

ANTHROPOLOGY

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The Optimized Summed Scored Attributes Method for the Classification of U.S. Blacks and Whites: A Validation Study*

ABSTRACT: Recently, Hefner and Ousley (2014) introduced the optimized summed scored attributes (OSSA) method that maximizes between-group differences in U.S. black and white populations by dichotomizing six cranial morphoscopic trait scores. This study tests OSSA using an independent skeletal sample (Hamann-Todd, $n = 208$) and positively identified forensic cases (Mercyhurst University, $n = 28$, and New York City Office of Chief Medical Examiner, $n = 38$). An evaluation of trait frequencies suggests shifting the heuristically selected sectioning point separating U.S. black and white populations from ≤ 3 to ≤ 4 . We found a total correct classification of 73.0% (B = 50.9%, W = 89.2%) using the originally suggested sectioning point of ≤ 3 , while the total correct classification increases to 79.2% (B = 80.2%, W = 78.5%) with a modified sectioning point of ≤ 4 . With the increased total correct classification and reduced classification bias between ancestry groups, we suggest the modified sectioning point of ≤ 4 be used when assessing ancestry in forensic unknowns.

KEYWORDS: forensic science, forensic anthropology, validation study, biological profile, ancestry estimation, optimized summed scored attributes

Introduction

Ancestry estimation is essential in the generation of an unknown person's biological profile (age, sex, stature, ancestry). Nonmetric traits have been pervasive in their use within the field of forensic anthropology and are continually used in active cases and in research (1). Recent work examining the 'gestalt' approach to ancestry estimation (2) shows that split decisions by researchers concerning the demographic information of an individual are established within seconds upon first viewing the cranium. Thus, initial impressions, based upon past experiences, bias the researcher either consciously or subconsciously. The aforementioned impressions are generally the product of a typology-based training and education, which has been ubiquitously taught in forensic anthropology (c.f. 3–5).

As a means to standardize the typological approach, Hefner (6) consolidated the various typological character lists into 11

traits, either binary or expanded into ordinal character states, to more adequately capture the range of normal human variation. Once the traits were standardized, Hefner (6) concluded that the traits could be used within a statistical framework to classify unknown individuals and thus provide a method that was *Daubert* (7) compliant and therefore admissible in court. Hefner (6) reported correct classifications ranging from 84 to 93% depending on the traits and statistical classification method utilized in the analysis. More recently, Hefner and Ousley (8) utilized a myriad of classification statistics to place the morphoscopic traits within a *Daubert* compliant framework. Hefner and Ousley (8) reported total correct classifications ranging from 66.4 to 87.8% across three ancestral groups (U.S. blacks, Hispanics, and whites). Of note, Hefner and Ousley (8) introduced a novel technique termed the optimized summed scored attributes (OSSA) method in which six traits (ANS, INA, IOB, NAW, NBC, and PBD) were recorded and then converted into dichotomous variables of 0 or 1 to estimate ancestry between U.S. blacks and whites (Table 1). The dichotomy of the variables was based on heuristically selected sectioning points derived from the frequency distributions of each trait in order to maximize group separation. The sectioning points to dichotomize the character states are available in Hefner and Ousley (8). Essentially, the summed OSSA scores can range from 0 to 6 with 3 or below corresponding to black ancestry and 4 and above to white ancestry.

Previously, the two primary authors (ARK and MWK) performed a variety of classification statistics on the Hefner (6) morphoscopic traits on an independent sample with total correct classifications between U.S. blacks and whites ranging from 73.3 to 86.6% depending on the trait combination and statistical method (9). These aforementioned results were comparable to

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TABLE 1—Trait names and abbreviations used for the OSSA method from Hefner and Ousley (8).

Trait	Abbreviation
Anterior Nasal Spine	ANS
Inferior Nasal Aperture	INA
Interorbital Breadth	IOB
Nasal Aperture Width	NAW
Nasal Bone Contour	NBC
Postbregmatic Depression	PBD

those attained by Hefner (6). Klates and Kenyhercz (9) also tested interobserver agreement between two observers experienced with the Hefner (6) traits. Of the six traits included in the OSSA method by Hefner and Ousley (8), three were found to have moderate agreement (IOB, NAW, PBD), one had fair agreement (INA), and two had slight agreement (ANS, NBC) when tested by Klates and Kenyhercz (9) using Cohen’s kappa.

The OSSA method is currently being used for active forensic casework in the United States, likely because of two main benefits of the method. First, standardized illustrations and descriptions capture the range of variation for traits commonly used in ancestry estimation, while avoiding the old typological approach. Second, the method relies on only a few traits and is quick and easy to use. The aim of the current study is to test the OSSA method on an independent skeletal sample and on positively identified forensic cases from U.S. blacks and whites.

Materials and Methods

The dataset is comprised of 274 U.S. black (B) and white (W) crania (Table 2). Data were obtained from a known historic

TABLE 2—Sample demographics by institution

Ancestry/Sex Group	Collection			Total
	HTH	DAFS	OCME	
Black Females (BF)	52	5	4	61
White Females (WF)	54	7	9	70
Black Males (BM)	50	0	6	56
White Males (WM)	52	16	19	87

HTH, Hamann-Todd Osteological Collection at the Cleveland Museum of Natural History; DAFS, The Department of Applied Forensic Sciences at Mercyhurst University; OCME, The Office of Chief Medical Examiner in New York City

TABLE 3—Trait frequencies by ancestral group and sample (%).

	ANS						INA						IOB									
	1		2		3		1		2		3		4		5		1		2		3	
	B	W	B	W	B	W	B	W	B	W	B	W	B	W	B	W	B	W	B	W	B	W
HTH	17.8	7.5	54.5	49.5	27.7	43.0	10.9	1.9	27.7	5.6	40.6	27.1	15.8	48.6	4.9	16.8	15.8	43.9	34.6	39.3	48.5	16.8
Forensic	40.0	7.8	46.7	27.5	13.3	64.7	20.0	0.0	20.0	0.0	40.0	5.9	20.0	45.1	0.0	49.0	13.3	37.3	33.3	58.8	53.4	3.9
Pooled	20.7	7.6	53.4	42.4	25.9	50.0	12.1	1.3	26.7	3.8	40.5	20.2	16.4	47.5	4.3	27.2	15.5	41.8	35.3	45.6	49.1	12.7
	NAW						NBC						PBD									
	1		2		3		0		1		2		3		4		0		1			
	B	W	B	W	B	W	B	W	B	W	B	W	B	W	B	W	B	W	B	W		
HTH	2.0	27.1	51.5	58.9	46.5	14.0	7.9	0.9	17.8	13.1	5.9	0.0	26.7	52.3	41.6	33.6	26.7	52.3	41.6	33.6		
Forensic	13.3	54.9	60.0	45.1	26.7	0.0	53.3	0.0	6.7	7.8	6.7	9.8	20.0	58.8	13.3	23.6	80.0	94.1	20.0	5.9		
Pooled	3.4	36.1	52.6	54.5	44.0	9.5	13.8	0.6	16.4	11.4	6.0	3.2	25.9	54.4	37.9	30.4	53.4	72.8	46.6	27.2		

sample, as well as positively identified modern forensic cases. The historic sample is comprised of 208 individuals from the Hamann-Todd Osteological Collection (HTH) (see Klales and Kenyhercz (9) for a full discussion of the sample). The modern, forensic sample is comprised of 66 individuals from the Department of Applied Forensic Sciences (DAFS) at Mercyhurst University and the New York City Office of Chief Medical Examiner (OCME) (Table 2). As per DAFS standard operating procedures, OSSA traits have been scored on each forensic case since 2008, while the OCME has routinely scored OSSA traits since 2009. Part of the OCME sample includes cases prior to 2009 that were scored post hoc from detailed photographs of the skull. It should be noted that there is no research to the authors’ knowledge that tests the reliability of scoring the OSSA traits from photographs. However, the author who scored the OCME cases (CWR) omitted any case in which he could not confidently score all six traits.

Hefner (6) concluded that there were no significant differences between sexes within the same ancestral group and that they can be pooled to increase sample sizes. In accordance with the original study, sexes were pooled for the following analyses. The six traits used in OSSA (Table 1) were scored in accordance with Hefner (6) and converted to their dichotomous OSSA scores following Hefner and Ousley (8). Trait frequencies were tabulated for each trait, as was the resulting summed OSSA score by group. Lastly, the OSSA sectioning point was heuristically adjusted to 4 to examine the effects on total correct classification.

Results

Trait Frequencies

The trait frequencies for the pooled forensic samples (DAFS, OCME) and the HTH sample are tabulated by ancestral group in Table 3. Figures 1 and 2 show the frequency of trait expression between the pooled forensic samples and the historic HTH sample by ancestral group. For ANS, the HTH sample has the same medians for blacks and whites at score 2, while the forensic sample shows a higher median and frequency of a score 3 for whites, while blacks remains at a score 2. The medians of the INA scores between samples remained consistent; however, whites show greater overall scores in the forensic sample as compared to the HTH. Similar to ANS, both groups in the HTH

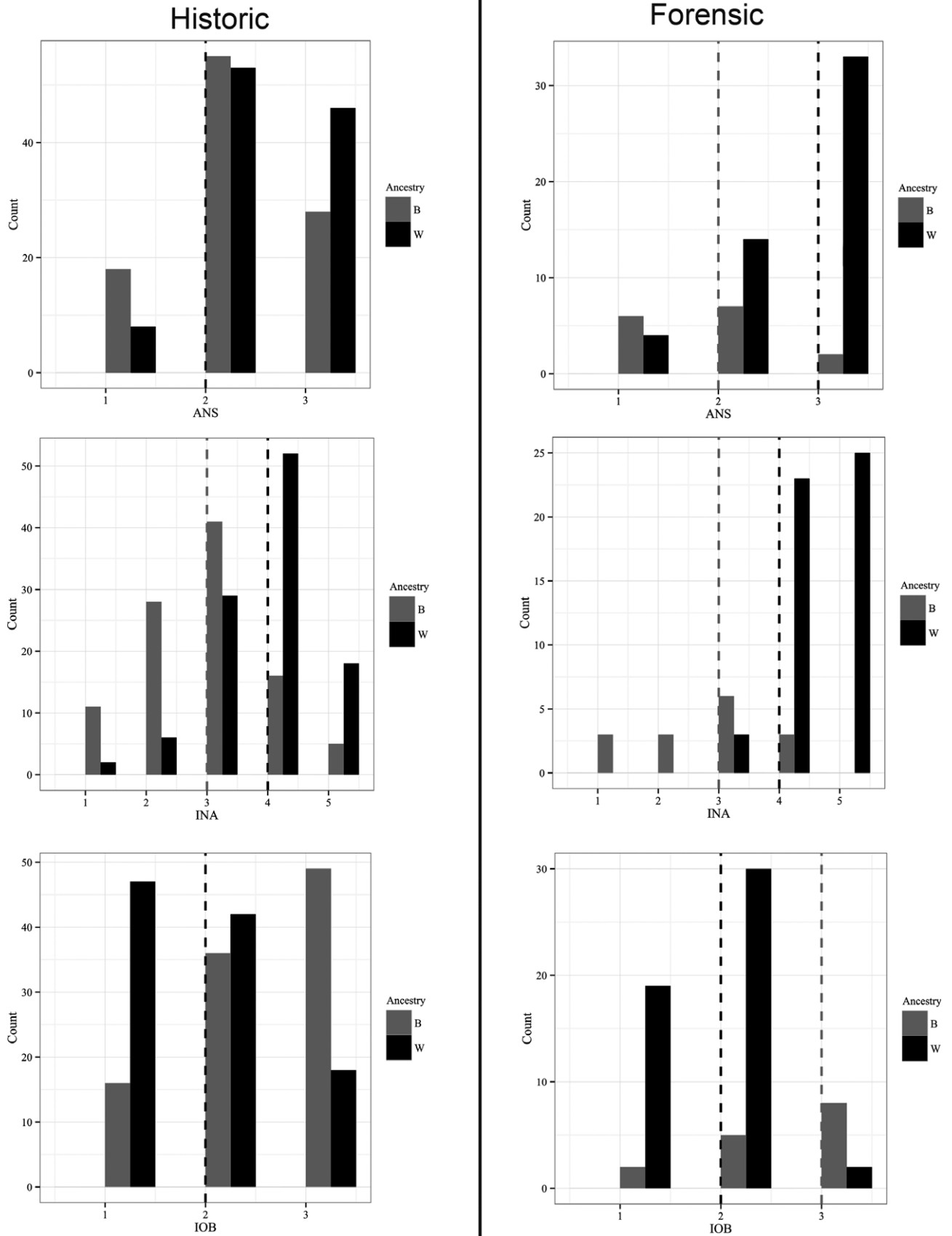


FIG. 1—Distribution of trait scores and the medians (dotted line) for the historic (HTH) and modern (forensic) samples. Note: If only one dotted line is present, the median for each ancestral group is the same.

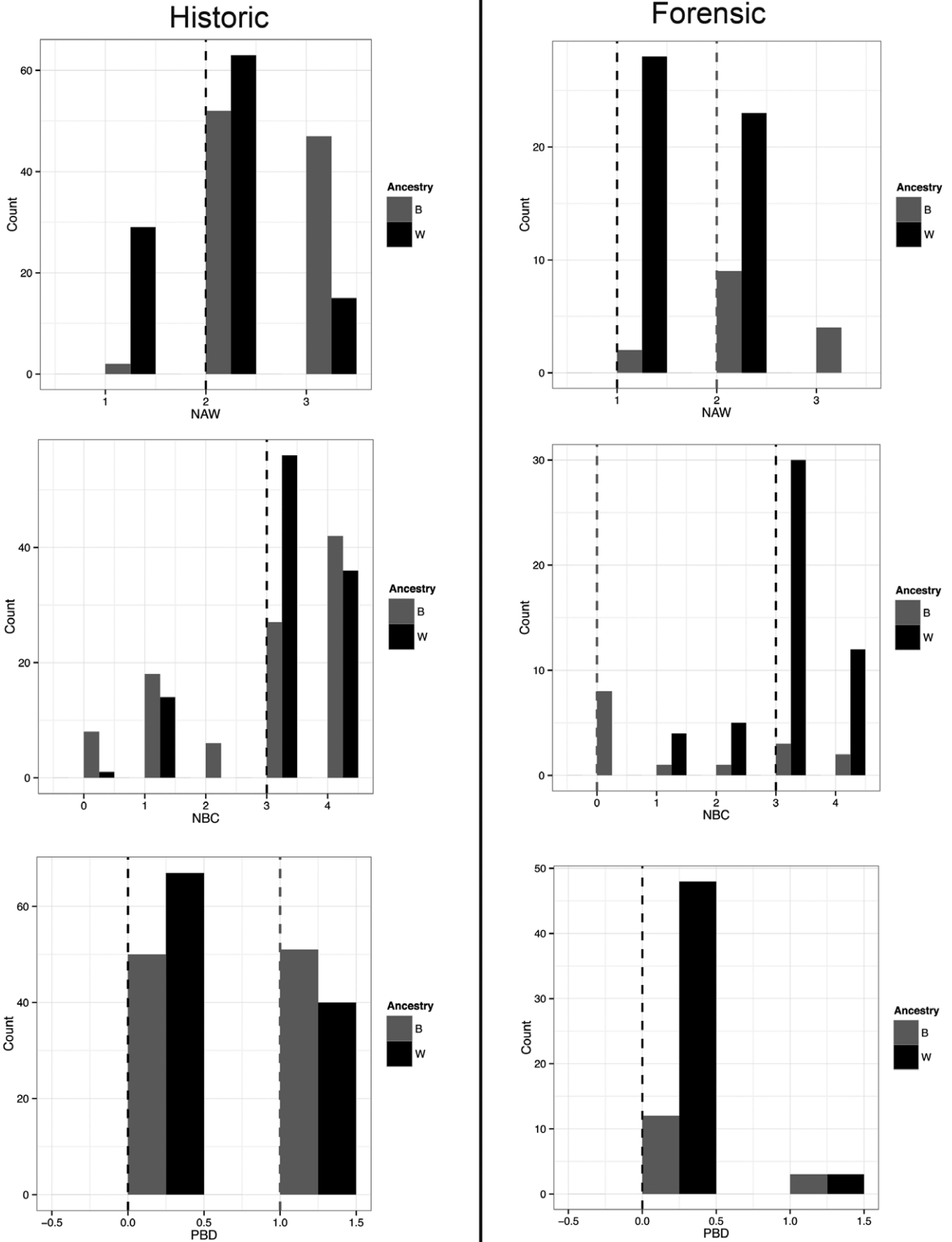


FIG. 2—Distribution of trait scores and the medians (dotted line) for the historic (HTH) and modern (forensic) samples continued. Note: If only one dotted line is present, the median for each ancestral group is the same.

sample have the same IOB median, while there is a divergence in the forensic sample. Specifically, the black median IOB increased to score 3, while the white median remained at score 2. The HTH sample’s distribution of NAW scores is comparable between groups, with each group’s median centering on a score 2. However, in the forensic sample, NAW scores for whites shifted lower with a median of score 1, and blacks remained at score 2. Notably, the NBC scores for the HTH sample were both 3, while the forensic sample sees a shift in blacks to a median score 0. The PBD of the HTH sample shows whites as having a median of 0 and blacks with a median of score 1, although in the forensic sample, both blacks and whites have a median score of 0, with very few instances of a score of 1 in either group.

Lastly, the HTH sample’s OSSA scores show blacks with a median of score 3 and whites with a median of score 5, while, in the forensic sample, the median for blacks remains at 3 and the median for whites shifts to score 6 (Table 4 and Fig. 3).

Classification

The HTH collection achieves a total correct classification of 68.3% (B = 50.5%, W = 85.0%) using the Hefner and Ousley (8) suggested OSSA sectioning point of ≤ 3 (Table 5). Shifting the sectioning point heuristically to ≤ 4 improves total correct classification of the HTH sample to 77.9% (B = 80.2%, W = 69.2%) and considerably reduces bias between ancestry

TABLE 4—OSSA score frequencies by ancestral group and sample (%).

	OSSA Score													
	0		1		2		3		4		5		6	
	B	W	B	W	B	W	B	W	B	W	B	W	B	W
HTH	4.0	0.0	3.0	0.9	22.8	3.7	20.8	10.3	29.7	15.9	16.8	42.1	3.0	27.1
Forensic	6.7	0.0	13.3	0.0	20.0	0.0	13.3	2.0	26.7	0.0	0.0	25.5	20.0	72.5
Pooled	4.3	0.0	4.3	0.6	22.4	2.5	19.8	7.6	29.3	10.8	14.7	36.7	5.2	41.8

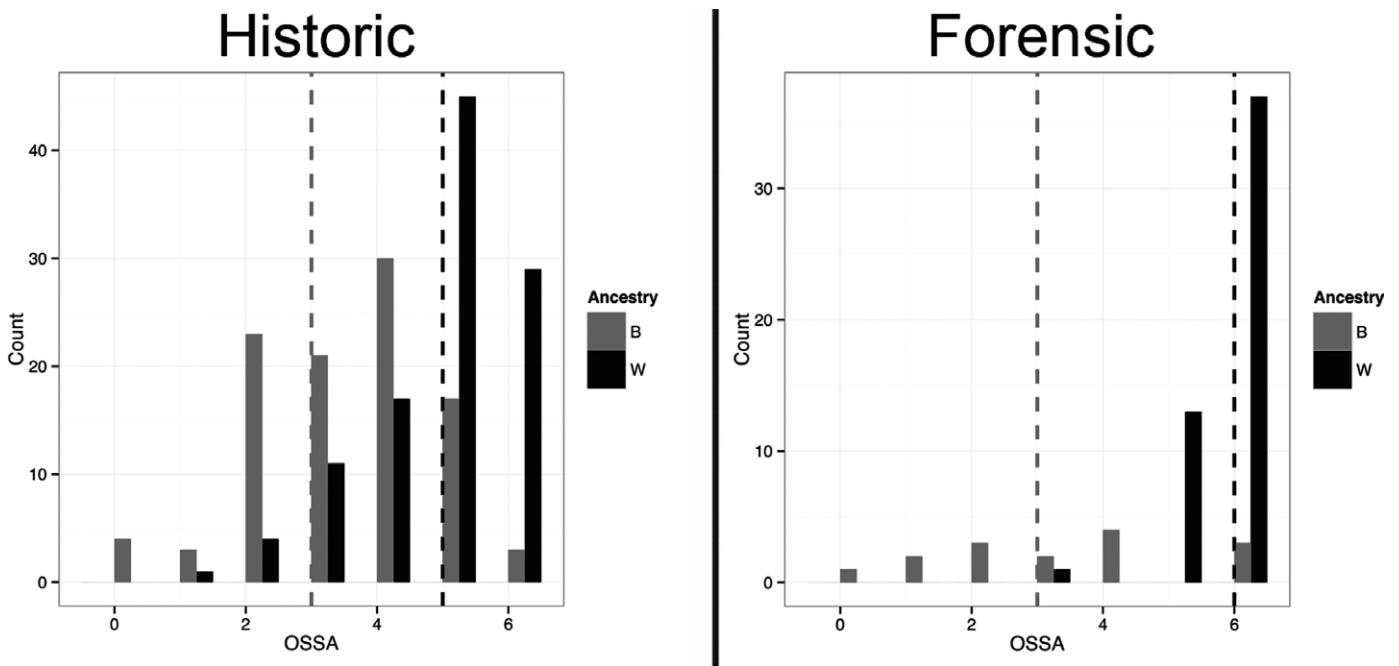


FIG. 3—OSSA score distributions for the historic (HTH) and forensic (modern) samples by ancestral group. Median is shown by the dotted lines.

TABLE 5—Classification percentages for each analysis.

Analysis	B (% Correct)	B (% Incorrect)	W (% Correct)	W (% Incorrect)	Total Correct (%)
HTH (sectioning point = 3)	50.5	49.5	85.0	15.0	68.3
HTH (sectioning point = 4)	80.2	19.8	69.2	30.8	77.9
Forensic (sectioning point = 3)	53.3	46.7	98.0	2.0	87.9
Forensic (sectioning point = 4)	80.0	20.0	98.0	2.0	93.9
Pooled (sectioning point = 3)	50.9	51.1	89.2	11.8	73.0
Pooled (sectioning point = 4)	80.2	19.8	78.5	21.5	79.2

groups (Table 5). The pooled forensic sample achieves a total correct classification of 87.9% (B = 53.3%, W = 98.0%) using the sectioning point of ≤ 3 (Table 5). When the sectioning point is shifted to ≤ 4 , the forensic sample total correct classification increases to 93.9% (B = 80.0%, W = 98.0%) again with a considerable decrease in bias between ancestry groups (Table 5). Pooling all samples yields a total correct classification of 73.0% (B = 50.9, W = 89.2%) using the sectioning point of ≤ 3 (Table 5). Using the adjusted sectioning point, the pooled samples total correct classification increases to 79.2% (B = 80.2, W = 78.5) (Table 5). U.S. blacks have higher classification accuracy than whites in the HTH sample (using the adjusted sectioning point), yet have lower correct classifications in the forensic sample. Heuristically adjusting the sectioning point to four in the modern sample also greatly decreased the classification bias between ancestral groups.

Discussion

For comparative purposes, the frequencies discussed herein will be of the pooled sample (historic and forensic) (Tables 3–5). In the current study, both blacks and whites exhibit more marked ANS, narrower IOB, and higher frequencies of intermediate NAW scores than those reported by Hefner (6). The differences in individual trait frequencies observed in the current study have resulted in a different distribution of OSSA scores than those reported by Hefner and Ousley (8). In comparison with the distribution of OSSA scores reported by Hefner and Ousley (8), the current study found that blacks showed more intermediate OSSA scores (2–4), while whites showed greater frequencies of higher OSSA scores (5 and 6). In fact, from the pooled white sample, 78.5% of individuals had OSSA scores of 5 or 6, in comparison with those reported by Hefner and Ousley (8), where 58.6% of white individuals had OSSA scores of 5 or above.

The different distribution of trait and composite scores noted in the current study also affected classification accuracies. Hefner and Ousley (8) reported a total correct classification of 86.1% using OSSA, while the current study found a lower total correct classification. Using the suggested sectioning point of 3, the pooled sample achieved a total correct classification of 73.0%; however, shifting the sectioning point to 4 increased total correct classification to 79.2%. Further, shifting the sectioning point to 4 resulted in less biased results; total correct classification of blacks rose from 50.9% (sectioning point = 3) to 80.2% (sectioning point = 4). Similar results occurred in each individual sample when the sectioning point was adjusted.

Given the changes in trait frequency expression noted, particularly in the modern black samples, there are two possible explanations: secular change in the distribution of trait expressions and/or increased admixture. Secular change may potentially explain these differences given the time disparity between the HTH and two modern samples. Metrically, Jantz and Meadows Jantz (10) found that over time the cranium has changed in both size and shape with the face becoming narrower and taller in both U.S. blacks and whites. Interestingly, Jantz and Meadows Jantz found that the direction and magnitude of secular change is the same in both blacks and whites. Using geometric morphometrics, Wescott and Jantz (11) examined U.S. black and white crania and reached the same conclusions as Jantz and Meadows Jantz—the cranium is getting narrower and taller. However, according to Wescott and Jantz (11), the majority of the shape

variation through time is contained within the cranial base. Finally, Truesdell (12) found that the expressions of a suite of nonmetric cranial traits (prognathism, orbit shape, nasal bridge, cranial form, nasal spine, nasal sill, and total nasal form) had changed through time in U.S. blacks and whites. In sum, metric, morphological, and nonmetric secular changes have been observed and may relate to changes in nutrition and greater access to health care, particularly at younger ages (10).

Additionally, increasing admixture might explain the temporal shift in trait expressions. While no data are available to substantiate intermarriage preference, intermarriage rates can act as a proxy (13). However, it should be made exceedingly clear that intermarriage does not necessarily reflect intermating and vice versa. Intermarriage has seen a steep rise from the 1980s through today with over 15.1% of all new marriages being classified as intermarriage, with a total intermarriage rate of 8.4% (compared to 3.2% in 1980) (14). Presumably, the new intermarriage rates in 2010 reflect births past 1980, although the birth years for marriages are not reported by Taylor and colleagues (14). Further, Passel et al. (15) noted that in the event of intermarriage, blacks most commonly marry a white partner; however, whites most commonly intermarry with Hispanics. The increase in intermarriage rates reflects the changing attitudes toward intermarriage. Given the trends in intermarriage, and assuming that the expression of cranial nonmetric traits is heritable, admixture could potentially explain the shift in the frequency of trait expressions, particularly in the modern samples. However, it should be noted that the results be interpreted with caution given the small sample sizes, particularly in the modern black samples.

Conclusions

U.S. blacks and whites express the cranial traits outlined by Hefner (6) and Hefner and Ousley (8) in different frequencies, which are particular to each group and can be used as a means of estimating ancestry. Through time, the expression of cranial traits has tended to become more intermediate, which might be explained through either secular change or admixture or a combination of both. Changing the suggested OSSA sectioning point from 3 to 4 improves total correct classification and reduces bias across the board, but especially in the modern sample. Given the changes in trait expression through time, it is suggested when examining modern forensic cases to increase the sectioning point to 4 for best classification accuracy. Furthermore, practitioners should have adequate experience in scoring the traits as defined by Hefner and Ousley (8) and be sufficiently familiar with the normal range of human variation to confidently score each of the traits.

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