given that the two groups uncommonly share the same geographic space. For researchers outside of New Mexico and Southern Florida, having an unknown skeleton assigned to the NMH/SFH group may be satisfactory, at least until specific research is conducted on HA in their area. For such researchers, it may be satisfactory to apply the AA/EA v. NMH/SFH equation, and, if a result of NMH/SFH is returned, consider analysis complete and provide an estimate of "Hispanic" to relevant authorities.

Many of the characteristics that separate HA from EA and AA would also identify Asian-derived populations, including Native Americans. At this time, it is unknown whether variation in Hispanic dentitions is different enough from the variation in other groups with significant Asian and Native American ancestry to make these groups discernable from each other dentally. Future research should explore this question.

Frequencies of correct assignment of individuals to groups are generally lower for the test sample than for the samples on which the discriminant equations is based. This is to be expected, as the variation in the test sample is not necessarily exactly the same as in the original sample. This drop in success is common to most if not all similar applications of discriminant functions.

Not every equation presented here has an equally excellent, or even acceptable, success rate. Perhaps that is not surprising given that they use very few observations, and that there has been admixture between these groups since their inceptions in the United States. Indeed, the groups "Hispanic American" and "African American" are defined in part by admixture. While a practitioner might wish for greater assurance in the application of these equations, at least their use is associated with an expectation of a success rate, along with a standard error.

These equations can also be applied to any other skeletal collection with known ancestries, and other researchers can test the accuracy presented here.

The traditional application of dental morphology to estimating ancestry in forensic contexts is non-statistical and has never been properly tested, so cannot meet the standards set forth in *Daubert v. Merrell Dow Pharmaceuticals* (No.92–102 509 US 579, 1993), our current standard for scientific evidence (28). The work presented here includes associated error rates and can be tested. It begins the process of bringing the use of dental morphology in forensic estimation of ancestry up to the standards set forth in the *Daubert* ruling.

## Example

Imagine that a researcher is developing a biological profile of the skeletal remains of an unknown individual. Using the trait descriptions in Turner et al. (14) the observations of dental morphological traits listed in Table 1 are made. The scores are then dichotomized, also according to Table 1. Table 5 lists the resulting scores for this hypothetical example. Notice that five of the characteristics are unobservable, a common situation.

The first step is to determine whether the individual is most like the group AA/EA or NMH/SFH. This will be done using equation 6 of Table 2, because it is the equation with the most terms for which we have all the data necessary. The equation is:

$$-2.049(\mathrm{LM1AF}=0)+-1.369(\mathrm{LI2SS}=1)+-2.930(\mathrm{UI2SS}=0)+-2.474(\mathrm{UM1MC}=0)+-2.374(\mathrm{UM1HC}=0)+4.912=3.543$$

Since the result is positive, the formula indicates that the individual is likely of the AA/EA group. Further, the interval of the result plus or minus the standard error contains only positive numbers.

The second step is to narrow from assignment to the AA/EA group to either AA or EA. This will be done using equation 7 of Table 3, again because it is the equation with the most terms for which we have all the data necessary. The equation is:

$$0.305(\mathrm{UCDR}=1)+1.308(\mathrm{UCTD}=1)+2.359(\mathrm{LCDR}=0)+4.254(\mathrm{LP3LC}=1)-4.653=1.214$$

The result is positive, indicating affiliation with AA. The standard error of the result includes negative numbers, so caution in accepting this assignment is necessary. The application of this equation to the test sample resulted in correct group assignment in more than 70% of cases. This is far from an extraordinary success rate, but it also is far better than chance. This accuracy can be improved upon if more characteristics are observable. This method is applicable in many cases where other data are not available, and derives from a method that is scientifically testable.

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## TABLE 1

Traits used in logistic discriminant functions, with their codes, breakpoints, numbers of observations, and frequencies in each group.

| | | | breakpoint | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| trait | tooth | code | absent | present | n | AA frequency | n | EA frequency | n | NMH frequency | n | SFH frequency |
| double shovel | maxillary first incisor | UI1DS | 0–1 | 2–6 | 90 | 0 | 145 | 0 | 80 | 0.275 | 185 | 0.335 |
| shovel shape | maxillary second incisor | UI2SS | 0–1 | 2–7 | 88 | 0.352 | 144 | 0.139 | 77 | 0.636 | 181 | 0.619 |
| double shovel | maxillary second incisor | UI2DS | 0 | 1–6 | 88 | 0 | 144 | 0.007 | 77 | 0.52 | 182 | 0.56 |
| shovel shape | maxillary canine | UCSS | 0–1 | 2–6 | 87 | 0.172 | 142 | 0.035 | 72 | 0.444 | 165 | 0.43 |
| distal accesory ridge | maxillary canine | UCDR | 0–1 | 2–5 | 89 | 0.764 | 143 | 0.392 | 76 | 0.711 | 176 | 0.58 |
| tuberculum dentale | maxillary canine | UCTD | 0–1 | >1 | 83 | 0.855 | 135 | 0.467 | 65 | 0.492 | 150 | 0.58 |
| hypocone | maxillary first molar | UM1HC | 0–4 | >4 | 89 | 0.191 | 143 | 0.266 | 80 | 0.75 | 182 | 0.841 |
| metacone | maxillary first molar | UM1MC | 0–4 | >4 | 90 | 0.267 | 145 | 0.407 | 81 | 0.901 | 187 | 0.893 |
| metacone | maxillary second molar | UM2MC | 0–4 | >4 | 83 | 0.133 | 136 | 0.103 | 65 | 0.32 | 172 | 0.593 |
| metaconule | maxillary second molar | UM2C5 | 0 | 1–5 | 73 | 0.37 | 125 | 0.12 | 58 | 0.344 | 132 | 0.28 |
| shovel shape | mandibular first incisor | LI1SS | 0 | 1–3 | 89 | 0.292 | 143 | 0.175 | 82 | 0.841 | 188 | 0.622 |
| shovel shape | mandibular second incisor | LI2SS | 0 | 1–3 | 90 | 0.333 | 144 | 0.132 | 81 | 0.852 | 189 | 0.646 |
| distal accesory ridge | mandibular canine | LCDR | 0–1 | 2–5 | 88 | 0.546 | 144 | 0.125 | 76 | 0.355 | 186 | 0.268 |
| lingual cusp complexity | mandibular anterior premolar | LP3LC | 0–3 | 4–9 | 83 | 0.928 | 140 | 0.114 | 77 | 0.065 | 186 | 0.145 |
| anterior fovea | mandibular first molar | LM1AF | 0–1 | 2–4 | 78 | 0.244 | 124 | 0.121 | 75 | 0.68 | 168 | 0.661 |
| deflecting wrinkle | mandibular first molar | LM1DW | 0 | 1–3 | 755 | 0.467 | 130 | 0.215 | 69 | 0.304 | 171 | 0.251 |
| protostylid | mandibular first molar | LM1PS | 0 | >0 | 82 | 0.073 | 138 | 0.036 | 76 | 0.566 | 179 | 0.291 |
| cusp seven | mandibular first molar | LM1C7 | 0 | 1–4 | 85 | 0.447 | 138 | 0.138 | 77 | 0.234 | 176 | 0.568 |
| fifth cusp | mandibular second molar | LM2C5 | 0 | 1–5 | 66 | 0.561 | 127 | 0.205 | 51 | 0.333 | 136 | 0.331 |
| cusp seven | mandibular second molar | LM2C7 | 0 | 1–4 | 83 | 0.181 | 133 | 0.068 | 60 | 0.183 | 150 | 0.493 |

## TABLE 2

A/EA v. SFH/NMH comparisons. Logistic discriminant function coefficients and intercepts for nine equations, along with each equation’s success rates for within sample and test group applications. A result >0 indicates AA/EA affiliation.

| | | | | | | | | | | | | | AA/EA | | sample NMH/SFH | | combined | | AA/EA | | test NMH/SFH | | combined | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **equation** | **LM1PS** | **UCSS** | **UI2DS** | **UM2MC** | **LI1SS** | **LM1AF** | **LI2SS** | **UI2SS** | **UM1MC** | **UM1HC** | **intercept** | **std error** | **n** | **correct** | **n** | **correct** | **n** | **correct** | **n** | **correct** | **n** | **correct** | **n** | **correct** |
| 1 | −2.284 | −1.084 | −3.274 | −1.406 | −1.222 | −1.929 | −0.130 | 0.020 | −1.528 | −2.842 | 5.670 | 7.122 | 171 | 0.918 | 166 | 0.916 | 337 | 0.917 | 15 | 0.867 | 9 | 0.889 | 24 | 0.875 |
| 2 | | −1.470 | −3.365 | −1.399 | −1.518 | −2.047 | −0.031 | 0.112 | −1.784 | −2.642 | 5.589 | 6.064 | 179 | 0.899 | 170 | 0.924 | 349 | 0.911 | 16 | 0.875 | 10 | 0.900 | 26 | 0.885 |
| 3 | | | −3.495 | −1.338 | −1.405 | −2.080 | −0.349 | −0.399 | −1.738 | −2.477 | 5.290 | 4.945 | 182 | 0.901 | 190 | 0.911 | 372 | 0.906 | 17 | 0.824 | 11 | 1.000 | 28 | 0.893 |
| 4 | | | | −1.404 | −1.384 | −2.111 | −0.432 | −3.586 | −1.773 | −2.505 | 5.234 | 4.472 | 182 | 0.901 | 193 | 0.922 | 375 | 0.912 | 17 | 0.647 | 11 | 1.000 | 28 | 0.786 |
| 5 | | | | | −0.971 | −2.206 | −0.540 | −3.158 | −2.379 | −2.451 | 5.013 | 3.558 | 194 | 0.923 | 222 | 0.878 | 416 | 0.899 | 17 | 0.706 | 12 | 1.000 | 29 | 0.828 |
| 6 | | | | | | −2.049 | −1.369 | −2.930 | −2.474 | −2.374 | 4.912 | 2.677 | 198 | 0.934 | 223 | 0.870 | 421 | 0.900 | 17 | 0.706 | 14 | 1.000 | 31 | 0.839 |
| 7 | | | | | | | −1.754 | −2.819 | −2.526 | −2.280 | 4.291 | 1.876 | 228 | 0.838 | 248 | 0.895 | 476 | 0.868 | 18 | 0.611 | 16 | 1.000 | 34 | 0.794 |
| 8 | | | | | | | | −3.261 | −2.430 | −2.466 | 3.661 | 1.429 | 229 | 0.856 | 252 | 0.881 | 481 | 0.869 | 18 | 0.667 | 16 | 0.938 | 34 | 0.794 |
| 9 | | | | | | | | | −2.395 | −2.247 | 2.686 | 0.794 | 232 | 0.866 | 262 | 0.733 | 494 | 0.796 | 20 | 0.750 | 19 | 0.579 | 39 | 0.667 |

## TABLE 3

AA v. EA comparisons. Logistic discriminant function coefficients and intercepts for nine equations, along with each equation's success rates for within sample and test group applications. A result >0 indicates AA affiliation.

| | | | | | | | | | | | | | AA | | sample EA | | combined | | AA | | test EA | | combined |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **equation** | **LI2SS** | **UI2SS** | **UM2C5** | **LM1DW** | **LM1C7** | **LM2C5** | **UCDR** | **UCTD** | **LCDR** | **LP3LC** | **intercept** | **std error** | **n** | **correct** | **n** | **correct** | **n** | **correct** | **n** | **Correct** | **n** | **correct** | **n** | **correct** |
| 1 | 0.656 | 0.676 | −0.230 | 1.006 | −0.076 | 0.780 | 0.997 | 0.864 | 1.405 | 4.013 | −5.856 | 9.564 | 40 | 0.925 | 95 | 0.947 | 135 | 0.941 | 3 | 0.667 | 2 | 1.000 | 5 | 0.800 |
| 2 | | 0.889 | −0.393 | 0.961 | −0.046 | 0.797 | 0.919 | 0.992 | 1.482 | 3.922 | −5.727 | 8.386 | 40 | 0.950 | 95 | 0.937 | 135 | 0.941 | 3 | 1.000 | 2 | 1.000 | 5 | 1.000 |
| 3 | | | −0.397 | 0.869 | −0.049 | 0.924 | 1.002 | 0.891 | 1.352 | 4.095 | −5.572 | 7.263 | 42 | 0.929 | 96 | 0.927 | 138 | 0.928 | 4 | 0.750 | 2 | 1.000 | 6 | 0.833 |
| 4 | | | | 1.150 | −0.248 | 0.913 | 1.080 | 0.973 | 1.256 | 4.275 | −5.833 | 6.272 | 48 | 0.938 | 101 | 0.931 | 149 | 0.933 | 5 | 0.600 | 2 | 1.000 | 7 | 0.714 |
| 5 | | | | | 0.507 | 1.343 | 0.598 | 0.925 | 2.155 | 3.429 | −4.867 | 4.676 | 52 | 0.885 | 110 | 0.927 | 162 | 0.914 | 7 | 0.714 | 2 | 1.000 | 9 | 0.778 |
| 6 | | | | | | 1.391 | 0.699 | 1.057 | 2.149 | 3.641 | −4.944 | 4.015 | 56 | 0.875 | 115 | 0.930 | 171 | 0.912 | 9 | 0.778 | 4 | 1.000 | 11 | 0.818 |
| 7 | | | | | | | 0.305 | 1.308 | 2.359 | 4.254 | −4.653 | 3.121 | 76 | 0.868 | 130 | 0.915 | 206 | 0.898 | 8 | 0.625 | 6 | 1.000 | 14 | 0.786 |
| 8 | | | | | | | | 1.408 | 2.465 | 4.287 | −4.596 | 2.506 | 76 | 0.868 | 131 | 0.916 | 207 | 0.899 | 8 | 0.750 | 6 | 1.000 | 14 | 0.857 |
| 9 | | | | | | | | | 2.355 | 4.686 | −3.810 | 1.755 | 81 | 0.926 | 140 | 0.886 | 221 | 0.900 | 9 | 0.667 | 8 | 1.000 | 17 | 0.824 |

## TABLE 4

NMH v. SFH comparisons. Logistic discriminant function coefficients and intercepts for nine equations, along with each equation's success rates for within sample and test group applications. A result >0 indicates NMH affiliation.

| | | | | | | | | | NMH | | sample SFH | | combined | | NMH | | test SFH | | combined | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **equation** | **LI2SS** | **LI1SS** | **UM2MC** | **LM1PS** | **LM2C7** | **LM1C7** | **intercept** | **std error** | **n** | **correct** | **n** | **correct** | **n** | **correct** | **n** | **correct** | **n** | **correct** | **n** | **correct** |
| 1 | 0.619 | 0.686 | −1.049 | 1.686 | −0.957 | −1.303 | −1.290 | 4.247 | 48 | 0.583 | 125 | 0.904 | 173 | 0.815 | 5 | 0.600 | 4 | 0.500 | 9 | 0.556 |
| 2 | | 1.082 | −1.117 | 1.641 | −0.969 | −1.325 | −1.030 | 2.831 | 49 | 0.571 | 126 | 0.897 | 175 | 0.806 | 5 | 0.600 | 4 | 0.500 | 9 | 0.556 |
| 3 | | | −1.106 | 1.773 | −0.899 | −1.187 | −0.397 | 2.154 | 49 | 0.490 | 128 | 0.898 | 177 | 0.785 | 6 | 0.333 | 5 | 0.800 | 11 | 0.545 |
| 4 | | | | 1.740 | −1.257 | −1.168 | −0.724 | 1.534 | 56 | 0.446 | 134 | 0.940 | 190 | 0.795 | 6 | 0.333 | 6 | 1.000 | 11 | 0.727 |
| 5 | | | | | −1.146 | −1.104 | −0.101 | 1.030 | 58 | 0.000 | 140 | 1.000 | 198 | 0.707 | 7 | 0.000 | 6 | 1.000 | 13 | 0.462 |

## TABLE 5

Dental morphology scores for an example individual.

| trait | score | trait | score |
|---|---|---|---|
| UI1DS | 0 | LI1SS | unobservable |
| UI2SS | 1 | LI2SS | 1 |
| UI2DS | 0 | LCDR | 0 |
| UCSS | 0 | LP3LC | 1 |
| UCDR | 1 | LM1AF | 0 |
| UCTD | 1 | LM1DW | 0 |
| UM1HC | 0 | LM1PS | 0 |
| UM1MC | 0 | LM1C7 | 0 |
| UM2MC | unobservable | LM2C5 | unobservable |
| UM2C5 | unobservable | LM2C7 | unobservable |