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Using the Seventh Rib Length and Depth Measurements as a Method to Estimate Ancestry and Sex in Adults

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USING THE SEVENTH RIB LENGTH AND DEPTH MEASUREMENTS AS A METHOD TO ESTIMATE ANCESTRY AND SEX IN ADULTS

A Thesis

Submitted to the Graduate Faculty of the Louisiana State University and Humanities and Social Sciences College In partial fulfillment of the Requirements for the degree of Masters in Anthropology

in

The Department of Geography and Anthropology

by

Alexandria M. Amaki
B.A., California State University, Chico, 2015
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Abstract

This study tested the correlation of dimensions of the left seventh rib (L7) to ancestry and sex in adult humans. The first hypothesis, based on Bergmann’s theory, is that Black (African-American) individuals will have smaller L7 dimensions than White individuals (Americans of primarily European descent). The second hypothesis is that males, due to sexual dimorphism, will have larger ribs than females. 299 individuals from the Hamann-Todd Skeletal Collection were used in the study, approximately evenly distributed among sex and ancestry groups. Five variables were examined, including three measurements (length, width, and width point), and two calculations (area and ratio). A Pearson’s correlation tested the precision of the measurements being taken. To further test intraobserver error, 29 individuals measured on the first day of data collection were remeasured on the last day, and those two sets of measurements were analyzed with a paired T-Test. Swarm plots were created to show the distribution of data separated by sex and ancestry, as well as by sex only. Two sample T-Tests were run on all the variables to look for differences in the means with ancestry and sex. Results found significant differences between ancestry groups for both sexes for length, width, width point, and the ratio, with Black individuals smaller than White individuals for all variables except width. Thus, the first hypothesis was only partially supported. The second hypothesis was fully supported; significant differences were found between sexes for all variables, with males being larger.

Lastly, non-linear models to estimate ancestry and sex from L7 dimensions were created based on results of the swarm plots, then tested on the main dataset and on a smaller dataset derived from contemporary individuals. From the models, ancestry was correctly estimated in 70% and 91.6% of males, and 65.1% and 66.6% of females, of the test samples, respectively; sex was correctly estimated in ~81% and ~89% of the test samples. Future research should focus on
testing inter-observer error, the symmetry of the ribs and applying the models to other population samples.
Chapter 1. Introduction

One of the goals of forensic anthropology is to reconstruct a person’s biological profile in order to assist with the identification of an individual. The biological profile consists of estimations of a person’s age, sex, ancestry, and stature. In forensic contexts, the remains of a person can become dispersed and elements can be lost or fragmented. The loss or fragmentation of elements such as the skull, os coxae, and postcranial long bones limits potential methods to generate these estimations. Research utilizing the ribs in estimating the biological profile has been done mostly to estimate sex and age of an individual. This study will utilize the left seventh rib (L7) to test whether or not rib measurements (i.e., length, width, and width point) and calculations based on those measurements (i.e., area and ratio) can be used to estimate ancestry and sex.

In adult humans, male and female skeletons will differ in their size and shape. Several studies (Phenice 1969, Walker 2005) focus on the morphological differences between the sexes. In past research, the os coxae, cranium, and mandible are the primary elements used when estimating sex in unknown individuals. For the os coxae, Phenice (1969) and Walker (2005) focus on several qualitative features, and Buikstra and Ubelaker (1994) compiled a list of five qualitative cranial features to estimate sex based on others’ research. The program FORDISC can also be used to estimate sex using measurements taken from the cranium, as well as several postcranial elements. Other elements that can be used to estimate sex in lieu of the skull and os coxae, and using quantitative methods are the femur, tibia, humerus scapula, radius, ulna, and clavicle (Steyn & Íşcan 1997, Rogers 1999, Spradley & Jantz 2011).

When estimating ancestry, the skull is the primary skeletal element that shows variation of traits from different ancestry groups. Rhine (1990) compiled a list of 45 different traits from
other researchers that could be used to estimate ancestry from the skull alone; in 2009, Hefner narrowed the list down to 11 traits. Other research to estimate ancestry using postcranial bones has focused on the os coxae, femur, and tibia (Baker et al. 1990, İşcan 1990, İşcan & Cotton 1990, Gilbert & Gill 1990). With regard to metric analysis for estimating ancestry, the program FORDISC can be used for the cranium and mandible and can distinguish seven different ancestral groups. To utilize FORDISC, the measurements are taken from a cranium and mandible and are input into the program; the measurements are then put through a discriminant function analysis and the observer is given an estimated ancestry of the unidentified individual based on comparisons to data in the FORDISC database (Ousley & Jantz 2013). Though these methods are most useful for a complete skull, when it is fragmented or absent, there are few other ways to estimate ancestry. Being able to utilize the ribs for ancestry estimation will add to the field of anthropology and assist in circumstances where the skull may not be available for analysis.

The current study utilizes the theory of ecogeographic patterning, which recognizes patterns among body size, shape, and climate. The theory of ecogeographic patterning is based on three rules: Bergmann’s rule, Allen’s rule, and Gloger’s rule. All three rules relate how the climate and geographical location of an individual can affect body size and shape (VanderWerf 2012). Allen’s rule applies to appendage length, and is often studied along with Bergmann’s rule, which focuses on body size. Gloger’s rule applies to the coloring of, for example, plumage or the fur of animals (Walsberg 1982, VanderWerf 2012, Gohli & Voje 2016). Specifically, in this study, Bergmann’s rule will be used, which states that warm-blooded animals will have smaller body sizes in warm climates and larger body sizes in cold climates (Bergmann 1847, as recorded in Holiday & Falsetti 1999). This theory brings about the first hypothesis of this study: that
individuals of African descent (i.e., those who socially may identify as “Black”) will have smaller rib dimensions (as exemplified in length, width, width point, area, and ratio) than Americans of non-African, primarily European, descent (i.e., those who socially may identify as “White”). These expected differences are based on potential evolutionary adaptations to the different climates in Africa and Europe. If this hypothesis is supported, it can lead to a new method in ancestry estimation. In situations where the skull or other commonly used postcranial bones are missing or fragmented, a method such as this will be a helpful tool for forensic anthropologists. The second hypothesis of this study is that males and females will differ in the size of L7, with males generally being larger than females. Therefore, the information obtained from the rib’s measurements can assist in the estimation of sex in unknown adults. If this hypothesis is true, being able to use the ribs will assist with sex estimation of unknown human adults when other methods cannot be utilized.

The sample of human skeletal remains used in this study came from the Hamann-Todd Osteological Collection, and are individuals with known information on sex and ancestry. Measurements were taken from individuals with a complete L7, and used to calculate the approximate area of the inner curvature of the rib and the ratio of the length to width. All variables then were analyzed statistically for variation between sex and ancestry. If significant relationships are found, models will be created to test the applicability and accuracy of using L7 dimensions to estimate sex and ancestry.

This thesis begins with a review of literature pertaining to rib anatomy and development, anthropological research using the ribs, methods for sex and ancestry estimation, and ecogeographic patterning. Next, the materials and methods used in the study are explained, as well as how the data were analyzed. Results of the analyses are presented, in addition to the
results from the models constructed to predict ancestry or sex. Lastly, the discussion section considers how this study supports the goals of forensic anthropology, any shortcomings within the study, and future research opportunities that can be investigated.
Chapter 2. Literature Review

Rib Anatomy and Development

Ribs provide support for the thoracic cavity and protect the organs that sit inside of the cavity. On each side of the torso, there are typically 12 ribs, but this number can vary between 11 and 13. Of the 12 ribs, one through seven are considered “true ribs” because they articulate directly with the sternum by their costal cartilage. Ribs eight through 10 are known as “false ribs” because they articulate with the sternum through a cartilaginous bar. Ribs 11 and 12 are termed “floating ribs” because they do not articulate with the sternum (Scheuer & Black 2004).

Each rib also exhibits four main components: body, tubercle, neck, and head. First, the body, or shaft of the rib, is the elongated curved portion, which makes up the largest segment. Next, the tubercle consists of two parts: a non-articulating portion, and an articular surface which contacts the transverse process of the vertebra. The neck of the rib connects the tubercle and head, and distinguishes itself with a slight inward curve. The head of the rib articulates with the demifacets of its numerically corresponding thoracic vertebra and the vertebra directly superior; exceptions to this typical anatomy are the first, eleventh, and twelfth thoracic vertebra, which have “whole” costal facets for their corresponding ribs (Waxenbaum et al. 2020).

Developmentally, ribs are formed from perichondral ossification, which is the mineralization of vascularized perichondrium tissue. From the mineralization, bone begins to form in primary ossification centers. The primary centers of ribs five through seven are first seen in the eighth to ninth weeks prenatal. By week 11 to 12 intrauterine, each rib has its primary ossification center, with the exception of rib 12 (Fazekas & Kosa 1978, Scheuer & Black 2004). After the fourth prenatal month, the ossification of the primary centers begins to slow, and from then until the onset of puberty, little change is seen in the structure of the ribs except for growth.
in size and curvature (Fazekas & Kosa 1978, Scheuer & Black 2004). Scheuer and Black (2004) suggest that the most important occurrence during juvenile torso development is that the torso becomes more active in respiratory mechanisms. With this development, the sternal ends of the ribs descend slightly in order to accommodate the diaphragmatic breathing seen in adults. This lowering of the ribs also transforms the shape of the thorax from a “pyramid shape” seen in infants, to a “barrel shape” seen in adults (Garcia-Martinez et al. 2015).

Secondary ossification centers develop postnatally and are often observed as epiphyses. Studying secondary ossification centers is difficult in the ribs because of the variation in the timing of when they develop and their order of fusion, and because the epiphyses are the smallest and most difficult to identify (Stevenson 1924, Scheuer & Black 2004). On the ribs, the secondary centers will appear around ages 12 to 14, and will be located at or near the sites of articulations, such as the head, tubercle, and articular surface of the tubercle (Scheuer & Black 2004). The first site that forms is the non-articulating part of the tubercle, which is first seen around ages 12 to 14, and fuses between ages 14 to 18. The epiphysis of the articulating region of the tubercle follows at puberty and fuses between the ages of 18 to 20. The last secondary center to appear is the head, between ages 17 to 18, which then fuses between ages 22 to 25 (Stevenson 1924, McKern & Stewart 1957, Scheuer & Black 2004). Of all the ribs, four through nine are the last rib heads to unite. Generally, the ribs will form starting with the first and twelfth ribs and progress inferiorly and superiorly, respectively, toward the sixth and seventh ribs (Stevenson 1924, McKern & Stewart 1957).

Bastir et al.’s (2013) and García-Martínez et al.’s (2015) studies of the human thorax suggest that the upper and lower portions of the thorax have different morphological growth patterns, and they seek to better understand its ontogeny. One of the first changes seen in the
thorax that may affect development starts with the lowering and shift in orientation of the upper ribs in infants during the change in respiration from diaphragmatic breathing to thoracic breathing. In the upper thorax, the development of the ribs may be affected by pulmonary kinematics or the development of the shoulder girdle. In the lower thorax, “… development could be influenced by diaphragmatic kinematics…, spine lordosis related to posture, thoraco-pelvic integration,” or the organs. (García-Martínez et al. 2015:424). Both studies utilized computer tomography (CT) reconstructions of rib cages from living subjects and assigned landmarks on the scans to illustrate rib curvature. The CT scans from both studies used a wide age range of individuals from newborns to full-grown adults. Both studies then estimated the morphological growth patterns of their samples by putting them through growth simulations and comparing the results to the adult rib samples. The results did show that there were different growth patterns in the upper and lower ribs due to the axial rib curvature. Bastir et al. (2013) concluded that the upper thorax, specifically ribs three through five, were altered more by respiratory changes and lung growth, and the lower thorax from the digestive system. García-Martínez et al. (2015) concluded that “intrinsic factors, such as rib torsion and axial rib curvature, are important factors during postnatal ontogeny” (2015:430). The 2015 study also questioned the reliability of their model with the first, eleventh, and twelfth ribs, but found that the first rib followed similar growth patterns of the upper ribs, and the eleventh and twelfth ribs followed the lower rib growth patterns, despite their stark differences in morphologies to the other ribs.

**Anthropological Research Using the Ribs**

Ribs have been studied for their use as an aging method. Íşcan and colleagues published two articles, one in 1984 using White male ribs and one in 1985 using White female ribs,
suggesting a method using the sternal end of the fourth rib. The method uses three traits to estimate age, including pit depth, pit shape, and rim and wall configurations. The pit depth is taken by measuring the “distance between the base of the pit and the adjacent anterior and posterior walls” (İşcan et al. 1984:148). The pit shape refers to the change in the walls of the pit from a “V” shape to a “U” shape. Rim and wall configurations begin with a smooth and even border; as a person ages, the wall then becomes irregular, thin, and sharp. In the original method, each of the traits could be divided into six stages (0-5), with zero being used for juveniles and adolescents who have no pit formation. After the traits were assigned a stage, the sum of the stages was taken. This sum ranged from 3 to 15, and each sum corresponded to an age range between 17 and 76 years old. The method subsequently was updated to no longer be based on composite scoring of the three traits. In 1993, İşcan, Loth and Wright produced rib casts, with descriptions, representing each of the stages. The descriptions were edited from the original İşcan et al. (1984, 1985) studies to better clarify the different stages. These casts and descriptions can be used as references when using this method to estimate age.

More recently, Hartnett (2010) tested the accuracy of İşcan et al.’s method using the sternal end of ribs from a modern autopsy sample, and sought to propose revisions to increase precision of the method. The revised descriptions came from and were subsequently named the Forensic Science Center (FSC) descriptions, and included minor changes in the wording, age ranges, and means per phase of İşcan et al.’s 1984 study. The most notable of the changes was the emphasis of bone density and quality with the age estimation. The study used a sample consisting of 630 individuals from the Maricopa County Forensic Science Center and the Barrow Neurological Institute; the samples were used to test the accuracy of İşcan’s descriptions and casts, as well as the FSC descriptions. One of the problems Hartnett found was that İşcan et al.’s
descriptions of the sternal rib ends could be interpreted differently by researchers, leaving room for error. The study therefore concluded that İşcan et al.’s method was not as accurate as previously thought, and, even with the revised descriptions, large age ranges are still needed to accommodate for human variation (Hartnett 2010).

İşcan (1985) also studied the sternal ends of the ribs and their calcification patterns to test if there was a correlation to an individual’s sex. For this study, the three measurements taken were the “maximum superior-inferior height (S-I), maximum anterior-posterior breadth (A-P), and maximum pit depth (P-D)” (İşcan 1985:1091). The data collected were then separated by “younger” and “older” age groups and one-way analysis of variance (ANOVA) tests were used to test the difference in means between the measurements and an individual’s sex. Overall, the results showed that the males were larger than the females in all aspects, except in the P-D of the “younger group.” The tests showed an accuracy of 82% in the “younger groups” and 89% in the “older groups” to determine sex. Also, even though the rib changes with age, the authors concluded that metric analysis can be used to determine sex in individuals aged in their teens to 70s, while non-metric variation would not be seen until the mid-20s.

Muñoz et al. (2018) tested İşcan’s methods to estimate sex using rib measurements and to develop new age at death estimates using the sternal end of the fourth rib. The study used individuals of Mexican descent from the Instituto de Ciencias Forenses in Mexico City; altogether, they had 444 males and 60 females with an age range of 17 to 92 years old. Two measurements were used for sex estimation: the “superior-inferior height” (SIH) or maximum distance from the most superior point to the most inferior point of the sternal end, and the “anterior-posterior breadth” (APB), or the maximum distance between the most anterior and posterior points of the sternal end. For age at death estimation, a phase described by İşcan (1984)
was assigned to each rib sample. The results of the sex estimation test yielded a 73-87% success rate. For age-at-death, estimations were successful an average of 43.17% in males and 31.21% in females. The study concludes with an emphasis on the importance of testing widely accepted methods on different populations.

In a study by Bellemare et al. (2006), the length of the rib, and other measurements, were compared between males and females to test for sexual dimorphism. Using 46 fresh cadavers, 23 males and 23 females, the third, sixth, and ninth ribs were measured using a lead wire that ran along the entirety of the rib. The length of the thoracic spine, the biacromial distance, and the length of the limbs were also measured to compare their correlations with the ribs as well. Using independent sample T-tests, or Mann-Whitney tests, and a linear regression, the measurements were tested for their differences in mean and medians with one another and with sex. Bellemare et al. (2006) found that although the lengths of the ribs were not statistically significant between the sexes, females had longer ribs, in relation to height, than males. The males, however, showed a correlation with rib length and the length of the axial skeleton, and females did not. The correlation to the axial skeleton may suggest that males and females differentiate on what regulates rib size during development. The study concluded that females would likely have a larger rib cage volume compared to males of equal height, which may be to allow for internal organ displacement that occurs during pregnancy (Bellemare et al. 2006).

Mann (1993) was able to create a method to side and sequence human ribs, given that the ribs are morphologically standard and there is no trauma or growths. For this method, the ribs are first sided using morphological traits. To side ribs three through 10, with the head of the rib oriented toward the practitioner and the “sharp” edge of the rib pointed inferiorly, the convexity of the rib points to the correct side. To sequence the ribs, the first rib is laid down, and behind it
ribs two through seven follow, increasing in size. Ribs eight through 12 then decrease in size. If the ribs are ordered correctly, the heads of the ribs should form a bell curve, assuming the ribs are of standard morphology and have no trauma or growths.

Ribs have also been used in paleoanthropology to study evolution of early hominins. Franciscus and Churchill (2002) examine Neandertal ribs and whether or not an inference can be made about the shape of the thorax of Neandertals, compared to that of Homo erectus and Homo sapiens. The study focused on the comparisons of the following skeletons: the Neandertal skeleton of Shanidar 3, which comes from the Shanidar Cave in northeastern Iraq, “other Near Eastern and European Neandertals; the Nariokotome specimen [a Homo erectus/ergaster specimen]; Levantine archaic/early modern humans; early and later European modern humans; and a sample of recent Euroamerican males” (Franciscus & Churchill 2002:1). Using 22 different measurements of the height and shape of the torso, Franciscus and Churchill (2002) concluded that Neandertals likely had a larger thoracic volume than modern humans. The larger thoracic volume would likely have been due to cold climate adaptation, increased activity levels, and genetic drift.

In a study by Ben-Dor et al. (2016), the correlation of a high protein diet and the change in size and shape of the thorax of Neandertals was examined. While evidence shows that Neandertals mostly consumed medium and large herbivores, the cold climate during the winter months on the European tundra would have made foraging for plants difficult. This created a niche to which the Neandertals adapted. According to the study, due to the Neandertals’ high protein diet, more amino acids were produced which in turn caused an increase in the size of their livers and kidneys. The skeleton then adapted to the larger organs giving the Neandertals a more ‘bell-shaped’ thorax and wider pelvis. The increase in thorax size is specifically seen
around rib eight, where the liver sits, making that rib the largest in the Neandertal as well. Ben-Dor et al. (2016) also note the hypothesis that low temperatures can affect the size of the liver and kidneys due to metabolism changes; however, their model takes into account the estimated total energetic expenditure to ensure the two hypotheses do not interfere with each other. The study concludes “that there is significant evidence to support a morphological adaption of Neandertals to a high level of protein consumption” (Ben-Dor 2016:8).

**Sex Estimation**

The estimation of sex is one of the first steps taken when putting together the biological profile of an unknown individual. The os coxae, followed by the crania, is favored when it comes to sexing unknown individuals, though other elements such as the long bones can also be used. In general, male traits are graded as more “robust” and females are graded as more “gracile” (Walker 2008). However, with the os coxae and the cranium there are several traits that are either present or absent. In forensic anthropology, most individuals will present as either male or female. If sex cannot be determined due to lack of usable elements, or features presenting as ambiguous, an individual will be labeled as undetermined sex.

Phenice (1969) developed a qualitative method to sex unknown individuals using features located on the pubis. The three features include the ventral arc, the subpubic concavity, and the medial aspect of the ischiopubic ramus. This technique is described as “accurate, rapid, highly objective, and [one] which does not require years of experience” (Phenice 1969:298). When the study was completed, only 11 of the 275 individuals used from the Terry Skeletal Collection were incorrectly sexed. The ventral arc is a feature present in female skeletons, which shows as a “slightly elevated ridge of bone which extends from the pubic crest and arcs inferiorly across the ventral surface to the lateral most extension of the subpubic concavity” (Phenice 1969: 298).
subpubic concavity presents, on females, as an upward curve on the ischiopubic ramus when viewing the pubis area dorsally. Lastly, the medial aspect of the ischiopubic ramus presents as a broad surface on males and a narrow surface on females. In order to accurately utilize this technique, all three features should be used together.

In a study by İşcan and Derrick (1984), they used three features of the sacroiliac joint to estimate sex visually. The sample size they used consisted of 17 males and 10 females. The three features were the iliac tuberosity, the post-auricular sulcus, and the post-auricular space (the greater sciatic notch). The post-auricular space was reported to be the most reliable and was even successful in sexing the two adolescents added to the sample. The post-auricular sulcus was present in nine out of 10 females, and three of the 17 males. The third structure, the iliac tuberosity, had the most variation and was the least reliable of the three, though, “the presence of a fossa instead of the tuberosity should […] be considered […] a female characteristic” (İşcan & Derrick 1984:97).

Buikstra and Ubelaker (1994) compiled a standards guide, which includes sexing methods using the pelvis and crania derived by other researchers. Along with Phenice’s (1969) method, the greater sciatic notch and the preauricular sulcus are both discussed as features useful in sexing unknown individuals. The greater sciatic notch is given a score between 1 and 5. For example, a “1” would indicate a “typical female” and would show a very broad sciatic notch, and a higher number would represent more “masculine” features, for instance a “5,” indicating a narrower sciatic notch. The preauricular sulcus is most commonly seen in females, and is given a score of “0” for absent, “1” for a broad sulcus that extends into the auricular surface, and “2-4” for a progressively narrower and smoothed sulcus with ridged walls.
Jordan Karsten (2018) did a study of the preauricular sulcus and its accuracy to estimate sex based on Buikstra and Ubelaker’s 1994 descriptions. The study used 500 left os coxae from the Hamann-Todd Skeletal collection, which included 261 males and 239 females. To test the differences between the males and females, a chi-square test was used, as well as a multiple regression to analyze any age or ancestry correlations. While the age and ancestry showed no significance to the preauricular sulcus, the results showed a 75.8% accuracy for sex estimation, with 62.84% of males being correctly assessed and 89.96% of females being correct. Karsten’s (2018) study indicates that the presence of a preauricular sulcus does not equate to a female, and that while a preauricular sulcus with a score of 1 has a high probability of female, the probability decreases quickly with scores of 2 or 3. One-third of the males in the study actually displayed preauricular sulci, and Karsten concluded that while the absence of the sulcus would strongly indicate male, a preauricular sulcus with a score of 4 would also be indicative a male individual.

The scoring system using four cranial and one mandibular trait, including the nuchal crest, mastoid process, supra-orbital margin, supra-orbital ridge/glabella, and the mental eminence, was originally published in Acsádi and Nemeskéri (1970) (as reported in Buikstra & Ubelaker 1994). In this method, each trait is given a score of 1-5, “1” being more female, “5” being more male, and “3” being ambiguous. The nuchal crest is graded on its robusticity, the mastoid process based on its overall volume, the supra-orbital margin on its sharpness versus roundedness, and the supra-orbital ridge/glabella and the mental eminence on their prominence.

Walker (2008) tested the reliability of traits outlined in Buikstra and Ubelaker (1994) using univariate and multivariate discriminant function analysis. The study utilized 304 modern crania from the Hamann-Todd Collection in Ohio, the Terry Collection in Washington D.C., and the Saint Bride’s Church Collection in London, as well as on an archaeological sample from the
Santa Barbara Channel in southern California. To test the intra-observer error, Walker scored 10 skulls on five separate occasions over the course of a month. For the inter-observer error, 20 volunteers, six trained osteologists and 14 students, also scored each of the 10 skulls. The scores from the 20 volunteers were put through a Kruskal-Wallis test to assess if there were any significant differences among observers. Aside from the mastoid process, the data showed that 96% of the scores were within one value of each other, and for the intra-observer error, Walker had a 99.5% accuracy for his scores falling in the same range. When the univariate test was run, it correctly estimated sex for 69-83% of the individuals, while the multivariate analysis gave an 89% accuracy for sex estimation. These results led Walker to conclude that using a logistic regression is the best approach when estimating sex, but also that using the scoring system can be recommended since it had a high reliability even with observers with little osteological training (Walker 2008).

Steyn and İşcan (1997) used a sample of 106 White South African individuals to test the viability of sex determination using measurements from the femur and tibia. The six measurements taken from the femora were maximum femoral length, head diameter, circumference, antero-posterior diameter, transverse diameter, and distal breadth. The tibia had seven measurements taken: physiological length, proximal epiphysal breadth, anteroposterior diameter, transverse diameter, circumference, minimum circumference, and distal epiphyseal breadth. The results of the study showed that the males were larger than females in all measurements, and the males had greater variation. After the comparative statistics tests were run, three femoral and five tibial measurements were selected for their percent contribution. “The accuracy of all the measurements ranged from 86% to 91%, with the combined method for the tibia and femur providing the best result [for sex estimation],” and “a 98% accuracy […] for
females…” (Steyn & Íşcan 1997:116). The study concluded with Steyn and Íşcan comparing their results with other studies using different populations, all of which showed similar accuracies in their results.

In a study by Spradley and Jantz (2011), quantitative sex estimation methods using the skull were compared to postcranial elements to test their effectiveness for sex estimation, and to determine which elements overall provide the most successful estimations. An advantage of using the postcranial elements for sex estimation, mentioned in the study, is that the methods tend to rely on quantitative data, which are less likely to be affected by subjectivity. The measurements taken in this study consisted of “…24 cranial, 10 mandibular, and 44 postcranial” (Spradley & Jantz 2011:290). The 13 elements used in the study were the cranium, mandible, clavicle, scapula, humerus, radius, ulna, os coxa, sacrum, femur, tibia, fibula, and calcaneus. For the statistics, ANOVA tests were run and significant differences in sex were found for the cranium, mandible, and all the postcranial elements. Overall, the humerus, clavicle, scapula, and femur were more accurate than the cranium in estimating sex in American Black individuals. For American White individuals, the radius, clavicle, femur, humerus, scapula, ulna, and tibia were more successful. The results of this study indicate that the cranium is not necessarily the second most accurate element to use when estimating sex using measurements, and that the use of postcranial elements should be utilized more when they are available.

**Ancestry Estimation**

Estimating the ancestry of an individual can assist in identifying him or her when unidentified remains are found. A person’s ancestry refers to the geographic region from which his or her ancestors originated. Most current ancestry estimation methods classify people into
three main groups, which correspond to broad geographic regions: Africa, Europe and the Middle East, and Asia and the Americas.

There is a current debate among anthropologists about whether or not ancestry estimation is an ethical practice in forensics (Bethard & DiGangi 2020, Dunn et al. 2020, & Stull et al. 2020). In a letter to the editor of the Journal of Forensic Sciences, Bethard and DiGiangi (2020) discuss that the use of morphoscopic traits should be ended in forensics due to lack of knowledge on the traits and that the traits encourage the concept of biological race. They also suggest giving an ancestry estimation can possibly obstruct the identification process due to law enforcement deeming the identification of a non-white individual less important. Stull et al. (2020) responded to the letter to explain how forensic anthropologists rely on traits that have a statistical grounding, while also acknowledging the negative past associated with early anthropological practices. They also mention that there is no data that shows a bias in the identification of non-white individuals by law enforcement, but the authors agree that the conversation surrounding the topic of ancestry estimation in forensics is important (Stull et al. 2020). Lastly, Dunn et al. (2020) provided an overview of past methodologies to estimate ancestry, and how they have been used to formulate the current methods and practices used by anthropologists today.

Methods to estimate ancestry can include two categories: metric and non-metric. Metric methods use measurements to make estimations. For example, Fordisc 3 is a program developed by Ousley and Jantz (2005) that performs a discriminant function analysis to estimate ancestry and sex in unidentified remains (Ousley & Jantz 2013). In Fordisc, measurements from the skull and mandible of an unknown individual are compared to measurements taken from known samples in the Forensic Data Bank. The skull is then assigned to the group to which it is statistically most similar. Non-metric methods use morphological traits that can be assessed as
ordinal categories or determined as present or absent. Non-metric methods are based on a qualitative assessment as opposed to quantitative (Hefner 2009).

The skull is the best element to estimate ancestry. Rhine (1990) compiled a list of 45 traits that can be assessed non-metrically from the skull and used for ancestry estimation. The classifications he used are “Anglo,” “Hispanic,” “Indian,” and “Black.” Based on his assessment, Rhine drew two conclusions. First, humans show variable cranial traits. Second, none of the traits that are listed should be used alone to assign ancestry. The fewer traits that are applied to the skull, the less support there is for an ancestry estimation.

Another study by Gill and Gilbert (1990) used the mid-facial skeleton to estimate the ancestry of Black and White Americans. This study used both metric and non-metric traits. The metric traits included the naso-maxillofrontal subtense, the maxillofrontal breadth, naso-zygoorbital subtense, and the zygoorbital breadth. The non-metric traits included the interorbital breadth and nasal bone shape. Gill and Gilbert (1990) found that by using these traits there was a high probability that the correct ancestry could be estimated.

Hefner (2009) also studied non-metric variation in the skull to estimate ancestry. In his study Hefner sought to improve non-metric ancestry analysis, test the accuracy on a large modern sample, and address disputes to the methods. Using 11 traits, four ancestral groups were assessed, including African, Asian, American-Indian, and European. The 11 traits are as follows: the anterior nasal spine, the interior nasal aperture, the interorbital breadth, the malar tubercle, the nasal aperture width, the nasal bone contour, nasal overgrowth, the postbregmatic depression, the supranasal suture, the transverse palatine suture, and the zygomaticomaxillary suture. To test the statistical significance of these traits among groups, frequency distributions were utilized. In the study, Hefner found that, when using all 11 variables, every individual in the sample of 747
exhibited traits from more than one ancestry group. Hefner (2009) concluded that using the idea of “typical” trait expressions in the four ancestry groups is not a reliable method to estimate ancestry.

A study by L’Abbé et al. (2011) utilized 13 nonmetric cranial traits to test their correlation to ancestry in a South African sample. For the study, the three main socially defined groups recognized in South Africa were represented: “White” or someone who is likely descended from colonial immigrants, “Black” or indigenous Africans, and “Colored” or someone who is likely descended from Eastern or Central African, or Malaysian slaves, the indigenous Khoisan, or modern Black and White people (L’Abbé et al. 2011). The goal of the study was to test if the nonmetric traits that were originally formulated using an American sample could be used by forensic specialists in South Africa. The sample consisted of 520 individuals, and the 13 traits were as follows: “nasal bone contour, nasal aperture width, anterior nasal spine projection, inferior nasal aperture form, nasal overgrowth, malar tubercle, interorbital breadth, zygomaticomaxillary suture, and transverse palatine suture shape..., alveolar prognathism, and zygomatic projection…, and the presence or absence of mandibular and palatine tori” (L’Abbé et al. 2011). The results showed that while most of the traits had a statistical significance, the South African sample was still very genetically heterogeneous, and L’Abbé et al. (2011) concluded that anthropologists cannot use morphological traits to estimate ancestry for a South African population. The study did note, however, that the traits described by Hefner (2009) had good repeatability in their intra- and inter-observer errors, and were recommended for future non-metric studies regarding ancestry.

Ancestry estimation using postcranial bones occurs less often, but there are methods that can be used to differentiate between the different ancestries. Īşcan and Cotton (1990) took 21
postcranial measurements from specimens at the Hamann-Todd Collection to search for a correlation with ancestry. Of the measurements taken in this study, six were from the pelvis, seven were from the femur, and eight were from the tibia. Of the 21 measurements, seven were determined to have a high success rate in estimating ancestry. In another study, Baker et al. (1990) compared a sample of 250 femora to estimate ancestry and sex using measurements of the intercondylar notch. The maximum height of the notch was taken from known specimens of American White and Black populations. However, in order to utilize this method to estimate sex or ancestry, either the sex or the ancestry must be known first.

Another study by Stewart (1962) used the anterior femoral curvature to differentiate among American Black, Native American, and White populations. To take the measurements, the femur was placed horizontally and the distance to the leveling points was taken. On the proximal end of the femoral shaft, the leveling point is on the medial side and above the lesser trochanter; on the distal end of the femur, the leveling point is on the lateral side of the shaft about 1-2 cm proximal to the lateral condyle (Stewart 1962:50-51). These points are the greatest anterior curvature of the diaphysis, the highest point of the cervical tubercle, and the highest point of the head. Stewart (1962) concluded that femoral curvature should not be used by itself as a way to estimate ancestry. However, by also including femoral torsion, Native Americans could be differentiated from Black and White populations.

**Ecogeographic Patterning**

Ecogeographic patterning theorizes that body size, appendage length, and coloring in warm-blooded species are influenced by climate, latitude, and altitude. There are three “rules” that researchers identified with regard to ecogeographic patterns: Bergmann’s rule, Allen’s rule, and Gloger’s rule. This theory and its rules are used in zoology and evolutionary biology, and
have been used to study migration patterns of early humans and Neandertals (Ruff 1991, VanderWerf 2012, Roseman & Auerbach 2014). The theory is based on thermoregulation in warm-blooded species and how their bodies have adapted to their specific climate in order to stay warmer or cooler (Tilkens et al. 2007). Thermoregulation, being able to maintain a consistent internal core temperature, is a trait seen in all endothermic, or warm-blooded, animals (Tattersall & Cadena 2010).

In 1847, biologist Carl Bergmann first proposed the idea that warm-blooded species in cold climates will be larger bodied, while in warm climates, they will be more narrow-bodied (as discussed in Holliday & Falsetti 1999). Joseph Allen’s 1877 work indicated that warm-blooded animals in cold climates will have shorter appendages than animals in warm climates (Tilkens et al. 2007). Shorter appendages and a larger body size are advantageous in cold climates because they decrease the surface area of an individual, thus limiting the heat loss. In warm climates, long appendages and smaller bodies are then beneficial, as they keep the individual cooler (Tilkens et al. 2007).

Researchers have completed studies testing Bergmann and Allen’s rules in modern humans. Holliday and Falsetti (1999) compared measurements of postcranial elements of African-American and European-American males and females from the Terry Collection. They hypothesized that although there is a shared temperate climate between the two samples, a difference in length should be seen that relates individuals to the continent from which their ancestors originated. Seven measurements were taken, including, skeletal trunk height, bi-iliac breadth, femoral bicondylar length, maximum humerus measurements, femoral head length, maximum tibia length, and maximum radius length. Holliday and Falsetti (1999) concluded that measurements in both sexes were consistent with Bergmann and Allen’s rules, with the results
showing 100% accuracy in classifying females, and 87% accuracy in males. That is, in regard to the Terry Collection, African-Americans had longer limbs, and shorter, more narrow torsos, than European-Americans.

In a study published in 1953, Roberts tested Bergmann’s rule, using indigenous populations from different parts of the world. Roberts looked for correlations among weight, stature, and mean temperature of the regions from which the populations originated. The data used for Robert’s study was acquired through published studies and physical reports. Overall, information from 134 populations from 10 different geographic regions were utilized for the study, though groups with less than 20 individuals were omitted, as were “sexually heterogeneous samples” (Roberts 1953:535). In the end, the mean weight and stature of 116 populations for males and 33 of the populations for females were calculated. The mean statures and body weights were then statistically compared to the geographic locations and their climates. While only some of the results were significant, Roberts (1953) concluded that Bergmann’s rule was demonstrated in the study with regard to height, but there was a great deal of variability seen in weight/body mass. Roberts discussed that a clearer definition of “body mass” and more data on the body composition of the indigenous populations were needed.

Katzmarzyk and Leonard’s (1998) research reevaluated Robert’s (1953) study. This study utilized 418 males and females from 10 different geographic regions. Information collected for each individual included body mass index (BMI), surface area/mass ratio, and relative sitting height. Katzmarzyk and Leonard (1998) found that Robert’s (1953) sample had a substantially higher correlation between individual body mass and annual temperature. While Katzmarzyk and Leonard still observed a correlation, their results compared to Roberts (1953) were less notable.
Foster and Collard (2013) also researched whether or not modern humans conformed to Bergmann’s rule. Using a similar methodology to Roberts, Foster and Collard examined 263 groups who were “believed to have resided in their present location since 1492” (Foster & Collard 2013:1). In the study, there were three sets of analyses, each of which compared modern human body size to temperature. The first analysis included the entire sample, the second controlled for the warm climate bias in the sample, and the third separated the northern and southern hemispheres. The first two analyses concluded that modern humans do conform to Bergmann’s rule, but only when there is a major difference in latitude and temperature between the groups (Foster & Collard 2013). When the third set was analyzed the northern hemisphere conformed to Bergmann’s rule, while the southern hemisphere did not. Overall, Foster and Collard (2013:15) suggest that “modern humans do conform to Bergmann’s rule but only when there are major differences in latitude and temperature among groups.”

Another study that tested Bergmann’s theory was done by Wells et al. (2019), with the hypothesis that other climate factors such as precipitation, temperature irregularity, and infectious disease would affect body composition in humans. The study looked at living individuals from non-industrialized regions and measured their height and weight, calculated body mass index, as well as took skin fold measurements from the triceps and subscapular region. The climate data used encompassed 113 years and recorded the annual average temperature and precipitation, and the inter-year irregularity in annual temperature. The researchers were looking for differences in lean mass versus adiposity or muscle versus fat storage in individuals from different regions. In the hot environments, the results showed individuals increased in both muscle and fat tissue when precipitation was high, likely due to the availability of resources. The cold environment sample indicated that precipitation had little
influence on body mass; however, the evidence did show that for those individuals, body mass increased during more unpredictable weather patterns. In cold environments, Wells et al. (2019) suggest that the increased body mass index during irregular temperatures is due to the body preparing for less resources availability. Wells et al. (2019) concluded that Bergmann’s theory does not fully account for the complex relationship between human body composition and climate, and that precipitation and temperature volatility are large factors in human body composition.

Ecogeographic patterning has also been applied to paleoanthropology research to understand hominin body adaptations and whether or not climate was an influence. For example, Ruff (1991) researched how early hominid body shape was affected by climate. He compared four fossil and two modern specimens: STS 14 (Australopithecus africanus), AL 288-1 (Australopithecus afarensis), Kebara 2 (Homo neanderthalensis), KNM-WT 15000 (Homo ergaster), and living African and European males; he also compared 71 living Sub-Saharan African, European, Southeastern Asian, and Northern Asian males and females. By measuring bi-iliac breadth for the breadth of the body and the stature, Ruff used a cylindrical model to estimate the surface area of each specimen. When the living populations were tested, Ruff (1991:85) found that “within similar climatic groups, absolute bi-iliac breadth shows little variation… [but] between groups absolute bi-iliac breadth increases from warmer to colder climates.” The heights and bi-iliac breadths were then calculated and estimated for the four fossils and two modern specimens. When compared to the living sample, STS 14, AL 288-1, and KNM-WT 15000 all fell within range of the tropical/subtropical populations, and Kebara 2 fell closest to the European and Northern Asian population. According to Ruff, while the evolution
of the hominid body size and shape probably had many influences, climate and geography likely played a part in that change over time as well.

Roseman and Auerbach (2015) examined whether or not natural selection on skeletal traits is prompted by the climate or other evolutionary processes. Four data sets were compiled for this study: the Goldman Data Set (1,538 skeletons), Auerbach’s Americas Data Set (2,749 skeletons), and two sets sampled from Europe and Africa, and Uganda and Kenya. The four data sets contained postcranial measurements, and represented populations from Eurasia, Africa, Oceania, and the Americas. After samples that had an undetermined sex, were poorly provenienced, or were duplicates were removed, 2,187 male individuals were left. The study utilized computer simulations using the samples to build models that show phenotype distribution to better understand which processes are responsible for human variation. Roseman and Auerbach (2015) drew three main conclusions: first, that population structure can affect human body size and shape; second, that evolutionary forces influence ecogeographic patterning; and lastly, that the uniqueness of human population history can mislead referential models. Overall, they suggest that in order to better understand phenotypic evolution, a combination of comparative, experimental, and theoretical work is needed.

Betti et al.’s (2014:66) study had two aims: the first, “to reaffirm the effect of neutral evolutionary processes… in determining human pelvic bone shape variation across populations,” and the second, “to evaluate the effect of climatic adaption on the size and shape of the os coxae.” The study consisted of 1,464 individuals, 922 males and 572 females, and 27 landmarks were used to measure the morphometric data collected. To test the hypothesis of neutral evolutionary processes being the cause inter-population differences of pelvic shape and size, linear and nonlinear models were created using a Mantel test to assess the correlation between
the phenotypic and geographic distance variables. For this study, the results indicated a significant correlation between coxal shape and neutral evolutionary processes. To test the difference in means between the coxal size and climate, ANOVA tests were run. The results of these tests showed a difference in means in the size of males with climate, but not in females. For correlation of climates and coxal shape, a Mantel test was also used and showed that the difference in shape changes were more related to population differences rather than to sex. The study concluded that while the os coxae follow Bergmann’s rule, genetic drift also showed a significant influence on the size of the os coxae. They suggest that “the two processes are compatible and not mutually exclusive” (Betti et al. 2014:72).

Lastly, in 2015, the author of the current research completed a pilot study on the left seventh rib (L7) using the donated skeletal collection housed at the Louisiana State University Forensic Anthropology and Computer Enhancement Services (LSU FACES) Laboratory. This pilot study was conducted to establish methods for measurements that were consistent and replicable for use in the current study, as well as to test if there were differences between the left and right-side length and width measurements. The pilot study samples consisted of 18 individuals, including both sexes and African and European ancestry groups. Results from paired T-tests found no significant differences between left and right sides for width; however, significant differences were found between left and right sides for length ($t = 4.0435$, $p = 0.0011$). These results indicate that left and right sides cannot be used interchangeably for length measurements if that variable is shown to be significant for estimating ancestry or sex.

To conclude, if Bergmann’s rule applies to modern humans, a difference in rib size between individuals of African and European/Middle Eastern ancestry should be observed (hereafter referred to as “Black” and “White” populations). The use of the terms Black and
White to describe ancestry was in part due to the fact that the Hamann-Todd Collection uses these terms to describe individuals who are of African and European ancestry, respectively. The research discussed shows that climate does have some effect on body size, which in turn, affects the heat regulation of warm-blooded animals. If a measurable difference in the rib length and depth between Black and White individuals can be determined, it may lead to a new method of ancestry estimation in forensic or bioarchaeological contexts. Most ancestry estimation methods use the skull or postcranial long bones, with little research conducted on the ribs as a possible element to utilize. From this review, the possibility of the ribs showing variation between Black and White individuals has potential.
Chapter 3. Materials & Methods

Materials

This study utilizes the left seventh rib (L7) of adult humans to test for correlations between the rib and an individual’s ancestry and sex. For the current study the Hamann-Todd Osteological Collection, which is housed at the Cleveland Museum of Natural History in Cleveland, Ohio, was used. This collection was chosen because of its well-documented specimens and the availability of skeletons of different ages, ancestries, and sexes. The Hamann-Todd Collection is a made up from a contemporary American population of over 3,000 individuals. Most of the collection was acquired from the Cuyahoga County Morgue and city hospitals in Cleveland, Ohio, and consisted of unclaimed bodies which were processed at a medical school by Todd and his assistants (Kern 2006:10-11).

Black and White males and females aged 25 years and older were included in this study. Individuals were selected based on two main qualities: the completeness of the left set of ribs, and lack of trauma to the left seventh rib (L7) specifically. Having a complete, or near complete, rib set is important to confidently order the ribs and ensure the measurements were taken from the left seventh rib. Lack of trauma to the L7 is an important quality since a fragmented or previously injured rib could affect measurement results and skew the sex or ancestry analysis. The two ancestry groups were selected with the expectation that they will show variation in their rib dimensions based on Bergmann’s rule. Males and females were also assessed to determine if the size differences could be attributed to human sexual dimorphism. The decision to use individuals 25 years and older was based on the fact that secondary ossification centers may still be fusing in individuals younger than 25. Older individuals with ossified cartilage were still
included in the sample; however, the measurement point at the sternal rib end was taken as close as could be determined to the original end of rib and excluded the ossified costal cartilage.

Coordinate calipers (Aichel type) shown in Figure 3.1 were used to take the measurements of the ribs. Coordinate calipers are similar to sliding calipers, except they have an extra measuring device that can take a depth measurement. The calipers used in this study have a measuring range of 20-300 mm and were able to accommodate all human rib measurement data. The measurements were taken to the nearest millimeter. Lastly, a digital camera and scales were used to take example photographs during the data gathering process.

![Coordinate Calipers](image)

**Figure 3.1. Coordinate Calipers**

**Methods/ Data Collection**

In order to collect the data, first the ribs had to be sided for each individual. To stay consistent throughout the study, the left side was always used. Then, using Mann’s (1993) methodology, the ribs were ordered and the seventh selected for measurements. As the last true rib, the seventh rib was chosen for the study because it is often the widest and longest rib of the chest, and therefore theorized to show the most variation. Once identified, each rib was placed
superior side down on a table, and three measurements were taken (Figure 3.2). The first measurement, named the “tuberculo-ventral chord” by Franciscus and Churchill (2002), or the “length,” (shown in red in the figure), measures the distance between the dorsal-most border of the articular tubercle and the ventral-most point of the sternal end. The second measurement, the “tuberculo-ventral subtense” (Franciscus and Churchill 2002), or “width,” (shown in green), is the perpendicular distance from the line created by “length” to the lateral edge of the rib body at the greatest depth. The last measurement, referred to in this study as the “width point measurement,” is based on locating the approximate point where the width and length intersect (i.e., the width point), then measuring the distance between that point and the sternal end of the rib (shown in orange).

![Figure 3.2. Length (#1, shown in red), Width (#2, shown in green), and Width Point (#3, shown in orange). Measurements (photograph by author of specimen from the LSU FACES Lab donated skeletal collection).](image)

Two calculations also were made based on the measurements, including the approximate “area” for the inner curvature of the rib, and ratio of the rib length to width. The inner curvature
area was estimated by calculating the area of a triangle from the length and width measurements, and using the formula

\[ \text{Area} = \frac{(h_b \times b)}{2} \]

where \( h_b \) = height (i.e., width), and \( b \) = base (i.e., length). The ratio, which gives an approximation of the curvature of the rib, was calculated by dividing the length by the width. To minimize measurement error in data collection, each of the measurements was taken three times, and the mean value was used in calculations and statistical analyses. To achieve the most consistent measurements, the calipers were reset to zero after each measuring, and the measurements were always taken in the same order for each rib (i.e., length, width, and width point), so the same point was not measured contiguously.

Intra-observer error was tested using a subsample of 28 individuals from the Hamann-Todd collection. Randomly selected individuals measured on the first day of data collection were re-measured on the last day, about two weeks apart, and variation in measurements was assessed statistically.

**Data Analysis**

To analyze the data collected in this study, the statistics programs STATA and Python were utilized. STATA was used to compile the data into summary statistics tables, and to run Pearson’s Correlation tests, two sample T-tests, and paired T-tests. Pearson’s Correlation was used to test consistency among the three measurement attempts, and a paired T-test was used to test consistency in measurements taken at the beginning and end of data collection. The two sample T-tests looked for difference in means between the rib measurements and ancestry or sex. For all tests, significance was determined if \( p < .05 \). Python was used to create swarm plots to visually show the distribution of the data for each variable, separated by sex and ancestry, then
by sex only. Based on those results, models were made to estimate sex or ancestry using the means and standard deviations of variables that showed the strongest correlation to sex or ancestry. The model then was tested using the data from the Hamann-Todd Collection and the contemporary LSU sample to check its accuracy in estimating the sex and ancestry of the individual.
Chapter 4. Results

A total of 299 individuals were measured from the Hamann-Todd skeletal collection. Of those 299, 75 were Black males, 74 Black Females, 75 White males, and 75 White females. Summary statistics are shown in Table 4.1 separated by sex and ancestry, and in Table 4.2 separated only by sex. From the summary statistics alone, the length and area means show noteworthy differences between the two sexes. For ancestry, the average width point and length showed the largest difference between Black and White individuals. The ratio, in relation to ancestry, exhibited larger values for White individuals compared to Black individuals for both sexes. This finding illustrates that the L7 in Black individuals has a slightly deeper curve. In regards to the ratio compared by sex, males have a slightly higher mean ratio at 3.5 than the females at 3.4.

Table 4.1. Summary Statistics from the Hamann-Todd Skeletal Collection (n=299) separated by sex and ancestry. Measurements described: Lmean (length mean), Wmean (width mean), WptMean (width point mean), Area, and Ratio.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Dev.</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lmean</td>
<td>74</td>
<td>202.5225</td>
<td>13.67764</td>
<td>163.3333</td>
<td>236.6667</td>
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<tr>
<td>Wmean</td>
<td>74</td>
<td>62.87838</td>
<td>7.161238</td>
<td>49.3333</td>
<td>79.66666</td>
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<tr>
<td>WptMean</td>
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<td>126.4099</td>
<td>11.86332</td>
<td>96.33334</td>
<td>155.6667</td>
</tr>
<tr>
<td>Area</td>
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<td>6366.298</td>
<td>849.6057</td>
<td>4836.556</td>
<td>9006</td>
</tr>
<tr>
<td>Ratio</td>
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<td>3.261978</td>
<td>.4293058</td>
<td>2.050209</td>
<td>4.385135</td>
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</table>

<table>
<thead>
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<th>Std. Dev.</th>
<th>Min</th>
<th>Max</th>
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<tr>
<td>Lmean</td>
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<td>209.3422</td>
<td>12.4948</td>
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<td>239</td>
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<tr>
<td>Wmean</td>
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<td>75.33334</td>
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<td>WptMean</td>
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<td>165.3333</td>
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</table>

(Table 4.1. cont’d).
(Table 4.1. cont’d.)

<table>
<thead>
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<th>Variable</th>
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<th>Mean</th>
<th>Std. Dev.</th>
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<td>Wmean</td>
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(-> Sex = Male, Ancestry = Black)

<table>
<thead>
<tr>
<th>Variable</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Dev.</th>
<th>Min</th>
<th>Max</th>
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<tr>
<td>Lmean</td>
<td>75</td>
<td>231.7378</td>
<td>14.25258</td>
<td>202</td>
<td>287</td>
</tr>
<tr>
<td>Wmean</td>
<td>75</td>
<td>62.58222</td>
<td>8.072512</td>
<td>36</td>
<td>75.66666</td>
</tr>
<tr>
<td>WptMean</td>
<td>75</td>
<td>153.3333</td>
<td>15.85037</td>
<td>115.6667</td>
<td>214.3333</td>
</tr>
<tr>
<td>Area</td>
<td>75</td>
<td>7243.219</td>
<td>968.6848</td>
<td>4254</td>
<td>9180.889</td>
</tr>
<tr>
<td>Ratio</td>
<td>75</td>
<td>3.777942</td>
<td>.6393246</td>
<td>2.669604</td>
<td>6.564815</td>
</tr>
</tbody>
</table>

(-> Sex = Male, Ancestry = White)

Table 4.2. Summary Statistics from the Hamann-Todd Skeletal Collection (n=299) separated by sex. Measurements described: Lmean (length mean), Wmean (width mean), WptMean (width point mean), Area, and Ratio.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Dev.</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lmean</td>
<td>149</td>
<td>205.9553</td>
<td>13.49222</td>
<td>163.3333</td>
<td>239</td>
</tr>
<tr>
<td>Wmean</td>
<td>149</td>
<td>61.06488</td>
<td>7.318133</td>
<td>41.33333</td>
<td>79.66666</td>
</tr>
<tr>
<td>WptMean</td>
<td>149</td>
<td>130.8054</td>
<td>12.19136</td>
<td>96.33334</td>
<td>165.3333</td>
</tr>
<tr>
<td>Area</td>
<td>149</td>
<td>6282.124</td>
<td>821.6652</td>
<td>4278</td>
<td>9006</td>
</tr>
<tr>
<td>Ratio</td>
<td>149</td>
<td>3.426874</td>
<td>.5214471</td>
<td>2.050209</td>
<td>5.656</td>
</tr>
</tbody>
</table>

(-> Sex = Female)

(Table 4.2. cont’d.)
Table 4.3 shows the Pearson’s correlation table tabulated to show repeatability among measurement attempts. Length is represented by L1, L2, and L3; width by W1, W2, and W3, and the width point measurement by Wpt1, Wpt2, and Wpt3. The length measurements show precision of approximately (~) .94, or 94%, across the measurements, which is the lowest of the three variables. Width shows precision scores of ~ .99 and .92, which averages to .955 or 95.5%. The width point scores are ~ .98 and .95; the average for these is .965 of 96.5%. These numbers show that the measurements were taken fairly consistently during the data collection process.

Table 4.3. Pearson’s Correlation Table

<table>
<thead>
<tr>
<th>Variable</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Dev.</th>
<th>Min</th>
<th>Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lmean</td>
<td>150</td>
<td>226.2778</td>
<td>14.39392</td>
<td>190</td>
<td>287</td>
</tr>
<tr>
<td>Wmean</td>
<td>150</td>
<td>65.05778</td>
<td>7.850462</td>
<td>36</td>
<td>83</td>
</tr>
<tr>
<td>WptMean</td>
<td>150</td>
<td>146.0578</td>
<td>16.03146</td>
<td>109.3333</td>
<td>214.3333</td>
</tr>
<tr>
<td>Area</td>
<td>150</td>
<td>7348.726</td>
<td>913.1287</td>
<td>4254</td>
<td>9535.167</td>
</tr>
<tr>
<td>Ratio</td>
<td>150</td>
<td>3.541243</td>
<td>.5817747</td>
<td>2.471861</td>
<td>6.564815</td>
</tr>
</tbody>
</table>

\[ \rightarrow \text{Sex} = \text{Male} \]
Results of the paired T-test examining variation in the measurements taken on the first day of data collection compared to the last day are presented in Table 4.4. From the results, the null hypothesis, that there are no notable differences in the measurements taken two weeks apart, can be rejected for the width (t = -3.1729, p = .0009), and width point (t = 6.0805, p < 0.0000). This result is not surprising considering that the point along the lateral edge of the rib where the width and width point measurements are taken can be somewhat subjective. For the length, the T-test results show that the null hypothesis fails to be rejected (t = -.9743, p = .3385).

Table 4.4. Results of the paired T-test comparing measurements taken the first and last day of data collection from the Hamann-Todd Collection (n=28). Variables described: LMean (length average from the first day), LMeanend (length average from the last day), WMean (width average from the first day), WMeanend (width average from the last day), WptMean (width point average from the first day), and WptMeanend (width point average from the last day).

<table>
<thead>
<tr>
<th>Variable</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>Std. Dev.</th>
<th>95% Conf. Interval</th>
</tr>
</thead>
<tbody>
<tr>
<td>WMean</td>
<td>28</td>
<td>63.17857</td>
<td>1.32254</td>
<td>6.998226</td>
<td>60.46494 - 65.8922</td>
</tr>
<tr>
<td>WMeanend</td>
<td>28</td>
<td>65.34524</td>
<td>1.172445</td>
<td>6.203996</td>
<td>62.93958 - 67.7509</td>
</tr>
<tr>
<td>diff</td>
<td>28</td>
<td>-2.166667</td>
<td>.5835539</td>
<td>3.087877</td>
<td>-3.36402 - .969313</td>
</tr>
</tbody>
</table>

\[
t = \frac{\bar{X}_{1} - \bar{X}_{2}}{S_{p}} = -3.7129
\]

degrees of freedom = 27

Pr(T < t) = 0.0005  Pr(|T| > |t|) = 0.0009  Pr(T > t) = 0.9995

(Table 4.4. cont’d.)
Swarm plots were created to give a visual representation of the data; they also reveal patterns with each of the variables. Figure 4.1 shows the distribution of data with sexes and ancestry groups separated. The females are represented by pink dots and males by green. In the length (Lmean) plot, an approximate diamond shaped distribution can be seen for both ancestries and their sex subsets, with many of the measurements clustering near the middle, then tapering
on each side. For width, width point, and area, the data show more variation within each ancestry group and sex subset than between them. In visually examining the variation in data between ancestry groups, the width mean shows the largest difference between Black and White individuals, with the ratio showing the smallest difference. This pattern is confirmed by the summary statistics (Tables 4.5 and 4.6).

Figure 4.1. Swarm plots showing the distribution of length (Lmean), width (Wmean), width point (Wptmean), area, and ratio by ancestry and sex.

(Figure 4.1. cont’d.)
(Figure 4.1. cont’d.)
The swarm plots in Figure 4.2 show the distribution of the variables separated by sex. Within each plot, ancestry is distinguished with Black individuals represented by orange dots and White individuals by blue. It is interesting to note how much intermingling can be seen in the data and that no new patterns emerge in any of the variables with regard to ancestry. The swarm plots also show that length (Lmean), width point (Wptmean), and ratio are more condensed (i.e., show less variation) than the width and area measurements. Males generally are larger than the females; though there is overlap for each variable, length (Lmean) and width point (Wptmean) show more distinct differences by sex.

Figure 4.2. Swarm plots showing the distribution of length (Lmean), width (Wmean), width point (Wptmean), area and ratio to sex.

(Figure 4.2. cont’d.)
(Figure 4.2. cont’d.)
Table 4.5 shows the results of the T-tests assessing the variation in the means of ancestry groups for all variables, with males and females separated. With the exception of area, significant differences were found for all other variables for both sexes (i.e., the length, width, width point, and ratio). Whites had larger lengths, width points, and ratios, while Blacks had larger widths. Thus, for those four variables, the null hypothesis, can be rejected.

Table 4.5. Results of the T-tests showing the length (LMean), width (WMean), width point (WptMean), area, and ratio

<table>
<thead>
<tr>
<th>Group</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>Std. Dev.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Black</td>
<td>74</td>
<td>202.5225</td>
<td>1.589994</td>
<td>13.67764</td>
<td>199.3537 - 205.6914</td>
</tr>
<tr>
<td>White</td>
<td>75</td>
<td>209.3422</td>
<td>1.442775</td>
<td>12.4948</td>
<td>206.4674 - 212.217</td>
</tr>
<tr>
<td>combined</td>
<td>149</td>
<td>205.9553</td>
<td>1.105326</td>
<td>13.49222</td>
<td>203.771 - 208.1395</td>
</tr>
<tr>
<td>diff</td>
<td>-6.8197</td>
<td>2.145708</td>
<td></td>
<td>-11.06012 - 2.57928</td>
<td></td>
</tr>
</tbody>
</table>

$\text{diff} = \text{mean(Black)} - \text{mean(White)}

\begin{align*}
\text{t} & = -3.1783 \\
\text{degrees of freedom} & = 147
\end{align*}$

$\text{H}_0: \text{diff} = 0 \\
\text{H}_1: \text{diff} < 0, \text{diff} > 0, \text{diff} \neq 0$

$\Pr(T < t) = 0.0009, \Pr(|T| > |t|) = 0.0018, \Pr(T > t) = 0.9991$

$\text{diff} = \text{mean(Black)} - \text{mean(White)}

\begin{align*}
\text{t} & = -5.0070 \\
\text{degrees of freedom} & = 148
\end{align*}$

$\text{H}_0: \text{diff} = 0 \\
\text{H}_1: \text{diff} < 0, \text{diff} > 0, \text{diff} \neq 0$

$\Pr(T < t) = 0.0000, \Pr(|T| > |t|) = 0.0000, \Pr(T > t) = 1.0000$

(Table 4.5. cont’d.)
(Table 4.5. cont’d.)

<table>
<thead>
<tr>
<th>Group</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>Std. Dev.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Black</td>
<td>74</td>
<td>62.87838</td>
<td>.832477</td>
<td>7.161238</td>
<td>61.21925 64.5375</td>
</tr>
<tr>
<td>White</td>
<td>75</td>
<td>59.27556</td>
<td>.8163832</td>
<td>7.070086</td>
<td>57.64888 60.90223</td>
</tr>
<tr>
<td>combined</td>
<td>149</td>
<td>61.06488</td>
<td>.5995248</td>
<td>7.318133</td>
<td>59.88014 62.24961</td>
</tr>
<tr>
<td>diff</td>
<td></td>
<td>3.602823</td>
<td>1.165875</td>
<td>1.298782</td>
<td>5.906863</td>
</tr>
</tbody>
</table>

\[ \text{diff} = \text{mean(Black)} - \text{mean(White)} \quad t = 3.0902 \]

Ho: diff = 0  
degrees of freedom = 147  
Pr(T < t) = 0.9988  
Pr(|T| > |t|) = 0.0024  
Pr(T > t) = 0.0012

(Cont’d.)

<table>
<thead>
<tr>
<th>Group</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>Std. Dev.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Black</td>
<td>75</td>
<td>67.53333</td>
<td>.7874389</td>
<td>6.819421</td>
<td>65.96433 69.10234</td>
</tr>
<tr>
<td>White</td>
<td>75</td>
<td>62.58222</td>
<td>.9321334</td>
<td>8.072512</td>
<td>60.72491 64.43954</td>
</tr>
<tr>
<td>combined</td>
<td>150</td>
<td>65.05778</td>
<td>.6409875</td>
<td>7.850462</td>
<td>63.79118 66.32438</td>
</tr>
<tr>
<td>diff</td>
<td></td>
<td>4.951111</td>
<td>1.220218</td>
<td>2.53981</td>
<td>7.362412</td>
</tr>
</tbody>
</table>

\[ \text{diff} = \text{mean(Black)} - \text{mean(White)} \quad t = 4.0576 \]

Ho: diff = 0  
degrees of freedom = 148  
Pr(T < t) = 1.0000  
Pr(|T| > |t|) = 0.0001  
Pr(T > t) = 0.0000

(Cont’d.)
(Table 4.5. cont’d.)

```
. by Sex, sort: ttest WptMean, by(Ancestry)

-> Sex = Female

Two-sample t test with equal variances

<table>
<thead>
<tr>
<th>Group</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>Std. Dev.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Black</td>
<td>74</td>
<td>126.4099</td>
<td>1.379083</td>
<td>11.86332</td>
<td>123.6614  129.1584</td>
</tr>
<tr>
<td>White</td>
<td>75</td>
<td>135.1422</td>
<td>1.265119</td>
<td>10.95626</td>
<td>132.6214  137.663</td>
</tr>
<tr>
<td>combined</td>
<td>149</td>
<td>130.8054</td>
<td>.9987552</td>
<td>12.19136</td>
<td>128.8317  132.779</td>
</tr>
<tr>
<td>diff</td>
<td></td>
<td>-8.732311</td>
<td>1.870466</td>
<td>-12.42879</td>
<td>-5.035834</td>
</tr>
</tbody>
</table>

diff = mean(Black) - mean(White)  \quad t = -4.6685  
Ho: diff = 0  \quad degrees of freedom = 147

Ha: diff < 0  \quad Pr(T < t) = 0.0000  
Ha: diff != 0  \quad Pr(|T| > |t|) = 0.0000  
Ha: diff > 0  \quad Pr(T > t) = 1.0000

-> Sex = Male

Two-sample t test with equal variances

<table>
<thead>
<tr>
<th>Group</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>Std. Dev.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Black</td>
<td>75</td>
<td>138.7822</td>
<td>1.455823</td>
<td>12.60779</td>
<td>135.8814  141.683</td>
</tr>
<tr>
<td>White</td>
<td>75</td>
<td>153.3333</td>
<td>1.830243</td>
<td>15.85037</td>
<td>149.6865  156.9802</td>
</tr>
<tr>
<td>combined</td>
<td>150</td>
<td>146.0578</td>
<td>1.308964</td>
<td>16.03146</td>
<td>143.4712  148.6443</td>
</tr>
</tbody>
</table>

diff = mean(Black) - mean(White)  \quad t = -6.2221  
Ho: diff = 0  \quad degrees of freedom = 148

Ha: diff < 0  \quad Pr(T < t) = 0.0000  
Ha: diff != 0  \quad Pr(|T| > |t|) = 0.0000  
Ha: diff > 0  \quad Pr(T > t) = 1.0000
```
(Table 4.5. cont’d.)

<table>
<thead>
<tr>
<th>Group</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>Std. Dev.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Black</td>
<td>74</td>
<td>6366.298</td>
<td>98.76466</td>
<td>849.6057</td>
<td>6169.46 – 6563.136</td>
</tr>
<tr>
<td>White</td>
<td>75</td>
<td>6199.073</td>
<td>91.2225</td>
<td>790.01</td>
<td>6017.308 – 6380.837</td>
</tr>
<tr>
<td>combined</td>
<td>149</td>
<td>6282.124</td>
<td>67.31343</td>
<td>821.6652</td>
<td>6149.105 – 6415.144</td>
</tr>
<tr>
<td>diff</td>
<td></td>
<td>167.2254</td>
<td>134.3811</td>
<td>-98.34298</td>
<td>432.7938</td>
</tr>
</tbody>
</table>

\[
\text{diff} = \text{mean(Black)} - \text{mean(White)} \quad t = 1.2444 \\
\text{Ho: diff} = 0 \quad \text{degrees of freedom} = 147
\]

- \( \text{Pr}(T < t) = 0.8923 \)
- \( \text{Pr}(|T| > |t|) = 0.2153 \)
- \( \text{Pr}(T > t) = 0.1077 \)

(Cont’d.)

-> Sex = Male

Two-sample t test with equal variances

<table>
<thead>
<tr>
<th>Group</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>Std. Dev.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Black</td>
<td>75</td>
<td>7454.233</td>
<td>97.84078</td>
<td>847.326</td>
<td>7259.281 – 7649.185</td>
</tr>
<tr>
<td>White</td>
<td>75</td>
<td>7243.219</td>
<td>111.8541</td>
<td>968.6848</td>
<td>7020.345 – 7466.093</td>
</tr>
<tr>
<td>combined</td>
<td>150</td>
<td>7348.726</td>
<td>74.55665</td>
<td>913.1287</td>
<td>7201.491 – 7496.051</td>
</tr>
<tr>
<td>diff</td>
<td></td>
<td>211.0133</td>
<td>148.6074</td>
<td>-82.65306</td>
<td>504.6797</td>
</tr>
</tbody>
</table>

\[
\text{diff} = \text{mean(Black)} - \text{mean(White)} \quad t = 1.4199 \\
\text{Ho: diff} = 0 \quad \text{degrees of freedom} = 148
\]

- \( \text{Pr}(T < t) = 0.9211 \)
- \( \text{Pr}(|T| > |t|) = 0.1577 \)
- \( \text{Pr}(T > t) = 0.0789 \)
(Table 4.5. cont’d.)

```
. by Sex, sort : ttest Ratio, by(Ancestry)

-> Sex = Female

Two-sample t test with equal variances

<table>
<thead>
<tr>
<th>Group</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>Std. Dev.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Black</td>
<td>74</td>
<td>3.261978</td>
<td>.0499058</td>
<td>.4293058</td>
<td>3.162516 - 3.361444</td>
</tr>
<tr>
<td>White</td>
<td>75</td>
<td>3.589572</td>
<td>.0640814</td>
<td>.5549615</td>
<td>3.461887 - 3.717257</td>
</tr>
<tr>
<td>combined</td>
<td>149</td>
<td>3.426874</td>
<td>.0427186</td>
<td>.5214471</td>
<td>3.342457 - 3.511291</td>
</tr>
<tr>
<td>diff</td>
<td></td>
<td>-.3275941</td>
<td>.08136</td>
<td>-.4883805</td>
<td>-.1668078</td>
</tr>
</tbody>
</table>

diff = mean(Black) - mean(White)  
Ho: diff = 0  
degrees of freedom = 147

  Ha: diff < 0  
Pr(T < t) = 0.0000  

  Ha: diff != 0  
Pr(|T| > |t|) = 0.0001

  Ha: diff > 0  
Pr(T > t) = 1.0000

-> Sex = Male

Two-sample t test with equal variances

<table>
<thead>
<tr>
<th>Group</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>Std. Dev.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Black</td>
<td>75</td>
<td>3.304545</td>
<td>.0460717</td>
<td>.3989924</td>
<td>3.212745 - 3.396345</td>
</tr>
<tr>
<td>White</td>
<td>75</td>
<td>3.777942</td>
<td>.0738228</td>
<td>.6393246</td>
<td>3.630847 - 3.925037</td>
</tr>
<tr>
<td>combined</td>
<td>150</td>
<td>3.541243</td>
<td>.0475017</td>
<td>.5817747</td>
<td>3.447379 - 3.635107</td>
</tr>
<tr>
<td>diff</td>
<td></td>
<td>-.4733968</td>
<td>.0870196</td>
<td>-.6453582</td>
<td>-.3014354</td>
</tr>
</tbody>
</table>

diff = mean(Black) - mean(White)  
Ho: diff = 0  
degrees of freedom = 148

  Ha: diff < 0  
Pr(T < t) = 0.0000  

  Ha: diff != 0  
Pr(|T| > |t|) = 0.0000

  Ha: diff > 0  
Pr(T > t) = 1.0000
```
The Table 4.6 shows results of the T-tests assessing the difference in means for all the variables and sex. Four out of five variables show significant differences (p < 0.05); thus, the null hypothesis can be rejected for those variables (length, width, width point, and area).

Table 4.6. T-tests showing the differences in means between Sex and length (LMean), width (WMean), width point (WptMean), and Area.

<table>
<thead>
<tr>
<th>Group</th>
<th>Obs</th>
<th>Mean (LMean)</th>
<th>Std. Err.</th>
<th>Std. Dev.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Female</td>
<td>149</td>
<td>205.9553</td>
<td>1.105326</td>
<td>13.49222</td>
<td>203.771  208.1395</td>
</tr>
<tr>
<td>Male</td>
<td>150</td>
<td>226.2778</td>
<td>1.175258</td>
<td>14.39392</td>
<td>223.9555 228.6081</td>
</tr>
<tr>
<td>combined</td>
<td>299</td>
<td>216.1505</td>
<td>.9976529</td>
<td>17.25103</td>
<td>214.1872 218.1138</td>
</tr>
<tr>
<td>diff</td>
<td></td>
<td>-20.32252</td>
<td>1.613724</td>
<td>-23.4983</td>
<td>-17.14674</td>
</tr>
</tbody>
</table>

\[
t = \frac{\text{diff}}{\text{Std. Err.}} = \frac{-20.32252}{1.613724} = -12.5936
\]

Ho: diff = 0
Ha: diff < 0

Pr(T < t) = 0.0000

Table 4.6. cont’d.)
(Table 4.6. cont’d.)

```
. ttest WptMean, by(Sex)

Two-sample t test with equal variances

<table>
<thead>
<tr>
<th>Group</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>Std. Dev.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Female</td>
<td>149</td>
<td>130.8054</td>
<td>.9987552</td>
<td>12.19136</td>
<td>128.8317 – 132.779</td>
</tr>
<tr>
<td>Male</td>
<td>150</td>
<td>146.0578</td>
<td>1.308964</td>
<td>16.03146</td>
<td>143.4712 – 148.6443</td>
</tr>
<tr>
<td>combined</td>
<td>299</td>
<td>138.4571</td>
<td>.9337114</td>
<td>16.14538</td>
<td>136.6196 – 140.2946</td>
</tr>
</tbody>
</table>

\[ \text{diff} = \text{mean(Female)} - \text{mean(Male)} \]
\[ t = -9.2553 \]
\[ \text{Ho: diff} = 0 \]
\[ \text{degrees of freedom} = 297 \]

\[ \text{Ha: diff < 0} \]
\[ \text{Ha: diff} \neq 0 \]
\[ \text{Ha: diff > 0} \]
\[ \Pr(T < t) = 0.0000 \]
\[ \Pr(|T| > |t|) = 0.0000 \]
\[ \Pr(T > t) = 1.0000 \]

. ttest Area, by(Sex)

Two-sample t test with equal variances

<table>
<thead>
<tr>
<th>Group</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>Std. Dev.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Female</td>
<td>149</td>
<td>6282.124</td>
<td>67.31343</td>
<td>821.6652</td>
<td>6149.105 – 6415.144</td>
</tr>
<tr>
<td>Male</td>
<td>150</td>
<td>7348.726</td>
<td>74.55665</td>
<td>913.1287</td>
<td>7201.401 – 7496.051</td>
</tr>
<tr>
<td>combined</td>
<td>299</td>
<td>6817.209</td>
<td>58.90768</td>
<td>1018.609</td>
<td>6701.281 – 6933.136</td>
</tr>
<tr>
<td>diff</td>
<td></td>
<td>-1066.602</td>
<td>100.4834</td>
<td></td>
<td>-1264.351 – -868.852</td>
</tr>
</tbody>
</table>

\[ \text{diff} = \text{mean(Female)} - \text{mean(Male)} \]
\[ t = -10.6147 \]
\[ \text{Ho: diff} = 0 \]
\[ \text{degrees of freedom} = 297 \]

\[ \text{Ha: diff < 0} \]
\[ \text{Ha: diff} \neq 0 \]
\[ \text{Ha: diff > 0} \]
\[ \Pr(T < t) = 0.0000 \]
\[ \Pr(|T| > |t|) = 0.0000 \]
\[ \Pr(T > t) = 1.0000 \]

(Continued)
Based on the results of the swarm plots, variables were selected to create nonlinear models to estimate ancestry and sex (Figures 4.3-4.5). The variables selected were those that showed the greatest differences in the means for each subset, and included length, width, and width point for the ancestry predictor models, and length, area, and width point for the sex predictor model. Due to the ancestry data being separated by sex, two ancestry models were created, one for males (Figure 4.3) and one for females (Figure 4.4).

![Non-linear model to estimate ancestry in males.](image)

Table 4.6. cont'd.

<table>
<thead>
<tr>
<th>Group</th>
<th>Obs</th>
<th>Mean</th>
<th>Std. Err.</th>
<th>Std. Dev.</th>
<th>[95% Conf. Interval]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Female</td>
<td>149</td>
<td>3.426874</td>
<td>.0427186</td>
<td>.5214471</td>
<td>3.342457 - 3.511291</td>
</tr>
<tr>
<td>Male</td>
<td>150</td>
<td>3.541243</td>
<td>.0475017</td>
<td>.5817747</td>
<td>3.447379 - 3.635107</td>
</tr>
<tr>
<td>combined</td>
<td>299</td>
<td>3.48425</td>
<td>.0320719</td>
<td>.5545746</td>
<td>3.421134 - 3.547366</td>
</tr>
<tr>
<td>diff</td>
<td>- .1143695</td>
<td>.0639084</td>
<td>-.2401401</td>
<td>.0114011</td>
<td></td>
</tr>
</tbody>
</table>
In the models for ancestry, the result of length divided by width, also referred to as the ratio, is divided by the mean of the ratios (3.54 for males and 3.43 for females), then that value is added to the result of width point divided by the mean of the width point (146.06 for males and 130.81 for females). That sum then is divided by the sum of the value of width divided by the mean of the width (65.06 for males and 61.06 for females) plus 1. Ancestry is estimated based on the result generated by the model, with a result of 0.9 or less being assigned as Black, and 1 or higher being assigned as White.

The model was tested for accuracy in estimating ancestry using the dataset from this study, as well as the data from the FACES Lab pilot study. Based on the Hamann-Todd dataset, the models showed an accuracy rate of 70%, or 105 out of 150, for males, and 65.1%, or 97 out of 149, for females. Using the FACES Lab sample, the model correctly estimated the ancestry of 11 of 12 males (91.6%), and 4 of 6 females (66.6%).

In the model for sex (Figure 4.5), for each variable, the measurement is divided by the mean for that variable calculated from the total data set; these values then are added together, and the sum is divided by three. Sex is estimated based on the result generated by the model, with a result of 0.9 or less assigned female, and a result of 1.0 or higher being male.
The model was tested for accuracy in sex estimation using the dataset from this study, as well as the data from the FACES Lab pilot study. Based on the Hamann-Todd dataset, the model showed an accuracy rate of 80.9% or 242 out of 299 individuals correctly sexed. Using the FACES Lab sample, the model correctly estimated the sex in 16 of 18 individuals (88.9%) accuracy.
Chapter 5. Discussion

This study sought to construct a new method of ancestry and sex estimation to be used when identifying unknown adult humans when other methods cannot be utilized. The first hypothesis of this study was that Black individuals would have smaller rib dimensions (i.e., length, width, width point, area, and ratio) than White individuals, due to evolutionary adaptation to varying climates. Results indicated that Black individuals, both males and females, did have smaller lengths, width points, and ratios, and the differences in these three variables were significant. However, Black individuals actually had larger widths. Additionally, when the model estimating ancestry was tested using the Hamann-Todd dataset, only in 70% of males and 65.1% of females was ancestry correctly estimated. From these findings, the first hypothesis is only partially supported. While the L7 does exhibit significant differences between Black and White individuals in certain dimensions, the variation does not unequivocally adhere to Bergmann’s rule. Additionally, it appears that the L7 dimensions examined in this study do not have a strong enough association to ancestry to confidently estimate ancestry for unknown individuals.

The second hypothesis of the study stated that males and females would differ in the size of L7, with males being larger than females, and that rib dimensions could be used to estimate sex in unknown adults. The results of this study indicate that there are indeed statistically significant differences for all of the variables and sex. L7 dimensions in males were larger than females, even though there was some overlap with every variable. The model used to estimate sex returned an 80.9% success rate when used on the Hamann-Todd dataset, and 88.9% success rate when used on the LSU FACES Lab dataset. Thus, this method could aid in estimating sex when the crania and os coxae are not available. The hypothesis in this case can be accepted; that is, there is an association between dimensions of the L7 and sex, with males larger than females.
This result also appears to contradict Bellemare et al.’s (2006) study which concluded that females had a larger rib cage volume. However, the measurements in this study were slightly different than those in Bellmare et al.’s study, which could account for the different results. Specifically, Bellemare et al. (2006) measured along the ribs using a metal wire (i.e., incorporating the curvature of the body), while the current study measured the linear distance between the rib head and sternal end using calipers. The rib length to axial skeleton height ratio was larger in females in Bellemare et al.’s (2006) study, yielding the conclusion that females have a larger rib cage volume, in comparison to males of the same height. In this study, the axial skeleton height was not taken into account, and the ratio variable used was to illustrate the approximate curvature of the rib.

Several concerns about the results of the current study include the use of the Hamann-Todd dataset to both construct and test the models for estimating ancestry and sex, as well as issues involving both intra- and inter-observer error. With regard to the former concern, for ancestry, even based on the same dataset, the modest results of 70% (males), and 65.1% (females) correct estimations may indicate rib dimensions are not consistently different enough between Black and White populations to reliably estimate the ancestry of unknown individuals. The results of testing the model on the smaller sample appear to corroborate this indication for females (i.e., still only 66.6% correct estimations). However, for males the smaller sample had a success rate of 91.6% correct estimations. The improved results for the sex estimation model (~81% correct estimation) are expected when using the main dataset, and the results are even better when tested against a different sample (~89% correct estimations). Though promising, these results still should be considered with caution due to the small sample size of the test
sample. The best way to ensure that the success rate for estimating sex from the L7 dimensions is valid is to test the model on other datasets.

With regard to potential methodological error (i.e., intra- and inter-observer), one observation made in this study was that, while the length showed little variation from the first day of measurements compared to the last day, the width and width point variables showed statistically significant variation, with width point having a more dramatic difference (i.e., nearly 13 mm, see Table 4.4). As the placement of the width point measurement is relatively subjective, this result is not surprising. Because of this subjectivity, the models to estimate sex and ancestry were made and tested with and without the width point measurement. The results showed that using the width point coefficient substantially improved the accuracy of the sex and ancestry estimations. Therefore, because width point may be an important variable in differentiating ancestry groups and sexes, efforts should be made to improve the precision in locating width point and taking its measurement. Such standardization would improve not only intra-observer error, but also would enable testing inter-observer error. Before the model can be validated as a method for estimating sex from L7 dimensions, it is important to know if the measurements can be taken consistently, and the results of this study can be replicated, by others.

Another important issue to consider regarding this possible new method of sex estimation is the viability of the ribs when recovered in forensic and archaeological contexts. In several studies, it has been noted that the distal and proximal ends of the ribs were often splintered and chewed by scavengers when the internal organs are accessed (Haglund 1988, Moraitis & Spiliopoulou 2010). Further, Haglund et al. (1988) also found that ribs were recovered from outdoor locations only about 68% of the time (the number of ribs recovered is not described). Understandably, the ribs found in multiple fragments or that are incomplete are prone to error for
estimating sex, if measurements can even be taken. Similarly, ribs with healed trauma also can result in incorrect estimations if the width or length is altered due to the trauma. For example, when a rib is broken, its shape can become morphed after healing and, thus, is no longer suitable to use with a model for sex estimation. For these reasons, ribs that showed any signs of healed trauma or that were fragmented were not used in the current study; therefore, it also is suggested that the model generated in this study not be applied to ribs with trauma or fragmentation.

To test asymmetry, all measurements were taken from both the left and right seventh ribs from a sample of 18 individuals from the donated skeletal collection housed at the Louisiana State University Forensic Anthropology and Computer Enhancement Services (LSU FACES) Laboratory. This collection is comprised of individuals donated from a contemporary forensic context, and includes individuals of varying ages from both sexes and African and European ancestry groups. This pilot study, conducted by the author, found significant differences in length measurements between right and left sides, with disparities as large as 10mm. These data suggest that the right side cannot be easily substituted for the left side if the latter is not available. However, the sample used to look at symmetry was very small (n=18). Moreover, the author found that taking measurements on the right rib was difficult because either the calipers or the rib had to be turned over; this change in positioning affected the ability to consistently locate the landmarks (particularly for width point) and, thereby, take the necessary measurements. Based on the potential asymmetry between left and right rib lengths, as well as on the difficulty in taking the width point measurement from the right side, it would not be recommended to use the right ribs to estimate sex using the model created in this study. Either a new model would have to be created that excludes width point or an accurate method of taking the width point from the right side would have to be established.
The partial rejection of the first hypothesis (i.e., that variation in the ribs exists between Black and White ancestry groups) could be related to a variable seen in other research. Concerning Bergman’s rule, many studies that utilize this theory also incorporate the variable of body mass into their research (Roberts 1953, Foster and Collard 2013, & Katzmarzyk and Leonard 1998, Wells et al., 2019). It is possible that Bergman’s rule may rely heavily on the body mass of individuals, and less so on the torso size and shape. This possibility is plausible since the muscle and fat stored on mammals would have an impact not only on their size, but on their thermoregulation as well. Also, though the muscle and fat distribution may have an effect on the skeletal structure in mammals, body mass and torso size/shape are not mutually interchangeable. Moreover, the use of a dataset where the individuals who, despite having different ancestral origins, are assumed to have lived their lives in similar latitudes, may also be having an effect on the results. Using two separate datasets, for example one derived from a European population and one from an African population, may show different results than the current study. In a study by De La Cova (2011) individuals from the Hamann-Todd Collection, as well as the Cobb and Terry collections, were compared for disparities in skeletal health between African American and European American males who were of low socioeconomic status. De La Cova found that African American individuals did have higher rates of tuberculosis and treponematosis. The higher rates of disease were likely due to poor living conditions that were available to people of color during the 1800s, as well as stressors individuals may have faced during the Civil War, Reconstruction and post-Reconstruction (De La Cova 2011). These skeletal collections were formed during the late 19th and early 20th centuries when it was anatomical law for hospitals to give unclaimed bodies to medical schools (De La Cova 2011). The study by De La Cova brings attention to the fact that some of the disparities observed among
individuals of African American and European American ancestries can actually be attributed to stressors and diseases African Americans faced during slavery and segregation.

Wells et al.’s (2019) study also brings up an important factor regarding Bergmann’s theory and body composition. That is, how the climate affects other important aspects of an individual’s life, such as rain and temperature affecting food production or disease affecting muscle and fat storage, may also contribute to an individual’s body size. Considering that the current study was completed on a modern sample from an industrialized nation, it is likely that the individuals in the study sample did not have to worry about average rainfall affecting their food intake or their thermoregulation outdoors in the same way that individuals from earlier or non-industrialized populations would have had to do. These considerations indicate areas where more research is needed to understand how rib development in less controlled environments may be impacted, or how affected the rib morphology is by changes in an individual’s body mass index.

Lastly, L’Abbé et al.’s (2011) study mentions the homogeneity of the population in South Africa and how, because of this, estimating ancestry within that population is more difficult. Further research that considers the intermingling of (or gene flow between) individuals from different ancestry groups in the US or regions of the US would be important to refine methods for ancestry estimation. It also would be interesting to use the models created in this study for datasets from Europe and Africa to determine if the results would show differences in correct estimations based on the possibility that these populations may have remained separated or more isolated from other groups than the sample used in this study.
Conclusion

To recap this study, the first hypothesis: that left seventh (L7) rib dimensions correlate to ancestry, and that Black individuals will have smaller L7 rib dimensions than White individuals, generally can be rejected. The second hypothesis: that L7 rib dimensions correlate to sex, and that males will have larger L7 rib dimensions than females, can be cautiously accepted. Use of the model provided in this study for sex estimation is cautiously recommended alongside other, more established, methods; however, more research is needed. Most importantly, the method for locating and subsequently measuring the width point needs to be standardized, and the model for sex estimation needs to be tested on other datasets to determine its reliability. Being able to use the left seventh rib to estimate sex gives forensic anthropologists an additional method to aid in human identification. When faced with cases where remains are dismembered and main elements are missing, this method can assist with providing more information for unknown individuals.

Though the first hypothesis has been rejected in this study, research using geographically diverse datasets may provide a different result. The use of American Black and White individuals from a similar geographic region may be contributing to the lack of successful results in this study. It is possible that the individuals included in this study, who may not be first generation immigrants, are acclimated to the climate in the US or represent a more homogenized population, and therefore do not show the variation expected for their ancestry groups as suggested by Bergmann’s theory. Regardless, in conclusion, use of the left seventh rib dimensions for estimating ancestry was not successful and Bergmann’s rule is not supported by the results of this study.
Bibliography


Vita

Alexandria M. Amaki was born in Ventura, California April 22, 1993. She was graduated from Adolfo Camarillo High School in 2011, and went on to achieve her degree in Anthropology from CSU, Chico, with a minor in Food Studies in 2015. While attending CSU, Chico she was also student worker for the Chico State Human Identification Lab and a member of Alpha Chi Sorority. She also attended the Betty’s Hope Archaeological Field School in Antigua the Summer of 2015. In 2017, she began her studies at Louisiana State University, Baton Rouge, to continue to pursue her interests in forensic anthropology and archaeology, and worked as a graduate assistant for the LSU Forensic Anthropology and Computer Enhancement Services Lab (FACES Lab). She plans to receive her Master’s this May 2021. After graduation, she will pursue a job in the field of anthropology, specifically in bioarchaeology or forensics.