

SEX ESTIMATION OF THE HUMAN SKELETON

History, Methods, and
Emerging Techniques

Edited by

ALEXANDRA R. KLALES



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CHAPTER 16

MorphoPASSE: Morphological pelvis and skull sex estimation program

Alexandra R. Klales

Forensic Anthropology Program, Department of Sociology and Anthropology, Washburn University, Topeka, KS, United States

Background and rationale

The primary goal asked of forensic anthropologists is the estimation of a person's biological profile to help law enforcement determine the identity of unknown human remains encountered in forensic contexts. Sex estimation is an important component of the biological profile, and many methods have been developed, tested, and utilized to estimate sex using different regions of the human skeleton. Despite the availability of quantitative methods for sex estimation, many forensic anthropologists continue to rely on qualitative traits for sex estimation. In a survey of biological anthropologists, most practitioners (63.6%) prefer using both qualitative and quantitative methods; however, when both are not used, qualitative methods (23.9%) were preferred nearly twice as often as metric methods (12.5%) (Klales, 2013).

Benefits of morphological methods include ease of use, relatively quick application, no need for specialized equipment, and applicability to fragmentary remains. Unfortunately, many of the qualitative methods used for sex estimation are based on subjective interpretations of skull and pelvic traits (Rogers & Saunders, 1994; Williams & Rogers, 2006). Because of this, attempts to standardize the use of morphological traits has resulted in the creation of methods that rely on standardized ordinal scoring and statistical methods of sex classification (e.g., Klales, Ousley, & Vollner, 2012; Walker, 2008), thereby making the methods compliant with the *Daubert* recommendations (Daubert vs. Merrell Dow Pharmaceuticals, 1993). According to the Klales (2013) survey, the most preferred traits for morphological cranial sex estimation are the traits depicted in Buikstra and Ubelaker (1994) and subsequently utilized by Walker (2008): nuchal crest, mastoid process, supraorbital margin, glabella, and mental eminence. Likewise, survey participants indicated that the three traits originally described by Phenice (1969) and then modified by Klales et al. (2012) are the most popular for morphological pelvic sex estimation (Klales, 2013): ventral arc, subpubic concavity/contour, and the medial aspect of the ischio-pubic ramus. Because the Walker (2008) and Klales et al. (2012) methods and the sex classification results obtained when using them have been found to be highly correlated with the metrics of the skull and pelvis, Kenyhercz, Fredette, Klales, and Dirmaat (2012)

recommend the use of both method types (quantitative and qualitative) for sex estimation. Given the survey results mentioned above, it would appear that most practitioners are, in fact, using both types of methods, albeit perhaps with a preference for qualitative methods.

Quantitative sex estimation methods were consolidated into the computer program *FORDISC* in 1993 (Jantz & Ousley, 2005). Cranial and postcranial metric data from 13 modern populations (eight male groups and five female groups) have been integrated into the interactive program (Jantz & Ousley, 2005). Forensic scientists can enter the measurements of their unknown individual into the program and then compare their case to those individuals within the known reference samples for sex and ancestry classification using linear discriminant function analysis and stature estimation using linear regression (see Chapter 12 of this volume for more information). Users are then provided with discriminant function classification accuracy, a posterior probability of group membership, and several typicalities that the practitioner can then interpret for combined sex and ancestry estimation. Within two short decades, *FORDISC* has become the number-one method for metric assessment of sex and ancestry (Klales, 2013). The ease of use and inclusive nature of the program is likely why *FORDISC* is the number-one method for metric assessment of sex and ancestry parameters of the biological profile (Klales, 2013).

Unfortunately, a similar program for morphological methods did not yet exist; therefore, practitioners must rely on the equations provided in the original publications and then must evaluate sample and statistical appropriateness when applying the method to their unknown individual. To remedy this, the *MorphoPASSE: Morphological Pelvis and Skull Sex Estimation* program was created through a National Institute of Justice-funded grant (2015-DN-BX-K014). The primary aim of the database project was to examine temporal changes, population variation, and the effects of asymmetry on sex classification using the eight most popular morphological traits of the skull (five used in the Walker, 2008 method) and the pelvis (three used in the Klales et al., 2012 method). The secondary aim of this project was to develop *MorphoPASSE*, a free, interactive morphological program, based on these standardized methods. With the program, practitioners can enter, compare, and analyze morphological traits of their unknown individual to a large sample with known demographic data in order to more accurately and more easily estimate sex.

About *MorphoPASSE*

Skull and pelvis score data in the *MorphoPASSE* program come from 15 different collections (Table 1) and contain individuals from five broad geographic ancestral backgrounds: Asian ($n=266$), African/Black ($n=685$), Hispanic ($n=320$), Native American ($n=117$), and European/White ($n=1207$) (Table 2). Both contemporary and historical samples are included, thereby making the database applicable to modern

Table 1 Skeletal samples included in MorphoPASSE.

<ul style="list-style-type: none"> • Antioquia Modern Skeletal Reference Collection • Arikara Collection at the University of Tennessee, Knoxville • Hamann-Todd Human Osteological Collection • Hartnett-Fulginiti Pubic Bone Collection • Khon Kaen University Human Skeleton Research Centre • Mercyhurst University Forensic Anthropology Laboratory • Nubian Collection at the University of Colorado • Osteological Collection of the National Autonomous University of Mexico 	<ul style="list-style-type: none"> • Pretoria Bone Collection • Robert J. Terry Anatomical Skeletal Collection • Santa María Xigui Cemetery • Texas State Operation Identification Collection • Texas State University Donated Skeletal Collection • University of the Philippines Skeletal Reference Collection • William M. Bass Donated Skeletal Collection
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Table 2 Sample sizes in MorphoPASSE by geographic population/ancestry group.

	Males	Females	Total
Asian	179	87	266
Black	367	318	685
Hispanic	198	122	320
Native American	59	58	117
White	694	513	1207
Total sample			2595

forensic casework, as well as bioarchaeological cases. Prior to the formation of the program, population variation, temporal variation, observer error, and the impacts of asymmetry were assessed. Data not collected as part of the grant was sourced from fellow researchers after observer error studies demonstrated that all traits are reliable with the exception of the mental eminence (Walls & Klales, 2018). The MorphoPASSE program and accompanying manual can be found here: <https://www.morphopasse.com/> and the database itself is accessible via R Studio's www.shinyapps.io/MorphoPASSE.

Scoring procedures

The five Walker (2008) and three Klales et al. (2012) traits should be scored using the MorphoPASSE manual (Klales & Cole, 2018), not the original publications, because modifications were made to the traits based on research from the grant. For example, Walker's (2008) traits were expanded to include descriptions for intermediate scores (2–4) and also revised to include real bone examples of the traits to accompany his original drawings (Fig. 1, example for the nuchal crest). The manual is freely available at www.MorphoPASSE.com.

1. Nuchal Crest

Abbreviation: NC

Description: Thick transverse nuchal crest along the squamous portion of the occipital bone, at the external occipital protuberance (EOP), for the attachment of the nuchal and trapezius muscles and the nuchal ligament. Note: inion is the furthest projection of the EOP and is sometimes erroneously used interchangeably with the term nuchal crest and EOP.

Scoring: View the skull in lateral position (left or right side) and palpate the surface noting any rugosity. When viewing this landmark laterally, the overall robusticity of the superior nuchal line can also be observed and should be considered. Note: Do not score this trait if an occipital bun is present and obscuring the region and also note (see images below) that the location of EOP on the posterior portion of the skull varies considerably based on vault shape.

Scores:

- 1- Smooth. EOP is not evident.
- 2- Slight roughening or traces of the nuchal lines. EOP is not evident.
- 3- Nuchal lines and EOP evident. EOP is rough and has a lip or edge with very slight posterior projection (i.e., you can catch a fingernail on it).
- 4- Nuchal lines and marked EOP. EOP is pronounced with clear posterior projection, but has not yet developed a pronounced hook or inferior projection.
- 5- Nuchal lines and EOP with rough surface. EOP is very pronounced and can be hooked with marked posterior/inferior projection. A ledge or ridge to either side of the EOP may be present.

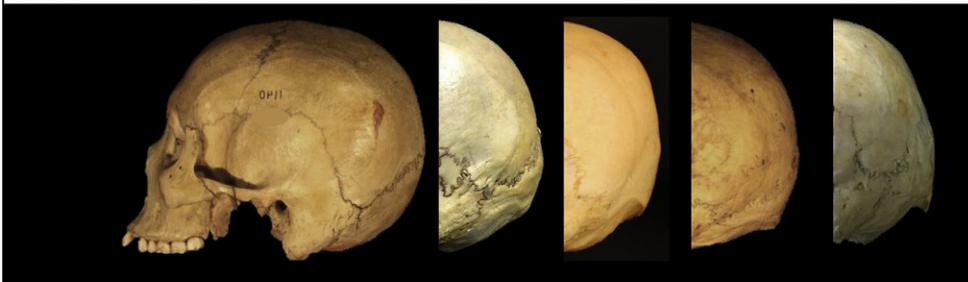
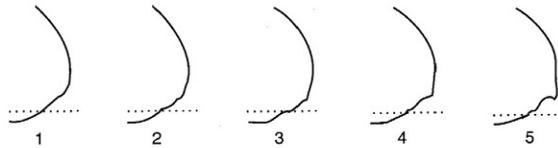
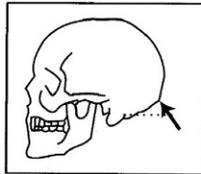


Fig. 1 Page 18 from the MorphoPASSE manual (Klales & Cole, 2018) showing modifications to Walker's (2008) nuchal crest trait.

The manual includes a description of the trait, scoring procedures, and special considerations followed by individual score descriptions from the original publications, modifications and revisions, schematic representations of each trait, and real bone specimen photos of each trait. Prior to scoring the traits, the analyst should become familiar with the range of variation present by minimally examining the real bone specimens provided in the manual. For each trait, the analyst should view the specimen and compare it to both the descriptions and figures (drawings and real bone examples) to score the specimen. For some traits, multiple features are being scored; therefore, weight or preference should be given to those listed as most important in the manual. For example, the mental eminence examines the tubercles, as well as the portion of the mandible occupied by the eminence. Likewise, the ventral arc examines the ridge of bone, as well as the overall bone shape and morphology. In the case of bilateral traits, both the left and right sides should be scored. Lastly, the manual includes a scoring form (page 29) and information on how the data can be accessed by outside researchers for additional projects.

Statistical options

In keeping consistent with [Walker \(2008\)](#) and [Klales et al. \(2012\)](#), MorphoPASSE allows the analyst to select the binary logistic regression (LR) equations provided in the original publications for sex classification and provides calculation of posterior probabilities of sex membership. In both these methods, the sex of the individual is treated as the binary dependent variable, and the skeletal indications are the ordinal independent variables. However, as [Konigsberg and Frakenberg \(2019: 385\)](#) recently pointed out, skeletal “indicators depend on the sex of the individual, rather than the sex of the individual depending on the indicators”; therefore, a different statistical approach may be more appropriate for these traits. Nonetheless, LR was chosen in these articles due to its numerous advantages over other classification methods (e.g., discriminant function analysis). The relaxed assumptions of LR do not require normally distributed data, and it remains robust despite normality deviations. LR does generally assume larger samples and that (1) variables are discrete, (2) there are no data outliers, (3) a linear relationship exists between each independent variable and the odds ratio, and (4) there is to be no collinearity among predictor variables. While not all of these assumptions are met, [Walker \(2008\)](#) and [Klales et al. \(2012\)](#) argued that practical criteria are more important than dogmatically adhering to the rules (see [Chapter 13](#) of this volume for a more in-depth discussion of this Measurement-Statistic debate).

Because of the collinearity of these 13 variables and the inability of LR to easily handle missing data, MorphoPASSE also includes random forest modeling (RFM). RFM is the recommended application in MorphoPASSE and is a flexible machine learning (ML) algorithm that creates a series of decision trees using bootstrap aggregating of random training subsets and then produces an average prediction based on the “forest.” Random

forest classification uses many random subsets of the variables and repeated sampling of the original data to produce hundreds of decision trees, called an ensemble, and the consensus of the ensemble is used to determine the best classification rules. Random forests can generally tolerate a large number of variables simultaneously, including “noisy” ones (Hefner & Ousley, 2014: 886). Thousands of random cut-off points in the sample are determined “on-the-fly” to determine the most accurate pooling of groups (i.e., the sexes in this case) (Hefner & Ousley, 2014; Williams, 2011). The more trees in the forest, the more robust or accurate the sex prediction. This approach prevents overfitting and only selects the most valuable input features, or traits and their scores, for classification. RFM is non-parametric whereby the model is based on the data entered (i.e., not specified a priori) and makes no assumptions about that data (e.g., requirement of normal distribution, sample size, etc.). Thus far, ML approaches, including decision trees/random forest models, have been mostly applied to continuous data for sex estimation; however, these statistical approaches have also shown great promise for morphological traits (binary, discrete, ordinal data) and combined morphological/metric ancestry estimation (Hefner & Ousley, 2014; Hefner, Spradley, & Anderson, 2014), but have yet to be widely applied in this capacity to sex estimation (see Chapter 13 of this volume).

Users may enter in any of the 13 variables (three unilateral and two bilateral skull traits and three bilateral pelvis traits) into MorphoPASSE to generate an “on-the-fly” prediction of sex membership based on the population and temporal-specific criteria selected by the practitioner. Posterior probabilities, determining how likely the entered individual’s score are to belong to each sex, are also provided to interpret the strength of the results. For example, a probability of 60% (i.e., close to random chance) should be interpreted as far less meaningful than a probability of membership of 85% or above for sex. Practitioners also have the option of utilizing the LR equations provided in the original Walker (2008) and Klales et al. (2012) articles rather than using the “on-the-fly” calculations.

Interface

On the input page, the analyst enters their name (or initials) and case identification number. Next, they select the statistical option to use—again RFM is the recommended approach. Then a temporal period, ancestry group, and/or region can be selected based on the case being analyzed. If none of these are selected (i.e., all listed as unknown), the program will use the entirety of the database sample. Lastly, at least one trait score must be entered for analysis. Once trait scores are entered, the total sample size used in the analysis will be displayed. The final step for classification is selecting the “run analysis” button at the top. Once the analysis is complete, the output page will come up automatically. A word document of the analysis and report can be downloaded.

Included in the output are the following: data entered, test parameters selected, model formula, case prediction/sex probability, test accuracy, training model accuracy, and

variable importance. *Case Prediction* provides the probability of sex membership. *Model* is the model summary. The type of RFM is classification, because sex is a binary variable. The number of trees is included along with the number of predictor variables considered at each node of the decision tree. The “*out of the bag*” (OOB) estimate of the error is based on bootstrap aggregation. At each iteration created with a subset of data, the unused data is tested in the tree to produce an average of errors for the entire set of decision tree. Model tuning *mtry* is the number of variables randomly sampled as candidates for each node and is also presented visually. The confusion matrix presents the accuracy of the model based on true negatives, true positives, false positives, and false negatives. *Variable Importance* (mean decrease in Gini coefficient) describes how important each of the variables is when classifying sex. The most important variable will be the one with the highest mean decrease in OOB error. Typically, pelvic traits will always be of more importance than skull traits due to the higher degree of sexual dimorphism in the pelvis. This information is also presented visually. *Model Training* provides cross-validated classification accuracy of the entire sample. The *Kappa* statistic provides the accuracy of the model taking into account random chance and will typically be lower than the accuracy. The details of model training, percent accuracy, and kappa statistic are only provided in the downloaded report. *Model Accuracy* tests the model on a hold-out sample from the database. The following are also provided: sensitivity/true positive, $(TP)/(TP + FN)$; specificity/true negative, $(TN)/(FP + TN)$; positive predictive value, $(TP)/(TP + FP)$; and negative predictive value, $(TN)/(FN + TN)$.

Conclusion

The MorphoPASSE program provides a free, user-friendly means by which to utilize the Walker (2008) and Kiales et al. (2012) traits and associated methods for reliable and valid sex estimation. In the future, the hope is that (1) additional morphological traits of the skull and pelvis, for example, the greater sciatic notch (Walker, 2005), will be added to the program, and (2) data can be sourced from additional worldwide populations to increase the sample size and global representativeness of the database. Moving toward databases and programs, like FORDISC and MorphoPASSE, will aid in the quest for standardization of our methods.

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References

- Buikstra, J. E., & Ubelaker, D. H. (1994). Standards for data collection from human skeletal remains. In *Proceedings of a seminar at the Field Museum of natural history*.
- Daubert v. Merrell Dow Pharmaceuticals, Inc. (1993). 509 U.S. 579.
- Hefner, J. T., & Ousley, S. D. (2014). Statistical classification methods for estimating ancestry using morphoscopic traits. *Journal of Forensic Sciences*, 59(4), 883–890.
- Hefner, J. T., Spradley, M. K., & Anderson, B. (2014). Ancestry assessment using random forest modeling. *Journal of Forensic Sciences*, 59(3), 583–589.
- Jantz, R. L., & Ousley, S. D. (2005). *FORDISC 3: Computerized forensic discriminant functions*. Version 3.0 Knoxville, TN: The University of Tennessee-Knoxville.
- Kenyhercz, M. W., Fredette, S. M., Klales, A. R., & Dirmaat, D. C. (2012). Metric and non-metric assessment of sex: Accuracy, correlation and corroboration. [Abstract]. *Proceedings of the American Academy of Forensic Sciences*, 18, 370.
- Klales, A. R. (2013). Current practices in forensic anthropology for sex estimation in unidentified, adult individuals. [Abstract]. In 19. *Proceedings American Academy Forensic Sciences*.
- Klales, A. R., & Cole, S. J. (2018). *MorphoPASSE: The morphological pelvis and skull sex estimation database manual*. Version 1.0 Topeka, KS: Washburn University.
- Klales, A. R., Ousley, S. D., & Vollner, J. M. (2012). A revised method of sexing the human innominate using phenice's nonmetric traits and statistical methods. *American Journal of Physical Anthropology*, 149(1), 104–114.
- Konigsberg, L. W., & Frakenberg, S. R. (2019). Multivariate ordinal probit analysis in the skeletal assessment of sex. *American Journal of Physical Anthropology*, 169(2), 385–387.
- Phenice, T. W. (1969). A newly developed visual method for sexing the os pubis. *American Journal of Physical Anthropology*, 30, 297–302.
- Rogers, T. L., & Saunders, S. (1994). Accuracy of sex determination using morphological traits of the human pelvis. *Journal of Forensic Sciences*, 39, 1047–1056.
- Walker, P. L. (2005). Greater sciatic notch morphology: Sex, age, and population differences. *American Journal of Physical Anthropology*, 127, 385–391.
- Walker, P. L. (2008). Sexing skulls using discriminant function analysis of visually assessed traits. *American Journal of Physical Anthropology*, 136, 39–50.
- Walls, M. M., & Klales, A. R. (2018). Testing the reliability of morphological sex estimation methods used in forensic anthropology. [Abstract]. In 24. *Proceedings American Academy Forensic Sciences*.
- Williams, G. (2011). *Data mining with rattle and R*. New York, NY: Springer.
- Williams, B. A., & Rogers, T. (2006). Evaluating the accuracy and precision of cranial morphological traits for sex determination. *Journal of Forensic Sciences*, 51(4), 729–735.