OSTEOMETRIC SORTING OF METACARPALS AND METATARSALS IN COMMINGLED HUMAN SKELETAL ASSEMBLAGES

A Thesis

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Anthropology

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by

Kristen A. Broehl

Spring 2018

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LIST OF SYMBOLS OR NOMENCLATURE

%TEM	relative (percent) technical error of measurement
BW	base mediolateral width measurement
HIL	CSUC Human Identification Lab Donated Forensic Collection
HUM.1/FEM.1	variable calculated ln(maximum length+epicondylar breadth+head diameter)
HUM.2/FEM.2	variable calculated ln(epicondylar breadth)
HUM.3/FEM.3	variable calculated ln(head diameter)
HUM/FEMEP	epicondylar breadth of humerus or femur
HUM/FEMHD	head diameter of humerus or femur
HUML/FEML	maximum length of humerus or femur
HW	head mediolateral width measurement
IAL	interarticular length measurement
LATF	lateral articular facet length measurement
LEN	length measurement
MC(s)/MT(s)	metacarpal(s)/metatarsal(s)
MC.1/MT.1	variable calculated ln(interarticular length+head width+base width)
MEDF	medial articular facet length measurement
MLNI	most likely number of individuals
MNI	minimum number of individuals
MOB	mini osteometric board

MXL	maximum length measurement
PSJ	Point San Jose Collection
pXRF	portable x-ray fluorescence
R	coefficient of reliability
r	correlation coefficient
TEM	technical error of measurement
UNM	University of New Mexico Maxwell Museum of Anthropology Documented Collection

ABSTRACT

OSTEOMETRIC SORTING OF METACARPALS AND

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Commingling of human skeletal remains impedes anthropological analyses. Therefore, researchers must develop methods for individuating remains. One such method is osteometric sorting, but most studies have not included frameworks for resolving commingling of hand and foot elements, such as metacarpals and metatarsals. This study uses a reference sample from the University of New Mexico's documented osteological collection to derive that data. Hypotheses relating to the concepts underlying osteometric sorting of paired, articulating, and other regions were tested, including (1) metacarpals and metatarsals show symmetry through no significant size differences between rights and lefts, (2) the lengths of facets where metacarpals and metatarsals articulate are correlated, and (3) metacarpal and metatarsal dimensions are correlated with humerus and femur dimensions. Statistical data for osteometric sorting was then derived, tested, and applied to the historic Point San Jose Collection to discern various types of medical discard that could explain its origin.

Most hypotheses were accepted, but symmetry for the metacarpals was rejected due to a right directional asymmetry that may reflect handedness of the population. The minor right-left differences did not prevent the application of osteometric pair-matching, which was powerful for sorting. Osteometric articulation and osteometric comparisons to the humerus and femur were moderately successful. The application of the methods to the Point San Jose collection suggests the presence of cadavers rather than surgical waste. While refinements of measurements and a larger, more diverse reference sample would improve the method, this study shows the utility of sorting metacarpals and metatarsals using osteometric methods.

CHAPTER I

INTRODUCTION

The Point San Jose (PSJ) Collection was discovered in a refuse pit at Fort Mason, part of the Golden Gate National Recreation Area in San Francisco. It is associated with the historical hospital on the base. Historically, Fort Mason was an army post called Point San Jose that was meant to protect Union commercial ships against potential Confederate attacks during the Civil War (National Park Service, 2016). Descriptive analyses of the remains by Willey et al. (2016) show that the assemblage is consistent with being disposed medical refuse or teaching specimens, although commingling has been an impediment to examination. Evidence of autopsy, dissection, and amputation are all present through saw cut marks and incised cut marks, but differentiating these sorts of circumstances has been difficult due to commingling. Knowing whether fairly complete skeletons or a number of isolated body parts comprise the assemblage would add evidence for and against various contextual possibilities.

Differentiating these behaviors could tell researchers more about the physicians who worked at the Point San Jose hospital, such as Dr. Edwin Bentley (Powell and Shippen 1892), and about general medical practices of the nineteenth century. A pit of surgical waste, however, provides different anthropological insights into the site's significance than would a pit of cadavers because dissections are a potential example of structural violence due to targeting the most marginalized groups of society with grave-robbing to supply corpses for medical training (Sappol 2002; Tward and Patterson 2002).

Identifying the context of the site is then necessary for drawing conclusions regarding the purpose of the remains and the motivation behind their subsequent disposal in a backyard pit.

Resolving commingling is obviously a significant goal that would aid in the analysis of the collection and the consideration of context. Sorting the hands and feet would be especially helpful since they represent the most frequent elements. The MNI based off the highest counted element, the right talus, is 22; thus there is a bias toward finding foot bones above other elements. This thesis will focus on testing whether sorting the metacarpals and metatarsals, which are also among the most frequent elements, can help interpret the PSJ collection.

Methods to address issues of commingling have been a topic of interest for anthropologists for decades. Commingling can obscure demographic data and context in bioarchaeological assemblages, or preclude identification and return of remains in forensic cases. Visual matching, osteometrics, trace element analysis, DNA, and other methods have been recommended for resolving cases of commingled remains. This study will focus primarily on osteometric sorting due to its statistical validity and objectivity, although additional sorting methods will be employed in conjunction with osteometric sorting to strengthen or supplement the results.

Research Questions

Osteometric sorting uses bone measurements to exclude elements that are too different to originate from the same individual, including pairs, articulations, and bones from other body regions. Studies of osteometric sorting have largely focused on major long bones, innominates, and sacra (Byrd 2008; Byrd and LeGarde 2014; Lynch et al. 2018; Thomas et al. 2013). One study examined pair-matching metacarpals using geometric morphometrics with success (Garrido-Varas et al. 2015), but the metacarpals and metatarsals have not yet been the subject of commingling studies using traditional osteometric techniques. This study will address the dearth of literature by developing the methodological framework for metacarpals and metatarsals from a reference sample and will apply the method to the commingling problem in the Point San Jose Collection. Broadly, this project investigates two main questions: Can dimensions of metacarpals and metatarsals be used in the resolution of commingling? Can resolving commingling of the metacarpals and metatarsals clarify context of the Point San Jose Collection?

To answer the first question, this thesis will test three hypotheses:

(1) I hypothesize that paired bones will show no statistical difference in dimensions. Osteometric sorting is dependent on the concept of symmetry between the left and right sides (Byrd 2008), so there should not be significant differences between the left and right MCs and MTs. Due to this symmetry, the mean left-right differences should be useful in osteometric sorting.

(2) I hypothesize that the dimensions of facets of articulating MCs and MTs are correlated. Facets represent the region where two articulating elements touch, so the facet lengths on each of the elements should be related and should be helpful in sorting articulating elements. Additionally, for visually assessing articulations, the confidence in a fit for joints involving the MCs and MTs are considered to have high to moderate

reliability (Adams and Byrd 2006). With the level of confidence in visual articulation, metric assessments of the joints could be similarly useful.

(3) I hypothesize that the lengths of MCs and MTs are correlated to the lengths of other long bones within an individual. MC and MT lengths have been shown to correlate with stature and sex, albeit with less strength than other limb bones (Byers et al. 1989; Falsetti 1995; Manolis et al. 2009; Meadows 1990; Meadows and Jantz 1992; Mountrakis et al. 2010; Musgrave and Harneja 1978; Scheuer and Elkington 1993; Smith 1997; Stojanowski 1999; Zaher et al. 2011), so they should also show correlations to other long bones that are correlated with stature or sex. As Byrd and Adams state, “a large humerus is associated with a large femur and a large metatarsal” (2016:232), so osteometric comparisons to other elements for osteometric sorting may be possible. Kanchan et al. (2010) have showed dimensions of the hands and feet to be correlated, but they used fleshed anthropometric data rather than skeletal measurements. Still, it shows the potential of the correlation of specific bones of the hands and feet within an individual.

To answer the second research question, the pattern of association, or lack thereof, for elements in the Point San Jose assemblage will be examined after sorting. The number of pair-matches, articulations, and other matched regions can help gauge how complete are the remains. Relatively complete remains, shown through many matches, could indicate the presence of cadavers, whether they were autopsied or dissected, while few element matches could indicate the presence of body parts rather than cadavers, as would be expected with either medical waste or a collection of anatomical specimens (Nystrom 2014).

Organization

The second chapter explores commingling in depth. It examines how commingling can impede anthropological analyses, such as how it impacts estimations of number of individuals, biological profile estimations, and identification efforts. It describes various methods developed to address commingling, including the numerous osteometric methods that exist, and also discusses examples of when sorting metacarpals and metatarsals could assist analysts in completing project goals.

Chapter III focuses on the background of the Point San Jose Collection and the history of nineteenth century medical practices. First, it describes the history of the Point San Jose army post, from its initial establishment during Spanish control of California to its use during the U.S. Civil War to its current role as a part of the Golden Gate National Recreation Area. It then briefly describes the excavation and analysis of the collection as well as the physicians that may be responsible for the pit. Finally, the chapter explores the various possible circumstances behind the collection's use and discard at the hospital and how resolving commingling of the metacarpals and metatarsals could help with analysis of context.

Chapter IV describes the materials and methods used in this thesis. It discusses the measurements collected, which were largely based on previous studies, as well as the samples that were used to develop and test the osteometric sorting techniques. It describes the analyses, including assessment of error, hypothesis testing, and osteometric sorting formulae. It ends with a description of the methods used to analyze the Point San Jose collection.

The fifth chapter describes the results from each test in the project. It starts with a review of intra- and inter-observer error for each of the measurements and the results from the three hypothesis tests. Then, it describes the osteometric sorting frameworks developed each for pair-matching, articulations, and comparisons of other regions. Last, the chapter includes the results from their application to the Point San Jose Collection, including the percentage of potential matches excluded by osteometric, pXRF, and visual sorting.

Chapter VI is a discussion of the thesis results. It considers the meaning of the error and osteometric sorting results in light of previous literature and the implications for commingling studies. It also compares four osteometric pair-matching methods in terms of power and accuracy. A discussion of the Point San Jose results includes what lessons PSJ sorting could provide and contextual analysis. The chapter closes with discussion of the limitations of the thesis and some brief concluding remarks regarding osteometric sorting of the MCs and MTs and analysis of the PSJ Collection.

CHAPTER II

COMMINGLING AND METHODS FOR RESOLUTION

Introduction

Commingling of human skeletal remains can occur in forensic and bioarchaeological contexts due to disasters (Mundorff et al. 2014; Steadman et al. 2014), mortuary practices (Glencross 2014), poor excavation or curation techniques (Simmons 1997a; Zejdlik 2014), and more. Sorting commingled remains is important because individualizing skeletons can improve the accuracy of analysis and help interpret the context of the assemblage. In archaeology, knowing how many individuals are represented, and by which elements or body parts, aids in refining the demographic profile of the collection and understanding the processes and decisions behind their burial. In forensic contexts, reconciling skeletal commingling is important because separating the remains of multiple unidentified victims aids in positive identification and the return of the remains to grieving family members. For these many reasons, researchers are tasked with developing methods that will help sort skeletal remains when commingling is encountered.

This chapter will explore the background of research in the commingling of human skeletal remains. It will first provide examples of how sorting aids anthropological analysis, and then will provide an overview of current methods for resolving commingling. Next, this chapter will examine specifically commingling of the hand and foot bones and the issues leading to the research questions addressed in the thesis.

Commingling and Anthropological Analysis

Successful sorting of commingled elements is significant for accurately estimating the number of individuals represented in an assemblage. The two estimation methods that are probably the most commonly-applied in forensic anthropology and bioarchaeology include the Minimum Number of Individuals (MNI) and Most Likely Number of Individuals (MLNI). The MNI is the least number of individuals that would lead to the observed assemblage and is usually estimated using the element of the highest count, though other observations, including age, sex, or re-associated elements, can be applied to refine the estimation (Adams and Konigsberg 2004). MNI estimations should also be accompanied by MLNI estimations when possible because MNI tends to underestimate the number of individuals when the recovery rate of elements is low (Adams and Konigsberg 2004). MLNI uses the number of paired and unpaired elements to calculate a range that includes the statistically most likely number of individuals present. Models for estimating the MLNI have been borrowed from the ecological and zooarchaeological literature, specifically capture-recapture studies that estimate the size of faunal populations (Adams and Konigsberg 2004). MLNI calculations can be more accurate than MNI in assemblages without a high degree of fragmentation, but the accuracy is also dependent upon correctly pair-matching left and right elements.

Reassociating elements, then, is crucial for increasing the accuracy of estimating the number of individuals present, which is often the first major step in skeletal analysis. Other analyses that can be improved by resolving commingling are demography, paleopathology, and context in bioarchaeology, and positive identification in medicolegal settings. Demography can be refined as highly diagnostic regions of the skeleton are associated with regions that provide less accurate information. The most accurate element present from the individual's reassociated remains can be used to build the biological profile. Comparing estimates from a wide range of age indicators rather than comparing the same indicators consistently between individuals has been shown to increase error in age modeling (Glencross 2014). MacInnes (2017) also found that sex estimations from pair-matched elements did not always match, and Harrington and Blakely (1995) found inconsistencies in demographic makeup when comparing results by element. Individual by individual rather than element by element analyses, therefore, tend to be better. Similarly, paleopathology studies usually assess the type and prevalence of pathologies within a population using the individual as the unit of analysis (Glencross 2014), requiring the resolution of commingling. Both demographic and paleopathological analyses can be completed successfully element by element instead of person by person (Osterholtz et al. 2014b), but it limits the questions that can be investigated and may sacrifice accuracy.

Sorting commingled assemblages can also provide evidence regarding archaeological context. An accurate demographic profile is important because an assemblage skewed towards a certain age or sex speaks to the origin or context of the sample. Additionally, knowing if there are any elements that are demonstrably unassociated with others in the collection through sorting methods can aid in contextual analysis because the presence of a partial skeleton or body parts versus an entire skeleton is often related to the behavior of the society (Osterholtz et al. 2014a).

In forensic cases, it is important to individualize skeletons to make sure all victims are accounted for and analyzed. In some disaster contexts, remains can be destroyed so that some victims are represented by only a few elements or fragments (Mundorff et al. 2014), and sorting can identify elements belonging to another victim. Reassociating elements is often a goal even if all victims have been accounted for because it allows a more complete skeleton to be returned to grieving family members.

Methods of Resolving Commingling

Since the sorting of commingled human remains is important in physical anthropology, many methods have been developed to attempt to segregate or match skeletal elements. One such technique involves visual assessment of potential pair-matches or articulations. For pair-matching, the size and shape of the bones and features are taken into consideration with the idea that the left and right sides of an individual are generally symmetrical. For articulations, the apparent fit of the joint is assessed. Both can be somewhat subjective, however, and the accuracy can be affected by the experience level of the practitioner, the size of the commingled sample, or on the element itself (Byrd and Adams 2016). Different studies have found that visual pair-matching of various elements ranges in accuracy from 75.6% to above 90%, and the making or rejecting of a specific match can vary between individuals (Adams and Konigsberg 2004; Byrd and Adams 2016; Garrido-Varas et al. 2015). Taphonomic signatures can also be visual indicators that are considered for both paired and articulating matches, but burial disturbances can lead to elements from a single individual undergoing different taphonomic changes, so it is only helpful for unique patterns across multiple bones (Byrd and Adams 2016).

To address some of the issues of visual methods, many researchers have advocated for the more objective approach of osteometric sorting. It involves quantitative rather than qualitative methods and generates statistical justification for evaluating the potential that two elements originate from the same individual. Osteometric methods of sorting commingled human remains have been applied to paired (Byrd 2008; Byrd and LeGarde 2014; Thomas et al. 2013; Vickers et al. 2015) and articulating (Buikstra et al. 1984; Byrd 2008; Byrd and LeGarde 2014) bones. It can also be used to assess whether elements from different regions of the body are from the same individual (Byrd 2008; Byrd and Adams 2003; Byrd and LeGarde 2014), a task for which visual methods are not generally useful (Byrd and Adams 2016). Length measurements have been shown to generate the most highly-correlated regression models for osteometric sorting, though adding breadth measurements can increase the reliability in some cases (Byrd 2008; Byrd and Adams 2016; Byrd and LeGarde 2014). It is important to note that osteometric sorting is only useful for separating elements and cannot be used to positively match elements (Byrd and Adams 2016). Therefore, it is essential that it is used in conjunction with other methods of sorting, such as visual matching of pairs that are not eliminated osteometrically. Also, like other metric analyses in osteological studies, researchers should try to use a reference sample that will represent the individuals in their collection, so it is important to make the reference populations as diverse as possible for age, sex, and ancestry, and to use a reference population that is from a similar time period when possible (Byrd 2008).

A number of variations for osteometric sorting have been suggested, with four major methods for osteometric pair-matching. Byrd (2008) and Byrd and LeGarde (2014) advocate a process in which an analyst must: perform a specific measurement on both the right (*a*) and left (*b*) elements of a potential pair and calculate the difference between the right and left for that measurement; sum the right-left differences for a series of measurements to calculate *D*;

$$D = \sum(a - b) \qquad [1]$$

calculate the absolute value of ($D - 0$), with the zero representing an average right-left difference of zero for the element; divide the value by the standard deviation of *D* for that element derived from a reference sample;

$$t = \frac{|D - 0|}{SD_{ref}} \qquad [2]$$

and compare this number to a two-tailed *t*-distribution to find a *p*-value to reject or fail to reject the null hypothesis that the bones originated from a single individual. The authors suggested an alpha level of 0.1 be used for rejections, although it will vary by project and individual preference. This method has been widely used in bioarchaeological and forensic assemblages since its development (Chew 2014; Jin et al. 2014; MacInnes 2017; Rodríguez et al. 2016; Winburn et al. 2017).

Later tests of this method by Vickers and colleagues (2015) revealed some potential issues with the original technique. They criticized the assumption of zero-difference between pairs and the potential that the distribution of *D* is nonnormal. In their sample, the method also led to higher numbers of false rejections than should be allowed given their chosen alpha level. They proposed a new approach to osteometric sorting, where a researcher would find the sum of the differences in measurements between the left and right of a potential pair, the same as for the Byrd (2008) and Byrd and LeGarde (2014) method, but then compare the result to the full range of the values derived from the reference sample. A value outside the range is evidence the elements are not from a single individual. Vickers et al. (2015) showed that their method was more accurate, in terms of lowering the number of false rejections, but led to less rejected matches and therefore more time invested in alternative sorting tequniques afterwards.

Thomas et al. (2013) also offered an alternative method of osteometric sorting with a more straightforward test of association than Byrd (2008) and Byrd and LeGarde's (2014), albeit with less sorting power. Researchers would perform a specific measurement on the left and right elements of a potential pair; calculate the absolute value of the difference; divide this value by the result of halving the sum of the left and right measurements to find *M*;

$$M = \frac{|L - R|}{(L+R)/2} \qquad [3]$$

and compare the calculated M to the M values derived for the measurement from a reference sample. A value above the threshold leads to the segregation of the potentially-paired elements.

Recently, Lynch and colleagues (2018) proposed some revisions to Byrd (2008) and Byrd and LeGarde's (2014) process in an attempt to address some of the criticisms. For this method, an analyst would calculate D as the sum of the absolute value of left-right differences for a number of measurements on an element.

$$D = \sum|a - b| \qquad [4]$$

The authors use the absolute value of differences for various measurements so that they aggregate to create the "true difference" between the sides (Lynch et al. 2018:372); in the original method, a mixture of larger left and right dimensions, creating some positive and negative values, would lead to some of the differences being cancelled out when they were summed. Lynch et al. (2018) also recommend using a half-normal transformation since using the true difference generates a non-normal distribution.

$$D = ((\ \sum|a - b|\ ) + 0.00005)^{0.33} \qquad [5]$$

The average D from a reference sample, rather than assuming a difference of zero, is subtracted from the test case's D, and the value is divided by the reference standard deviation to calculate a t value

$$t = \frac{D - \bar{x}}{SD_{ref}} \qquad [6]$$

that can be compared to a one-tailed t-distribution to find a p-value that rejects or fails to reject the null hypothesis of the two elements originating from a single individual. In the original method, a two-tailed distribution is used, but a one-tailed is needed here since using the absolute value introduces positive directionality. Lynch et al.'s (2018) results showed slightly higher numbers of exclusions and reduced numbers of false exclusions compared to using Byrd (2008) and Byrd and LeGarde's (2014). This method also improved upon the original method because it used computer-automated sorting, which can reduce time investments involved with calculating the value of *D* or *t* by hand for each potential match.

In addition to pair-matching, osteometrics are useful for testing possible articulating matches. Buikstra and colleagues (1984) demonstrated that subtracting the values of particular measurements on articulating portions and comparing the result to confidence intervals derived from a reference sample provided evidence for whether the two elements originated from the same individual. Later, Byrd (2008) and Byrd and LeGarde (2014) advocated for an approach with the same premise but that utilized a *t*-test rather than confidence intervals, giving a representation of the strength of the fit. For their method, a researcher would: take a specific measurement (*i*) on one bone (*c*) and a measurement (*j*) on the potentially articulating bone (*d*); subtract the values to find *D*;

$$D = c_i - d_j \qquad [7]$$

derive a value of *t* by subtracting the reference mean value of *D* from the observed *D* and dividing the absolute value of the result by the reference standard deviation of *D*;

$$t = \frac{|D - x_{ref}|}{SD_{ref}} \qquad [8]$$

and compare this value to a two-tailed t-distribution to find a p-value to reject or fail to reject the null hypothesis that the bones originated from a single individual.

Unlike visual methods, osteometric sorting allows researchers to test the likelihood that a set of non-paired and non-articulating elements comes from separate individuals. The method requires that an analyst take specified measurements on one element, calculate the natural log of the sum of the measurements (x_a), and enter the value into a regression formula derived from a reference sample that produces a predicted value for the natural log of the sum of measurements for the potential match (y_p). Originally, Byrd and Adams (2003) recommended comparing the result to a prediction interval and segregating elements when the value fell outside of the interval. More recently, Byrd (2008) and Byrd and LeGarde (2014) advocated entering x_a, y_p, the actual dependent y value for the case (y_a), standard error of the regression model (SE), sample size used to develop the regression equation (N), reference sample mean of the independent variable (x), and the reference sample standard deviation of the independent variable (SD) into an equation to obtain a t-value.

$$t = |y_p - y_a| / [SE \text{ x } \sqrt{[1 + (1/N) + (x_a - x)^2 / (N \text{ x } SD)^2]}] \quad [9]$$

The t-value then is compared to a two-tailed t-distribution to find a p-value to reject or fail to reject the null hypothesis that the bones originated from a single individual. They suggested using a t-test rather than prediction intervals because the p-value would give an indication of the strength of the fit. Lynch (in press) later introduced automated sorting using this method, which reduced time investments from hand-calculated tests and increased accuracy because the computer could calculate numerous formulae based on available measurements and choose whichever was best.

Since using the size of elements for sorting using osteometrics was successful, researchers tested and verified the feasibility of geometric morphometrics for pair-matching in skeletal assemblages. Size and shape data are attained through landmarks on the bone, and match predictions are generated based on similarity. The method is accurate (Garrido-Varas et al. 2015; McCormick 2016), but linear measurements sometimes outperform geometric morphometrics (McCormick 2017).

Recently, researchers have shown that trace element analysis using portable X-ray fluorescence (pXRF) can assist with resolution of commingling. pXRF uses x-rays to move electrons between shells of an atom and measures the fluorescent x-rays that are emitted as a consequence to characterize the concentrations of elements within the bone (Finlayson et al. 2017; Gonzalez-Rodriguez and Fowler 2013; Perrone et al. 2014). The elemental concentrations for bones within an individual should be similar and can be used to segregate individuals that have significantly different values. More research into the effects of diagenesis is needed, however.

Widespread in disaster contexts is the use of DNA for identification and sorting efforts. It is an indispensable method because certain DNA sequences are unique to individuals and shared between all elements within the individual, and matches with reference samples can lead to positive identification. However, DNA can be degraded or contaminated, and it is a fairly expensive tool (Fowler and Thompson 2015). For this reason, many disaster response teams will employ anthropological methods of sorting commingled remains to the furthest extent so they can sample for DNA strategically. As many elements as possible from a site are reassociated so they need only sample unresolved elements and specific elements per reassociated group (Parsons et al. 2007; Puerto et al. 2014). Traditional anthropological methods are also important for testing the validity of genetically generated matches (Arlotti et al. 2003).

Sorting Commingled Hand and Foot Elements

Although all of the methods described are helpful in sorting commingled remains, a lot of research has focused on osteometric standards. This is likely because element measurements provide statistical validity, are an affordable and widespread skill among anthropologists, and have been shown consistently to be accurate for sorting by prior studies (Fowler and Thompson 2015). These studies, discussed above, have researched osteometric sorting mainly of major long bones (e.g. femur, tibia, fibula, humerus, radius, ulna), the scapulae, vertebrae, and the innominates. Few researchers have included elements of the hands and feet in their studies, though with some exceptions. Thomas et al. (2013) included data on pair-matching the calcaneus, Byrd (2008) and Byrd and LeGarde (2014) considered osteometrics for articulating the ankle joint (tibia and talus), and Anastopoulou et al. (2018) developed formulae for sorting articulating calcanei and tali. Garrido-Varas et al. (2015) performed a study on sorting commingled metacarpals with success, but the methods incorporated geometric morphometrics rather than traditional osteometrics. Sorting of hand and foot bones, specifically osteometric sorting, then presents a relatively unexplored region in the literature.

Few studies have considered them, but the ability to test association of the hands and feet could prove important in many circumstances. Reassociating hand and foot bones, for example, could be useful in estimations of MLNI. While its calculation is usually based on larger elements with higher survivability rates and usefulness in demographic estimations (Adams and Konigsberg 2004), it may be useful to use certain bones of the hands and feet if there is a bias of what elements are present or if there is significant fragmentation of elements typically used for MLNI that precludes pair-matching them. Some tarsals and metatarsals have been noted by practitioners to be more likely found complete than other long bones, particularly when they are encased by footwear (Bidmos and Asala 2003; Byers et al. 1989). Additionally, in some disaster contexts, it is desirable to identify all remains even if all victims have already been accounted for (Byrd and Adams 2016; Kontanis and Sledzik 2014), in which case matching elements of the hands and feet to identified individuals would likely be necessary.

In other disaster or bioarchaeological settings, several individuals at a site may only be represented by a few elements or body parts. Testing whether recovered hand and foot elements belong with other elements within the assemblage could lead to another identification if it is found that they represent a different person. An example of where this could be useful is in mass grave excavations like in the Balkans. After years of war and ethnic violence that led to 40 thousand missing people in the 1990s, many mass graves have been located and excavated; however, in an attempt to confound the evidence, perpetrators exhumed many of the graves and relocated the bodies to a secondary burial (Jugo and Wastell 2015). Taphonomic studies have shown that exhumations performed by individuals without osteological expertise often overlook small bones, such as in the hands and feet or fragments, leaving them behind in, or near, the primary burial context (Roksandic 2001). This was often seen in the Balkans, and leaves analysts with the task of determining whether these elements belong to victims still present in the grave or remains that were removed (Connor 1998a; Saul and Saul 2005; Skinner 1998). Elements also became commingled due to burning, dismemberment, or natural decomposition processes (Connor 1998b; Connor and Gould 1999; Harrington 1998a,b; Simmons 1997b). DNA is essential in the region for positive identifications and reassociation of remains split between multiple graves, but anthropological methods are employed in conjunction with DNA for resolving commingling within a site for strategic sampling, or to evaluate the accuracy of potentially identified genetic matches within and between sites (Arlotti et al. 2003; Jugo and Wastell 2015; Parsons et al. 2007). Improved sorting methods for elements of the hands and feet could further support the approach in contexts with high numbers of these bones.

Some bioarchaeological assemblages have also been found that contain body parts rather than full skeletons, such as in situations of medical discard, so it is important to attempt to determine whether the recovered hands and feet are associated with other elements in the assemblage or if they represent disarticulated body regions of another individual. Willey and colleagues (2016) describe one such medical collection where commingling has obscured context since the completeness of individuals is unknown; the collection and issues of commingling will be discussed in detail in later chapters.

Research Questions

With the utility of sorting hands and feet in many instances, it is important to develop methods that assist in their segregation. An attempt at understanding the variation within and between individuals, rooted in evolutionary theory, helps inform processes of sorting commingled assemblages. Low-level theory, like statistical induction theory, can then be applied by using past observations (skeletal reference samples) to derive methods and estimate the probability that current observations (forensic cases or bioarchaeological samples) will be correctly assessed (Boyd and Boyd 2011). Osteometric sorting can specifically be useful because it can add statistical evidence for separating certain bones (Byrd and Adams 2016), or can be used to eliminate potential matches to reduce the ones that a practitioner assesses with other methods, thereby helping lower the time investment in the sorting process of large assemblages (Byrd et al. 2003; Vickers et al. 2015). A major question of this study is then: Can dimensions of metacarpals and metatarsals be used in the resolution of commingling?

Summary

Commingling can significantly impede anthropological analyses or forensic identification. Osteometric sorting is one of many methods to address commingled human skeletal assemblages. It is useful for reducing the number of potential matches that need to be assessed by other methods and for adding statistical support to associations. Multiple osteometric pair-matching procedures have been introduced, as well as comparisons for articulating elements and non-paired and non-articulating elements. Since most methods have not developed the statistical frameworks for osteometric sorting of the metacarpals and metatarsals, this thesis will focus on using a reference sample to derive the necessary data with which to apply the methods to the hand and foot elements.

CHAPTER III

HISTORY OF THE POINT SAN JOSE COLLECTION

Introduction

The Point San Jose Collection is a medical skeletal assemblage with uncertain context due to extensive commingling. Although multiple explanations have been suggested for the collection's use and discard, including autopsied remains, dissected cadavers, medical waste, and teaching specimens (MacInnes 2017; Pershan 2015; Willey et al. 2016), it has been difficult to evaluate the various explanations due to lack of isolated individuals. Resolving commingling could therefore aid researchers in analysis. It is an appropriate collection for exploring commingling of hands and feet specifically due to the high frequency of such elements. This chapter will describe the background of the collection, including the history of the base where it was found and the excavation and analyses. Then, the potential background of the collection will be explored through contextual clues and the lens of nineteenth century medical practices. Finally, some of the research questions of this thesis will be discussed, specifically how de-commingling the hands and feet may support analyses.

History of Point San Jose Military Reservation

In 1797, Spanish forces established *La Batteria San José* to further fortify their control over California while they were at war with Britain, though only five cannons are believed to have been there. When Mexico became independent of Spain in 1821, they gained control of the battery, but it was completely abandoned before the United States acquired California in the late 1840s (Freeman et al. 1999; Sebby 2009). The site remained abandoned, but United States officials recognized its strategic value and wanted to claim it for potential military purposes in the future (Sebby 2009).

The Point San Jose Military Reservation was established at the site of *La Batteria San José* in 1851 by a presidential order from President Millard Fillmore, partially in response to the California gold rush because it was intended to help protect shipments of gold sailing from the west to the east coast. However, the base, nicknamed Black Point due to the dark underbrush that covered the area, was not actively utilized by the military and became a popular location for squatters to occupy and build homes (National Park Service 2016; Sebby 2009). At the outbreak of the Civil War, San Francisco was an essential city for commerce that the government wanted to make sure would not be lost. Fears of Confederates attacking commerce ships, or of Britain attempting to take control of California while the United States forces were focused on the war on the east coast, led the military to strengthen its fortifications at a number of military bases in the San Francisco region, including Point San Jose (Freeman et al. 1999; National Park Service 2016; Sebby 2009). All the civilian residents were evicted and the army occupied the base (National Park Service 2016; Sebby 2009).

In 1882, Point San Jose was renamed Fort Mason (Figure 1) after a former military governor of California, Colonel Richard Barnes Mason (National Park Service 2016; Sebby 2009). After the Civil War, the army continued to occupy the base, but its

Figure 1 Photograph of Fort Mason in 1910. Provided by NPS/GGNRA.

role in harbor defense was not significant. Its next major role came after the 1906 earthquake that hit San Francisco, when it was designated as a temporary City Hall, an army command post, and a refugee camp for civilians displaced by the earthquake and subsequent fires. In World Wars I and II, Fort Mason also served as a significant port for the shipment of troops and supplies to Pacific fronts. Fort Mason's importance to military operations continuously declined after the wars, and was among the underused Bay Area federal lands that were transferred to National Park Service control after President Richard Nixon signed a law creating the Golden Gate National Recreation Area in 1972 (National Park Service 2017; Sebby 2009). Fort Mason continues to serve as the park's headquarters (National Park Service 2017).

Point San Jose Collection

The Point San Jose Ossuary Pit was discovered in October 2010 while a historic building at Fort Mason was being renovated by the National Park Service. It was found just behind the post's historical hospital, used from the mid—1800s to early 1900s, while digging around the building to address lead-contaminated soil. The pit contained thousands of skeletal elements, mostly commingled without complete individuals, but with some body parts still articulated (Figure 2), along with a number of medicinal bottles and metal waste (Fagan 2010; MacInnes 2017; Pershan 2015). The top layer,

Figure 2 Photographs from excavation of PSJ Ossuary Pit. Pit levels showed varying degrees of articulation. Provided by NPS/GGNRA.

which extends beyond the pit to below the nearby Steward's Quarters, was made of crushed sandstone, suggested to be a hygienic seal, and provides the very latest possible date of the pit's creation as 1891, when the Steward's Quarters was added to the hospital (MacInnes 2017). The medicinal bottles provide the earliest possible date for the pit, as they were briefly issued by the army starting in the early 1860s (MacInnes 2017; Pershan

2015). Although there is an almost 30-year range when the pit could have been created, an examination of all associated artifacts led National Park Service archaeologists to conclude the pit was created around the 1870s (MacInnes 2017).

In the summer of 2016, the Point San Jose Collection was loaned to California State University, Chico for osteological analyses. Due to the high degree of commingling, most analyses had to be performed element-by-element rather than individual-by-individual as would be ideal. Analyses showed, using an age and sex based MNI, that a minimum of 25 individuals were present in the assemblage, but the MLNI showed there could be as many as 59 individuals represented. Both sexes were represented, Asian individuals were more frequent than their representation in the 1870 census, ages were skewed towards the very young and middle-aged adults, and statures were shorter than the 19th century United States average. The amount of pathology was relatively low, and the majority of elements with pathology were changes associated with joint disease. A number of elements exhibited saw cut marks or incised cut marks, showing that the collection is medical-related (Willey et al. 2016).

Many physicians served at the Point San Jose hospital during its operation, but National Park Service archaeologists believe the pit was most likely associated with Dr. Edwin Bentley because he was the surgeon stationed at Point San Jose the longest around this time, and the years he was stationed as post-surgeon there, at least 1871 through 1874, are within the range suggested for the pit's origin (MacInnes 2017; Pershan 2015; Powell and Shippen 1892). He is also known to have collected medical specimens that were of pathological interest (Bentley 1870c; Lamb 1916). This thesis will proceed with the assumption that Dr. Bentley is in fact the individual responsible for the collection of skeletal remains; even if it was another surgeon that collected the remains, the motivations behind the gathering and subsequent discard of the assemblage would likely be similar since they would all be army surgeons that likely followed similar protocols and medical practices of the time.

Dr. Edwin Bentley was an expert surgeon and pathologist when pathology was a relatively young medical specialization (Michael 1955). He received a medical degree from the University Medical College of New York City (now NYU School of Medicine) in 1849 and practiced medicine in his home state of Connecticut until enlisting in the US Volunteers' army as a surgeon near the start of the Civil War in 1861. He served as an army physician in various cities, including running the military hospital system in Alexandria, Virginia during the war, and was appointed as an Assistant Surgeon of the Regular Army in 1866 (Cobb 1980; Powell and Shippen 1892). In 1869, Bentley was transferred to San Francisco. At various points during his time in the city, he was associated with the hospital at Point San Jose, the hospital in the Presidio, and Alcatraz Island, and he often reviewed cases from the City and County Hospital of San Francisco (Bentley 1870b; Powell and Shippen 1892; Otis 1871:100). He was concurrently a Professor of Descriptive and Microscopic Anatomy and Pathology at the Medical College of the Pacific (Cobb 1980; Michael 1955), and physician colleagues described how his pathology skills were "not excelled, if equaled, on this coast" (Gibbons and Gibbons 1872:225). In 1875, he was transferred away from San Francisco and was stationed in various cities, including Little Rock where he helped found the medical school at the University of Arkansas. In 1888, he retired from the army and practiced medicine in Arkansas until his death (Cobb 1980; Powell and Shippen 1892).

Exploring Context of the Point San Jose Collection

One major goal of the analyses of the Point San Jose Collection is to clarify the context of the assemblage. The saw and incisded cut marks, as well as the close association with the post's hospital, clearly show the collection is medical-related. However, its exact origins are not known. This section will examine the suggested contexts of the assemblage and the evidence thus far. It will also discuss how resolving commingling of the hands and feet could potentially aid researchers in attempts at determining context.

A number of possibilities have been proposed as to why the remains at Point San Jose were collected and ultimately discarded. One suggestion is that the remains represent dissected cadavers. There are quite a few bioarchaeological examples of cadavers from a similar time period as the Point San Jose Collection in the United States (Halling and Seidemann 2017; Harrington and Blakely 1995; Owsley et al. 2017). Medical schools in the 19th century needed bodies which they could dissect in demonstrations for students learning anatomy, but public views of dissection were negative because, religiously, it was viewed as a mutilation of the body and identity which could impede resurrection of the dead since they were no longer whole (Hildebrandt 2008; Hulkower 2011; Sappol 2002; Tward and Patterson 2002). Throughout the country, physicians and students, as well as professional "resurrectionists" that profited from selling cadavers to medical schools, started robbing graves to meet growing demand for corpses (Hulkower 2011; Sappol 2002). In an attempt to curb illegal disinterment, many states passed anatomy laws that provided cadavers to medical schools from criminals that were executed or died in custody, and later, when supply still did not meet demand, from unclaimed bodies from hospitals and almshouses. This association of dissection with poverty and criminality led to further societal disapproval surrounding it, but as long as resurrectionists targeted pauper and minority cemeteries rather than the graves of white, prominent individuals, then society largely ignored the body-snatchers (Breeden 1975; Savitt 1982). Dissection can then be viewed from the perspective of structural violence in regards to both death and life in nineteenth century America. Not only did the marginalized face the postmortem harm to their identity through nonconsensual dissection, but the threat of theft of their family member's bodies, or of their own upon death, led to anxieties among the living (Nystrom 2014; Savitt 1982).

California's history with anatomical education and disenfranchisement largely mirrors the rest of the country. Laws criminalizing the unauthorized disinterment of dead persons appeared as early as 1854 (Hittell 1870:486), but the state's 1872 Penal Code specifically addressed disturbing graves for selling or dissecting bodies, reflecting the nationwide body-snatching phenomenon (Deering et al. 1906:125-126). Acts pertaining to the acquisition of cadavers for medical education were passed just before and during Dr. Edwin Bentley's stint in San Francisco. "An Act to promote the study of anatomy" was passed in 1864 and said that certain officials "may surrender the dead bodies of such persons as are required to be buried at the public expense," but stipulated bodies could only be "those persons who have died during their term of service in the State prison, or been executed for crime" (Hittell 1870:62-63). The law made exceptions for those deceased that requested to be buried during their last sickness, were claimed by family or friends within 36 hours of death, or were travelers. An amendment to that act that passed in 1866 removed the constraint that the bodies be from criminals (California 1866:327), and thereby allowed the transfer of any unclaimed remains. In 1870, a version of the law passed with almost identical language to the previous ones except that it said officials "shall" surrender the bodies (California 1870:405), as opposed to "may" used previously, and lowered the unclaimed period to 24 instead of 36 hours. Bentley himself praised anatomy laws in an address to the San Francisco Medical Society:

> Well may medicine rejoice that with the advancing tide of progress she has lost no opportunities. That relic of barbarism which so long obstructed the study of anatomy—a superstitious reverence for the dead—has within the nineteenth century given place to reason and religion, and material for dissection is supplied by law in most of the enlightened cities of both hemispheres; and now is open wide the door for the study of those foundation principles on which pathology in all its forms most securely rests (Bentley 1870a:293-294).

Dissection could explain the Point San Jose assemblage since a number of cut marks were found on various elements in the collection (Willey et al. 2016). Bentley is known to have used postmortem demonstrations in his teaching (Cobb 1980). Additionally, illicit procurement of cadavers would account for the lack of proper burials for the individuals in the ossuary pit. Analysis found the pit was composed of individuals of Asian and European ancestry; while in many states resurrectionists targeted mainly African American cemeteries or other disenfranchised groups (Breeden 1975; Humphrey

1973; Savitt 1982), California had a low African population, so they may have targeted Asian and indigent European cemeteries instead (MacInnes 2017; Willey et al. 2016). The significant marginalization of the Chinese in 19th century San Francisco (Trauner 1978) would likely have made them targets.

Due to saw marks of the cranium and sternum, autopsy was another explanation offered for the Point San Jose Collection's context. Autopsies were generally viewed with less contempt than dissection due to the differing intent. Dissections were a spectacle and associated with poverty; autopsies were usually more private and used to determine cause of death or confirm diagnoses (Sappol 2002), although doctors often used the process as an opportunity to link observations during the illness with observations of organs, or to collect pathological specimens (Elizondo-Omaña et al. 2005; Lamb 1916). Evidence of autopsy may or may not exemplify structural violence in a bioarchaeological context. Some autopsies were legally sanctioned, so were likely buried in a cemetery as typical for the time (Nystrom 2014). The Point San Jose ossuary pit, however, does not likely reflect a legal and respectful autopsy due to the secretive nature of the discard pit. Physicians sometimes stole bodies with interesting illnesses to autopsy, or could have used cadavers to teach the autopsy process (Nystrom 2011; Sappol 2002). In these cases, corpses were likely illegally obtained like for dissection.

Another potential origin for the Point San Jose Collection is that it represents a pathological collection or "curio cabinet" that was discarded by Bentley or another physician when no longer wanted (Willey et al. 2016). Many Civil War-era surgeons, including Bentley, are known to have collected specimens that may be of anatomical or pathological interest for the purpose of research or teaching. Hammond (1862), Surgeon General of the army, requested at the beginning of the Civil War that army surgeons collect and send specimens of morbid anatomy, samples that would demonstrate surgical or medical principles, to the newly-formed Army Medical Museum. Subsequent Surgeon Generals would even send out periodic reminders for army physicians to send specimens, and some physicians were known to travel to battle sites during the war or offer autopsy services to other hospitals with the goal of finding a unique specimen to save (Lamb 1916:16-17,20,22). Museum records show that Bentley contributed a number of samples during the Civil War from his time working in the Alexandria, Virginia hospital system (Lamb 1916:23). Like other medical officers (Lamb 1916:16), he also collected specimens over his career that were for his personal research or teaching rather than for the museum, such as body parts found in his former Connecticut home (New York Times 1869), soft tissue and skeletal pathology samples he presented to the San Francisco Medical Society (Bentley 1870c) that "possess rare merit, and serve to illustrate important principles in pathology" (Gibbons and Gibbons 1871:565), and a book with preserved anomalous intestinal tissue at the University of Arkansas (Ampezzan 2016).

If the Point San Jose Collection represented specimens from this sort of curio cabinet, one might expect to find many unassociated body parts or even single elements rather than complete individuals and a high frequency of pathological elements due to selectivity towards interesting cases; however, the collection showed a fairly low level of pathology, with only about 20% of observable bones displaying pathological changes and approximately 68% of the pathological elements being attributed to joint disease (Willey et al. 2016). This seems to suggest that the Point San Jose assemblage was not for researching or teaching pathology. Alternatively, the assemblage could represent unwanted remains that were discarded after morbid specimens were collected from them. In this case, researchers might expect remains to be more complete but with some missing body parts. For example, Willey et al. (2016) suggest that the relatively low number of crania found in the assemblage could represent skulls being more highly selected for as curios. It could also explain the low level of pathology in the collection if many of the affected elements were kept.

A final suggestion for the context of the Point San Jose Collection is that it was medical waste, such as from amputation or other surgical procedures (Willey et al. 2016). While axial elements are present in the assemblage, the most numerous elements are limb bones, and such selectivity could represent surgical procedures. There are also some saw marks that appear to be consistent with amputation, but an in-depth analysis of these marks is still in progress. As discussed above, some surgical specimens were saved by physicians as morbid specimens, but others were likely just considered refuse (Nystrom 2014), especially if they were not seen to contain valuable anatomical or pathological data. If the collection is largely composed of medical discard, a number of unassociated body regions would be expected that could differentiate it from dissected or autopsied cadavers. If the results indicate the collection is likely not medical discard, the saw marks could indicate removal of pathological specimens or practice of surgical cuts on cadavers.

Of course, not all of the categories discussed are mutually exclusive. For example, the collection could conceivably be dissection cadavers but with some body parts kept by the physician as "curios" or teaching specimens if they offered pathological knowledge. It is possible that remains from multiple categories are represented (Owsley et al. 2017). Individuating remains through resolving commingling could show which explanation, or explanations, best accounts for the remains from Point San Jose.

Research Questions

Commingling has been a significant obstacle in attempts to understand the origin of the Point San Jose Collection. A previous graduate thesis by Heather MacInnes (2017) attempted to address some of the commingling for the femora, humeri, radii, ulnae, tibiae, and innominates in the collection. Although she was able to match and reject some potential pair-matches and articulations, she was not able to sort the assemblage enough to say anything meaningful about the collection's context. The current thesis intends to build upon that work by addressing commingling of the hands and feet, specifically metacarpals and metatarsals. Resolving commingling for these elements may provide more insight into the assemblage's origins because elements of the hands and feet were among the most numerous elements. Of the fourteen most frequent elements, ten were hand and foot bones; six of the ten most frequent elements were either metacarpals or metatarsals specifically (Willey et al. 2016). Therefore, one research question in this thesis is: Can resolving commingling of the metacarpals and metatarsals in the Point San Jose Collection help illuminate context? This project will focus on gauging completeness of remains to narrow down possible contexts, such as discerning surgical waste versus cadavers.

Summary

The Point San Jose Collection was discovered in Fort Mason in a pit associated with the post's historical hospital. Saw and incised cut marks as well as other artifacts in the pit support that the assemblage is some sort of medical collection, but the lack of individuation of the remains obscures the context. The possibility that it is surgical waste or dissected/autopsied cadavers will be explored by attempting to resolve commingling of the metacarpals and metatarsals in the collection since they are among the most frequent elements. Identifying the type of medical discard could help illuminate medical practices during the nineteenth century, including the possibility of evidence for structural violence through dissection of marginalized groups during the 19th century.

CHAPTER IV

MATERIALS AND METHODS

Introduction

The methodology for this project involved applying techniques developed by previous researchers for osteometric sorting (Byrd 2008; Byrd and LeGarde 2014; Lynch et al. 2018; Thomas et al. 2013; Vickers et al. 2015) to elements of the hands and feet. This study tested applications to the metacarpals and metatarsals because they are frequent in the Point San Jose Collection and because previous studies have shown strong correlations with other long bones. Data were used to develop the statistical framework of the six osteometric tests described in chapter II. The various methods were compared for exclusionary power and low levels of false rejections to suggest the best osteometric methods for sorting MCs and MTs.

The research required taking measurements of metacarpals and metatarsals on a reference sample in order to develop the statistical frameworks for testing possible associations between two elements. Using remains of known individuals allowed for an investigation of the metric relationships between elements within the human skeleton and captured the variation between individuals. After establishing what is considered typical variation within individuals, the method, along with other sorting procedures, was applied to the Point San Jose collection in an attempt to build upon previous sorting efforts for the collection and to better understand the context of the assemblage.

Measurements

A series of measurements on the metacarpals and metatarsals were taken to see which proved most useful in osteometric sorting. The dimensions were largely based on previous publications that utilized metrics of MCs and MTs. However, deciding on the measurements to use for this study was difficult since so many different definitions have been used by different authors (Byers et al. 1989; Case and Ross 2007; Case et al. 2015; Falsetti 1995; Manolis et al. 2009; Meadows 1990; Meadows and Jantz 1992; Mountrakis et al. 2010; Musgrave and Harneja 1978; Robling and Ubelaker 1997; Scheuer and Elkington 1993; Smith et al. 1997; Stojanowski 1999; Zaher et al. 2011;). Recently, for example, Case and colleagues (2015) suggested using a mini-osteometric board (MOB) for measuring metacarpals to decrease both inter-observer error and time investments. A MOB was not readily available for this study, so measurement definitions were primarily derived from earlier studies that utilized sliding calipers. Definitions and the reasons for picking each measurement are described below. An intra- and inter-observer error component, described later in this chapter, was incorporated into the study to assess repeatability of measurements.

For each MC and MT, measurements included length (LEN), maximum length (MXL), interarticular length (IAL), head mediolateral width (HW), base mediolateral width (BW), and articular facet length for digits two through five (MEDF and LATF), and were taken using Mitutoyo digital sliding calipers. The calipers were zeroed between each measurement to avoid the common type of human error described by Adams and Byrd (2002). Descriptions of measurements are below, and sample illustrations are in Appendix A. Multiple length measurements were used to determine which definitions have the lowest errors and strongest sorting power. Also, each length corresponds to a different dimension that may show variation between elements from different individuals that could help in pair matching.

Length was defined as the dimension from the most proximal point of the base to the most distal point of the head (Case and Ross 2007; Case et al. 2015; DeSilva et al. 2014; Meadows 1990). The long axis of the bone should stay parallel to the long axis of the sliding calipers (perpendicular to the arms of the calipers) with the arms of the calipers in a medial-lateral direction. For MT5, the medial surface of the bone was considered the long axis, following Byers et al. (1989) and Robling and Ubelaker (1997).

Maximum length was considered the maximum dimension of the element. Move the MC/MT within the arms of the calipers to find the maximum length. It is based on Cordeiro et al.'s (2009) maximum lengths for MT1 and MT2 as well as Byrd and Adam's (2015) osteometric sorting measurements. This length measurement was used because it was thought it may provide less error than the above measurement of length since there should be no subjectivity in how to position the bone. Often, length and maximum length were virtually the same measurement, but that was not always the case, particularly for some of the MTs.

Interarticular length was the length from the center of the proximal articular surface to the apex of the head (Byers et al. 1989; Musgrave and Harneja 1978; Scheuer and Elkington 1993; Stojanowski 1999; Zaher et al. 2011). For each of the MCs, Musgrave and Harneja's (1978) landmarks, further clarified in Scheuer and Elkington

(1993), described that the midpoint of the proximal ends were used. These included: the "center of the proximal articular surface" for MC1; where the "notch for articulation with the trapezoid consisting of a narrow anterior part and a wider posterior part, both running in a distal/proximal direction diagonally from the respective anterior and posterior surfaces of the bone…meet to form a slight ridge" for MC2; the "point lying as near as possible to the longitudinal axis on the ridge that runs in an anteroposterior direction across the base and separates the articular facet for the capitate from that for metacarpal 2" for MC3; the "point as close as possible to a hypothetical center of the base" for MC4; and, for MC5, the "most distal point in the concavity in the mediolateral plane" of the articular facet for the hamate (Scheuer and Elkington 1993:771).

Studies that used the interarticular length for MTs did not define specific points that could be considered the midpoint of the proximal articular surface, so the center was estimated. For MT5, the interarticular length was considered the functional length from Byers et al. (1989), which was from the apex of the head to the midpoint along the ridge formed between the facets for MT4 and the cuboid. Interarticular length was used because it is a common measurement used in previous studies of MC and MT metrics.

Head mediolateral width was defined as the width from the most lateral to the most medial points of the distal end. It is the maximum width obtainable with the arms of the sliding calipers on both sides of the distal end and parallel to the long axis of the bone. Many previous publications use a mediolateral width of the distal articular surface (Robling and Ubelaker 1997; Scheuer and Elkington 1993; Smith 1997); however, the current definition includes non-articular projections, if they create the maximum width of the distal end, because it is adapted from Case et al.'s (2015) MOB measurement that showed less error than previous definitions. In the measurement for this study, the arms of the calipers are meant to mimic the uprights of the MOB. Even with the MOB, the authors suggest that head width for some MCs may show too much error for use in studies of asymmetry, but it was included in this thesis to further test that conclusion.

The *base mediolateral width* was the width from the most lateral to the most medial points of the proximal end. It was the maximum width obtainable while keeping the arms of the sliding calipers in the mediolateral plane and parallel to the long axis of the bone (Case et al. 2015; Scheuer and Elkington 1993; Smith 1997; Stojanowski 1999). The head and base of the MTs were not always in the same plane; in this case, the superior surface of the element was defined in reference to the head, as in Robling and Ubelaker (1997).

Articular facet lengths, for rays two through five for the MCs and MTs, were defined as the palmar-dorsal or plantar-dorsal length of the medial and lateral articular facets near the proximal end of the elements. The maximum palmar/plantar-dorsal length was measured while staying parallel to the proximal margin of the base. If there was more than one facet on the relevant surface (for example, MC4 usually has two round facets laterally), one measurement that encompassed both facets was performed to get a length for the whole articulating area. This measurement was not based on any previous studies, but was developed specifically to examine the relationship between articulating surfaces on adjacent elements.

In addition to measurements of the MCs and MTs, a few measurements of the humeri and femora were taken for correlating osteometrics of the hand and foot elements to other regions of the body. Measurements on the humerus included maximum length, epicondylar breadth, and maximum vertical diameter of the head, while measurements on the femur included maximum length, epicondylar breadth, and maximum diameter of the head (Moore-Jansen et al. 1994).

For this study, only a few measurements each for the MCs, MTs, humerus, and femur were taken. If this study shows promise for applications in commingled collections, then further measurements could be added to possibly increase the strength of exclusions. For example, many osteometric studies of MCs and MTs use a midshaft diameter and a measure of head and base height in addition to the widths (Case et al. 2015; Robling and Ubelaker 1997; Scheuer and Elkington 1993). Measurements such as capitulum-trochlea breadth and anterior-posterior breadth of the head for the humerus, and anterior-posterior and transvers subtrochlear diameters of the femur, have also been used for osteometric sorting (Byrd 2008; Byrd and LeGarde 2014).

Samples

The documented skeletal collection at the University of New Mexico's Maxwell Museum of Anthropology (UNM) was used as the reference sample on which measurements were taken to determine what amount of variation can exist within an individual and subsequently to develop osteometric sorting methods for MCs and MTs. The collection was established in 1984, so individuals in the sample all died during or after that year. All individuals in the collection were donated by pre-death arrangements, by family members after death, or by investigators when a deceased's next of kin was unknown. Information such as sex, age-at-death, ancestry, stature, year of birth, cause of death, and other details are documented for most individuals in the collection (Maxwell Museum 2018).

Maxwell Museum staff provided a list of 110 individuals that were randomly sampled from the individuals over 17 years old in the collection. Only individuals older than 17 were included because that is the age when the epiphyses of the MCs and MTs should all be fused (Scheuer and Black 2004). The order of the list of individuals was then randomized, since it was in numerical order when provided, and as many were measured as possible over three weeks spent at UNM.

Each of the measurements described previously were performed on the MCs, MTs, humeri, and femora of 86 individuals in the collection, split approximately evenly between females and males (44 and 42, respectively). Individuals ranged in age from 18 to 94, with a median age-at-death of 67 years, and birth years between 1890 and 1975 (with one unknown birth year). The individuals in the sample were predominately of European ancestry (n=74), but there were a few individuals of African (n=3), Hispanic (n=2), and unknown (n=7) ancestry.

Measurements that would have been impacted by pathological or taphonomic changes were excluded. Additionally, many individuals were missing some of their MCs and MTs. When analyses were completed, therefore, the actual sample sizes for each test varied.

A second sample served as a holdout sample and consisted of five other individuals from the UNM documented collection and 13 individuals from the forensic skeletal collection at the California State University, Chico Human Identification Laboratory (HIL). The HIL forensic collection consists mainly of skeletal remains that were donated by families of individuals after identification, but some are from law enforcement when identification efforts were not successful. The 18 individuals from UNM and HIL were used to test the power and accuracy of the methods derived from the reference sample. Fourteen males and four females between the ages of 18 and 94 were included. Eleven of the individuals were born between the years 1906 and 1964. One individual was determined to be archaeological and was born in the late 1800s, and six individuals' birth years are unknown. Fifteen are of European ancestry, one each are of African and Hispanic ancestry, and one ancestry is unknown.

The final sample included in this thesis was the Point San Jose Collection (PSJ). The results from previously described samples were used towards the process of analyzing and interpreting the PSJ Collection. Osteometric sorting, along with other pair-matching and sorting techniques, was applied to the resolution of commingling for the hands and feet in this collection. As described in chapter III, PSJ is a Civil War-era medical or teaching collection that was discovered in 2010 near the building that was the historical hospital at the Point San Jose army base, now Fort Mason in the Golden Gate National Recreation Area (Willey et al. 2016). The MNI for the collection was 22 individuals, from the right talus, or 25 using age and sex based evidence. However, despite their frequency, most hand and foot bones were not included in sorting efforts

(Willey et al 2016; MacInnes 2017), so this thesis attempted to individuate metacarpals and metatarsals to help clarify the context of the collection.

Analyses: Error

In metric skeletal studies, it is important to evaluate how much measurement error may have impacted the results of the research. For this study, it is especially important because measurements of the MCs and MTs are not among skeletal dimensions commonly learned or used by practitioners. Therefore, a number of elements were re-measured and indices of error calculated. These indices included the relative Technical Error of Measurement (%TEM) and a coefficient of reliability (R); acceptable levels of error will vary by study, measurement, and experience level of the observer, but 5% TEM and R>0.95 have been suggested as values indicative of good quality control (Goto and Mascie-Taylor 2007; Ulijaszek and Kerr 1999). The median percent difference was included to allow comparisons of error between this study and Case et al.'s (2015) study.

To assess intra-observer error, error that occurs between measurements of a single case performed by a single observer on different occasions, a sample of 11 individuals from the UNM documented collection and eight individuals from the HIL forensic collection were re-measured by the author a minimum of 1.5 weeks after the measurement originally was performed. To assess inter-observer error, error between measurements of a single case performed by at least two different people, an independent observer was given minimal instruction on how to complete the measurements and then, with no input from the author, measured the 13 individuals in the HIL sample and 22 stand-alone elements from the PSJ collection. For the analyses, actual sample size varies since some elements were excluded due to pathology, taphonomy, or lack of presence.

No measurements in this study were removed due to high error, but their impacts on the study were considered. The author both developed and applied the osteometric sorting frameworks utilizing the measurements, so high interobserver error would not impact the results, but would have implications for their use by other researchers. For dimensions with intraobserver error that is higher than ideal, measurement error would become a component of human variation that is built into the statistical frameworks developed (Goto and Mascie-Taylor 2007). Lack of quality measurements can lead to more variance for a variable, and more variance could decrease the power of sorting models, but it should not increase false rejections since the inconsistency in levels of asymmetry caused by error would be incorporated into models.

Analyses: Hypothesis Tests

A number of hypotheses relating to concepts underlying osteometric sorting were tested using the UNM reference sample. These analyses could show whether or not the method would be useful for MCs and MTs. Osteometric pair-matching is based on the idea that humans display right-left symmetry within the body. To test this assumption for the MCs and MTs, paired *t*-tests for right-left pairs were performed in SPSS v.24 for each of the dimensions of the elements in the original sample. The tests were performed on males and females separately. Measurements with high levels of asymmetry between antimeres potentially could reduce the efficacy of osteometric sorting.

Osteometric articulation methods are based on the idea that joining elements must share size similarities between articulating regions. Since facets are areas where adjacent MCs and MTs touch, the facet lengths of articulating elements should be related. To test this, a correlation test was completed in SPSS v.24 for males and females in the original sample. Correlations were completed for facets between MC2 and MC3, MC3 and MC4, MC4 and MC5, MT2 and MT3, MT3 and MT4, and MT4 and MT5 for left and right elements. Correlation coefficient (*r*) values greater than or equal to 0.7 were considered strong, values below 0.7 but greater than or equal to 0.5 were moderate, and values below 0.5 but greater than 0.2 were indicative of weak relationships.

Osteometric comparisons of non-paired and non-articulating elements rely on correlations in size between multiple elements in the body. MC and MT lengths have previously been shown to correlate with stature and sex like other long bones, although with less strength. Still, since the MCs and MTs and other limb bones are correlated with similar variables, they should show correlations with each other, and this correlation would be useful in estimating whether elements could have come from a single individual. To test this, correlations were performed in SPSS v.24 for males and females in the reference sample. The tests compared the natural log of interarticular lengths of all of the MCs and MTs to the natural log of maximum lengths of the humeri and femora. Interarticular length was tested because bone lengths tend to show the highest correlations (Byrd and Adams 2003), so at least one length should be included in sorting methods, and of the three MC/MT lengths the interarticular length was least likely to be affected by taphonomy or pathology and is therefore present for testing more often. The natural log of the summed measurements was used since that is how variables in the osteometric sorting method are calculated. Since width or breadth measurements sometimes increase the strength of correlations (Byrd and Adams 2003), correlation tests were also performed comparing the natural log of the summed interarticular length, head width, and base width for MCs and MTs to the natural log of the summed maximum length, head diameter, and epicondylar breadth for humeri and femora.

For hypothesis testing, the males and females were separated to prevent violations of the test parameters. When developing each of the osteometric sorting methods, however, individuals of all sexes and ancestries were combined into one sample since, in an actual commingling scenario, the demographics of the sample may be unknown.

Analyses: Osteometric Sorting

Osteometric Pair-Matching

The UNM reference sample was used to develop osteometric sorting frameworks for the MCs and MTs. For pair-matching, LEN, MXL, IAL, HW, and BW were considered. First, following Byrd (2008) and Byrd and LeGarde (2014), the measurements from the left and right paired elements of each individual in the reference sample were subtracted and the differences for a series of measurements were summed to find *D* (equation [1]). *D* was calculated using each measurement and using various combinations of measurements (LEN+MXL+IAL+HW+BW, IAL+HW+BW, and HW+BW) because fragmentation could prevent certain ones from being usable.

Microsoft Excel was used to find the standard deviation of *D* for each combination of measurements for each element which would be used for the application of the method.

The accuracy of the method was tested using the holdout sample by finding *D* for each potential pair and dividing the absolute value of the result minus zero by the reference sample standard deviation to calculate *t* (equation [2]) in Excel. The value of *t* was compared to the critical values for a two tailed t-distribution using $N - 1$ degrees of freedom. An alpha-level of 0.05 was used to determine statistically significant differences between the left and right elements of the pair; Byrd (2008) and Byrd and LeGarde (2014) recommend a 0.10 cutoff, but 0.05 was used for all tests in this study to be more conservative in preventing false exclusions. Pairs with *t*-values above the critical *t*-value (with low *p*-values) were segregated. The proportion of rejections were noted as a measure of how powerful the method was in excluding elements from different individuals. Pairs known to be from the same individual, but that would be considered too different to be from one individual in real applications of the test, were false rejections.

The same steps were taken for Lynch et al.'s (2017) method, except with their slightly altered equations. *D* was calculated for each individual in the reference sample by summing the absolute value of right-left differences, and performing a half-normal transformation for skewed distributions (equation [5]). The mean and standard deviation for various measurement combinations, the same as for the Byrd (2008) and Byrd and LeGarde (2014) method above, were calculated in Excel for use in testing associations. Individuals in the holdout sample were used to test the method on known pairs and non-pairs by calculating *t* as the reference mean subtracted from *D* and dividing the result by the reference standard deviation (equation [6]). The value of *t* was compared to the critical value for a one-tailed *t*-test with $N - 1$ degrees of freedom and alpha level 0.05; values of *t* above the critical values were considered exclusions, and the number of true and false exclusions were noted.

Thomas et al.'s (2013) osteometric pair-matching method involves calculating the *M* statistic by dividing the absolute value of left-right differences for a specific measurement by the halved value of the sum of the left and right measurements (equation [3]). *M* was computed for each measurement on each element for each individual in the reference sample using Microsoft Excel, and the upper 95th percentile and maximum value of *M* were calculated in SPSS v.24. These ranges were considered the acceptable maximum of *M* values for elements originating from the same individual, with the decision about which range (95th percentile or maximum) to use depending on how conservative rejections have to be for the purposes of a particular project. The holdout sample was used to test the accuracy of these ranges by calculating *M* for elements known to be matches or not and noting the number of false and true rejections. In this sample, the 95th percentile was used. The accuracy and power of various measurements were then compared to see which measurements should be prioritized for sorting when present.

The final parameters developed for osteometric pair-matching were from Vickers et al. (2015). They found that Byrd (2008) and Byrd and LeGarde's (2014) method led to too many false rejections and criticized its assumption of zero-difference between pairs. Following Vickers et al.'s (2015) new suggested method, *D* was calculated on the reference sample the same way as for Byrd (2008) and Byrd and LeGarde (2014) outlined above. The absolute value was taken and the full range of values became the cutoff for sorting; elements in the test sample outside the range were considered too different to come from the same individual and were segregated.

Osteometric Articulations

Following Byrd (2008) and Byrd and LeGarde (2014), the value of *D*, which was calculated by subtracting the facet lengths of two articulating elements (equation [7]), was computed for each of the articulating pairs in the original sample. The facet length on the higher-numbered digit was subtracted from the facet length on the lower-numbered digit to calculate *D* (for example, the facet length on MC3 was subtracted from the facet length on MC2). The average *D* and standard deviation of *D* for the reference sample were developed in Excel to use in testing potential matches. *D* was then calculated for known pairs and non-pairs in the test sample and *t*-values were calculated by subtracting the average *D* from the potential pair's *D* and dividing the result by the standard deviation of *D* (equation [8]). Values of *t* were compared to the critical values of a two-tailed *t*-distribution at an alpha level of 0.05 using $N - 1$ degrees of freedom. A *t*-value with a low *p*-value led to segregation of the elements. The proportion of true and false rejections were noted.

Osteometric Comparisons to Humerus and Femur

Following Byrd (2008) and Byrd and LeGarde (2014), osteometric methods for comparisons of the MCs and MTs with other bone regions were developed. A number of variables (Table 1), calculated as the natural log of the sum of a series of measurements on the MCs, MTs, humeri, or femora, were computed using SPSS v.24 and then used to develop regression formulae. Various combinations of measurements were used to address fragmented humeri and femora, including the summed length, epicondylar breadth, and head diameter (variables HUM.1 and FEM.1), and epicondylar breadth (HUM.2, FEM.2) and head diameter (HUM.3, FEM.3) each independently. The variable used for the MCs and MTs included only interarticular length, head width, and base width summed. Ideally, regression formulae would be developed to compare numerous measurements on the MCs and MTs with numerous measurements on the other elements to account for varying fragment conditions, but would have led to too many

Table 1 Calculation of variables used for osteometric comparisons to humerus and femur.

Variable	Calculation
MCx.1	ln(MCxIAL+MCxHW+MCxBW)
MTx.1	ln(MTxIAL+MTxHW+MTxBW)
HUM.1	ln(HUML+HUMEP+HUMHD)
HUM.2	ln(HUMEP)
HUM.3	ln(HUMHD)
FEM.1	ln(FEML+FEMEP+FEMHD)
FEM.2	ln(FEMEP)
FEM.3	ln(FEMHD)

combination possibilities for the purposes of this study. The interarticular length + head width + base width variable was chosen because it would allow the greatest number of MCs and MTs to be measureable while still including a length measurement. It would also be ideal to compare MCs and MTs with numerous elements within the body, such as the radius, ulna, tibia, and fibula, but this study used just the humerus and femur to test whether comparisons with the MCs and MTs were even useful. Consistent with Lynch (in press), there were no differences for comparisons of the same or opposite sides (left-left and right-right versus left-right and right-left) so formulae were developed that could be used for both instances.

The holdout sample was used to test the power and accuracy of the method. Since there were too many regression equations to test each individually, three were chosen as examples, including the formulae with the highest, lowest, and an intermediate correlation coefficient. These tests should provide a general idea of how well equations with similar r values perform. Series of measurements for known matches and non-matches were summed and transformed with the natural log to obtain the actual x and y values, and x was entered into the appropriate regression formula to obtain the predicted y value. Actual and predicted y values were compared by calculating a value of t (equation [9]) that could be compared to a two-tailed t-distribution with $N - 2$ degrees of freedom. A p-value below 0.05 rejected the null hypothesis that the two bones originated from the same individual, and the number of false and true rejections were noted.

Case Study: Point San Jose Collection

The methods developed in this study were applied to the Point San Jose Collection in an attempt to understand the context of the assemblage while also evaluating the usefulness of the methods in a non-simulated scenario. Each available measurement was taken for the MCs, MTs, humeri, and femora. Using Microsoft Excel, each potential match for pair-matching, joint articulation, and comparisons to other regions was assessed using the appropriate formula and data derived from the reference sample. The percentage of potential pairs that could be excluded using osteometrics was calculated to show how helpful or not osteometric sorting was in the process of resolving commingling in the PSJ Collection.

Visual assessment of all potential pair and articular matches was completed separately. Normally, visual matching could be used just to compare potential matches that are not excluded osteometrically to reduce time investment in the sorting process, but it was completed for all elements in this study since it could allow an approximation, although not perfect, of how many false osteometric rejections there were for the newly-developed frameworks. Potential pairs and articulations were considered matched, possibly matched, not matched, or unable to be determined/ambiguous based on visual clues. Visual matching was not used for comparisons of the MCs and MTs to the humeri and femora as it is generally not useful.

Results from the osteometric and visual methods were compared, and results that complemented each other were considered confirmed. For example, if a visually matched pair was not osteometrically excluded it was considered a confirmed pair, or if all potential pairs for an element were excluded osteometrically and had no visual matches it was considered a confirmed non-pair. The methods in conjunction could also change classifications; for example, possible matches could become confirmed matches through articulation to a matched pair, and indeterminate matches (possibly matched or ambiguous) could become non-matches if osteometrics suggested segregation. Process of elimination was of course another important line of evidence, as osteometric and visual methods do not usually exclude all potential matches, but an element being matched to another led to its exclusion.

In some cases, elements were unable to be compared osteometrically or visually (for example, MC/MT head to base comparisons) or were otherwise not confidently matched or rejected. Portable x-ray fluorescence was used to help sort these cases when possible. It was also used to try to exclude additional humeri and femora that were not excluded osteometrically. All MCs, MTs, humeri, and femora were scanned for three minutes with a Bruker Tracer IV Series pXRF device, with a connected vacuum, as close to the center of the element's shaft as possible. Trace element concentrations previously shown to be useful in sorting commingled remains, including silicon, phosphorus, potassium, calcium, manganese, iron, cobalt, lead, and strontium (Finlayson 2017; Gonzalez-Rodriguez and Fowler 2013; Perrone et al. 2014), were used to evaluate the likelihood that elements originated from the same individual using Perrone et al.'s (2014) suggested procedure. Confidence intervals (95%) were created using elemental concentrations of remains matched through osteometric and visual means. Elements potentially originating from the same individual as the confidence interval were compared. If values fell far outside the confidence intervals for many of the above trace elements, they were considered not to originate from the same individual and were rejected. In closed samples, the confidence intervals could be used for associations. Since PSJ is an open sample, it was used more conservatively, for rejecting potential matches that consistently fell far outside the confidence intervals formed by a group of three or more elements.

Evidence from all methods was considered for sorting. The minimum number of individuals (MNI) represented by each MC and MT in the PSJ Collection was then calculated to see if sorting helped improve estimations of how many individuals are present in the pit. The number of matches versus single elements present was also considered to attempt to get at questions of context.

Summary

Using a mixture of previously developed and novel measurements, the frameworks for osteometric sorting were derived for metacarpals and metatarsals. A reference sample from the documented osteological collection at the University of New Mexico was used to develop the methods, and a test sample was used to test how powerful and accurate each of the methods and measurements were. Based on those results, osteometric sorting, in conjunction with other sorting techniques, were applied to the metacarpals and metatarsals of the Point San Jose Collection in an attempt to assist with skeletal analysis of the assemblage.

CHAPTER V

RESULTS

Introduction

This chapter presents the results from the various tests described in the Materials and Methods chapter. This includes an examination of intra- and inter-observer error, tests of the research hypotheses, and the development and testing of various osteometric methods for the metacarpals and metatarsals. Finally, this chapter presents the results from the application of various sorting methods, with an emphasis on osteometric sorting, to the metacarpals and metatarsals in the commingled Point San Jose Collection.

Measurement Error

Quantifying measurement error is an important aspect of studies incorporating metrics. Measurements with too much error may impact study results or may not be applicable to other research. This study used the relative technical error of measurement (%TEM) and coefficient of reliability (R) to consider the amount and impact of error on osteometric sorting procedures. While the cutoff for what is considered too much error is somewhat arbitrary and accepted levels of error vary by study, measurements with less than 5%TEM and greater than 0.95 R value have been suggested as values indicative of low error and served as guidelines for this project.

Intra-Observer Error

Intraobserver error is a description of how repeatable a specific measurement is for an individual observer. After some time has passed since taking measurements initially, they are repeated by the same person on the same elements to make sure the observer is performing measurements consistently.

The results from the intraobserver error test are in Appendix B. A majority of the dimensions were below the suggested 5% TEM and above the suggested R threshold of 0.95, with more than half of the measurements below 1% TEM. Measurements with greater than 5% TEM or less than 0.95 for R included MC2 medial facet, MC3 base width, MC3 medial facet, MC3 lateral facet, MC4 medial facet, MC4 lateral facet, MC5 lateral facet, MT2 lateral facet, MT3 base width, MT3 medial facet, MT3 lateral facet, MT4 base width, MT4 medial facet, MT4 lateral facet, MT5 base width, and MT5 medial facet. Most of the dimensions with higher error were facet lengths, although a few of the base widths also showed greater error than desired.

Although some measurements showed higher error than would have been ideal, no measurements were excluded from this study. Measurement error is a component of measured human variation and should therefore be built into the osteometric sorting methods that are developed as if they represent actual intra-individual variation. As shown below, there did not appear to be a relationship between higher error and higher false exclusions, so removing the measurements would not improve the accuracy of the study results. Using measurements with lower error could, however, lead to the development of sorting methods with increased power.

Inter-Observer Error

Interobserver error is the amount of error present for a single measurement that was taken by two different people independently and shows the degree of repeatability between multiple researchers. The results from the interobserver error test are in Appendix B. Almost all of the measurements were below 5% TEM but only two-thirds were above an R of 0.95. Again, most of the measurements with high error were facet lengths and some base widths, although some head widths were also below 0.95 for R. Measurements with high interobserver error would not have affected the results of this study because both the measurements used to develop and test the osteometric sorting methods were performed by the author. However, interobserver error is an important consideration for other researchers looking to use the methods in their own studies.

Results of Hypothesis Tests

A number of hypotheses relating to the theoretical foundations of osteometric sorting were developed and tested for the metacarpals and metatarsals. Concepts tested include the symmetry of paired elements for pair-matching, the relationships of dimensions between articulating elements, and the relationships of dimensions between MCs/MTs and other regions of the skeleton.

Symmetry of Paired Elements

The first hypothesis in this study was that there are no statistically significant differences in size between antimeres. Pair-matching is predicated upon overall left-right symmetry within the skeleton, so this research sought to investigate how much symmetry actually exists for MCs and MTs in the UNM reference sample. Paired t-tests are a simple way to investigate this question since they can detect differences between dependent variables that could tell how well osteometric pair-matching techniques will work for elements. Results from the t-tests, including sample sizes, means, and *p*-values, can be viewed in Tables 2 and 3.

For the MCs, 12 out of 31 measurements were statistically significantly different for males, and 15 of 31 were significant for females. For each of these dimensions, the mean for the right was larger than the left, usually by less than one millimeter. At least one dimension on each metacarpal for both males and females showed a significant difference, though which ones were different tended to vary by sex. Females appeared to have more asymmetry in length measurements compared to males, while males seemed to show more differences for the widths. For the MTs, two of 31 *t*-tests were significant for males, and seven of 31 for females. Both of the significant dimensions for males were on MT4, while females showed asymmetry for all of the measurements on MT1 and for one measurement each on MT4 and MT5. There was variation in whether the mean for the left or right was larger, except for females' MT1 which showed a consistently larger mean for the left.

<u>Size Relationships for Articulating Elements</u>

The second hypothesis in this study was that facets where MCs and MTs articulate are strongly correlated. Relationships between measurements at joints form the basis for osteometric sorting of articulating elements because articulating regions need to

Table 2 Results of paired sample *t*-Tests comparing right and left MC/MT dimensions (males)

n	Measurement	Mean	*p*-value	n	Measurement	Mean	*p*-value
27	LMC1LEN RMC1LEN	47.7444 48.0759	0.053	35	LMT1LEN RMT1LEN	63.2843 64.1220	0.417
26	LMC1MXL RMC1MXL	47.9138 48.2015	0.110	34	LMT1MXL RMT1MXL	66.9315 68.3471	0.185
36	LMC1IAL RMC1IAL	45.2042 45.4725	0.073	39	LMT1IAL RMT1IAL	61.5787 62.4982	0.307
33	LMC1HW RMC1HW	16.6379 16.9761	**0.003**	27	LMT1HW RMT1HW	21.5841 22.1070	0.235
31	LMC1BW RMC1BW	16.3655 16.6635	**0.009**	32	LMT1BW RMT1BW	20.9794 21.3788	0.391
38	LMC2LEN RMC2LEN	70.2963 70.5558	**0.049**	34	LMT2LEN RMT2LEN	79.3515 79.1332	0.177
38	LMC2MXL RMC2MXL	70.5987 70.7974	0.123	33	LMT2MXL RMT2MXL	79.1888 79.1042	0.593
39	LMC2IAL RMC2IAL	67.1897 67.2108	0.880	39	LMT2IAL RMT2IAL	75.2585 75.1674	0.549
37	LMC2HW RMC2HW	15.5457 15.8397	**0.001**	32	LMT2HW RMT2HW	12.2134 12.2809	0.491
38	LMC2BW RMC2BW	19.2013 19.4463	**0.006**	39	LMT2BW RMT2BW	16.8905 16.9146	0.804
37	LMC2MEDF RMC2MEDF	15.3773 15.8195	**0.004**	36	LMT2LATF RMT2LATF	15.5725 15.4719	0.878
37	LMC3LEN RMC3LEN	69.2673 69.5568	0.160	39	LMT3LEN RMT3LEN	74.0379 73.8918	0.374
37	LMC3MXL RMC3MXL	69.3727 69.7251	0.082	38	LMT3MXL RMT3MXL	74.5876 74.5495	0.812
39	LMC3IAL RMC3IAL	65.2156 65.2877	0.584	39	LMT3IAL RMT3IAL	72.0679 72.2051	0.402
39	LMC3HW RMC3HW	15.0362 15.4074	**0.000**	30	LMT3HW RMT3HW	10.4237 10.3720	0.580
41	LMC3BW RMC3BW	15.0773 15.1790	0.428	41	LMT3BW RMT3BW	14.9383 15.1102	0.154
32	LMC3MEDF RMC3MEDF	11.3969 11.8034	0.290	38	LMT3MEDF RMT3MEDF	16.7903 16.1442	0.198
40	LMC3LATF RMC3LATF	15.7970 16.1730	**0.001**	40	LMT3LATF RMT3LATF	8.6475 8.8490	0.178
34	LMC4LEN RMC4LEN	58.6379 58.9041	0.102	29	LMT4LEN RMT4LEN	72.5172 72.5417	0.900
34	LMC4MXL RMC4MXL	59.0153 59.2156	0.188	29	LMT4MXL RMT4MXL	72.6538 72.8593	0.249

n	Measurement	Mean	*p*-value	n	Measurement	Mean	*p*-value
36	LMC4IAL RMC4IAL	57.7617 57.8517	0.513	34	LMT4IAL RMT4IAL	69.3038 69.7494	**0.018**
42	LMC4HW RMC4HW	13.0229 13.4086	**0.000**	28	LMT4HW RMT4HW	10.5379 10.4296	0.298
38	LMC4BW RMC4BW	13.0634 13.1171	0.582	39	LMT4BW RMT4BW	16.2265 15.8059	**0.004**
31	LMC4MEDF RMC4MEDF	9.9648 10.4529	**0.002**	42	LMT4MEDF RMT4MEDF	8.3929 8.5536	0.285
31	LMC4LATF RMC4LATF	11.1290 11.0745	0.865	31	LMT4LATF RMT4LATF	11.1158 11.4497	0.094
32	LMC5LEN RMC5LEN	53.9628 54.0941	0.380	29	LMT5LEN RMT5LEN	73.6534 73.8369	0.336
32	LMC5MXL RMC5MXL	54.1700 54.2797	0.462	29	LMT5MXL RMT5MXL	74.4383 74.6255	0.337
32	LMC5IAL RMC5IAL	52.9581 53.0731	0.442	34	LMT5IAL RMT5IAL	61.8944 62.2474	0.067
38	LMC5HW RMC5HW	12.5900 12.7676	0.084	26	LMT5HW RMT5HW	11.0142 11.0838	0.619
38	LMC5BW RMC5BW	14.6316 14.9755	**0.001**	39	LMT5BW RMT5BW	21.0310 20.9515	0.639
32	LMC5LATF RMC5LATF	9.9809 10.3650	**0.005**	42	LMT5MEDF RMT5MEDF	10.3836 10.6867	0.075

fit well together. Correlation tests are one simple way to test for such relationships, specifically for articulating MCs and MTs in the reference population. Strong correlations should indicate more accuracy for sorting. The results of the correlation tests can be found in Table 4. The majority of the articulating facets for both males and females showed strong correlations ($r \geq 0.7$). A few, four for males and two for females, showed moderate correlations ($0.7 > r \geq 0.5$). One correlation test for males, for the facets connecting left MC4 and MC5, showed a weak relationship ($0.5 > r \geq 0.2$). All of the correlation tests were statistically significant.

Table 3 Results of paired sample *t*-tests comparing right and left MC/MT dimensions (females)

n	Measurement	Mean	*p*-value	n	Measurement	Mean	*p*-value
21	LMC1LEN RMC1LEN	43.7448 44.3271	**0.001**	29	LMT1LEN RMT1LEN	62.2997 60.0472	**0.021**
21	LMC1MXL RMC1MXL	43.7981 44.3981	**0.001**	25	LMT1MXL RMT1MXL	66.1244 63.6688	**0.040**
36	LMC1IAL RMC1IAL	41.5686 41.9303	**0.003**	35	LMT1IAL RMT1IAL	60.6989 58.8777	**0.036**
32	LMC1HW RMC1HW	14.7406 15.1250	**0.000**	16	LMT1HW RMT1HW	21.1850 20.2456	**0.042**
20	LMC1BW RMC1BW	14.3345 14.5720	**0.039**	23	LMT1BW RMT1BW	20.2222 19.0435	**0.003**
35	LMC2LEN RMC2LEN	65.4594 65.8163	**0.003**	29	LMT2LEN RMT2LEN	74.0052 73.9862	0.922
34	LMC2MXL RMC2MXL	65.6488 65.9826	**0.003**	29	LMT2MXL RMT2MXL	74.1555 74.1976	0.821
36	LMC2IAL RMC2IAL	62.5697 62.7739	0.126	36	LMT2IAL RMT2IAL	70.9422 71.0647	0.476
35	LMC2HW RMC2HW	13.9271 14.2297	**0.000**	29	LMT2HW RMT2HW	11.2879 11.2297	0.510
31	LMC2BW RMC2BW	16.9045 16.9974	0.412	32	LMT2BW RMT2BW	15.4869 15.3313	0.387
34	LMC2MEDF RMC2MEDF	13.8065 14.1174	0.067	32	LMT2LATF RMT2LATF	12.4588 13.7334	0.146
34	LMC3LEN RMC3LEN	64.4935 64.9779	**0.023**	29	LMT3LEN RMT3LEN	68.7283 68.7121	0.913
34	LMC3MXL RMC3MXL	64.6197 65.1668	**0.010**	28	LMT3MXL RMT3MXL	69.2289 69.2857	0.689
39	LMC3IAL RMC3IAL	60.8767 60.9890	0.340	35	LMT3IAL RMT3IAL	67.4900 67.6246	0.251
36	LMC3HW RMC3HW	13.1542 13.5333	**0.000**	30	LMT3HW RMT3HW	9.7323 9.7447	0.859
37	LMC3BW RMC3BW	13.3443 13.4343	0.394	33	LMT3BW RMT3BW	13.4164 13.7433	0.170
32	LMC3MEDF RMC3MEDF	9.8928 10.1044	0.256	30	LMT3MEDF RMT3MEDF	13.1400 13.8337	0.413
38	LMC3LATF RMC3LATF	14.0353 14.5392	**0.000**	37	LMT3LATF RMT3LATF	7.5854 7.5516	0.901
34	LMC4LEN RMC4LEN	54.4097 54.5765	0.162	28	LMT4LEN RMT4LEN	68.3739 68.5221	0.656
33	LMC4MXL RMC4MXL	54.6906 54.9367	**0.035**	28	LMT4MXL RMT4MXL	68.5221 68.7593	0.179

n	Measurement	Mean	*p*-value	n	Measurement	Mean	*p*-value
37	LMC4IAL RMC4IAL	53.5351 53.7432	0.070	34	LMT4IAL RMT4IAL	65.7138 66.0797	**0.023**
39	LMC4HW RMC4HW	11.6900 11.8449	**0.005**	28	LMT4HW RMT4HW	9.6146 9.5889	0.792
34	LMC4BW RMC4BW	11.6394 11.5559	0.408	34	LMT4BW RMT4BW	14.8974 14.8018	0.663
32	LMC4MEDF RMC4MEDF	8.9828 8.9791	0.982	36	LMT4MEDF RMT4MEDF	7.4397 7.5486	0.661
34	LMC4LATF RMC4LATF	9.6847 9.4068	0.154	26	LMT4LATF RMT4LATF	10.4615 10.6581	0.424
36	LMC5LEN RMC5LEN	50.0903 50.3542	0.063	24	LMT5LEN RMT5LEN	68.7896 68.5983	0.388
36	LMC5MXL RMC5MXL	50.2747 50.5281	0.059	24	LMT5MXL RMT5MXL	69.2942 69.2704	0.909
38	LMC5IAL RMC5IAL	49.2803 49.4808	0.088	32	LMT5IAL RMT5IAL	58.8347 59.0631	0.275
37	LMC5HW RMC5HW	11.2246 11.3395	0.093	26	LMT5HW RMT5HW	10.2892 10.2831	0.951
37	LMC5BW RMC5BW	13.1200 13.3030	0.087	31	LMT5BW RMT5BW	18.9171 18.9429	0.872
33	LMC5LATF RMC5LATF	8.7303 8.9494	**0.031**	35	LMT5MEDF RMT5MEDF	9.2897 9.7214	**0.028**

Size Relationships of Non-paired and Non-articulating Elements

The third hypothesis that was tested in this research is that the size of the MCs and MTs is correlated with the size of other bones in the body, a concept which is the basis for osteometric sorting of non-paired and non-articulating elements. Dimensions with strong correlations should have more sorting power since they would indicate stronger relationships. Only correlations between the MCs and MTs with each of the humeri and femora were tested in the current research. Results showed all statistically significant correlations (Tables 5 and 6).

Table 4 Correlation coefficient test results for articulating facets.

	Males			Females		
Articulation	***N***	***r***	***p***	***N***	***r***	***p***
LMC2MEDF-LMC3LATF	38	0.893	**0.000**	37	0.860	**0.000**
LMC3MEDF-LMC4LATF	32	0.781	**0.000**	32	0.751	**0.000**
LMC4MEDF-LMC5LATF	33	0.424	**0.014**	33	0.797	**0.000**
RMC2MEDF-RMC3LATF	40	0.919	**0.000**	37	0.840	**0.000**
RMC3MEDF-RMC4LATF	35	0.873	**0.000**	35	0.782	**0.000**
RMC4MEDF-RMC5LATF	31	0.745	**0.000**	34	0.727	**0.000**
LMT2LATF-LMT3MEDF	38	0.641	**0.000**	31	0.758	**0.000**
LMT3LATF-LMT4MEDF	41	0.578	**0.000**	39	0.546	**0.000**
LMT4LATF-LMT5MEDF	33	0.819	**0.000**	32	0.814	**0.000**
RMT2LATF-RMT3MEDF	35	0.975	**0.000**	32	0.735	**0.000**
RMT3LATF-RMT4MEDF	41	0.693	**0.000**	35	0.924	**0.000**
RMT4LATF-RMT5MEDF	37	0.538	**0.001**	31	0.644	**0.000**

For females, all but one test (MC1.1-HUM.1) showed strong correlations. Marginal differences existed in *r* values between tests with and without width measurements but exhibited no consistency as to which was higher. Metacarpal and metatarsal dimensions showed stronger relationships with the femora than the humeri. Males had weaker correlations compared to females, with a some strong and some moderate correlations for comparisons without widths. Adding widths usually increased the strength of *r* for comparisons and led to correlations that were mostly strong, though still with some moderate. Metatarsals had stronger correlations with the femora than with the humeri, but metacarpals showed some stronger relationships with the femora and some with the humeri.

Table 5 Correlation coefficient test results for natural logs of MC/MT IAL and HUML/FEML.

		Males		Females	
		lnHUML	**lnFEML**	**lnHUML**	**lnFEML**
lnMC1IAL	*r*	0.771	0.767	0.764	0.786
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	66	70	73	62
lnMC2IAL	*r*	0.670	0.756	0.852	0.917
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	74	76	71	60
lnMC3IAL	*r*	0.646	0.683	0.815	0.885
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	73	75	74	62
lnMC4IAL	*r*	0.643	0.635	0.767	0.829
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	70	72	74	63
lnMC5IAL	*r*	0.701	0.649	0.753	0.809
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	66	70	73	63
lnMT1IAL	*r*	0.678	0.753	0.847	0.876
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	73	76	70	62
lnMT2IAL	*r*	0.705	0.769	0.846	0.891
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	73	76	71	63
lnMT3IAL	*r*	0.684	0.731	0.827	0.875
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	73	76	69	61
lnMT4IAL	*r*	0.649	0.687	0.821	0.890
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	69	71	66	59
lnMT5IAL	*r*	0.628	0.668	0.769	0.840
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	69	72	66	59

Development of Osteometric Sorting Frameworks

The reference sample, which was used for testing the hypotheses, was also used to establish the statistical framework for each of the osteometric sorting approaches described in chapter IV. Each method was then performed on the 18-individual test sample that simulated a commingled assemblage. In evaluating the methods, power

Table 6 Correlation coefficient test results for MC.1/MT.1 and HUM.1/FEM.1

		Males		Females	
		HUM.1	**FEM.1**	**HUM.1**	**FEM.1**
MC1.1	*r*	0.799	0.744	0.619	0.740
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	48	53	41	31
MC2.1	*r*	0.771	0.797	0.820	0.838
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	63	63	52	46
MC3.1	*r*	0.763	0.767	0.831	0.880
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	66	67	56	51
MC4.1	*r*	0.697	0.669	0.761	0.822
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	63	65	56	53
MC5.1	*r*	0.734	0.663	0.761	0.813
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	60	64	59	53
MT1.1	*r*	0.631	0.663	0.830	0.868
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	48	51	40	42
MT2.1	*r*	0.703	0.724	0.825	0.908
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	52	55	43	45
MT3.1	*r*	0.731	0.741	0.866	0.892
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	52	56	46	46
MT4.1	*r*	0.759	0.803	0.831	0.883
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	54	58	37	45
MT5.1	*r*	0.736	0.767	0.831	0.868
	p	**0.000**	**0.000**	**0.000**	**0.000**
	N	55	59	37	38

(ability to exclude high proportions of potential matches) and accuracy (low levels of false exclusions) were considered.

<u>Osteometric Pair-Matching</u>

A summary of the test sample in regards to pair-matching is in Appendix C. For each element, the sample's number of potential matches and actual matches are listed. The potential matches are how many element-to-element comparisons would need to be done based on comparing every left element present to every right element, and the actual matches are how many of the lefts truly match with one of the rights in the sample. For example, the test sample MC1 assemblage consisted of 14 lefts and 14 rights leading to 196 potential matches. Thirteen of these potential matches were known pairs and is the number of actual MC1 matches in the sample. Therefore, two MC1s, one left and one right, did not have a pair present. Appendix C also shows the number of potential and actual matches for each measurement, or combination of measurements, used for pair-matching. The values are different than the sample potential and actual values because these are considered according to the actual variables that are being tested. For example, out of the 196 potential left-right MC1 pairs in the whole sample, only 121 of these possibilities could be compared using the length measurement alone since pathology or taphonomy on some of the elements precluded taking that particular measurement. Of the sample's 13 actual matches, only 10 of the actual matches could be tested using length.

Appendix D shows the values that are needed to test potential matches in a commingled assemblage using the Byrd (2008) and Byrd and LeGarde (2014) method. These data include the standard deviation of *D* and the sample size of the original sample that dictates degrees of freedom in the *t*-test. Table 7 summarizes the results from applying the method to the test sample, including the percent of variable potential matches that were correctly excluded, the percent of sample potential matches that were correctly excluded, and the percent of variable actual pairs that were falsely segregated using the method. The table includes the proportion of exclusions for both actual

Table 7 Percent exclusions for osteometric pair-matching in test sample using Byrd (2008) and Byrd and LeGarde (2014).

	Variable % Excluded	Sample % Excluded	Variable % False Exclusions	Variable % Excluded	Sample % Excluded	Variable % False Exclusions
	Length (LEN)			Maximum Length (MXL)		
MC1	72.7	44.9	0.0	71.8	40.3	0.0
MC2	84.7	79.0	0.0	84.2	78.6	0.0
MC3	68.7	63.8	0.0	68.1	63.3	0.0
MC4	73.5	73.5	7.1	75.0	75.0	7.1
MC5	78.0	78.0	15.4	79.1	79.1	7.7
MT1	72.8	72.8	0.0	78.1	78.1	7.7
MT2	79.5	69.6	0.0	81.0	70.8	9.1
MT3	82.6	67.1	0.0	82.1	66.7	0.0
MT4	79.7	59.8	0.0	79.7	59.8	0.0
MT5	81.0	65.8	0.0	82.1	66.7	0.0
	Interarticular Length (IAL)			Head Width (HW)		
MC1	71.4	66.3	0.0	67.3	57.7	16.7
MC2	83.7	78.1	0.0	67.9	63.3	23.1
MC3	73.5	73.5	0.0	65.8	65.8	15.4
MC4	76.0	76.0	7.1	50.5	50.5	0.0
MC5	75.8	75.8	0.0	40.1	40.1	0.0
MT1	73.2	73.2	0.0	68.2	58.5	18.2
MT2	80.0	70.0	0.0	51.1	47.9	8.3
MT3	83.6	67.9	0.0	47.2	35.4	10.0
MT4	76.6	57.4	0.0	44.6	34.0	0.0
MT5	70.7	66.3	0.0	44.5	33.8	16.7
	Base Width (BW)			LEN+MXL+IAL+HW+BW		
MC1	59.6	47.4	9.1	83.8	42.3	10.0
MC2	60.2	56.2	7.7	86.2	80.5	7.7
MC3	45.1	41.8	23.1	72.8	62.8	0.0
MC4	59.3	55.1	15.4	73.6	68.4	15.4
MC5	45.1	45.1	0.0	79.1	79.1	0.0
MT1	58.9	58.9	0.0	72.6	67.4	0.0
MT2	53.8	50.4	0.0	79.0	69.2	0.0
MT3	34.7	32.5	0.0	79.2	55.4	10.0
MT4	32.9	30.9	0.0	78.2	50.4	0.0
MT5	46.3	46.3	0.0	83.3	54.2	0.0

	Variable % Excluded	Sample % Excluded	Variable % False Exclusions	Variable % Excluded	Sample % Excluded	Variable % False Exclusions
	IAL+HW+BW			HW+BW		
MC1	72.3	48.0	10.0	66.2	43.9	20.0
MC2	80.1	74.8	7.7	65.8	61.4	7.7
MC3	74.2	68.9	7.7	61.0	56.6	15.4
MC4	71.4	66.3	15.4	66.5	61.7	7.7
MC5	73.1	73.1	0.0	51.1	51.1	0.0
MT1	77.6	66.5	0.0	66.7	57.1	0.0
MT2	77.1	67.5	0.0	55.7	48.8	0.0
MT3	76.2	53.3	0.0	49.4	34.6	0.0
MT4	74.5	48.0	0.0	46.7	32.8	0.0
MT5	80.8	61.3	0.0	73.6	55.8	9.1

comparisons by variable and for the total sample because the former allows assessments of relative exclusionary power without other factors (taphonomy, pathology) impacting the outcome, but the latter is what would be considered in an actual commingled assemblage. The Byrd (2008) and Byrd and LeGarde (2014) method correctly excluded 68.7-84.7% of length comparisons, 68.1-84.2% of maximum length comparisons, 70.7-83.7% of interarticular length comparisons, 40.1-68.2% of head width comparisons, 32.9-60.2% of base width comparisons, 72.6-86.2% of length+maximum length+interarticular length+head width+base width comparisons, 71.4-80.8% of interarticular length+head width+base width comparisons, and 49.4-73.6% of head width+base width comparisons.

The information to be used in osteometric tests of MCs and MTs using the Lynch et al. (2018) method can be viewed in Appendix D, including sample size, average *D*, and standard deviation of *D* from the original sample. This method properly excluded 68.7-82.7% of valid comparisons for length, 67.6-82.1% for maximum length, 68.0-83.7% for interarticular length, 34.1-64.6% for head width, 25.0-61.8% for base width, 74.6-89.8% for all measurements combined, 77.7-89.8% for interarticular length, head width, and base width combined, and 46.2-76.9% for head width and base width combined (Table 8).

The framework for the Thomas et al. (2013) method can be found in Appendix D. For each measurement, the data include the number of elements in the original sample used to derive the standards and the *M* statistic's 95th percentile and maximum value from the original sample that could be used in an actual osteometric sorting test. In applying the method to the test sample using the 95th percentile, it correctly segregated 65.9-83.6% of length comparisons, 66.5-83.6% of maximum length comparisons, 67.6-83.6% of interarticular length comparisons, 33.5-74.2% of head width comparisons, and 30.7-66.7% of base width comparisons (Table 9).

The data that can be used for the Vickers et al. (2015) method is available in Appendix D. For each measurement combination, the maximum value for the absolute value of right-left differences, to be used in actual tests, and the sample size are listed. Testing the method on the test sample (Table 10) led to 37.1-77.6% of potential matches rejected using the length variable, 50.5-80.6% using maximum length, 30.8-75.7% using interarticular length, 12.6-61.5% using head width, 4.4-55.1% using base width, 44.6-82.7% using all measurements, 45.6-70.3% using interarticular length+head width+base width, and 9.0-67.0% using head width+base width.

Figures 3 through 10 provide visual comparisons of percent exclusions by variable for all four osteometric pair-matching methods. For single measurements, the Byrd (2008) and Byrd and LeGarde (2014) procedure tended to lead to more exclusions,

Table 8 Percent exclusions for osteometric pair-matching in test sample using Lynch et al. (2018)

	Variable % Excluded	Sample % Excluded	Variable % False Exclusions	Variable % Excluded	Sample % Excluded	Variable % False Exclusions
	Length (LEN)			**Maximum Length (MXL)**		
MC1	70.2	43.4	0.0	70.9	39.8	0.0
MC2	82.7	77.1	0.0	82.1	76.7	0.0
MC3	68.7	63.8	0.0	67.6	62.8	0.0
MC4	71.9	71.9	0.0	72.4	72.4	0.0
MC5	74.2	74.2	0.0	76.9	76.9	0.0
MT1	73.7	73.7	0.0	78.6	78.6	7.7
MT2	77.1	67.5	0.0	79.5	69.6	0.0
MT3	82.1	66.7	0.0	81.5	66.3	0.0
MT4	79.2	59.4	0.0	79.7	59.8	0.0
MT5	79.0	64.2	0.0	81.5	66.3	0.0
	Interarticular Length (IAL)			**Head Width (HW)**		
MC1	70.9	65.8	0.0	61.3	52.6	16.7
MC2	83.7	78.1	0.0	61.7	57.6	15.4
MC3	71.4	71.4	0.0	51.5	51.5	7.7
MC4	74.5	74.5	7.1	45.9	45.9	0.0
MC5	75.3	75.3	7.7	34.1	34.1	0.0
MT1	73.7	73.7	0.0	64.6	55.4	18.2
MT2	76.2	66.7	0.0	48.0	45.0	8.3
MT3	82.1	66.7	0.0	42.8	32.1	10.0
MT4	76.6	57.4	0.0	37.9	28.9	0.0
MT5	68.0	63.8	0.0	44.5	33.8	16.7
	Base Width (BW)			**LEN+MXL+IAL+HW+BW**		
MC1	51.9	41.3	0.0	81.8	41.3	0.0
MC2	60.2	56.2	7.7	89.8	83.8	7.7
MC3	44.5	41.3	23.1	74.6	64.3	0.0
MC4	53.3	49.5	7.7	81.9	76.0	7.7
MC5	42.3	42.3	0.0	81.3	81.3	7.7
MT1	58.0	58.0	0.0	75.5	70.1	0.0
MT2	61.8	57.9	8.3	85.7	75.0	0.0
MT3	36.0	33.8	0.0	83.9	58.8	0.0
MT4	25.0	23.4	0.0	80.6	52.0	0.0
MT5	39.6	39.6	0.0	88.5	57.5	0.0

	Variable % Excluded	Sample % Excluded	Variable % False Exclusions	Variable % Excluded	Sample % Excluded	Variable % False Exclusions
	IAL+HW+BW			HW+BW		
MC1	77.7	51.5	0.0	63.1	41.8	10.0
MC2	89.8	83.8	7.7	60.7	56.7	7.7
MC3	84.6	78.6	15.4	55.5	51.5	23.1
MC4	84.1	78.1	7.7	67.0	62.2	7.7
MC5	78.6	78.6	7.7	46.2	46.2	0.0
MT1	83.3	71.4	0.0	66.1	56.7	0.0
MT2	88.6	77.5	0.0	66.2	57.9	9.1
MT3	82.1	57.5	0.0	48.8	34.2	0.0
MT4	81.8	52.7	0.0	49.4	34.8	0.0
MT5	81.9	62.1	0.0	76.9	58.3	0.0

but marginally when compared with Lynch et al. (2018) and Thomas et al. (2013). For the two variables combining lengths and widths (LEN+MXL+IAL+HW+BW and IAL+HW+BW), Lynch et al. (2018) performed best. The Vickers et al. (2015) method consistently performed relatively poorly.

Osteometric Joint Articulation

Appendix D summarizes the data derived from the original sample that can be used to perform osteometric articulation tests, including sample size, average *D*, and the standard deviation of *D*. Appendix C summarizes the number of potential and actual matches for each type of articulating pair within the test sample, as well as the number of potential and actual matches by variable. Results in Table 11 from the test sample commingling simulation show that this method of osteometric sorting correctly excluded between 6.3% and 51.0% of the MCs and MTs that could be compared using the facets. The tests performed much better for the MCs than they did for the MTs, but, within each

Table 9 Percent exclusions for osteometric pair-matching in test sample using Thomas et al. (2013).

	Variable % Excluded	Sample % Excluded	Variable % False Exclusions		Variable % Excluded	Sample % Excluded	Variable % False Exclusions
MC1LEN	66.9	41.3	0.0	MT1LEN	71.9	71.9	0.0
MC1MXL	67.3	37.8	0.0	MT1MXL	79.9	79.9	7.7
MC1IAL	67.6	62.8	0.0	MT1IAL	75.4	75.4	0.0
MC1HW	56.5	48.5	8.3	MT1HW	67.7	58.0	18.2
MC1BW	55.1	43.9	0.0	MT1BW	56.7	56.7	0.0
MC2LEN	82.1	76.7	0.0	MT2LEN	77.6	67.9	0.0
MC2MXL	81.6	76.2	0.0	MT2MXL	76.7	67.1	0.0
MC2IAL	82.7	77.1	0.0	MT2IAL	78.6	68.8	0.0
MC2HW	69.4	64.8	15.4	MT2HW	51.1	47.9	16.7
MC2BW	62.8	58.6	7.7	MT2BW	66.7	62.5	8.3
MC3LEN	65.9	61.2	0.0	MT3LEN	83.6	67.9	0.0
MC3MXL	66.5	61.7	0.0	MT3MXL	83.6	67.9	9.1
MC3IAL	69.9	69.9	0.0	MT3IAL	83.6	67.9	0.0
MC3HW	57.1	57.1	7.7	MT3HW	46.7	35.0	10.0
MC3BW	39.0	36.2	23.1	MT3BW	30.7	28.8	0.0
MC4LEN	68.9	68.9	0.0	MT4LEN	79.2	59.4	0.0
MC4MXL	73.5	73.5	0.0	MT4MXL	78.1	58.6	0.0
MC4IAL	70.4	70.4	0.0	MT4IAL	72.9	54.7	0.0
MC4HW	41.8	41.8	0.0	MT4HW	33.8	25.8	0.0
MC4BW	58.2	54.1	7.7	MT4BW	31.3	29.3	0.0
MC5LEN	74.2	74.2	15.4	MT5LEN	81.5	66.3	0.0
MC5MXL	77.5	77.5	7.7	MT5MXL	80.0	65.0	0.0
MC5IAL	74.2	74.2	7.7	MT5IAL	70.2	65.8	0.0
MC5HW	33.5	33.5	0.0	MT5HW	74.2	56.3	0.0
MC5BW	39.6	39.6	0.0	MT5BW	35.8	35.8	18.2

element group, there did appear to be an association between strength of correlation and power in osteometric sorting.

Table 10 Percent exclusions for osteometric pair-matching in test sample using Vickers et al. (2015).

	Variable % Excluded	Sample % Excluded	Variable % False Exclusions	Variable % Excluded	Sample % Excluded	Variable % False Exclusions
	Length (LEN)			**Maximum Length (MXL)**		
MC1	62.8	38.8	0.0	66.4	37.2	0.0
MC2	77.0	71.9	0.0	80.6	75.2	0.0
MC3	50.5	46.9	0.0	50.5	46.9	0.0
MC4	66.3	66.3	0.0	66.8	66.8	0.0
MC5	71.4	71.4	0.0	69.2	69.2	0.0
MT1	37.1	37.1	0.0	54.9	54.9	0.0
MT2	75.2	65.8	0.0	74.8	65.4	0.0
MT3	60.0	48.8	0.0	63.6	51.7	0.0
MT4	77.6	58.2	0.0	77.6	58.2	0.0
MT5	76.9	62.5	0.0	73.8	60.0	0.0
	Interarticular Length (IAL)			**Head Width (HW)**		
MC1	62.1	57.7	0.0	44.6	38.3	0.0
MC2	70.4	65.7	0.0	34.2	31.9	0.0
MC3	69.4	69.4	0.0	53.1	53.1	7.7
MC4	65.8	65.8	0.0	17.3	17.3	0.0
MC5	64.3	64.3	0.0	12.6	12.6	0.0
MT1	30.8	30.8	0.0	61.5	52.7	18.2
MT2	75.7	66.3	0.0	33.3	31.3	0.0
MT3	61.5	50.0	0.0	30.6	22.9	0.0
MT4	69.8	52.3	0.0	28.7	21.9	0.0
MT5	50.2	47.1	0.0	29.7	22.5	9.1
	Base Width (BW)			**LEN+MXL+IAL+HW+BW**		
MC1	39.0	36.2	0.0	44.6	38.3	0.0
MC2	55.1	51.4	7.7	72.4	67.6	0.0
MC3	11.0	10.2	0.0	57.4	49.5	0.0
MC4	51.6	48.0	7.7	65.4	60.7	0.0
MC5	22.5	22.5	0.0	61.5	61.5	0.0
MT1	50.9	50.9	0.0	50.0	46.4	0.0
MT2	4.4	4.2	0.0	76.2	66.7	0.0
MT3	11.6	10.8	0.0	66.7	46.7	0.0
MT4	5.8	5.5	0.0	76.4	49.2	0.0
MT5	35.4	35.4	0.0	82.7	53.8	0.0

	Variable % Excluded	Sample % Excluded	Variable % False Exclusions	Variable % Excluded	Sample % Excluded	Variable % False Exclusions
	IAL+HW+BW			HW+BW		
MC1	45.6	42.3	0.0	43.5	37.2	0.0
MC2	65.3	61.0	0.0	46.4	43.3	7.7
MC3	67.0	62.2	0.0	36.3	33.7	0.0
MC4	64.3	59.7	0.0	48.4	44.9	8.3
MC5	54.4	54.4	0.0	28.6	28.6	0.0
MT1	63.5	54.5	0.0	58.9	50.4	0.0
MT2	58.6	51.3	0.0	9.0	7.9	0.0
MT3	58.9	41.3	0.0	20.8	14.6	0.0
MT4	69.7	44.9	0.0	15.6	10.9	0.0
MT5	70.3	53.3	0.0	67.0	50.8	9.1

Table 11 Percent exclusions for osteometric articulations in test sample.

	Variable % Excluded	Sample % Excluded	Variable % False Exclusions
LMC2-LMC3	49.0	45.7	0.0
LMC3-LMC4	41.1	35.2	8.3
LMC4-LMC5	29.6	27.5	0.0
RMC2-RMC3	50.5	46.9	0.0
RMC3-RMC4	51.0	51.0	0.0
RMC4-RMC5	42.3	42.3	7.1
LMT2-LMT3	18.9	15.4	0.0
LMT3-LMT4	6.3	6.3	0.0
LMT4-LMT5	27.1	23.8	15.4
RMT2-RMT3	7.1	5.8	0.0
RMT3-RMT4	22.5	21.1	0.0
RMT4-RMT5	18.4	18.4	0.0

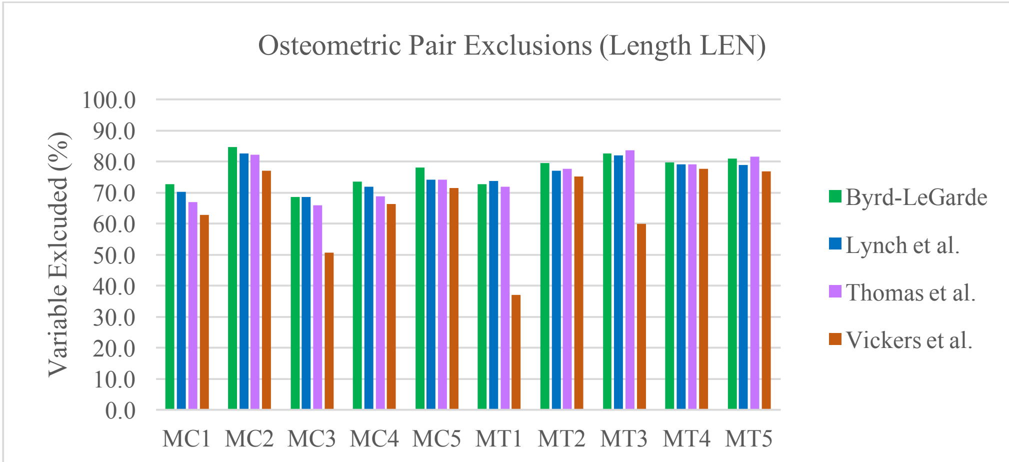

Figure 3 Percent exclusions by variable for test sample pair-matching (LEN).

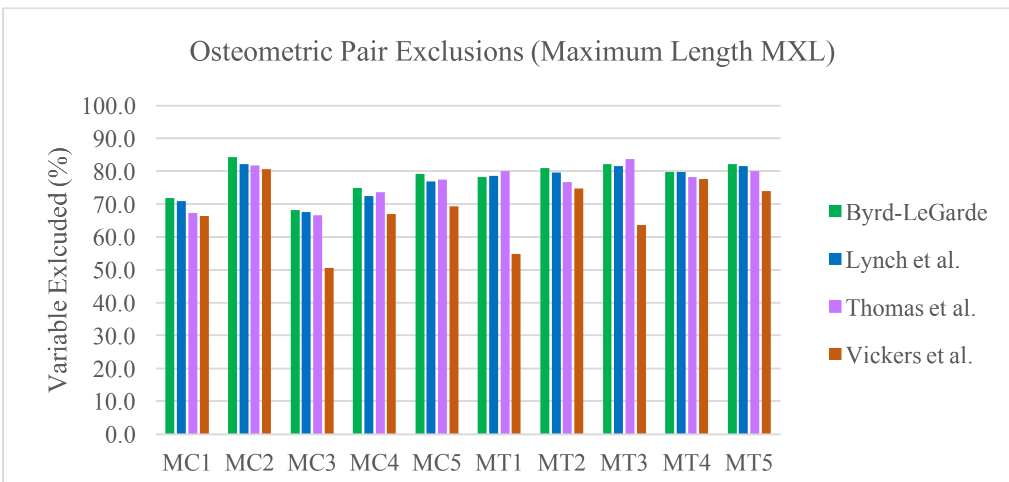

Figure 4 Percent exclusions by variable for test sample pair-matching (MXL).

<u>Osteometric Comparisons of Other Regions</u>

Data needed for osteometric comparisons of the MCs and MTs to the humeri and femora, including regression formulae, sample sizes, *r*, the standard errors of the equations, and means and standard deviations for each independent variable, are available

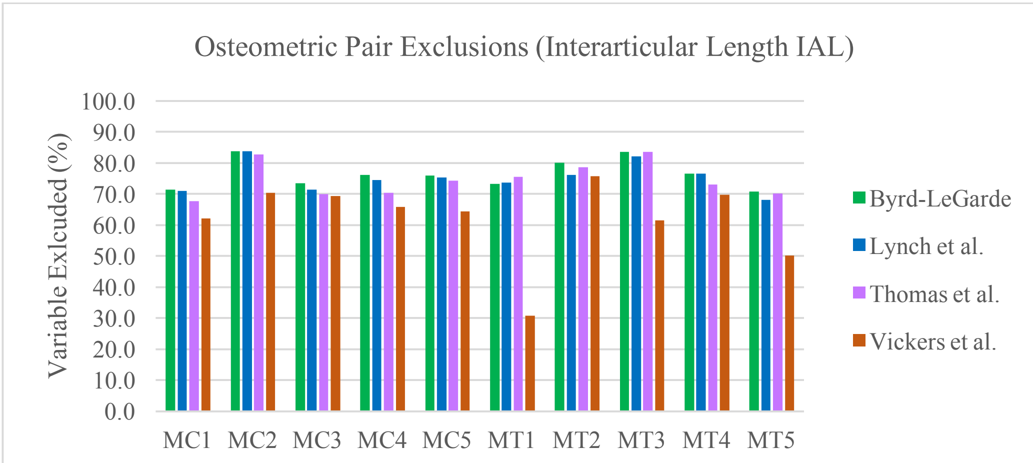

Figure 5 Percent exclusions by variable for test sample pair-matching (IAL).

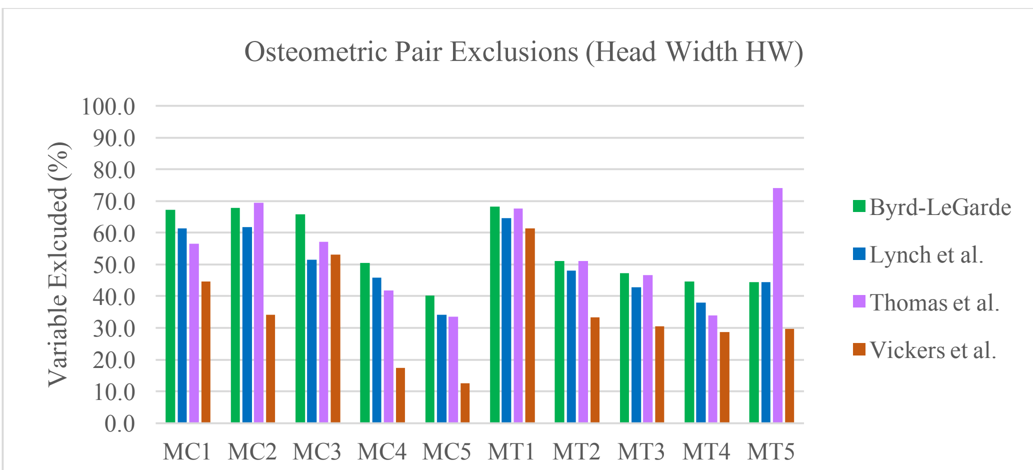

Figure 6 Percent exclusions by variable for test sample pair-matching (HW).

in Appendix D. For the three equations that were tested on the holdout sample, which included the ones with the lowest and highest values for *r*, between 22.1% and 36.7% of valid comparisons were excluded and no true matches were falsely rejected (Table 12). Formulae with higher *r* values did show more sorting power, although ideally this trend

Table 12 Percent exclusions for MC/MT to humerus/femur comparisons in test sample.

Comparison	Variable % Exclusions	Sample % Exclusions	Variable % False Exclusions
MC4.1-HUM.2	30.4	26.6	0.0
MT4.1-HUM.3	22.1	15.8	0.0
MT2.1-FEM.1	36.7	26.8	0.0

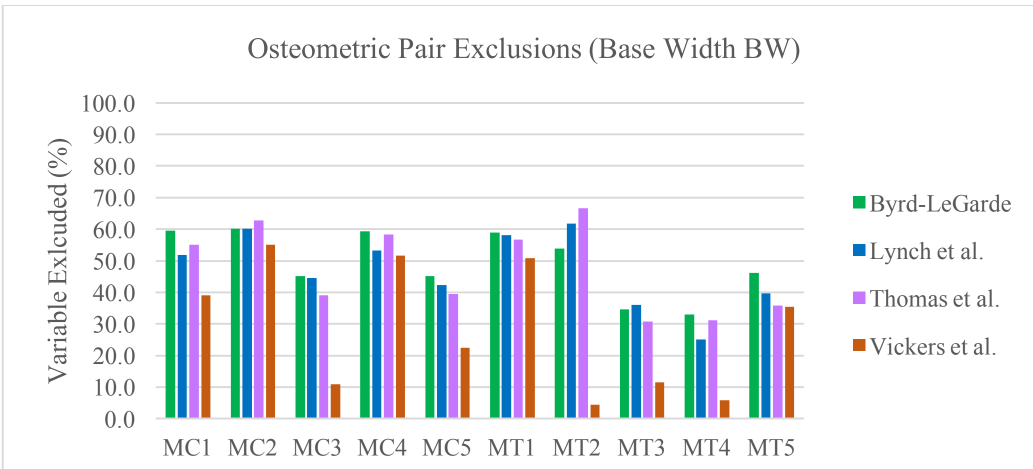

Figure 7 Percent exclusions by variable for test sample pair-matching (BW).

would be tested with all equations rather than just three. Usually, regression equations incorporating all three measurements for the humeri and femora had slightly higher *r* values than those equations using just head diameter or epicondylar breadth.

Analysis of Point San Jose Collection

The osteometric sorting frameworks that were developed as described above were then used to assist with sorting the commingled PSJ collection. Hand and foot bones were among the most frequent elements, so this project focused solely on the

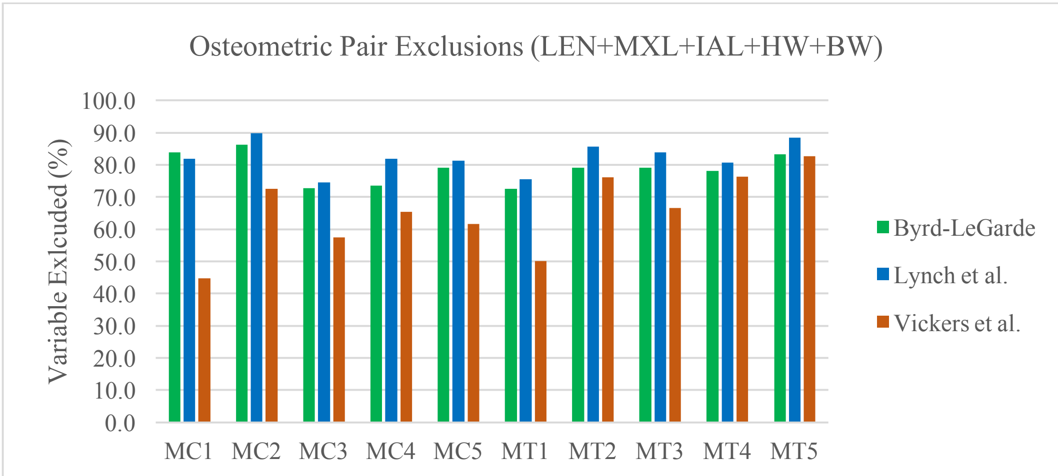

Figure 8 Percent exclusions by variable for test sample pair-matching (LEN+MXL+IAL+HW+BW).

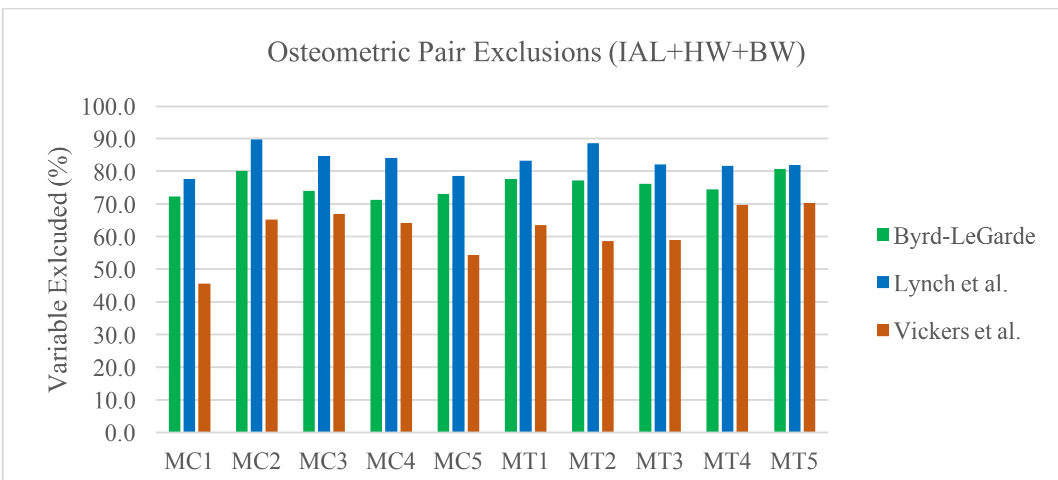

Figure 9 Percent exclusions by variable for test sample pair-matching (IAL+HW+BW).

metacarpals and metatarsals. For pair-matching, the Lynch et al. (2018) method was chosen out of the four approaches due to its relatively low number of false exclusions without sacrificing exclusionary power. The Byrd (2008) and Byrd and LeGarde (2014) procedures were used for osteometric articulations and comparisons of other regions. For

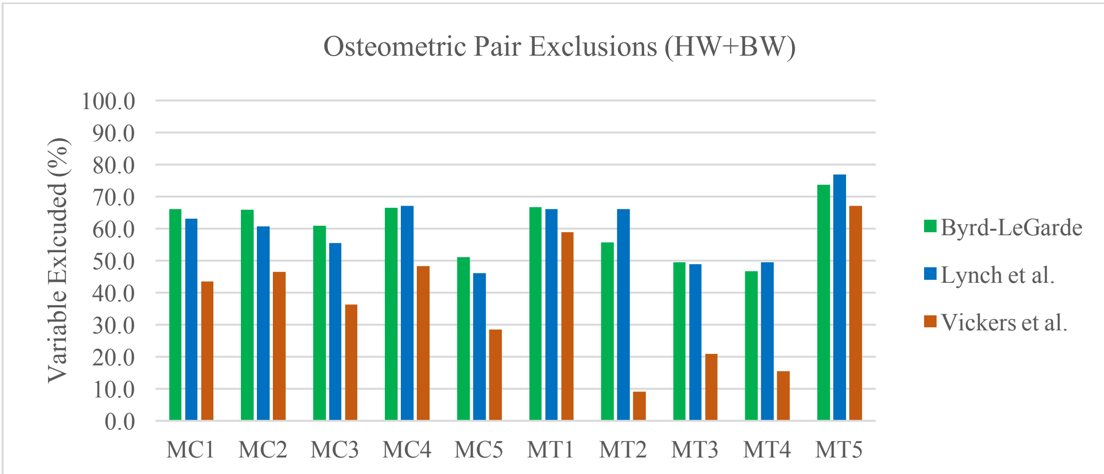

Figure 10 Percent exclusions by variable for test sample pair-matching (HW+BW).

pair-matching and comparisons to other regions, where multiple frameworks were available using different variables, variables with high power and low levels of inaccurate exclusions on the test sample were prioritized when available. In pair-matching with Lynch et al.'s (2018) method, that meant the variable combining all measurements was used when possible, followed by IAL+HW+BW, length alone, maximum length alone, interarticular length alone, HW+BW, base width alone, and finally head width alone if no other measurements were obtainable. In osteometric comparisons to the humerus and femur, the formula with the highest *r* for the dimensions present was selected. Visual assessment of potential pair-matches and articulations was used in conjunction with osteometrics, and pXRF data was used to eliminate some potential matches.

Figures 11 through 14 display the proportion of potential matches in the PSJ Collection that could be excluded using osteometric sorting for the MCs and MTs. For osteometric pair-matching, 18.5-73.6% of potential pairs were segregated, with the

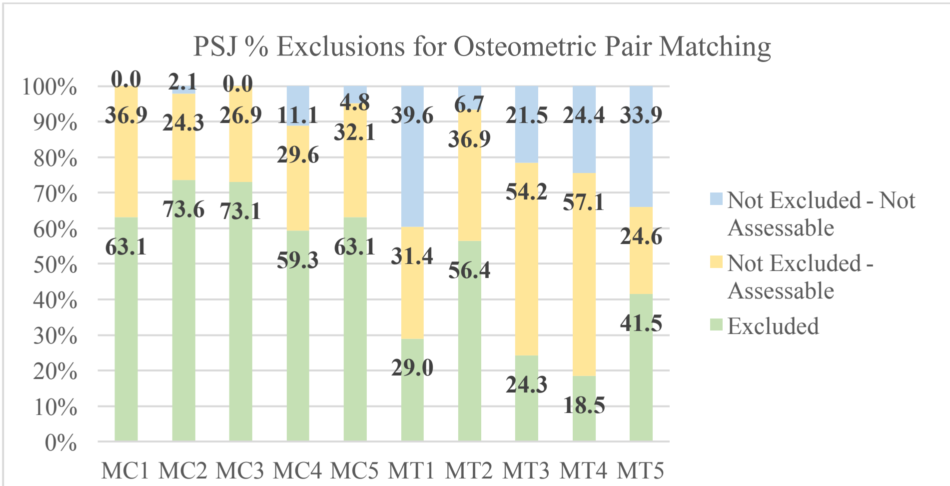

Figure 11 Percent exclusions for pair-matching in PSJ.

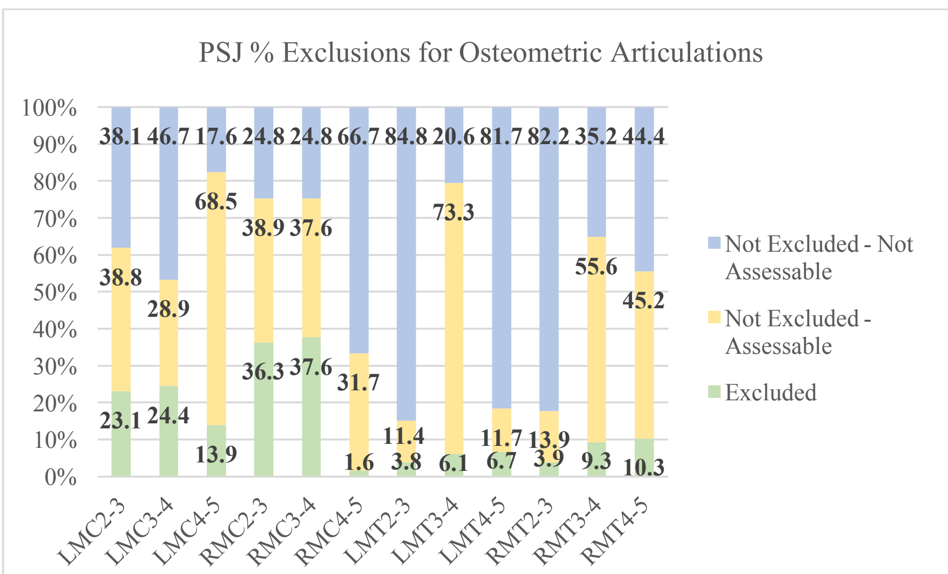

Figure 12 Percent exclusions for osteometric articulations in PSJ.

MCs having the most segregations. For osteometric articulations, the amount of exclusions ranged from 1.6% for RMC4-RMC5 to 37.6% for RMC2-RMC3. Osteometric comparisons of the MCs and MTs to other regions led to the segregation of 1.4 to 22.7% of potential matches for the humeri, and 0.5 to 23.2% for the femora.

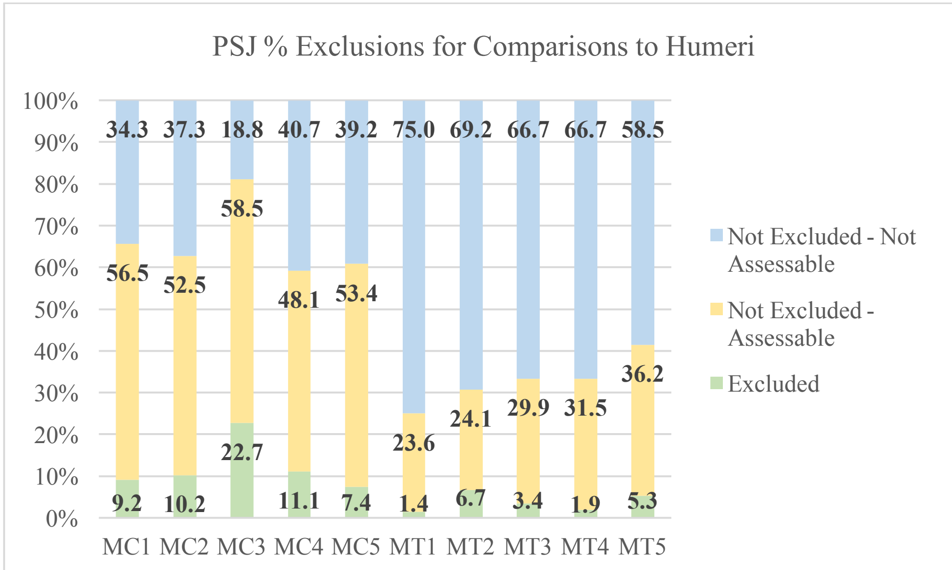

Figure 13 Percent exclusions for osteometric comparisons to humeri in PSJ.

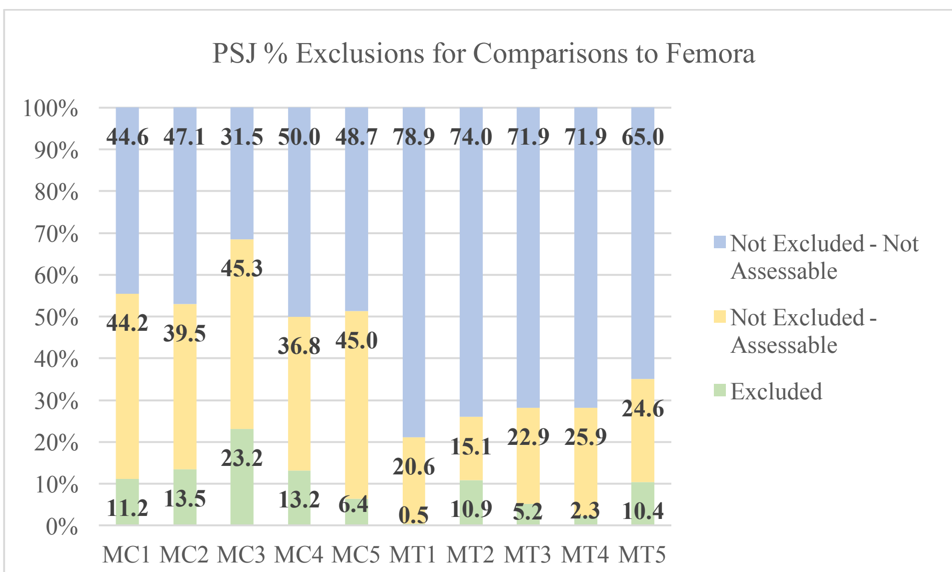

Figure 14 Percent exclusions for osteometric comparisons to femora in PSJ.

Comparisons with the femur tended to lead to more exclusions than comparisons with the humerus, and the MCs had more exclusions than the MTs. Visual methods largely confirmed the osteometric results and allowed affirmative matches to be made. pXRF data was not used often. It did help exclude some potential pairs or humeral and femoral matches for the MCs, but there were not many MC groups with at least four elements with which to do comparisons. Sorting efforts for the MTs did not lead to enough groups of associated elements for the pXRF confidence interval system to be useful in sorting them. Figure 15 shows an example of the use of pXRF for this thesis. Individuals A, B, and C were humeri that were not osteometrically excluded from matching a group of metacarpals (Individual 4). Individual C's elemental concentrations fell far outside Individual 4's confidence intervals for multiple elements, so it was considered too dissimilar to match. Most comparisons to the humerus and femur did not have enough osteometric exclusions to be particularly useful.

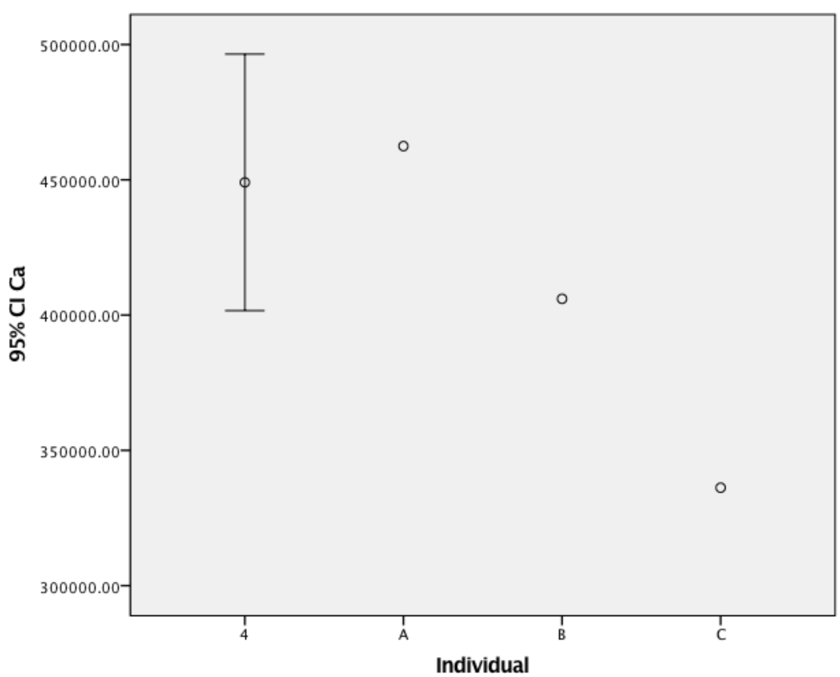

Figure 15 Example of pXRF confidence intervals excluding (Individ. C) and not excluding (A and B) potential humerus matches to MC group (4). Other elements also suggested exclusion but Ca is used as an example.

All combined methods led to 29 MC and 31 MT pairs, at least 27 unpaired MCs and 14 unpaired MTs, and 32 MCs and 60 MTs that were unable to be confidently sorted. The unpaired elements were not always identified, but a minimum was estimated based on the number of lefts and rights that were present that could still potentially match after sorting efforts were completed in addition to elements shown to be unpaired. For articulations, only twelve MC2-3, nine MC3-4, three MC4-5, nine MT2-3, nine MT3-4, and ten MT4-5 matches were made, leaving most MCs and MTs unsorted for articulations. Five of the 60 matched pairs, or about 8%, were considered strong visual matches but would have been osteometrically excluded, and two of 52, or about 4%, were strong visual articulations but osteometric exclusions. These percentages give an approximate false rejection rate, although these figures could be lower or higher depending on how many of the unsorted elements do or do not have an actual match present. While osteometrics and pXRF helped exclude some potential humerus and femur matches, none were shown to be positively matched or unmatched, and visual clues were not useful for evaluating potential error.

Table 13 shows the MNI that was calculated from each MC without sorting, based on the assumption that all left and right elements belong together, and the MNI from each MC after using all methods of sorting. Sorting increased the MNI for four of five MC rays. While there were some confirmed paired and non-paired elements for the MTs, there were not enough to increase the MNI for any of the elements like with the MCs, and MC2 ended up with a larger MNI than any of the MTs. The overall MNI for the MCs and MTs after sorting is 20, calculated from the MC2.

Table 13 MNI for each MC before and after sorting.

	Original MNI	MNI Sorted
MC1	13	14
MC2	18	20
MC3	13	16
MC4	9	11
MC5	12	12

Table 14 shows the minimum representation of each individual based on known matches and segregations of the metacarpals. Only MCs two through five are included since MC1 does not articulate with MC2 and therefore was not compared osteometrically. The figure does not show all the known pairs and articulations for the third, fourth, or fifth MCs because it was built from MC2, which had the largest MNI, and they could not always be confidently associated with or segregated from the MC2s. There could, of course, be more individuals represented by MCs in the assemblage that could not be isolated, or there could be individuals that are represented by other elements besides metacarpals.

Summary

Most hypotheses in this study were accepted, but the hypothesis of no significant size differences for left and right MCs was rejected due to larger right sides for many measurements. Overall, the osteometric sorting methods showed moderate to strong power when applied to the test sample. Most variables for sorting had low numbers of false rejections, but needs to be tested on a larger sample. The methods were helpful for sorting the MCs in the PSJ Collection, but it was not as useful for sorting the MTs.

Table 14 Minimum representation of MCs for each individual in PSJ. "•" indicates presence. "x" indicates absence. Blank indicates indeterminate.

	RMC2	RMC3	RMC4	RMC5	LMC5	LMC4	LMC3	LMC2
Individual 1	•	•	•	•	x	x	x	x
Individual 2	•	•					•	•
Individual 3	•	•	•			•	x	•
Individual 4	•	•	•			x	x	x
Individual 5	•	•	•			•	x	•
Individual 6	•	•	•			x	x	•
Individual 7	•	•					•	•
Individual 8	•	•					x	x
Individual 9	•	x					x	•
Individual 10	x	x	•	•	•	•	•	•
Individual 11	•	x				•	•	•
Individual 12	•							
Individual 13	•	•					•	•
Individual 14	•	•					•	•
Individual 15	•							x
Individual 16	•	x					x	•
Individual 17	•							
Individual 18	•							•
Individual 19	•							
Individual 20	x	x					•	•

CHAPTER VI

DISCUSSION

Introduction

This chapter will discuss the results for the various tests performed in this study. The measurements, methods, and overall utility of sorting MCs and MTs will be evaluated and contextualized with prior research. Additionally, there will be a discussion on how the results from osteometric sorting of MCs and MTs in the Point San Jose case study helped contribute to the analysis of the assemblage.

Measurement Error

Overall, most of the measurements used in this study showed high intra-observer repeatability through their low percent TEM and high R value, but the inter-observer results were more mixed. A majority of the measurements with high error for both were facet length measurements. This was not too surprising because the facets are small measurements. Prior studies have shown that small measurements tend to decrease precision because the same magnitude of error (measured by TEM) has a bigger relative impact (measured by %TEM) on smaller dimensions than larger ones, and reliability (measured by R) is often correlated with size, with smaller measurements showing less reliability (Jamison and Ward 1993). Besides size, factors such as poor measurement definitions, lack of reliable landmarks, and inexperience can increase error (Jamison and Ward 1993). In this case, only researchers with in-depth knowledge of MC and MT articulations could perform the measurements because some of the elements had facets for carpals and tarsals that could easily be mistaken as part of the MC/MT facets. For example, the lateral facets on MT2 usually only have a slight ridge separating the articular regions for MT3 and the cuneiform and could easily be overlooked if one did not know to search for it. Even still, facets were variable and could be difficult to delineate, increasing the likelihood of measurement error.

The three lengths showed the lowest %TEM and the highest R for both intra- and inter-observer error, with the maximum length usually outperforming the other two. Of the lengths, interarticular had the most error, but not so much as to render it unhelpful in studies of asymmetry or osteometric sorting. Most of the head widths and base widths showed low intra-observer error, but showed mixed results for inter-observer error. While overall the error in this research seems to be lower than the error for the same or similar measurements in the study by Case et al. (2015), shown by comparing median percent difference for caliper measurements, there tended to be similar results in terms of low error for lengths but mixed results for widths.

Measurements with higher levels of intraobserver error than ideal did not produce more false rejections, but did tend to lead to less power in sorting. Those with high interobserver error would not impact the results of analyzing the PSJ collection in this study. All the measurements, for both developing the osteometric methods and applying them to PSJ, were taken by the author. However, outside researchers that may be looking to apply these methods to a commingled assemblage should be aware of which measurements had between-researcher discrepancies that could impact the results of their tests. In this study, the independent observer had little instruction in the measurement definitions prior to participating in the research. Prior studies show that experience level can impact the amount TEM (Perini et al. 2005), so it is unknown if measurements with low intraobserver error but high interobserver error represent poor definitions or just ones that require more experience. To use some of the measurements in this study in practical applications, future research would need to focus on improving measurement reliability, or practitioners would need much training and practice prior to research.

Osteometric Pair-Matching

The first hypothesis in this study was that there would be left-right symmetry within individuals shown by a lack of statistically significant differences between left and right elements. The results reveal a mixture of rejecting and failing to reject the null hypothesis of no difference.

For the MCs, about half of the dimensions, a minimum of one measurement per MC, showed statistical differences in both males and females, though the means were usually less than one millimeter apart, leading to the rejection of the hypothesis of no differences for the hands. Side differences may be related to handedness, with right dominance leading to increased biomechanical loading and subsequent increased stress on the right upper limb. Handedness information was available for only some of the individuals in the UNM sample, so the effect of handedness could not be examined in this particular sample; however, some noticeable trends can be contextualized with prior research. All the significantly different measurements, and almost all the nonsignificant ones, showed a larger measurement mean for the right MC compared with the left MC. This finding is fairly consistent with previous studies that examined hand asymmetry since many noted a tendency for larger dimensions or increased density in the right compared to the left, for both significant and non-significant differences, in osteological or anthropometric measurements of the hand (Cashmore 2009; Kimura 1990; Krishan and Sharma 2007; Kušec et al. 1990; Lazenby et al. 2008; McLeod and Coupland 1992; Nathena et al. 2015; Özener 2010; Plato et al. 1980; Purves et al. 1994). Studies of other upper limb bones tend to also find right-favored asymmetry (Auerbach and Ruff 2006; Latimer and Lowrance 1965; Münter 1936; among others).

Some studies showed that a group of left-handed individuals did not have larger left elements in the upper limb, but rather showed practically no asymmetry while a right-handed group and even an ambidextrous group showed pronounced asymmetry with larger rights (Plato et al. 1980; Purves et al. 1994). The studies suggest two explanations for this observation. It is possible that left-handed individuals used both their left and right hands often due to a natural inclination for their left hand but a cultural preference for right dominance, which led to decreased asymmetry. They also suggest there may be a biological component that leads populations to have inherently larger right hands but an environmental component (handedness) that augments asymmetry in right-handed individuals and mitigates asymmetry in left-handed individuals. Other studies find left-handed individuals have larger left upper limb bones, but not to the same extent as right-handed directional asymmetry (Özener 2010; Roy et al. 1994). Either way, the fact that many metacarpal dimensions in the current study population are larger in the right hand seems to be supported by other research identifying environmental and possibly biological factors leading to right directional asymmetry.

There were some sex differences in the asymmetry of the MCs. Females tended to show asymmetry in lengths and some widths of elements, while males tended to show asymmetry in the widths but not too often in the lengths. Similar trends, with females displaying more length asymmetry and males displaying more breadth asymmetry, have been noted for the humerus and radius (Auerbach and Ruff 2006; Münter 1936).

For the MTs, only two dimensions for males (MT4IAL, MT4BW) and seven dimensions for females (MT1LEN, MT1MXL, MT1IAL, MT1HW, MT1BW, MT4IAL, MT5MEDF) showed statistically significant differences. Overall, then, the hypothesis of left-right symmetry is accepted for the feet, except for the first metatarsal in females for which the hypothesis should be rejected. There is variation among significantly different dimensions in whether the mean for the left or right is larger, except for the MT1 in females which consistently has a higher mean for the left element. The significant differences between the means for the right and left MT1 for females is more surprising than the differences in dimensions of the hands and is more difficult to explain, especially since the magnitude of the difference in means is larger at up to 2.5 millimeters. This could be caused by a gendered activity putting more stress on the left foot in females but not in males. It is also possible that some individuals included in the sample had some sort of pathology or condition that increased asymmetry but it was not visually identifiable or included in the individuals' medical histories. There has also been some evidence that other lower limb elements exhibit "crossed symmetry," where the asymmetry in the lower limb is opposite what is seen in the upper limb, but these have seemingly not looked at metatarsals specifically, and the magnitude of asymmetry in the lower limb is generally less than that of the upper limb (Auerbach and Ruff 2006; Kanchan et al. 2008). It also seems strange that only one metatarsal was affected.

The previous studies that examined asymmetry of the feet were mixed, with some reporting no directional trends (Robling and Ubelaker 1997), some finding larger left (Mascie-Taylor et al. 1981) or right (Ewunonu et al. 2014; Gawlikowska et al. 2007; Krishan and Sharma 2007) dimensions, though not necessarily statistically significant, and others finding mixed results (Levy and Levy 1978; Mountrakis et al. 2010; Pomerantz and Harris 1980). Some found statistical differences whether it was for the right or left, but for some there was just a trend in directionality discussed. These studies all covered a wide range of demographics, so it is possible that a closer investigation of sex, age, ancestry, or cultural affiliation could reveal subtle patterns, but, unlike for the MCs, currently seem to show no consistent trend. What may be the most likely explanation for the females' MT1 asymmetry in the current research, due to the conflicting results between prior studies, is that there was some sort of sampling bias where females with high asymmetry of MT1 were included by random chance. The sample sizes of some of the tests were also somewhat small, with the sample size of female MT1 measurements not exceeding 35 and as low as 16, and could have led to the contradictory findings.

Despite the presence of asymmetry in some of the antimeres, all the osteometric pair-matching methods were successful in eliminating potential matches within the simulated commingled test sample to reduce the number of pairs that would need to be examined using alternative sorting methods. However, the accuracy and power of each of the measurements and methods varied.

Accuracy was assessed by comparing the proportion of excluded actual pairs and non-excluded actual pairs in the test sample. It is important to note that there was a small sample size, with only 9 to 14 actual matches available for each variable, so looking at the percentages can be misleading. One false exclusion for a single variable would lead to approximately 7-11% of true pairs being separated. Ideally, accuracy would be examined using a larger sample, but for this study the percentages could at least give an idea of how accurate the measurements and methods are comparatively. Within each method, head width, base width, and HW+BW led to the highest number of false exclusions and could potentially impact sorting applications. The highest accuracies were produced by the three single length measurements, although the two measurement combinations integrating lengths and widths also had low levels of mistaken rejections. For methodological comparisons, the Vickers et al. (2015) method was the most accurate, followed by the Lynch et al. (2018) method, the Thomas et al. (2013) method, and finally the Byrd (2008) and Byrd and LeGarde (2014) method.

The relative exclusionary power of each measurement and method was examined by comparing the percentage of known non-pairs that were properly excluded from the test sample. Within the Byrd (2008) and Byrd and LeGarde (2014) and Lynch et al. (2018) methods, the LEN+MXL+IAL+HW+BW and IAL+HW+BW combinations were the most powerful for sorting. In fact, using the Lynch et al. (2018) method and either of these two variables produced the most exclusionary power of any method in this study. However, with the Vickers et al. (2015) method, any of the length measurements by themselves led to the most segregations. Using the Thomas et al. method (2013), or any other method while comparing single measurements, lengths performed better than widths. Between the three length measurements, there was variation in which performed best, although interarticular length was least likely to be affected by pathology or taphonomy and therefore measureable more often.

Out of the four methods, the Vickers et al. (2015) method performed the worst. For all but one measurement (MC3HW) where it was second-to-last in performance, it had the lowest quantity of segregated pairs. The results from each of the other three methods were more complicated. When using the variables LEN+MXL+IAL+HW+BW or IAL+HW+BW, the Lynch et al. (2018) method outperformed the others. When only a single measurement was available, the Byrd (2008) and Byrd and LeGarde (2014) method tended to, but not always, exclude more potential matches. It was usually closely followed by the Lynch et al. (2018) and Thomas et al. (2013) methods, though which was more powerful between the two varied. The main exception to this was for comparisons of head width, where both the Byrd (2008) and Byrd and LeGarde (2014) and Thomas et al. (2013) methods consistently outperformed Lynch et al. (2018) and the difference in percentage of exclusions was pronounced rather than the marginal differences seen in other one-measurement comparisons.

The fact that Vickers et al. (2015) led to higher accuracies but lower power is unsurprising since the method, using the full range of left-right differences from the reference population, was developed with the understanding that decreasing the likelihood of falsely excluding an actual pair would also reduce actual exclusions. That the Lynch et al. (2018) method led to higher accuracy than the Byrd (2008) and Byrd and LeGarde (2014) method is also consistent with Lynch et al.'s (2018) paper and is likely due to fixing some of the shortcomings of the original method. As shown by the statistically significant differences between the left and right for many elements in this study, Byrd (2008) and Byrd and LeGarde's (2014) assumption of zero difference between pairs in the calculation of t is problematic, an issue that Lynch and colleagues (2018) addressed with their revision of the method. Also, by summing the absolute value of left-right differences, size information was not lost for variables combining multiple measurements if some had a mix or larger left and right dimension. In the study by Lynch and colleagues (2018), however, the new method consistently led to higher numbers of exclusions than the original method, regardless of which or how many measurements were used. It was surprising, then, that the Lynch et al. (2018) method did not perform best for comparisons using single measurements, although it did perform best for variables combining multiple measurements.

Osteometric Joint Articulations

The second hypothesis that was tested in this study was that the lengths of the medial and lateral facets where metapodials articulate are correlated. With the majority of articulating pairs showing strong correlations, and the rest showing statistically significant correlations even though they are not necessarily strong, the null hypothesis of no correlation could be rejected and the research hypothesis accepted. As discussed in regards to error, however, the osteometric sorting method could be problematic due to the variability of facets on certain elements and the high error for some measurements. The method was not very powerful, eliminating as little as 6.3% of the test sample potential matches, for LMT3-LMT4, and only eliminating 51.0% at its best, for RMC3-RMC4. Still, excluding even a small part of a large commingled collection could prove helpful in reassociating elements. It would likely be best, though, if future research investigated the utility of other measurements, such as lengths or base heights, that potentially have less error and more power.

Osteometric Comparisons of Other Regions

The final hypothesis that was tested in this research was that dimensions of the MCs and MTs are correlated with dimensions of other skeletal elements, specifically the humerus and femur. Results revealed moderate to strong correlations, all statistically significant, leading to the rejection of the null hypothesis of no relationship and the acceptance of the research hypothesis of size relationships between the MCs and MTs and other appendicular elements. Consistent with prior research (Byrd and Adams 2003), adding widths in addition to lengths for comparisons tended to have either no effect or a small positive effect on correlation strength. The osteometric sorting regression formulae developed to test whether MCs or MTs and humeri or femora could originate from a single individual were fairly successful, correctly segregating 22.1% of test sample potential matches with the equation with the lowest r and 36.7% with the highest. While not as powerful for sorting as the pair-matching methods, reducing potential matches in a commingled sample by approximately one-fifth to one-third could prove useful. The correlation coefficients for the equations in this study ranged from 0.628 to 0.888, while those of Byrd (2008) and Byrd and LeGarde's (2014) models comparing the humerus, radius, ulna, femur, and tibia ranged from 0.79 to 0.99. As expected then, comparisons of the MCs and MTs were less strong than other long bone correlations, but there is much overlap.

Analysis of Point San Jose Collection

Osteometric sorting, as well as some other methods to resolve commingling, were fairly successful in sorting the PSJ Collection. With a number of known matches and non-matches but still many unsorted elements, conclusions about context are limited. However, there are still some important considerations that PSJ sorting highlighted, and some interpretations of context that are possible.

Application of Osteometric Sorting to PSJ

In deciding which metric pair-matching method to use for sorting this assemblage, the Lynch et al. (2018) method seemed to be the most appropriate. Using multiple measurements, it was the most powerful. While Byrd (2008) and Byrd and LeGarde (2014) tended to perform better for a one measurement threshold, the difference in percent exclusions was minimal and worth the sacrifice when considered with Lynch et al.'s (2018) reduction in false exclusions. Vickers et al. (2015) had even lower numbers of false exclusions, but much less power in excluding pairs. For variables where the percentage of exclusions was close to the percentage for Lynch et al. (2018), the number of false exclusions was not greatly affected, but where the false exclusions were reduced the number of exclusions was significantly cut and therefore not worth the trade-off.

Which method is chosen depends on the goals and needs of a specific project. If researchers are most concerned with accuracy, then Vickers et al. (2015) would be the appropriate choice. For methods that allow for simpler comparisons, Thomas et al. (2013) or Vickers et al. (2015) make more sense. In this case, the Lynch et al. (2018) method was chosen because it seems to allow some of the highest levels of segregation while also keeping false rejections reasonably low. Since each variable displayed different levels of exclusionary power, the most powerful yet accurate of the measurements available for potential matches were used for comparison. For pair-matching, they were prioritized in the following order: (1) LEN+MXL+IAL+HW+BW, (2) IAL+HW+BW, (3) LEN, (4) MXL, (5) IAL, (6) HW+BW, (7) BW, and (8) HW. For comparing the humerus and the femur, the regression equation with the highest r based on available measurements for the potential match was used.

Osteometric sorting of the MCs and MTs in the PSJ Collection was overall successful. Between 18.5% and 73.6% of potential pair-matches were excluded, so when elements were not excluded osteometrically and were positively matched using visual clues, there could be high confidence in those matches. Of course, most sorting methods will always retain some level of uncertainty, and this is especially true of the PSJ Collection since it is an open sample where the actual number and identities of individuals are unknown (Byrd 2008). Still, the agreement of methods lends credence to sorting conclusions. Using all methods combined, including a couple rejections based on pXRF data, over half of all MCs and MTs were successfully sorted by being positively shown to be paired or unpaired. Metacarpals, however, showed higher success in sorting. Osteometric assessment of articulations was moderately successful for the metacarpals, with up to one-third of potential matches being excluded, but it was fairly useless for the metatarsals, with no more than 10% excluded. Visual matching was the most helpful tool for articulation of both MCs and MTs, especially because some unique dark red staining patterns from iron artifacts sometimes helped to show congruency. Comparisons of the MCs and MTs to the humeri and femora were also moderately successful, with 7.4 to 23.2% of matches for the MCs being excluded, and 0.5 to 10.9% of matches for MTs being excluded. pXRF led to some further exclusions for the humeri and femora, but not enough to confidently sort them. Approximately 8% of probable pair-matches and 4% of probable articulations were osteometrically excluded, so the methods appear to be performing about as accurately as would be expected with an alpha level of 0.05, although the pair-matching error was slightly high and comparisons of other regions could not be evaluated.

For four out of five MC rays, the MNI estimation from that element was increased based on sorting outcomes. MC2 had the most known individuals represented, with an MNI of 20. This MNI is below the MNI estimated for the entire collection, which was 22 for a simple MNI based on the right talus or 25 based on age and sex indicators (Willey et al. 2016). Even though sorting of the MCs and MTs did not alter the estimated number of individuals present for the entire sample, the increase in MNI within the MCs and MTs does illustrate the importance of sorting commingled remains for more accurate analyses.

The application of the sorting methods to the PSJ Collection highlights a few important concepts when it comes to sorting skeletal remains. First, the success of osteometric sorting, as well as other sorting techniques, often depends on the condition of the skeletal remains (Byrd and Adams 2003). A higher proportion of potential metacarpal matches than metatarsal matches were segregated for all three osteometric approaches, despite most variables displaying no major performance differences for the MCs and MTs in the test sample. However, the PSJ MTs had more fragmentation and taphonomic wear than the MCs, leading to a much higher proportion of potential matches that were unable to be assessed. Differences in taphonomy could explain why sorting was so much more successful with the MCs than the MTs and show why having many frameworks utilizing various element dimensions is ideal.

The sorting process for hand and foot elements in the PSJ Collection also exemplifies the importance of using many sorting methods in combination. While osteometric sorting was effective and useful, mainly for pair-matching and comparisons of the humerus and femur, neither method could use osteometrics alone. Osteometric sorting can significantly reduce the number of potential matches, but other methods are needed to positively associate elements. Since visual methods are not generally useful for non-paired and non-articulating elements, osteometrics was the main tool available for sorting. Still, it only segregates a portion of potential matches, so other methods, such as pXRF in this case, are needed to further sort elements. Visual matching could potentially be used alone for pair-matching, but the method's subjectivity can lead to less confidence in outcomes and more time invested in sorting large assemblages, issues addressed by osteometrics through its ability to lend support to suggested pairs or confidently segregate those that were too ambiguous to reject visually, and through its ability to reduce the total pairs that need visual matching. There were a few potential pairs that could not be compared by visual or osteometric methods due to fragmentation of elements, but trace element evidence suggested segregation. PSJ sorting efforts then demonstrate the importance of using multiple lines of evidence in individuating remains.

Resolution of Commingling and PSJ Context

A number of metacarpals and metatarsals in the collection were effectively sorted, with many having pair-matches and/or articular matches. Sorting was, however, more fruitful for the metacarpals than for the metatarsals and MC2 resulted in the largest MNI, so most of the conclusions drawn are based on the MCs.

Suggested origins of the collection include medical waste associated with a functioning hospital, autopsied individuals, dissected cadavers, or a discarded collection of teaching specimens. Saw and cut marks on elements within the collection seem to be consistent with autopsy, dissection, and amputation, although a thorough analysis to differentiate them has not been completed (Willey et al. 2016). The clandestine nature of the pit is consistent with either dissection, which was often practiced illicitly, or surgical leftover, since it would be trash. It does not appear consistent with sanctioned autopsies since the individuals are not buried according to cultural customs, but could still have been cadavers used for practicing or teaching autopsies. Low levels of pathology led analysts to conclude that it was not a pathological collection or "curio cabinet" but could still represent the unwanted or uninteresting elements from a collection.

Many of the MCs that are known not to have a pair-match are articulated with elements that do have matches (Figure 14). In these cases, single elements rather than whole hands are missing. Only a few individuals (Individual 1, for example) show evidence of being represented by only one rather than two hands. It seems, then, that the origin of the PSJ Collection is not explained by medical waste associated with typical hospital functioning, such as amputation. If PSJ represented medical waste many more unpaired than paired hands would be expected. These results also strengthen the supposition that it is not a collection of teaching specimens since more single elements or body parts would be present from physicians saving specific elements with pathological or anatomical anomalies. These two explanations cannot definitively be ruled out for all individuals from the pit because numerous types of medical "waste" may have been discarded at once, but it suggests that the Point San Jose Collection was largely formed by other activities.

Therefore, the most likely explanation as to the origin and function of the PSJ assemblage is that a number of cadavers were dissected and/or autopsied for teaching or research purposes and then discarded. Sawed elements in the assemblage that appear similar to surgical cuts could be from practicing amputation procedures or retaining pathological specimens on cadavers, which was also common for physicians, particularly army surgeons that would have been stationed at Point San Jose. During the time period, it was common for physicians and medical schools to acquire cadavers through illegal means, such as postmortem theft, and then secretly dispose of the remains to conceal their actions, which could explain why the remains were discarded in a pit behind the hospital rather than properly buried.

Limitations

There were limitations to this research that could affect the implementation of the methods or the PSJ analysis. Even though osteometric sorting can decrease the time commitment of visual matching in large assemblages, a lot of time still needs to be invested due to the equations and t-tests being performed by hand. Ideally, osteometric sorting of the MCs and MTs could be incorporated into Lynch's (in press; Lynch et al. 2018) new computer-automated approaches to sorting so that measurements can be inputted and the computer will suggest segregation or lack of segregation based on a reference sample. It would likely decrease time investments even more. Also, the computer-automation of comparing non-paired and non-articulating elements (Lynch in press) was more powerful than previous methods because the computer could create countless measurement combinations from the reference sample and then make decisions about which to apply based on power and accuracy. The Byrd (2008) and Byrd and LeGarde (2014) method relied on the creation of regression formulae that would account for only a fraction of the possible combinations due to fragmentation.

Another limitation in this thesis was the reference sample. Most methods of osteometric sorting use a reference sample composed of hundreds of individuals, but the current study used only 86. The inclusion of more individuals would allow for a better understanding of what is typical versus atypical variation. The UNM sample was also overwhelmingly composed of individuals of European ancestry, so incorporating a more diverse sample would improve the validity for application to many assemblages. For PSJ specifically, using a reference sample that included many individuals of Asian and European ancestry that lived during the 19th century would have been ideal.

Conclusion

Commingling can obstruct anthropological analyses of bioarchaeological and forensic assemblages, so resolving commingling is an important step to investigation. Osteometric sorting is one avenue to address it. Although some measurements had high levels of error, the osteometric sorting techniques developed for the metacarpals and metatarsals in this thesis were found to be useful overall. Osteometrics could exclude a high percentage of potential pair-matches, and a moderate number of articulations and comparisons to other regions. While some of the techniques could use improvements, this study has shown that osteometric sorting is an important tool for addressing commingling of the MCs and MTs. It is especially significant in assemblages with a high concentration of hand and foot elements, such as the Point San Jose Collection. While the ability to draw conclusions regarding PSJ context was limited, the number of associated metacarpals did show that the majority of individuals in the assemblage were likely from teaching or research cadavers rather than surgical waste or a pathological collection.

Future research should address some of the limitations of this research. It should increase the reference population size by collecting data on other samples of varying sexes, ages, ancestries, and birth years. This diversity would allow the application of the methods to more samples. Since some of the measurements showed a high propensity for error, research should also focus on improving definitions. Facets would probably not be included in future research, and widths would need to be further tested to see if experience level improves inter-observer error, but other measurements, such as base and width heights or diaphysis diameters, should be incorporated to test their utility in osteometric sorting.

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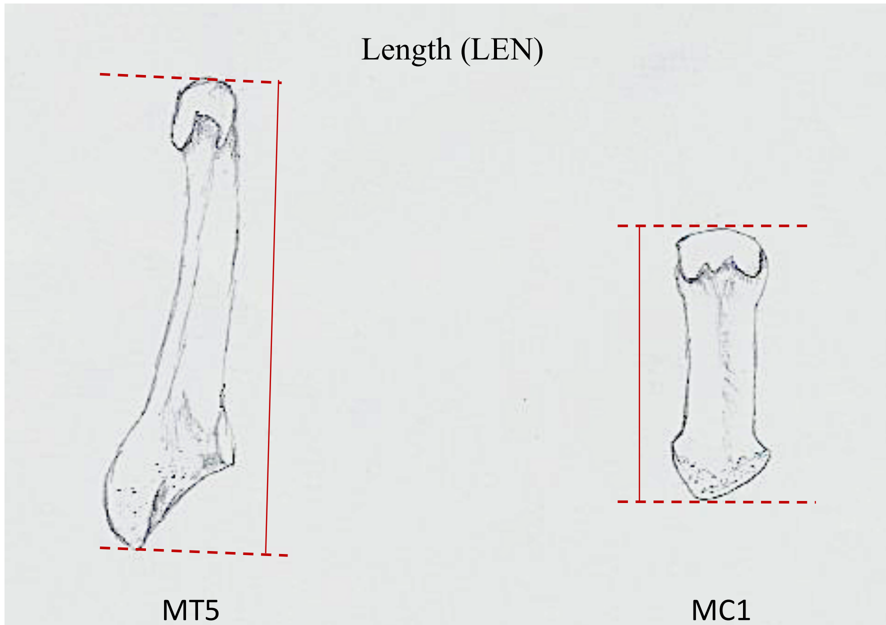
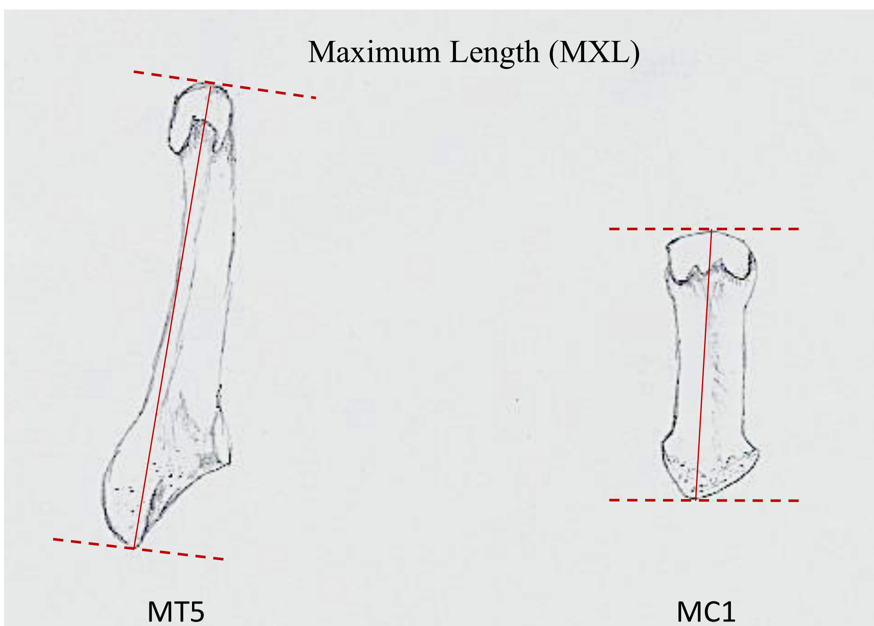
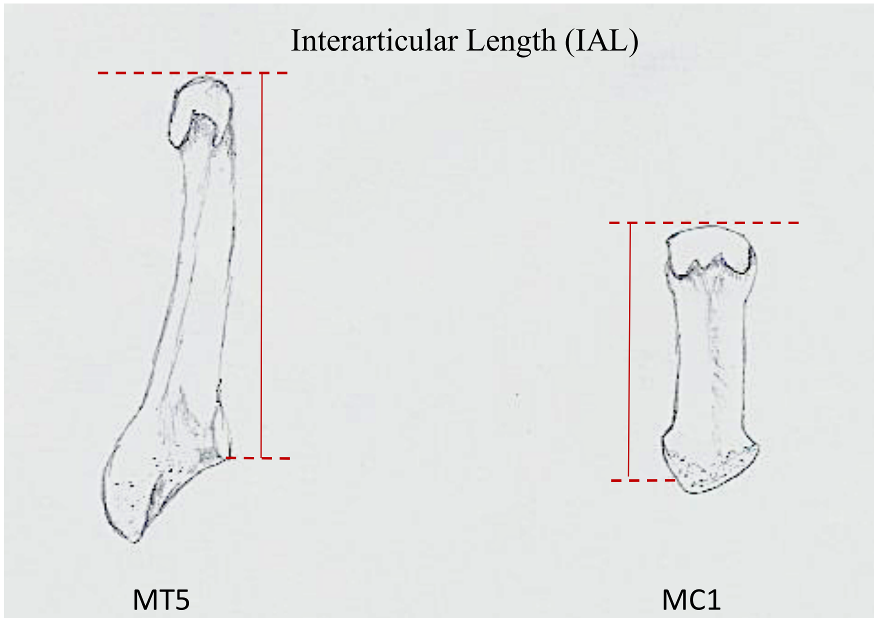
APPENDIX A



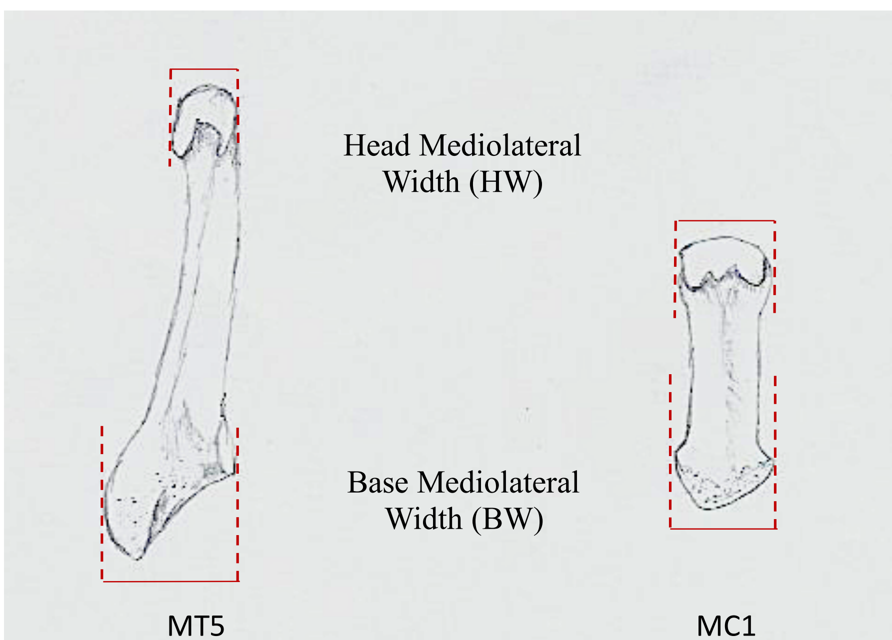
Example of length measurements.



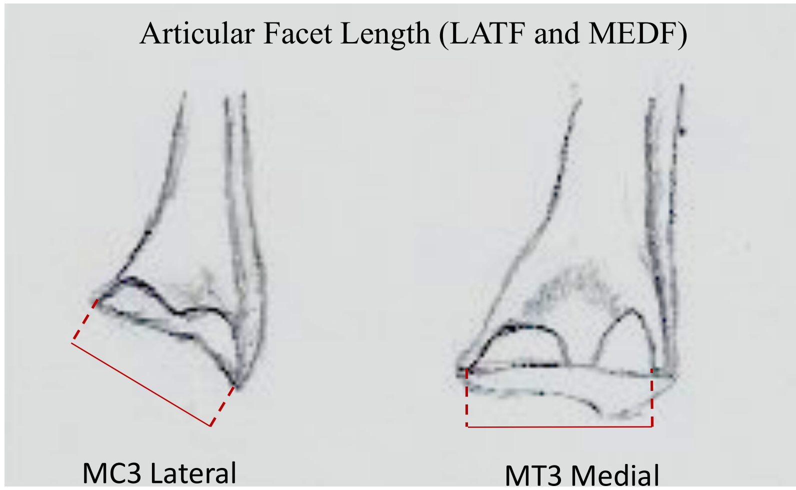
Example of maximum length measurements.



Example of interarticular length.



Example of head and base mediolateral widths.



Example of lateral and medial facet lengths.

APPENDIX B

Results for intra-observer error tests.

Measurement	*N*	Median Absolute Diff.	Median % Diff.	TEM	%TEM	R
MC1LEN	25	0.040	0.093	0.040	0.100	0.999
MC1MXL	24	0.010	0.022	0.017	0.038	0.999
MC1IAL	31	0.080	0.166	0.118	0.275	0.999
MC1HW	26	0.025	0.167	0.045	0.286	0.999
MC1BW	27	0.060	0.438	0.149	0.989	0.990
MC2LEN	34	0.140	0.197	0.112	0.163	0.999
MC2MXL	34	0.020	0.030	0.128	0.187	0.999
MC2IAL	34	0.060	0.097	0.099	0.150	0.999
MC2HW	34	0.050	0.335	0.089	0.608	0.995
MC2BW	33	0.200	1.158	0.268	1.523	0.975
MC2MEDF	33	0.310	1.867	0.754	**5.142**	**0.824**
MC3LEN	34	0.035	0.056	0.062	0.093	0.999
MC3MXL	34	0.010	0.015	0.031	0.046	0.999
MC3IAL	35	0.120	0.185	0.152	0.240	0.999
MC3HW	34	0.035	0.274	0.078	0.555	0.996
MC3BW	34	0.115	0.880	0.489	3.438	**0.874**
MC3MEDF	33	0.260	2.643	0.762	**7.337**	**0.876**
MC3LATF	33	0.350	2.468	0.440	2.887	**0.923**
MC4LEN	35	0.140	0.255	0.331	0.582	0.995
MC4MXL	35	0.010	0.019	0.052	0.091	0.999
MC4IAL	35	0.130	0.260	0.267	0.477	0.996
MC4HW	35	0.030	0.211	0.035	0.288	0.999
MC4BW	35	0.130	1.088	0.284	2.352	0.951
MC4MEDF	34	0.345	3.517	0.364	3.824	**0.903**
MC4LATF	34	0.150	1.587	1.089	**11.120**	**0.777**
MC5LEN	33	0.060	0.129	0.075	0.142	0.999
MC5MXL	33	0.010	0.020	0.026	0.050	0.999
MC5IAL	33	0.100	0.206	0.115	0.222	0.999
MC5HW	34	0.075	0.661	0.115	0.964	0.985
MC5BW	34	0.110	0.811	0.227	1.647	0.962
MC5LATF	34	0.215	2.238	0.293	3.163	**0.941**
HUML	32	0.000	0.000	0.559	0.176	0.999
HUMEPBR	35	0.000	0.000	0.521	0.885	0.992
HUMHD	33	0.330	0.785	0.430	0.974	0.989
MT1LEN	33	0.180	0.264	0.388	0.624	0.993
MT1MXL	32	0.010	0.017	0.068	0.103	0.999
MT1IAL	34	0.085	0.152	0.192	0.317	0.998
MT1HW	29	0.100	0.552	0.225	1.061	0.981
MT1BW	30	0.295	1.513	0.363	1.762	0.974
MT2LEN	32	0.075	0.091	0.106	0.138	0.999
MT2MXL	32	0.020	0.025	1.250	1.634	0.958

Measurement	*N*	Median Absolute Diff.	Median % Diff.	TEM	%TEM	R
MT2HW	32	0.080	0.725	0.134	1.159	0.982
MT2BW	33	0.090	0.623	0.116	0.745	0.992
MT2LATF	32	0.430	2.767	2.353	**15.688**	**0.313**
MT3LEN	32	0.100	0.150	0.116	0.164	0.999
MT3MXL	32	0.010	0.015	0.063	0.089	0.999
MT3IAL	33	0.070	0.112	0.202	0.292	0.998
MT3HW	34	0.040	0.417	0.094	0.927	0.980
MT3BW	33	0.370	2.619	0.945	**6.678**	**0.540**
MT3MEDF	34	0.455	2.926	2.502	**16.219**	**0.268**
MT3LATF	35	0.130	1.635	1.931	**22.956**	**0.040**
MT4LEN	34	0.095	0.143	0.109	0.157	0.999
MT4MXL	34	0.010	0.015	0.046	0.066	0.999
MT4IAL	34	0.120	0.174	0.339	0.506	0.995
MT4HW	34	0.060	0.579	0.084	0.845	0.987
MT4BW	36	0.410	2.515	0.566	3.787	**0.868**
MT4MEDF	35	0.150	1.822	1.190	**14.845**	**0.447**
MT4LATF	32	0.300	2.718	0.396	3.505	0.910
MT5LEN	31	0.280	0.411	0.371	0.526	0.995
MT5MXL	31	0.010	0.015	0.026	0.036	0.999
MT5IAL	33	0.160	0.260	0.192	0.317	0.998
MT5HW	33	0.080	0.768	0.129	1.213	0.982
MT5BW	31	0.360	1.817	0.672	3.417	**0.872**
MT5MEDF	35	0.240	2.388	0.440	4.204	**0.924**
FEML	31	0.000	0.000	0.454	0.102	0.999
FEMEPBR	35	0.000	0.000	0.414	0.522	0.996
FEMHD	32	0.155	0.374	0.175	0.395	0.998

Results for inter-observer error tests.

Measurement	*N*	Median Absolute Diff.	Median % Diff.	TEM	%TEM	R
MC1LEN	18	0.030	0.058	0.100	0.220	0.999
MC1MXL	17	0.010	0.025	0.022	0.048	0.999
MC1IAL	20	0.110	0.243	0.121	0.277	0.999
MC1HW	19	0.030	0.222	0.094	0.587	0.997
MC1BW	21	0.060	0.381	0.086	0.553	0.997
MC2LEN	20	0.095	0.136	0.109	0.156	0.999
MC2MXL	20	0.015	0.025	0.065	0.094	0.999
MC2IAL	20	0.400	0.576	0.630	0.946	0.989
MC2HW	20	0.060	0.419	0.250	1.699	0.961
MC2BW	20	0.480	2.479	0.760	4.311	**0.804**
MC2MEDF	20	0.455	3.234	0.550	3.715	**0.893**
MC3LEN	20	0.050	0.074	0.084	0.122	0.999
MC3MXL	20	0.010	0.014	0.035	0.050	0.999
MC3IAL	21	0.100	0.143	1.549	2.356	**0.926**
MC3HW	21	0.060	0.395	0.360	2.540	**0.887**
MC3BW	20	0.210	1.487	0.788	**5.570**	**0.630**
MC3MEDF	19	0.540	5.241	0.479	4.594	0.965
MC3LATF	19	0.500	3.849	0.674	4.412	**0.815**
MC4LEN	20	0.125	0.206	0.234	0.400	0.998
MC4MXL	20	0.025	0.041	0.076	0.129	0.999
MC4IAL	20	0.235	0.408	0.215	0.373	0.998
MC4HW	20	0.050	0.389	0.174	1.399	0.959
MC4BW	20	0.210	1.700	0.395	3.277	**0.927**
MC4MEDF	20	0.575	5.823	0.456	4.719	**0.763**
MC4LATF	20	0.350	3.032	0.868	**8.614**	**0.902**
MC5LEN	20	0.080	0.137	0.103	0.191	0.999
MC5MXL	20	0.020	0.037	0.018	0.034	0.999
MC5IAL	20	0.125	0.223	0.362	0.689	0.995
MC5HW	20	0.090	0.778	0.282	2.324	**0.882**
MC5BW	20	0.285	2.151	0.531	3.885	**0.760**
MC5LATF	19	0.530	5.585	0.583	**6.366**	**0.666**
HUML	17	0.000	0.000	1.372	0.416	0.999
HUMEPBR	19	0.000	0.000	0.429	0.701	0.996
HUMHD	19	0.890	2.098	0.981	2.138	0.963
MT1LEN	20	3.340	4.879	2.503	3.819	**0.820**
MT1MXL	20	0.060	0.080	0.125	0.185	0.999
MT1IAL	20	1.050	1.670	1.103	1.750	0.959
MT1HW	19	0.310	1.383	0.638	3.035	**0.864**
MT1BW	19	0.420	2.239	0.450	2.131	0.972
MT2LEN	19	0.150	0.175	0.177	0.222	0.999
MT2MXL	19	0.010	0.014	0.093	0.116	0.999

Measurement	*N*	Median Absolute Diff.	Median % Diff.	TEM	%TEM	R
MT2HW	19	0.140	1.316	0.163	1.404	0.966
MT2BW	20	0.135	0.860	0.221	1.386	0.983
MT2LATF	18	0.410	2.465	4.030	**28.516**	**0.134**
MT3LEN	19	0.150	0.185	0.248	0.335	0.998
MT3MXL	19	0.020	0.026	0.162	0.218	0.999
MT3IAL	19	0.590	0.814	0.533	0.738	0.990
MT3HW	20	0.045	0.442	0.060	0.585	0.994
MT3BW	20	0.195	1.315	0.950	**6.667**	**0.589**
MT3MEDF	19	8.940	138.226	5.226	**36.708**	**-0.041**
MT3LATF	20	0.205	2.670	0.329	4.077	**0.905**
MT4LEN	19	0.220	0.311	0.178	0.247	0.999
MT4MXL	19	0.010	0.014	0.038	0.052	0.999
MT4IAL	19	0.860	1.341	0.819	1.168	0.980
MT4HW	20	0.080	0.708	0.079	0.078	0.992
MT4BW	20	1.755	12.004	1.454	**9.949**	**0.363**
MT4MEDF	21	0.310	4.540	0.361	4.534	**0.912**
MT4LATF	19	0.560	5.000	0.596	**5.140**	**0.778**
MT5LEN	19	0.390	0.505	0.435	0.585	0.996
MT5MXL	19	0.010	0.016	0.012	0.016	0.999
MT5IAL	20	0.635	1.125	0.674	1.057	0.984
MT5HW	19	1.870	14.088	1.645	**13.392**	**0.080**
MT5BW	21	0.580	2.674	0.666	3.272	**0.870**
MT5MEDF	21	0.470	4.224	0.652	**5.984**	**0.653**
FEML	12	0.500	0.097	1.118	0.240	0.999
FEMEPBR	16	0.000	0.000	0.454	0.548	0.995
FEMHD	16	0.215	0.518	0.285	0.613	0.996

APPENDIX C

Summary of test sample makeup for pair-matching.

L-R Pairs	Sample Potential Matches	Variable Potential Matches	Sample Actual Matches	Variable Actual Matches
MC1	196		13	
LEN		121		10
MXL		110		10
IAL		182		13
HW		168		12
BW		156		11
LEN+MXL+IAL+HW+BW		99		10
IAL+HW+BW		130		10
HW+BW		130		10
MC2	210		14	
LEN		196		13
MXL		196		13
IAL		196		13
HW		196		13
BW		196		13
LEN+MXL+IAL+HW+BW		196		13
IAL+HW+BW		196		13
HW+BW		196		13
MC3	196		13	
LEN		182		12
MXL		182		12
IAL		196		13
HW		196		13
BW		182		13
LEN+MXL+IAL+HW+BW		169		12
IAL+HW+BW		182		13
HW+BW		182		13
MC4	196		14	
LEN		196		14
MXL		196		14
IAL		196		14
HW		196		14
BW		182		13
LEN+MXL+IAL+HW+BW		182		13
IAL+HW+BW		182		13
HW+BW		182		13
MC5	182		13	
LEN		182		13
MXL		182		13
IAL		182		13
HW		182		13
BW		182		13
LEN+MXL+IAL+HW+BW		182		13
IAL+HW+BW		182		13

L-R Pairs	Sample Potential Matches	Variable Potential Matches	Sample Actual Matches	Variable Actual Matches
MT1	224		13	
LEN		224		13
MXL		224		13
IAL		224		13
HW		192		11
BW		224		13
LEN+MXL+IAL+HW+BW		208		11
IAL+HW+BW		192		11
HW+BW		192		11
MT2	240		13	
LEN		210		11
MXL		210		11
IAL		210		11
HW		225		12
BW		225		12
LEN+MXL+IAL+HW+BW		210		11
IAL+HW+BW		210		11
HW+BW		210		11
MT3	240		13	
LEN		195		11
MXL		195		11
IAL		195		11
HW		180		10
BW		225		13
LEN+MXL+IAL+HW+BW		168		10
IAL+HW+BW		168		10
HW+BW		168		10
MT4	256		14	
LEN		192		10
MXL		192		10
IAL		192		10
HW		195		11
BW		240		13
LEN+MXL+IAL+HW+BW		165		9
IAL+HW+BW		165		9
HW+BW		180		10
MT5	240		13	
LEN		195		10
MXL		195		10
IAL		225		12
HW		182		12
BW		240		11
LEN+MXL+IAL+HW+BW		156		9
IAL+HW+BW		182		11
HW+BW		182		11

Summary of test sample makeup for osteometric articulation.

	Sample Potential Matches	**Sample Actual Matches**	**Potential Matches by Variable**	**Actual Matches by Variable**
LMC2-LMC3	210	14	196	13
LMC3-LMC4	196	13	168	12
LMC4-LMC5	182	13	169	12
RMC2-RMC3	196	14	182	13
RMC3-RMC4	196	14	196	14
RMC4-RMC5	196	14	196	14
LMT2-LMT3	240	15	196	13
LMT3-LMT4	240	15	240	15
LMT4-LMT5	240	15	210	13
RMT2-RMT3	240	15	196	13
RMT3-RMT4	256	16	240	15
RMT4-RMT5	256	16	256	16

APPENDIX D

Data for osteometric pair-matching with Byrd (2008) and Byrd and LeGarde (2014) method.

Pair	Avg. D	SD	*N*	Avg. D	SD	*N*
	Length (LEN)			**Maximum Length (MXL)**		
MC1	0.390	0.800	48	0.369	0.831	47
MC2	0.306	0.727	73	0.263	0.700	72
MC3	0.383	1.204	71	0.446	1.178	71
MC4	0.216	0.806	68	0.223	0.760	67
MC5	0.201	0.825	68	0.186	0.801	68
MT1	-0.294	1.249	69	-0.193	1.035	66
MT2	-0.138	0.972	64	-0.038	0.935	63
MT3	-0.091	0.924	68	0.002	0.884	66
MT4	0.051	0.970	57	0.221	0.917	57
MT5	0.014	1.042	53	0.092	1.017	53
	Interarticular Lenth (IAL)			**Head Width (HW)**		
MC1	0.298	0.784	72	0.360	0.574	65
MC2	0.109	0.825	75	0.298	0.435	72
MC3	0.092	0.767	78	0.375	0.435	75
MC4	0.149	0.747	73	0.275	0.444	81
MC5	0.161	0.763	70	0.147	0.521	75
MT1	-0.293	1.295	77	0.115	0.527	54
MT2	0.001	0.977	76	0.012	0.509	62
MT3	0.136	0.865	74	-0.020	0.443	60
MT4	0.406	0.965	68	-0.067	0.523	56
MT5	0.234	1.270	65	0.032	0.607	52
	Base Width (BW)			**LEN + MXL + IAL + HW + BW**		
MC1	0.295	0.536	51	2.003	2.707	41
MC2	0.177	0.569	69	1.208	2.298	61
MC3	0.096	0.730	78	1.416	3.357	65
MC4	-0.011	0.588	72	0.881	2.430	65
MC5	0.265	0.624	75	0.998	2.584	67
MT1	-0.205	0.973	65	-0.677	3.953	46
MT2	-0.055	0.800	72	-0.430	3.144	49
MT3	0.241	1.051	74	-0.162	2.905	50
MT4	-0.269	1.077	73	-0.002	3.097	47
MT5	-0.033	0.975	70	0.441	3.119	43

	IAL + HW + BW			HW + BW		
MC1	1.048	1.321	46	0.642	0.938	46
MC2	0.681	1.194	62	0.463	0.938	64
MC3	0.550	1.308	72	0.479	0.959	73
MC4	0.374	1.144	69	0.231	0.762	72
MC5	0.601	1.184	68	0.397	0.762	72
MT1	-0.324	1.830	48	-0.090	1.137	48
MT2	-0.196	1.538	54	-0.067	1.101	55
MT3	0.068	1.409	51	0.038	0.991	54
MT4	-0.177	1.537	53	-0.465	1.209	54
MT5	0.305	1.855	46	0.050	1.173	47

Data for osteometric pair-matcing with Lynch et al. (2018) method.

Pair	**Avg. D**	**SD**	***N***	**Avg. D**	**SD**	***N***
	Length (LEN)			**Maximum Length (MXL)**		
MC1	0.839	0.213	48	0.848	0.221	47
MC2	0.795	0.245	73	0.777	0.239	72
MC3	0.878	0.295	71	0.872	0.294	71
MC4	0.798	0.242	68	0.779	0.255	67
MC5	0.799	0.258	68	0.794	0.240	68
MT1	0.841	0.300	69	0.826	0.265	66
MT2	0.854	0.260	64	0.814	0.273	63
MT3	0.836	0.235	68	0.807	0.247	66
MT4	0.849	0.260	57	0.844	0.237	57
MT5	0.887	0.260	53	0.897	0.224	53

	Interarticular Lenth (IAL)			Head Width (HW)		
MC1	0.810	0.220	72	0.722	0.246	65
MC2	0.789	0.236	75	0.706	0.196	72
MC3	0.770	0.247	78	0.707	0.224	75
MC4	0.749	0.249	73	0.643	0.229	81
MC5	0.781	0.240	70	0.679	0.223	75
MT1	0.856	0.279	77	0.693	0.223	54
MT2	0.831	0.281	76	0.688	0.203	62
MT3	0.795	0.263	74	0.636	0.213	60
MT4	0.865	0.255	68	0.662	0.231	56
MT5	0.923	0.282	65	0.697	0.222	52
	Base Width (BW)			**LEN + MXL + IAL + HW + BW**		
MC1	0.696	0.258	51	1.404	0.270	41
MC2	0.744	0.120	69	1.351	0.226	61
MC3	0.736	0.238	78	1.430	0.295	65
MC4	0.693	0.245	72	1.324	0.250	65
MC5	0.733	0.226	75	1.364	0.257	67
MT1	0.857	0.246	65	1.456	0.320	46
MT2	0.758	0.120	72	1.434	0.257	49
MT3	0.810	0.264	74	1.384	0.274	50
MT4	0.823	0.332	73	1.485	0.239	47
MT5	0.827	0.287	70	1.508	0.221	43
	IAL + HW + BW			**HW + BW**		
MC1	1.136	0.202	46	0.931	0.239	46
MC2	1.110	0.185	62	0.936	0.239	64
MC3	1.125	0.198	72	0.944	0.219	73
MC4	1.060	0.210	69	0.869	0.209	72
MC5	1.111	0.205	68	0.920	0.209	72
MT1	1.207	0.242	48	0.995	0.223	48
MT2	1.153	0.202	54	0.941	0.203	55
MT3	1.115	0.231	51	0.942	0.206	54
MT4	1.206	0.218	53	0.989	0.230	54
MT5	1.242	0.225	46	0.997	0.251	47

Data for osteometric pair-matching with Thomas et al. (2013)

Measurement	*N*	***M*** **95%**	***M*** **Max**	Measurement	*N*	***M*** **95%**	***M*** **Max**
MC1LEN	48	0.0429	0.0517	MT1LEN	69	0.0390	0.1036
MC1MXL	47	0.0429	0.0498	MT1MXL	66	0.0262	0.0734
MC1IAL	72	0.0444	0.0586	MT1IAL	77	0.0320	0.1222
MC1HW	65	0.0982	0.1326	MT1HW	54	0.0523	0.0633
MC1BW	51	0.0799	0.1100	MT1BW	65	0.1074	0.1245
MC2LEN	73	0.0246	0.0324	MT2LEN	64	0.0273	0.0360
MC2MXL	72	0.0241	0.0288	MT2MXL	63	0.0272	0.0322
MC2IAL	75	0.0252	0.0457	MT2IAL	76	0.0266	0.0315
MC2HW	72	0.0554	0.1252	MT2HW	62	0.0853	0.1107
MC2BW	69	0.0615	0.0877	MT2BW	72	0.0630	0.3709
MC3LEN	71	0.0392	0.0772	MT3LEN	68	0.0239	0.0538
MC3MXL	71	0.0385	0.0770	MT3MXL	66	0.0206	0.0487
MC3IAL	78	0.0263	0.0291	MT3IAL	74	0.0238	0.0488
MC3HW	75	0.0743	0.0806	MT3HW	60	0.0873	0.1134
MC3BW	78	0.1138	0.1869	MT3BW	74	0.1775	0.4186
MC4LEN	68	0.0333	0.0367	MT4LEN	57	0.0255	0.0355
MC4MXL	67	0.0280	0.0342	MT4MXL	57	0.0278	0.0345
MC4IAL	73	0.0314	0.0361	MT4IAL	68	0.0350	0.0485
MC4HW	81	0.0909	0.1460	MT4HW	56	0.1204	0.1318
MC4BW	72	0.0980	0.1221	MT4BW	73	0.1453	0.2596
MC5LEN	68	0.0335	0.0454	MT5LEN	53	0.0259	0.0341
MC5MXL	68	0.0314	0.0473	MT5MXL	53	0.0260	0.0354
MC5IAL	70	0.0308	0.0428	MT5IAL	65	0.0401	0.0706
MC5HW	75	0.0946	0.1257	MT5HW	66	0.0410	0.0483
MC5BW	75	0.1023	0.1537	MT5BW	52	0.1234	0.1429

Data for osteometric pair-matching with Vickers et al. (2015).

Pair	Max D	*N*	Max D	*N*	Max D	*N*
	LEN		**MXL**		**IAL**	
MC1	2.51	48	2.42	47	2.7	72
MC2	2.21	73	1.97	72	3	75
MC3	5.2	71	5.2	71	1.91	78
MC4	2.2	68	2.17	67	2.1	73
MC5	2.34	68	2.47	68	2.22	70
MT1	6.42	69	4.95	66	7.38	77
MT2	2.76	64	2.48	63	2.25	76
MT3	3.9	68	3.54	66	3.44	74
MT4	2.42	57	2.36	57	3.13	68
MT5	2.62	53	3.08	53	4.59	65
	HW		**BW**		**LEN+MXL+IAL+HW+BW**	
MC1	2.28	65	1.72	51	7.57	41
MC2	2.06	72	1.51	69	9.52	61
MC3	1.22	75	3.06	78	13.35	65
MC4	1.9	81	1.44	72	7.36	65
MC5	1.9	75	2.34	75	9.59	67
MT1	1.26	54	2.61	65	17.27	46
MT2	1.49	62	4.94	72	7.88	49
MT3	1.29	60	4.86	74	10.6	50
MT4	1.38	56	4.09	73	7.59	47
MT5	1.7	52	2.57	70	6.93	43
	IAL+HW+BW		**HW+BW**			
MC1	4.16	46	2.97	46		
MC2	5.34	62	3.33	64		
MC3	3.71	72	3.31	73		
MC4	3.42	69	2.37	72		
MC5	4.83	68	3.13	72		
MT1	5.9	48	3.13	48		
MT2	6.02	54	5.78	55		
MT3	5.17	51	4.18	54		
MT4	3.79	53	4.7	54		
MT5	5.9	46	3.02	47		

Data for osteometric articulations.

	Avg D	SD	N
LMC2-LMC3	-0.409	0.672	75
LMC3-LMC4	0.507	1.299	64
LMC4-LMC5	0.079	0.888	66
RMC2-RMC3	-0.571	0.682	77
RMC3-RMC4	0.725	1.126	70
RMC4-RMC5	0.024	0.789	65
LMT2-LMT3	-0.461	2.018	66
LMT3-LMT4	0.24	1.416	80
LMT4-LMT5	0.706	0.874	65
RMT2-RMT3	-0.461	2.141	67
RMT3-RMT4	0.17	1.08	76
RMT4-RMT5	0.685	1.295	68

Data for osteometric comparisons to other regions – regression equations.

Model	*N*	*r*	*r^2*	SE
HUM.1=0.812(MC1.1)+2.551	89	0.822	0.676	0.042
HUM.2=0.972(MC1.1)-0.105	98	0.813	0.661	0.054
HUM.3=0.894(MC1.1)-0.055	98	0.813	0.661	0.047
HUM.1=0.937(MC2.1)+1.752	115	0.858	0.736	0.037
HUM.2=1.087(MC2.1)-0.899	128	0.812	0.659	0.052
HUM.3=1.056(MC2.1)-1.047	130	0.830	0.668	0.046
HUM.1=0.869(MC3.1)+2.121	122	0.859	0.739	0.038
HUM.2=0.967(MC3.1)-0.280	128	0.812	0.659	0.052
HUM.3=0.952(MC3.1)-0.505	138	0.814	0.663	0.048
HUM.1=0.845(MC4.1)+2.335	119	0.810	0.657	0.044
HUM.2=0.943(MC4.1)-0.053	135	0.790	0.625	0.057
HUM.3=0.956(MC4.1)-0.404	135	0.796	0.633	0.051
HUM.1=0.845(MC5.1)+2.371	119	0.821	0.675	0.042
HUM.2=0.974(MC5.1)-0.149	132	0.816	0.666	0.053
HUM.3=0.923(MC5.1)-0.222	137	0.788	0.621	0.050
FEM.1=0.780(MC1.1)+2.995	84	0.812	0.659	0.044
FEM.2=0.805(MC1.1)+0.910	94	0.830	0.689	0.042
FEM.3=0.957(MC1.1)-0.316	94	0.866	0.750	0.043
FEM.1=0.930(MC2.1)+2.089	109	0.869	0.756	0.035

Model	***N***	***r***	***r^2***	**SE**
FEM.3=1.090(MC2.1)-1.190	126	0.828	0.686	0.048
FEM.1=0.889(MC3.1)+2.338	118	0.880	0.775	0.037
FEM.2=0.828(MC3.1)+0.643	134	0.805	0.649	0.046
FEM.3=1.000(MC3.1)-0.709	134	0.835	0.697	0.050
FEM.1=0.840(MC4.1)+2.666	118	0.829	0.688	0.044
FEM.2=0.840(MC4.1)+0.693	133	0.819	0.671	0.045
FEM.3=1.000(MC4.1)-0.583	134	0.832	0.692	0.051
FEM.1=0.837(MC5.1)+2.714	117	0.824	0.679	0.044
FEM.2=0.849(MC5.1)+0.690	132	0.825	0.681	0.044
FEM.3=0.986(MC5.1)-0.482	133	0.818	0.669	0.052
HUM.1=0.799(MT1.1)+2.358	92	0.826	0.682	0.041
HUM.2=0.832(MT1.1)+0.246	101	0.714	0.510	0.061
HUM.3=0.839(MT1.1)-0.082	105	0.746	0.556	0.055
HUM.1=0.908(MT2.1)+1.861	99	0.841	0.707	0.039
HUM.2=0.961(MT2.1)-0.340	112	0.764	0.583	0.060
HUM.3=0.937(MT2.1)-0.529	113	0.742	0.550	0.057
HUM.1=0.885(MT3.1)+2.024	98	0.848	0.719	0.039
HUM.2=0.867(MT3.1)+0.146	112	0.747	0.558	0.061
HUM.3=0.882(MT3.1)-0.218	113	0.729	0.532	0.058
HUM.1=0.836(MT4.1)+2.259	95	0.801	0.641	0.043
HUM.2=0.879(MT4.1)+0.104	108	0.727	0.529	0.064
HUM.3=0.828(MT4.1)+0.040	109	0.628	0.465	0.061
HUM.1=0.787(MT5.1)+2.495	88	0.793	0.628	0.044
HUM.2=0.872(MT5.1)+0.149	98	0.736	0.541	0.063
HUM.3=0.752(MT5.1)+0.396	100	0.655	0.429	0.062
FEM.1=0.801(MT1.1)+2.655	97	0.849	0.721	0.037
FEM.2=0.774(MT1.1)+0.805	106	0.791	0.626	0.044
FEM.3=0.854(MT1.1)-0.137	103	0.757	0.573	0.054
FEM.1=0.912(MT2.1)+2.145	103	0.888	0.788	0.035
FEM.2=0.866(MT2.1)+0.388	116	0.795	0.632	0.048
FEM.3=1.001(MT2.1)-0.809	114	0.788	0.621	0.057
FEM.1=0.868(MT3.1)+2.406	102	0.883	0.779	0.036
FEM.2=0.787(MT3.1)+0.807	115	0.768	0.590	0.050
FEM.3=0.906(MT3.1)-0.314	114	0.755	0.570	0.061
FEM.1=0.867(MT4.1)+2.426	100	0.876	0.767	0.036
FEM.2=0.791(MT4.1)+0.797	112	0.758	0.575	0.051
FEM.3=0.898(MT4.1)-0.264	111	0.740	0.547	0.062
FEM.1=0.810(MT5.1)+2.692	93	0.851	0.724	0.038
FEM.2=0.779(MT5.1)+0.863	102	0.779	0.606	0.048
FEM.3=0.874(MT5.1)-0.143	102	0.752	0.565	0.059

Data for osteometric comparisons of other regions – independent variables.

Variable	***N***	**Mean**	**St Dev**
MC1.1	105	4.321	0.076
MC2.1	141	4.587	0.065
MC3.1	152	4.517	0.075
MC4.1	150	4.388	0.075
MC5.1	149	4.344	0.074
MT1.1	112	4.638	0.072
MT2.1	125	4.616	0.072
MT3.1	126	4.545	0.076
MT4.1	121	4.537	0.075
MT5.1	110	4.510	0.077