

THE FAULTS IN THE METHODS: PROBLEMS WITH CURRENT SEX
ESTIMATION METHODS FOR HISPANIC INDIVIDUALS AND POTENTIAL
SOLUTIONS

by

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DEDICATION

To the individuals who have died while crossing the border and remain unidentified

Though you may be lost, know that we seek to bring you safely home, no matter where
home may be for you

Know that we haven't given up on you

ACKNOWLEDGEMENTS

Thank you, all the friends and family who have stood by me (and listened to me ramble about my fascination with bones)

Thank you, all the professors who have stood in front of me and taught me everything that I now know (and for expecting a hair under too much of me)

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Thank you, Dad, for helping me gain an appreciation for experiential learning as well as classroom learning (and getting me used to the feeling of a tool in my hands)

Perhaps most importantly...

Thank you, dear reader, for choosing to read this thesis. I hope you read this, learn many things, and use it to propel your own research forward.

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ABSTRACT

A key piece of information that can be obtained from human skeletal remains is the biological sex of an individual. This can be estimated using several methods, such as analyzing the structure of the pelvic bones or the dimensions of the skull or other skeletal elements. Most of these methods were designed and tested on primarily white individuals. However, the sexual dimorphism that these methods rely on occurs in different proportions in different ancestral groups. For instance, individuals with Hispanic ancestry tend to have more gracile features than white individuals and can be misclassified by an observer who is unfamiliar with Hispanic remains (Jantz, 2004; Spradley et al., 2008). Additionally, there is not as much research concerning Hispanic individuals as there is white or even black individuals. What research is available is fraught with problems. Incomplete or fragmentary skeletal remains, unknown identity, and large gender disparities all contribute to the lack of available research in this field. This thesis will examine the problems facing research into Hispanic sex estimation and current efforts to combat these problems, as identified in current literature. It will also argue for a more long-term solution to these problems. If the current research is not bolstered and used by the forensic community, such as researchers and medical examiners, then individuals may be misclassified. In such cases, they may never be returned to their loved ones, who will not receive closure over their deaths.

I. An Introduction

A crucial means of identifying deceased individuals is the biological profile, which includes age, ancestry, biological sex, and stature. When looking at skeletal remains, building a biological profile involves taking measurements of the skeleton and classifying the size and shape of various parts of the skeleton. These data are then compared to known skeletal samples, and a profile is estimated based on that comparison. The biological sex of an individual is a key part of this profile in forensic contexts because, once you estimate it, you can remove approximately half of the population as a possible identification. However, there are several problems with these methods. The majority of samples available for research and comparison are older white male individuals (Forensic Anthropology Center, n. d.; Personal Communication, Wescott, 2020). The samples that are a majority or entirely non-white may be small, have individuals who are incomplete, unidentified, or fragmented, or may have a large sex disparity. Skeletal elements or features used for sex estimation can be morphologically different based on other parts of the biological profile.

With this in mind, can the methods used to estimate the biological sex of Hispanic individuals be improved? If so, how can we improve them? Hispanics are now the largest and fastest growing minority population in the United States (US Census, 2008). Additionally, the U.S. Customs and Border Patrol's strategy for preventing undocumented border crossers (UBCs) from crossing illegally into this country results in countless Hispanic deaths every year (De Leon, 2015). If these techniques can be improved and are not, many Hispanic individuals may be misidentified or remain unidentified. These individuals may never be returned to their families, given their

preferred last rites, or buried under their real names, preventing their families from fully receiving closure over their deaths (De Leon, 2015).

To answer this question, a thorough review of the available literature must be performed, and key trends must be identified. Additionally, more studies must be conducted to create appropriate methods for estimating a biological profile for Hispanic individuals. Eventually, a large sample of Hispanic remains with biological, anthropological, and forensic data must be collected for use in research projects without requiring physical human remains.

II. Some Background Knowledge

Before discussing the specific problems associated with sex estimation in any great deal of depth, I first need to define some terms and concepts. Since anthropologists study humans, many observations can and have been used in rhetoric that hurts, insults, or marginalizes certain groups of people. Because of this, we use vocabulary with very specific definitions.

First and foremost, a distinction must be made between ‘estimation’ and ‘determination.’ Forensic anthropologists estimate every aspect of the biological profile, including sex from the skeleton. This is because we don’t know for sure whether our conclusion based on the data is correct or not. If we attempt to determine sex, we eliminate the possibility that we may be wrong in our conclusions. Given that we are looking primarily at the bones, not the genitalia, secondary sex characteristics, or DNA, of an individual, we must always be open to the possibility of being wrong in our conclusions. Our estimations also come with probabilities and error statements, which allows other researchers and anthropologists to attempt our methods to obtain similar results.

Next, a distinction is also made between ‘gender’ and ‘sex.’ Gender refers to how a person expresses their sex. This is more of a cultural question than biological sex; most expressions of sex are best seen in living individuals. This also extends to wider cultural questions, such as gender roles, familial patterns, or norms of sexuality. Sex, on the other hand, refers to a person’s biological phenotype and is used when describing humans biologically (Prince, 2005). This is frequently examined with human skeletal remains.

Since the bones alone cannot tell us how someone expressed their sex, an anthropologist can examine certain features of the skeleton to estimate their biological sex.

Many methods exist in the academic literature to estimate sex from human skeletal remains. It has long been known in anthropology that certain bones are very sexually dimorphic, or reliably variable between biological sexes, which include the

pelvis and the skull (Buikstra & Ubelaker, 1994; France, 1989).

As such, methods have been created to estimate the sex of an

individual's remains using these

bones (Jantz & Ousley, 2005;

Phenice, 1969; Walker, 2008).

The pelvis is the most sexually dimorphic bone in the body, most notably because of female's

ability to give birth. This causes the female pelvic bones to widen

and stretch, which in turn causes certain features to be present

which don't appear on male

pelvises. These traits were compiled by

Phenice (1969) and the method published in his paper is considered the most accurate

way to estimate sex by most anthropologists. The traits include the ventral arc, subpubic

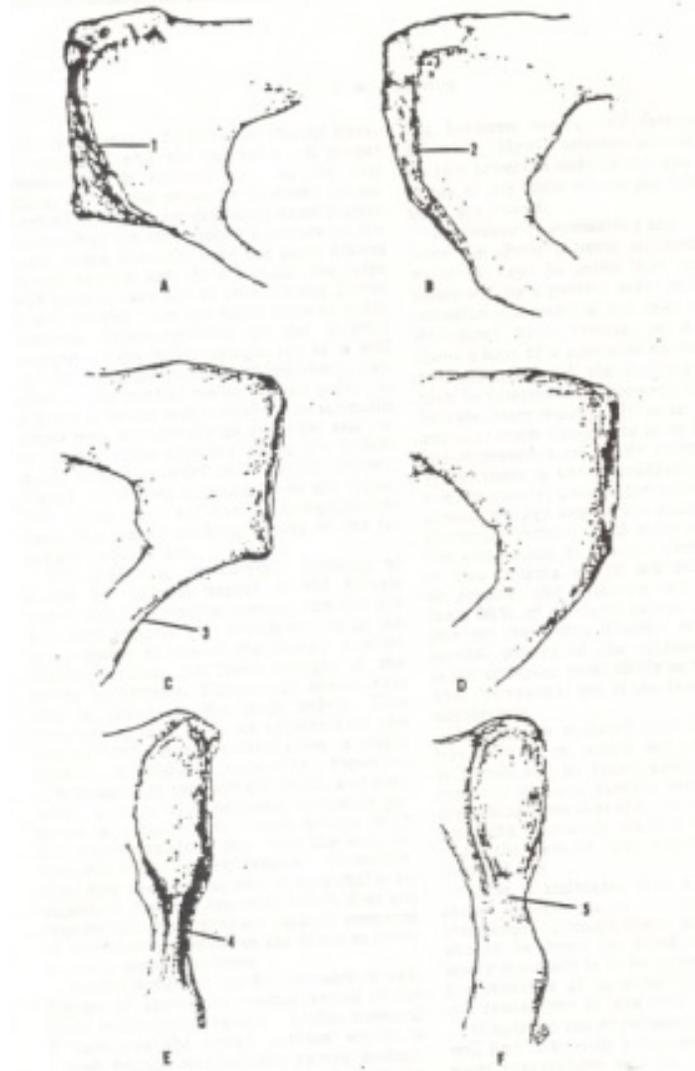


Figure 1- Comparisons between male (right) and female (left) pubic bones. A shows the ventral arc, C shows the subpubic concavity, and E shows the ischiopubic ramus ridge (Phenice, 1969:299)

concavity, and the ischiopubic ramus ridge (fig. 1). The ventral arc is a curved line of bone on the most forward side of the pubic region of the pelvic bone. It noticeably pulls away from the edge of the bone at the bottom, leaving a signature triangular shape. The subpubic concavity describes how the area between the pubic region and base of the pelvic bone curves in slightly. The ischiopubic ramus ridge is a pinched ridge of bone that runs from the pubic symphysis, the area where the two pelvic bones connect, down towards the base of the pelvis (Phenice, 1969).

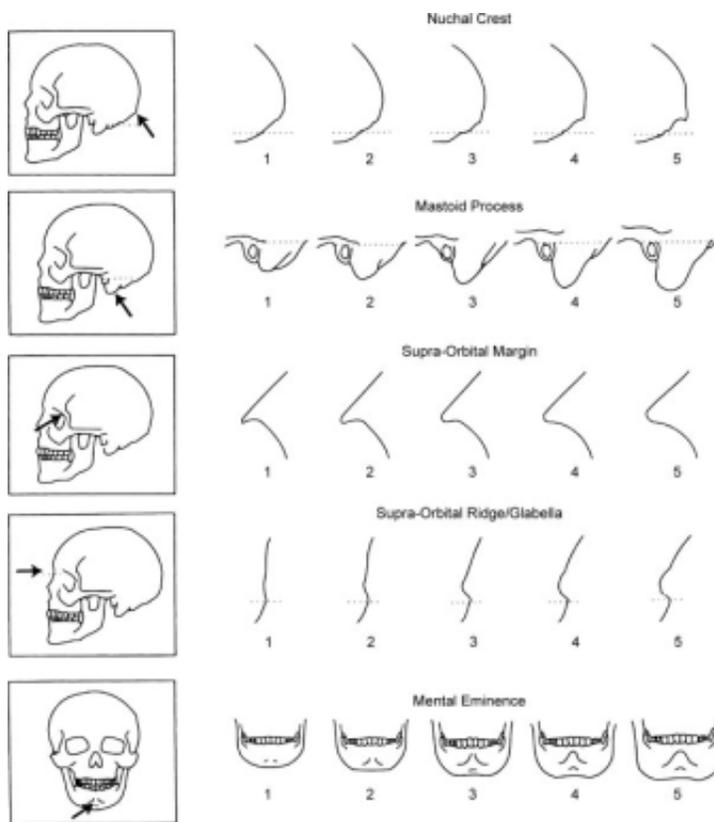


Figure 2- Features used in Walker (2008). The leftmost depictions represent clearly female individuals, and the rightmost depictions represent clearly male individuals (Walker, 2008:41)

The skull, on the other hand, doesn't have many uniquely male or uniquely female features. Instead, many muscle attachment sites are noticeably larger in males than in females (Walker, 2008). The traits that Walker uses in his method are the nuchal crest, the mastoid process, the glabella, the supraorbital margin, and the mental eminence (Fig. 2).

The nuchal crest is a site at the back of the skull where the nuchal, or neck, muscles attach. The mastoid process is a site just behind the ear that serves as an attachment site for jaw muscles. The glabella is a ridge of bone located just above and between the orbital sockets (which is to say, the eye

sockets). The supra-orbital margin describes the thickness of the upper edge of the orbital sockets. This edge is typically blunter in male individuals. The mental eminence is a raised area of bone on the mandible, or the lower jaw. This area marks the site where the mandible fuses in early childhood. The trained eye can use these features to estimate the sex of an individual. Walker (2008) used these traits to make discriminant functions that can estimate the probability of an individual being male or female. As this is more comparative than the method in Phenice (1969), the results from these functions are statistically less reliable than other methods (Spradley & Jantz, 2011). However, there are times when a skull is the only bone an anthropologist has access to. Additionally, an anthropologist should always use multiple methods to estimate anything related to human skeletal remains unless absolutely necessary.

A third method of estimating sex involves analyzing dimensions of bones using statistical techniques. In most populations, male individuals tend to be larger and have more developed muscles, although this varies between cultures and populations. This is reflected in the skeleton; male individuals tend to have larger bones and more rugose, or defined and rough, muscle attachments. France (1989) has written extensively on discriminant functions that can estimate sex using various bones. However, the most common method involves using a computer program. Fordisc 3 (Jantz and Ousley, 2005) is a statistical program developed by researchers at the Forensic Anthropology Center at the University of Tennessee in Knoxville. It uses osteometric measurements that a researcher gathers, along with its own databank, to create a discriminant function that is unique to the gathered data (Jantz and Ousley, 2012). The program then checks that function by estimating the sex of several individuals in its reference sample using that

function and shows how many individuals taken from each reference group were classified correctly or incorrectly. The conclusions that Fordisc displays are the posterior probability and several typicality probabilities. The posterior probability is the probability that the individual in question belongs to one of the chosen reference groups, assuming that they do belong to a chosen group. The typicality probabilities, on the other hand, do not assume that the individual belongs to a chosen reference group. The F typicality converts the Mahalanobis distance, a measure of how similar the data is to a group mean, into an F ratio, a ratio of between-group and within-group variance. It is considered to be the most conservative typicality ratio. The Chi typicality uses a chi-square distribution of the Mahalanobis distance and assumes the sample size is very large. It always directly varies with the Mahalanobis distance. The R typicality simply compares the unknown individual to each reference group and calculates the Mahalanobis distance. This is seen as possibly the most useful typicality by the creators of Fordisc (Jantz & Ousley, 2012).

All this talk of discriminant functions raises a fair question: what is a discriminant function? A discriminant function is an equation using multiple variables and a constant, usually in the following form (McLachlan, 1992):

$$N = aX + bY + cZ + k$$

The solution to this equation will fall above or below some critical value, which is determined using an arbitrary constant (k). Some researchers will opt to choose this constant to make the critical value zero, as this helps to simplify later operations. A binary answer can be estimated based on that solution (McLachlan, 1992). Walker lays out his process for estimating the probability of an individual being male or female in his

paper explicitly. Since his equations have a critical value of zero, he was able to estimate the probability of an individual being male or female using two equations:

$$p_f = \frac{1}{1 + e^{-y}}$$

$$p_m = 1 - p_f$$

where p_f is the probability that a skull belongs to a female, p_m is the probability that a skull belongs to a male, y is the solution from one of his discriminant functions, and e is a constant used as the base for natural logarithms (2.71828) (Walker, 2008).

Another pair of words whose definitions are similar but have very different anthropological connotations are ‘race’ and ‘ancestry.’ Simply put, biological anthropologists can estimate the ancestral population that a set of human skeletal remains belongs to. They cannot and will not, however, estimate the ‘race’ of an individual. This is due to many factors, including anthropology’s checkered past when it comes to ‘race’ and the current social and political climate surrounding the concept. The first anthropological experiments and theories about ‘race’ were less than scientific to say the least (American Anthropology Association, 2007, Broca, 1864). To cover the vast injustices done with these experiments would take an entire book, one that I’m sure has already been written. To summarize, many experiments in biological anthropology and archaeological theories around the nineteenth century attempted to justify the horrors of colonialism by proving white Europeans to be superior to all other humans. Eventually, these lines of thinking were corrected, but the damage was done; many atrocities were committed in the name of race and many anthropologists today avoid investigating the

topic today. As for the current climate surrounding race, I'm sure you don't need me to tell you how dicey it is. I could go on and on about social inequality, poverty rates, incarceration rates, and the like (ACLU, n. d., Kaiser Family Foundation, n. d.), but honestly you could turn on the news and watch for an hour to get a similar experience.

However, 'race' is listed on most formal identifying documents, for better or worse. Your driver's license or medical records list your 'race.' School applications ask for your 'race' while you're applying. The United States Census asks for not just your 'race,' but where your family comes from. Most missing persons have their 'race' listed when they are reported missing. To have the best possible chance of identifying a set of remains, 'race' needs to be estimated (Spradley & Weisensee, 2012). However, if anthropologists will not estimate 'race', how will investigators know whether they have the remains of a six-foot-tall white man or a six-foot-tall black man?

Most biological anthropologists will opt to estimate 'race' by estimating their ancestry. Darwin's theory of Natural Selection states that populations adapt to their environments over many generations. Certain traits are more useful in certain environments than others, and individuals with those traits have a higher likelihood of surviving to produce offspring (Darwin, 1860). A classic example of this is the peppered moth, which evolved to have darker wings during the industrial revolution in England (Grant, 1999). An example in human biology is known as Allen's rule, which states that populations who live in colder climates can adapt to have smaller, more compact proportions than populations near the equator in order to more efficiently conserve heat (Allen, 1877). Additionally, if a small group of individuals is cut off from a larger population for several generations, the future generations will exhibit the founders' traits

more frequently than the base population; this is known as the Founder's Effect (Templeton, 1980). These factors, among many others, shape the skeletal structure of humans whose ancestors hailed from certain regions of the world. The skull is used most frequently to estimate ancestry because many features vary consistently in size and shape between populations (Spradley & Weisensee, 2012). However, this variation can also affect the features of the skull associated with sex. This can cause misclassification issues with populations that an observer is unfamiliar with.

III. The Problems in the Current Research

However, many problems exist in the research of sex estimation surrounding Hispanic individuals. One of the large problems is that there aren't nearly as many available samples of individuals who are confirmed to be of Hispanic ancestry as there are samples of individuals with white ancestry. Most collections of human skeletal remains that are available for study are predominately of European or American White ancestry, which is to say, white. For instance, the WM Bass Donated Collection located at University of Tennessee, has an ancestral demographic of 93 percent white individuals, 4 percent black individuals, 2 percent Hispanic individuals, and 1 percent other or mixed ancestral groups (Forensic Anthropology Center, n. d.). In another example, the Donated Collection at Texas State University has a demographic of 94 percent white individuals, 3 percent black individuals, 3 percent Hispanic individuals, and less than one percent other ancestral groups (Personal Communication, Wescott, 2020).

Hispanic individuals are currently the largest and fastest growing minority population in the United States (US Census, 2008). As a result, forensic professionals, including anthropologists, will see an increase in the number of cases featuring Hispanic individuals (Spradley, Jantz, Robinson, & Peccerelli, 2008). Despite this, there are only a handful of Hispanic majority samples that are routinely researched. Of these, only two are held in the United States: the Operation Identification (OpID) collection at the Forensic Anthropology Center at Texas State University (FACTS) and the collection of UBCs at the Pima County Medical Examiner's Office (PCOME) in Arizona. Both collections are current, but the individuals are largely unidentified, so neither their ancestry nor sex is confirmed. This presents a problem for using these individuals as a

sample to develop or test a new method: there are no confirmed data to compare the results to.

Another complicating factor is that many remains of UBCs recovered by both FACTS and PCOME are only partially complete. The elements that are found frequently have extensive taphonomic damage due to weathering or have been scavenged by local wildlife. This makes data collection difficult, as key features may be incomplete or missing altogether, or certain bones may be too damaged to take proper osteometric measurements (Fowler & Hughes, 2018). One of the most reliable methods relies on taking measurements of long bones and using discriminant function analysis to estimate sex (Spradley & Jantz, 2011). Several studies examine discriminant function analysis of postcranial elements (France, 1989), as well as long bones of Hispanic individuals specifically (Fowler & Hughes, 2018, Spradley, Anderson, & Tise, 2015; Tise, Spradley, & Anderson, 2013). However, if the remains are too fragile or badly damaged to get precise measurements, then these methods become nigh impossible to use. While Fordisc can create its own discriminant function using the data that you are able to feed it (Jantz & Ousley, 2012), even that has its problems. First, the function that Fordisc generates becomes less accurate as less data is given to the program. Secondly, as of version 3.1 (Jantz & Ousley, 2005), Fordisc can only estimate sex from postcranial measurements of American Black and American White individuals, due to the lack of Hispanic osteometric data currently in the Forensic Databank.

Yet another factor that must be considered is that there is a disparity within the demographic of individuals who are found. Most UBCs are males between the age of 18 and 40 (Anderson, 2008). Other Hispanic-majority samples face a similar problem, with

more individuals who have been confirmed male than female. This trend tends to produce samples that have a higher proportion of males than females, as seen in many studies of the remains of UBCs (Fowler & Hughes, 2018; Hurst, 2012; Klales & Cole, 2017; Spradley et al., 2015; Tise et al., 2013). This is a problem because researchers investigating new methods will see a broader range of variation in male individuals than in female individuals. This gives researchers a clearer picture of what is typical in males, but a more indistinct picture of what is typical in females.

Additionally, anthropologists must a basic assumption about these individuals: they all have Hispanic ancestry. Most unidentified human remains found in border counties of the United States are UBCs, but not all. It has been estimated that approximately 90 percent of these human remains are from Mexico or Central America. The remaining 10 percent could be immigrants from other countries or American citizens who died in the desert and were mistaken as Hispanic individuals by local law enforcement agencies. Most border counties in Texas have a Justice of the Peace rather than a county medical examiner, and do not have the education or incentive to estimate ancestry for every set of unidentified human skeletal remains that are found. Therefore, to conserve space in their morgues, they presume that they are UBCs and bury them as such (McQuade, 2020). Therefore, a small percentage of individuals in the OpID or PCOME collections may not be Hispanic in origin.

This assumption must be made to make a model that both encompasses the scope of what anthropologists are seeing and limits the scale to something that is manageable. An example of this can be seen in many theoretical physics experiments. For example: if a physicist fired a bullet and dropped a bullet at the exact same time from the exact same

height, which bullet would hit the ground first? If the physicist neglected air resistance, wind, the recoil of the gun, the time delay between firing the gun and dropping the bullet, so on and so forth, they would find that the two bullets hit the ground at exactly the same time. The only force acting on the bullets would be gravity, pulling the bullets towards the Earth with the same acceleration. However, this is not a situation that reflects the real world. In the real world, there are countless other variables to consider in even this simple thought experiment. If all of these variables were to be taken into account, the two bullets would likely not hit the ground at the same time. However, this observation does not disprove the fact that acceleration due gravity is the same for all objects close to the surface of the Earth. The same can be said for the situation at the border. If all of the variables that change the demographic are taken into account, our methods become a lot less clear and harder to accurately use. However, this does not mean that our methods are inherently flawed; it just proves that there are variables that we had not considered in our model.

There has also been an increase in minors crossing the border in recent years, both accompanied and unaccompanied (Fowler & Hughes, 2018). This presents a challenge as most methods used to develop a biological profile do not work well on adolescents. As their bones are still growing and skeletal markers still developing, they tend to be more androgynous than a typical adult. Their bones also contain organic material than adult bones, so they tend to decompose faster and more easily.

One problem facing estimation methods using the skull in particular is that certain features on the skull are variable between different ancestral populations (Hefner, 2009; Spradley & Weisensee, 2012). For example, Hispanic skulls tend to have more gracile

features than white skulls (Duecker, 2014, Hurst, 2012). If an examiner is blindly following the method laid out in Walker (2008), or is unfamiliar with the differences between the populations, then they can misclassify less robust male skulls as female (Spradley et al., 2008; Jantz, 2004). Since the estimation of sex can effectively remove half of the population from consideration for positive identification, a misclassification can mean that the individual may be misidentified or remain unidentified. If an individual remains unidentified, their families will never know what happened to them. If an individual is misidentified, but is later identified correctly, that will cause even more hurt to a grieving family. Either way, the best policy is to use the proper methods to correctly identify an individual the first time. Even if using the skull to estimate sex is less accurate than other methods, however, it is sometimes the only element recovered, and therefore the only option available to estimate a biological profile.

A problem also exists facing estimation methods using the pelvis. The method most commonly used, as detailed in Phenice (1969), assumes that all individuals will express the extreme of the traits presented by their biological sex. For example, according to Phenice (1969), all females will exhibit a heavily defined subpubic concavity, and all males will exhibit noticeable bowing outward in the same region. However, all human traits exist on a gradient. While female pelvic bones do exhibit an incurvature in the subpubic region, for example, not all bones exhibit an incurvature as deep as shown in Phenice (1969). Scoring these traits based on their extremes fails to encompass the wide range of human variation present (Klales et al., 2012).

One could argue that DNA could be used to identify biological sex, however there are even problems there. Aside from the long wait times to obtain DNA results, the

individual's DNA may be too degraded to collect data from (Fowler & Hughes, 2018). Additionally, there are ethical concerns regarding the collection of DNA. Firstly, the process is destructive. While many Americans wouldn't think twice about that, many cultures and religions have the belief that the dead should be laid to rest and not be disturbed thereafter, or their loved one will not rest in peace. This belief can be seen in the struggles of Native Americans to protect their burials from white governments and archaeologists. A good example of this is the Kennewick Man, a nearly complete set of human remains found in Kennewick, Washington that was dated to 7000 BCE (Stafford, 2014). The Umatilla tribe, one of the local Native American Tribes, requested custody of the remains. However, several anthropologists sued the United States Government for the right to study the individual, claiming that the remains were of Caucasian descent. In 2004, the US Court of Appeals denied the request of several tribes to reclaim the remains on the basis that they were unable to show evidence of kinship. Recently, the remains were found to be genetically closer to modern Native Americans, and were reburied in 2017, but not before the skeleton was examined and had samples taken against the wishes of the tribes (Black, 2018). Secondly, many families have security concerns when it comes to having their DNA or their loved one's DNA registered, even if it is only used to identify their loved one's remains. It may be used to find their family members who live in America legally or illegally, who may then be forcefully deported (Fowler & Hughes, 2018; Stevens, 2011).

Another solution one could argue for is the combination of existing samples. For instance, a sample of Hispanic individuals may be made up of individuals from the PCOME and the Forensic Anthropology Data Bank (FDB). The FDB contains Hispanic

individuals who have ancestral backgrounds from America, Puerto Rico, Cuba, or other countries. However, even if you know the ancestral background of the individuals from the FDB, you don't know the background of the individuals from the PCOME. Therefore, you run the risk of obscuring the context of the whole sample. If the individuals from the PCOME have backgrounds from Mexico, then your sample will be unevenly weighted for each ancestral background (Bertoni, Budowle, Sans, Barton, & Chakraborty, 2003).

This leads naturally to the question of what the term Hispanic means in a forensic context. The U.S. Census Bureau defines a Hispanic individual as an individual from Mexico, Puerto Rico, Cuba, Central or South America, or an individual who has other Hispanic or Latinx origins (Ramirez, 2003). Sanchez (2013:233) defines his ethnicity as a *mestizaje*, or coming together, of “two geographical or historical axes, namely, a cross Atlantic European-American axis and a Latin American-North American Axis.” While these are useful general definitions, they are still general. For forensic purposes, they are based primarily on geography and do not account for biological processes. Birkby and colleagues (2008:31) define specifically Southwest Hispanic individuals specifically as individuals who “display the impact of European (particularly Spanish) gene flow on the Native American gene pool.” Rhine (1990:13), in decidedly less palatable terms, defines Hispanic as a “biological category indicating varying combinations of European and Amerindian stocks,” noting that it replaced the term Mestizo. These definitions come with their own problems, in that they are also very general in terms of proportions of European and Native American ancestry. This isn't meant in a gatekeeping, ‘If you're not at least 50 percent Native American, you aren't truly Hispanic,’ fashion. An identification bias has been demonstrated in Hispanic populations. Hispanic individuals with more

European features are more likely to be identified than individuals with more Native American ancestry (Hughes, Algee-Hewitt, Clausing, & Anderson, 2015).

IV. Discussion

In the past decade, some research has been done investigating the use of current methods to estimate the biological profile of Hispanic individuals. These articles showcase recent research being done into sex estimation methods. While, in general, the results are not as accurate as the original methods' published results, these methods have been found to be more accurate on Hispanic individuals than the original methods.

Klales and Cole published an article in 2017 that examined the methods detailed in Walker (2008) and used them on a primarily Hispanic sample of 61 individuals. This sample was largely comprised of individuals from the OpID and Donated Collections at Texas State University. Walker (2008), by comparison, boasts a sample size of 304 individuals, the majority of whom are of European or English ancestry. While Klales and Cole's (2017) sample size was significantly smaller, it had an even distribution of male and female individuals. For the function in Walker (2008) examined by Klales and Cole (2017), the accuracy for male individuals was 88.4% and 86.4% for female individuals, (Walker, 2008). However, when looking at Hispanic individuals, Klales and Cole (2017) found that the accuracy for males was 70.4% and 77.8% for females. This is a statistically significant difference, which warranted further examination. Therefore, they developed discriminant functions of their own using their own data. While these are less accurate than Walker (2008) on white individuals, likely due to low sample sizes, several outperform Walker's accuracies on Hispanic individuals. One equation, for example, boasts an accuracy of 81.5% on both male and female individuals (Klales & Cole, 2017).

Drs. Tise, Spradley, and Anderson have published two separate papers on estimating sex using discriminant functions and postcranial bone measurements

(Spradley et al., 2015; Tise et al., 2013). While this type of work is normally done using Fordisc, one of the weaknesses of that program is the lack of postcranial Hispanic data. Rather than generate a new discriminant function for every individual, Tise et al. (2013) developed functions based on single bones that could be applied to any Hispanic individual. To generate these functions, they used a sample of 142 individuals from the PCOME and the Forensic Data Bank at University of Tennessee, Knoxville; however, 114 of those individuals were classified or identified as male. Their results show an average accuracy of 83.32% for univariate functions and 83.14% for multivariate functions (Tise et al., 2013). Spradley et al. (2015) reexamined these results with a different sample; the total came to 150 individuals from the PCOME and cemetery collections from Zimapan, Hildago and Merida, Yucatan. Of this total, 110 had been positively identified as male. These results show an average accuracy of 87.73% for univariate functions and 87.82% for multivariate functions (Spradley et al., 2015). While these accuracies are high, and several formulae were developed that can apply to different remains in varying conditions, the samples did have a heavy bias towards male individuals. This means that the researchers could see a wider range of variability in the male individuals than in the female individuals.

In response to an increase in popularity of scientific techniques using discriminant function analysis during the early 21st century, Klales et al. (2012) sought to apply this analysis to the nonmetric method detailed in Phenice (1969). To recap from the previous section, while the pelvic bones have been shown to be the most sexually dimorphic bones in the body, Phenice (1969) assumes that all individuals will clearly exhibit the traits used in the method. This effectively turns the features of the pelvic bones into a binary system,

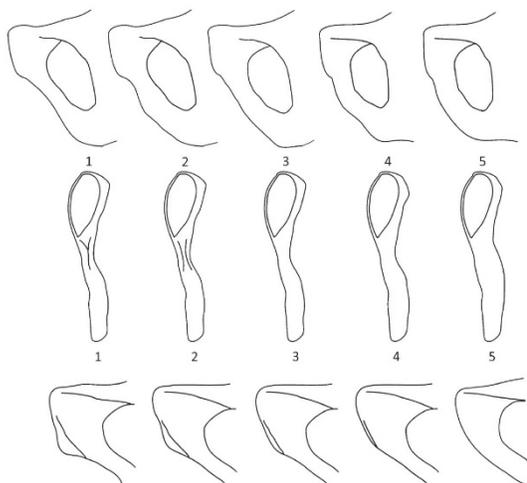


Figure 3- The scoring system of Phenice (1969) traits developed in Klales et al. (2012, p. 107). The scale ranges from 1-5; 1 being most feminine, 5 being most masculine. The traits, from top row down: subpubic concavity, ischiopubic ramus ridge and ventral arc

rather than a gradient, which is more accurate to human biology. Additionally, several validation studies of Phenice (1969) had been performed since it was published, and most failed to reproduce Phenice's accuracy rates (Klales et al., 2012). Klales et al. (2012) translated Phenice's more binary approach into a five-level gradient (figure 3) similar to Walker (2008) and developed discriminant

functions that were able to provide a probability that an individual was male or female. While the accuracy of Klales et al.'s discriminant functions fell short of the accuracies published in Phenice (1969), these functions have reported sex biases and methods to estimate the probability of an individual being male or female, which were missing from Phenice's article. Klales later calibrated and used this discriminant function to estimate sex of Hispanic individuals in Klales et al. (2017).

Because this research is newer and more niche in nature, it is typically not taught much in introductory methods classes. However, it is available to researchers and investigators, frequently at the cost of a subscription to a scholastic journal. While the debate about monetizing research in itself could take up another book, the implications for this thesis are that this research is less available for researchers and investigators who lack the funds to access this research. The removal of these fees to access research can greatly increase the amount of research currently being done.

Going forward, more needs to be done to ensure large, high quality samples for research. The current samples are spread out across universities and museums across North and Central America. To obtain a large sample of individuals, a researcher would need to request permission from several organizations. This takes no small amount of time and energy, especially if said researcher wanted to coordinate all of their proposals to be submitted on the same day.

I propose a potential solution that could remedy this problem, as well as some of the problems outlined previously: a large database containing data on Hispanic remains that have been found or identified to date. This data would include photographs, radiographs, and CT scans of the remains, osteometric measurements, scans of skeletal elements for 3D printing remains, and digitized notes collected by forensic anthropologists. In essence, this database would have all the data that a researcher would need to investigate and develop methods that primarily estimate a biological profile of Hispanic remains without necessitating access to the physical bones themselves. This database would be available primarily in English and Spanish, as most researchers of Hispanic individuals speak one or both languages. However, the notes could be translated into other languages if a researcher requests.

This will solve two main problems that I have already touched upon. First, a large, centralized database allows researchers to get a large sample of Hispanic individuals without obtaining permission from several separate, smaller samples. This database would have population affinity for positively identified individuals, so researchers could filter through individuals if they want to look at a specific population of Hispanic individuals. Theoretically, this could also aid in solving the sex disparity in

samples. Since many separate samples are consolidated into one database, a researcher does not have to sacrifice sample size to have an equal distribution of male and female individuals. The other main problem this solves is the general lack of integrity of the remains. These remains are frequently fragile or fragmentary. The ability to 3D-print remains allows researchers to examine them without fear of damaging the original remains. Unfortunately, the fragmentary nature of the remains cannot be fixed with current technology. However, the bone fragments can be printed separately or reconstructed remains can be printed as one unit, if the data for either is on the database.

Some issues with this solution could include privacy and security of data and the inability to use the original remains. The privacy or security of data is a very important topic to discuss. If all this data is centralized, but not private, then what could stop the government or other entity from taking advantage of this data to target Hispanic individuals, either in rhetoric or biased laws? If the data is not secure, then eventually some entity will more than likely either steal the data to make a profit or usurp the database to promote violent or racist rhetoric. To address these concerns, the database could be housed by a university or a nongovernmental organization with the hardware to maintain it. This could theoretically prevent some extreme faction of the government from taking advantage of the data under the pretense of the database being funded by taxpayers, provided the database is not funded by the government. The only people who would have access to the information would be researchers who request access for the purposes of developing or testing new techniques or theories. This would probably deter most malicious entities from trying to gain legal access to the data. Additionally, the database would be kept to the highest standards of cybersecurity in order to prevent

malicious entities hacking into the system.

The concerns about inability to use the original remains may seem relatively minor compared to concerns about security of data. However, while casting technology has improved over the years, most casts cannot pick up little details on bone like small fractures, poorly defined features, staining, or textures very well. On the other hand, many remains of Hispanic individuals that are available for study are UBCs who are currently waiting to be identified and returned to their families; once they are returned, researchers cannot use the physical bones anymore. Therefore, models will need to be available if a researcher wishes to handle physical bones. Casts cannot be feasibly made of every Hispanic individual and sold to researchers because of privacy of the remains; additionally, it is very immoral to profit off of peoples' suffering in general, not just in anthropological disciplines. Scans of remains can be stored as data in this database and printed by any 3D printer that has access to them. Many laboratories have some level of access to a 3D printer, and details missed in the replications can be supplemented by notes, radiographs, and CT scans.

While this solution is by no means a perfect one, it is a solution that helps to balance the needs of researchers with the needs of families whose loved ones are still unidentified. If this solution is implemented and taken advantage of by researchers, we could see a large influx of new discoveries and methods that become as accurate and prolific as current techniques.

V. Conclusion

In conclusion, while forensic anthropologists have many techniques for estimating the sex of an individual, many of these techniques do not work as well on Hispanic individuals. This is for many reasons, such as fragility of remains, small samples, and most methods being developed primarily with samples that are not of Hispanic ancestry. While some steps towards Hispanic-specific methods have been made, these steps are hampered by the limitations of the samples. My proposed solution is to create a database containing a large amount of biological data and images of identified Hispanic remains which can serve as a large sample for future research. While this solution does have some drawbacks, I believe it is a large step towards identifying more unidentified Hispanic remains, both of undocumented immigrants and documented citizens. Every human being has the right to be remembered, and this is a step towards that ideal.

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