A Synergistic Forensic Approach to Population Affinity Estimation

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DEDICATION

I dedicate this work to all the unidentified individuals whose story has yet to be fully told. To the many children we continue to be found buried on the grounds of Indian Boarding Schools. To all victims of racial injustice. I also would like to dedicate my work to my late father, Steven Allen Buck, and my late grandparents, Clyde and Nancy Buck, for your nurturing of my curiosity is what got me to this point in my life, and I shall continue this path in your honor. This work also exists to serve all indigenous peoples, to remind this globalized world that you still exist, that you were not erased. Lastly, I wish to dedicate this work to Kendrick Lee, a child taken too soon, who reminded me again of why I do what I do.

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ABSTRACT

Through analyzing the 20 skulls from the South Texas Applied Forensic Science center I aim to ascertain a better picture of the demography of our donors and what that means regarding the issue of ancestry estimation in Forensic Anthropology. I will also be analyzing genetic methods of ancestry estimation and how both forensic anthropology and forensic genetics can work synergistically to create new statistical software with greater accuracy. With our globalized society it is becoming more and more unlikely that we can fit ourselves neatly into the racial categories that the offices of jurisprudence would like us to fill, thus we should be tailoring our methods and practices to more reflect ourselves as biological populations of the species Homo sapiens rather than placing ourselves within antiquated racial typologies such as: Black, White, Asian, and Hispanic.

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Introduction

Crime shows have taken over our popular culture in the past few decades, flawlessly solving each crime within their allotted timeslot on air. While we all would like this expediency to be true, it is just not feasible. Bones, a crime drama focusing on forensic anthropology, identifies one of the most ambiguous factors of the biological profile, ancestry, almost immediately. While there are features on the osteological elements of a person that can proffer hints at ancestry, overall, they are quite unreliable at identifying various groups within our diverse population in the current age of globalization (Thomas et al. 2017). This proves to be quite problematic in the assemblage of the biological profile of human remains. Within forensic Anthropology we have quite reliable methods for ascertaining sex, age, and height; all of which are population dependent. If we are better able to define what population the individual came from then we are better equipped at providing law enforcement with a concise biological profile that they can then cross-reference with missing persons reports (Ferguson et al. 2011, Christensen et al. 2014). The forensic in forensic anthropology and even forensic genetics or genomics, which we will discuss later in more depth, means that you are of the courts or working on behalf of the courts. It is in this

space that we must enact expert testimony and the only way to do that is with accurate methods and objective rather than subjective frames.

In our journey to standardizing methods, we have made use of skeletal collections comprised of donated bodies with stated individual ancestry that we then try to match via our metric and non-metric analyses in Forensic Anthropology. It would be nearly impossible to make any improvement in the discipline if we learned solely from open cases, which are time sensitive and require the utmost proficiency. In working with skeletal collections, like the Robert J. Terry collection housed in the Smithsonian, we have a sufficient population from which to collect data. Innovations within the discipline of forensic Anthropology are made this way, by examining skeletal collections mostly comprised of individuals from archaeological origin or that were purchased from certain populations in typical colonial fashion (Hefner 2009, Ross et al 2010, Spradley & Jantz 2016). While we have learned a great deal by using these sets of remains, there is an issue regarding their ability to accurately measure our current populations. Since many of the individuals comprising collections such as the Terry collection are archeological in origin or are representative of populations from a century ago, they do not necessarily represent current populations, which can cause misclassification when we use them in our statistical software.

We have begun to circumvent this issue within the past two decades by borrowing a technique from our academic peers in medical science using cadavers for research. Just as medical students can step into an anatomy lab and dissect a medical cadaver gaining insights into the beauty that is our physiology, forensic science can also ascertain a great scope of knowledge from those who go before us. For instance, we would not know as much about the post-mortem interval or trauma identification if it were not for the altruistic gift of

individuals full anatomy. Once these initial inquiries are investigated, the skeletal remains of the same individuals are still of much value. We have used these donated skeletal remains to compile huge data sets like that of FORDISC.

The underrepresented populations in our current skeletal collections have much to do with our medical and social history (Halperin 2007 & Shiefer 2019). Much of the early advancements in medicine came at a gruesome cost of failed experimentations before a salient discovery surfaced or a technique improved upon. Anthropology itself began within the grasp of colonialism and racism, and quite often skewed its findings to place those of European origin, most hailing from the British Isles, France, Germany, and Colonial America above the rest of the world's populations. We have since reformed or abolished theories established in this manner by our predecessors. Alas we must bear in mind that even though we are aware of the predominant ideologies of the past, those we work with and the public we sometimes work for can still be inculcated within these ideologies. In relation to whole body donations, the crucial piece of our advancement in the discipline, we are met with the issues of medical history. While racism in and of itself is dubious, medical racism, as well as classism, have played a major role in the protraction of medical donations. We will dive deeper into the early days of American and British medicine and how anatomical donation has been treated through the last few centuries.

My focus of this study is the twenty skeletal remains that were on loan to the University of Houston's department of Anthropology from the Southeast Texas Applied Forensic Science Facility (STAFS) located at Sam Houston State University in Huntsville, Texas. Initially I posited that overall, I would see a prevalence of female donors in relation to male donors, surmising that females would tend to be more altruistic. Those initial

inquiries into the donated skeletal remains sparked within me the curiosity of examining our current methodologies of population affinity estimation. The literature on population affinity estimation constantly reinforces that certain populations within our skeletal collections are just not as robust as others (Dudzik 2019, Go & Hefner 2020). This made me want to look further at the actual demography of our donors and if such a record existed, so we can better tailor our donation programs to populations we have scant information on. We now live in an age staunchly affixed among technology and software algorithms are now the reigning proxy for ascertaining aspects of the biological profile such as ancestry (Ross et al. 2010, Go & Hefner 2020). Before you can gain insight from these algorithms one must still obtain physical measurements from the skeletal material. Regarding ancestry, the most valuable measurements are obtained from the skull. This is because components of the skull are both genetically and environmentally acted upon therefore creating variation among populations.

After introducing and discussing the history of anatomical donation I will discuss the issue of population affinity estimation within the discipline of Forensic Anthropology along with a history of racial typology within the discipline. In doing so I will also discuss the issues of biological race theory and how that helped create the groups we use today with population affinity estimation. I will also introduce forensic genetic methods of population affinity estimation. Then I will look at the donated skeletal collection that I used in my study, discussing sample size, and then presenting the data obtained from my research. I will present craniometric data processed by FORDISC 3.1 along with interviews conducted with board certified forensic anthropologists. After presenting my data I will then discuss my findings and how using PCR (Polymerase Chain Reaction) analysis of our RNA (ribonucleic acid) and DNA (deoxyribonucleic acid) can further help us in population affinity estimation

via use of Single Nucleotide Polymorphisms (SNPs) and Insertion/Deletion Polymorphisms (InDels), also known as Ancestry Informative Markers (AIMs). Once I have discussed the data and what it means in relation to our issue with population affinity estimation, I will discuss the improvements we could see going forward if we were to couple our current standard methods with more genomic analysis. The hypotheses I will be exploring are: 1) that both sex and population affinity trends of anthropological skeletal collections resembles the demography seen among medical anatomical gifts, 2) that the minority populations will show lower rates of classification within the discrete categories used in Fordisc 3.1, and 3) that we can better classify unknown individuals utilizing a synergistic approach with forensic genetics. With a species as varied as ours, it is impossible to fit ourselves into neat discrete categories, race categories, of which the body of jurisprudence currently demands. We should be focused on re-examining how we categorize unknown individuals, especially with the help of genetics.

History of Body Donation

In 18th Century Britain the only way for anatomists to obtain cadavers legally was from a criminal sentenced to execution. This was written into law in the Murder Act of 1752, where criminals hanged for murder were to undergo anatomization and dissection after hanging. The ideology of this comes from what was known as the Bloody Code where legal death occurred on the sentencing of the death penalty, medical death occurred via anatomization, and spiritual death was carried out via dissection (Hurren 2013). This treatment of the criminal came from the widely popular belief in the Christian resurrection, so destroying the body of the criminal completely bars them from resurrecting when the time comes, thus destroying the individual. The individuals tasked with performing the dissection on the criminal corpse were referred to as penal surgeons. These professionals assigned two stages to death of the criminal corpse, "Name of Death" where the individual was in the process of dying and "Absolute Death" where the individual had in fact expired (Hurren 2013). Anatomists in provincial England would check expiration by applying a cloth dipped in hot water and a swan feather caressing the neck. To make doubly sure of expiration they would make an incision into the sternum and watch the individual bleed out.

One bizarre case of expiration came from Sir William Blizzard, a London anatomist, charged to examine the expiration of William Sawyer who was hanged. Sawyer was hung at eight in the morning and transported to the surgeon's hall around 9:20am. Blizzard monitored Sawyer's expiration from 9:40am to 11am. By 11:40am Blizzard was unsatisfied with Sawyer's expiration, so he immersed Sawyer's heart and lungs in 100-degree Celsius water until Blizzard was satisfied no motion occurred. Blizzard declared Sawyer truly dead at noon, four hours after his execution. William Hey, a surgeon for Leeds infirmary boosted public relations by offering public dissections of criminals, such as Mary Bateman who was convicted of murder and witchcraft in 1809 (Hurren 2013). Mary's dissection lasted three days, during which time Dr. Hey made 80 pounds 14 shilling for Leeds Infirmary from the dissection lectures.

During the 18th and 19th centuries in America there was a growing demand for cadavers as the hands-on approach of anatomical dissection became a favored educational technique in medical schools. Before America's emancipation from England, it was codified in British law that murderers were to be dissected after hanging (Halperin 2007). Most anatomical specimens were procured in this manner, from the executed criminal. Once dissection took hold in the pedagogy of medical schools, the number of executed criminals

fell short of the demand, thus the practice of grave robbing took hold. This was especially the case in America. Most bodies were procured from potter's graves or African American cemeteries where people could not afford to install a mort safe (Halperin 2007). These body snatchers or night doctors, the monikers given by the public, had refined the practice so well that they could extract a body in under an hour. The public were mum to the exhumations of the poor and black communities as they were seen to be a burden on the public and in this manner, they were paying their debt to society. Every so often though, a white body was exhumed, and this did cause a stir in the public milieu. Such was the case in February 1788 when a white body was stolen from Trinity Church in New York, which caused a hostile takeover of New York Hospital on April 13th, 1788 (Halperin 2007). The New York legislature passed an act preventing any further exhumations of corpses for dissection following this riot. Similar acts were passed in Indiana and Ohio in 1879 due to the discovery of congressman John Scott Harrison's body being wheeled into an anatomical suite at Ohio Medical college and a friend of the family being found in a pickling tank at Cleveland Homeopathic Medical College the day following his interment.

It was especially prominent in America for doctors to advertise pro bono medical care to slave owners to fix the maladies of their slaves. Professionals, such as Dr. T. Stillman, would either have slave owners bring their slaves in or if the slave was too ill, the doctor would even offer to pay for the slave which would then become property of the medical institution (Halperin 2007). This in turn provided the medical institution with living subjects that would double as anatomical teaching aides once expired. Not only were African American slaves victimized by this medical torment, but indigenous peoples as well. In 1840 Dr. Weideman was fined in Texas for the public de-fleshing of two native American

corpses, victims of a conflict between the indigenous and European settlers (Halperin 2007). Post-civil war, with the emancipated north, there was still racial prejudice. Northern medical colleges would procure bodies of African Americans from the south, which were cleverly disguised as barrels of turpentine or hardware supplies shipped to hardware stores up north for pick up. Due to this imbalance of procured bodies medical mythology of people known as Night Doctors, specifically Needle Men in New Orleans arose in the black communities of the South (Halperin 2007). These men were said to give their patients cascara or magnesia to hasten death so they could sell their corpse to a medical school. This era of medical history is part and parcel of the mistrust that has accrued over time between the African American community and the medical establishment in America.

The Pennsylvania Anatomy Act of 1883 was very crucial for the curbing of a growing phenomenon of grave robbing in America to satiate the growing demand for anatomical specimens for medical schools. Dr. William Forbes is credited with the creation and passing of this anatomy act, even though Senator McKnight, also schooled in medicine, was the "true actor" in the passing of this anatomy act (Wright 2016). Dr. Forbes was staunched in a heated court case involving three men accused of grave robbing to supply Dr. Forbes' dissection suite. The weight of this robbery came about due to the location of the robbery, "Lebanon Cemetery in Philadelphia", an African American cemetery (Wright 2016). Due to this trial, Forbes' predecessor Dr. Pancoast, met with then senator McKnight to discuss how the medical school could thwart this nasty blemish placed upon the anatomy school. Senator McKnight had three requirements of this new anatomy act: statewide distribution of unclaimed bodies to medical schools, creation of an advisory board that oversaw distribution of the unclaimed bodies, and prevention of body trafficking or any

unauthorized use (Wright 2016). This Act was one of many adopted by each state, but so much attention was placed on this Act due to the nature of events surrounding its enactment. This anatomy act highlighted the blatant abuse of black and poor populations to balance the ever-growing demand of anatomical subjects. While America was dealing with its own dubious medical practices, England was tackling the very same issues but had been for a slightly longer period.

The English Anatomy Inspectorate was formed during the passing of the British Anatomy Act of 1833 as a regulating body. The inspectorate was comprised of three inspectors, one for Scotland, one for Ireland, and one to oversee England and Wales (MacDonald 2009). These inspectors oversaw the licensure for anatomical examination, receipt of notices and certificates of unclaimed bodies which were recorded and reported to the secretary of state every quarter, as well as visitation and examination of the anatomy suites to which these bodies were to be distributed. James Somerville was appointed to the position of inspector over England and Wales in 1832 and credited with the creation of an ordered system of tracking bodies, akin to the chain of custody we see today in the legal system (MacDonald 2009). Somerville's main priority was the prevention of grave robbing, which seemed to go very well. The curbing of this practice unfortunately narrowed the influx of bodies for anatomical dissection and Somerville soon feared anatomists would retaliate. There was money to be made in the procurement of corpses. St. Bartholmew's Hospital school would pay workhouses and prisons five pounds per body and were able to override the authority of the inspectorate as it was legal under the anatomy act (MacDonald 2009). Rather than make enemies with the anatomists, Somerville decided to help anatomists procure bodies outside the limitations placed on the inspectorate by the anatomy

act. Somerville would doctor burial records, so it seemed the body was never at a medical school, nor had it been disturbed. Somerville was relieved of his position in 1842 and replaced with John Bacot. Inspector John Alcock was also appointed after Somerville's dismissal as the metropolitan inspector for England and Wales, while John Bacot was over the provinces of Britain (MacDonald 2009). Alcock believed that the role of the inspectors should not be in the forefront but rather in the background. Bacot succeeded Alcock in 1844 and continued with this idea of inspectors being a background voice but maintaining the anatomy act.

In the anatomy act it was stated that next of kin could wish to bury the body of an unclaimed decedent, and thus burial societies began to form among the poor. People would claim bodies just for the purpose of burying them instead of letting them be anatomized. The inspectorate viewed these societies as problematic, and rightly so as they hindered the legally proclaimed use of unclaimed bodies for anatomization (MacDonald 2009). In one instance Bacot was informed of relatives coming to King's Medical college to claim a body, so he had the anatomists rebury the body and fix the death certificate, so it looked as if the body was never there. Before 1844 there were no laws prohibiting workhouses from selling the bodies of workers to schools or hospitals (MacDonald 2009). Bacot was known to have paid workhouse masters and undertakers for producing bodies that he would then provide medical establishments. Bacot defended his use of undertakers saying that the job of inspector was impossible for one man to execute across all of London. The gross negligence and corruption of the very institution put in place to regulate the trafficking of bodies for medical dissection, in this case in England, can be likened to the state of body procurement

in America around the same time. It only further explains the social regulation of procured bodies, predominantly from the poor and disenfranchised.

We can trace the history of human dissection all the way back to Galen who first used barbary macaques and other animals to understand human anatomy. During the Middle Ages the human anatomy was considered part of the material world and was not seen as important as the eternal soul (Gregory & Cole 2002). We can then speed up to the 15th century during the Italian Renaissance, a time when the human figure was greatly studied, and we find that a group of Italian and French professors begin dissecting cadavers for lectures on the human form. The most prominent student at the time, Andrew Vesalius, was the prominent figure in the early years of modern anatomy. He engendered the use of direct observation of dissection as a greater study of the human form compared to the traditional teaching method of studying the ancient texts alone. His book "De Humani Corporis Fabrica Libri Septem" was the first to really showcase the human form in all its splendor. Of course, during the time of the renaissance up to the 19th century there was popular belief that desecration of the body would impede the spiritual resurrection as told by the Christian faith tradition (Gregory & Cole 2002). This widely held belief stagnated the advancement of medical science through medical dissection and potentially led to the rise of the grave robbing era. It is in the 19th century that clinical pathology became an integral part of medicine, with dissection being its teaching implement, so medical schools began requesting bodies. This is when the demand for bodies outweighed the legal supply of available bodies, and the illegal transport and exhumation of corpses became the mainstay of the supply chain.

Grave robbing became a necessary evil in the eyes of the medical establishment. Before the influx of grave robbing the only way to obtain corpses for dissection was from an executed criminal. This was the case in both Britain and the United States. The demand for cadavers in the United States most likely began in 1745 when the University of Pennsylvania created the first formal anatomy course (Tward & Patterson 2002). At this time the only cadavers available were the executed criminals, which was mandated in Massachusetts by the Body of Liberties. Also, during this time dueling became a very popular act, and the state of Massachusetts decided to pass a law in 1784 that bequeathed slain duelists to surgeons if not buried in a public place with a stake driven through the body. In 1790 a federal law on cadaver supply was passed allowing federal judges to add dissection to the death sentence for murder (Tward & Patterson 2002). Once medical schools embraced the idea of teaching anatomy via dissection the demand for bodies grew, which gave rise to illegal procurement of them. The New York Doctor's Riot of 1788 was a response to this illegal procurement of bodies, when medical students were seen waving an arm at passersby. Citizens violently rioted the school and seven people died. Due to the intensity of the riot, New York legislators passed a law in 1789 forbidding grave robbing and urging the use of criminal corpses.

One of the biggest blemishes in British medical history is that of the Burke and Hare murders. These individuals would lure people to their cabin to stay overnight where they would murder them and sell the corpse to anatomists. After this horrific episode the Warburton Anatomy Act of 1832 came to pass and allowed unclaimed bodies to be donated to anatomists to curtail the rise of grave robbing in Britain (Tward & Patterson 2002). Across the pond in Massachusetts news of the Burke and Hare murders created another legislative response in the enactment of the Anatomy Act of 1831. At the beginning of the 20th century cadavers were almost exclusively supplied via unclaimed bodies. It was not until 1968 when the Uniform Anatomy Gift Act was passed and adopted by all fifty states that individuals could allocate their bodies to medical science (Tward & Patterson 2002). Medical Examiner offices still have the right to donate unclaimed bodies to medical or anthropological research facilities since the burden of burial cost is placed on the state for these individuals' deemed wards of the state.

Fastforward to the 21st Century and we can look at how medical schools procure their cadavers. One such study looked at the sociodemography of the pool of whole-body donors among the University of California system namely: Davis, Irvine, Los Angeles, and San Francisco (Asad et al 2014). Building upon older studies, they assumed the donor population would be comprised mostly of elderly, educated white males. After examining the information of the donors, the researchers discovered this was the case, but that there was in fact a second meaningful group of donors. This second group is comprised of older, single educated women who are migrants or who were first born Americans (Asad et al 2014). These results are quite interesting, especially in relation to whole-body donations to places such as anthropological research facilities.

Medical science donation appears to use more of an active recruitment style as opposed to the more passive recruitment style of anthropological research facilities, where an individual would have to know of the institution. As it turns out there are many paths to choose from when one says they wish to donate their body to science. One of my hypotheses is that the demography of skeletal samples I have examined will be comprised of mostly elderly white males. After reviewing the recorded ancestry from the registrants of my

skeletal sample I found this to be true, except for a few Hispanic males and one Hispanic female. Since the demographics seem to be similar, then perhaps the methods of recruitment used by medical schools to obtain cadavers could also be used by forensic facilities like Anthropological research facilities. Since there is a data gap in the software algorithms, we use for ancestry estimation, mostly among Asian and Hispanic populations, perhaps we could use recruitment techniques to attain data from these underrepresented groups. This of course is met with social issues, including both social and medical racism, as well as cultural taboos.

Another study of whole-body donation demography was conducted at the Alpert medical school at Brown University. In this study the researchers looked more closely at the rate of donation from doctors and willingness to donate from medical students rather than investigating ethnicity, gender, and age (Jedrzejewski & Ritter 2016). Even though the researchers focused on physician donations, they did provide demography for the total study population. Between 2003-2014, the researchers found that women comprised over half of the donor population, 52% precisely, while men comprised just 48%; and when looking at donor ethnicity most donors, 98%, are white (Jedrzejewski & Ritter 2016). One thing to note about this study in relation to their ethnicity composition is that the only other groups listed in the makeup of the study population are: African American, Native American, and White Latino, these groups comprising only: 0.8%, 0.6%, and 0.4% respectively (Jedrzejewski & Ritter 2016). While it is possible these are the only groups who donated to Alpert medical school's program it is worth noting that there are no individuals listed as non-white Latino or Asian. This study does not reveal if any recruitment effort was used to gain body donations for the program.

The researchers also investigated the breakdown of marital status and occupation. Most donors were married, 67%, followed by widowed individuals at 45% of the study population (Jedrzejewski & Ritter 2016). The only occupational categories included in this study were split into Industry; Office work, hospitality, and retail; and healthcare. Of the healthcare workers nurses were more likely to donate than their doctor counterparts comprising half of the donors from the healthcare group, 49%, of total whole-body donations; while that number is substantial, only 7% of the study population was comprised of healthcare workers (Jedrzejewski & Ritter 2016). After reviewing this study, I found some similar issues that have arisen with forensic anthropological studies and donor groups. We also have a lack of representation from Latino and Asian populations in our current standardized software for ancestry estimation. Given that this study did not discuss recruitment of its donors, I am unable to ascertain if these groups were excluded from recruitment or if these groups are just simply not apt to donate.

One study based out of Baltimore used a telephone survey to ascertain individual's willingness to whole-body donation. Questions were asked about individual demographics as well as attitudes toward donating and patient treatment in a hospital setting. When looking at the data in the chart provided in the article it should be noted that race/ethnicity is demarcated into only three categories: African American, Caucasian, and Other (Boulware et al 2004). When looking at percentages African American households were the most respondent to the survey with a representation of 47% of the study population with Caucasians being a close second at 42%, and the Other category only comprising 9% of the study population. Many of the responses stated to come from most of the population are that "patients have sometimes been deceived or mislead at hospitals" and "hospitals have

sometimes done harmful experiments on patients without their knowledge" (Boulware et al 2004). This is interesting given most of the study population are African American, a group with a long history of medical and social disenfranchisement. Incidents such as the Tuskegee experiments along with the medical establishment's miseducation that African Americans do not perceive pain the same way that Caucasians do have led to this mistrust in the medical establishment.

It was not stated that this study was confined to examining trends between two ethnic groups, yet the data suggest that is what happened in this study. Once again, a racial/ethnicity category of Other is implemented. Obfuscating data points from these individuals only creates more focus on the clearly defined categories, African American and Caucasian. Just as in forensic Anthropology there seems to be this emphasis on studying comparisons between African American and Caucasian ethnic groups when looking at the sample sizes of each group, which underrepresents and fails other ethnicities.

Social and Biological Paradigm on the Issue of Race

While we as forensic Anthropologists are tasked with gaining identity from the biological material presented to us, we must also look to the sociocultural aspect of identity as well. This is the quagmire everyone falls victim to when entering a discourse on Race. Wade et al (2014) look at the permeability of race into the political realm of the nation-state in Latin America, namely: Brazil, Mexico, and Colombia. It is touted that Race is not so much in the foreground in these countries as it is in the United States, but rather guised in the infrastructure of the government, such as the favelas of Brazil often being predominantly Afro-Brazilian or Indigenous. In this manner issues of Race are based on economic and

political motives to continue the narrative of Otherness. Derogatory terms such as "mestizo" or the idea of "mestizaje" or mixture are in fact not quite as demeaning in Latin American society (Wade et al 2014). The people of Latin America are aware of the past events that created modern day Latin America. They see this mixing of Amerindian, African, and European backgrounds as a unifying diversification of the population. In this way they see the mixture blur the lines on racial differences. Geneticists in Latin America are very concerned with using race in genomics for fear of giving rise to nationalist notions of what race is, of presenting one race as being in some way beneficial over others. Of course, this is a true dilemma for scientists when engaging with the public and the government, but geneticists like Sergio Pena reject race as a "valid concept, genetically and medically" (Wade et al 2014). Instead, geneticists view what society calls races as simply populations of our species Homo sapiens. We as scientists should be viewing identity objectively as biological populations, like the geneticists, instead of subjectively through the social lens of Race. This of course is quite the conundrum for anthropologists as we are the bridge between the biological and the social, but we must maintain our objectivity. Our loyalty, our duty is to the unknown individual on our table, and we should not be persuaded by outside influence however much of it we may encounter.

For a moment we should step back in time to before the marvelous inventions of modern transportation. The six habitable continents were for the most part isolated, thus the populations inhabiting them were relatively homogenized to breeding within the population and these populations over time developed adaptations, physically and genetically to survive the environment in which they lived. When referring to African, Amerindian, or European in a genetic sense, we are not activating the social milieu of identity, rather the temporal and

biological evidence that is telling us a particular individual belongs to or came from a certain population which can be geographically fixed and traced as the individual or the individual's family migrates. Fast forward to the era of modern transportation marvels and we are now a significantly globalized species with access to pretty much any place in the world, thus the once mostly homogenized populations have become intermixed creating the "mestizaje" examined in relation to genomics in Latin America Wade et al (2014). It is unfortunate that the discourse of Race is so enmeshed in the sociopolitical realm. As forensic scientists we are plugged into the political atmosphere working for the judicial system and ass such we must contend with non-scientists where it is our duty to voice science which dismantles the biological race concept, a long-standing idea in the mind of the public.

History of Human Variation in Biological Anthropology

To understand where we distilled our current classification system for affinal groups from we must first look at American Anthropology at the turn of the century, 1918 to be exact. This was the year Ales Hrdlicka founded the American Journal of Physical Anthropology. This was a time where traditional European anthropological thought brewed a racial anthropology that typified populations in a biological deterministic fashion. Another contender for biological determinism was Earnest Hooton. Hooton saw race as "continental groups" or in taxonomies "based on head shape" (Caspari 2009). Hrdlicka came from a background in French Anthropology being familiar with the works of Francis Galton in biometrics using media to fill the cranial cavity to measure volume of the braincase. In this way one could categorize a skull to its appropriate race, European skulls having the largest volume hence most intelligent and superior. Another influential individual would be Andres Retzius who created the cephalic index which categorizes individuals by skull shape instead of braincase volume. While these were significant strides in the discipline at the time they were investigated, we now refute the validity of braincase volume being a reliable method of attaining an affinal group for an individual.

The cephalic index is a valuable tool, but today with the level of interbreeding between populations of Homo sapiens we can see aspects of the entire index in one population. This is the preponderance of interbreeding, a concept that was considered taboo back in 1918. Hrdlicka and Hooton were what we call polygenists, having a belief in "once pure races that had separate evolutionary histories, but was complicated by an understanding that present human variation could not be accommodated within a few racial types" (Caspari 2009). Hooton had a view where human variation was much like a cascade event. Pure races would end up interbreeding and from them would spawn a hybrid race and so on and so forth thus explaining the variation of man.

The other school of thought at the time was propagated by Franz Boas, who challenged the ideology of race at the time. Boas was interested in "geographic variation" and even the same "biometrics" of Francis Galton that intrigued Hrdlicka and Hooton (Caspari 2009). Geographic variation is what distinguishes Boas from Hrdlicka and Hooton in that it looks towards environmental factors for the anthropometric findings in skull shape. In viewing variation as a geographically plastic concept then you make an incredibly good case for one species adapted to various environs (Caspari 2009). This is opposite the views of polygenists who saw each race as a potentially distinct species, such as "Homo sapiens afer" and "Homo sapiens europus" to use Linnaeus' nomenclature (Caspari 2009). This

concept of races as separate species fueled the fervor of biological determinism at the time and eventually spilled over into the public zeitgeist. A huge momentous ideological movement that cemented race science in the minds of citizens was the boisterous science of eugenics, of whom Francis Galton was a proponent.

This era of our history in Physical Anthropology is particularly important in the discipline of Forensic Anthropology in that we promoted the ideas that melanated individuals were a distinct species, H. sapiens afer, who were perceived to be lazy and have low cognitive function, whereas Europeans, H sapiens europus, were the smartest of the species. We allocated a great deal of the early years of the discipline to figuring out the differences between white and black, which is indicated in the skeletal collections we utilize in our statistical software. There is a great disparity in sample sizes of white and black Americans compared to: Asian, Latin, or Polynesian samples which tend to have less, sometimes only samples from one sex of the population. This disparity can be partly explained due to the way in which Physical Anthropology thrived, via governmental funding thus governmental research. It was at that time that we as scientists fueled an already embedded social idea of Otherness that was fueled by various populist political movements of the time. It was around this time that we had tremendous disdain for Italian and Jewish immigrants in the United States mixed with our freshly repealed social custom of slavery, many groups were targeted, and the science of anthropometry was an instrumental factchecker for the racial supremacy zeitgeist of the time. In 1982 Nei and Roychoudhury found only 9-11% of total genetic heterozygosity at 86 loci that aid in population affinity estimation (Caspari 2009). One handicap early biological (physical) anthropologists had was the absence of the synthesized human genome. Ever since the advent of the Human Genome

Project we have been gradually accumulating data which shows just truly how similar we are to one another. Indeed, one method for determining the origin of an individual we have at our disposal as Forensic Anthropologists comes from bioarcheologists and paleoanthropologists. Strontium isotope analysis can show us where an individual was living perimortem as well as if the individual had migrated.

While forensic anthropology comes out of the wider scope of biological anthropology, there seems to be less focus on the biological/genetic component of population affinity, and more emphasis placed on the social structures of race and ancestry. Within the last three decades we have seen a slight shift in the nomenclature surrounding the issue of identity. The decade spanning 1990-2000 saw a paper published by Lieberman et al showing from a survey that "50% of physical anthropologists accepted and 42% rejected the race concept", while around the same time it was accepted to categorize racial identity within the confines of "the big three: Black, White, and Asiatic (including American Indian)" (Ross & Pilloud 2021). In these early years of reforming our nuances around this issue we moved from outright calling this category race and instead began to use the word ancestry. These nomenclature changes occurred around the time the Human Genome Project was fully underway and near completion. It seems the change of nomenclature may have been predicated on the advancements from our colleagues in genetics, as now we have the road map so to speak of us, therefore, to speak of our identity as ancestry instead of race connotes a longer history that is more tangible than just the label of racial category. While this is a shift in ideology around the concepts of social understanding of biological phenotypes, it still engenders the notion of discrete categories with which to place individuals.

Ancestry is not just a single individual's line of succession, that would be their lineage, which is not quite individualistic either. In the wider social realm, we often think of ancestry as being an individual roadmap of concrete geographical locations from which those before us came. We, as a society, do not dive deeper into the conceptual aspects of this social phenomenon, looking at it as a biologist or biological anthropologist would, in terms of population structure. Yes, ancestry does involve those traceable geographic histories, but what we do not necessarily think about are the "microevolutionary forces (e.g., drift, flow, and selection)" which are enacted upon individuals who migrate to a certain degree but are far more accentuated in the future generations after the migration (Ross & Pilloud 2021). One of the best examples of this is the transatlantic slave system. This massive migration of African populations into the populations found in the New World created the Creole, the Afro-Caribbean, the Hispanic. I did not focus on the European aspect of this movement because the European colonizers were the driving force of these sudden gene flow and genetic drift events. The populations under stress, the indigenous of the New World and the Africans, were not venturing out themselves to make these lasting connections, rather they were forcibly placed within the same environment and as a means of survival, and perhaps just out of mutual attraction or love, they mated and successfully reproduced.

I must take the time now to explain that these were and never have been pure homozygous populations. The populations of individuals we find living in Africa are just as genetically close to our common ancestors as the rest of us who came about from our radiating the globe to create the population of H. sapiens we see today. It has been shown that cranial morphology "conforms" to a "neutral evolutionary model" (Ross & Pilloud 2021). This means that, for example, the tribes found along the west coast of Africa: Dogon,

Bakongo, Yoruban had for centuries, prior to European involvement, exchanged mates between the tribes. While this was mostly for economic and political reasons it has genetic and biological ramifications. Neutral molecular evolution theory holds that the changes we see at the molecular level, changes in the genomic sequence, do not affect fitness of the individual. This would also translate socially as genotypic features that do not enhance mating chance therefore, they would not be sexually selected for. These neutral mutations are due to random genetic drift, that is upended when you have forced migration of populations, which occurred during the Transatlantic slave trade. Once the populations from Africa and the New World were forced together, along with European involvement in gene flow, we get the terms Hispanic and Latin. This poses a great issue as these terms "have no biological basis" and "Hispanic" specifically has only been added categorically to things like the US census to assess individuals from "Spanish-speaking countries" (Ross & Pilloud 2021). For some reason, here in the United States and globally have accepted using linguistic categorizations as a proxy for what we think race categories are or can be. Given the long-standing anti-immigration sentiment of our country throughout its history I find this categorization to be a means of tracking the migration of peoples deemed politically problematic, but these people have been here long before the advent of geopolitical borders, and unfortunately these categories of Hispanic and Latin only exist because of European global expansions that forcibly placed disparate populations together. It's as if there has been an experiment gone awry and now it must be closely monitored, wherever it goes.

The take home point here is that geography is and cannot be a defining property of one's identity in the forensic context, especially now that we are a fully globalized species. Geography does play a part, how we socially configure ourselves into nation-sates, but the underlying genetic chains that sync us to populations are far more robust and telling of just who we are. We view these chains as phenotypic, visual, traits that we use to explain the diversity we encounter. Looking at osteology specifically, we as forensic anthropologists should be exploring the mechanisms and evolution of these "automorphies", characters seen in one group and defining if they are indeed "hyperostotic" or "hypostotic" (Ross & Pilloud 2021). As anthropologists we must view the entirety of the human population as beginning in Africa, and from this we should begin our approach to population affinity estimation. Initially we changed to fit our new environments to survive, then after the age of exploration we began to establish geographic populations which gave rise to modern global populations. Our genetic variation is "clinal" and "discontinuous", being linked to our earliest global migrations, "founder effects", and "microevolutionary forces" which have been compounded by "Transatlantic Slave Trade" and the global dissemination of European prowess (Ross & Pilloud 2021). Throughout the last ten years we have focused on creating or perfecting statistical programs to assess identity via racial categories and in doing so we allow ourselves to fall into the biological fallacy that races exist, because socially we still use this system. It is problematic to use a system such as race classification in a statistical analysis because it is not an empirical analysis with pure populations to test against. Therefore, there will always be a greater margin of error if taken at face value.

Human Variation & Secular Change

The zygomaxillary suture has been studied as a potential marker for population affinity. Sutures, in relation to osteology are distinguishers of ontogeny and interaction with surrounding musculature. This suture is said to have a "passive role" in growth of the craniofacial region "maintaining constant articulation between the maxilla and zygomatic bones (Maddux et al. 2015). To differentiate suture shape a scoring system was utilized. Using the Martindale & Gilbert method the suture is either angled or curved, and this shape was utilized to differentiate certain populations. Many North American samples, including those from the Arctic region, seem to possess an angled suture whereas curved sutures seem most prominent in African and Aboriginal Australian samples. The difference in suture shape across populations is thought to be influenced by factors such as "genetic drift, gene flow, and secular change" (Maddux et al. 2015). This difference in shape can be seen between old world populations, such as Africa, and new world populations, such as Amerindian groups. This suggests possible secular change due to climate and environmental factors and potential influence from diet as mastication throughout the period of development could determine the shape the suture takes.

It should also be noted that potential early trauma to the region is another potential confounding factor in the shape of the suture. Hefner (2003) determined that zygomaxillary suture morphology is "correlated" with other facial features such as: "nasal aperture breadth, interorbital breadth, and nasal bone structure" among Asian, African, and European populations. This is logical in that all corelating features are acted upon by the zygomatic in conjunction with musculature during mastication and other daily activities involving the masseter muscles. While Amerindian and African populations show a specific suture shape, populations in Europe and Asia have "relatively equal numbers of angled and curved sutures" (Maddux et al. 2015). Due to this extreme differentiation between populations, only marked difference in Amerindian and African/Australian populations, this method of assessment should be used cautiously and in conjunction with more robust methods of skeletal assessment.

Not only are there traits found within the crania that indicate potential affinal group, but these traits can also be indicative of within group variation temporally and socially. "Craniometric traits in humans are indicative of low heritability values and high plasticity" (Nagaoka et al. 2012). When a trait exhibits high plasticity that means the trait or traits involved are highly susceptible to environmental influence, which usually is of no detriment. The low heritability values also assume a neutral genetic function also indicating the trait is more environmentally driven, but still not being positively or negatively selected for or against as to become ubiquitous or eliminated in a population.

A great way to express this plasticity in cranial traits is by looking at a case study from Japan. The case study looks at a sample of crania from Edo period Japan and examines secular trends in "cranial dimensions" (Nagaoka et al. 2012). Secular trends occur within a population over time, usually as a result of improved diet or other environmental factors. Regarding head form there are two prominent forms "dolichocephalic", elongated and narrow, or "brachycephalic", being blunt or flattened and broader (Nagaoka et al. 2012). Of the crania examined the Hitotsubashi crania exhibited more dolichocephalic than the Tentokuji and Shirogane crania that were more brachycephalic. The hitotsubashi crania were dated to the early Edo period comprised of "townsmen" while the Tentokuji and Shirogane crania were from late Edo period and comprised of the "samurai class" (Nagaoka et al. 2012). This indicates that secular change is not only between generations, but it also occurs within the social strata. In this case of a trend toward brachycephaly, it is highly manipulated by environment especially diet during childhood. The Hitotsubashi crania were of townsmen who compose the lowest socioeconomic strata in Japanese society, the artisans and peasantry. These individuals would not have good quality food or water as the higher

Samurai class of the Tentokuji and Shirogane samples. The Shoguns however displayed "exceptionally high and narrow face with extremely narrow and prominent nose, high and roomy orbit, highly reduced upper and lower jaws" (Nagaoka et al. 2012). These features are strikingly like European features, which the Japanese aristocracy would be familiar with after the ingression of the Portuguese missionaries and subsequently the British and Americans.

In such fashion these phenotypic features are associated with success and become sexually selected among the aristocracy, and perhaps in the lower social milieu. Before exposure to the western world the Japanese diet did not consist of much dairy consumption, but after World War II the American occupation introduced milk into the population causing "increase of height" in Japanese (Nagaoka et al. 2012). What we can discern from these examples from both Edo and Showa periods is that diet effects secular trends tremendously. By changing the interface, we share with our surrounding environment we inevitably change our cranial space, perhaps not always to the extent of influencing our osteology directly. This tech boom in Japan is but one example of modern influence on secular trends.

The advancement of technology has globalized almost just as much as we humans have. This technology is unfortunately often relegated to the upper class of developing countries furthering the socioeconomic divide. As seen in this Japanese example, I would expect to see marked differences in crania of the same affinal group that are of opposing social strata. If this is the case, then non-metric analysis is quite arbitrary in discerning population affinity. Social identifiers which are sometimes recovered with remains could add conjecture to the identity of the individual in question and should be assessed after skeletal assessment. It should be noted that secular trends or "change" is defined as "changes

in the skeletal measurements of two successive populations from the same geographical region, resulting from shifts in living standards or exposure to a new environmental factor over a short timeframe" (Saini 2019). This means that in order to see these traits expressed you must wait until the next generation is born. It is initially the dietary and social improvements of the parents that initiates the secular change in the infant. There are possibly epigenetic factors involved as well, since the process begins with parental interaction with their changed environment.

These effects of dietary and social improvement can be further seen more specifically within the neurocranium. A study conducted by Saini (2019) examined cranial chord variables in a North Indian population. This study is cogently relatable to the Houston metropolitan area as we have one of the largest populations of Gujarati Indians in the United States along with other Indian sub-populations. It should be noted that sub-population here is not meant to subjugate one group or pronounce some inherent social strata. Subpopulations, in this context, are regional groups that share common environs and customs; but show slight deviations from neighboring sub-populations, which comprise the population of a country or region. This can best be described by clinal difference. In India for example, the more North you go the less eumelanin is present in individuals and the north is at a higher elevation resulting in shorter and stouter individuals. Going southward, closer to the equator, you see the opposite as in the North of the country, you get darkerskinned individuals who tend to be tall and thinner.

While these phenotypic variables are easily seen in extant individuals, there are changes that occur in the skeleton, more specifically the neurocranium, as well. Saini (2019) found that Glabella-Bregma chord was the most dimorphic measure in both contemporary

and "sub-recent" samples. This is in accordance with the general notion that males tend to have more pronounced glabellar regions, thus the male glabella-bregma chord would be larger than in the female samples which tend to show more gracile features. This "implies that the measurements vary according to sex and population" (Saini 2019). When assessing the identity of an unknown individual, namely population affinity, it is directly correlated to a sexual dimorphic paradigm. If this paradigm is misinterpreted, then it is possible to misinterpret the estimated affinal group. It has been noted that there is a "positive secular trend[s] in craniofacial measurement" which "have been apparent all over the world in the last century" (Saini 2019). This positive trend is due significantly to the urbanization and industrialization of much of the world in a rapid timespan. Add to this the necessity of migration and you get sub-populations that emerge outside of the natal population, hence Indian Americans, I.e., Gujarati or Keralan Indians living in America or outside India in general.

Spradley et al. (2016) show similar sexual dimorphic trends in Mexican migrants. These positive trends are generally "greater in developing countries and lower socioeconomic classes" (Saini 2019). The marked difference in these specific classifications is due to the rapid change occurring. Developing countries often have rapid increase in infrastructure and food security, barring dictatorships or corrupt governments. In such places where improvements to infrastructure or dietary requirements are stagnated it "modifies the capacity for populations to achieve the maximum potential size of bones" (Saini 2019). Usually in such circumstances either peri-liberation or after independence from dictatorship individuals tend to flee the suppressed region for better opportunity. This better opportunity in a more developed country enhances all aspects of an individual but is better biologically
interpreted in the generations to come. Of course, eventually as the generations come along in the novel environment, they will reach an equilibrium within the newly formed subpopulation within that environment. If a mutual level of urbanization and industrialization is achieved between the natal population and the extrinsic sub-population, then one would see a narrow similarity between them. "Thus, variables need to be updated at regular intervals to measure the extent of secular changes in them" (Saini 2019). This can be achieved via anatomic gifts presented to anthropological research facilities or via forensic cases. Using active forensic cases would slow the process if an unknown individual were representative of a new or understudied population or sub-population.

Forensic Anthropological Methods Assessing Population Affinity

Cunha and Ubelaker (2020) provide a broad scope view of evaluating ancestry in relation to forensic anthropology while championing interdisciplinary approaches. Initially they discuss the early classifications doled out by Linnaeus and Blumenbach, who categorized humans in a metaphysical hierarchy such as the Great Chain of Being and then further split Homo sapiens into regional species, i.e., Asian or African. This classification system was rooted in racial bias, a product of colonialism, which spilled over into the modern era of eugenics and race theory. While we no longer see these ideas as scientifically sound, they did have a great impact on discipline. After discussing the history of ancestry evaluation, Cunha and Ubelaker (2020) discuss the skeletal assessment methods of determining ancestry, which usually focuses on cranial aspects, but postcranial elements are also informative of ancestry such as the femur and tibia. Metric values are seen as more reliable than the non-metric measurements as non-metric measurements are subject to individual interpretation and can have observer bias. A poignant point brought up in this

article is that ancestry evaluation is a critical aspect of compiling the biological profile of an individual. There are sexually dimorphic trends in bone morphology, this applies just as well to populations, so that sexually dimorphic traits are population specific. By initially determining the ancestry one can then more precisely evaluate the other parameters of the biological profile: sex, stature, and age. There is discussion of current software algorithms used such as: FORDISC, CranID, and AncesTrees. While FORDISC is currently the standard software in the US, its use abroad should be cautioned. Most of the cases that build up FORDISC's database use forensic cases from the United States and may not reflect populations aboard thus giving out a skewed evaluation. Since the software uses compiled databases, some populations are underrepresented, this lack of certain populations in the databases opens opportunity for misclassification. This is where the interdisciplinary cooperation with forensic genetics and genomics comes in. Cunha and Ubelaker (2020) highlight several polymorphisms: short tandem repeats (STRs), single nucleotide polymorphisms (SNPs), and insertion/deletions (InDels). All these genetic markers, referred to as Ancestry Identification Markers (AIMs) can narrow the likelihood of ancestry down to certain global populations. A strong trace chemical approach is the analysis of the strontium isotope found within the dentition of an individual. This can determine the migration status of an individual as well as determine where an individual has lived for the past ten years. Cunha and Ubelaker (2020) strongly voice a push towards interdisciplinary work on ancestry evaluation.

In a letter to the editor Bethard and DiGangi (2020) are offering a critical look at our current standard practices in forensic anthropology regarding ancestry estimation and the effect our findings could have. The overall argument in this letter is a moratorium on the use

of morphoscopic traits in the ancestry estimation process. The reasoning behind this movement is due in part to our lack of understanding of how these traits form, and that these traits help bolster the now debunked biological race concept. As mentioned in the letter, we as forensic anthropologists are obligated to identify these individuals without hindrance, yet it is possible that once our work is done in the identification process some individuals get lost on the side of police investigations (Bethard & DiGangi 2020). It is noted that no such studies have been done on the correlation between ancestry identification by forensic anthropologists and positive identifications carried out by law enforcement. Non-metric traits were discussed, and non-metric traits should not be utilized so readily as they are generally best assessed based on observer experience. What this means is that someone who focuses their work on a specific population would be able to identify the non-metric traits associated with that population, therefore having a higher probability of correctly identifying that individual; but if the individual comes from a population unfamiliar to the observer, then use of non-metric traits can be obfuscating. As this letter to the editor imposes this moratorium on morphoscopic traits of the skeletal biology, this letter does not speak on the genomic aspect of ancestry identification which is less likely to be misconstrued by social bias.

One of the first software designed to assess population affinity via craniometrics was CranID. The majority of the CRANID5 database come from the Howells skeletal collection, which while encompassing samples from different regions of the world does not carry with it equal sample size across the regions housed in the collection. Since the first edition of the CRANID5 database other samples from different regions have been added to give a total of 66 samples, of which most have male and female samples (Wright 2008). Initially Wright's

chapter looks at the history of craniometry going back to Franz Boas and the use of cranial length and breadth to assess race in the early 20th Century. Given the technological reach of the time this was the best that could be done in relation to social mores regarding classification of peoples. This bivariate measurement unfortunately does not encapsulate the intricate and complex geometry of the human skull, which is of course three dimensional. Multivariate analysis, such as use of the 29 measurable traits implemented in CRANID5, allows a greater statistical probability of correctly placing an individual within their affinal group. Wright (2008) does caveat this though with four possibilities for a skull to come up indeterminate or misclassified. This first of which is user error in that the measurements were done improperly. More importantly though is the acknowledgment that the area the individual is from may not be adequately represented in the database. The person is an anomaly in their group or has deformations that complicate assessment, and the possibility that the individual is of a multi-populational background is quite likely. Given that we live in such a globalized world admixture is now the norm. If people of biracial or multiracial backgrounds are problematic in our current databases, then this poses a huge issue moving forward. While the assessment of CRANID5 is favorable, its use of "nearest neighbor analysis" is not so forthcoming (Wright 2008). In the second repatriation case mentioned, Wright (2008) used linear discriminant analysis in FORDISC 2.0 which gave an identity of European and initially CRANID5 identified it as Siberian. The first eight samples from CRANID5 pointed toward mongoloid origin, which is of course an antiquated term, but this suggests broadly an Asian origin. It was not until utilizing nearest neighbor analysis that a southern Japanese male skull would correlate to the unidentified skull, which was determined to be of Japanese origin.

Manthey et al. (2018) references another study within their research that assessed secular changes in German and US crania, which showed differences. This research was conducted to show that more population specific data is needed with FORDISC3.1 when used outside the US. The software is composed of the Terry skeletal collection (which is dated to the 19th century), and both forensic cases and the William Bass skeletal collection from the 20th century. In Manthey et al's (2018) research they note that 19th century Euro-Americans more closely line up with 20th century Italians, have a shorter cranial base and wider cranial breadth. When comparing the modern US population, the modern US population has a narrower cranial breadth and more robust glabellar region. When they ran the Italian crania through FORDISC3.1, they show that misclassification occurred among the sexes. Italian males were being classified as female in the FORDISC3.1 software. This problem is why estimating ancestry as accurately as possible is necessary for establishing a biological profile. Sexual dimorphism is different among populations, Manthey et al. (2018) mention a study done comparing three European populations: German, Italian, and Lithuanian. In that study Germans and Italians were seen to be closer together than the Lithuanian group to either German or Italian population.

In the Ancestry section of chapter 5 by Komar & Buikstra (2008) there is discussion of some of the issues surrounding ancestry in forensic anthropology along with the current methods used that are accepted by the Daubert standard set by the courts. Early in this section they reference Ousley and Jantz who say that "there are no races, only populations" and that "race can and should be used in its social context". If we only look at populations, then we can begin to see that even in our definitions within the biological race concept (Caucasian, African, Asian, Hispanic), there is slight difference among the local populations of these larger groups, for instance between European-Americans and European German and Italian populations. Komar and Buikstra (2008) also discuss the issues surrounding the use of Hispanic as a category among Caucasian and African American as Hispanic is an ethnic categorization rather than a biological one, therefore includes populations of European descent with those of greater indigenous genealogical affinity. We can go back to the first half of the 20th century to the work of Sherry Washburn and his legacy of stewarding us into a new Physical Anthropology, one that moved away from the Race concept and typology and ushered Physical, now Biological, Anthropology into evolutionary science utilizing population genetics (Caspari 2003). FORDISC is mentioned as the best algorithm in use that meets the Daubert standard, although caution should be used when using it on individuals possibly from underrepresented populations. There were at least two studies done, one on a Spanish sample dated between 1500-1700 and a Nubian Meroitic sample, where use of the FORDISC software yielded difficult and misleading interpretations.

The research conducted by Manthey et al. (2016) aimed to highlight the sexual dimorphism between modern German and Euro-American populations. While FORDISC 3.1 has Euro-American and even some European, including German, samples they are mostly from the 19th century. Manthey et al. (2016) show that either 19th or 20th century German skulls are indistinguishable from 19th century Americans, yet 20th Century Euro-Americans seem more robust than their 19th Century Euro-American and German counterparts. Only three measurements were assessed in this study: mastoid height, bizygomatic breadth, and glabella subtense. It is noted that one theory for this sexual dimorphism between populations is the "umbilical cord blood testosterone" that is passed from mother to fetus, which is

known to cause a more masculine shape to the facial region (Manthey et al. 2016). With strong evidence towards higher testosterone uptake during fetal development, the discrepancies found with FORDISC 3.1, and international use is the differentiation between populations. Even though there are representatives from the ancestral group within the FORDISC 3.1 algorithm they are not necessarily representative of the temporal population due to environmental factors. Manthey et al. (2016) anchor this further by positing that the secular change between the German 19th and 20th century samples occurred later than the secular change among the 19th and 20th century Euro-Americans. If this is indeed the case it only bolsters the idea of environmental factors playing a role in shaping some of the facial morphometrics used to ascertain not only ancestry, but even sex.

In this study conducted by Spradley and Jantz (2016), Spradley and Jantz compared the efficacy of the standard interlandmark distances found in Buikstra and Ubelaker's 'Standards for Data Collection from Human Skeletal Remains' and newer non-standard interlandmark distances. The groups used in the analysis of this study were American White, American Black, and Hispanic. The Interlandmark distances were measured using a Microscribe digitizer, which allows for 3D measurements. It should be noted that due to the cost of such instruments, this type of analysis is not necessarily available to all research facilities and researchers or practicing forensic anthropologists. 31 landmarks were chosen for study. Due to the 3D measuring ability of the Microscribe a total of 465 non-metric landmarks are possible for measurement from the 31 metric landmarks chosen from Buikstra and Ubelaker's Standards. After computing the landmarks, they were then able to ascertain Procrustes coordinates and centroid sizes for comparative analysis. When calculating mahalanobis distances the non-standard interlandmark distances provided larger distances than the standard landmarks from Buikstra and Ubelaker or geometric morphometric landmarks. The conclusion made with this study is that geometric morphometric landmarks are not necessarily better for identifying ancestry (Spradley & Jantz 2016). In fact, the nonstandard interlandmark distances are more accurate. The higher accuracy of the nonstandard landmarks is most likely because there are more of them to measure. Spradley & Jantz (2016) does state that this approach is more applicable to cases where taphonomy and trauma may have removed sections of measurable distances. When there are only fragmented remains it is more likely to narrow possible identification of remains when you have more measurements.

There has been some effort outside the US to compile samples representative of populations outside the US to better assess international cases, one such skeletal collection is that maintained at the University of Coimbra in Portugal. It should be noted that all the individuals in this collection were exhumed according to Portuguese law for unclaimed individuals. Most of these individuals were buried, yet unclaimed. The age range of this collection, when the article was published, was 25-99 years (Ferreira 2014). From the date of publication to the present, with the expected accrual of 20 individuals per year the age range could have expanded. It should also be noted that this collection is majority female, which is not common among our skeletal collections. The preservation of this collection is quite good since they were interred for a period. Almost all bones are present, some with prostheses. The only real issue occurs when looking at the older samples in relation to dental analysis as many individuals are edentulous. Depending on the degree of tooth loss, useful measures like palate breadth are unmeasurable if the alveolar channels are completely resorbed.

Dudzik (2019) approaches the issue of Ancestry estimation in relation to craniometrics with a multi-faceted approach. Their study advocates the use of geometric morphometric analysis in combination with standard craniometrics to better assess group affinity of an unknown individual. The problem explored exclusively in this study is the misclassification of Hispanic and Asian populations in the FORDISC 3.1 software. Data from Hispanic individuals is often misclassified as Asian, more specifically as Japanese, given the data in FORDISC 3.1 (Dudzik 2019). When using geometric morphometric measurements, you can enhance the relationships between groups because you are assessing them in a 3-dimensional coordinate space. The most important aspect being the Mahalanobis distance. When assessing the craniometrics on their own Hispanics had the shortest distance between the Japanese samples. In comparison to the Procrustes analysis, the Hispanic group had a longer distance between Asian groups and was closer to the American White and American Black centroids. In fact, using Geometric Morphometrics showed a correct identification rate of about 89% among Hispanic and Japanese samples. While this is greater than the classification rate of craniometrics on their own, the equipment needed to ascertain geometric morphometric data is still quite costly. Currently a G2X digitizer is the standard equipment used. While bigger cities and jurisdictions have the funds and facilities to use this equipment, the smaller counties that are underfunded do not. While we can see improvement in analysis of our data with novel technologies, we must keep in mind the accessibility of such technologies for all practitioners in order to improve population affinity estimation throughout the discipline.

Forensic Genetic Methods Assessing Population Affinity

Forensic Genetics complements forensic Anthropology very well in the ascertainment of identification of the unknown individual as we can ascertain SNPs, InDels, and STRs from bone samples. In this study by Bulbul et al (2018) they present a way to improve distinction between southwest Asian populations. One of the populations FORDISC is known to have higher misclassification with is the Asian population. This of course could simply be due to the vastness of the Asian continent and the numerous subpopulations that call it home. A point of focus in this study was southwest Asia, which is noted to have a great deal of genetic drift through the region due to lack of natural barriers between populations such as a large ocean or difficult mountainous regions (Bulbul et al 2018). This study was able to show software's ability to differentiate central/northern European groups from the Southwest Asian groups. There were 86 single nucleotide polymorphisms (SNPs) that were found to distinguish Southwest Asians, some of which even showed a strong relationship between Kuwaiti/Yemenite groups and Ethiopian Jews. The panels used to assess these genetic markers are highly accurate at grouping individuals into four major groups: European, Asian, African, and American. The three AISNP panels used in this study were: ALFRED, Frog-kb, and Kidd Lab 55, which has the largest amount of reference population samples. There was a two-step reduction process, a first tier and second tier, where initially one narrows down via the four major groups and then even further to region specific populations. Frog-kb is a web-based statistical software, so much like our anthropological software it only gives you the highest likelihood not an exact match. Populations that are in close contact, whether it be due to trade or seasonal migration, will experience genetic drift. This can become an issue if samples from each micro-group or the microhaplotype for each are not sufficiently assessed. One example of this would be Turkey where you have Turkish and Turkish Cypriots present in the population. This can be further confounded due to our highly globalized society where borders have become increasingly obfuscated genetically speaking.

Wang et al. (2019) presented a novel sequencing panel designed to assess genetic ancestry of cancer patients to better assist in the treatment of their cancer, namely liver cancer in this study. While this study is focused on using ancestry identification markers to help reveal population admixture in relation to medicine and the treatment of liver cancer, this same panel could be used forensically as well. This study aims to identify those within the Hispanic population, the sample group of which comes from south Texas. The 250 ancestry identification markers that compose the panel were used to assess the population admixture present in everyone within this study (Wang et al. 2019). The panel breaks up the population into: African, East Asian, and European populations, which are the migrating populations that interbred with Amerindian populations comprising the group we know as Hispanic/Latino. While the most exciting part of this study was indeed the efficacy of using either normal or tumor tissue to assess ancestry, the assessment and efficacy of this "UT-AIM250 panel" could potentially be used in the forensic context of identifying unknown remains (Wang et al. 2019).

Genetic materials have been used to sort out paternity issues along with disease susceptibility for at least the last two decades. Some of the very same genetic material and methods are just recently being posited for forensic application. Zeng et al. (2016) focused

on studying the informativeness of single nucleotide polymorphisms (SNPs) in relation to deciphering population affinity. Often in forensic practice autosomal short-tandem repeats (STRs) are used when a surviving relative of a victim is available, and a confirmation of relatedness is given or in pursuit of paternity. While this is acceptable in the case of assessing a sibling or parent-child relationship, this is not the best genetic marker to look to for assessing population affinity due to a "relatively high mutation rate" and the fact that most "common alleles" of STRs are found throughout the global population (Zeng et al. 2016). This high ambiguity of alleles could lead to a high frequency of misclassifying individuals. In contrast, SNPs have a "relatively low" mutation rate and the SNP allele location is "often identical by descent" (Zeng et al. 2016). It is due to the low mutation rate of the SNPs that allow the replication to pass generation to generation, thus becoming a sort of tracking number. Zeng et al (2016) comprised their study into four populations in the United States: African American, Caucasian, Chinese, and Mexican, which they crossreferenced with SNPs from HapMap global samples of: Yoruban, Han Chinese, Japanese, Italian and samples from the 1000 genome project of: Yoruban, Han Chinese, British, Columbian, and Mexican. The global populations selected to trace and assess the United States populations is indicative of the populations that shape the United States due to the forces of Colonialism. The study concluded that all populations tested fit into their expected groups.

One of the biggest populations with a high rate of admixture would be the Hispanic ethnic population. Given the complex history of the Americas, especially Central and South America, individuals from these regions would be expected to have a high chance of admixture. The "Setser80" AIM panel was compiled to address identification of Hispanic

individuals specifically (Sester et al. 2020). It is likely a better approach to form regional specific panels initially to ascertain substantial trends in the population, thus gaining better understanding of potential admixtures. By narrowing the AIMs in the panel to more population specific polymorphisms you also are decreasing the white noise often attributable to statistical error. This narrow selection also can help rule out outliers or potentially new members of the population. For example, if an individual has just migrated from Portugal to Brazil one would expect to see polymorphisms that would show Portuguese ancestry as the Portuguese have major influence on the population of Brazil, but this individual would not be likely to show polymorphisms indicative of the indigenous, African, or Japanese populations which have also shaped the modern population of Brazil.

A common occurrence in forensic anthropology is the taphonomic effects of time on the skeletal elements in relation to the environment in which they are dispatched. The longer biological elements are left to decay the higher the rate of DNA and RNA degradation. This can inhibit the use of some genetic tests, but not all of them. It has been shown that "Indels... produce much more balanced peak patterns (within locus, the two alleles for a heterozygote show similar peak heights) than those of single base extension SNP tests" (Romanini et al. 2015). These Indels, insertion-deletion polymorphisms, can be found within bone and are indicative of a point in DNA replication where a base pair or segment of DNA is deleted, and a modified base pair or segment is inserted in its place. Such tests are reliable to ascertaining single group affinity, I.e., an individual is African, but when presented with an individual of admixed background there showed "markedly lower probabilities" which can be improved by utilizing "PCA plots" to better understand the makeup of an admixed individual (Romanini et al 2015). In the study conducted by Romanini et al (2015) they utilized a 46 AIMs-Indel multiplex to assess the genetic background of the samples with "95%" of the markers being successfully typed. This high percentage of statistical probability shows that this method is reliable in conjunction with aged remains. It can be inferred that if such robusticity is seen in analyzing aged bone, then it should work just as well on remains that are more taphonomically recent. Such analyses can be helpful in cases where the possibility of an admixed background is likely and could help narrow down the highest proportions of populations present in the genetic makeup of the individual.

Methods

Skeletal Analysis

I assessed the 20 skulls on loan to the Department of Anthropology at the University of Houston from the Southeast Texas Applied Forensic Science facility (STAFS) of Sam Houston State University. The skulls were examined using both digital and spreading calipers for osteometric measurements. Since I am assessing population affinity, the only skeletal material I focused on was the skull as the skull currently holds the most data used to assess population affinity via anthropometry. I used Buikstra and Ubelaker's "Standards for Data Collection from Human Skeletal Remains" as a reference guide for which cranial measurements to assess. A list of the measurements taken from the skulls is found in Appendix I and I will discuss the measurements used in the statistical software analysis via FORDISC 3.1 3.1 and why they are seen as significant for estimating population affinity.

Due to an initially high error rate using all twenty-seven measurements taken, and accounts from subjects interviewed stating FORDISC 3.1 3.1 must have at least thirteen

measurements for statistical confidence, I made the decision to restrict my analysis to 14 measurements: glabello-occiptal length, maximum cranial breadth, basion-bregma height, bizygomatic breadth, palate breadth (external), nasal height, nasal breadth, orbit height (left), orbit breadth (left), biorbital breadth, interorbital breadth, nasion-bregma chord (frontal chord), bregma-lambda chord (parietal chord), and lambda-opisthion chord (occipital chord). The reason for restricting the measurements was not only due to a high error rate in analyzing the initial twenty-seven measurements, but to be more accurate with what we should expect to see in the field. I was fortunate to record my data using anatomically gifted skeletons, most of which were complete. There were however two individuals, STAFS 2009-004 and STAFS 2010-008 who had skull trauma that obfuscated several landmarks. STAFS 2009-004 had blunt force trauma to the cranium, making it impossible to locate all necessary landmarks for the chord measures, however the nasofacial region was intact for measurement. STAFS 2010-008 had a gunshot trajectory through the parietals, entering from the posterior right parietal region and exiting on the left subparietal region obliterating the left temporal bone making it impossible to accurately measure maximum cranial breadth as this measurement is situated along the temporal bone's borders and surrounding area. These two cases are what we should expect in the field.

We will rarely be presented with a completely intact skeleton. In relation to war crimes or acts of genocide obliterating these features would be another step in masking the social identity of the individual and group being subdued. Here in the United States, and even globally, the fascination with crime shows has expanded the potential ways in which murderers hide the identity of their victims, thus we should be prepared to experience an increase in the likelihood of less skeletal landmarks for population affinity estimation.

Another reason for selecting these 14 landmarks is the relation they potentially have with "secular change" within and between populations (Manthey 2016). Secular change is the change in anatomical structures, usually dealing with height and morphology of osteological elements, between populations. Manthey explains the secular change between native Germans and German immigrants to the United States and how the first-generation American born individuals show noticeable change in their head shape from that of their native German counterparts. These changes in morphology are thought to be initiated by the environment, especially diet. This is clear when Manthey discusses the secular change between 19th century American and German individuals and 20th Century American and German individuals. As we moved deeper into the industrial revolution and the rise of the age of technology, we have improved many aspects of our environment that allow optimal nutrition and thus change the way in which we develop overall.

Measurements were taken twice to ensure proper recording and lower observer error. Once recorded, measurements from the skulls were compiled into an excel spreadsheet which was then imported into SPSS (Statistical Package for the Social Sciences) for sample analysis. Demographic analysis was done through SPSS of the sample group, such as sex differences and correlations between the measurements and stated ancestries versus the estimated affinal group calculated by the databanks in the software.

Forensic Anthropological Software Analysis

The measurements taken from the 20 skulls were also put into the standard statistical software package, FORDISC 3.1, to assess the statistical probability of ancestry. FORDISC 3.1 is the standard software used by American Forensic Anthropologists and is compiled of

two datasets; the Forensic Data Bank, mostly American forensic samples from the William M. Bass Donated Skeletal Collection with the newest sample population coming from Guatemala, and the Howell's data bank, which is comprised of more archaeological specimens from around the globe. These data banks in conjunction with the statistical package in FORDISC 3.1 use what is known as "discriminate function analysis" (Ousley & Jantz). This type of analysis takes an unknown individual and compares their biometrics to all individuals within groups of interest. So, if one is trying to find out if an individual is either White male or Guatemalan male, those groups are selected, and the analysis runs a distance measurement, the Mahalanobis distance, of the unknown individual to all samples in the database to find the sample with the most similar biometrics. The mahalanobis distance is "multivariate measures of likeness or difference over a set of traits (usually metric) for purposes of organization and comparison among populations" (Howells 1971). This type of distance measure is orthogonal in nature, plotted within a Euclidean space, thus being able to be mapped in a three-dimensional cluster or forest. If an individual does not have statistical probability of similarity to an individual in the groups in query, then the individual is listed as undetermined. This does not mean that the unknown individual does not have affinity with these groups, but perhaps that the individual is of an admixed population affinity.

Distance measures are not without their own limitations. Within the population, say the United States, which is a diverse population there are subpopulations fueling that diversity. When examining at the whole population level you can expect to see "higher variance in gene frequencies" of "small subpopulations" within the subpopulation in comparison of larger populations (Howells 1971). It should be noted that large population

and subpopulation in relation to the issue of multi-affinal individuals should be seen as a homogenous/indigenous population and migrated populations respectively. These migrated populations are akin to what the political sphere likes to term the –American, such as Congolese-American or Filipino-American. These are scoped identities, which crania are not conducive to "fine-grain population studies" but are quite useful in "distance studies" (Howells 1971). Even though there is a noticeable diversity in the appearance of the Gestalt among different populations, the general shapes of the Gestalt within populations are quite uniform and sexually dimorphic. This is in part due to environmental factors. In order to assess more exactly the specific population of an individual you would need to assess the genetic makeup of the individual, which we will discuss in the Discussion section.

While using discriminate function analysis is quite reliable with a high rate of accuracy, the use of certain groups of individuals does pose some limitations. In the Howell's database for example many of the individuals comprising the samples outside the United States are at this time dated, archaeological specimens, and not as accurate as modern individuals due to secular change in populations over time. One instance of this secular change is the increased mobility of humans to travel and live anywhere in the world. Once highly homogenous populations have become more diverse with people vying for economic betterment. This migration of people often from the global South to the global North improves health conditions, i.e., a more balanced diet, which changes the way the next generation appears biologically. Environment plays a significant role in changes of the skeleton via secular change. One important group in Howell's database that shows this is the White groups, there is White19s and White20s. The White19s denotes 19th century

individuals and the White20s denotes 20th century individuals. We will examine this secular change further in the results section.

Interviews

After acquiring IRB (Institutional Review Board) approval for human subjects, I began to pool a collection of certified Forensic Anthropologists from the American Board of Forensic Anthropology's active Diplomate list. After looking through all the active Diplomates I compiled a pool of 60 candidates. Outreach was conducted via email correspondence. Once the subject agreed to be interviewed and sent back the signed consent forms for audio/video recording of the interview we established a date and time for the interview. Due to varied locations of many candidates and the still present COVID-19 pandemic most of these interviews were conducted via Zoom or Microsoft Teams, whichever software the subject was more comfortable with. The interview sessions were allowed to run 90 minutes (about 1 and a half hours) but averaged around 45 minutes. The reason for the length of session was to allow more of a dialogue instead of just discrete question and answer format. The interview process followed a 14-question questionnaire. Below is the list of questions asked to the subject:

- 1) What methods of identifying ancestry are you familiar with?
- 2) During your career have you seen a shift in the methodology of estimating ancestry?
- 3) Are you familiar with the software AncesTrees?
- 4) Are you familiar with the software CranID?
- 5) Are you familiar with the software FORDISC 3.1 3.1?

6) Of the software you have used, how accurate would you say it has been at estimating ancestry?

7) Do you believe that ancestry estimation is still an important part of the biological profile?

8) Do you believe use of archaeological skeletal materials should be incorporated in the datasets used to compile a software algorithm?

9) Would you say there is prejudice placed on certain remains when ancestry estimation is compiled?

10) Would you say there is a great relationship between Forensic Anthropologists and genetics currently?

11) How much reliance would you say is placed upon forensic DNA assessment in relation to skeletal analysis?

12) Have you had any experience in using single nucleotide polymorphisms (SNPs), insertion/deletion polymorphisms (InDels), or other ancestry identification markers from genomic material in relation to estimating ancestry?

13) Do you think institutions like the Body Farms are reaching out to the populations we are lacking proper data for?

14) Do you think we could have better methods for advocating anatomical gifting to forensic research?

These questions were asked to initially know what current standard methods are in practice among board certified Forensic Anthropologists and secondly to peer into the ethical dilemma presented with estimating population affinity, the potent miasma of Race Science. As Forensic Anthropologists we focus on analyzing the osteology and what it can tell us, but fundamentally within our training in Biological Anthropology we should be familiar with everything listed in these questions, except for questions: 7,8,9,13, and 14, which are all opinion-based questions not necessarily indicative of former training in the discipline.

While conducting the interviews I not only recorded the sessions but also took written notes as well. This was important as some interviews had technical issues where portions or whole interviews were not recorded. This was an instance where working on the research during a pandemic had its challenges. Most of the interviews I had to conduct from my home office space and many of my subjects did the same. This enhanced the interview experience in that both parties were able to carry the process as a friendly conversation rather than strictly a formal interview setting. Once all the interviews had been done, I went back through and transcribed them from my shorthand notations. Once the answers to the questionnaire were transcribed for each subject, I could then assign a numeric value to certain answers and then conduct a quantitative analysis of them via SPSS (Statistical Package for the Social Sciences). In total I had only 7 of the 60 potential candidates go through the interview process. The reason for such a low turnout of subjects is mostly due to the time at which the outreach process took place. I began doing the outreach in the latter half of the Spring 2021 semester once IRB approval was granted. This is around the time of semester finals for most universities in the United States and so the subjects who are involved in university education were not available and had projects coming up in the summer interim period. Other subjects, who work under the auspices of the office of the medical examiner, stated they were too busy with casework for an interview.

There were three international subjects of interest, all of whom did not respond back after several attempts. Given the COVID-19 global pandemic I was ambitious in recruiting individuals from outside the United States to participate, but my outlook on a response was very slim. Perhaps had the interview process been facilitated during the fall and outside the scope of a global pandemic there may have been greater turnout for the interview sessions. It should be noted that one subject was willing to participate but did not have the time for the length of the interview session and asked if they could receive the questionnaire by email and fill it out. Due to the low turnout of subjects, I allowed this to be a way of conducting the interview gaining the proper consent for participation, but not for audio/visual recording of the subject.

<u>Results</u>

Osteometric Data

After collecting the osteometric data from the crania, the data was input into both datasets within the Fordisc software, the Forensic Data Bank and Howells data bank. One interesting discrepancy between the two data banks is the way in which populations are classified. Within the Forensic Data Bank populations are classified into: White, Black, American Indian, Chinese, Japanese, Hispanic, and Guatemalan; whereas Howells's data bank shows continental grouping, but then further differentiates by ethnic group or tribe. For example, within the Howells data bank American Indian is subdivided into categories such as: Arikara and Eskimo and African is subdivided into categories such as: Dogon and Ethiopian. Of the twenty individuals in the sample from the STAFS collection twelve individuals classified into categories congruous to the individual's stated ancestry at time of body bequeathal. It should be noted that these twelve individuals that classified correctly were all the stated ancestry European, whereas all 3 of the Hispanic individuals misclassified when ran through both data banks. While it is possible that these individuals are indeed outliers in their respective populations, meaning that they are representative of their stated ancestries and are anomalous to the samples in the data banks; I present the possibility that there is more likelihood that these individuals are of mixed background. Being of mixed ancestry would also explain these discrepancies between stated ancestry and the results of the Fordisc assessments.

Graphs 1a-7a below represent the seven individuals who misclassified in the forensic data bank analysis. The dendrograph shows each potential affinal group as an ellipse where each cluster of color-coded dots indicates individual samples forming the population represented by the ellipse. The unknown individual, or the individual we are imputing data from, is indicated by the black square with a white X. This is plotted via calculation of the Mahalanobis distance of the unknown individual in relation to all individual samples within the groups of interest. For instance, Graph 7a represents STAFS 2010-001 with stated ancestry as European. When selecting potential groups to run against it was kept in mind that this individual is of American origin and by stating European ancestry all groups with historical interaction with Europeans were selected. This individual was run across: White male, Black male, American Indian male, Hispanic male, and Guatemalan male populations in the forensic data bank. The categories of Chinese male and Japanese male could have also been selected due to potential interaction with European populations, but this sample group being analyzed did not have any stated ancestries of Asian origin.

It has been noted that Fordisc does misclassify individuals of potential Hispanic origin as Japanese in origin, so to negate this misclassification Asian sample populations were not consulted (Dudzik 2019, Hughes 2019, Go 2020). The result from the forensic data bank shows this individual being of Guatemalan origin. Graph 6a, STAFS 2011-004, also presented with the stated ancestry being European and classified differently under forensic data bank analysis. When ran across the same populations as Graph 7a, which all cases were applied to, STAFS 2011-004 classified as a Hispanic male. While Fordisc has added a sample of Guatemalan males it is not clear if individuals placed in the Hispanic category that could classify as Guatemalan were eliminated from the Hispanic category or added to the

Guatemalan sample. Failure to do so could further cause misclassification where the individual classifying as Hispanic could be Guatemalan. With this possibility in mind, I still conclude that the possibility of admixture is still greater than the possibility of misclassification. In table 1 you can more easily see the misclassification between the data banks and stated ancestry of the individuals.

Graph 5a, STAFS 2011-014, presented as European and when analyzed in the forensic data bank showed highest affinity to the Guatemalan sample. Graph 4a, STAFS 2011-024, presented as a Hispanic male, but showed highest affinity to the Black male sample in the forensic data bank. Graph 3a, STAFS 2012-007, is special in that it is the only female case in the STAFS sample group to misclassify. Given that there is more disproportionality between male and female representation among and between sample populations, one would expect to see higher misclassification within female analyses. STAFS 2012-007 presented as Hispanic female, showing highest affinity to white female. Graph 2a, STAFS 2013-046, presented as a Hispanic male and when analyzed in the forensic data bank showed highest affinity to the white male sample population. Lastly Graph 1a, STAFS 2012-036, presented as European and classified as white male in the forensic data bank analysis. This is of course not indicative of misclassification per se, but the anomaly with this case comes with the second analysis ran in the Howells data bank.

STAFS #	Sex	Stated Ancestry	FDB est. Pop.	Howells est.
				Pop.
2009-004	Male	European	Unclassifiable	Unclassifiable
2009-010	Male	European	White Male	White Male 20s
2009-013	Male	European	White Male	White Male 19s
2009-014	Male	European	White Male	White Male 20s

Table 1: Stated Ancestry & Population membership estimations

2010-001	Male	European	Guatemala	Guatemala
			Male	Male
2010-002	Male	European	White Male	White Male 20s
2010-003	Male	European	White Male	White Male 20s
2010-004	Male	European	White Male	White Male 20s
2010-008	Male	European	White Male	White Male 20s
2010-015	Female	European	White Female	White Female
				20s
2011-004	Male	European	Hispanic Male	Guatemala
				Male
2011-012	Female	European	White Female	White Female
				20s
2011-014	Male	European	Guatemala	Guatemala
			Male	Male
2011-023	Male	European	White Male	White Male 20s
2011-024	Male	Hispanic	Black Male	White Male 20s
2012-004	Male	European	White Male	White Male 20s
2012-007	Female	Hispanic	White Female	White Female
				20s
2012-036	Male	European	White Male	Unclassifiable
2013-038	Female	European	White Female	White Female
				20s
2013-046	Male	Hispanic	White Male	White Male 20s

When reading the dendrographs from Fordisc 3.1 you can see there are several ellipses overlapping one another, quite like a Venn diagram gone awry. Within these ellipses are what look like little colored clouds, some of which dissipate out past the borders of the ellipses. Individuals outside the ellipse are considered outliers for the respective populations represented by each ellipse. For instance, within the forensic data bank when assessing males is: blue dots represent white males, light blue triangles represent American Indian males, purple symbols represent Guatemalan males, green squares represent Hispanic males, and red triangles represent Black males. When analyzing males through the Howells data bank populations are shown as: dark blue upside-down triangles for Eskimo, blue for Arikara, magenta for Peruvian, green for Guatemalan, purple for black males from the 19th century, periwinkle for Black males of the 20th century, light green for white males of the 19th century, and red for white males of the 20th century. The same categories were applied when analyzing female samples, except in the case for Guatemalan samples as the Guatemalan sample utilized in Fordisc is comprised of only males. The unknown individual being analyzed is demarcated by a black box with a white X inside it. This black box is then placed within the confines of an ellipse if it shows membership to that population or if it is assessed as an outlier, it will be placed outside the borders of the ellipses. In some cases, we can see the individual seemingly floating between two ellipses or clusters of colors or even falling on the border of an ellipse. These individuals are classified into a discrete category as that is how the software is setup, but this placement could be indicative of a multipopulation background or an individual who is of mixed race.

Forensic Data Bank Population Affinity Results



Graph 1a (STAFS 2012_036)



Graph 2a (STAFS 2013_046)



Graph 3a (STAFS 2012_007)



Graph 4a (STAFS 2011_024)



Graph 5a (STAFS 2011_014)



Graph 6a (STAFS 2011_004)



Graph 7a (STAFS 2010_001)

The dendrographs 1b-7b below represent the analyses done against the Howells data bank. Graph 6b, STAFS 2010-001, presented as European and misclassified again as Guatemalan male. This continuity in misclassification only supports the possibility that the individual is of a mixed background. The Guatemalan sample found in the Howells data bank is the same sample that was added to the forensic data bank, therefore with this sample population there is equal assessment across data sets, but with more categories to contend with in the Howells data bank than in the Forensic Data Bank. With that in mind it is paramount that when analyzing unknown remains to narrow the possibility as much as possible to eliminate possible inter-population misclassification, where the unknown individual is just an outlier genetically and morphologically speaking.

This outlier status could be indicative of environmental factors acting on the biological plasticity of the individual representative of secular change (Manthey 2018, Harvati et al. 2006, Hubbe et al. 2009, Saini 2019, Nagaoka 2012). Graph 5b, STAFS 2011-004, classified as Guatemalan male in the Howells analysis. Graph 4b, STAFS 2011-014, classified as a Guatemalan male as this individual did in the forensic data bank analysis. Graph 3b, STAFS 2011-024, classified as a white male 20th century in the Howells analysis. Graph 2b, STAFS 2012-007, classified as a white female from the 20th century sample in the

Howells data bank. This would be congruent with the analysis compiled in the forensic data bank where this individual classified as a white female. The individuals within the forensic data bank are compiled from modern forensic casework and donated skeletons from places such as the William M. Bass Collection comprised of modern donated specimens to anthropological research facilities. Therefore, all the individuals comprising the forensic data bank would be at least from the 20th Century if not the 21st Century. In the case of the Howells data bank samples are grouped, at least for white and black Americans, into nineteenth and twentieth century samples.

Graph 1b, STAFS 2013-046, also showed congruous misclassification as a white male from the 20th Century. Lastly Graph 7b, STAFS 2012-036, showed the most interesting phenomenon as it failed to classify in the Howells data bank utilizing all the same measures analyzed in the forensic data bank analysis. This unsmeasurability is due to either an extreme outlier or potentially that the samples indicative of the groups in question do not accurately represent the sum of the groups. With that in mind it is likely that STAFS 2012-036 would classify as a white male within both analyses, coincidentally there is not any trauma to this individual that would obfuscate the measurements input in the analyses, all fourteen measurements were utilized in both analyses. This allowed for the potential of one measurement to classify as abnormal from the population samples while still maintaining the minimum required measurements for statistical analysis.

Once the analysis was run if any measure showed to have three or more standard deviations from the norm of the population samples it was thrown out to better assess classification. In the case of STAFS 2012-036, this individual had two measurements that showed three or more standard deviations from the norm. Running the data with fourteen

measures yielded an unable to classify. Noting two measures had three or more standard deviations I removed them to see if this would increase the statistical congruity, but the result was the same unable to classify. It is likely that the sample in the Howells data set has a higher percentage of dated remains than the samples in the forensic data bank. Given that these individuals in the STAFS sample are modern, born at least in the 20th century, they are more likely to classify discretely within the forensic data bank. Again, the reason for this is temporal and secular change over time (Manthey 2018, Harvati et al. 2006, Hubbe et al. 2009, Saini 2019, Nagaoka 2012). The STAFS sample is more closely related temporally to the samples comprising the forensic data bank therefore they would more than likely share the same skeletal morphology. Of course, this differentiation is still further expanded upon if the individual is a recent migrant. Migrants should be expected to misclassify unless a robust sample from their native lands is represented in the statistical computation, otherwise they will most likely not resemble endemic individuals who share a background with the migrant's native population.

Howell's Population Affinity Results



Graph 1b (STAFS 2013_046)







Graph 3b (STAFS 2011_024)



Graph 4b (STAFS 2011_014)



Graph 5b (STAFS 2011_004)



Graph 6b (STAFS 2010_001)



Interview Data

Unlike the data acquired from the crania, I wanted to obtain data from the individuals within the field to see if there were any discrepancies or consistencies of methodology in praxis. This was not an assessment of who does it best or a conclusion to a right and wrong paradigm, but rather to look at this problem from within the institutions that steward it. The interview questionnaire was structured so that I could understand more in depth the standard methods being used across the country and on a different level the ideology of each subject in relation to the debate of population affinity estimation in forensic cases. In the paragraphs to follow I will give synopses of the interviews. To keep within the parameters of anonymity location of these subjects is omitted, but I will state if subject is male or female.

Subject 1 is a female who is a consulting agent that mainly works within academia. Subject uses the overall gestalt of the skull, looking at nonmetric traits in conjunction with metric data collection using the software FORDISC. Subject has seen a shift towards more statistical data collection rather than reliance on just nonmetric analysis, what the individual looks like overall. Subject is not familiar with AncesTrees. Subject is not familiar with CranID. Subject is familiar with FORDISC 3.1, subject stated that FORDISC is the standard statistical software they use in analyzing population affinity via craniometric data. The subject is only familiar with FORDISC. Within this statistical software estimation of population affinity is high among individuals of European and African ancestry, but weak at estimating populations outside those regions or individuals with ancestry from those respective regions. When asked if ancestry estimation, population affinity, is important and should remain part of the biological profile the subject said it is still important to the biological profile.

When the connection between stature, sex, and population affinity was brought up subject agreed that they are correlated. When asked about the use of archaeological skeletal data in building the algorithms for population affinity software the subject said that they should not be used in relation to forensic cases but are helpful when archaeological context is needed. The example of identifying First Nations burials, which repatriation would be queried. When asked if there is prejudice placed on skeletal remains once population affinity has been deduced subject responded yes, but it is getting better. A case was shared where remains of an African American young female were found in a garbage bag. Subject recalled that this case seemed to slow down after population affinity was deduced and the investigation was handed over to law enforcement. Subject also speculated that investigators assumed the decedent was a prostitute and that coupled with population affinity placed this individual within a certain level of prioritization. When asked about the relationship between Forensic Anthropologists and Forensic Geneticists, the subject responded that they have a

good relationship. That most of the genetics work is usually sent off-site, usually to the DNA lab at the University of North Texas. When asked about the degree to which DNA assessment is used in relation to skeletal analysis, the subject replied stating DNA analysis is only used to identify specific individuals. This usually occurs when they have a high likelihood of identification, where family members give DNA samples and a match is confirmed, usually via mitochondrial DNA analysis.

When asked about experience using genetic markers of population affinity subject responded having experience with single nucleotide polymorphisms in relation to Hispanic versus African population affinity. When asked about anthropological research facilities reaching out to individuals from populations where data is lacking in software, such as FORDISC, the subject stated they do not know much about how they operate. Even though they do not know how the facilities conduct recruitment, they also responded by stating that they most likely were not doing that sort of outreach. When asked if we could improve our methods of advocating anatomical gifting, the subject said we should. They also asked if I had any ideas on how to go about improving anatomical gifting to our anthropological research facilities. To which I responded given the relationship between minorities and the medical establishment I understand the hesitation for involvement in this type of research. With that being said, we should look at genome-wide associated studies and perhaps we could gain more favor by building a genomic database in conjunction with craniometric data to provide a more robust statistical package for population affinity estimation.

Subject 2 is also a female who works within academia and under the auspices of the medical examiner's office, but mostly works within the medico-legal field instead of predominantly teaching. Subject stated that they use macromorphoscopic and non-metric

methods, based on experience, to ascertain an estimate of ancestry. Subject 2 uses osteometric data. When asked about a possible change or improvement to the methodology the subject stated that there has been more use of 3D-ID and other software, a greater push towards use of algorithms instead of just observer's experience. Subject 2 had heard of AncesTrees, but did not know exactly what type of statistical software it was and had no experience using it. Subject was not familiar with CranID.Subject was familiar with using FORDISC and uses this software as the standard. When asked about the accuracy of the software subject 2 responded, if your sub-population is present in the software then FORDISC is very accurate. When asked about the importance of population affinity estimation in relation to the biological profile, the subject responded that it is still important when compiling the biological profile. When asked about using archaeological skeletal material in our datasets that compile software on ancestry estimation the subject responded that we should use them, but in context.

When asked if the subject thought that prejudice is placed on certain remains once ancestry is compiled the subject responded no, that the report they make goes directly to the medical examiner. Once the report is completed the forensic anthropologist does not have much involvement unless asked to testify in court. When asked about the relationship between Forensic Anthropologists and Forensic Geneticists, the subject replied that it is getting better. When asked about the reliance placed on forensic DNA assessment versus a full skeletal analysis, the subject responded that there is not really a preference. DNA analysis is only done when there is a probable identity that can be validated by DNA analysis, otherwise DNA is not used too much. When asked if the subject had any experience in using SNPs, InDels, or any other ancestry identification markers the subject

responded to only having experience in harvesting samples to be tested. When asked about outreach from anthropological research facilities to populations we are lacking data for in our software subject responded saying no I don't think they are doing any kind of outreach like that. When asked if we could improve methods for anatomical gifting to forensic research the subject stated they don't think we can. Given the past many communities have with the medical establishment makes it difficult to build trust, so it would take many years to improve and possibly never will.

Subject 3 is a male who works solely under the auspices of the medical examiner. When asked about methods the subject uses, subject responded with, metric and morphological assessment, mainly Hefner & Ousley's methods. When asked about seeing a change in the methodology over their career, the subject stated that there has been a move towards more data driven methods instead of heavy reliance on non-metric, experiencebased assessment. Subject is not familiar with AncesTrees nor have they used it. Subject is not familiar with CranID nor have they used it. Subject is familiar with FORDISC and uses it frequently as the standard. When asked about the accuracy of the software used to compile an ancestry estimate subject 3 responded saying that they do not have any numbers to speak of, but generally it (Fordisc) works good for broad population categories. When asked if ancestry estimation is still important for the biological profile subject responded yes, it is. It helps narrow down the search. When asked about using archaeological data in the datasets used to compile software subject responded that there is some utility in context, but that in forensic cases we should not use archaeological data. When asked if the subject felt that prejudice was placed upon certain remains once ancestry was compiled, the subject

responded that they were not sure. That the prejudice, if any, would be tied to the investigators not from the scientists doing the assessment.

When asked about the relationship between Forensic Anthropologists and Forensic Geneticists the subject responded that there is a very close relationship. When asked about reliance on forensic DNA analysis in relation to skeletal analysis, the subject responded that mitochondrial study is done, but it is not done frequently. Only if there is a probable match for identification. When asked if the subject had any experience using SNPs, InDels, or any other ancestry identification markers the subject responded that they did, only experience with mitochondrial (Y-STR) analysis. When asked if the subject thought that anthropological research facilities were reaching out to the populations we are lacking data for subject 3 responded that they are not sure. The subject is not familiar with how they operate. When the subject was asked if they thought we could improve our methods for advocating anatomical gifting for forensic research, the subject responded that they were not sure.

Subject 4 is a female who works under the auspices of the medical examiner's office and works within academia. When asked what methods the subject uses, the subject responded with morphomacroscopic traits, FORDISC, and a dental analysis method. When asked if the subject has seen a change in the methodology, the subject responded that they have seen a change from more non-metric analysis to more statistical analysis via programs like FORDISC. Subject has heard of AncesTrees, but has not used it.Subject has heard of CranID, but has not used it. Subject uses FORDISC as the standard program for osteometric analysis. When asked about the accuracy of the software the subject uses, they responded saying that it is good for assessing approximation but not for exact identification. When asked if the subject believes ancestry is still important to the biological profile, the subject responded that it is but if prejudice towards certain groups can be found to occur then perhaps, we should remove it from assessment. When asked if we should be using archaeological data in our software programs, the subject responded that if you are looking at archaeological populations, then yes. If you are dealing with a forensic case, then it should not be used. When asked if the subject thought prejudice was placed on certain remains when ancestry is compiled, subject responded not that they've seen in their office, but that's not to say that it doesn't happen. The subject stated that they have not seen proof of it yet.

When asked about the relationship between Forensic Anthropologists and Forensic Geneticists the subject responded that their office is smaller, so if DNA analysis is needed then it is usually sent out to UNT. Subject's office does not have a geneticist on staff. When asked about the reliance on DNA analysis in comparison to skeletal analysis, the subject responded saying that the only time they use DNA is for personal identification of the remains of an individual. When asked if the subject had any experience using SNPs, InDels, or other ancestry identification markers, the subject stated they did not in relation to forensics, but they did with their bioarcheological research. When asked if the subject thought anthropological research facilities were reaching out to populations we lack sufficient data for, the subject responded they are not sure how outreach is done at these facilities. Subject does work with First Nations people in their respective state, but not in a capacity to advocate anatomical gifting. When asked if the subject thinks we can improve our methods for anatomical gifting for forensic research, the subject responded that they
think this is a good question to look at. That perhaps we could, but the social issues surrounding minority populations and scientists might make it difficult.

Subject 5 is a male who is a consultant and professor. Subject is familiar with craniometric, morphoscopic, non-metric (dentition), metric (dentition), and forensic genealogy. When asked about changes in the methodology over the course of their career, the subject responded that there is a move towards more digital software, which is more ubiquitous. Subject mentioned software such as rASUDAS and AncesTrees. The subject stated that they were familiar with AncesTrees, possibly used it in one case. Subject is familiar with CranID, but has not used it. Subject stated as a U.S. practitioner of Forensic Anthropology Fordisc is the standard, note that subject 5 distinguishes working with the software as a U.S. practitioner and not using it outside the United States. Subject did not have an answer to describe accuracy of ancestry estimation using software. Subject noted that personally they reject ancestry as part of the biological profile. When asked if they think ancestry is still important to the biological profile, the subject responded stating that it is problematic and based in the now debunked Biological Race Theory. When asked about using archaeological samples in our datasets for compiling forensic software, the subject stated that we should not. Subject went on to say that archaeological samples are distinct from modern populations therefore not useful for forensic cases. When asked if the subject thought that there is prejudice placed on certain remains once ancestry is assessed the subject responded that this is the important question. Subject added that they think this question is more important than assessing the methods associated with estimating ancestry.

When asked about the relationship between forensic Anthropologists and forensic Geneticists, the subject responded saying it is just beginning in their opinion. When asked

about the reliance placed on DNA analysis in relation to skeletal analysis the subject responded by stating that DNA is the bulk of IDs, more so than skeletal analysis. When asked if the subject had experience using SNPs, InDels, or any other ancestry identification markers from genomic material, the subject responded stating that this is usually done by the medical examiner's office. Subject stated that they usually only harvest the bone sample or recommend the site from which a sample should be harvested. When asked if the subject thought anthropological research facilities are reaching out to populations we have deficient data for, the subject responded stating they do not know. Subject recommended that I should ask the individual institutions. When asked if the subject thought we could have better methods at advocating anatomical gifting for forensic research subject 5 responded that they do not know and asked my thoughts on the matter.

Subject 6 is also male, but mainly does work under the auspices of the US military and Department of Defense. When asked about the methodology used, the subject responded stating metrically and morphoscopically in relation to the skull. When asked about the change in methodology throughout the subject's career, the subject responded that they have seen a transition from non-metric typological assessment to more statistical metric assessment. The subject also stressed the need to move away from the typological approach. Subject responded that they are not familiar with AncesTrees. The subject even inquired about the developer and where they could access the software. Subject responded that they are not familiar with CranID. The subject asked me to describe the software. Subject responded that they were familiar with Fordisc, stated that this is the standard software they use. Subject stated that Fordisc is relatively accurate with the proper interpretation of the analysis output. Subject responded stating that the importance of population affinity

estimation depends on the particulars of each case. When asked about the use of archaeological skeletal remains in formation of our data within statistical software, the subject responded saying we should utilize this data. When asked about the possibility of prejudice post population affinity estimation, the subject responded saying not to their knowledge and that it is highly unlikely.

When asked about the relationship between forensic anthropologists and forensic geneticists, the subject responded that they are separate spheres that should do more collaborative research together. Subject was asked about the reliance placed on DNA assessment and skeletal analysis and responded saying that DNA is a stronger line of evidence, and more weight is placed on genetic evidence. They were asked if they had any experience with SNPs, InDels, or any type of ancestry identification markers. The subject responded that this is beyond their purview, but they can interpret results. Subject stated they had no experience in conducting the tests or harvesting samples. When asked if the subject thought anthropological research facilities were doing outreach to populations we have insufficient data for the subject responded that they do not believe they are recruiting for skeletal donation. Subject also stated that labeling is the biggest issue in population affinity estimation. When asked about their thoughts on improving advocacy of anatomical gifting the subject stated they were not sure but emphasized that our biggest issue is the labeling of our data.

Subject 7 is a female who works under the auspices of the medical examiner's office. This subject was too busy with case work to do a sit-down interview, so I allowed this individual to respond to the questionnaire and send it back to me via email. This was allowed due to the small turnout of interviewees. Since this was a written response from the

subject it has been scripted to uphold anonymity. The subject is most familiar with methods using human skeletal remains including osteometrics of the cranium and postcranium and morphoscopics/morphology (primarily of the cranium, including the dentition). Subject 7 stated that while ancestral affinity can be discerned from DNA (in the form of haplogroups or likelihood ratios based on populations) or using genetic genealogy, the subject is less familiar with these methods. The subject has seen a few different shifts in methodology, one involving a movement away from the term "race" to "ancestry," and one towards more statistical support for ancestry estimation. The methodologies have not changed in any significant manner, but the goals have shifted. For example, there is now an emphasis to study broader population histories, microevolution, quantification of metric or morphoscopic characteristics associated with ancestral histories and providing statistical support for our ancestry estimations. The subject is not familiar with the AncesTrees software. The subject has heard of CranID, but is not familiar with it. The subject is familiar with Fordisc as well as 3D-ID, both of which have large, modern samples from North and South America which are most applicable to the subject's casework.

Subject 7 states that there are numerous factors affecting the accuracy of an ancestry estimation. Subject states that if the craniometrics of an unknown individual are congruous to a group within the software database, the ancestry classification accuracy will be much higher than if the unknown individual belongs to a group that is not well represented in the database. The subject adds that it also depends on how familiar the analyst is with the software. The subject states that if an analyst does not know how to adequately account for the various statistical assumptions, remove outliers, remove groups that do not classify well, and interpret the results correctly, the accuracy of the ancestry estimation can be greatly

hampered. For example, if an unknown decedent belongs to a well-represented group in the Fordisc database and if the analyst properly measured the cranium and properly ran the statistical analyses, then the ancestry estimation should have a high classification accuracy.

The subject further explained that whether the ancestral classification matches the unknown individual's self-identified race is more difficult to determine. Subject believes population affinity estimation is still an important piece of the biological profile. The subject stated they think archaeological skeletal material should be incorporated into craniometric databases, however, there should always be a way to separate archaeological data from modern forensic data for analytical purposes. Archaeological metric data is not applicable to forensic cases, but if presumed historic/archaeological skeletal remains are discovered, having the ability to assess ancestry based on archaeological data is still important. The subject stated they did not understand what question 9 was asking. The subject tried to answer stating, if you are asking whether certain social races are prioritized in the assessment of ancestry I would disagree. The subject stated they treat every set of human remains with the same care and diligence regardless of their estimated ancestry, social status, age, or any other factor. The subject does not know how they would quantify "great," but they do think that there is a positive and growing relationship between forensic Anthropologists and forensic Geneticists, particularly in reference to genetic genealogy.

If forensic geneticists are being asked to assist with an identification, it is because there is a presumed identity of the unknown decedent. The subject further explained that geneticists can then compare the DNA of the unknown decedent to a family reference sample. However, if there is no presumed identification for an unknown decedent, a DNA analysis is limited in what it can provide. In this circumstance, a biological profile that

includes an estimated ancestry may provide information that leads to a presumed identity that can then be tested using DNA. However, if genealogists become involved, they can use historical records and investigative techniques to generate possible familial relationships. If a DNA profile is uploaded into CODIS, then it is a matter of luck whether that profile matches one already in the system.

The subject does not think Forensic Anthropologists frequently rely on DNA for skeletal analyses since they are two different processes and require different expertise. The subject has not personally used SNPs or InDels to make an identification since they are not a geneticist, but I have read the reports of our forensic geneticists regarding familial DNA comparisons to identify unknown decedents. The subject is not familiar with the specific recruitment and body donation processes at the various anthropological research facilities. The subject imagines there is always room for improvement when it comes to informing the public about anatomical gifting, particularly in relation to forensic research facilities, but I am not familiar with the means by which this is done.

Discussion

Most of the subjects interviewed agree that ancestry, in relation to the biological profile, is still a nascent piece of the puzzle when presented with unidentified skeletal remains. Understanding the hesitancy to use this category, especially in recent times with cases of social injustice I.e., the inhumane detainment of border crossers or the recent death of George Floyd. Social injustices such as these heighten public sensitivities to racial identifiers and thus can create bias in juries. If we focus more on the recent up-tick in police violence against African Americans, then one can see the hesitation to utilize population

affinity in the identification of unknown skeletal remains (DiGangi 2021, Bethard & DiGangi 2020). Unfortunately, the scope of this research does not encompass analysis of social mores within law enforcement as it pertains to population affinity of decedents and successful closing of cases or the unfortunate possibility of the case going cold. Subject 5 mentioned NamUS, a US based missing and unidentified persons database, and most individuals within that database are non-white. After browsing the first few hundred profiles it became clear that a portion of these individuals looked to be migrants, of whom presumably no next of kin were available or aware of the individual's passing. Another explanation for some of these individuals is estrangement from family or the harsh reality that no one wanted to be burdened by them. This does not necessarily indicate negligence on the investigative side.

The movement to eradicate population affinity estimation altogether would greatly affect the potential identification of the unidentified especially in NamUS. Just like narrowing down a pool of suspects, one must narrow the pool of affinal populations in hope of finding next of kin who can positively identify the decedent. If we do not attempt to narrow down what would essentially be a global search cases would potentially go on for years, and they do. The best approach to combat this issue with population affinity is a synergistic approach combining both forensic anthropological methods and forensic genetics. While Fordisc is relatively good at assessing remains with high probability of being White or African American, it has more difficulty differentiating between other groups due to sample sizes and it stands to reason a growing rate of admixture. Fordisc used outside the United States classifies poorly, and this is due once again to secular changes among and between populations (Manthey 2016, Manthey et al. 2018). Most of the samples

in the forensic data bank within Fordisc are individuals that resided within the United States. Therefore, fordisc classifies best within the population of the United States.

The misclassification issues incurred by Fordisc could be alleviated with the use of genetically assessed AIMs, ancestry identification markers, which can further specify population affinity of the unknown individual (Romanini et al. 2015, Zeng et al. 2016, Bulbul et al. 2018). Most of the subjects interviewed stated that there is a good relationship between forensic anthropologists and geneticists or that the relationship is strengthening. Some, like Subject 7, see genetic analysis as solely in the realm of the geneticist, but we must not forget the unique position we as forensic anthropologists hold. We assess the skeletal remains of individuals, the reliquaries of genetic material. As biological anthropologists we should have a familiarity with population genetics. Currently forensic anthropologists hold somewhat of a finite position within the Office of the Medical Examiner, but if we were to utilize our knowledge of genetics or perhaps further our training in this area, we could widen our toolkit making ourselves more broadly applicable within the medico-legal industry. This of course is in no way meant to eclipse geneticists' involvement in the process, but rather ease the burden of caseloads already put on institutions like the University of North Texas DNA lab.

A synergistic approach like this would be most beneficial in cases of suspected Hispanic origin where Fordisc has a high likelihood of misclassification. There are a few promising AIM panels that show a high percentage of correct classification for Hispanic populations (Wang et al. 2019, Setser et al. 2020). By utilizing genetic analyses, we can obtain specimens from living individuals which is easier to recruit for than anatomic gifting. Much of the data needed for such a data bank already exists in the multitude of genomewide associated studies conducted for medical research as well as for population demographics. Also, by compiling genetic data for population affinity we are also tracing potential genetic contributions to the morphological skeletal features we obtain metrics for (Ross & Pilloud 2021). In this manner we can begin to decipher the potential evolutionary factors for the variations we see in skeletal elements, namely the skull.

Conclusion

Since our earliest histories as societies, we have been enamored in pointing out the Other. Initially this came from survival instinct due to the inherent danger in the unknown. With the advent of city-states and the monopolization of power arose the ideologies we know today as Race, which attempted to discern a hierarchical ranking of humans based on phenotypic features driving social cognizance. These social ideologies which tried zealously to explain human biology for socio-political benefit have so permeated all facets of society so that we are ensnared in their terminology. We no longer classify with terms like negro or mongoloid, rather we have reinvented the terms into something more palatable, African American and Asian-American for instance. No matter how much political correctness we place in the terminology we use there is still going to be prejudice placed upon these terms if racism exists. To devoid ourselves of using population affinity in the biological profile as akin to not dealing with the issue of racism and what it fully entails. We as forensic anthropologists are bound to work within the purview of the courts which still utilize discrete categories to classify individuals.

As forensic anthropologists, scientists in general, it is our duty to educate the public on the realities found in our science. Namely we should be expounding the genetic Truth of

our species in that race does not originate in our biology, but rather we have a deeply rooted social programming to categorize individuals with a long history of subjugating the Other. In the broadest description of our job, we as forensic anthropologists are story tellers, the skeleton is our text. By removing population affinity from that text, you are deleting a very important chapter from that individual's story. In the event of homicide or missing persons, we owe these individuals the due diligence to obtain their Truth so that they can be reunited with their next of kin. By taking a synergistic approach to the issues surrounding population affinity estimation we can improve our statistical assessments ensuring unidentified individuals have the best chance at being identified. This synergistic approach could also be the catalyst for an internationally robust software that could be used with confidence outside the United States.

We currently do not have an international databank that we can utilize in the case of a mass fatality incident such as a Tsunami disaster or terroristic acts such as the events of 9/11. Here in the United States, we have devised a quite useful technology within the Fordisc software, but its efficacy dissolves once used outside the United States. Given current global affairs, the subjugation of the Rohingya sub-population in Southeast Asia, the Taliban takeover in Afghanistan, and the continuous migrant crises among central American countries show us that across the globe there are groups that we as forensic anthropologists are potentially to encounter post-mortem in human rights cases and cases for crimes against humanity. Many of these populations being subdued are not very well represented in our current models, which needs to change. This can be fixed and improved by working synergistically with genetics. Sherry Washburn was once the pioneer of moving physical anthropology into the biological anthropology of today (Caspari 2003). Just as he shifted

disciplinary thought from the biological race concept to one based in populational genetic theory, we as students as practitioners within the field of Biological Anthropology should disseminate this into the public sphere and most importantly within the court system.

Humans do not fit neatly into categorical boxes to be checked off a list. We are each a unique sequence of genetic division; our differences being comprised in less than 1% of our genetic sequence. We are 99% genetically the same with each other, and the phenotypic or visual differences we see are just survival mechanisms our genetic makeup produced to give us the best chance of survival in the environment in which we find ourselves. The marked differences we see within our osteology are not indicative of things like intelligence, but rather access to basic resources necessary for development or simply environmental differences that drive genetic change.

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<u>Appendix I</u>

- 1. <u>Glabello-Occiptal Length (GOL)</u>- distance between glabella and opisthocranion in the midsagittal plane, measured in a straight line.
- 2. <u>Nasio-Occipital Length (NOL)</u>- distance between nasion and opisthocranion in the midsagittal plane, measured in a straight line.
- 3. <u>Basion-Bregma Height (BBH)</u>- direct distance from the lowest point on the anterior margin of foramen magnum to bregma.
- 4. <u>Maximum Cranial Breadth (XCB)</u>- maximum width of the skull perpendicular to midsagittal plane wherever it is located, with the exception of the inferior temporal lines and the area immediately surrounding them.
- 5. <u>Maximum Frontal Breadth (XFB)</u>- maximum breadth at the coronal suture perpendicular to the midsagittal plane.
- 6. <u>Bifrontal Breadth (FMB)</u>- breadth across the frontal bone between frontomalare anterior on each side, most anterior point on the fronto-malar suture.
- 7. <u>Bizygomatic Breadth (ZYB)</u>- Direct distance between most lateral points on the zygomatic arches.
- 8. <u>Biauricular Breadth (AUB)</u>- least exterior breadth across the roots of the zygomatic process, wherever found.
- 9. <u>Maxillo-Alveolar Breadth (MAB)</u>- maximum breadth across the alveolar borders of the maxilla measured on the lateral surfaces at the location of the second maxillary molars.
- 10. <u>Biasterionic Breadth (ASB)</u>- direct measurement from asterion to asterion.
- 11. <u>Bijugal Breadth (JUB)</u>- external breadth across the malars at the jugalia, the deepest points in the curvature between the frontal and temporal process of the malars.
- 12. <u>Bimaxillary Breadth (ZMB)</u>- breadth across the maxillae, from one zygomaxillare to the other.
- 13. <u>Cheek Height (WMH)</u>- minimum distance, in any direction, from the lower border of the orbit to the lower margin of the maxilla, mesial to the masseter attachment.
- 14. <u>Nasion-Prosthion Height (NPH)</u>- direct distance from nasion to prosthion.
- 15. <u>Basion-Prosthion Length (BPL)</u>- direct distance from basion to prosthion.
- 16. <u>Basion-Nasion Length (BNL)</u>- direct distance from basion to nasion.
- 17. <u>Nasal Height (NLH)</u>- direct distance from nasion to the midpoint of a line connecting the lowest points of the inferior margin of the nasal notches.
- 18. <u>Nasal Breadth (NLB)</u>- maximum breadth of the nasal aperture.
- 19. <u>Biorbital Breadth (EKB)</u>- direct distance between right and left ectoconchion.
- 20. Interorbital Breadth (DKB)- direct distance between right and left dacryon.
- 21. <u>Orbit Height left (OBH)</u>- direct distance between the superior and inferior orbital margins.

- 22. <u>Orbit Breadth left (OBB)</u>- laterally sloping distance from dacryon to ectoconchion.
- 23. <u>Nasion-Bregma Chord, Frontal Chord (FRC)</u>- direct distance from nasion to bregma taken in the midsagittal plane.
- 24. <u>Bregma-Lambda Chord, Parietal Chord (PAC)</u>- direct distance from bregma to lambda taken in the midsagittal plane.
- 25. <u>Lambda-Opisthion Chord, Occipital Chord (OCC)</u>- direct distance from lambda to opisthion taken in the midsagittal plane.
- 26. <u>Zygomaxillary Subtense (SSS)</u>- the projection or subtense from subspinale to the bimaxillary width.
- 27. <u>Nasio-Frontal Subtense (NAS)</u>- the projection or subtense from nasion to the bifrontal breadth.