TECHNICAL NOTE

ANTHROPOLOGY

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Improving Nonmetric Sex Classification for Hispanic Individuals*

ABSTRACT: Current techniques used by forensic anthropologists for the identification of unknown human skeletal remains have largely been created using U.S. Black and White samples. When applied to Hispanics, these techniques perform poorly and can lead to misclassifications; consequently, there is an imperative need for population-specific standards for Hispanics. This research examines the classification accuracies obtained by the original Walker (Am J Phys Anthropol, 136, 2008) and Klales et al. (Am J Phys Anthropol, 149, 2012) methods for nonmetric sex estimation and provides recalibrated regression equations specifically for Hispanics. Ordinal data were collected for five skull and three pelvic traits from a sample of 54 modern Hispanic individuals. Recalibration of the Klales et al. equation improved accuracy (90.3% vs. 94.1%), while recalibration of the Walker method equation decreased accuracy (81.5% vs. 74.1%), but greatly improved sex bias (22.2% vs. −7.4%), thereby making the recalibrated equations more appropriate for use with Hispanics.

KEYWORDS: forensic science, forensic anthropology, Hispanics, border crossers, nonmetric traits, sex estimation, pelvis, skull

The term "Hispanic," as a defined group of peoples, is problematic from a forensic anthropological perspective for a number of reasons. Most importantly, because the term is applied to all Spanish-speaking groups regardless of geographic origin, the varied biological backgrounds of the populations in which the term encompasses are ignored (1). According to Spradley and colleagues (2), "the term Hispanic is a social construct with no precise genetic meaning and is defined by the U.S. Census Bureau as an individual originating from Mexico, Puerto Rico, Cuba, South or Central America, or other Hispanic/Latino origins." In the United States, individuals originating or descending from these varied regions are collectively referred to as "Hispanic" despite their vastly different population histories. The result is often difficulty identifying these individuals and increased misclassifications in forensic contexts (2).

There has been a marked increase in the number of Hispanic individuals illegally crossing the U.S.–Mexico border in the American Southwest, primarily through Texas, Arizona, and New Mexico. Increasing border security and implementation of several "operations" during the 1990s attempted to limit the number of individuals illegally entering the U.S. from the southern border. However, these measures did not stop illegal crossings from occurring, but instead caused illegal immigrants to seek more perilous routes into the U.S., often through dangerous desert terrain and stifling climates. The result has been an increased number of undocumented border crosser (UBC) deaths in the American Southwest due to heat-related illness. For a more in-depth discussion of the factors contributing to the rise in UBCs, see Anderson (3).

As forensic anthropologists, we are tasked with helping to identify UBCs that die during their journey. However, most of the techniques currently used in the identification of unknown individuals were created using U.S. Black and White populations. Spradley and colleagues (2) have shown that when some of these techniques are applied to Hispanic individuals, the performance of these methods is generally poor, indicating the need for population-specific standards for Hispanic individuals. The primary goals of this research were therefore to examine the classification accuracies obtained by the original Walker (4) and Klales et al. (5) methods for nonmetric skull and innominate sex estimation, and to present new logistic regression formulae that are more appropriate for Hispanic individuals than those equations provided by the original publications (4,5).

Materials and Methods

Skull and innominate data were collected from a sample (n = 61) of Hispanic individuals housed at the Forensic Anthropology Center at Texas State, Texas State University, San Marcos, TX. The majority of individuals (n = 44) are UBCs originating from the ongoing Operation Identification (ID) project. The goal of Operation ID is to identify UBCs through comprehensive skeletal analysis, DNA sampling, and personal effects to return these individuals to their families (6). The remaining individuals (n = 17) are from the Texas State University Donated Skeletal Collection or from local medical examiner's offices. Individuals within the donated collection are positively identified and therefore have known demographic information including sex and ancestry. The demographic information of the UBCs from Operation ID had to be inferred based on a number

of variables. Ancestry or geographic descent was based on information that was indicative of a migrant person, including clothing, associated personal effects, foreign currency, written documents, religious and cultural artifacts, and geographic location of the remains upon discovery. Metric analyses also indicated Hispanic or Guatemalan ancestry in a number of individuals ($n = 10$) using FORDISC software (7). Sex was determined via DNA for a portion of the individuals ($n = 13$). The remaining sex assignments were based on external genitalia (if present), FORDISC results, or from associated artifacts that were indicative of gender, which should be noted does not always correlate with biological sex; however, in some cases, it was the only information available to infer sex. In four cases, sex could not be reliably determined from any of the information available; therefore, these four individuals were excluded from all further analyses. Additionally, only individuals with all three skull traits required for Walker (4) equation 1 and all three innominate traits required for the Klales et al. (5) equation were used. Therefore, the final sample sizes were $n = 54$ for the Walker (4) method (27 females and 27 males) and $n = 51$ for the Klales et al. (5) method (25 females and 26 males).

The traits of each individual's skull and innominate were assigned ordinal scores by the primary author (ARK) based on the descriptions and illustrations found in Walker (4) and Klales et al. (5), respectively. The Walker's (4) skull traits include the nuchal crest (N), mental eminence (ME), glabella (G), supraorbital margin (SO), and the mastoid process (M). The Klales et al. (5) traits, modified from Phenice (8), include the ventral arc (VA), subpubic contour/concavity (SPC), and the medial aspect of the ischio-pubic ramus (MA). The left side of the skull and the left innominate were scored in accordance with the original publications; however, if the left side was missing or damaged, the right side was substituted. Side substitution occurred for two females and two males for the pelvis. Frequency distributions were calculated for each trait score by sex, and a chi-square test was used to test for significant differences in score frequencies between males and females.

Population-specific methods are typically preferred and recommended for sex estimation (9). When a new method is developed, and prior to applying it to groups other than those from which it was created, the external validity must be tested. According to Bracht and Glass (10), "to the extent and manner in which the results of an experiment can be generalized to different subjects, settings, experimenters, and, possibly, tests, the experiment possesses *external validity*." The goal is to determine whether the experimental method can be applied to a target population (i.e., all groups for which the method is being used). For sex estimation methods, external validation determines whether the method can be broadly applied to all groups, in this case all populations of males and females, or whether the method must be recalibrated to include population-specific applications. To determine this, external validation studies must be carried out using different population groups and different observers. The original Phenice (8) method has been externally validated nearly a dozen times in the last 45 years. The results have been mixed with some validations proving the method provides accurate estimations in different populations, while others found much lower accuracy rates than originally presented by Phenice (8) (see (5) for a full discussion). More recently, the Walker (4) and Klales et al. (5) methods have been validated as well (11–13). When a particular method performs poorly during external validation (i.e., the original method cannot be generalized beyond the samples and parameters from which it was created), the method

should be recalibrated to include population-specific parameters. For both the Walker (4) and Klales et al. (5) methods, recalibration can be accomplished through the creation of new sample-specific equations that can be applied to a specific population. The sex prediction model can be improved by recalibrating the predictor (i.e., trait) coefficients and the constant, thereby making the methods population specific, in this case ancestrally and temporally specific.

For this research, the external validity (i.e., accuracy) of the original methods was tested on a sample comprised of a different ancestral group (Hispanic), and in some cases a different temporal period (i.e., modern), than the original samples from which the two methods were initially created. The scores for each individual were first entered into the original discriminant function equation provided by Walker (4) and the original logistic regression equation provided by Klales et al. (5) to test their external validity for this sample of modern Hispanic individuals. Classification accuracy using Walker (4) was tested based on his first equation (equation 1, table 9 in (4)), which Walker recommends using based on its high classification accuracy (87.4% combined sexes) and low sex bias (2.0%). This equation utilizes only glabella, the mastoid, and the mental eminence [(G × −1.375) + (M × −1.185) + (ME × −1.151) + 9.128]. Classification accuracy using the Klales et al. (5) method was based on the equation 2.726 (VA) + 1.214 (MA) + 1.073 (SPC) − 16.312. Next, the equations were recalibrated to generate population-specific regression formulae for modern Hispanics, as both original publications provide equations developed using only individuals of European/White and African/Black descent that are mostly from historic time periods. Classification accuracies between the validation and recalibration tests were compared to determine whether population-specific formulae are more appropriate for Hispanic individuals or whether the original methods performed well enough to be used (i.e., are externally valid). All calculations were completed with SPSS (14) and Microsoft Excel software (15).

Results and Discussion

Frequencies

Frequency distributions for the traits of the skull and innominate are presented in Figs 1 and 2. Males and females differed significantly in score frequencies for all traits at the $p < 0.05$
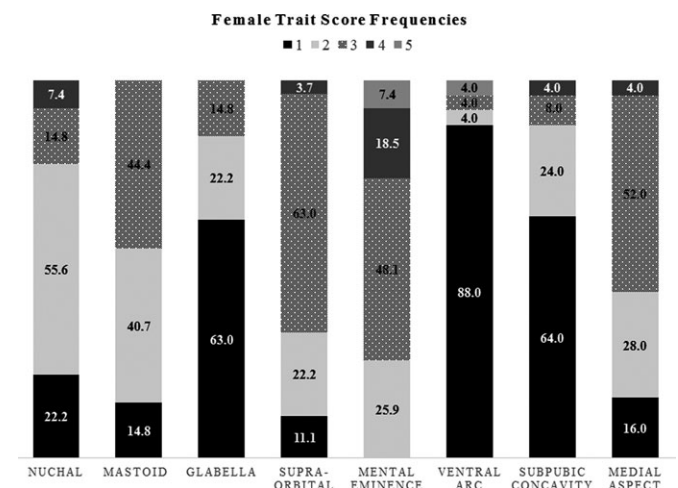

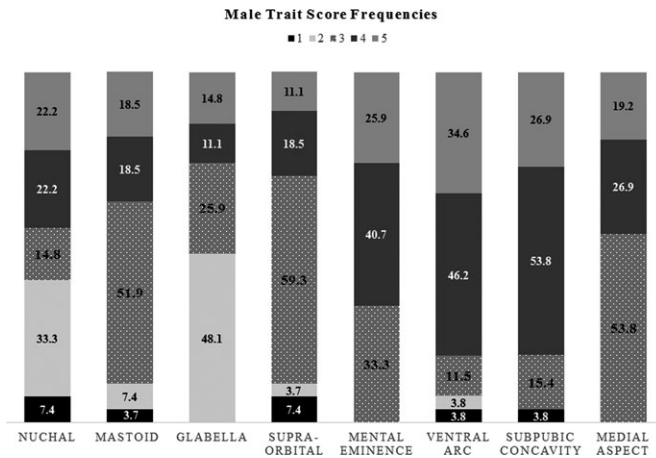FIG. 1—*Female score frequencies (%) for each trait.*

FIG. 2—*Male score frequencies (%) for each trait.*

level. For the skull, males were more variable than females in score frequency for all traits except the ME. Females were predominantly assigned scores of one, two, or three for the N, M, and G, while scores of either two or three were most often assigned to females for the SO and ME. No females scored above a three for M or G. The males received variable scores for N, with the majority of individuals receiving a score of two. Most males also scored a two for G, three for M and SO, and four for ME. No males scored a one for G, and no males scored a one or two for ME. With regard to the innominates, males were again more variable than females in score frequency for all traits except the MA. Females overwhelmingly were assigned a score of one for the VA and SPC, while a score of three was most often assigned for the MA. Males were most often assigned scores of four or five for the VA and SPC. As was the case for females, a score of three was most often assigned to males for the MA and no males scored below a three for this trait.

Validation

Using the Klales et al. (5) method, only one of the 25 females misclassified as male (96.0% accuracy) (Tables 1 and 2). This misclassified individual was very young. The iliac crest was not completely fused, nor was the epiphysis along the ischio-pubic ramus, which suggests an age range of less than 23 years (16). Of the 24 females that classified correctly, one classified as female with only a 78.1% probability. The remaining 23 females classified correctly with high probabilities (>99.9%). Of the 26 males, four misclassified as female (84.6% accuracy) (Tables 1 and 2). One of these four individuals misclassified as female with a probability of 55.0%, which is essentially chance. The remaining three individuals misclassified as female with probabilities greater than 78.1%. Of the 22 individuals that correctly classified as male, three did so with a probability of only 81.0% and one did so with a probability of only 73.4%. The remaining 18 individuals correctly classified as male with high probabilities (>92.6%). Overall accuracy for combined sexes using the Klales et al. (5) method was 90.3%. The disparity in classification accuracy between males and females indicates a sex bias in favor of females (−11.4%).

Using the Walker (4) method, eight of the 27 females misclassified as male (70.4% accuracy) (Tables 1 and 3). Of the eight females that incorrectly classified as male, seven classified as male with probabilities >85.0%, while one classified as male

with a probability of 65.0%. Of the 19 females that correctly classified, 14 classified as female with probabilities >86.0%, while five classified as female with probabilities only around 65.0%. Of the 27 males, only two misclassified as females (92.6% accuracy) (Tables 1 and 3). Of the two males that were incorrectly classified, one classified as female with a probability of 85% and one classified as female with a probability of 64.0%. Of the 25 males that correctly classified, 19 classified as male with probabilities >85.0%, while six classified as male with probabilities only around 65.0%. The disparity in classification accuracy between males and females indicates a high sex bias (22.2%) in favor of males.

Recalibration

The classification accuracy for combined sexes using the Klales et al. (5) method increased from 90.3% to 94.1% when using all three traits and recalibrating the logistic regression equation based on this sample of Hispanic individuals (Table 2). The sex bias decreased by over half, and males instead of females are favored using the recalibrated equation (−11.4% vs. 4.2%). Classification accuracies for each trait and each trait combination are presented in Table 4. Individually, accuracy was highest using the SPC (92.5%) followed by the VA (92.3%); however, the higher sex bias of the SPC suggests that the VA is the more appropriate trait to use of the two when only one trait is considered. The low classification accuracy of the MA (73.1%) combined with an incredibly high sex bias (−56.0%) indicates that this trait should not be used alone. With regard to trait combinations, accuracy was highest using all three traits (94.1%) and the VA/SPC combined (94.2%). Combination of the VA and the MA gives a classification accuracy somewhat lower than the VA/SPC/MA and VA/SPC combinations (92.2% vs. 94.1/94.2%), but with a lower sex bias (0.3%). Overall, each trait and each trait combination, with the exception of the MA, produces high classification accuracy (over 92.0%) and low sex bias (≤ 8.3%).

The results obtained in the current study are similar to the results of the original study by Klales et al. (5). In the original publication, the VA and SPC were found to perform well individually (88.5% and 86.6% accuracy), while the MA performed poorly (75.8%). When only two traits are considered, the combination of the VA and SPC gave the highest classification accuracy (93.5%) and lowest sex bias (4.8%) in the original study and in the present research. The combination of all three traits was found to give the best results due to even higher classification accuracy (95.5%) and low sex bias (7.0%) in the original study. In the current study, accuracy for all three traits was comparable at 94.1% using the recalibrated equation and sex bias was lower at 4.2%. Like the original study, the authors of this research recommend using all three traits in combination for Hispanics due to their high classification accuracy and low sex bias.

The classification accuracy for combined sexes using the Walker (4) method decreased by 7.4% when recalibrating Walker (4) equation 1 (81.5% vs. 74.1%); however, sex bias was considerably lower (22.2% vs. −7.4%) with females instead of males being favored (Table 3). Classification accuracy for each trait and each trait combination is presented in Table 5. With regard to individual traits, classification accuracy was highest for the M (72.2%), but with an incredibly high sex bias (33.3%). Accuracy was second highest for the ME (70.4%), which notably had the lowest sex bias relative to the other traits (−7.4%). This is interesting considering several studies have

TABLE 1—*Validation classification accuracy for each individual in the sample using the Walker (4) and Klales et al. (5) methods. The probability of being female (F) and male (M) is provided, as is the final sex classification using the method. Bolded sexes indicated individuals that were misclassified. Missing values indicate that the individual did not have all traits present to be scored.*

Specimen	Sex	Walker method			Klales et al. method		
		Prob F	Prob M	Classification	Prob F	Prob M	Classification
1	Female	0.96	0.04	Female	1.00	0.00	Female
2	Female	0.64	0.36	Female	1.00	0.00	Female
3	Female	0.87	0.13	Female			
4	Female	0.96	0.04	Female	1.00	0.00	Female
5	Female	0.96	0.04	Female	1.00	0.00	Female
6	Female	0.14	0.86	**Male**	1.00	0.00	Female
7	Female	0.87	0.13	Female	1.00	0.00	Female
8	Female	0.04	0.96	**Male**	1.00	0.00	Female
9	Female	0.14	0.86	**Male**	1.00	0.00	Female
10	Female	0.64	0.36	Female	1.00	0.00	Female
11	Female	0.96	0.04	Female	1.00	0.00	Female
12	Female				0.10	0.90	Female
13	Female	0.87	0.13	Female	1.00	0.00	Female
14	Female	0.63	0.37	Female	1.00	0.00	Female
15	Female	0.87	0.13	Female	1.00	0.00	Female
16	Female	0.87	0.13	Female	1.00	0.00	Female
17	Female	0.69	0.31	Female			
18	Female	0.12	0.88	**Male**	1.00	0.00	Female
19	Female	0.87	0.13	Female	1.00	0.00	Female
20	Female	0.12	0.88	**Male**	1.00	0.00	Female
21	Female	0.01	0.99	**Male**	0.01	0.99	**Male**
22	Female	0.96	0.04	Female	1.00	0.00	Female
23	Female	0.69	0.31	Female	1.00	0.00	Female
24	Female	0.35	0.65	**Male**	1.00	0.00	Female
25	Female	0.17	0.83	**Male**	0.78	0.22	Female
26	Female	0.87	0.13	Female			
27	Female	0.87	0.13	Female	1.00	0.00	Female
28	Female	0.99	0.01	Female	1.00	0.00	Female
29	Male	0.00	1.00	Male	0.00	1.00	Male
30	Male	0.00	1.00	Male	0.19	0.81	Male
31	Male	0.35	0.65	Male	0.01	0.99	Male
32	Male	0.35	0.65	Male			
33	Male	0.02	0.98	Male	0.95	0.05	**Female**
34	Male	0.02	0.98	Male	0.01	0.99	Male
35	Male	0.00	1.00	Male	0.55	0.45	**Female**
36	Male	0.01	0.99	Male	0.07	0.93	Male
37	Male	0.00	1.00	Male	0.00	1.00	Male
38	Male	0.14	0.86	Male	0.07	0.93	Male
39	Male	0.35	0.65	Male	0.00	1.00	Male
40	Male	0.14	0.86	Male	0.07	0.93	Male
41	Male	0.35	0.65	Male	0.00	1.00	Male
42	Male	0.00	1.00	Male	0.19	0.81	Male
43	Male	0.00	1.00	Male	0.78	0.22	**Female**
44	Male	0.00	1.00	Male	0.27	0.73	Male
45	Male	0.00	1.00	Male	0.02	0.98	Male
46	Male	0.14	0.86	Male	0.19	0.81	Male
47	Male	0.00	1.00	Male	0.07	0.93	Male
48	Male	0.36	0.64	Male	0.01	0.99	Male
49	Male	0.64	0.36	**Female**	1.00	0.00	**Female**
50	Male	0.35	0.65	Male	0.00	1.00	Male
51	Male	0.01	0.99	Male	0.00	1.00	Male
52	Male	0.85	0.15	**Female**	0.00	1.00	Male
53	Male	0.01	0.99	**Female**	0.00	1.00	Male
54	Male	0.04	0.96	**Female**	0.07	0.93	Male
55	Male	0.04	0.96	**Female**	0.02	0.98	Male

shown the ME to perform poorly compared to the other Walker (4) traits, especially when compared to the M and G (12,13). In the current study, G achieved a classification accuracy of 68.5% with an extremely high sex bias of −33.3%. The N also achieved a classification accuracy of 68.5% with a high sex bias (−18.5%). The SO achieved the lowest classification accuracy (61.1%) and the highest sex bias (55.6%). With regard to trait combinations, the vast majority of accuracies fell between 70.0%

and 80.0%. Exceptions to this include the N/G/ME/SO and N/G/ME/M/SO combinations, which achieved classification accuracies of 81.5% with no sex bias (0.0%).

In the current study, none of the Walker (4) traits or trait combinations achieved a classification accuracy that approaches those reported by Walker (4) or that meets the minimum threshold of 85% for adult sex estimation according to DiGangi and Moore (17). In the original publication, G obtained the highest

TABLE 2—*Classification accuracy and sex bias (%) using the innominate traits.*

	Males	Females	Combined	Sex Bias
Validation*	84.6	96.0	90.3	−11.4
Recalibration[†]	96.2	92.0	94.1	4.2

*Using the original Klales et al. (5) logistic regression equation and all three traits.

[†]Using the recalibrated logistic regression equation and all three traits.

TABLE 3—*Classification accuracy and sex bias (%) using the skull traits.*

	Males	Females	Combined	Sex Bias
Validation*	92.6	70.4	81.5	22.2
Recalibration[†]	70.4	77.8	74.1	−7.4

*Using the original Walker (4) discriminant equation 1 and three traits.
[†]Using the recalibrated regression equation and three traits.

combined classification accuracy (82.6%) with a fairly low sex bias (3.4%); however, in the present study, G had the second lowest classification accuracy (68.5%) and had an incredibly high sex bias (−33.0%). The classification accuracy for M was second highest (78.6%) with nearly no sex bias (0.1%) in Walker (4), but performed best in the present research albeit with a high sex bias. As was the case in the current study, the SO achieved the lowest classification accuracy in the original study (68.8%) but with a significantly lower sex bias than in the current study (1.7% vs. 55.5%). With regard to trait combinations, Walker (4) only reports classification accuracies using logistic regression for certain trait combinations (G/M, G/M/ME, SO/G/N/M, and SO/G/N/M/ME), thereby making direct comparison difficult. As mentioned previously, Walker (4) recommends using his equation 1, which utilizes the combination of G/M/ME, based on its high combined sex classification accuracy (87.5%) and low sex bias (2.0%). However, in the current study, the G/M/ME combination achieved a classification accuracy of only 74.1%. Because the N/G/ME/SO and N/G/ME/M/SO combinations achieved the highest classification accuracies in the current study (81.5%) with no sex bias, the authors recommend using either of these combinations for Hispanics.

In conclusion, classification accuracy and sex bias improved for the innominate when using the recalibrated equations specifically for Hispanic individuals. These results are not surprising given that similar results were obtained in another study using modern South African, Thai, and U.S. samples (13). Classification accuracies were high for all groups except the Thai (75.9%) when using the original Klales et al. (5) equation, but in all three of these groups, the authors found that classification accuracies increased when applying population-specific equations rather than the original equations from the study by Klales et al. (5). Interestingly, the skull recalibration decreased overall accuracy in the current study; however, absolute sex bias was reduced by 14.8%, thereby making the recalibrated equation more appropriate for use with modern Hispanics. Although the recalibrated equation performed worse, the original equation achieved a classification accuracy of only 81.5%, which is much lower than the accuracy achieved by Walker (4) in his original study using European Americans, African Americans, and English (87.5%). Although Walker (4) cautioned against using his method on populations different than those from which it was developed, others have failed to achieve the classification accuracy cited by Walker (4). Lewis and Garvin (11) tested Walker's (4) method using a U.S. sample representative of that used in the original publication, so as to more directly test the accuracy of the Walker's (4) method without adding confounding factors, such as secular change, which could affect results. Accuracy rates ranged from 13.3% to 96.6% depending on the experience of the observer, trial number, sex, ancestry, and equation utilized. The majority of their accuracy rates fell between 70.0% and 80.0% for equation 1. Lewis and Garvin (11) suggest that the lower accuracy rates may be attributed to the difficulty in scoring the ME due to the ambiguity of how to score this trait. Garvin et al. (12) have also discussed the difficulty with scoring the ME and how this can affect classification accuracy and interobserver agreement.

The disparate results between the classification accuracies of the innominate and skull in the current study indicate that the innominate displays a much higher degree of sexual dimorphism compared with the skull in this group of Hispanic individuals. These findings are not surprising given that the pelvis has long been considered the single best indicator of sex from the skeleton. The classification accuracies using the original and recalibrated Walker's (4) equations are discouraging and fall below the 85% classification accuracy threshold for use in adult sex estimation (17). The authors suggest giving more weight to the innominate traits than the skull traits when estimating sex in Hispanic individuals and perhaps excluding the cranial traits altogether unless the skull is all that is available for analysis. Best et al. (18) demonstrated that there is no significant relationship between the sexual dimorphism of the skull and pelvis regardless of whether size or shape is analyzed; therefore, it stands to reason that the analyst should utilize the bones that are most sexually dimorphic in the population being analyzed—in this case, the innominates.

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TABLE 4—*Classification accuracy (%) by innominate trait/trait combinations using recalibration logistic regression equations.*

Variable	Male	Female	Combined	Sex Bias	Equation
VA	92.3	92.3	92.3	0.0	$1.722(VA) - 4.336$
SPC	96.3	88.5	92.5	7.8	$2.113(SPC) - 5.855$
MA	100.0	44.0	73.1	−56.0	$2.724(MA) - 8.164$
VA SPC	96.2	92.3	94.2	3.9	$0.800(VA) + 1.262(SPC) - 5.536$
VA MA	92.3	92.0	92.2	0.3	$1.427(VA) + 1.656(MA) - 8.619$
SPC MA	96.3	88.0	92.3	8.3	$1.838(SPC) + 1.116(MA) - 8.513$
VA SPC MA	92.2	92.0	94.1	4.2	$0.807(VA) + 0.972(SPC) + 1.282(MA) - 8.641$

TABLE 5—*Classification accuracy (%) by skull trait/trait combinations using recalibration logistic regression equations.*

Variable	Male	Female	Combined	Sex Bias	Equation
SO	88.9	33.3	61.1	55.6	$0.914(SO) - 2.662$
M	88.9	55.6	72.2	33.3	$1.656(M) - 4.676$
ME	66.7	74.1	70.4	−7.4	$1.222(ME) - 4.261$
N	59.3	77.8	68.5	−18.5	$0.906(N) - 2.327$
G	51.9	85.2	68.5	−33.3	$1.836(G) - 3.824$
N M	66.7	81.5	74.1	−14.8	$0.543(N) + 1.411(M) - 5.404$
N G	74.1	74.1	74.1	0.0	$0.604(N) + 1.638(G) - 5.013$
N ME	74.1	74.1	74.1	0.0	$0.650(N) + 0.914(ME) - 4.867$
N SO	70.4	77.8	74.1	−7.4	$0.883(N) + 0.885(SO) - 4.868$
M G	63.0	85.2	74.1	−22.2	$0.888(M) + 1.342(G) - 5.362$
M ME	70.4	81.5	75.9	−11.1	$1.384(M) + 0.787(ME) - 6.649$
M SO	81.5	63.0	72.2	18.5	$1.511(M) + 0.637(SO) - 6.122$
G ME	70.4	77.8	74.1	−7.4	$1.591(G) + 0.497(ME) - 5.040$
G SO	63.0	88.9	75.9	−25.9	$1.990(G) + 1.117(SO) - 7.397$
SO ME	70.4	70.4	70.4	0.0	$1.008(SO) + 1.301(ME) - 7.437$
N M G	77.8	74.1	75.9	3.7	$0.503(N) + 0.725(M) + 1.302(G) - 6.161$
N M ME	81.5	77.8	79.6	3.7	$0.395(N) + 1.236(M) 0.649(ME) - 6.794$
N G SO	81.5	77.8	79.6	3.7	$0.636(N) + 1.829(G) + 1.189(SO) - 8.985$
N ME SO	74.1	74.1	74.1	0.0	$0.572(N) + 0.942(ME) + 0.894(SO) - 7.366$
N G ME	70.4	77.8	74.1	−7.4	$0.558(N) + 1.546(G) + 0.229(ME) - 5.498$
G M ME	70.4	77.8	74.1	−7.4	$1.217(G) + 0.832(M) + 0.292(ME) - 5.946$
G M SO	85.2	74.1	79.6	11.1	$1.600(G) + 0.643(M) + 1.057(SO) - 8.266$
ME M SO	70.4	77.8	74.1	−7.4	$0.876(ME) + 1.217(M) + 0.783(SO) - 8.757$
N M G ME	77.8	74.1	75.9	3.7	$0.457(N) + 0.709(M) + 1.269(G) + 0.087(ME) - 6.305$
N M G SO	81.5	77.8	79.6	3.7	$0.564(N) + 0.323(M) + 1.655(G) + 1.127(SO) - 9.196$
N G ME SO	81.5	81.5	81.5	0.0	$0.580(N) + 1.750(G) + 0.222(ME) + 1.211(SO) - 9.507$
M G ME SO	74.1	81.5	77.8	−7.4	$0.552(M) + 1.462(G) + 0.457(ME) + 1.180(SO) - 9.641$
N G ME M SO	81.5	81.5	81.5	0.0	$0.525(N) + 1.607(G) + 0.175(ME) + 0.296(M) + 1.153(SO) - 9.595$

Using the data and results from these analyses, a free, interactive morphological database will be developed where practitioners can enter, analyze, and compare morphological traits from unknown human skeletal remains to a large modern sample with known demographic data. This will allow sex estimations to be more easily and accurately made in a manner compliant with *Daubert* (19). The database will be available in the fall of 2017 and will include the data from the research presented here.

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