User Manual

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OsteoSort.net

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PAIR-MATCHING

Pair-matching follows the procedures by **Lynch *et al.* (1)** and **Byrd and LeGarde (2)**. The summed difference between left and right homologous measurements is calculated from a reference sample and case comparison. The reference sample is used as a representative of the left-right differences seen in a population. The comparison D-value has zero or the mean of the reference D-values subtracted, which is then divided by the standard deviation of reference D-values to produce a t-statistic. This t-statistic is compared to a t-distribution to produce a p-value where the degrees of freedom are equal to the reference sample minus one. Any p-value that is less than or equal to the alpha level is considered too different in size to have originated from a single individual, and any p-value greater than the alpha level indicates a similarity in size, suggesting the elements may belong to a single individual. It is important to note that a p-value greater than the alpha level does not confirm the elements originated from a single individual, but rather, indicates a comparison that cannot be excluded.

Using this methodology various statistical variations can be produced by manipulating the D-value, mean, and alpha level **(Figure 1)**. Multiple variations of the D-value can be calculated including the summed differences **(Model A and B)**, absolute value of summed differences **(Model C; 1)**, and Boxcox transformed absolute value of summed differences **(Model D; 1)**. The default model **(Model D)** is the absolute D-value with a Box-Cox transformation using the mean of the reference and an alpha level of 0.05.

$$D = \sum a_i - b_i \qquad D = \sum a_i - b_i \qquad D = \sum |a_i - b_i| \qquad D = \left(\left(\sum |a_i - b_i| \right) + 0.00005 \right)^{\lambda}$$

$$\bar{x} = 0 \qquad \bar{x} = \frac{\sum D_{ref}}{N} \qquad \bar{x} = \frac{\sum D_{ref}}{N} \qquad \bar{x} = \frac{\sum D_{ref}}{N}$$

$$t = \frac{D_{com} - \bar{x}}{S_{D_{ref}}} \qquad t = \frac{D_{com} - \bar{x}}{S_{D_{ref}}} \qquad t = \frac{D_{com} - \bar{x}}{S_{D_{ref}}} \qquad t = \frac{D_{com} - \bar{x}}{S_{D_{ref}}}$$

$$\textbf{(A)} \qquad\qquad \textbf{(B)} \qquad\qquad \textbf{(C)} \qquad\qquad\qquad \textbf{(D)}$$

Figure 1 – Pair-matching statistical models using a mean of 0 (A), mean of reference D-values (B), mean of reference and absolute D-values (C), and Box-Cox transformation mean of reference absolute D-values (D).

ARTICULATION

Articulation-matching follows the procedure by **Byrd and LeGarde (2)**. Given the similarity to pair-matching the same procedures apply here. However, unlike pair-matching, specific measurements are used for articulation-matching. These measurements include:

- **Hum_06 – Uln_11**
- **Hum_06 – Rad_04**
- **Hum_07 – Sca_03**
- **Hum_07 – Sca_04**
- **Fem_04 – Osc_17**
- **Fem_03 – Tib_02**

While it is possible to manipulate the statistical model it is currently recommended to use the original statistical model where the sum of difference between measurements is calculated for the reference sample and comparison **(Figure 2)**. The comparison D-value has the mean of the reference D-values subtracted, which is then divided by the standard deviation of reference D-values to produce a t-statistic. This t-statistic is compared to a t-distribution to produce a p-value where the degrees of freedom are equal to the reference sample minus one. A p-value that is less than or equal to the alpha level is considered too different in size to have originated from a single individual, and a p-value greater than the alpha level indicates a similarity in size, suggesting the elements may belong to a single individual. It is important to note that a p-value greater than the alpha level does not confirm the elements originated from a single individual, but rather, indicates a comparison that cannot be excluded.

$$D = \sum a - b$$

$$\bar{x} = \frac{\sum D_{ref}}{N}$$

$$t = \frac{D_{com} - \bar{x}}{S_{D_{ref}}}$$

Figure 2 – Articulation-matching model using the sum difference of measurements and the mean of the reference D-values.

ASSOCIATION

Two methods of association are supported. The original following the procedure by **Byrd and LeGarde (2)**, and an ordination method by **Lynch (4)**.

The original association approach calculates the natural log of the sum of measurements of a bone from reference data with known associations. This sum of measurements is considered an acceptable index of the size of the bone. A simple linear regression model is calculated between each bone types reference data where the independent variable is the bone you are using to associate with another type. The natural log of the sum of measurements is calculated for each bone within a case comparison **(Figure 3)**.

$$X = log_e \sum x_i$$
$$Y = log_e \sum y_i$$

Figure 3 – Association calculation for the independent and dependent bones.

Testing the null hypothesis that the bones are similar in size is based on checking that the case comparisons fall within a prediction interval calculated from the regression model. Originally a 90% prediction interval was recommended. The natural log summed value from the independent bone in a case comparison is used to predict what the dependent natural log summed value is. A 90% prediction interval around that point estimate is calculated and compared to the dependent natural log value from the case comparison. If that case comparison falls between the upper and lower bounds of the point estimates prediction interval, the null hypothesis is accepted.

The latest way to test the hypothesis is to calculate a t-statistic from the case comparison where y^ is the predicted value from the regression, y_i is the dependent natural log of summed measurements from the case comparison, S.E. is the standard error of the model, N is the sample size of the reference data, x_i is the independent natural log of summed measurements from the case comparison, x is the

independent natural log of summed measurements of the reference data, and s_x is the standard deviation of the independent natural log of summed measurements of the reference data **(Figure 4)**.

$$t = |y^{\wedge} - y_i| \bigg/ \left[(S.E.) * \sqrt{\left[1 + \left(\frac{1}{N}\right) + (X_i - X)^2 / (N * S_x{}^2)\right]}\right]$$

Figure 4 – t-statistic calculation from the case comparison.

This resulting t-statistic is compared to the t-distribution producing a p-value where the degrees of freedom are equal to the sample size minus 2. If the p-value is less than or equal to the alpha level the case comparison is excluded. If the p-value is greater than the alpha level it is considered too similar in size to be excluded.

The ordination model conducts two independent principal component analyses on each elements reference sample. The resulting principal components from both analyses, which can be specified by *n* components or a percentage of cumulative variance, are used in a canonical correlation analysis to identify the variation that correlates best between the two elements. The first canonical variates are subsequently used in simple linear regression to produce an algebraic equation. Each element in the case comparison has the measurement multiplied by the respective coefficient in the principal components analysis to produce principal components that are then multiplied by the respective coefficients from the canonical correlation analysis. The independent canonical variate is then used in the algebraic equation to predict what the dependent canonical variate score would be. If the case comparison dependent canonical variate score falls within the prediction interval it is considered too similar to be excluded and if the dependent value falls outside of the prediction interval it is considered too dissimilar to be from a single individual.

The statistical models can be manipulated by choosing which measurements can be included and which prediction interval level or alpha level will be applied. The default uses the ordination method with all measurements and a 0.95 prediction interval.

METHODS

OUTLIER

Identifying outliers is relatively simple. There are two approaches which can be applied. The first calculates the mean and standard deviation and the medium and quartiles of measurements within an element. These can be separated into standard deviation or quartile groups to identify who has the largest and smallest measurements relative to the assemblage. The second approach calculates the stature for each maximum length measurement and the mean and standard deviation and the medium and quartiles of the statures. These can be separated into standard deviation or quartile groups to identify who is the shortest and tallest relative to the assemblage. This allows comparison with existing antemortem data to quickly identify particular individuals. The stature data includes the following:

- **FDB-19th-century-cstat-any**
- **FDB-19th-century-cstat-white-male**
- **FDB-19th-century-cstat-white-female**
- **FDB-19th-century-cstat-black-male**
- **FDB-19th-century-cstat-black-female**
- **FDB-20th-century-fstat-any**
- **FDB-20th-century-fstat-white-male**
- **FDB-20th-century-fstat-white-female**
- **FDB-20th-century-fstat-black-male**
- **FDB-20th-century-fstat-black-female**
- **FDB-20th-century-fstat-hispanic-male**
- **Trotter-any-male**
- **Trotter-white-male**
- **Trotter-black-male**
- **Genoves-cstat-mexican-female (femur and tibia only)**
- **Genoves-cstat-mexican-male (femur and tibia only)**

SHAPE

Currently two methods for pair-matching with shape analysis are supported **(5)**. The complete (non-fragmentary) method relies on using photographs of specimens taken on a light box at a 90-degree angle from a copy stand. No particular height is required, but the height for each specimen must be the same. This allows the capture of size information in addition to shape. The light box differentiates the element from the background making the element appear nearly black. It is recommended to use a camera lens with minimal amount of barrel distortion. Each specimen must be placed in the same orientation in the photograph.

Photographs for each side should be saved separately, which will aid in utilizing the interface described below. Each photograph is converted to a binary matrix where the outline is traced with 0's. The resultant binary matrices have the 0's converted to coordinate indices based on the dimensions of the photograph. These coordinates are run through elliptical Fourier analysis with 40 harmonics. The coefficients are then used in inverse elliptical Fourier transformation to produce new coordinates with a specified number of landmarks per outline. These outlines can be optionally scaled to the centroid size that was captured prior to running elliptical Fourier analysis to remove size information.

The new coordinate configurations are run through iterative closest point, and after each round of iterations, K-nearest neighbor search is used to determine 50% or more landmark correspondences. A specimen is chosen as the starting mean, which has a Euclidean distance matrix calculated between itself to determine the two landmarks that are furthest apart. One of these landmarks is then shifted so the first landmark in the matrix is the furthest point at the long axis of the specimen. All specimens are similarly shifted to match this alignment with the landmark correspondences. A new mean is estimated after every iteration and the iterations are repeated *x* number of times until registration in a shape-size space is achieved.

Distances between each left to right specimen are calculated using either Hausdorff, Segmented-Hausdorff, or Procrustes calculations. The default for this program is the Segmented-Hausdorff with 6 segments. The lowest distance is accepted as the most probable match.

For a complete technical overview of the method, please read ***An Automated Two-Dimensional Form Registration Method for Osteological Pair-matching*** **(5)**.

The fragmentary method uses the same photograph collection procedure described above. However, the procedure differs in that the fragmented portion of a specimen should be placed outside of the photograph frame. Twenty rows and columns with values of 1 are appended to the resulting binary matrices. These rows serve the purpose of producing a linear line for the fragment margin and are subsequently removed after tracing, which produces a fragmented outline. Each outline is translated so the centroid is 0. The outlines are registered together using iterative closest point in a pairwise manner rather than estimating a mean as described above.

A modification of the average Hausdorff distance is utilized given the fragmented outlines. Each specimens' matrix has the Euclidean distance between the first and last coordinates and the first and second coordinates. If the first distance is four times greater than the second distance the matrix is shifted so the last coordinate takes the position of the first. Every two coordinates overlapping have their distance calculated and compared to one another. Any index that is greater than four times the previous is saved as the fracture margins.

The average Hausdorff distance is used where any coordinate correspondence to the fracture margins are ignored, which allows the distance analysis between fragmented outlines where they overlap. A dilated distance can be calculated where the average is multiplied by the standard deviation, which further separates true- and false-pairs for larger commingled assemblages. The lowest distance is accepted as the most probable match.

ANTEMORTEM

This method allows the association of postmortem stature point estimates to known antemortem statures **(6)**. A t-statistic is calculated using the formula described above under association, but with the introduction of antemortem statures as case comparisons. A p-value is derived from the t-distribution, which is used to test the strength of evidence associating the antemortem stature to postmortem stature point estimate. If the p-value is less than or equal to the alpha level, the case comparison is excluded. If the p–value is greater than the alpha level, it is considered too similar to be excluded.

In this calculation $y^\wedge$ is the predicted bone length point estimate from the regression model, y_i is the bone length from the case comparison, S.E. is the standard error of the model, N is the sample size of the reference data, x_i is the known antemortem stature from the case comparison, x is the mean of the postmortem statures from reference data, s_x is the standard deviation of the postmortem statures in the reference data **(Figure 5)**.

$$t = |y^\wedge - y_i| \Big/ \left[(S.E.) * \sqrt{\left[1 + \left(\frac{1}{N} \right) + (X_i - X)^2 / (N * S_x{}^2) \right]} \right]$$

Figure 5 – t-statistic calculation from the case comparison.

REFERENCE DATA

The reference sample consists of data for the scapula, clavicle, humerus, ulna, radius, os coxa, femur, tibia, and fibula. The populations represented include European American, African American, and Asian. The reference is comprised of individuals from the Forensic Data Bank, Terry Collection, Hamann-Todd Collection, Trotter World War II data, and Defense POW/MIA Accounting Agency case work. The data is not split by population for pair-matching, articulation, and association as current research suggests there is little if any difference between populations in the amount of asymmetry and proportion. Further, it is not always possible to identify sex and ancestry from every element in an assemblage, so combining demographics allows a more practical reference data set for realistic commingled situations.

SINGLE COMPARISON

USER INTERFACE

The single comparison interface allows an analyst to conduct a one-to-one case comparison. The three methods currently supported include pair-matching, articulation, and association. Selecting between these options will dynamically generate the user input interface **(Figure 6)**. Under pair and association, the **measurements** dropdown menu allows the selection of standard or supplement measurements. Under articulation there is no measurement selection as the method depends on one specific measurement per bone. The **predictor** dropdown menu allows the selection of which element will be used as the independent variable with bone1 indicating the left column and bone2 indicating the right column. See the CoRA Measurement Guide for definitions and references for the measurement numbers.

Figure 6 – Single comparison interface.

SINGLE COMPARISON

STATISTICAL PARAMETERS

The statistical parameters tab allows the manipulation of the statistical models **(Figure 7)**. **PCA-CCA-Regression** switches between simple linear regression and the ordination approach. The ordination approach is the default. **Use alpha levels for regression** will calculate a t-statistic for the simple linear regression and use a p-value rather than prediction interval for excluding. The **Prediction Interval Level** slider allows setting the interval for the regression models. The **Alpha Level** slider will change the cut-off point for excluding comparisons for pair-matching, articulation, and association if using simple linear regression. The default is 0.05, but commonly 0.10 can be applied. The alpha level must be evaluated in light of the assemblage being analyzed. As a general rule the smaller the alpha level the better the accuracy will be and the higher the alpha level the more exclusions can be made. A balance between the two must be chosen by the analyst.
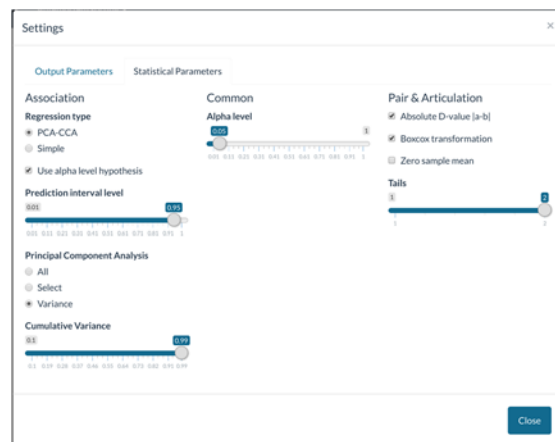
Figure 7 – Single comparison statistical parameters.

Absolute D-value (|a-b|) checkbox selects whether the summed absolute value of differences between measurements will be calculated or the summed difference between measurements (a-b). This applies not only to the case comparison, but to the reference data. The **zero sample mean** checkbox will change the reference mean to zero within the t-statistic calculation. This tests the hypothesis that there are zero differences between paired elements. The default option is the mean of the reference.

SINGLE COMPARISON

OUTPUT PARAMETERS

This tab allows the selection for using excel files and a plot for output **(Figure 8)**. The default is set to excel files. This will split the results by exclusions and non-exclusions.
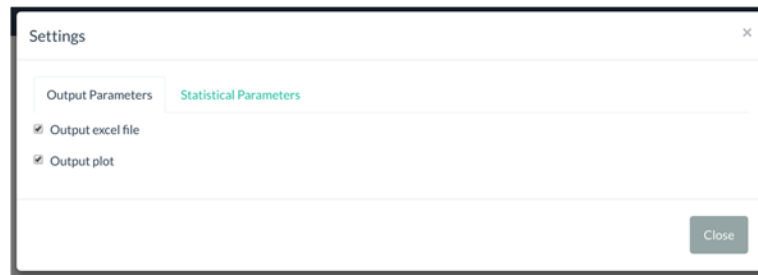
Figure 8 – Single comparison output parameters.

INTERPRETING RESULTS

For pair-matching and articulation-matching if the case comparison p-value is less than or equal to the alpha level (0.05 default) than the comparison is excluded **(Figure 9)**. If the case comparison is greater than the alpha level it is considered not excluded or a "potential match". However, caution must be applied when interpreting a non-exclusion as this does not confirm that the two elements originate from the same individual. That assessment must be made independent of OsteoSort. For association if the case comparison falls outside of the prediction interval (0.90 default) than the case comparison is considered excluded (Figure 8). If the case comparison falls within the prediction interval it is considered not excluded or a "potential match".

The graph indicates the distribution of reference data and where your comparison falls within the reference. For pair-matching and articulation-matching a histogram is produced with a red line indicating your individual. If no red line is visible the comparison is completely outside of the reference distribution. For association a scatterplot is produced with lines indicating the prediction interval, mean, and a blue dot indicating where the comparison falls within the reference data. Similarly, if no blue dot is visible the comparison falls outside of the reference data.
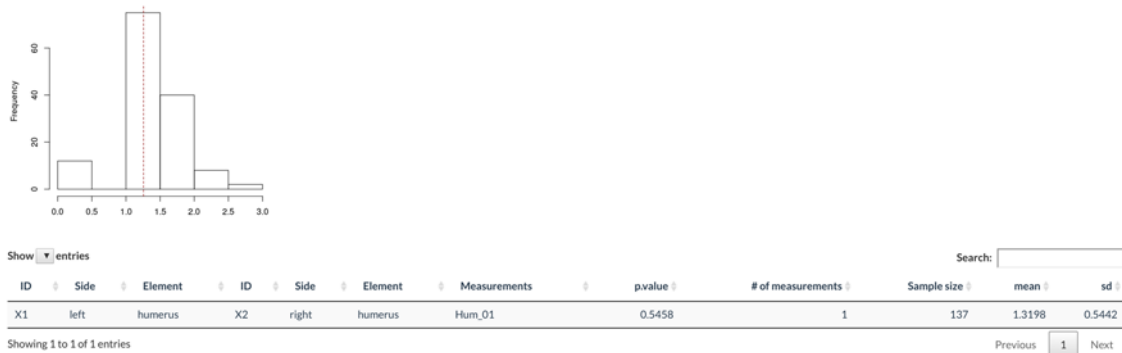
(A)
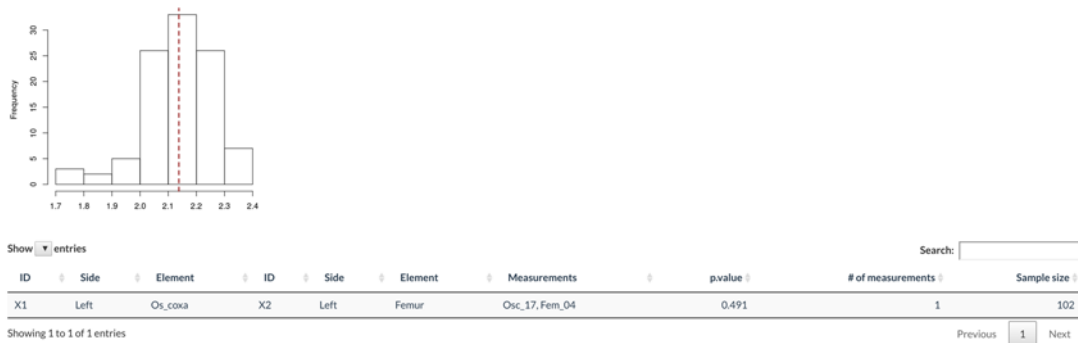
(B)
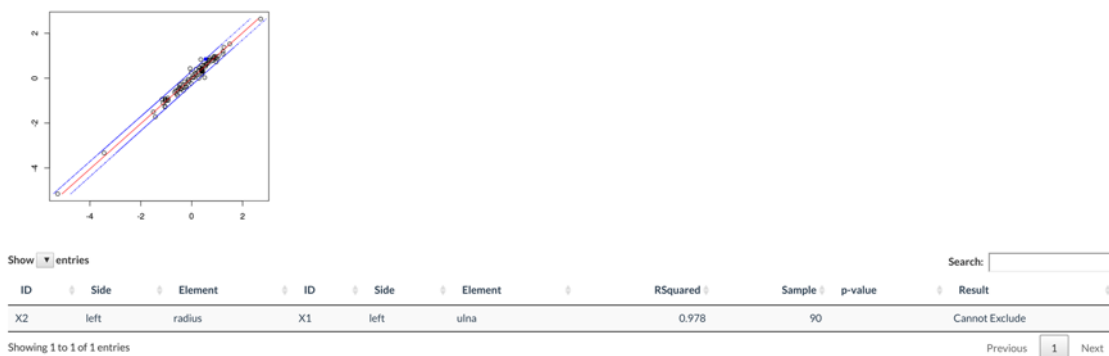
(C)

Figure 9 – Single comparison pair-match (A), articulation (B), and association (C) results.

SAVING RESULTS

After selecting the appropriate options for output files clicking **save results** will compress the data into a .zip archive and prompt you for saving.

MULTIPLE COMPARISON

USER INTERFACE

The multiple comparison interface allows an analyst to conduct one-to-many comparisons. The three methods currently supported include pair-matching, articulation, and association. Selecting between these options will dynamically generate the user input interface **(Figure 10)**. Under pair and association, the **measurements** dropdown menu allows the selection of standard or supplement measurements. Under articulation there is no measurement selection as the method depends on one specific measurement per bone. The **predictor** and **predicted** labels indicate which side will be used as the independent and dependent variables. See the CoRA Measurement Guide for definitions and references for the measurement numbers. The **Browse** button allows you to upload a .CSV file based off of the template containing your measurement data for a full assemblage. **Clear Data** button will clear the uploaded data, allowing another dataset to be uploaded.

Figure 10 – Multiple comparison interface.

MULTIPLE COMPARISON

TEMPLATE

Using multiple comparison requires uploading data in .CSV format. A template is provided through OsteoSort with the column names required for uploading data.

STATISTICAL PARAMETERS

The statistical parameters tab allows the manipulation of the statistical models **(Figure 11)**. **PCA-CCA-Regression** switches between simple linear regression and the ordination approach. The ordination approach is the default. **Use alpha levels for regression** will calculate a t-statistic for the simple linear regression and use a p-value rather than prediction interval for excluding. The **Prediction Interval Level** slider allows setting the interval for the regression models. The **Alpha Level** slider will change the cut-off point for excluding comparisons for pair-matching, articulation, and association if using simple linear regression. The default is 0.05, but commonly 0.01 can be applied. The alpha level must be evaluated in light of the assemblage being analyzed. As a general rule the smaller the alpha level the better the accuracy will be and the higher the alpha level the more exclusions can be made. A balance between the two must be chosen by the analyst.
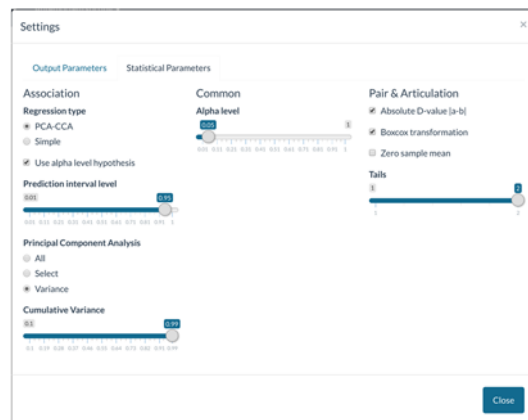
Figure 11 – Single comparison statistical parameters.

Absolute D-value (|a-b|) checkbox selects whether the summed absolute value of differences between measurements will be calculated or the summed difference between measurements (a-b). This applies not only to the case comparison, but to the reference data. The **zero reference sample** mean checkbox will change the reference mean to zero within the t-statistic calculation. This tests the hypothesis that there are zero differences between paired elements. The default option is the mean of the reference. **Calculate research statistics** will generate performance statistics based on the assumption that the correct pair-match or association has the same **ID** in the .CSV data.

MEASUREMENT PARAMATERS

The measurements tab allows the manipulation of which measurements to include in all three analyses **(Figure 12)**. Manipulating the measurement slider will indicate the minimum number of measurements required before a comparison will be analyzed. The default is one measurement.

MULTIPLE COMPARISON
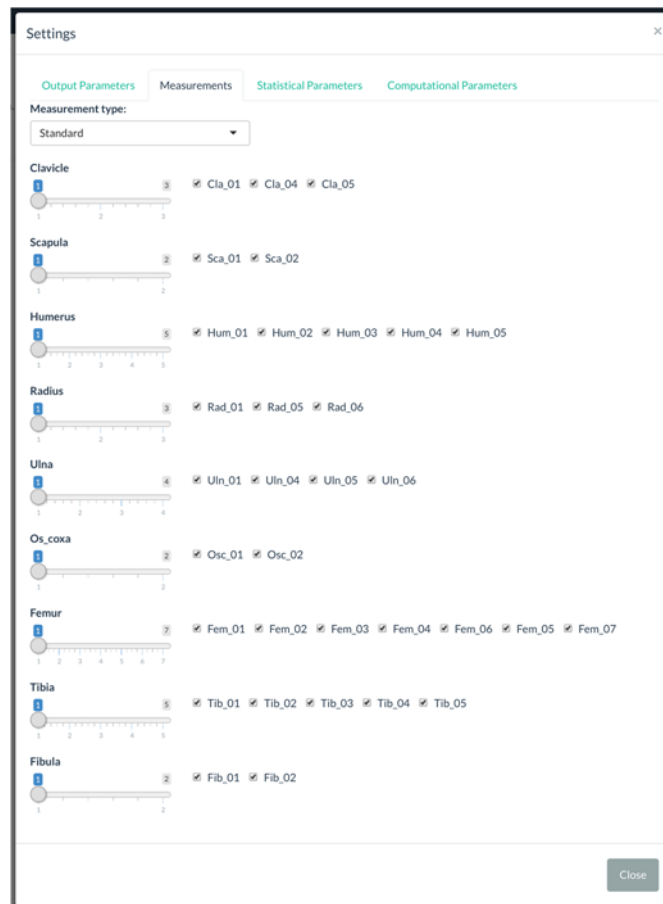
Figure 12 – Multiple comparison measurement parameters.

OUTPUT PARAMETERS

This tab allows the selection for using excel files and plots for output **(Figure 13)**. The default is set to excel files. This will split the results by exclusions and non-exclusions. **WARNING**: Plots will generate a plot for every comparison made. This is disabled by default.

MULTIPLE COMPARISON

Figure 13 – Multiple comparison output parameters.

COMPUTATIONAL PARAMETERS

The computational parameters allow the setting of cores to be used for parallel processing **(Figure 14)**. The default is one.

Figure 14 – Multiple comparison computational parameters.

INTERPRETING RESULTS

For pair-matching and articulation-matching if the case comparison p-value is less than or equal to the alpha level (0.05 default) than the comparison is excluded **(Figure 15)**. If the case comparison is greater than the alpha level it is considered not excluded or a "potential match". However, caution must be applied when interpreting a non-exclusion as this does not confirm that the two elements originate from the same individual. That assessment must be made independent of OsteoSort. For association if the case comparison falls outside of the prediction interval (0.90 default) than the case comparison is considered excluded **(Figure 15)**. If the case comparison falls within the prediction interval it is considered not excluded or a "potential match". Given the large amount of comparisons, graphs are not generated for multiple comparison.

Statistical analysis complete.
Number of comparisons conducted: 82302
Total specimens tested: 575
Number of specimens with 1 or more potential matches: 575
Total number of potential matches: 23442
Mean number of potential matches per specimen: 81.5 (14.2 %)
Standard deviation of potential matches: 48.8
Total number of exclusions: 58860 (71.5 %)

Not excluded Excluded

Show 10 ▾ entries   Search: [   ]

ID	Side	Element	ID	Side	Element	Measurements	p.value	# of measurements	Sample size	mean	sd
CIL 2003-116G-01X-232C201	left	humerus	CIL 2003-116G-01X-232C202	right	humerus	Hum_01, Hum_02, Hum_03, Hum_04, Hum_05	0.3933	5	137	1.8289	0.3492
CIL 2003-116G-05X-219D201	left	humerus	CIL 2003-116G-01X-232C202	right	humerus	Hum_01, Hum_02, Hum_03, Hum_04, Hum_05	0.1977	5	137	1.8289	0.3492
CIL 2003-116G-05X-219F201	left	humerus	CIL 2003-116G-01X-232C202	right	humerus	Hum_01, Hum_02, Hum_03, Hum_04, Hum_05	0.1591	5	137	1.8289	0.3492
CIL 2003-116G-07X-217C201	left	humerus	CIL 2003-116G-01X-232C202	right	humerus	Hum_01, Hum_02, Hum_03, Hum_04, Hum_05	0.0531	5	137	1.8289	0.3492
CIL 2003-116G-07X-237C201	left	humerus	CIL 2003-116G-01X-232C202	right	humerus	Hum_02	0.3654	1	137	0.8294	0.495
CIL 2003-116G-08X-223F201	left	humerus	CIL 2003-116G-01X-232C202	right	humerus	Hum_01, Hum_02, Hum_03, Hum_04, Hum_05	0.4664	5	137	1.8289	0.3492
CIL 2003-116G-10X-256D201	left	humerus	CIL 2003-116G-01X-232C202	right	humerus	Hum_02	0.1946	1	137	0.8294	0.495
CIL 2003-116G-11X-24?D201	left	humerus	CIL 2003-116G-01X-232C202	right	humerus	Hum_01, Hum_02, Hum_03, Hum_04, Hum_05	0.2011	5	137	1.8289	0.3492
CIL 2003-116G-12X-252A201	left	humerus	CIL 2003-116G-01X-232C202	right	humerus	Hum_01, Hum_02, Hum_03, Hum_04, Hum_05	0.0651	5	137	1.8289	0.3492
CIL 2003-116G-12X-252D201	left	humerus	CIL 2003-116G-01X-232C202	right	humerus	Hum_02	0.9439	1	137	0.8294	0.495

Showing 1 to 10 of 23,442 entries   Previous 1 2 3 4 5 ... 2345 Next

(A)

Statistical analysis complete.
Number of comparisons conducted: 161428
Total specimens tested: 1140
Number of specimens with 1 or more potential matches: 1139
Total number of potential matches: 99953
Mean number of potential matches per specimen: 175.5 (15.4 %)
Standard deviation of potential matches: 56.3
Total number of exclusions: 61475 (38.1 %)

Not excluded Excluded

Show 10 ▾ entries   Search: [   ]

ID	Side	Element	ID	Side	Element	Measurements	p.value	# of measurements	Sample size
CIL 2003-116G-01X-232C401	left	femur	CIL 2003-116G-01X-232C901	left	os_coxa	Fem_04, Osc_17	0.8734	1	102
CIL 2003-116G-01X-233E401	left	femur	CIL 2003-116G-01X-232C901	left	os_coxa	Fem_04, Osc_17	0.5394	1	102
CIL 2003-116G-01X-234A401	left	femur	CIL 2003-116G-01X-232C901	left	os_coxa	Fem_04, Osc_17	0.0617	1	102
CIL 2003-116G-01X-235A401	left	femur	CIL 2003-116G-01X-232C901	left	os_coxa	Fem_04, Osc_17	0.1671	1	102
CIL 2003-116G-04X-56A401	left	femur	CIL 2003-116G-01X-232C901	left	os_coxa	Fem_04, Osc_17	0.5392	1	102
CIL 2003-116G-04X-56B401	left	femur	CIL 2003-116G-01X-232C901	left	os_coxa	Fem_04, Osc_17	0.645	1	102
CIL 2003-116G-04X-56C401	left	femur	CIL 2003-116G-01X-232C901	left	os_coxa	Fem_04, Osc_17	0.9434	1	102
CIL 2003-116G-04X-56D401	left	femur	CIL 2003-116G-01X-232C901	left	os_coxa	Fem_04, Osc_17	0.322	1	102
CIL 2003-116G-04X-56E401	left	femur	CIL 2003-116G-01X-232C901	left	os_coxa	Fem_04, Osc_17	0.6076	1	102
CIL 2003-116G-04X-56G401	left	femur	CIL 2003-116G-01X-232C901	left	os_coxa	Fem_04, Osc_17	0.892	1	102

Showing 1 to 10 of 99,953 entries   Previous 1 2 3 4 5 ... 9996 Next

(B)

Statistical analysis complete.
Number of comparisons conducted: 140
Total specimens tested: 24
Number of specimens with 1 or more potential matches: 22
Total number of potential matches: 28
Mean number of potential matches per specimen: 2.5 (10.4 %)
Standard deviation of potential matches: 1.2
Total number of exclusions: 112 (80 %)

Not excluded Excluded

Show 10 ▾ entries   Search: [   ]

ID	Side	Element		ID.1	Side.1	Element.1		RSquared	Sample	Result	
90	left	ulna		2	left	radius		0.979	90	Cannot Exclude	
90	left	ulna		4	left	radius		0.979	90	Cannot Exclude	
91	left	ulna		7	left	radius		0.979	90	Cannot Exclude	
91	left	ulna		8	left	radius		0.979	90	Cannot Exclude	
91	left	ulna		9	left	radius		0.979	90	Cannot Exclude	
92	left	ulna		7	left	radius		0.979	90	Cannot Exclude	
92	left	ulna		8	left	radius		0.979	90	Cannot Exclude	
92	left	ulna		9	left	radius		0.979	90	Cannot Exclude	
93	left	ulna		4	left	radius		0.979	90	Cannot Exclude	
93	left	ulna		7	left	radius		0.979	90	Cannot Exclude	

Showing 1 to 10 of 28 entries   Previous 1 2 3 Next

(C)

Figure 15 – Multiple comparison pair-match (A), articulation (B), and association (C) results.

SAVING RESULTS

After selecting the appropriate options for output files selecting **save results** will compress the data into a .zip archive and prompt you for download.

OUTLIER METRIC ANALYSIS

USER INTERFACE

The outlier metric analysis interface allows an analyst to conduct one-to-many comparisons **(Figure 16)**.

Browse allows the upload of data in the specified .CSV template described above.
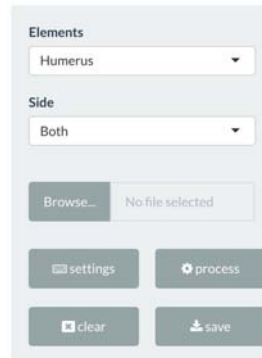

Figure 16 – Outlier metric analysis user interface.

MEASUREMENT PARAMETERS

Allows the selection of which measurement to use for outlier analysis **(Figure 17)**. Only one measurement per element may be used.
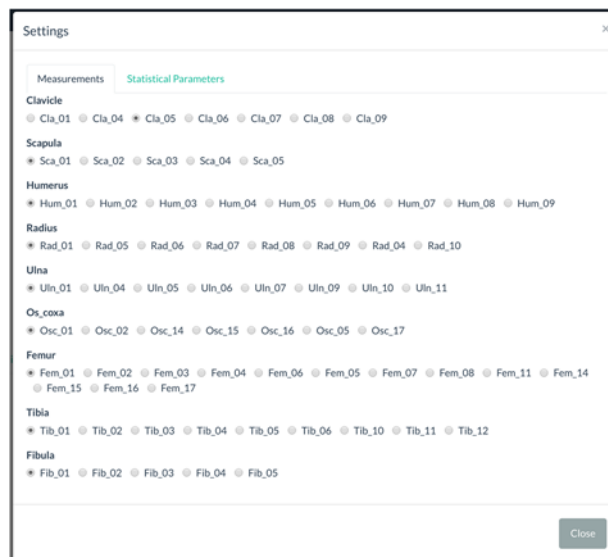

Figure 17 – Measurement parameter user interface.

OUTLIER METRIC ANALYSIS

STATISTICAL PARAMETERS

The statistical parameters allow the selection of standard deviations or quartiles for identifying outliers **(Figure 18)**. Selecting one will dynamically switch the sliding between standard deviations and interquartile ranges, which allow the setting of where the outlier cutoff should fall. The default is 2 for standard deviations and 1.5 for interquartile range. Selecting the slider will create a second allowing a cutoff range to be specified for the outliers to fall between.
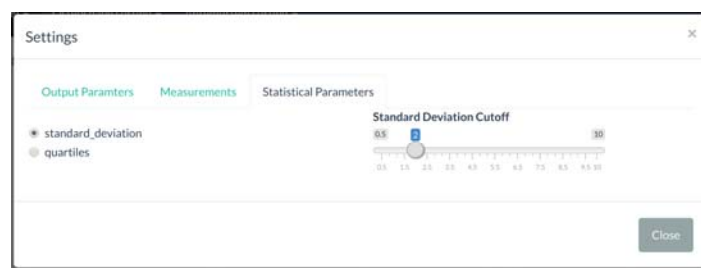
Figure 18 – Statistical parameter user interface.

OUTPUT PARAMETERS

This tab allows the selection for using excel files and a plot for output **(Figure 19)**. The default is set to excel files. This will split the results by exclusions and non-exclusions.
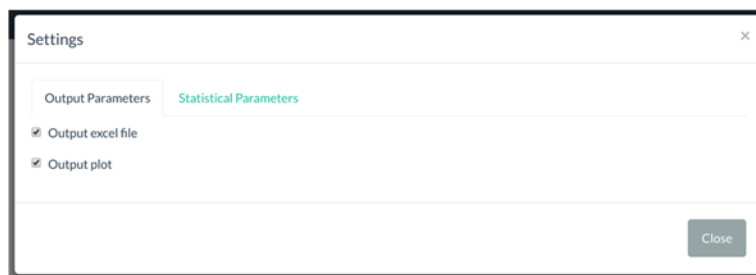
Figure 19 – Outlier metric comparison output parameters.

INTERPRETING RESULTS

The results produce a table with three tabs **(Figure 20)**. The first two specifies the outliers above and below the standard deviation or interquartile cutoff values or ranges. The third specifies the elements

that are not outliers. The graph indicates the distribution of the assemblage with the mean indicated by the red dashed line, and the cutoff values indicated by the blue dashed lines.

Figure 20 – Outlier metric analysis results.

SAVING RESULTS

Save results will compress the data into a .zip archive and prompt you for download. This includes the graph and excel files split by outlier groups.

OUTLIER STATURE ANALYSIS

USER INTERFACE

The outlier stature analysis interface allows an analyst to conduct one-to-many comparisons **(Figure 21)**. Population allows the selection of reference population for the calculating stature. Browse allows the upload of data in the specified .CSV template described above.
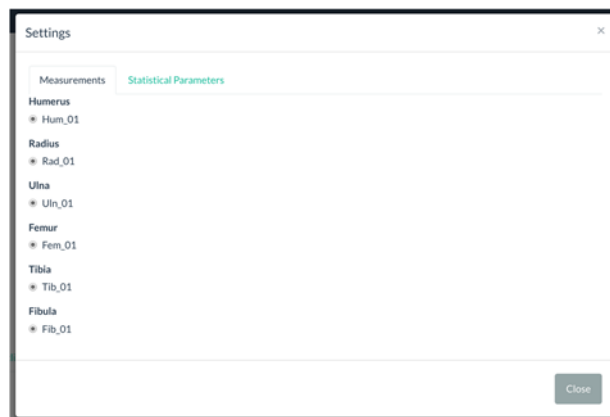
Figure 21 – Outlier stature analysis user interface.

MEASUREMENT PARAMETERS

Allows the selection of which measurement to use for outlier analysis **(Figure 22)**. Only one measurement per element may be used.

Figure 22 – Measurement parameter user interface.

OUTLIER STATURE ANALYSIS

STATISTICAL PARAMETERS

The statistical parameters allow the selection of standard deviations or quartiles for identifying outliers **(Figure 23)**. Selecting one will dynamically switch the sliding between standard deviations and interquartile ranges, which allow the setting of where the outlier cutoff should fall. The default is 2 for standard deviations and 1.5 for interquartile range. Selecting the slider will create a second allowing a cutoff range to be specified for the outliers to fall between.

Figure 23 – Statistical parameter user interface.

OUTPUT PARAMETERS

This tab allows the selection for using excel files and a plot for output **(Figure 24)**. The default is set to excel files. This will split the results by exclusions and non-exclusions.
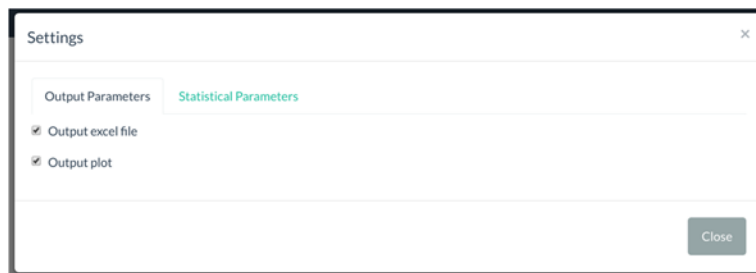
Figure 24 – Single comparison output parameters.

INTERPRETING RESULTS

The results produce a table with three tabs **(Figure 25)**. The first two specifies the outliers above and below the standard deviation or interquartile cutoff values or ranges. The third specifies the elements

that are not outliers. The graph indicates the distribution of the assemblage with the mean indicated by the red dashed line, and the cutoff values indicated by the blue dashed lines.
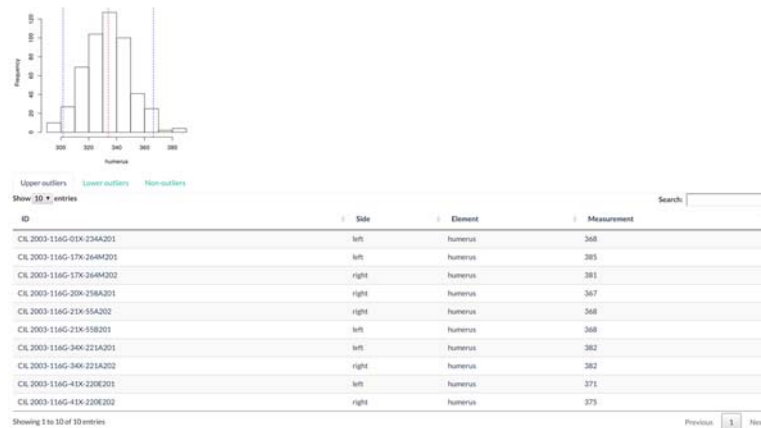

Figure 25 – Outlier metric analysis results.
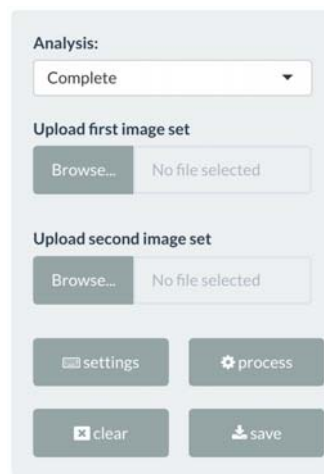
SAVING RESULTS

Save results will compress the data into a .zip archive and prompt you for download. This includes the graph and excel files split by outlier groups.

USER INTERFACE

This interface allows an analyst to conduct one-to-many comparisons. **Analysis** specifies whether complete or fragmented analysis should be conducted. The **browse** buttons will allow batch image uploading for each side respectively **(Figure 26)**. The **slider** allows choosing which specimen will be utilized as the starting mean shape **(Figure 26)**. **Clear Data** button will clear the uploaded images, allowing additional images to be uploaded.

(A)
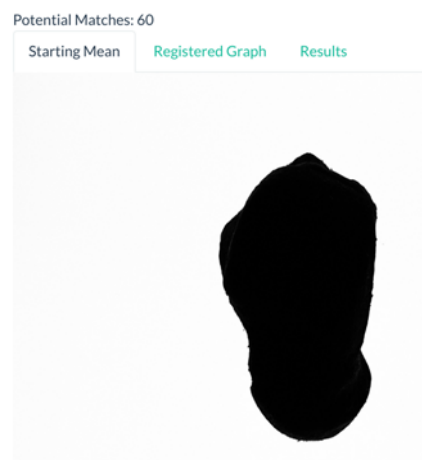
(B)

Figure 26 – Two-dimensional shape analysis user interface (A) and mean shape selection (B).

STATISTICAL PARAMTERS

The statistical parameters tab allows the manipulation of the registration and distance analysis procedures **(Figure 27)**. The defaults should work in most instances. The **number of mean iterations** slider defines how many iterations around the estimated mean should be used for registration. The **number of iterative closest point iterations** slider defines the number of iterations between each specimen and the mean shape for each iteration of the estimated means described previously. The **number of elliptical Fourier analysis harmonics** slider defines the number of harmonics for use with calculating coefficients. The **number of landmarks during elliptical Fourier transformation** slider defines the number of landmarks from approximately the outline shape using the coefficients.

The **black and white threshold level** slider is the threshold on a scale of 0 to 1 of which colors of each image to convert to 0's. The check box **mirror left images to right** will mirror the images uploaded to first input to the second. The **scale to centroid size** option will scale the specimens to their original centroid size from the photograph after the elliptical Fourier transformation, which removes size information.

The check box for **transformation type** is the type of transformation to use in iterative closest point. **Distance calculation** check box indicates the type of distance to use for comparisons. If **Hausdorff** is selected, the additional check box for average or maximum will appear allowing the selection of which type of Hausdorff to calculate. Similarly, the slider for **number of regions** will appear allowing the selection of how many regions to use in the **Segmented-Hausdorff** distance.

Finally, the **number of shortest distance matches** specifies how many matches per specimen to return based on lowest distance. **Hide distance** will omit the distances from the output to aid on objectively analyzing the results rather than relying on what the distance is.
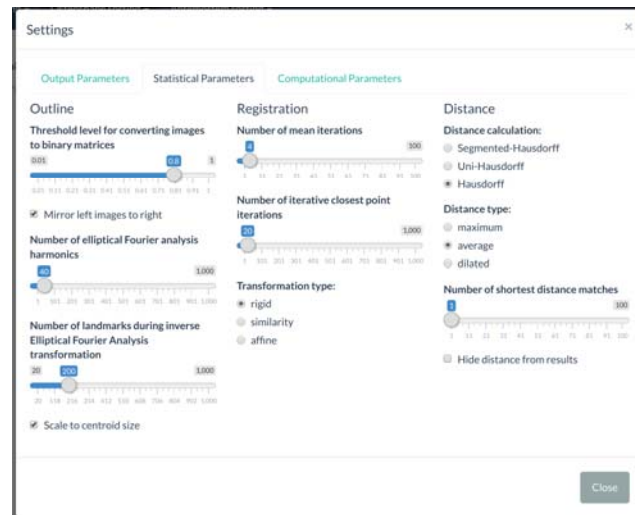
Figure 27 – Two-dimensional statistical parameter user interface.

OUTPUT PARAMETERS

The output parameters tab allows the selection of outputting results in **excel** format, a general **plot** showing the form registration, and the option to output the landmark coordinates in **TPS** format **(Figure 28)**.
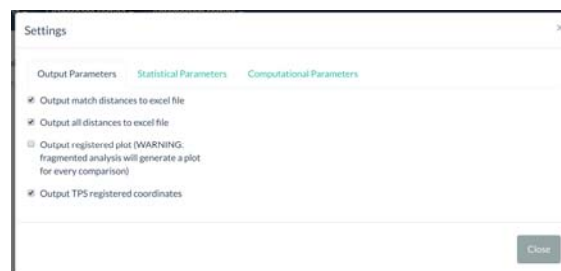
Figure 28 – Two-dimensional comparison output parameters.

COMPUTATIONAL PARAMETERS

The computational parameters allow the setting of cores to be used for parallel processing **(Figure 29)**.

The default is one.

Figure 29 – Two-dimensional computational parameters.

INTERPRETING RESULTS

The results are presented in two tabs. The first is the registered graph showing how well all of the specimens registered to the estimated mean shape **(Figure 30)**, and the second is the results tab showing the lowest distance matches **(Figure 30).**

Potential Matches: 60

Starting Mean | Registered Graph | Results

(A)

Potential Matches: 60

Starting Mean | Registered Graph | Results

Show 10 ▾ entries

Search:

ID	Match-ID	Distance
58.JPG	A58.JPG	0.00284359669242109
57.JPG	A57.JPG	0.00329407786852332
56.JPG	A56.JPG	0.00368821673306556
55.JPG	A55.JPG	0.00307577457529685
54.JPG	A54.JPG	0.0040410814803445
53.JPG	A53.JPG	0.00532668384536486
52.JPG	A52.JPG	0.00329707134213439
51.JPG	A51.JPG	0.00272913141677162
50.JPG	A50.JPG	0.00296152405832197
49.JPG	A37.JPG	0.00392993451596759

Showing 1 to 10 of 60 entries

Previous | 1 | 2 | 3 | 4 | 5 | 6 | Next

(B)

Figure 30 – Two-dimensional registered shape-size space (A) and the lowest distance matches (B).

TWO-DIMENSIONAL COMPARISON

SAVING RESULTS

Save results will compress the data into a .zip archive and prompt you for download. This includes the files selected under the **output parameters**. The lowest distance is accepted as the most likely match, and the number of potential matches is based on the **statistical parameters** selected.

ANTEMORTEM SINGLE COMPARISON

USER INTERFACE

The single comparison interface allows an analyst to conduct a one-to-one case comparison **(Figure 31)**. **Stature metric** allows the selection of the stature metric you wish to input, and similarly, will output in that stature format. **Population** allows the selection of the reference population to use with the regression formula and stature estimation. **Postmortem ID** and **Antemortem ID** refer to the ID of the skeletal element and known antemortem stature respectively. Upon change the element type the measurement name will dynamically change. **Side** allows selecting a side, but this does not change any of the analytics as it is purely for organizing results. The **Process** button will begin the analysis.

Figure 31 – Antemortem single comparison interface.

STATISTICAL PARAMETERS

The statistical parameters tab allows the selection of which model type to use for excluding a potential match **(Figure 32)**. Both **prediction interval** and **alpha level** will produce identical results.

ANTEMORTEM SINGLE COMPARISON

Figure 32 – Antemortem single comparison statistical parameters.

OUTPUT PARAMETERS

The output parameters tab allows the selection of saving the results in excel format, as well as saving a plot showing the regression model and relationship of antenortem stature to postmortem element within that regression space **(Figure 33)**.

Figure 33 – Antemortem single comparison output parameters.

INTERPRETING RESULTS

The results return a table with various statistical results **(Figure 34)**. The **t-statistic** and **p-value** are the interpretable statistics of the comparison. The **point estimate** for the postmortem element is returned along with the **prediction interval**. The **R-squared** is the fitness of the stature estimation model. Within the plot that is returned, the predicted point estimate is represented by the **blue circle**, and the known antemortem stature is represented by the **red circle**. The distance between these two is reflected in the p-value. The closer the two points within the regression space, the higher the p-value will be.
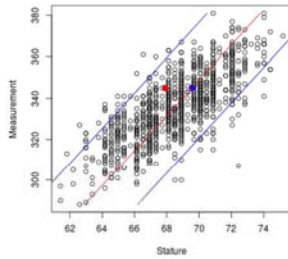
Statistical analysis complete.

id	antemortem_stature	id	side	element	postmortem_measurement	t-statistic	p-value	sample_size	lower_PI	point_estimate	upper_PI	Rsquared	Result
X1	67.9	X2	Left	humerus	345	1	0.32	1009	66.3	69.57	72.85	0.55	Cannot Exclude

Show ▾ entries   Search: [ ]

Showing 1 to 1 of 1 entries   Previous | 1 | Next

Figure 34 – Antemortem single comparison results.

SAVING RESULTS

Save results will compress the data into a .zip archive and prompt you for download. This includes the files selected under the **output parameters**. The lowest distance is accepted as the most likely match, and the number of potential matches is based on the **statistical parameters** selected

ANTEMORTEM MULTIPLE COMPARISON

USER INTERFACE

This interface analysis an analyst to conduct multiple pairwise comparisons between skeletal elements and known antemortem statures **(Figure 35)**. The **stature metric** specifies which metric the antemortem statures are uploaded as. The **population** dropdown specifies which reference population to use for the stature regression model. The **antemotrem stature** upload uses a standardized template as described below. The **postmortem measurements** upload uses the same measurement template as the other methods in OsteoSort.

Figure 35 – Antemortem multiple comparison user interface.

TEMPLATES

Two templates are used for antemortem comparison. The first is the standard template for metric measurements and the second is for known antemortem statures. Both are .csv templates and can be accessed from the help tab in OsteoSort.

STATISTICAL PARAMETERS

The statistical parameters tab allows the selection of which model type to use for excluding a potential match **(Figure 36)**. Both **prediction interval** and **alpha level** will produce identical results. **Research statistics** will calculate research statistics where correct associations share the same **ID** numbers in the templates.

ANTEMORTEM MULTIPLE COMPARISON
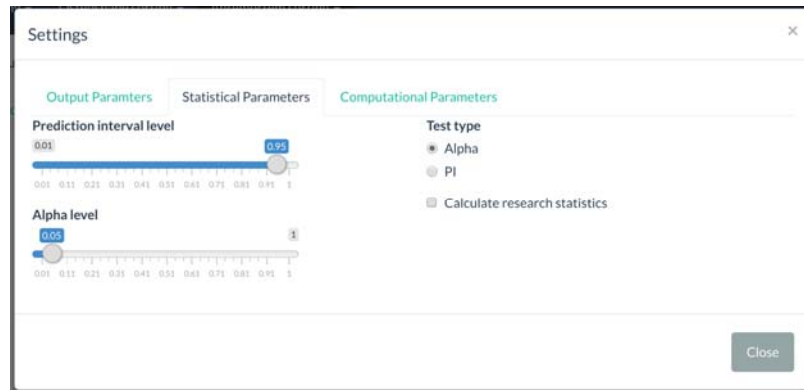
Figure 36 – Antemortem multiple comparison statistical parameters.

OUTPUT PARAMETERS

This tab allows the selection for using excel files and plots for output **(Figure 37)**. The default is set to excel files. This will split the results by exclusions and non-exclusions. **WARNING**: Plots will generate a plot for every comparison made. This is disabled by default.
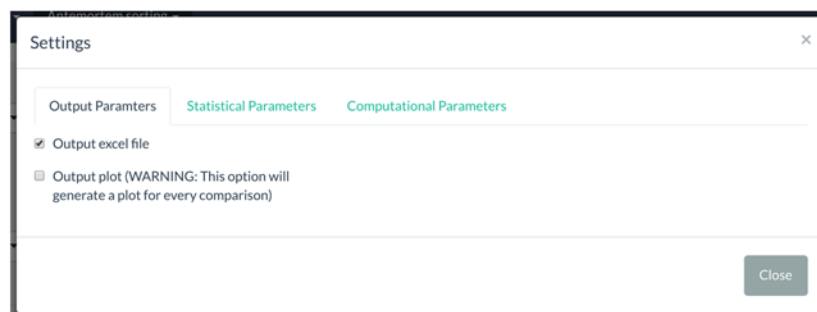
Figure 37 – Antemortem multiple comparison statistical parameters.

COMPUTATIONAL PARAMETERS

The computational parameters allow the setting of cores to be used for parallel processing **(Figure 38)**.
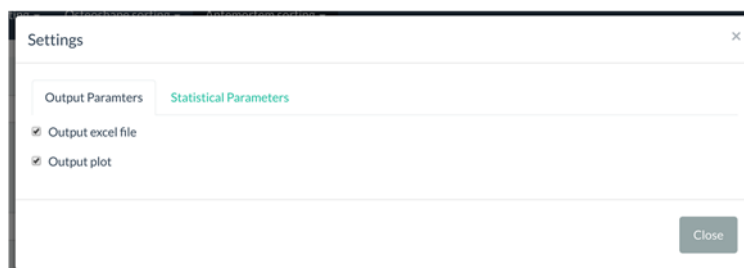
The default is one.
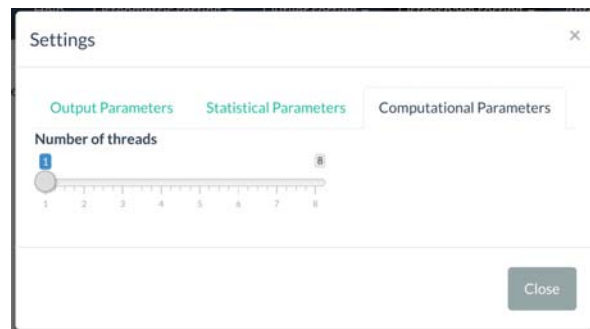
Figure 38 – Antemortem multiple comparison computational parameters.

INTERPRETING RESULTS

The results return a table with various statistical results **(Figure 39)**. The **t-statistic** and **p-value** are the interpretable statistics of the comparison. The **point estimate** is returned along with the **prediction interval**. The **R-squared** is the fitness of the stature estimation model. Individual **plots** generated will be available when saving the results.

Statistical analysis complete.
Number of comparisons conducted: 18445
Antemortem specimens: 155
Postmortem specimens: 119
Total number of potential matches: 10525
Total number of exclusions: 7920 (42.9 %)

Not excluded   Excluded

Show 10 ▾ entries   Search:

id	antemortem_stature	id	side	element	postmortem_measurement	t-statistic	p-value	sample_size	lower_PI	point_estimate	upper_PI	Rsquared	Result
1	185.5	1	Left	humerus	359	1.09	0.27	1009	172.56	180.87	189.19	0.55	Cannot Exclude
4	186.7	1	Left	humerus	359	1.38	0.17	1009	172.56	180.87	189.19	0.55	Cannot Exclude
6	181.6	1	Left	humerus	359	0.17	0.86	1009	172.56	180.87	189.19	0.55	Cannot Exclude
7	180.34	1	Left	humerus	359	0.13	0.9	1009	172.56	180.87	189.19	0.55	Cannot Exclude
8	177.8	1	Left	humerus	359	0.72	0.47	1009	172.56	180.87	189.19	0.55	Cannot Exclude
9	177.8	1	Left	humerus	359	0.72	0.47	1009	172.56	180.87	189.19	0.55	Cannot Exclude
11	172.72	1	Left	humerus	359	1.92	0.05	1009	172.56	180.87	189.19	0.55	Cannot Exclude
13	174.6	1	Left	humerus	359	1.48	0.14	1009	172.56	180.87	189.19	0.55	Cannot Exclude
15	179	1	Left	humerus	359	0.44	0.66	1009	172.56	180.87	189.19	0.55	Cannot Exclude
16	175.3	1	Left	humerus	359	1.31	0.19	1009	172.56	180.87	189.19	0.55	Cannot Exclude

Showing 1 to 10 of 10,525 entries   Previous 1 2 3 4 5 … 1053 Next

Figure 39 – Antemortem multiple comparison results.

SAVING RESULTS

Save results will compress the data into a .zip archive and prompt you for download. This includes the files selected under the **output parameters**. Results will be split based on those excluded and those not excluded.

CORA MEASUREMENT GUIDE

This is an edited copy of the CoRA measurement guide containing only the measurements currently used in OsteoSort. Measurements are from a variety of sources and are referenced with the measurement description.

CLAVICLE

Cla_01. Maximum Length of the Clavicle: The maximum distance between the most extreme ends of the clavicle. *Instrument*: osteometric board.

Comment: Place the bone on the osteometric board and place the sternal end of the clavicle against the vertical end board. Press the movable upright against the acromial end and move the bone up, down and sideways until the maximum length is obtained (Martin and Knussmann 1988: 197, #1; Langley *et al.* 2016: 73, #38).

Cla_02. Maximum Diameter of the Clavicle at Midshaft: The maximum diameter of the bone measured at midshaft. *Instrument*: sliding caliper.

Comment: Determine the midpoint of the diaphysis on the osteometric board and mark it with a pencil. Place the bone between the two arms of the caliper and rotate the bone until the maximum diameter is obtained (Langley *et al.* 2016: 73, #39).

Cla_03. Minimum Diameter of the Clavicle at Midshaft: The minimum diameter of the bone measured at midshaft. *Instrument*: sliding caliper.

Comment: Determine the midpoint of the diaphysis on the osteometric board and mark it with a pencil. Place the bone between the two arms of the caliper and rotate the bone until the minimum diameter is obtained (Langley *et al.* 2016: 74, #40).

Cla_04. Sagittal (Anterior-Posterior) Diameter at Midshaft: The distance from the anterior to the posterior surface at midshaft. *Instrument:* sliding caliper.

Comment: Determine the midpoint of the diaphysis on the osteometric board and mark it with a pencil. Then determine sagittal diameter (Moore-Jansen *et al.* 1994, #36).

Cla_05. Vertical (Superior-Inferior) Diameter at Midshaft: The distance from the superior to the inferior surface at midshaft. *Instrument:* sliding caliper.

Comment: Taken perpendicular to sagittal diameter (Moore-Jansen *et al.* 1994, #37).

Cla_06. Maximum Width at the Distal End: The maximum width of the distal end of the clavicle where the calipers are in contact with the rough attachment area, taken perpendicular to the shaft. Avoid angling the calipers (Byrd and Adams 2015, #37A). *Instrument*: sliding caliper.

Cla_07. Breadth at the Inflexion Point at the Distal End: Anchor the caliper in the concave curve of the inflexion point at the distal end of the clavicle and place the other jaw of the caliper on the opposite side usually on or near the tubercle (Byrd and Adams 2015, #37B). *Instrument*: sliding caliper.

Cla_08. Maximum Thickness at the Inflexion Point at the Distal End: The maximum thickness in the same vertical plane as the previous measurement (take perpendicular to breadth at the inflection point measurement) (Byrd and Adams 2015, #37C). *Instrument*: sliding caliper.

Cla_09. Maximum Anterior-Posterior Width at the Proximal End: The maximum anterior-posterior width of the proximal end (be sure to hold in anatomical position) (Byrd and Adams 2015, #37D). *Instrument*: sliding caliper.

SCAPULA

Sca_01. Height of the Scapula (Anatomical Height): The distance from the most superior point of the cranial angle to the most interior point on the caudal angle (Martin and Knussmann 1988:197, #1; Langley *et al.* 2016: 74, #41). *Instrument*: sliding caliper or osteometric board.

Sca_02. Breadth of the Scapula (Anatomical Breadth): The distance from the midpoint on the dorsal border of the glenoid fossa to midway between the two ridges of the scapular spine on the vertebral border. *Instrument*: sliding or spreading caliper.

Comment: Project a line through the obtuse angle of a triangle formed by the vertebral border and the two ridges of the spine, dividing it into two equal halves. The medial measuring point is located where this line intersects the vertebral border (Hrdlicka 1920: 131; Langley *et al.* 2016: 74, #42).

Sca_03. Glenoid Cavity Height: The distance from the most superiorly located point on the margin of the glenoid cavity to the most inferiorly located point on the margin, taken perpendicular to glenoid cavity breadth. Often a distinct rim is visible (look at the fossa from the side and take the measurement at the apex of the ridges). In cases of severe lipping, this measurement should not be taken (Martin and Knussmann 1988: 198, #12; Langley *et al.* 2016: 74, #44; Byrd and Adams 2015, #39A). *Instrument*: sliding caliper.

Sca_04. Glenoid Cavity Breadth: Maximum distance from the ventral to dorsal margins (anterior/posterior) of the glenoid cavity, taken perpendicular to glenoid cavity height. In cases of severe lipping, this measurement should not be taken (Martin and Knussmann 1988: 198, #13, Langley *et al.* 2016: 74, #43). *Instrument*: sliding caliper.

Comment: Place one flat surface of the jaw of the calipers on the anterior side of the glenoid fossa and place the flat surface of the other jaw on the posterior side with both jaws oriented parallel to the long axis of the bone (Byrd and Adams 2015, #39B).

Sca_05. Minimum Length from Scapular Notch to Axillary Border: This measurement is the minimum distance from the superior border (typically in the notch) to the axillary border. Anchor a jaw of the

caliper in the notch and use the other jaw to find the minimum distance to a point on the axillary border (Byrd and Adams 2015, #39D). *Instrument*: sliding caliper.

HUMERUS

Hum_01. **Maximum Length of the Humerus:** The distance from the most superior point on the head of the humerus to the most inferior point on the trochlea. *Instrument*: osteometric board.

Comment: Place the humerus on the osteometric board so that its long axis parallels the instrument. Place the head of the humerus against the vertical end board and press the movable upright against the trochlea. Move the bone up, down and sideways to determine the maximum distance (Hrdlicka 1920:126; Langley *et al.* 2016: 74, #45).

Hum_02. **Epicondylar Breadth of the Humerus:** The distance from the most laterally protruding point on the lateral epicondyle to the corresponding projection on the medial epicondyle (Martin and Knussmann 1988: 199, #4; Langley *et al.* 2016: 74, #46). *Instrument*: osteometric board or sliding calipers.

Hum_03. **Vertical Diameter of Head:** The distance between the most superior and inferior points on the border of the articular surface. *Instrument*: sliding caliper.

Comment: Do not include arthritic lipping which may be present on the perimeter of the joint surface. This diameter is not necessarily the maximum head diameter (Martin and Knussmann 1988: 200, #10; Langley *et al.* 2016: 74, #47).

Hum_04. **Maximum Diameter of the Humerus at Midshaft:** The maximum diameter of the humeral shaft at midshaft. *Instrument*: sliding caliper.

Comment: Determine the midpoint of the diaphysis on the osteometric board and mark with a pencil. Using sliding calipers to measure with one hand, rotate the bone with the other hand until the maximum diameter is obtained. (Martin and Knussmann 1988: 199, #5; Langley *et al.* 2016: 74-75, #48).

Hum_05. **Minimum Diameter of the Humerus at Midshaft:** The minimum diameter of the humeral shaft at midshaft. *Instrument*: sliding caliper.

Comment: Determine the midpoint of the diaphysis on the osteometric board and mark with a

pencil. Using sliding calipers to measure with one hand, rotate the bone with the other hand until the minimum diameter is obtained. (Martin and Knussmann 1988: 199, #6; Langley *et al.* 2016: 75, #49).

Hum_06. **Total Breadth of the Capitulum-Trochlea:** The breadth of the capitulum and trochlea at the distal humerus. One end of the sliding calipers is positioned parallel to the flat, spool-shaped surface of the trochlea (medial), and the other end is moved until it comes into contact with the capitulum (lateral) (Byrd and Adams 2003, #41A). *Instrument*: sliding caliper.

Hum_07. **Anterior-Posterior Breadth of the Head:** The maximum breadth of the humeral head taken in the anterior-posterior direction on the articular surface. This measurement is taken perpendicular from the vertical diameter of the humeral head (Byrd and Adams 2003, #42A). *Instrument*: sliding caliper.

Hum_08. **Minimum Diameter of the Diaphysis:** The minimum diameter of the humeral diaphysis taken in any direction perpendicular to the shaft. This measurement should be taken on the oval part of the shaft, superior to the flattening observed around the olecranon fossa and the lateral supracondylar ridge. Often it is found near midshaft (Byrd and Adams 2003, #44B). *Instrument*: sliding caliper.

Hum_09. **Maximum Diameter of Diaphysis at the Deltoid Tuberosity:** The maximum diameter of the diaphysis within the length of the deltoid tuberosity. Rotate and slide the element to find the maximum diameter (Byrd and Adams 2015, #44D). *Instrument*: sliding caliper.

RADIUS

Rad_01. **Maximum Length of the Radius:** The distance from the most proximally positioned point on the head of the radius to the tip of the styloid process without regard to the long axis of the bone. *Instrument*: osteometric board.

Comment: Place the proximal end against the vertical upright of the osteometric board and press the movable upright against the distal end. Move the bone up, down and sideways to obtain the maximum length (Martin and Knussmann 1988: 201, #1; Hrdlicka 1920: 127; Langley *et al.* 2016: 75, #50).

Rad_04. **Maximum Diameter of the Head:** The maximum diameter of the radial head measured on the margin of the head that articulates with the ulna. The bone is rotated until the maximum distance is obtained (Montagu 1960: 68; Langley *et al.* 2016: 75, #53; Byrd and Adams 2003, #47D). *Instrument*: sliding caliper.

Rad_05. **Anterior-Posterior (Sagittal) Diameter at Midshaft:** The distance between anterior and posterior surfaces at midshaft. *Instrument:* sliding caliper.

Comment: Determine the midpoint of the diaphysis on the osteometric board and mark with a pencil. Measure sagittal diameter at that point. This measurement is almost always less than the medial-lateral diameter (Moore-Jansen *et al.* 1994, #46).

Rad_06. **Medial-Lateral (Transverse) Diameter at Midshaft:** The distance between medial and lateral surfaces at midshaft. *Instrument:* sliding caliper.

Comment: Perpendicular to anterior-posterior diameter (Moore-Jansen *et al.* 1994, #47).

Rad_07. **Maximum Diameter at the Radial Tuberosity:** The maximum shaft diameter on the radial tuberosity. Position the calipers around the tuberosity and rotate the bone until the maximum distance is obtained (Byrd and Adams 2003, #47A). *Instrument*: sliding caliper.

Rad_08. **Maximum Diameter of the Diaphysis Distal to the Radial Tuberosity:** The maximum shaft diameter distal to the radial tuberosity, positioned along the interosseous crest. The bone should be rotated to find the maximum distance (Byrd and Adams 2003, #47B). *Instrument*: sliding caliper.

Rad_09. **Minimum Diameter of the Diaphysis Distal to the Radial Tuberosity:** The minimum shaft diameter anywhere distal to the radial tuberosity. The bone may be rotated to find the minimum distance (Byrd and Adams 2003, #47C). *Instrument*: sliding caliper.

Rad_10. **Breadth of the Distal Epiphysis:** The maximum distance from the ulnar notch to the lateral aspect of the styloid process. The medial protrusions (articular borders of the ulnar notch) are placed against the vertical endboard of the osteometric board (sliding calipers may also be used) and the movable portion is applied to the lateral surface of the styloid process to find the maximum breadth (Byrd and Adams 2015, #47E). *Instrument*: sliding caliper.

CORA MEASUREMENT GUIDE

ULNA

Uln_01. **Maximum Length of the Ulna:** The distance between the most proximal point on the olecranon and the most distal point on the styloid process. *Instrument*: osteometric board.

> *Comment*: Place the proximal end of the ulna against the vertical end board. Press the movable upright against the distal end while moving the bone up, down and sideways to obtain the maximum length (Hrdlicka 1920; 127; Martin and Knussmann 1988: 204, #1; Langley *et al.* 2016: 75-76, #54).

Uln_04. **Anterior-Posterior (Dorso-Volar) Diameter:** The maximum diameter of the diaphysis where the crest exhibits the greatest development in the anterior-posterior (dorso-volar) plane (Moore-Jansen *et al.* 1994, #49). *Instrument:* sliding caliper.

Uln_05. **Medial-Lateral (Transverse) Diameter:** The distance between medial and lateral surfaces at the level of greatest crest development. *Instrument:* sliding caliper.

> *Comment:* Taken perpendicular to anterior-posterior diameter (Moore-Jansen *et al.* 1994, #50).

Uln_06. **Physiological Length of the Ulna:** The distance between the deepest point on the articular surface of the coronoid process on the guiding ridge and the most inferior point on the distal articular surface of the ulna. *Instrument*: spreading caliper.

> *Comment*: Do not include the styloid process or the groove between the styloid process and the distal articular surface (Martin and Knussmann 1988: 204, #2; Langley *et al.* 2016: 76, #57).

Uln_07. **Minimum Circumference of the Ulna:** The least circumference near the distal end of the bone (Martin and Knussmann 1988: 204, #3; Langley *et al.* 2016: 76, #58). *Instrument*: tape.

Uln_08. **Olecranon Breadth:** The maximum breadth of the olecranon process, taken perpendicular to the longitudinal axis of the semilunar notch (Martin and Knussmann 1988: 206, #6; Langley *et al.* 2016: 76, #59). *Instrument*: sliding caliper.

Uln_09. **Minimum Diameter of the Diaphysis including Interosseous Crest:** Locate the minimum diameter of the diaphysis along the portion of the bone that includes the interosseous crest. This measurement may not necessarily include the interosseous crest, but should be taken on that part of the shaft that exhibits the crest. This measurement is not always near the distal end of the crest (Byrd and Adams 2003, #51A). *Instrument:* sliding caliper.

Uln_10. **Minimum Diameter of the Diaphysis:** This measurement will be found near the distal epiphysis of the ulna. The bone should be rotated in order to locate the minimum distance (Byrd and Adams 2003, #51B). *Instrument:* sliding caliper.

Uln_11. **Breadth of the Semilunar Notch:** This is a measure of only the distal surface of the semilunar notch (the base). *Instrument:* sliding caliper.

Comment: In order to obtain the distance, one end of the calipers is positioned within the radial notch (approximate midpoint), roughly parallel to the shaft. The other end of the calipers is applied to the medial edge of the semilunar notch to obtain the maximum distance. Calipers can be angled (Byrd and Adams 2003, #51C).

OS COXA

Osc_01. Maximum Innominate Height: The distance from the most superior point on the iliac crest to the most inferior point on the ischial tuberosity (Martin and Knussmann 1988: 213, #1). *Instrument*: osteometric board or spreading caliper.

Comment: When using an osteometric board, place the ischium against the vertical end board and press the movable upright against the iliac crest. Move the ilium sideways and up and down to obtain the maximum distance (Hrdlicka 1920: 135; Langley *et al.* 2016: 77, #64).

Osc_02. Maximum Iliac Breadth: The distance from the anterior superior iliac spine to the posterior superior iliac spine (Martin and Knussmann 1988: 213, #2; Langley *et al.* 2016: 77, #65). *Instrument*: spreading caliper.

Osc_05. Minimum Iliac Breadth (WIB): The minimum distance measured from the area below the anterior inferior iliac spine to the most inward curvature of the greater sciatic notch (Langley *et al.* 2016: 77, #66; Byrd and Adams 2015, #59D). *Instrument*: sliding caliper.

Osc_14. Thickness of the Ilium at the Sciatic Notch: Position one end of the calipers along the arcuate line, adjacent to the apex of the auricular surface. Slide the opposing end of the calipers to the posterior surface of the ilium to obtain the measurement (Byrd 2008, #59A). *Instrument:* sliding caliper.

Osc_15. Maximum Breadth of the Ischium: Position one end of the calipers in the obturator foramen and place the other end on the ischial tuberosity. Move the calipers around to find the maximum distance (Byrd and Adams 2015, #59B). *Instrument:* sliding caliper.

Osc_16. Minimum Breadth of the Pubis: Position the calipers along the iliopubic ramus; rotate and slide the calipers to find the minimum distance. Use the pointed edges of the calipers instead of the flat so as not to obstruct the measurement (Byrd and Adams 2015, #59C). *Instrument:* sliding caliper.

Osc_17. Maximum Diameter of the Acetabulum: The maximum distance of the acetabulum taken at any two points along the articular border of the lunate surface (look at the acetabulum from the side and take the measurement at the peaks of the ridges). This distance is commonly found in line with the iliac crest and the ischial tuberosity (Byrd 2008, #59E). *Instrument:* sliding caliper.

FEMUR

Fem_01. Maximum Length of the Femur: The distance from the most proximal point on the head of the femur to the most distal point on the medial or lateral femoral condyle (Martin and Knussmann 1988: 216, #1). *Instrument*: osteometric board.

Comment: Place the femur parallel to the long axis of the osteometric board and resting on its posterior surface. Press the medial or lateral condyle against the vertical end board while applying the movable upright to the femoral head. Move the bone up, down, and sideways until the maximum length is obtained (Hrdlicka 1920: 128; Langley *et al.* 2016: 78, #75).

Fem_02. Bicondylar Length of the Femur: The distance from the most proximal point on the head of the femur to a plane drawn between the inferior surfaces of the distal condyles . *Instrument*: osteometric board.

Comment: Place the femur on the osteometric board so that the bone is resting on its posterior surface. Press both distal condyles against the vertical end board while applying the movable upright to the head of the femur (Martin and Knussmann 1988: 216, #2; Hrdlicka 1920: 128; Langley *et al.* 2016: 78, #76).

Fem_03. Epicondylar Breadth of the Femur: The distance between the two most projecting points on the epicondyles. *Instrument*: osteometric board.

Comment: Place the femur on the osteometric board so that it is resting on its posterior surface. Press one of the epicondyles against the vertical end board while applying the movable upright to the other condyle. (Martin and Knussmann 1988: 218, #21; Langley *et al.* 2016: 79, #77).

Fem_04. Maximum Diameter of the Femur Head: The maximum diameter of the femur head measured on the border of the articular surface. *Instrument*: sliding caliper.

Comment: Rotate the arms of the caliper around the femur head to find the maximum diameter. (Dwight 1905: 21; Montagu 1960: 70; Langley *et al.* 2016: 79, #78).

Fem_05. Anterior-Posterior (Sagittal) Subtrochanteric Diameter of the Femur: The anterior-posterior

diameter of the proximal end of the diaphysis measured perpendicular to the transverse diameter at the point of the greatest lateral expansion (See definition #65 for approximate location on the femoral shaft for this measurement). This diameter is oriented perpendicular to the anterior surface of the femur neck (Martin and Knussman 1988: 217, #10; Langley *et al.* 2016: 80, #80). *Instrument*: sliding caliper.

Fem_06. Medial-Lateral (Transverse) Subtrochanteric Diameter of the Femur: The transverse diameter of the proximal portion of the diaphysis at the point of its greatest lateral expansion. *Instrument*: sliding caliper.

Comment: The transverse diameter is oriented parallel to the anterior surface of the femur neck. Close attention should be paid to assessing this plane in femoral necks with a significant degree of torsion. In cases where this cannot be determined (e.g. where the lateral surfaces remain parallel) this measurement is recorded in the region 2-5 cm below the lesser trochanter (Martin and Knussman 1988: 217 #9; Langley *et al.* 2016: 79-80, #79).

Fem_07. Anterior-Posterior (Sagittal) Midshaft Diameter: The distance between anterior and posterior surfaces measured approximately at the midpoint of the diaphysis, at the highest elevation of linea aspera. *Instrument:* sliding caliper.

Comment: The sagittal diameter should be measured perpendicular to the anterior bone surface (Moore-Jansen *et al.* 1994, #66).

Fem_08. Medial-Lateral (Transverse) Midshaft Diameter: The distance between the medial and lateral surfaces at midshaft, measured perpendicular to the anterior-posterior diameter (Moore-Jansen *et al.* 1994, #67). *Instrument:* sliding caliper.

Fem_11. Circumference of the Femur at Midshaft: The circumference measured at the midshaft. *Instrument*: tape.

Comment: If the linea aspera is unusually hypertrophied at midshaft, this measurement should be recorded approximately 10 mm above the midshaft (Martin and Knussmann 1988: 217, #8; Langley

et al. 2016: 80, #83).

Fem_14. Minimum Anterior-Posterior Diameter of the Diaphysis: The minimum anterior-posterior diameter anywhere along the diaphysis. The linea aspera and condyles should be utilized in order to orient the bone in anatomical position (use the condyles to orient) (Byrd and Adams 2003, #68A). *Instrument*: sliding caliper.

Fem_15. Minimum Medial-Lateral Diameter of the Diaphysis: The minimum medial-lateral diameter anywhere along the diaphysis. The linea aspera and condyles should be utilized in order to orient the bone (should be taken in a perpendicular orientation to 68A) (Byrd and Adams 2003, #68B). *Instrument*: sliding caliper.

Fem_16. Minimum Superior-Inferior Neck Diameter: The minimum distance from the superior surface to the inferior surface on the femoral neck (Seidemann *et al*. 1998). Place caliper in the saddle of the neck (superior) and close inferior caliper arm, moving as necessary to find the minimum (Byrd and Adams 2015, #68D). *Instrument*: sliding caliper.

Fem_17. Maximum Diameter along the Linea Aspera: The maximum shaft diameter at any point along the linea aspera. As the bone should be rotated to obtain the maximum distance, the measurement does not necessarily have to include the linea aspera, though it likely will (Byrd and Adams 2003, #68E). *Instrument*: sliding caliper.

TIBIA

Tib_01. **Length of the Tibia:** The distance from the superior articular surface of the lateral condyle of the tibia to the tip of the medial malleolus (Martin and Knussmann 1988: 220, #1). *Instrument*: osteometric board.

Comment: An osteometric board with a hole for the intercondylar eminence makes this measurement easier to take. Place the tibia on the osteometric board resting on its posterior surface with the longitudinal axis of the bone parallel to the board (Hrdlicka 1920: 129). If using an osteometric board without a hole, place the tibia on the osteometric board so that it the long axis is parallel to the board. The measurement is taken from the lateral condyle to the tip of the medial malleolus (Langley *et al.* 2016: 81, #86).

Tib_02. **Maximum Proximal Epiphyseal Breadth of the Tibia:** The maximum distance between the two most projecting point on the margins of the medial and lateral condyles of the proximal epiphysis. *Instrument*: osteometric board.

Comment: Place the tibia on the osteometric board resting on its posterior surface. Press the lateral condyle against the vertical end board, and place the movable upright against the medial condyle. Tibiae exhibiting marked torsion may have to be rotated to obtain the maximum breadth (Martin and Knussmann 1988: 221, #3; Langley *et al.* 2016: 81, #87).

Tib_03. **Maximum Distal Epiphyseal Breadth:** The distance between the most medial point on the medial malleolus and the lateral surface of the distal epiphysis. *Instrument*: osteometric board.

Comment: Place the two lateral protrusions of the distal epiphysis against the fixed side of the osteometric board and move the sliding board until it contacts the medial malleolus (Martin and Knussmann 1988: 221, #6; Langley *et al.* 2016: 81, #88).

Tib_04. **Maximum Diameter at the Nutrient Foramen:** The distance between the anterior crest and the posterior surface at the level of the nutrient foramen (Moore-Jansen *et al.* 1994, #72). *Instrument:* sliding caliper.

Tib_05. **Medial-Lateral (Transverse) Diameter at the Nutrient Foramen:** The straight line distance from the medial margin to the interosseous crest at the level of the nutrient foramen (Moore-Jansen *et al.* 1994, #73). *Instrument:* sliding caliper.

Tib_06. **Circumference at the Nutrient Foramen:** The circumference measured at the level of the nutrient foramen (Moore-Jansen *et al.* 1994, #74). *Instrument:* tape.

Tib_10. **Maximum Anterior-Posterior Diameter Distal to the Popliteal Line:** This measurement should be taken at the most distal point of the popliteal line where it intersects with the margin of the diaphysis. The calipers are rotated to find the maximum distance (this is the maximum diameter of the diaphysis at this point). Note that the correct location may be difficult to determine in very gracile individuals (Byrd and Adams 2003, #74A). *Instrument:* sliding calipers.

Tib_11. **Minimum Anterior-Posterior Diameter:** Locate the minimum anterior-posterior distance at any point on the tibial shaft. Use the medial malleolus and anterior crest to orient the bone, particularly when torsion is present (Byrd and Adams 2003, #74B). *Instrument:* sliding calipers.

Tib_12. **Maximum Anterior-Posterior Distance of the Distal Articular Surface:** Locate the maximum anterior-posterior distance of the distal articular surface by viewing the element from the side to *find the peaks of the articular surface* and measuring the distance between them. Use the medial malleolus to orient the bone (Byrd and Adams 2015, #74F). *Instrument:* sliding calipers.

FIBULA

Fib_01. Maximum Length of the Fibula: The maximum distance between the most superior point on the fibular head and the most inferior point on the lateral malleolus (Martin and Knussmann 1988: 222, #1). *Instrument*: osteometric board.

Comment: Place the fibula on the osteometric board and place the tip of the lateral malleolus against the vertical end board. Press the movable upright against the proximal end of the bone while moving it up and down and sideways to obtain the maximum length (Langley *et al.* 2016: 82, #92).

Fib_02. Maximum Diameter of the Fibula at Midshaft: The maximum diameter at the midshaft. (Martin and Knussmann 1988: 222, #2). *Instrument*: sliding caliper.

Comment: Find the midpoint on the osteometric board and mark with a pencil. Place the diaphysis of the fibula between the two arms of the caliper while turning the bone to obtain the maximum diameter (Langley *et al.* 2016: 82, #93).

Fib_03. Maximum Diameter of the Diaphysis: This measurement should only be taken along the interosseous crest. Avoid measurements of the shaft near the epiphyses (Byrd and Adams 2015, #76A). *Instrument:* sliding calipers.

Fib_04. Minimum Diameter of the Diaphysis: The minimum distance at any point along the diaphysis (Byrd and Adams 2015, #76B). *Instrument:* sliding calipers.

Fib_05. Maximum Breadth at the Distal End: Place the one jaw of the caliper on the posterior portion (tubercle) and extend the other jaw to the opposite side (just above the malleolar articular surface) to find the maximum distance (Byrd and Adams 2015, #76C). *Instrument:* sliding calipers.

TECHNICAL REQUIREMENTS

Supported operating systems include Linux, macOS, and Windows 7/8/10 with R version 3.3.X or greater. 8 gigabytes of RAM or greater is recommended. All performance analyses published were conducted on Linux systems with 32-64 gigabytes of RAM.

REFERENCES

REFERENCES

1. Lynch, JJ, Byrd, J, LeGarde, CB. The Power of Exclusion using Automated Osteometric Sorting: Pair-Matching. Journal of Forensic Sciences 2018. (In Press)

2. Byrd JE, LeGarde CB. Osteometric sorting. In: Adams BJ, Byrd JE, editors. Commingled Human Remains: methods in recovery, analysis, and identification. San Diego, CA: Academic Press, 2014:167-191.

3. Lynch, JJ (A). An analysis on the choice of alpha level in the osteometric pair-matching of the os coxa, scapula, and clavicle. Journal of Forensic Sciences 2018. (In Press)

4. Lynch, JJ (B). The automation of regression modeling in osteometric sorting: an ordination approach. Journal of Forensic Sciences 2018. (In Press)

5. Lynch, JJ (C). An automated two-dimensional form registration method for osteological pair-matching. Journal of Forensic Sciences 2018. (In Press)

6. Adams BJ, Byrd JE. Interobserver variation of selected postcranial skeletal measurements. Journal of Forensic Sciences 2002;47:1193-202.

7. Adams BJ, Byrd JE. Resolution of small-scale commingling: a case report from the Vietnam war. Forensic Science International 2006;156-63-9.

8. Anastopoulou I, Karakostis FA, Borrini M, Moraitis K. A statistical method for reassociating human tali and calcanei from a commingled context. Journal of Forensic Sciences 2017. (In Press)

9. Byrd JE (2008). Models and methods for osteometric sorting. In Recovery, Analysis, and Identification of Commingled Human Remains, edited by B.J. Adams and J.E. Byrd. Pp. 1992;20. Humana Press, New Jersey.

10. Byrd JE, Adams BJ (2003). Osteometric sorting of commingled human remains. Journal of Forensic Sciences, 48(4):1-8. Byrd JE, Adams BJ (2015). Updated measurements for osteometric sorting. DPAA CIL document, dated 16 December 2015.

11. Chew KR. The use of osteometric sorting techniques to aid in the resolution of a large scale commingling: the piggot ossuary site. Master's Thesis, Raleigh, NC: North Carolina State University 2014.

12. Dwight T (1905). The size of the articular surfaces of the long bones as characteristics of sex; an anthropological study. American Journal of Anatomy, 4: 19-32.

13. Ericka N, Abbe L. A case of commingled remains from rural South Africa. Forensic Science International 2005;151(2-3):201-206.

14. Finlayson JE, Bartelink EJ, Perrone A, Dalton K. Multimethod resolution of a small scale case of commingling. Journal of Forensic Sciences 2016.

15. Garrido-Varas C, Rathnasinghe R, Thompson T, Savriama Y. A new method to pair-match metacarpals using bilateral symmetry and shape analysis. Journal of Forensic Sciences 2015;60:118-123.

16. Genoves S. Proportionality of the long bones and their relation to stature among Mesoamericans. American Journal of Physical Anthropology 1967;26(1):67-77.

17. Giles E and Klepinger LL. Confidence intervals for estimates based on linear regression in forensic anthropology. Journal of Forensic Sciences 1988;88(5):1218-22.

18. Hrdlicka A (1920). Anthropometry. The Wistar Institute of Anatomy and Biology: Philadelphia.

19. Karell MA, Langstaff HK, Halazonetis DJ, Minghetti C, Frelat M, Kranioti EF. A novel method for pair-matching using three-dimensional digital models of bone: mesh-to-mesh value comparison. International Journal of Legal Medicine 2016;130:1315-22.

20. Langley NR, Jantz LM, Ousley SD, Jantz RL, Milner GS (2016). Data Collection Procedures for Forensic Skeletal Material 2.0. The University of Tennessee and Lincoln Memorial University: Tennessee. http://fac.utk.edu/wp-content/uploads/2016/03/DCP20_webversion.pdf

21. LeGarde CB. Asymmetry of the Humerus: the influence of handedness on the deltoid tuberosity and possible implications for osteometric sorting. Master's Thesis, Missoula, MT: The University of Montana 2012.

22. Martin R, Knussmann R (1988). Anthropologie: Handbuch der vergleichenden Biologie des Menschen. Stuttgart: Gustav Fischer. Montagu MFA (1960). A Handbook of Anthropometry. Charles C. Thomas, Springfield, Illinois.

23. Mccormick K. A biologically informed structure to accuracy in osteometric reassociation. PhD dissertation, Knoxville, TN, The University of Tennessee Knoxville 2016.

24. Moore-Jansen PM, Ousley SD, Jantz RJ. Data Collection Procedures for Forensic Skeletal Material. Report of Investigations No.48 1994; Department of Anthropology, University of Tennessee, Knoxville.

25. Okrutny E CJ. Postcranial osteometric assessment of Korean ancestry. Master's Thesis, Orlando, FL, University of Central Florida 2012.

26. Osterholtz AJ, Baustian KM, Martin DL, editors. Commingled and Disarticulated Human Remains: Working Toward Improved Theory, Method, and Data. Ny, Springer, 2014.

27. Parkinson EW, Craig-atkins E. Joint articulation in resolving commingled human remains: osteometric analysis of the acetabulofemoral and tibio-femoral articular surface areas. Poster presented at the 86th Annual Meeting of the American Association of Physical Anthropologists 2017.

28. Pankakhyo MN. Evaluation of the methodology for addressing commingled human remains from the lewis jones cave ossuary. Master's Thesis, Tuscaloosa, AL, The University of Alabama 2013.

29. Rodriguez JM, Hackman L, Martinez W, Medina CS. Osteometric sorting of skeletal elements from a sample of modern Colombians: a pilot study. International Journal of Legal Medicine 2016;13-(2):541-50.

30. Seidemann RM, Stojanowski CM, Doran GH. The use of the supero-inferior femoral neck diameter as a sex assessor. American Journal of Physical Anthropology 1998; 107:305–313.

31. Snow C, Folk E. Skeletal assessment of commingled skeletal remains. American Journal of Physical Anthropology 1970;32:423-7.

32. Thomas, RM, Ubelaker DH, Byrd JE. Tables for the metric evaluation of pair-matching of human skeletal elements. Journal of Forensic Sciences 2013;58(4):952-956.

33. Trotter M and Gleser GC. Estimation of stature from long bones of American whites and negroes. American Journal of Physical Anthropology 1952;10:463-514.

34. Vickers S, Lubinski P, DeLeon LH, Bowen JT. Proposed method for predicting pair matching of skeletal elements allows too many false rejections. Journal of Forensic Sciences 2014;60(1):102-106.

35. Jang YR, Jung-Min L, Jeong-Sang P, Na-Hyok L. The new method of implementing 3D scanners and X-ray on Commingled Remains Recovered from a Korean War Recovery Site. Poster presented at the 68th Annual Scientific Meeting 2016.

36. Jantz RL, Hunt DR, Meadows L. Maximum length of the tibia: How did Trotter measure it? American Journal of Physical Anthropology 1994;93:525-528.

37. Jantz RL, Hunt DR, Meadows L. The measure and mismeasure of the tibia: Implications for stature estimation. Journal of Forensic Sciences 1995;40:758-761.

38. Jantz RL, Moore Jansen PM. A data base for forensic anthropology: Structure, Content and Analysis. Knoxville, TN: Report of Investigations No. 47, Department of Anthropology, University of Tennessee, Knoxville, 1988.