

THE MORPHOLOGICAL AND OSTEOMETRIC SORTING OF HUMAN  
COMMINGLED ASSEMBLAGES: TALI AND CALCANEI

by

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## LIST OF ABBREVIATIONS

<b>Abbreviation</b>	<b>Description</b>
CAB	Breadth of the calcaneus
CAF	Fraction of the most superior point of the arc of the posterior articular facet of the calcaneus
CAL	Length of the posterior articular facet of the calcaneus
CAS	Subtense of the most superior point of the arc of the posterior articular facet of the calcaneus
CAW	Width of the posterior articular facet of the calcaneus
CSTJ	Clinical subtalar joint
FACTS	Forensic Anthropology Center at Texas State
LI	Lincoln Index
MLNI	Most Likely Number of Individuals
MNI	Minimum Number of Individuals
SEE	Standard Error of the Estimate
TAB	Breadth of the talus
TAF	Fraction of the most superior point of the arc of the posterior articular facet of the talus
TAL	Length of the posterior articular facet of the talus
TAS	Subtense of the most superior point of the arc of the posterior articular facet of the talus
TAW	Width of the posterior articular facet of the talus
TXSTDSC	Texas State University Donated Skeletal Collection

## ABSTRACT

The accurate sorting of elements from a commingled assemblage can be important to estimating the number of individuals represented by those particular elements, and to gain a better understanding of the actual assemblage. Many methods of sorting utilize visual matching, particularly in smaller assemblages, while others use osteometric sorting methods specific to the re-association of elements of the same side or pair-matching elements of opposite sides. The purpose of this study was to create a method utilizing morphological variation of the clinical subtalar joint (CSTJ) of tali and calcanei, in combination with using simple and multiple regression models to make predictions of matching elements in order to accurately sort elements of a larger commingled assemblage.

Facet patterns were categorized into four types, with varying anterior and middle articular facets, though a fifth type is acknowledged. Type A consisted of a missing anterior facet, but a separate middle facet. Type B had separate anterior and middle facets. Type C had a continuous anterior and middle facet, but with a significant angle between them. Type D also consisted of a continuous anterior and middle facet, but this facet was flat. Type E typically consists of the anterior, middle, and posterior articular facets all being fused together, but was not observed in this assemblage.

Five measurements from each element were utilized in the creation of simple and multiple regression equations and include the length and width of the posterior articular facet, the breadth of the element, and the fraction and subtense of the most superior point

of an arc on the posterior articular facet. These regression equations were created using 120 individuals from the Texas State Donated Skeletal Collection. These equations utilized the left talus to predict measurements of the calcaneus from the left side, as well as the right talus to predict measurements of the calcaneus from the right side for re-association. The left talus was then used to predict measurements of the right talus, and measurements of the left calcaneus was used to predict measures of the right calcaneus for pair-matching. The absolute value of the differences between element measurements was taken, and then all measurement differences were combined into an average to predict element matches, rather than matching elements from measurement to measurement. Elements were then ranked by lowest average difference up to 1.5mm average difference.

A holdout test consisted of 30 individuals with varying degrees of element presence. Out of 120 elements, only 85 elements were present. Using the predictions generated via the regression equations as well as elimination of potential matches via facet pattern the left elements were re-associated with 84.6% accuracy, the right elements were re-associated with 93.8% accuracy, the calcanei were pair-matched with 93.8% accuracy, the tali were pair-matched with 93.3% accuracy, and the solo elements were classified as solo with 66.7% accuracy. These results are similar to other metric methods of re-associating tali and calcanei, but are less accurate than analyses for pair-matching using two- or three-dimensional shape comparisons. Overall this method worked well in predicting ranked matches, as well as eliminating potential matches using facet patterns.

## 1. INTRODUCTION

The commingling of human skeletal remains occurs when the skeletal elements of two or more individuals have mixed. Commingling of elements can be a result of mass disasters, particularly in a forensic context, or it can be due to mass deaths caused by famine or disease, or even just the tradition of burying the dead in ossuaries. This mixing of elements can be an issue when attempting to understand the original number of individuals that make up an assemblage. If the original context is known, forensic identifications can be facilitated more easily, while with bioarchaeological assemblages the demography of the buried population can be appropriately studied. To accurately estimate the original assemblage it is necessary to be able to sort these commingled elements into their respective individuals. In situations where preservation is good this can be accomplished by extracting DNA from skeletal elements, and establishing which elements are from the same person. While DNA is a useful tool in matching elements to individuals, destructive analyses are often not permitted. Furthermore, DNA extractions are time-consuming and expensive, and sometimes do not yield results. Therefore, matching elements to the proper individual in commingled contexts is frequently carried out using visual and metric methods.

One main goal in dealing with commingled assemblages is estimating a minimum number of individuals (MNI). This is typically estimated by observing which feature, landmark, or portion of an element is most represented from one side of the body for a particular age group. Combining that observation with observations from other age groups that may be present can give the researcher an MNI for their assemblage. An MNI is a basic estimate for a mixed context, as it is just the minimum estimate of how many

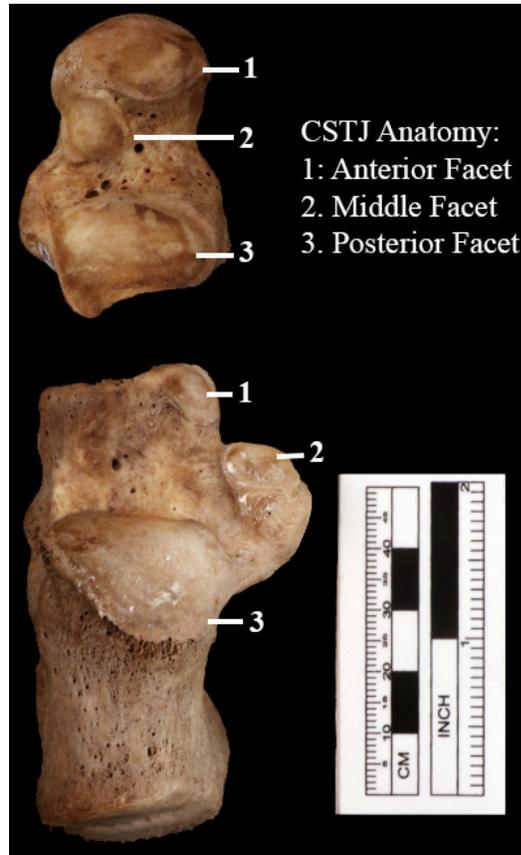
individuals are represented by the elements present. Another estimate that can help give information on the commingling event is a Most Likely Number of Individuals (MLNI) estimate which estimates the original number of individuals in an assemblage, rather than just the bare minimum (Konigsberg and Adams 2014). Calculating an MLNI per element could be useful in further understanding the demographic makeup of the commingled assemblage at present.

The type of methods used often depend on the assemblage size, which bones are present, and the condition of the bones. In most cases a combination of general morphology (e.g., age, sex, pathology), articulation congruency, bone size and shape, and taphonomic condition can be used to re-associate disarticulated elements (Adams and Byrd 2006, Rodríguez et al. 2016). However, for large assemblages and when matching of different skeletal elements is necessary, osteometric sorting, which uses measurements and statistical models, is a valuable tool in combination with the aforementioned processes (Byrd and Adams 2003, Byrd and LeGarde 2014).

This research project will focus on tali and calcanei because the preservation of these elements is fairly common in mass graves and other commingling events due to the small size and compact nature of these bones (Anastopoulou et al. 2017). In historic mass graves and forensic mass burials, these tarsals are also often protected by footwear. Since Golda (2015) shows these elements do not have a high survivorship when the individual is left to decompose on the surface, this method is useful for primary mass burials, where the survivorship of these tarsals is typically higher.

The purpose of this study is to develop a method for grouping commingled human calcanei and tali that combines morphological patterns of the clinical subtalar joint

(CSTJ) and a multivariate method of osteometric sorting. A diagram displaying the anatomy of the CSTJ for a talus and calcaneus can be found in Figure 1.



**Figure 1. Diagram of the CSTJ anatomy depicting the location of the anterior, middle, and posterior facets.**

The goal of the current research is to develop statistical models to associate tali and calcanei from the ipsilateral and contralateral sides. These models would predict potential matches for particular elements. This list of matches would then be narrowed down by eliminating potential matches based on facet patterns. This could help save time, since visually comparing elements based on size and shape, muscle attachment sites, pathologies, or color and texture of elements in large assemblages can be very time consuming. If a list of potential matches is predicted by the regression equations, and

facet pattern types are used to narrow down that list, less time can be spent comparing elements visually. This current research aims to combine the re-association of elements of the same side and pair-matching of elements of the opposite side in order to group elements into a distinct individual. For the remainder of this document, re-association will refer to the re-association of two different elements from the same side, such as the reuniting of a left talus with a left calcaneus of the same individual. Pair-matching will refer to the matching of the same element from the opposite side of the individual, such as the pairing of a right and left talus. Grouping elements into an individual could aid in MLNI estimates in real life scenarios when the initial number of individuals is unknown. This method will be developed and tested on a modern U.S. reference population.

## **Literature Review**

### *Visual Methods of Sorting*

The sorting of small commingling events can typically be completed using visual sorting methods which can include observations of taphonomy in the form of staining, or postmortem damage, or visually assessing size and shape of elements, their muscle markings, or their articular surfaces (Nikita and Lahr 2011, Adams and Byrd 2006, Konigsberg and Adams 2014). In a test of visual pair-matching, Konigsberg and Adams (2014) found that the more likely errors to occur were from overlooking true pairs rather than pairing unrelated elements. They also found that when a commingled assemblage is large, in this case over 15 individuals, visual matching is less reliable and reasonable.

One preliminary study has shown that visual pair-matching of a large commingled assemblage of humeri, 287 left, and 293 right, could be accurately pair-matched by five

researchers with 84% to 99% accuracy (LeGarde 2019). The number of Confident Matches differed between researchers, and it took anywhere from 35 hours to 50 hours of sorting. While true pairs were not necessarily known, since these elements did not come from identified individuals, labels were not covered, so elements from the same bundle could have biased the participants in their matching. The full report on accuracy was also pending DNA results, so those numbers could change.

Visual re-association tends to occur by attempting to articulate elements that are suspected to belong to the same individual. According to Adams and Byrd (2006), articulation of elements is one of the most reliable methods of determining individual association, but the degree of confidence of a re-association depends on the elements that are being articulated. Once again, in smaller contexts this might not be as much of an issue, but articulating elements from larger assemblages could pose problems since sometimes there is not a close fit between elements (Adams and Byrd 2006). In that particular study, the visual re-association was only occurring in a context that included two individuals, so re-association of elements was completed fairly easily.

These visual methods of sorting can be accurate when resolving a smaller commingled assemblage, but the researcher must be highly familiar with the variation that can occur for the particular elements they are working with. These visual methods have also proven to be time consuming, especially when attempting to sort the skeletal remains of tens to hundreds of individuals. Since there can be issues with only using visual sorting, the utilization of other types of sorting methods could help improve accuracy of true pairings as well as costing less time.

### *Osteometric Sorting*

As discussed previously, commingled skeletal elements can be sorted into individuals using information such as sex, age, physique, and rearticulating joints when the number of commingled remains are relatively small. However, when the samples are larger, osteometric sorting through comparisons of element shape and size can greatly aid in sorting commingled remains (Byrd and LeGarde 2014, Rodríguez et al. 2016, Lynch 2018a). Different statistical models are appropriate for different types of elements, and for pair-matching versus re-association.

Byrd and Legarde (2014) utilize the differences between right side bone measurements and left side bone measurements and compare those differences to zero while using a reference standard deviation of the sum of differences. They then evaluate the deviation from zero using t-distributions with two tails, where the p-values determine the strength of evidence for a pair-match. For re-association, they use a similar method but compare the difference in sizes of the adjoining portions of two elements. The difference between those areas is taken and compared to a mean difference calculated from reference data, and the process with t-distributions is repeated. Rodríguez et al. (2016) employed those osteometric sorting methods and found that they were relatively reliable, but they also stated that all elements should be compared to individuals from the same population. While this is useful information, this seems like it would be an issue in the case mass disasters or burials where the original populations may be unknown or mixed.

When commingled assemblages are too large to use traditional osteometric sorting methods in a timely manner, an automated method can be used instead. The

program OsteoSort, which is an osteological sorting package in the statistical program R, can pair-match, estimate articulations, and associate elements using standard or supplemental measurements (Lynch 2018a). This program utilizes a multivariate ordination approach to calculate the best regression fit between combinations of elements. Since it is automated, numerous analyses can be run consecutively without taking up copious amounts of time while also improving on accuracy of matches. This program can be very useful and save the researcher valuable time, as long as the elements utilized are actually part of the program. The current research was initially going to attempt to use particular measurements of tali and calcanei in OsteoSort for re-associations and pair-matching, but those elements were not available for comparison at the time of data analysis, 2017-2018. OsteoSort can perform many analyses though, some of which include shape analysis of whole and fragmentary elements to produce most probable matches (Lynch 2017, Lynch 2018b), but this will be discussed further in the ‘Additional Methods of Sorting’ section of the Introduction.

The resolution of larger commingled contexts do not rely only visual or osteometric sorting for pair-matching or re-association methods. Typically, most osteometric methods include a visual sorting aspect, since confirming matches requires observing the elements. Previously, Nikita and Lahr (2011) used a combination of measurements, as well as variation in bone formation or resorption at muscle attachment sites, and severity of osteoarthritis to pair-match long bones. All of those variables were compared from right to left side, and the potential matches were given if their differences were below a user-defined level. Potential matches were then visually assessed, whether one match was identified, or more potential matches were suggested. This method pair-

matched from 35% accuracy to 100% accuracy based on differing levels of asymmetry for measurements, muscular attachments, and level of osteoarthritis and it cut down on the amount of visual matching that would have been necessary.

The objective of the current research is to combine both visual and metric methods so that true groupings can be made. The true groupings will be formed using morphological variation of the CSTJ in combination with regression analyses utilizing five measurements on tali and calcanei to re-associate elements, as well as pair-match. A combination of morphological variation and osteometric sorting could potentially cut down on time. When it comes down to making final matches, it is at the discretion of the researcher to make the final call on true pairs, regardless of whether elements were included in predictions or not.

#### *Additional Methods of Sorting*

While traditional visual and metric methods have shown to produce high accuracies in regard to true matching, there are additional types of sorting that can be of use. In particular, the use of two-dimensional outline form data taken from photographs for whole bones (Lynch 2017) and from fragmentary skeletal remains (Lynch et al. 2018b), as well as mesh-to-mesh value comparisons of three-dimensional models of bone (Karell et al. 2016) have been found to have high pair-matching accuracies. These digital methods do not require a lot of handling or manipulation of the elements, which could be especially important in contexts where skeletal remains are fragile.

The two-dimensional methods used by Lynch (2017, and 2018b) focused on the pair-matching of tali and calcanei. These methods only require a particular photograph setup, and then the images can be run through OsteoSort where the size and shape of the

elements can be repeatedly compared to obtain the most probable match for an element. The whole bone analysis had a 98.4% accuracy for pair-matching calcanei, and a 98.2% accuracy for pair-matching tali (Lynch 2017). A slightly adjusted method for fragmentary elements was also developed, and had up to 98% accuracy for fragmented and complete commingled assemblages (Lynch 2018b).

The mesh-to-mesh value comparison utilized CT scans as well as 3D surface scan data to pair-match humeri (Karell et al. 2016). The authors used a manual method which utilized the mirror-image of right humeri, and then compared left humeri to the mirror-images one by one. The manual method had a 100% accuracy for pair-matching humeri, while the automated method that was developed which compared all meshes to each other, had a lower accuracies with 95% sensitivity and 60% specificity.

These shape analysis methods have high accuracy rates, but can be equally as time consuming as traditional methods of sorting (Lynch 2018b). While the two-dimensional methods are automated, they require photos of all available elements and then the processing of the data is still time consuming. The three-dimensional approaches require CT scans or 3D scanning of elements, so the three-dimensional models take a bit of time to create in the first place. Manipulation of those scans manually adds more time to the method, and while the automated approach could potentially be faster it needs improvement with its accuracy of pair-matching (Karell et al. 2016). Regardless, these methods may still be faster than trying to visually pair-match all elements from a large commingled assemblage.

#### *MNI and MLNI*

The preservation of the bones recovered and the scale of the commingling event

(small versus large-scale) are important factors in estimating MNI and MLNI. Initially developed for zooarchaeological applications, these approaches have been adapted for use with human skeletal remains. While MNI calculations for human remains are not particularly different from calculations for zooarchaeological material, the Lincoln Index (LI) was originally developed for studies of living animals (Adams and Konigsberg 2004). The LI was applied on land animals, but it was based on the Petersen Method of capture-recapture techniques in fisheries in order to estimate the size of the living population (Adams and Konigsberg 2004, Peterson and Cederholm 1984, Adams 1951). These estimates were then adapted for use to pair match human and non-human skeletal remains by Adams and Konigsberg (2004) and Konigsberg and Adams (2014).

Calculating MLNI requires that elements from opposite anatomical sides be pair-matched with full accuracy. Adams and Konigsberg (2004) determined that if pair-matching is accurate, MLNI can be a very accurate and useful tool in determining the original number of deceased individuals present in an assemblage, even when recovery of skeletal elements is low due to poor preservation. They also state that some important criteria for choosing elements to calculate MLNI involve the potential for sex and age estimation, as well as the likelihood of survival. Typically, these calculations seem to be made using long bones or the os coxa. Tali and calcanei can still be useful for MLNI estimates since they can be used in population-specific sex estimation (Steele 1976, Gualdi-Russo 2007, Peckmann et al. 2015a, and Peckmann et al. 2015b) while generally age is limited to adult versus subadult determinations.

While MLNI is an important estimation, sometimes these estimations are not completed using only the elements that estimated the MNI. Pair-matching elements that

are not the most frequently occurring is still important when it is possible to combine MLNI estimates. MLNI calculations from different elements that do not overlap, such as tibiae or humeri, can be used in conjunction to come to a conclusion about the MLNI for the whole context (Adams and Konigsberg 2004). MLNI focuses on pair-matching, but if these matched elements can also have re-associations via articulations, the researcher can gain a better understanding of the individuals represented. Grouping elements accurately is important to the overall assessment of the commingling event, regardless of whether those groups focus on the calculation of the MLNI. For the purposes of this research, MNI and MLNI estimates will not be the focus since the test sample is set, but the accurate grouping of elements into individuals will be tested.

#### *Methods for Grouping Tarsal Bones*

The accurate association of elements of individuals in a commingled context is important to gaining understanding of the demographic makeup of the context. Aside from visual matching by size, gross morphology, and taphonomy, metric methods can aid in the re-association of tarsals. Anastopoulou et al. (2017) used measurements on the articular facets of tali and calcanei, as well as measurements of the talar trochlea to create regression analyses to estimate the association of these tarsals. The authors were able to correctly associate elements of the same side with 89% accuracy without the trochlea measurements. Anastopoulou et al. (2017) suggested that they were also able to predict the dimensions of elements of the opposite side. Furthermore, they found that sex was not a significant factor, so their method can be used without first estimating sex. This is important because many commingled assemblages are mixed in regard to sex, and while there are ways to estimate sex from tali and calcanei, this method can still be useful when

sex cannot be estimated (Steele 1976, Gualdi-Russo 2007, Peckmann et al. 2015a, and Peckmann et al. 2015b).

Anastopoulou et al. (2017) also used the morphological compatibility of articular surfaces between the tarsals to aid in their final re-associations. While it was not the primary step in estimating matches, it did contribute to the overall sorting method. The patterns of articular facets on the adjoining tali and calcanei are important in determining whether they are associated. While it may be assumed that size and shape of the corresponding talar and calcaneal facets would be similar within individuals, there is evidence of varying patterns between elements in the same individual (Jung et al. 2015, Anjaneyulu et al. 2014).

Jung et al. (2015) classified calcaneal CSTJ facets into three categories based on the relationship between the anterior, middle, and posterior articular facets (Table 1). Other clinical studies (Sharada et al. 2012, Mol et al. 2012) have described additional facet patterns but typically only for calcanei, and unfortunately the associated talar facet patterns were not discussed in these studies. These additional types and their descriptions can be found in Table 2. The facet pattern types from Jung et al. (2015) and Sharada et al. (2012) will be re-classified for this current research.

According to the literature most facet pattern types are present throughout populations in different geographic regions, but typically the most frequently occurring patterns differ from population to population (Jung et al. 2015). In European populations, the Type A from Jung et al. (2014) is the most common calcaneal facet pattern while Type B is the most common talar facet pattern. Since 90.7% of the sample in the current research from the Texas State University Skeletal Collection (TXSTDSC) consists of

individuals of European ancestry, the frequency of the facet pattern types in this study will certainly be of interest. While Type 4 of the Sharada et al. (2012) study is observed on both elements amongst other studies (Mol et al. 2012, Bilodi 2006, Garg et al. 2013) it was not observed in the TXSTDSC and therefore will not be included in this current research. With those studies in mind, looking at the patterns of articular facets alone does not accurately match associated tali and calcanei, but could probably be useful in the elimination of potential matches for these tarsals.

**Table 1. Descriptions and pairs of CSTJ facet patterns by Jung et al. (2015).**

Type	Description	Matches
A	Separate anterior, middle, separate anterior, middle, and posterior articular facets.	A calcanei – A tali A calcanei – B tali
B	Partially connected anterior and middle facets, but the posterior articular facet is separate.	B calcanei – B tali B calcanei – C tali
C	Anterior and middle articular facets are fully fused, while the posterior articular facet is separate.	C calcanei – C tali

**Table 2. Descriptions of CSTJ facet patterns of calcanei by Sharada et al. (2012).**

Type	Description
3	Two facets, but the anterior facet is on the sustentaculum tali.
4	Just a single fused facet (anterior, middle, and posterior are all fused).

## Research Questions

The current research examines the usefulness of morphological variation of the CSTJ in combination with a multivariate method of osteometric sorting in order to group commingled human tali and calcanei. This combination of visual and metric sorting is used to address the following research questions.

1) Does the combination of matching facet patterns, and the statistical models used to predict measurements reliably associate tali and calcanei from the same anatomical side

with minimal false positive (Type 1 errors) and false negative (Type 2 errors) findings?

Type 1 errors will occur when the correct match is present but not identified. Type 2

errors will occur when a match is identified that is not actually a correct match or a match

is identified when there is no corresponding element present.

2) Does this combination of matching facet patterns and osteometric sorting reliably

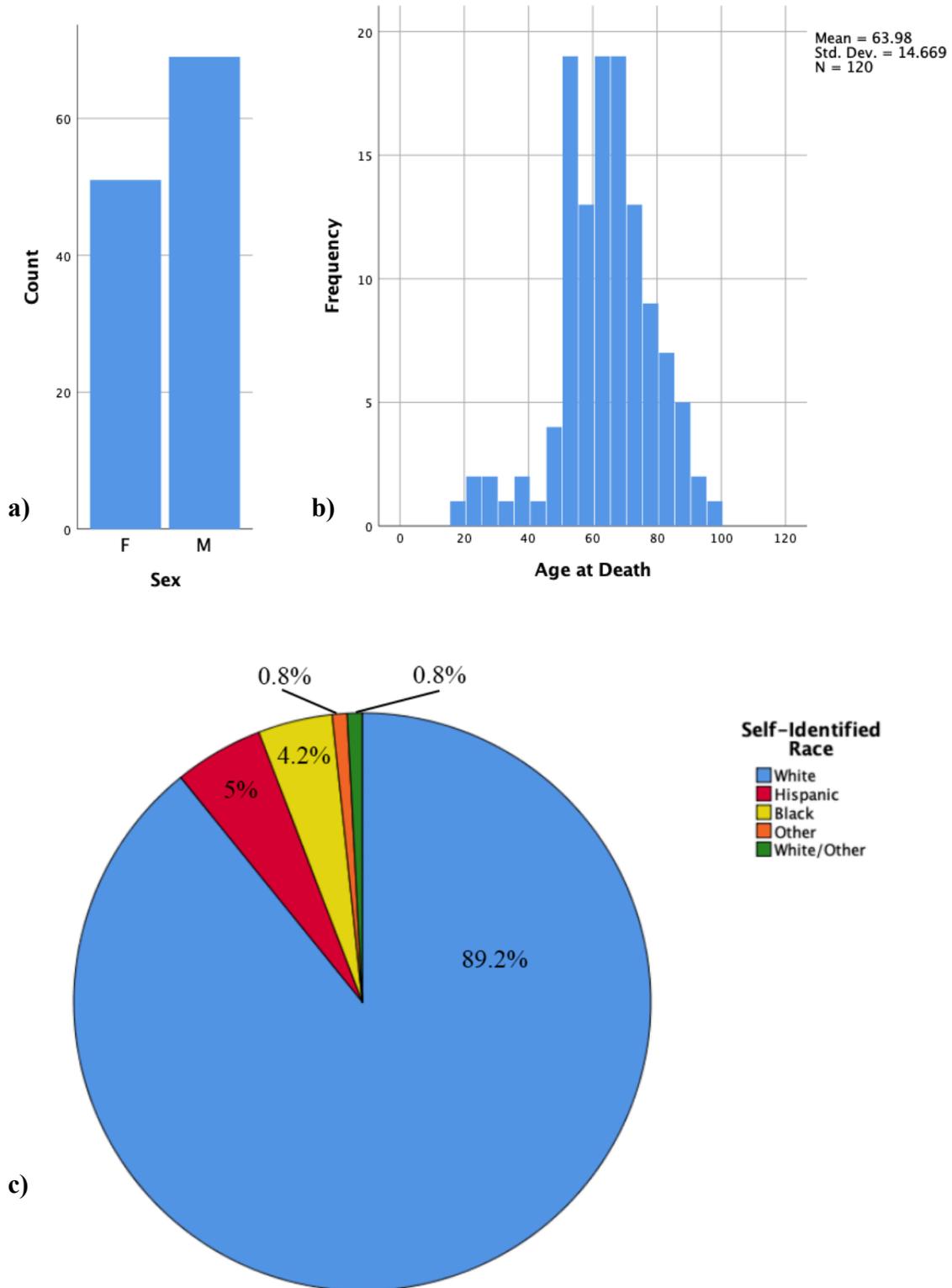
match elements of opposite anatomical sides with minimal Type 1 and Type 2 errors?

## 2. MATERIALS AND METHODS

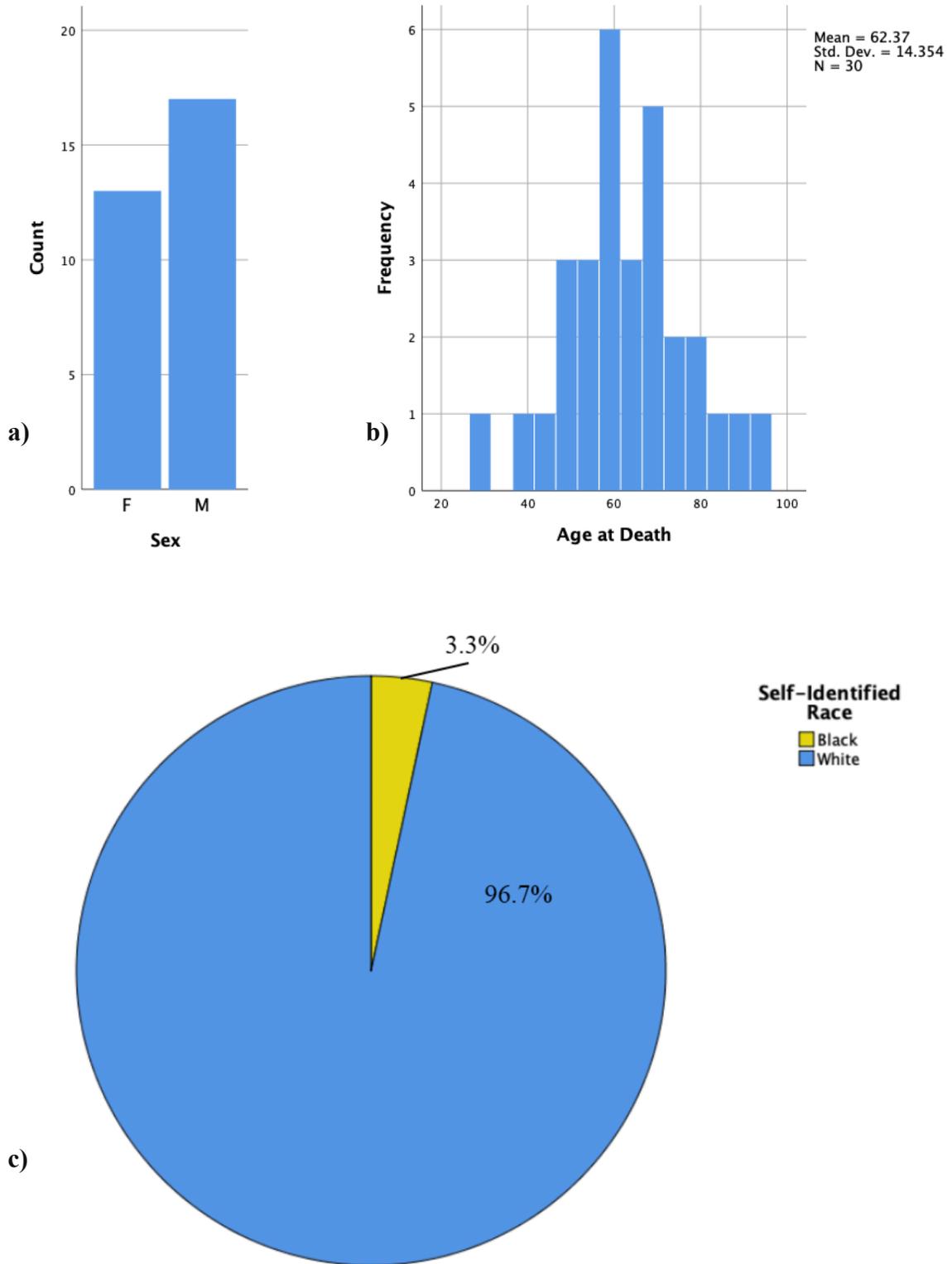
### Materials

Tali and calcanei from 150 known-age and known-sex individuals in the Texas State University Donated Skeletal Collection (TXSTDSC) were used to create the method of interest. Sex was not a factor in the selection process, nor was ancestry. All individuals had a full set of complete calcanei and tali or at least complete CSTJ areas. Any individuals with extensive pathologies or taphonomic damage were excluded from this research. Of the 150 individuals, 120 were used to develop the regression equations while a holdout sample consisting of 30 individuals with varying completeness of a set of elements was used to test the equations.

While the Forensic Anthropology Center at Texas State (FACTS) was created in 2006, the TXSTDSC was started in 2008 with the first donor accepted to the willed body donation program (Wescott 2018). There are currently over 400 individuals in the TXSTDSC, and around 60% are male. The majority of individuals, over 90%, identified as White in life. Still, the current method did not use sex or ancestry as factors for the selection of individuals for the creation of the regression equations, and therefore included males and females, and 12 individuals who self-identify as non-white. All individuals were adults. Demographic data for the sample used to create regression equations can be visualized in Figure 2, while the demographic data for the holdout sample can be visualized in Figure 3. There was only one individual who self-identified as non-white in the holdout sample, but this was unintentional. See Appendix A for a list of the donors and demographic data used to create the regression equations, and Appendix B for a list of the donors and demographic data used in the holdout sample.



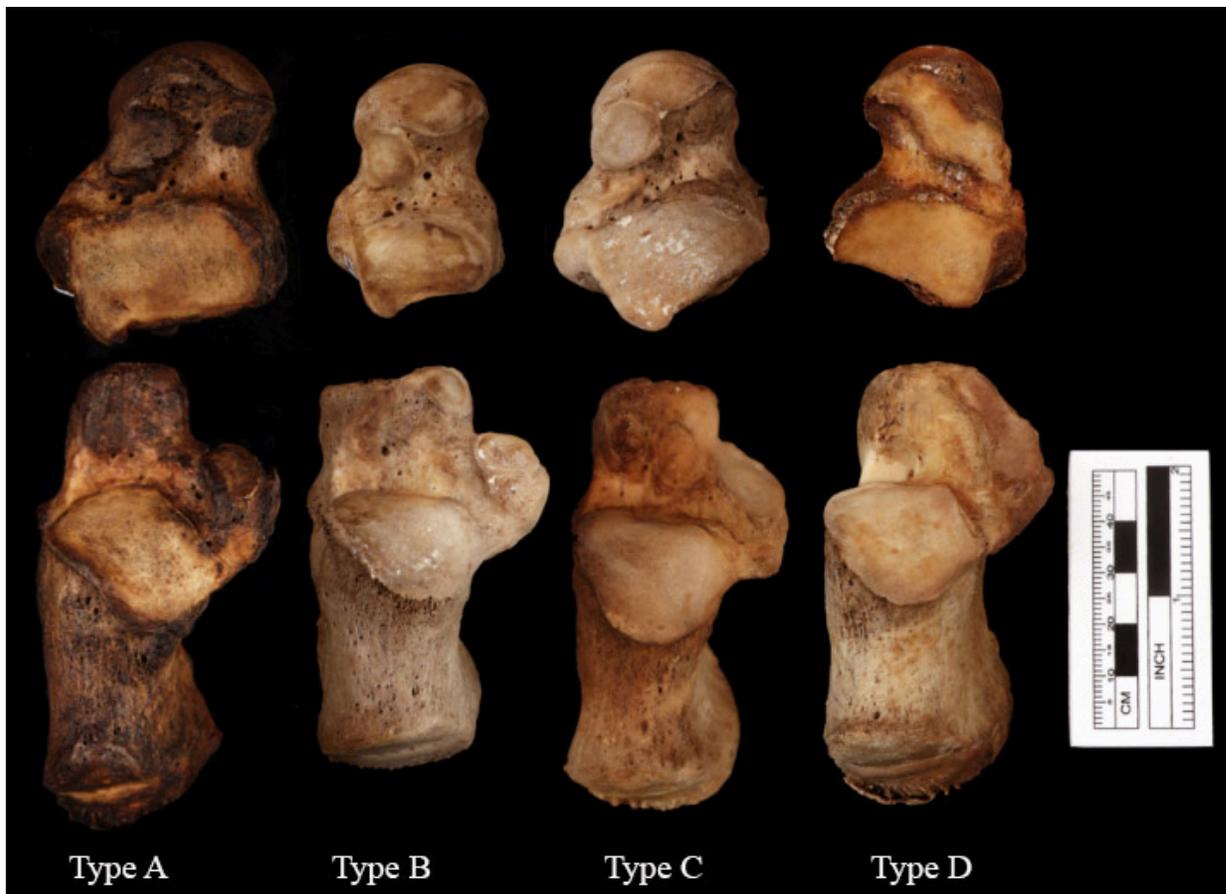
**Figure 2. Demographic data of the individuals used to create the regression equations: (a) number of individuals per sex (F=female; M=male), (b) distribution of the age at death in years for individuals, (c) Self-Identified race of the individuals.**



**Figure 3. Demographic data of the individuals used in the holdout sample test: (a) number of individuals per sex (F=female; M=male), (b) distribution of the age at death in years for individuals, (c) Self-Identified race of the individuals.**

## Facet Pattern Classification

Talocalcaneal facet patterns were classified into four categories based on Jung et al. (2015), as well Sharada et al. (2012) and are displayed in Figure 4. There is an additional type that was recognized in the literature, but not actually observed in the TXSTDSC and was therefore excluded from this research, though the description was included for cases where this pattern is actually present. The descriptions for each pattern type can be found in Table 3.



**Figure 4. Facet Patterns of tali and calcanei from the CST joint.**

**Table 3. Descriptions of the facet pattern types used in this research.**

<b>Type</b>	<b>Description</b>
A	There are two articular facets present – there is no anterior facet, but the middle facet and posterior articular facets are present.
B	Three articular facets are present – there is an anterior facet, middle facet, and a posterior articular facet. All facets are separate.
C	These elements have two articular facets present, one of which is the posterior articular facet – the anterior and middle facets are fused, but there is a constriction between the two facets on calcanei, or a noticeable angle on tali.
D	Two articular facets are present, one of which is the posterior articular facet – the anterior and middle facets are fused, there is no constriction on the calcaneal facet, and for both elements the facet is fairly flat.

### **Data Collection – Measurements**

Three measurements were collected on tali, as well as calcanei following Martin (1988), and two were new to this study. These measurements can be found in Table 4, and Figure 5. The length (CAL, TAL), width (CAW, TAW), and breadth (CAB, TAB) of each element was taken using a sliding caliper to the nearest 0.1mm, while fraction and subtense were collected with a Microscribe digitizer to the nearest 0.01mm. The fraction (CAF, TAF) and subtense (CAS, TAS) were taken as an arc and calculated the most superior point of the posterior articular facets. The purpose of taking the most superior point of the arc of the posterior articular facet was that visually some elements are flatter while others have a higher peak. The fraction and subtense were collected by setting the digitizer to autoscan at 0.5ms and dragging the point of the digitizer through the middle of the facet lengthwise. The start and end points for this line were designated by marking the points that were used to measure the length of the facet. The digitizer point was dragged from the lateral edge of the facet, to the medial edge to maintain consistency in the calculation of the fraction.

In addition to the fraction and subtense, the angle of the arc at the most superior

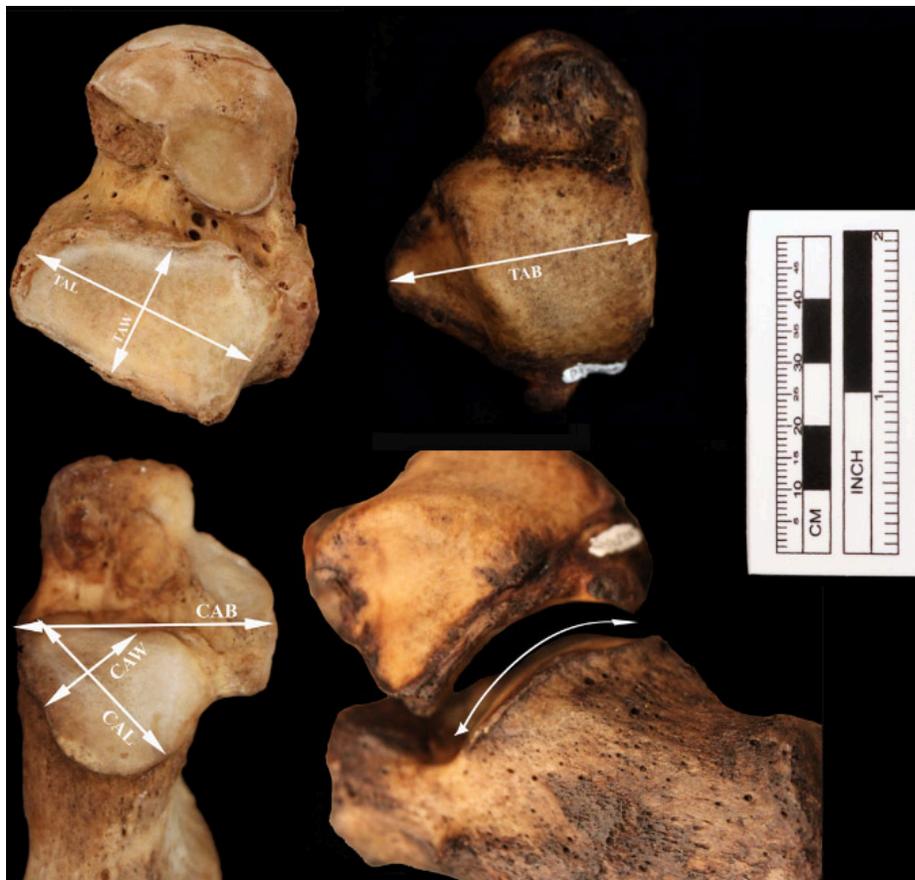
point was calculated. However, this variable had a low correlation with other variables and did not aid in the predictions made by the regression equations. As a result, the angle was dropped and is not used in any of the sorting models.

**Table 4. Measurement descriptions and abbreviations used in this research.**

Measurement	Abbreviation	Description	Reference
Length of the posterior articular facet on the talus	TAL	This measurement is taken transversely across the middle of the posterior articular facet of the talus.	Anastopoulou et al. 2017 following Martin 1988
Width of the posterior articular facet of the talus	TAW	This measurement is taken from anterior to posterior, in the middle of the posterior articular facet of the talus.	Anastopoulou et al. 2017 following Martin 1988
Breadth of the talus	TAB	This measurement is the distance between the most medial point of the posterior process, and the most lateral point on the lateral process of the talus.	Martin 1988
Subtense of the posterior articular facet of the talus	TAS	This measurement is taken at the most superior point of the posterior articular facet of the talus.	Unique to this study
Fraction of TAS	TAF	This measurement is taken in tandem with TAD, and is the location where TAD is taken across the articular facet.	Unique to this study
Length of the posterior articular facet of the calcaneus	CAL	This measurement is taken transversely across the middle of posterior articular facet of the calcaneus.	Anastopoulou et al. 2017 following Martin 1988
Width of the posterior articular facet of the calcaneus	CAW	This measurement is taken perpendicular to CAL, in the middle of the posterior articular facet of the calcaneus.	Anastopoulou et al. 2017 following Martin 1988

**Table 4. Continued**

Breadth of the calcaneus	CAB	This measurement is taken as the distance between the most medial point on the sustentaculum tali, and the most lateral point on the dorsal articular facet of the calcaneus.	Martin 1988
Subtense of the posterior articular facet of the calcaneus	CAS	This measurement is taken at the most superior point of the posterior articular facet of the calcaneus.	Unique to this study
Fraction of CAS	CAF	This measurement is taken in tandem with CAS, and is the location where CAS is taken across the articular facet.	Unique to this study



**Figure 5. Measurements of the talus above, measurements of the calcaneus below, and the line indicating how fraction and subtense are collected on bottom right.**

## **Statistical Analyses**

The data were analyzed in the SPSS software package (IBM Inc., Armonk NY, USA; version 26 for MAC) and a Shapiro-Wilks test was run to assess the normality of the data. To check for intra-observer error, measures were taken on 10 individuals twice, with over two weeks between the first and second measurements. Paired-samples t-tests were used to assess the intra-observer error. Then, simple and multiple regression analyses were run to create the equations for re-association and for pair-matching using 120 individuals. The re-association equations used the talus measures to predict calcaneus measures, while the pair-matching equations used the left elements to predict the right elements. Type 1 and Type 2 errors from the final sort and groupings were assessed.

## **Test Sample**

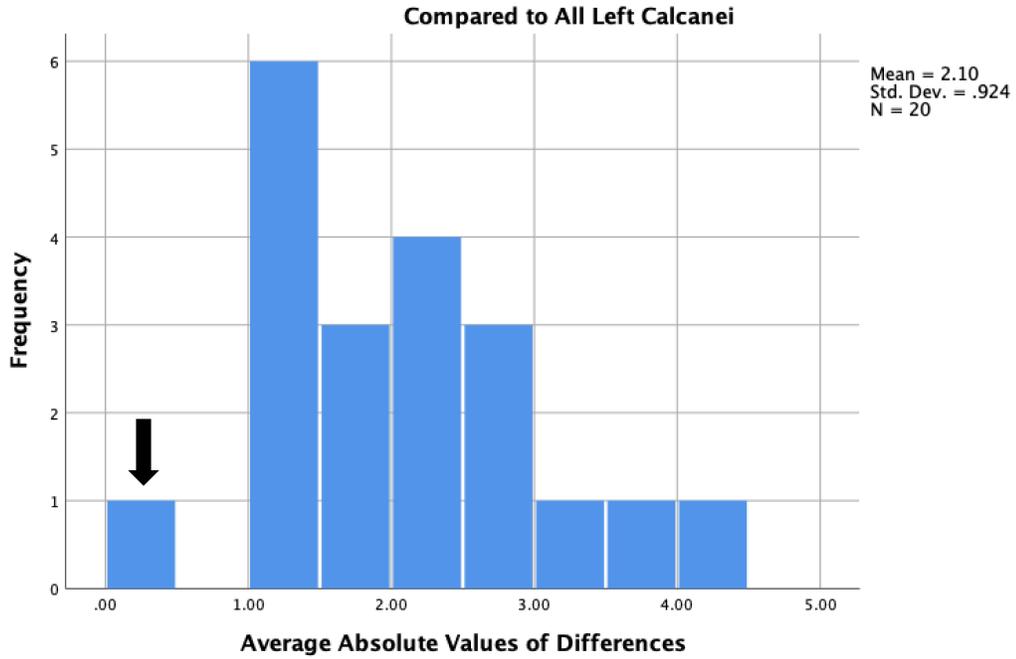
Only 85 out of 120 elements ended up being used from the holdout sample, so all four elements were present in the assemblage for some individuals, while others may have been represented by three or less elements. Since this particular method focuses on the re-association of two elements, and the pair-matching of two elements, any pairings that included a right talus and a left calcaneus or vice versa were changed by a colleague to either match sides or match elements. The donation number of each individual was obscured by the same colleague, and a randomized bone ID was assigned to each element. These elements and their codes can be found in Table 5.

**Table 5. List of donations and the elements that were present for this test.**

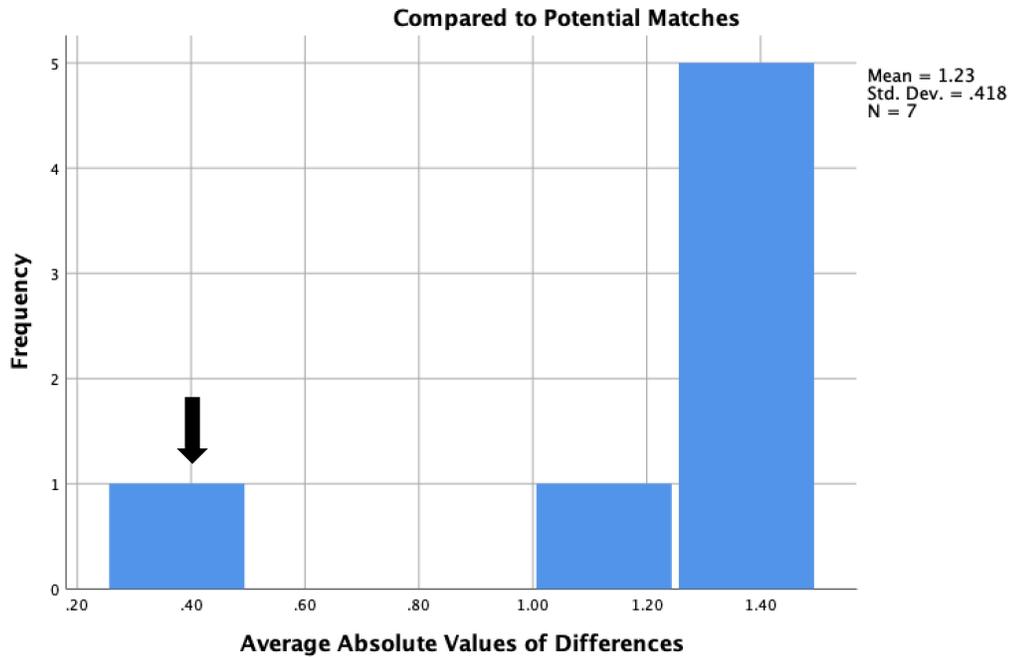
	<b>L Cal</b>	<b>L Tal</b>	<b>R Cal</b>	<b>R Tal</b>
2012.004	52	-	23	24
2012.006	53	64	3	-
2012.012	5	6	70	51
2012.013	43	-	42	62
2012.015	76	35	-	21
2012.016	17	69	-	67
2012.018	19	18	40	-
2013.014	20	71	56	65
2013.015	-	61	57	10
2013.050	58	-	26	68
2013.054	28	83	27	-
2013.055	33	79	48	45
2014.013	38	-	81	-
2014.014	80	12	72	-
2014.016	-	4	25	47
2014.017	-	-	37	60
2014.042	-	-	-	85
2014.043	-	36	-	13
2014.044	73	-	29	-
2014.047	-	49	1	41
2014.049	2	7	-	-
2014.056	-	77	-	-
2014.060	63	-	46	54
2014.062	75	39	9	34
2014.064	50	78	30	84
2014.065	-	-	74	59
2015.012	-	-	-	44
2015.060	66	22	82	32
2016.009	11	55	15	14
2016.051	-	31	16	8

To test the method using the holdout group, elements were sorted by side, measured, and their facet patterns classified. The regression equations were used to predict measurements for a paired element. The difference between actual measurements of the elements in the assemblage and predicted measurements was calculated, the absolute value of each difference was taken, and then the average of the combinations of those values was taken per element. This multivariate method made it possible to rank elements from the lowest average difference up to a cutoff of 1.5mm average difference.

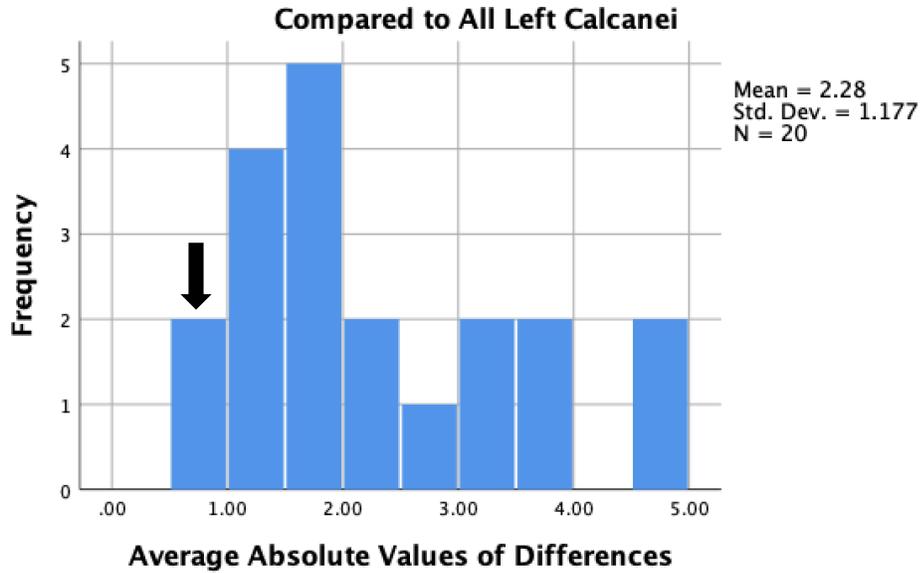
Two examples are provided below. Figures 6 and 7 depict histograms showing the true match for talus 7 using the prediction measurements from the multiple regression equation for left re-associations. Figure 6 depicts the average of the absolute values of differences between talus 7 and all left calcanei. Figure 7 depicts those values of only the potential matches below 1.5mm average difference. None of these potential matches had mismatching facet patterns, therefore none were eliminated. An example of the template for comparisons for talus 7 can be observed in Appendix C. Figures 8 through 10 depict histograms showing the true match for talus 12 using the prediction measurements from the multiple regression equation for left re-associations. Figure 8 depicts the average of the absolute values of differences between talus 12 and all left calcanei. Figure 9 depicts those values of only the potential matches below 1.5mm average difference. Figure 10 depicts the potential matches that were left over after the comparison of facet patterns. This resulted in the elimination of two potential matches, which put the true match for talus 12 as the first ranked potential match.



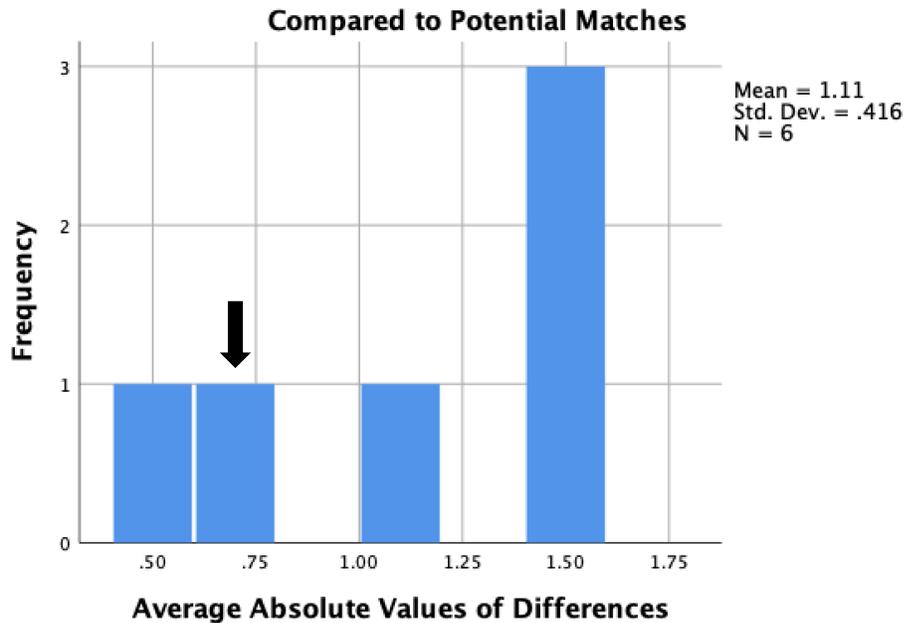
**Figure 6. Histogram comparing talus 7 to all left calcanei using the average of the absolute values of the differences between the talus and calcaneal elements. The black arrow indicates the true match.**



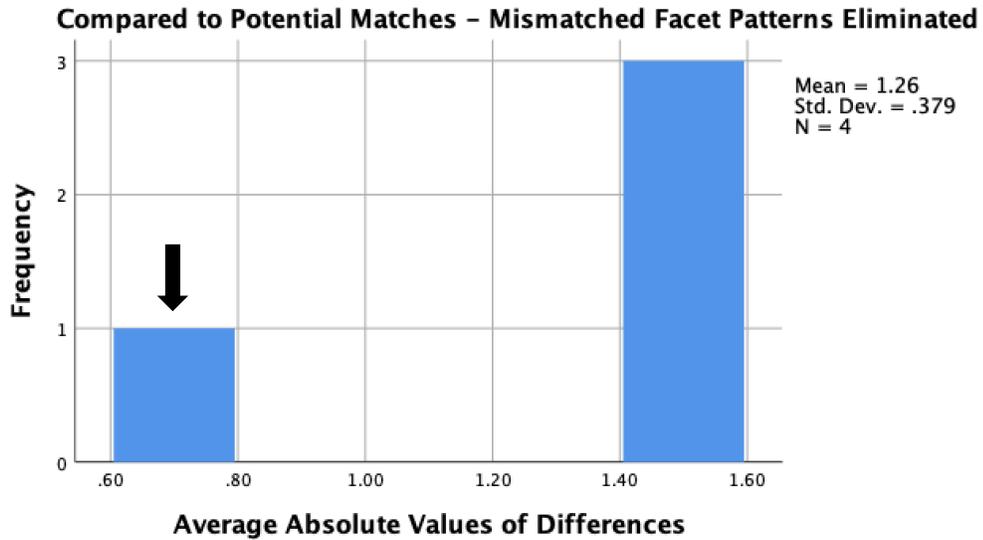
**Figure 7. Histogram comparing talus 7 to the potential matches predicted using the average of the absolute values of the differences between the talus and calcaneal elements. The black arrow indicates the true match.**



**Figure 8. Histogram comparing talus 12 to all left calcanei using the average of the absolute values of the differences between the talus and calcaneal elements. The black arrow indicates the true match.**



**Figure 9. Histogram comparing talus 12 to the potential matches predicted using the average of the absolute values of the differences between the talus and calcaneal elements. The black arrow indicates the true match.**



**Figure 10. Histogram comparing talus 12 to the potential matches predicted where calcanei with mismatching facet patterns have been removed. The black arrow indicates the true match.**

After potential matches were ranked and elements with mismatched facet patterns eliminated, an initial sort using the simple regression predictions was completed. First, elements that had the lowest average differences were assessed and as matches were confirmed, potential matches were eliminated for remaining elements. Final matches were made based on other typical sorting techniques. This process was repeated for the multiple regression predictions. Once final matches for the multiple regression predictions were made, an initial round of combining the results of the re-associations and pair-matchings was completed. Any groupings with conflicting matches were reassessed and a final round of the combined sorting methods was completed.

### 3. RESULTS

The results of the Shapiro-Wilks test showed that all measured variables used to create the regression equations were normally distributed. The descriptive statistics for these measurements are displayed in Table 6.

**Table 6. Descriptive statistics of the measured variables.**

	N	Range	Mean		Std. Deviation
	Statistic	Statistic	Statistic	Std. Error	Statistic
L Cal Length of PAF	120	12.80	30.5678	0.25627	2.80728
L Cal Width of PAF	120	14.69	21.9648	0.21413	2.34568
L Cal Breadth	120	17.00	42.5449	0.29613	3.24394
L Cal Fraction	120	9.21	18.7103	0.17799	1.94978
L Cal Subtense	120	4.85	5.4519	0.08190	0.89712
R Cal Length of PAF	120	13.90	30.7143	0.27352	2.99627
R Cal Width of PAF	120	13.64	22.1303	0.22197	2.43156
R Cal Breadth	120	16.40	42.5528	0.30187	3.30686
R Cal Fraction	120	8.42	18.7799	0.16976	1.85966
R Cal Subtense	120	4.63	5.5188	0.08438	0.92436
L Tal Length of PAF	120	13.10	30.6248	0.24521	2.68611
L Tal Width of PAF	120	10.40	21.9916	0.20080	2.19963
L Tal Breadth	120	14.70	44.2675	0.31496	3.45019
L Tal Fraction	120	9.75	17.9829	0.17300	1.89515
L Tal Subtense	120	5.03	5.7397	0.08171	0.89508
R TAL Length of PAF	120	14.60	30.1524	0.24711	2.70694
R TAL Width of PAF	120	10.50	22.2391	0.21786	2.38655
R TAL Breadth	120	15.61	44.2589	0.32182	3.52532
R TAL Fraction	120	8.35	17.9786	0.17355	1.90117
R TAL Subtense	120	4.56	5.6812	0.08583	0.94026

## Intra-observer Error

The results of the paired-samples t-tests to check the intra-observer error are displayed in Table 7. All of the comparisons were statistically significant. All elements were assigned the same facet pattern from the first classification to the second.

**Table 7. Intra-observer error per measurement.**

	Paired Differences					t	df	Sig. (2-tailed)
	Mean	Std. Deviation	Std. Error Mean	95% Confidence Interval of the Difference				
				Lower	Upper			
L CAL Length	0.05300	0.72243	0.22845	-0.46380	0.56980	0.232	9	0.822
L CAL Width	-0.17000	0.69025	0.21828	-0.66377	0.32377	-0.779	9	0.456
L CAL Breadth	0.22800	0.68833	0.21767	-0.26440	0.72040	1.047	9	0.322
L CAL Fraction	0.41300	1.43743	0.45455	-0.61527	1.44127	0.909	9	0.387
L CAL Subtense	0.13500	0.42438	0.13420	-0.16858	0.43858	1.006	9	0.341
R CAL Length	0.16800	0.91473	0.28926	-0.48636	0.82236	0.581	9	0.576
R CAL Width	-0.50700	1.23408	0.39025	-1.38981	0.37581	-1.299	9	0.226
R CAL Breadth	0.47000	0.80748	0.25535	-0.10764	1.04764	1.841	9	0.099
R CAL Fraction	-0.12900	1.35681	0.42906	-1.09960	0.84160	-0.301	9	0.771
R CAL Subtense	0.18600	0.29148	0.09217	-0.02251	0.39451	2.018	9	0.074
L TAL Length	0.02400	0.67905	0.21474	-0.46177	0.50977	0.112	9	0.913
L TAL Width	-0.02000	0.80905	0.25584	-0.59876	0.55876	-0.078	9	0.939
L TAL Breadth	-0.52500	0.92044	0.29107	-1.18344	0.13344	-1.804	9	0.105
L TAL Fraction	-0.56500	1.43628	0.45419	-1.59245	0.46245	-1.244	9	0.245
L TAL Subtense	-0.10900	0.33408	0.10565	-0.34799	0.12999	-1.032	9	0.329
R TAL Length	-0.05800	1.00859	0.31895	-0.77950	0.66350	-0.182	9	0.860
R TAL Width	-0.05200	0.79095	0.25012	-0.61781	0.51381	-0.208	9	0.840
R TAL Fraction	0.07800	1.48860	0.47074	-0.98688	1.14288	0.166	9	0.872
R TAL Subtense	-0.05700	0.23824	0.07534	-0.22742	0.11342	-0.757	9	0.469

## Facet Patterns

The facet patterns were more complicated than originally thought, and as such their classifications were not as cut and dry. The frequency of each facet pattern is shown in Table 8. The most frequent pattern type in calcanei was Type B, while the most frequent pattern type in tali was Type C. Facet pattern combinations between articulating elements were generally as follows: Type A calcanei – Type A tali, Type B calcanei – Type B tali, Type B calcanei – Type C tali, Type C calcanei – Type C tali, Type C calcanei – Type D tali, Type D calcanei – Type D tali. Due to issues with choosing one type for a classification, percentages for each combination were excluded.

Elements from opposite sides tended to have matching facet patterns, and if they were different it was typically only shifted one type, so that a left calcaneus might have a Type B pattern while a right calcaneus might have a Type C pattern. This mismatch of patterns occurred in around 10.8% of the calcaneal pairs that had clearly classifiable facet patterns. This was 10 out of 103 pairs, and only one out of those 103 pairs were shifted by two types. The mismatch of pattern types in tali with clearly classifiable facet patterns occurred 10.7% of the time, with six out of 75 pairs shifted by one type and one out of the 75 pairs shifted by two types.

**Table 8. Frequencies of facet patterns per element.**

Facet Type	L CAL	L TAL	R CAL	R TAL	Total CAL	Total TAL
A	2.5 % (3/120)	3.3% (4/120)	1.7% (2/120)	1.7% (2/120)	2.1% (5/240)	2.5% (6/240)
A or B	0%	4.2% (5/120)	0.8% (1/120)	5.8% (7/120)	0.4% (1/240)	5% (12/240)
B	55.8% (67/120)	17.5% (21/120)	54.2% (65/120)	17.5% (21/120)	55% (132/240)	17.5% (42/240)
B or C	5% (6/120)	7.5% (9/120)	2.5% (3/120)	5.8% (7/120)	3.7% (9/240)	6.7% (16/240)
C	25.8% (31/120)	45.8% (55/120)	25.8% (31/120)	42.5% (51/120)	25.8% (62/240)	44.2% (106/240)
C or D	4.2% (5/120)	14.2% (17/120)	8.3% (10/120)	16.7% (20/120)	6.3% (15/240)	15.4% (37/240)
D	6.7% (8/120)	7.5% (9/120)	6.7% (8/120)	10% (12/120)	6.7% (16/240)	8.7% (21/240)

**Re-association Regression Equations**

The simple regression equations to re-associate elements from the same side are displayed in Table 9, as well as each equation’s Standard Error of the Estimate (SEE), Pearson’s Correlation (r), and r-squared values. The same information for the multiple regression equations are in Table 10.

**Table 9. Simple regression equations for re-associating elements of the same side.**

	Regression Equation	SEE	r	r <sup>2</sup>
<i>Left</i>	CAL = 2.05 + 0.93TAL	1.23	0.89	0.79
	CAW = 0.91 + 0.96TAW	1.04	0.9	0.81
	CAB = 5.89 + 0.83TAB	1.54	0.88	0.78
	CAF = 5.42 + 0.74TAF	1.36	0.72	0.52
	CAS = 0.72 + 0.82TAS	0.51	0.82	0.68
<i>Right</i>	CAL = 1.01 + 0.99TAL	1.37	0.89	0.79
	CAW = 2.23 + 0.9TAW	1.17	0.88	0.77
	CAB = 6.00 + 0.83TAB	1.58	0.88	0.78
	CAF = 4.09 + 0.82TAF	1.03	0.84	0.7
	CAS = 0.91 + 0.81TAS	0.52	0.83	0.68

**Table 10. Multiple regression equations for re-associating elements of the same side.**

	Regression Equation	SEE	r	r <sup>2</sup>
<i>Left</i>	CAL = -1.51 + 0.56TAL + 0.21TAW + 0.21 TAB + 0.06TAF + 0.01TAS	1.14	0.92	0.84
	CAW = 1.18 + 0.05TAL + 0.95TAW - 0.05TAB - 0.05TAF + 0.21TAS	1.04	0.9	0.81
	CAB = 5.58 + 0.2TAL + 0.26TAW + 0.59TAB - 0.90TAF + 0.08TAS	1.46	0.9	0.81
	CAF = 0.74 + 0.10TAL + 0.04TAW + 0.10TAB + 0.53TAF + 0.05TAS	1.27	0.77	0.59
	CAS = -0.09 - 0.10TAL + 0.02TAW + 0.07TAB + 0.03TAF + 0.78TAS	0.5	0.84	0.71
<i>Right</i>	CAL = -3 + 0.62TAL + 0.22TAW + 0.19TAB + 0.16TAF - 0.20TAS	1.15	0.93	0.86
	CAW = 1.29 + 0.24TAL + 0.83TAW - 0.04TAB - 0.26TAF + 0.22TAS	1.09	0.9	0.81
	CAB = 4.76 + 0.26TAL + 0.12TAW + 0.52TAB + 0.25TAF + 0.01TAS	1.44	0.9	0.82
	CAF = 3.84 + 0.03TAL + 0.01TAW - 0.001TAB + 0.82TAF - 0.12TAS	1.04	0.84	0.7
	CAS = 0.43 + 0.004TAL - 0.05TAW + 0.04TAB - 0.01TAF + 0.80TAS	0.52	0.83	0.69

### Pair-Matching Regression Equations

The simple regression equations for pair-matching opposite side elements are included in Table 11, which also include the SEE, r value, and r<sup>2</sup> values. The multiple regression equations that predict the opposite element are included in Table 12.

**Table 11. Simple regression equations for predicting right element measurements from the left side in order to pair-match elements.**

Regression Equation	SEE	r	r <sup>2</sup>
Right CAL = 1.09 + 0.97CAL	1.26	0.91	0.83
Right CAW = 1.14 + 0.96CAL	0.95	0.92	0.85
Right CAB = 0.90 + 0.98CAB	0.93	0.96	0.92
Right CAF = 6.17 + 0.67CAF	1.32	0.71	0.5
Right CAF = 0.70 + 0.89CAS	0.48	0.86	0.74
Right TAL = 3.07 + 0.88TAL	1.3	0.88	0.77
Right TAW = 0.47 + 0.99TAW	0.98	0.91	0.83
Right TAB = 1.29 + 0.97TAB	1.11	0.95	0.9
Right TAF = 6.64 + 0.63TAF	1.48	0.63	0.4
Right TAS = 0.32 + 0.93TAS	0.43	0.89	0.79

**Table 12. Multiple regression equations for predicting right element measurements from the left side in order to pair-match elements.**

Regression Equation	SEE	r	r <sup>2</sup>
Right CAL = -1.36 + 0.80CAL - 0.002CAW + 0.16CAB + 0.05 CAF + 0.06CAS	1.24	0.91	0.84
Right CAW = 0.08 + 0.09CAL + 0.89CAW + 0.06CAB - 0.08CAF - 0.24CAS	0.92	0.93	0.86
Right CAB = 0.58 + 0.02CAL - 0.06CAW + 0.96CAB + 0.08CAF + 0.09CAS	0.92	0.96	0.93
Right CAF = 2.02 - 0.01CAL - 0.07CAW + 0.17CAB + 0.49CAF + 0.39CAS	1.23	0.76	0.58
Right CAS = -0.01 - 0.03CAL + 0.02CAW + 0.03CAB + 0.01CAF + 0.85CAS	0.48	0.86	0.74
Right TAL = 1.02 + 0.72TAL - 0.06TAW + 0.14TAB + 0.07TAF + 0.21TAS	1.27	0.89	0.79
Right TAW = -0.97 + 0.11TAL + 0.90TAW - 0.03TAB + 0.10TAF - 0.04TAS	0.96	0.92	0.85
Right TAB = 1.31 + 0.03TAL + 0.10TAW + 0.92TAB - 0.03TAF - 0.07TAS	1.11	0.95	0.91
Right TAF = -1.55 - 0.01TAL - 0.10TAW + 0.33TAB + 0.27TAF + 0.44TAS	1.13	0.82	0.66
Right TAS = 0.17 - 0.04TAL + 0.03TAW + 0.04TAB - 0.05TAF + 0.94TAS	0.42	0.9	0.81

### Sample Test

The simple and multiple regression predictions tended to have anywhere from one to 12 predicted matches. Facet patterns did manage to eliminate potential matches for most elements. The sorting from the simple regression predictions and the multiple regression predictions ended up being the same. The initial groupings from the combination of regression predictions and facet pattern elimination is displayed in Table 13, in congruence with the resulting groupings from the final sort. In the initial grouping there were six Type 1 errors where a match should have been made, and there were two Type 2 errors, where a false match was made. In the final grouping, there were three Type 1 errors, and only one Type 2 error (Table 14). In both groupings, there was a match that was made when it should have been by itself. After the final grouping, the left elements were re-associated with 84.6% accuracy, the right elements were re-associated with 93.8% accuracy, the calcanei were pair-matched with 93.8% accuracy, the tali were pair-matched with 93.3% accuracy, and the solo elements were classified as solo with

66.7% accuracy (Table 14).

Out of the seven instances where all four elements were present, all were properly matched after the first attempt. In the initial grouping, 14 individuals had three elements present, and five errors occurred. There were six individuals that only had two elements present, whether it was a pair on one side or a pair of elements from opposite sides, with only one error occurring. There were three individuals that were only represented by one element, and one error occurred that involved matching with a proper group of three other elements.

After the initial grouping, there were about seven errors total, and two were resolved in the final set of groupings. Calcaneus 28 was predicted with a fairly similar average difference to re-associate with either talus 61 or talus 83. Both seemed likely, but the decision was originally made to re-associate it with talus 61. Then, when comparing the rest of that grouping, it was found that while talus 61 matched with talus 10, and talus 10 re-associated with calcaneus 57, calcaneus 28 was actually paired with Calcaneus 27. When all the groupings were complete, it was confirmed that 61, 57, and 10 seemed to actually group together and was then decided that calcaneus 28 probably went with talus 83 instead, which resolved the issue of a different right calcaneus being included in the group.

The remainder of the issues involved the exclusion of codes 81, 17, and 1, as well as the incorrect match of talus 77 to talus 24, which led to its inclusion in a group when it was actually a solo element. While talus 77 was originally thought to have no association, calcaneus 52 was not fully eliminated from the match and it was thought that potentially an error had been made when re-associating which kept talus 77 in the group,

allowing for Type 2 errors. Calcaneus 81 was not on the prediction list as a match for calcaneus 38, but when actually sorting the elements it was evident that visually they did match based on taphonomic coloring and texture. Since it was not part of the prediction though, it was still counted as a Type 1 error.

A similar issue occurred with calcaneus 1, it did not show up as a prediction for talus 41 which lead to its exclusion from that group of elements. It was noticed visually that they likely matched, since there actually was similar osteoarthritis on the elements, but the posterior articular facet measurements were just too different between the two to allow it to be a prediction. Calcaneus 17 did appear as the last prediction before the cutoff value for talus 69 for both the simple and multiple regression predictions, but it was ultimately not chosen as a match for the talus. This was no fault of the equations, but the fault of the author.

**Table 13. Depictions of the initial groupings on the left, and final groupings on the right with Type 1 errors highlighted in blue, Type 2 errors highlighted in red. Elements that were changed and ended up correct have an asterisk next to the code. Elements with parentheses indicate what the correct placement in a grouping should have been.**

Initial Groupings				Final Groupings			
L Cal	L Tal	R Cal	R Tal	L Cal	L Tal	R Cal	R Tal
52	77	23	24	52	77	23	24
53	64	3	-	53	64	3	-
5	6	70	51	5	6	70	51
43	-	42	62	43	-	42	62
76	35	-	21	76	35	-	21
(17)	69	-	67	(17)	69	-	67
19	18	40	-	19	18	40	-
20	71	56	65	20	71	56	65
28	61	57/(27)	10	-*	61	57*	10
58	-	26	68	58	-	26	68
(28)	83	(27)	-	28*	83	27*	-
33	79	48	45	33	79	48	45
38	-	(81)	-	38	-	(81)	-
80	12	72	-	80	12	72	-
-	4	25	47	-	4	25	47
-	-	37	60	-	-	37	60
-	-	-	85	-	-	-	85
-	36	-	13	-	36	-	13
73	-	29	-	73	-	29	-
-	49	(1)	41	-	49	(1)	41
2	7	-	-	2	7	-	-
-	(77)	-	-	-	(77)	-	-
63	-	46	54	63	-	46	54
75	39	9	34	75	39	9	34
50	78	30	84	50	78	30	84
-	-	74	59	-	-	74	59
-	-	-	44	-	-	-	44
66	22	82	32	66	22	82	32
11	55	15	14	11	55	15	14
-	31	16	8	-	31	16	8

**Table 14. Frequency of correct matches per association as well as Type 1 and Type 2 errors.**

<b>Type of Sorting</b>	<b>Correct</b>	<b>Type 1 Errors</b>	<b>Type 2 Errors</b>
<b>Left Re-association</b>	11/13 (84.6%)	1	1
<b>Right Re-association</b>	15/16 (93.8)	1	-
<b>Calcaneus Pair-Match</b>	15/16 (93.8%)	1	-
<b>Talus Pair-Match</b>	14/15 (93.3%)	-	1
<b>Solo elements</b>	2/3 (66.7%)	-	1

## 4. DISCUSSION

The purpose of this study was to create a method that would be successful in reuniting tali and calcanei from ipsilateral and contralateral sides from a commingled assemblage. This was accomplished by looking at morphological variations in the CSTJ area, as well as utilizing measurements from the posterior articular facet, and the breadth of each element. While most elements were successfully grouped with the rest of the available elements from the same individual, there were a few instances where successful matches were not made and there was one instance in which an element was incorrectly paired.

### **Facet Patterns**

The most common pattern for calcanei was Type B, while the most common talus facet pattern was Type C. This followed Jung et al. (2012), where the higher frequencies of Type B calcanei and Type C tali were linked to European populations. Since the majority of the individuals used in the current research are White, these frequencies may be connected to a European ancestry. These particular facet patterns are known to be associated with one another, and this research further supports this articulation. There were issues with classifying facet patterns, particularly with tali, since even though the current literature has shown five types of patterns per element there seem to be elements that do not quite fit the descriptions and images that were found. Elements were classified anyways, so that even a general elimination might occur in instances where the facet pattern was potentially a Type A or B, and neither would pair with Type D. Classification of the morphological variation of these facets was useful in the matching of elements, especially for the re-association of elements. Since elements from opposite sides tended

to have matching facet pattern types, the use of these patterns for pair-matching was still helpful in eliminating potential matches.

### **Regression Equations and Multivariate Predictions**

The measurements in this research were chosen because most of them are contained to one area, and generally breadth measurements can be estimated if needed. If the whole posterior articular facet is present, then four measurements are available, though the fraction and subtense might be difficult to collect via digitizer on more friable elements.

The regression formulae show that there were high correlations between the length, width, breadth, and subtense measurements but that fraction measures were typically not as high. There were definitely issues with collecting the fraction and subtense since using a digitizer is so precise, and any unsteadiness meant extra data was collected, or possibly data was left out. Another issue was due to the fact that the articular surfaces are not smooth and even surfaces. Frequently, articular surfaces have slight dips and, since the digitizer is fairly precise, it recorded these surface irregularities. The use of a coordinate caliper was attempted before using a digitizer, but it was less precise and equally difficult to use. While the method of data collection could have been an issue, the lower correlations of the subtense and fraction measurements could just be due to the fact that the measurements themselves do not correlate well. They did seem to enhance the multiple regression equations, but alone they would not be useful in predicting a true pair.

### **Test Sample**

One thing to discuss with this test sample is the fact that they are all from donors, which means the taphonomy of many of these individuals is rather unique. While some

donors decompose on the surface for about a year, whether in the sun or the shade, others might have been buried or stayed out at the decomposition facility for shorter or longer amounts of time. This definitely has effects on the elements and helped make them more unique from one another. Some elements very visibly matched others based on color and texture alone, but in mass burial contexts this likely would not be the case. For bioarchaeological material, many elements end up being the same color because they are buried for anywhere from 50 years to thousands of years. This means that the color and texture of most of these elements is probably very similar, eliminating those variables as factors for sorting. Even in forensic settings, where a mass burial may occur, if all individuals are buried in the same grave within a small enough amount of time, it is likely that the elements will all stain similarly and have similar texture. Utilizing methods of sorting using measurements and morphological aspects of the elements can aid in accurate sorting of an assemblage that cannot be segregated based on taphonomic staining and texture.

The purpose of varying the presence of elements from the individuals in this holdout sample was to reflect real life scenarios in which not all elements are preserved. Some research includes test samples that have all paired elements present when testing a method (Anastopoulou et al. 2017, Lynch 2017). While this may be good as a baseline test, it would be ideal to apply these methods to actual commingled assemblages, or simulated assemblages that more accurately match real world commingling events. The current research attempted to replicate a realistic commingled assemblage, but the actual survivorship of tali and calcanei in a commingled context may not be as high as in this sample. Repeating this test with more individuals and less elements present might better

reflect real world commingling events.

The regression formulae predicted the correct potential matches in almost every type of association, except in two instances. For the elements that were actually matched, both regression equations predicted the matches that were present. The difference related to the ranking of each possible match. The facet patterns then narrowed down the list, effecting rankings further. As expected, at no point did facet patterns eliminate a true match. This allowed for even less time spent visually sorting elements.

In situations where an element had true matches, only one Type 1 error was typically made per type of association. There was similar error occurring with individuals represented by only one element, especially in the case where talus 77 was added to a group which meant a Type 2 error occurred. Since the elements that had no associations still had predicted potential matches, identifying their solo nature was difficult. These errors did not reflect the findings of Konigsberg and Adams (2014) during the process of visual matching in that true pairs are overlooked more often than the pairing of unrelated elements. The pair-matching of unrelated elements only occurred once but was counted as a Type 2 error for a re-association, pair-match, and incorrect pairing of a solo element. There was also only one error made overlooking a true pair.

With these results in mind, the research questions addressed in this study are answered. The first research question focused on the re-association of elements of the same side, and while more errors were made for the left re-association of elements than the right, there were still only minimal Type 1 and Type 2 errors. The same can be said for the second research question regarding the pair-matching of elements. Only one Type 1 error was made when pair-matching calcanei, and only one Type 2 error was made

when pair-matching tali.

Calculation of the MNI and MLNI estimates was not the focus of this research, but was still calculated for the hold out sample. The MNI is 23 based on right calcanei. Using the pair-matches of tali and calcanei in the holdout sample, the MLNI from the final sorting of elements was 29 individuals. The original assemblage consisted of 30 individuals, so even though errors occurred with pair-matching, this MLNI calculation was very close and obviously more accurately represents the number of individuals present than the MNI. This estimate follows the accuracy of MLNI calculations described in Adams and Konigsberg (2004), which tended to only be off by one individual for three of four calculations. One calculation estimated the correct original number of individuals. The grouping of tali and calcanei in the current research, while not fully accurate, still allowed a very similar MLNI estimate of the holdout assemblage.

While the combined method of visual and osteometric sorting generally had high accuracy in predicting potential matches, the process of predicting, ranking, and eliminating potential matches for each element and then grouping the elements into potential individuals was very time consuming. This process would have taken even longer when comparing elements measurement by measurement. These comparisons were briefly explored, but using the average absolute value of the difference of the measurements was still more time efficient and accurate.

In comparison to other research, this study probably took just as long to set up, collect data, and test as other methods of osteometric sorting. The accuracy rates for re-association were not extremely different from Anastopoulou et al. (2017) who had about 89% accuracy while the current research had around 84% accuracy for left re-

associations and 94% accuracy for right re-associations. The current research had high accuracy rates for pair-matching at around 93% accuracy, but were still lower than the shape analysis methods of pair-matching tali and calcanei which had a minimum of 98% accuracy (Lynch 2017, Lynch 2018b). The size of the commingled assemblage might be the most important factor to consider when assessing what methods to use for sorting commingled remains. Any method used will be time consuming, it is will be the choice of the researcher whether more time will be spent visually sorting elements, collecting images whether two or three-dimensional, or taking measurements.

Overall, with varying presence of elements for 30 individuals, the combination of the morphological variation of the CSTJ and the predictions created by the regression equations performed well. In the end, the final matches do need to be selected by a researcher so someone who has experience with re-articulating elements as well as visual pair matching is probably the best to perform this type of sorting.

## 5. CONCLUSION

Overall, the results of this sample test indicate that this particular metric method of sorting combined with morphological aspects of the elements for elimination, works fairly well for a commingled assemblage of tali and calcanei with varying degrees of element presence.

It is important that the researcher is familiar with the elements they are sorting, and the variation that can occur on articular surfaces and with general shape and size. While this method was useful in predicting most matches, the final decision was made by the researcher when deciding which elements actually belonged to another, and that is where a few of the errors occurred. Due to asymmetry of the articular facets either due to pathology or just because of biomechanics, there were errors in matching some of the elements using the combination of measurements. To avoid the total exclusion of matching true pairs, it is recommended that elements with that are deemed to have no match in the sorting process are visually compared again in case there is any asymmetry or pathology that might be inhibiting elements as predicted potential matches.

When working with large commingled assemblages, sometimes multivariate methods may not be utilized. If the researcher can choose areas of elements with high survivorship, then multivariate analyses can often be more useful than univariate methods. This research showed the importance of using metrics and morphological variation when sorting a larger commingled assemblage. Once variables are chosen, and data collection standardized, a combined method could potentially save time, and improve accuracy of re-association or pair-matching when sorting through commingled contexts.

### *Future Research*

To allow greater accuracy of this method, it is beneficial to further explore the extent of the facet pattern variation. Facet patterns were useful in the elimination of matches before any sort of articulating or visual comparison was done, but there was confusion with some of the patterns. Additionally, it would be ideal to test the usefulness of this combination of morphological variation of the CSTJ and the measurements used in the current research in the newest release of OsteoSort. Tali and calcanei will be available for sorting, so it will be valuable to compare the accuracy of the current method against OsteoSort, and to generally utilize it as a tool for osteometric sorting.

## APPENDIX SECTION

**Appendix A.** List of donors used to develop method, and their demographics.

<b>TXSTDSC #</b>	<b>Sex</b>	<b>Race</b>	<b>Age at Death</b>
2008.001	M	H	81
2008.003	M	W	77
2009.007	F	W	65
2009.008	F	W	53
2009.011	F	W	79
2010.004	F	W	53
2010.009	M	W	63
2010.011	M	W	91
2010.012	M	W	54
2010.014	F	B	63
2010.015	M	H	64
2011.001	M	W	40
2011.003	M	W	66
2011.004	F	W	68
2011.005	M	W	80
2011.006	F	W	53
2011.007	M	W	87
2011.008	M	W	53
2011.009	F	W	54
2011.010	M	W	63
2011.012	F	W	53
2011.013	M	W	65
2011.014	M	W	51
2011.016	M	B	84
2011.020	F	W	73
2011.021	F	W	56
2011.022	M	W	56
2011.023	F	W	66
2011.026	M	W	34
2012.019	M	W	18
2012.023	M	W	56
2012.027	F	W	58
2012.028	M	W	75
2012.032	F	W	47
2012.033	M	W	72
2012.034	M	O	72
2012.035	F	W	63

2012.036	F	W	42
2012.037	M	B	49
2012.038	M	W	50
2012.039	M	W	57
2012.040	F	H	67
2012.041	M	W	60
2012.043	M	W	71
2012.045	M	W	65
2012.046	M	W	60
2012.047	M	W	68
2012.050	M	W	64
2013.005	M	W	54
2013.007	M	W	76
2013.008	F	W	68
2013.010	F	W	83
2013.011	M	W	64
2013.016	M	W	53
2013.019	M	W	60
2013.023	M	W	63
2013.024	F	W	53
2013.025	M	W	62
2013.027	M	W	69
2013.029	F	W	71
2013.033	M	W	52
2013.034	F	W	79
2013.036	M	W	88
2013.037	M	W	64
2013.039	F	W	90
2013.044	M	W	64
2013.045	M	W	52
2013.046	M	W	55
2013.059	M	W	58
2013.061	M	W	61
2013.065	M	W	61
2014.001	F	H	72
2014.003	F	W	64
2014.005	F	W	88
2014.006	M	W	74
2014.007	F	W	79
2014.009	M	W	70
2014.020	M	W	83

2014.022	M	B	57
2014.024	M	W	70
2014.025	M	W/O	61
2014.027	M	W	56
2014.028	F	H	68
2014.032	F	W	69
2014.037	F	W	73
2014.038	M	W	79
2014.039	F	W	70
2015.005	F	W	39
2015.014	M	W	70
2015.015	M	W	71
2015.023	M	W	69
2015.024	F	W	67
2015.025	F	W	68
2015.026	F	W	21
2015.027	M	W	70
2015.031	F	W	55
2015.032	F	W	73
2015.035	F	W	69
2015.037	F	W	55
2015.039	M	W	85
2015.041	F	W	57
2015.043	F	W	97
2015.055	M	W	81
2015.056	M	W	65
2015.066	F	W	56
2016.001	F	W	79
2016.002	M	W	73
2016.008	F	W	52
2016.012	M	W	88
2016.015	F	W	53
2016.018	F	W	71
2016.021	M	W	52
2016.022	F	B	68
2016.028	M	W	83
2016.041	F	W	77
2016.046	F	W	47
2016.056	M	W	30
2017.011	F	W	91
2017.061	F	H	23

2017.079	M	W	30
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**Appendix B.** List of donors used in the holdout sample, and their demographics.

<b>TXSTDSC #</b>	<b>Sex</b>	<b>Race</b>	<b>Age at Death</b>
2012.004	F	W	63
2012.006	M	W	58
2012.012	F	W	64
2012.013	M	W	48
2012.015	M	W	62
2012.016	M	W	47
2012.018	M	W	59
2013.014	M	W	58
2013.015	F	W	55
2013.050	M	W	71
2013.054	F	W	94
2013.055	M	W	57
2014.013	M	B	29
2014.014	M	W	78
2014.016	F	W	59
2014.017	M	W	68
2014.042	F	W	67
2014.043	M	W	73
2014.044	M	W	73
2014.047	F	W	69
2014.049	M	W	56
2014.056	F	W	69
2014.060	M	W	59
2014.062	M	W	53
2014.064	F	W	89
2014.065	M	W	43
2015.012	F	W	40
2015.060	F	W	49
2016.009	F	W	84
2016.051	F	W	77

I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD
	Code - L TAL	49	4	71	35	12	69	78	79	77	36	39	64	61	31	83	7	55	18		22
	Predicted TAL Length	29.59	28.88	31.26	33.65	32.52	34.1	28.21	31.24	29.32	31.04	31.91	30.28	26.24	28.17	25.93	28.48	29.94	33.25	27.15	29.2
	Predicted TAL Width	22.56	21.96	21.75	26.1	24.41	24.82	19.63	21.63	21.4	23.2	23.85	22.39	19.95	21.65	19.64	20.49	21.11	24.54	21.29	20.8
	Predicted TAL Breadth	41.96	41.4	44.08	45.02	45.72	47.05	39.86	43.86	41.84	42.1	44.67	41.39	37.8	40.11	38.25	42.1	42.49	46.59	39.86	40.61
	Predicted TAL Fraction	18.19	17.16	19.74	21.8	20.59	20.32	18.37	19.47	17.07	20.44	18.01	17.97	16.16	18.28	16.51	17.33	18.99	20.77	17.51	18.92
	Predicted TAL Subtense	5.76	5.15	6.05	7.73	6.78	5.6	6.13	5.42	4.55	5.54	5.21	5.56	4.38	5.05	5.65	5.97	5.51	5.46	5.34	5.53
	Code - Actual L CAL	20	58	19	33	80	28	66	75	52	17	53	76	2	50	63	73	11	43	5	38
	Length of PAF	33.3	32.4	33.6	30.9	31.8	27.1	30.1	31.3	29.1	35	31.4	32.5	27.6	29.1	34.2	31.3	29.8	30.1	25.4	33.5
	Width of PAF	21.6	24.1	22.4	20.9	23.6	20.3	23.7	25.4	22.4	24.8	23.1	25.7	20.7	19.9	22.5	24	20.8	23.3	21.3	22
	Breadth	44.1	44.6	45	43.4	46	38.3	41	43.5	39.5	43	42	48	42.1	38.1	45.9	39.9	40.5	41.4	40.5	43.3
	Fraction	19.84	21.01	23.16	20.51	19.85	16.5	17.95	17.58	15.79	18.61	18.76	22.04	17.15	18.79	23.17	14.96	19.51	18.68	14.9	21.51
	Subtense	5.89	5.97	5.24	5.51	5.9	4.83	5.35	4.44	5.33	5.27	5.61	6.93	5.61	6.5	5.97	4.79	5.92	4.9	4.92	6.13
Comparison 7 AND	Length	20	58	19	33	80	28	66	75	52	17	53	76	2	50	63	73	11	43	5	38
	Width	-4.82	-3.92	-5.12	-2.42	-3.32	1.38	-1.62	-2.82	-0.62	-6.52	-2.92	-4.02	0.88	-0.62	-5.72	-2.82	-1.32	-1.62	3.08	-5.02
	Breadth	-1.11	-3.61	-1.91	-0.41	-3.11	0.19	-3.21	-4.91	-1.91	-4.31	-2.61	-5.21	-0.21	0.59	-2.01	-3.51	-0.31	-2.81	-0.81	-1.51
	Fraction	-2	-2.5	-2.9	-1.3	-3.9	3.8	1.1	-1.4	2.6	-0.9	0.1	-5.9	0	4	-3.8	2.2	1.6	0.7	1.6	-1.2
	Subtense	-2.51	-3.68	-5.83	-3.18	-2.52	0.83	-0.62	-0.25	1.54	-1.28	-1.43	-4.71	0.18	-0.96	-5.84	2.37	-2.18	-1.35	2.43	-4.18
		0.08	0	0.73	0.46	0.07	1.14	0.62	1.53	0.64	0.7	0.36	-0.96	0.36	-0.53	0	1.18	0.05	1.07	1.05	-0.16
ABS value	7 AND	20	58	19	33	80	28	66	75	52	17	53	76	2	50	63	73	11	43	5	38
	Length	4.82	3.92	5.12	2.42	3.32	1.38	1.62	2.82	0.62	6.52	2.92	4.02	0.88	0.62	5.72	2.82	1.32	1.62	3.08	5.02
	Width	1.11	3.61	1.91	0.41	3.11	0.19	3.21	4.91	1.91	4.31	2.61	5.21	0.21	0.59	2.01	3.51	0.31	2.81	0.81	1.51
	Breadth	2	2.5	2.9	1.3	3.9	3.8	1.1	1.4	2.6	0.9	0.1	5.9	0	4	3.8	2.2	1.6	0.7	1.6	1.2
	Fraction	2.51	3.68	5.83	3.18	2.52	0.83	0.62	0.25	1.54	1.28	1.43	4.71	0.18	0.96	5.84	2.37	2.18	1.35	2.43	4.18
	Subtense	0.08	0	0.73	0.46	0.07	1.14	0.62	1.53	0.64	0.7	0.36	0.96	0.36	0.53	0	1.18	0.05	1.07	1.05	0.16
AVG diff		2.10	2.74	3.30	1.55	2.58	1.47	1.43	2.18	1.46	2.74	1.48	4.16	0.33	1.34	3.47	2.42	1.09	1.51	1.79	2.41

Appendix C. Screenshot of the comparison tables used for predicting matches, with talus 7 compared to all left calcanei.

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