Metric Methods for the Biological Profile in Forensic Anthropology: Sex, Ancestry, and Stature

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ABSTRACT

The biological profile, conducted by a forensic anthropologist, is necessary for severely decomposed or skeletonized remains. The biological profile consists of estimates of sex, age, ancestry, and stature. It is crucial to have a correct estimate of sex, as this designation will narrow down the search through missing persons reports by half (e.g., searching through NamUs). However, sex estimates can be population specific, necessitating accurate ancestry estimation. When estimates of age and stature are added, the search narrows further. If these estimates are incorrect, the unidentified human remains may never be identified. These biological profile components are estimated based on either metric or nonmetric methods (visual observation and recording of categorical data). While age is inherently nonmetric, stature is inherently metric. Estimates of sex and ancestry can take a metric or nonmetric approach. The purpose of this review article is to review metric methods in forensic anthropology (sex, ancestry, and stature), to provide general knowledge of why and how these metric methods work, and to highlight that estimates of sex, ancestry, and stature do not subscribe to a “one size fits all” model. *Acad Forensic Pathol.* 2016 6(3): 391-399

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INTRODUCTION

Metric methods of sex, ancestry, and stature play an important role in building the biological profile for unidentified human remains—the first step toward a positive identification. Because they involve well-defined measurements, metric methods for the biological profile have less potential for inter- and intraobserver error than nonmetric methods. The purpose of this article is to review the current status of metric methods for sex, ancestry, and stature estimation within forensic anthropology.

Sex, ancestry, and stature estimates depend on methods derived from the most appropriate reference data for use in forensic practice. In some cases, sex is more straightforward than ancestry as the outcome is one of two groups (for biological sex) while the outcome for ancestry estimation is one of multiple groups. Stature is an estimate along a continuum. For sex and stature, the best estimates are usually provided by population specific formulae. For example, formulae derived from one population group (e.g., Mexican-Americans) may not work well for another group due to differences in sexual size dimorphism. Moreover, an estimate of sex helps narrow down search parameters by approximately 50% when searching through missing persons reports for an identification hypothesis. An accurate estimation of ancestry and stature can narrow down search parameters even further.

This article contains three sections: sex, ancestry, and stature. Each section contains background information on each topic, describes the most appropriate method and data needed to make an informed estimation, and provides practical considerations on how to make the best estimation possible for each topic. Simple, straightforward conclusions are included at the end of each section to highlight the main points to consider when estimating sex, ancestry, and stature.

DISCUSSION

Sex Estimation

The pelvis provides the best estimate of sex based on

differences in sexual size and shape dimorphism between males and females. Because females have the potential for childbirth, their pelvises differ not only in size, but also in shape. Although the pelvis is the best estimator of sex, the second best indicators are postcranial bones. While using postcranial bones may seem counter to traditional teachings and older texts, Spradley and Jantz demonstrated, using large samples of individuals who self-reported as American black and white, that the long bones outperform the cranium in sex estimation achieving classification rates between 92-94% (1). Measurements of postcranial bones are often entered into a discriminant function formula (multivariate) or a sectioning point (univariate) that yields a score indicating male or female. As for the skull, it is usually measurements from the cranium (craniometrics) that are used in conjunction with a discriminant function program, Fordisc 3.1 (2), for an estimate of sex and ancestry.

Better results from the cranium can be achieved using three-dimensional (3D) computed tomography (CT) scans, computer automated analyses, automatic landmark detection, and linear discriminant function analysis. Abdel Fatah et al. was able to achieve 97% correct classification for sex from the cranium with 11 variables (3). These 11 variables consist of both standard and nonstandard measurements, meaning some of the variables could only be derived from the use of CT scans. In cases where there is a cranium only, this method is highly useful for sex estimation.

Postcranial bones

Although Spradley and Jantz demonstrated that postcranial bones outperform the skull in sex estimation, the formulae they provided are most applicable to Americans that identify as black or white. Moore et al., following the methodology outlined in Spradley and Jantz (1), developed population specific sex estimation criteria for Columbians (4). In 2013, Albanese developed nonpopulation specific methods for sex estimation using the clavicle, humerus, radius, and ulna and logistic regression (5). As many methods are population specific, sometimes population affiliation may not be accurately estimated if skeletal remains

are fragmentary. Albanese's method worked well in general, with the exception of small males that were classified as female. Population groups that are nutritionally stressed during growth and development may produce individuals that do not reach their genetic potential for height (6). Spradley et al. found that Hispanic males, particularly migrants that died crossing the U.S./Mexico border, were more often classified as female using formulae derived from other population groups (7). For individuals working with populations that may contain smaller, gracile males, population specific methods will work best.

Gulhan et al. set out test the applicability of population-specific equations in a Turkish population for the purpose of assisting with mass fatalities (8). While not providing specific classification functions for the end user, Gulhan et al. did suggest that population-specific equations for the femur work best on a Turkish population. Frutos developed a univariate method of sex estimation from the superior-inferior femoral neck diameter for rural Guatemalans (9). These particular groups of Guatemalans were victims of genocide during the Civil War in the 1980s. Frutos was also able to develop sex estimation formulae from the clavicle, scapula, and humerus for these rural Guatemalans, with the humerus providing the highest classification accuracy (9-11). Overall, Frutos found that rural Guatemalans tend to be smaller than other North American groups, necessitating population-specific formulae for sex estimation (9).

Pelvic Bones

The pelvis provides a high degree of reliability using macroscopic, nonmetric data in conjunction within a statistical framework. However, several researchers have published metric methods for estimating sex from the pelvis. Mestekova et al. (12) using ten measurements from a French sample, tested a method proposed by Murial et al. (13), and achieved accuracies ranging from 92-97%. Bytheway and Ross utilized 36 landmarks and geometric morphometric methods (GM) and achieved classification rates between 98-100% (14). Measurements of the pelvis are often difficult and ambiguous due to the lack of

identifiable and well-defined landmarks. Further, if enough of the pelvis is present to directly measure or collect landmark data, then a visual observation of nonmetric traits using statistical methods could also be employed with high accuracy (e.g., Klales et al. [15]) without the need for collecting measurements or landmark data.

Short, Flat, and Irregular Bones

Although the pelvis and long bones, followed by the cranium, are the most popular bones for sex estimation, in cases of extreme fragmentation or incomplete skeletal recovery, other bones may be informative for sex estimation.

Cranial bones

Focusing on specific bones of the cranium, Saini et al. used the mastoid process to estimate sex in Indian population with 87% accuracy (16). Further, Jung and Woo used the mastoid process and GM analysis in American whites, also with 87% accuracy (17). Saini et al. used measurements that can easily be obtained with calipers, while Jung and Woo used GM analysis, which requires a digitizer and is not easily extrapolated for use in forensic practice. Although both show promise for using the mastoid process in sex estimation, as this portion of the cranium is compact and often found intact in fragmentary crania.

Sternum

Hrytl proposed that the length of the manubrium compared to the sternum provides a ratio of 1:2 in females and 2:1 in males (18). Although Bongiovanni and Spradley found that Hrytl's law holds true, there is too much overlap between males and females for the ratio to prove useful (19). Rather, it is metric analysis in the form of discriminant function analysis that was a more reliable indicator of sex using a recent American sample (19). Franklin et al., using data derived from multislice computed tomography in a Western Australian population, found that sex could be estimated from eight standard sternal measurements with accuracies ranging from 72-85% (20).

Scapula and Clavicle

Dabbs and Moore-Jansen utilized metric data from the scapula from the Hamann-Todd Collection, with birth years from the late 19th and early 20th century, to develop new criteria for sex estimation from the scapula (21). Dabbs and Moore-Jansen used a training sample that yielded results up to 94%; however, the test sample from a more recent cadaver collection in Kansas yielded classification rates of 83%. The discrepancy between the two classification rates could be that the test sample had more recent birth years than the training sample.

Using data derived from CT images from living people, Torimitsu et al. found that standard measurements of the scapula provided classification rates up to 95% for a Japanese population, although no test sample was utilized (22). Using a contemporary Spanish sample, surface scans, linear measurements and quantification of volume and curves of the clavicle, Mediavilla et al., was able to achieve classification rates of 85-100% for sex (23). Mediavilla et al. further suggest that volume alone provided a 92% correct classification.

In addition to the previously described methods, there are other published sex estimation methods including the use of hand, foot, and other bones (24-29). Use of hand, foot, and other bones such as patella, should only be used when no other highly diagnostic bones are available.

Summary of Sex Estimation

While the pelvis provides the best estimate of sex, the best metric method for sex estimation falls with the long bones, clavicle, and scapula. However, the single best bone for sex estimation will depend on the population at hand. Multivariate methods such as discriminant functions are more robust than univariate sectioning points.

Ancestry Estimation

Ancestry estimation, or estimation of geographic origin, is most commonly accomplished through sta-

tistical analysis of measurements from the cranium (craniometrics). However, postcranial measurements can also be used for ancestry estimation. Ancestry estimation has been shaped by long-term evolutionary trends and is best explained in terms of population genetic theory. Early humans traveled in small groups and migrated to various geographic areas across the earth. Over several hundred thousand years, evolutionary forces such as natural selection and genetic drift shaped differences in physical appearance of these various human groups (e.g., skin color, hair color, height). While there is more gene flow in recent human history, geographic, language, and cultural barriers (e.g., religion) still shape mating practices in the modern world. Population groups living in close geographic proximity are more similar to one another while populations groups living far apart are more dissimilar, a concept referred to as isolation by distance (IBD) (30).

Because underlying genetics shape human morphology, it is possible to use cranial and postcranial measurements to estimate where in the world someone comes from—based on IBD and assortative mating. Further, in the United States there is a concordance between socially constructed, bureaucratic racial categories (e.g., U.S. Census Bureau categories) and population substructure. Therefore, it is possible to estimate socially constructed racial categories from the human skeleton (31). The estimation of ancestry is an estimation and should always be expressed with a degree of probability. Further, populations are constantly changing due to migration and relaxation of barriers to gene flow. Moreover, ancestry estimation involves statistically classifying one individual into one of many groups. Therefore, when attempting to estimate ancestry, it is important to have appropriate reference groups for comparison purposes.

Reference Data

Obtaining reference data can be difficult. In the early 2000s, the Hispanic population began to increase and by 2014 Hispanics became the second largest population group in the U.S. (32). However, there was little skeletal data available for individuals considered

Hispanic and little understood about the biological variation of these individuals. Due to the forethought of early anatomists, skeletal collections representing American blacks and whites born during the late 19th and early 20th centuries were readily available for study by forensic anthropologists (33). Several skeletal collections derived from body donation programs have been able to pick up where these anatomical collections have left off, including the William M. Bass Donated Skeletal Collection at the University of Tennessee (<https://fac.utk.edu/wm-bass-donated-skeletal-collection/>), the University of New Mexico Documented Skeletal Collection (http://www.unm.edu/~osteolab/coll_doc.html) and the Texas State Donated Skeletal Collection (<http://www.txstate.edu/about>).

Even with the more recent skeletal material, the collections still primarily contain American whites followed by American blacks with very few Hispanic or Asian-American groups. Due to increases in U.S./Mexico border crossing deaths over the past decade, standardized data collection of these deaths, particularly in Arizona and Texas (34), has allowed for a better understanding of the biological variation of individuals from Latin America and how to better estimate sex and ancestry for this diverse group.

Ross et al. found that Cubans, a group that would be considered Hispanic in the U.S., were more similar to American blacks and precontact Cubans (35). Using migrants that died crossing the U.S./Mexico border, thought to be Mexican, Spradley et al. found that this group displays an intermediate position between Native American and American whites (7). Thus Ross et al. and Spradley et al. were able to demonstrate variation among different groups considered Hispanic highlighting the importance of appropriate reference group selection.

Cranial and Postcranial Ancestry Estimation

Osteometric data, measurements that capture the overall size and shape of the skeleton, are the most commonly used data for estimation of ancestry (2, 36, 37). However, craniometric data (measurements

from the cranium) are more often used than postcranial metrics. Sex estimation can be performed with single measurements through univariate methods like sectioning points, even though multivariate methods are more robust. Ancestry estimation is a multivariate endeavor and the Scientific Working Group for Forensic Anthropology (SWGANTH) guidelines suggest that the best practice is to use multivariate methods to estimate ancestry (38).

Fordisc 3.1 is a discriminant function program that contains craniometric data from recent population groups and uses standard, well-defined measurements for the estimation of ancestry (2). The program has a user-friendly interface where measurements from an unknown skull are entered into the program and then statistically compared to the reference groups. The program provides statistical output (Mahalanobis d^2 and posterior probabilities) that the user must interpret to ascertain which reference group the unknown is most similar to. Fordisc 3.1 is arguably the most widely used program for ancestry estimation. The authors of the program strive to continually update the program with current reference data. Recently, Spradley and Jantz suggested that nonstandard measurements, measurements calculated from landmark data collected by a 3D digitizer, provide better estimates of ancestry (39). Further, these nonstandard landmarks provide better estimates for Hispanic groups, likely because they capture craniofacial variation that standard, caliper-driven measurement cannot capture (39).

When the cranium is not available, postcranial metrics can provide reliable results. Using long bone lengths, trunk height, and bi-iliac breadth measurements, Holliday and Falsetti achieved good classification rates for ancestry estimation for American whites and blacks (40). However, estimating trunk height and bi-iliac breadth required all vertebrae and both innominants to be present. Using postcranial data from three groups, American blacks and whites and Hispanics, Spradley ran a discriminant function analysis for each postcranial bone, with classification accuracies reaching 75% (41). However, when all postcranial bones were combined, classification rates increased as high as 85%. Liebenberg et al., exploring ancestry estimation among

three South African groups, also found that a combination of postcranial measurements worked better than using individual bones and achieved classification rates of 85% (42). Further, both Liebenberg et al. and Spradley found that results obtained from postcranial metrics were similar to results obtained using cranio-metric data from the same groups (41, 42).

Summary of Ancestry Estimation

It is possible to achieve good ancestry estimation with cranial or postcranial metric data, provided that the reference data is appropriate. Unlike sex estimation methods that provide an outcome of male or female, ancestry estimation requires user interpretation of statistical output for classification of an individual into one of many groups. Therefore, the user needs to have a working knowledge of multivariate statistics in order to make a sound estimation.

Stature

There are two main methods of stature estimation: mathematical models and the anatomical method (43). For mathematical models, it is usually long bone lengths regressed on stature that provides a prediction formula for stature estimation. In these cases, a measurement of the femur or measurements from a combination of bones are entered into a formula and a stature estimation is generated along with a confidence interval or prediction interval. Konigsberg et al. gives a discussion of inverse calibration and regression of stature on long bone lengths (44). The anatomical method consists of an estimation of stature based on measurements of various skeletal elements from the cranium to the foot. These skeletal measurements are then summed and a soft tissue and age correction factor may be applied (45).

Mathematical Models

Early mathematical stature formulae, such as Trotter and Gleser's formulae, were derived from measured stature from World War II dead and the Terry collection (46). However, in current practice, the Trotter and Gleser method is no longer applicable for current

forensic cases due to secular changes in long bone length in the American population as regression-based stature equations are often population-specific and even period-specific (47). Ousley reviewed the merits of developing stature equations from measured (e.g., Trotter and Gleser) versus forensic stature (e.g., driver's license) (48). Ousley concluded that

...forensic stature estimation is less precise than Trotter and Gleser stature estimation but is more accurate for modern forensic cases because a forensic stature is the only stature available for a missing person.

Further, Trotter and Gleser used standard errors to provide ranges for stature. Ousley recommends using formulae that provide prediction intervals (48).

While most stature formulae are population specific, they are also period-specific. Secular change, short-term generational change in human morphology, has been shown to affect heights (49). Fordisc 3.1, in addition to ancestry estimation, also estimates stature and it does so "on the fly" (50). Fordisc 3.1 will allow a user to enter all available postcranial measurements into the program. Based on the reference data in Fordisc and the measurements selected, the program will provide multiple stature equations and the end user can choose the one with the highest R squared value. When estimating stature in Fordisc 3.1, the user also has the option of selecting from "20th Century Forensic Stature," "Trotter Measured Stature," or "19th Century Cadaver Stature," depending on the need for estimation. Additionally, a prediction interval is provided.

Albanese found that using century specific equations in Fordisc did not provide better results (51). However, the test sample used for the basis of these conclusions had birth years ranging from the late 19th to the early 20th century.

Anatomical Method

The anatomical method is best suited for all population groups as it lacks the temporal sensitivity of

mathematical stature and accounts for any differences in long bone proportionality among groups. In 1956, Fully developed an anatomical method of stature estimation (52). In 2006, Raxter et al. published a test of the Fully method providing clear definitions for employing the method (45). Further, in 2007, Raxter et al. published a technical note urging anyone using the formula to use an age-specific equation as stature can decline with age (53). Maijanen tested eight different versions of the anatomical method (54) and found that the Raxter et al. (45, 53) modification of the Fully technique had a low error rate and that anatomical models in general work well for individuals with body proportions outside of the normal range of human variation. The revision of the Fully method by Raxter et al. includes measurements of cranial height, vertebral heights, sacral height, long bone lengths, and a measurement from the articulated calcaneus and talus (45, 53). While this is the best method to use, according to SWGANTH, it also requires a complete skeleton, which is not always available.

Summary of Stature Estimation

Mathematical methods provide a good stature estimate for incomplete skeletal remains, although it is important to keep in mind the population group and the time period that was used to develop the method. The anatomical method provides the best estimate of stature and is not population or time period-specific and should be used when the complete skeleton is available.

CONCLUSION

It is important to remember that estimation of sex, ancestry, and stature are estimations, approximations of reality. These approximations may be close to reality if we use the best method, based on the most appropriate reference data with regard to population group and time period. Metric estimations of sex are more robust if multivariate approaches are utilized, such as a classification function derived from a discriminant function analysis. However, if dealing with fragmentary remains, then univariate sectioning points may be the only option.

Ancestry estimation is inherently multivariate and using a single metric is considered unacceptable practice (38). Craniometric data, in conjunction with multivariate statistical models, are highly reliable for ancestry estimation. The ancestry classification is predicated on the assumption that the unknown individual belongs to one of the reference groups (50), therefore it is important to be familiar with the demographic structure of the population at hand and have the ability to interpret statistical output.

The best stature estimation method is the anatomical method (38), in particular the modification of the Fully technique (45, 53). However, this technique requires a nearly complete skeleton. If the Fully method can't be used, postcranial metrics can be entered into Fordisc 3.1. Fordisc 3.1 contains reference data from forensic cases around the country and donated skeletal collections, therefore making it applicable for forensic casework.

No matter what methods are used for sex, ancestry, and stature estimations, they should always be based on the best possible reference data.

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