



Automated Osteological Sorting of Human Commingled Remains

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Origin



Large commingled assemblages:

- USS *Oklahoma*
- Comparison growth:

	Left	Right	Pair-matches	Associations
Humeri	289	294	84,966	2,057,990
Ulnae	196	201	39,396	1,475,252
Radii	190	175	33,250	1,368,020
Femora	343	344	117,992	2,353,662
Tibiae	311	310	96,410	2,168,532
Fibulae	245	254	62,230	1,803,386
Os coxae	282	264	74,448	1,947,582
Scapulae	206	209	43,054	1,534,670
				15,260,800 comparisons



Figure 1. USS *Oklahoma* recovery

Origin



Computerized automation:

- Pair-matching
- Articulation
- Association
- Outlier identification
- Antemortem stature association



Figure 2. Historical sorting of *Oklahoma* service members

What is it?



OsteoSort vs. OsteoShiny

- Development: R, C++, Shiny
- Free open source code licensed with GNU General Public License version 2
- Source code:
www.github.com/jjlynch2/OsteoSort
www.github.com/jjlynch2/OsteoShiny
- Installation instructions:
www.osteocoder.com

```
> library(OsteoSort)
> ls(package=OsteoSort)
 [1] "add.alpha"                "analytical_temp_space"
 [3] "antestat.input"           "antestat.regtest"
 [5] "art.input"                "art.ttest"
 [7] "dilated_directional_hausdorff_rcpp" "e_dist"
 [9] "efa"                      "fragment_margins"
[11] "hausdorff_dist"           "i_efa"
[13] "m.row"                   "match.2d"
[15] "match.3d"                "max_directional_hausdorff_rcpp"
[17] "mean_directional_hausdorff_rcpp" "metricsort"
[19] "minimum_euclidean_distances_indices" "outline.images"
[21] "output_function"         "pca_align"
[23] "pm.input"                "pm.ttest"
[25] "randomstring"            "readtps"
[27] "reg.input"               "reg.multitest"
[29] "remove_fragmented_margins" "shiftmatrices"
[31] "statssort"               "writetps"
```

Figure 3. OsteoSort R package

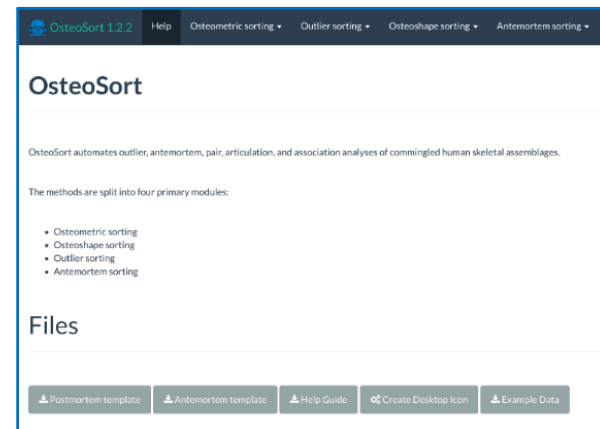


Figure 4. OsteoShiny GUI

What is it?



Web vs. Local

- Online tools: www.osteosort.net
- R package installation
- Installation on internal webserver



Figure 5. OsteoSort online GUI

What is it?



Measurement standards:

- Standard nomenclature
- Cheat sheet:
www.osteocoder.com/projects/measurement-standards
- Help guide provides definitions

Search:

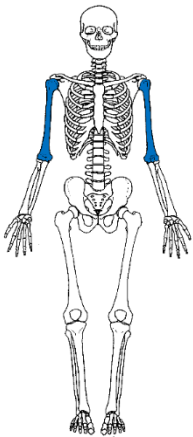
	CoRA 2017	Bulkstra & Ubelaker 1994	UTK 1994	UTK 2016	Byrd & Adams Supplemental 2003	Simmons 1990	Holland 1992	Holland 1995	Howells 1973
Hum_01	40		40	45					
Hum_02	41		41	46					
Hum_03	42		42	47					
Hum_04	43		43	48					
Hum_05	44		44	49					
Hum_06					41A				
Hum_07					42A				
Hum_08					44B				
Hum_09					44D				

Showing 1 to 9 of 9 entries (filtered from 231 total entries)

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Figure 6. CoRA standardized measurement variable names

Osteometric Sorting



Pair-matching:

- Homologous measurements
- t -distribution
- Null hypothesis: both elements are similar enough to have come from a single individual

$$D = \sum a_i - b_i$$

$$t = \frac{D - \tilde{x}}{S_{Dref}}$$

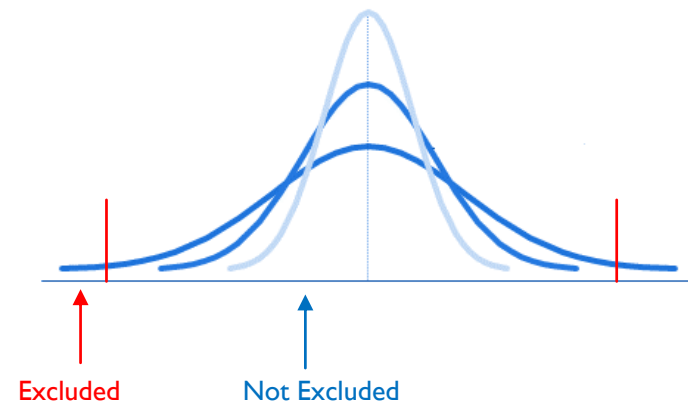
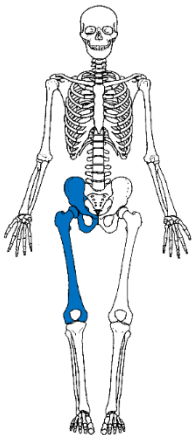


Figure 7. t -distribution

Osteometric Sorting



Articulation:

- Minimal difference measurements
- t -distribution
- Null hypothesis: both measurements are similar enough to have come from a single individual

$$D = a_i - b_j$$

$$t = \frac{D - \tilde{x}}{S_{Dref}}$$

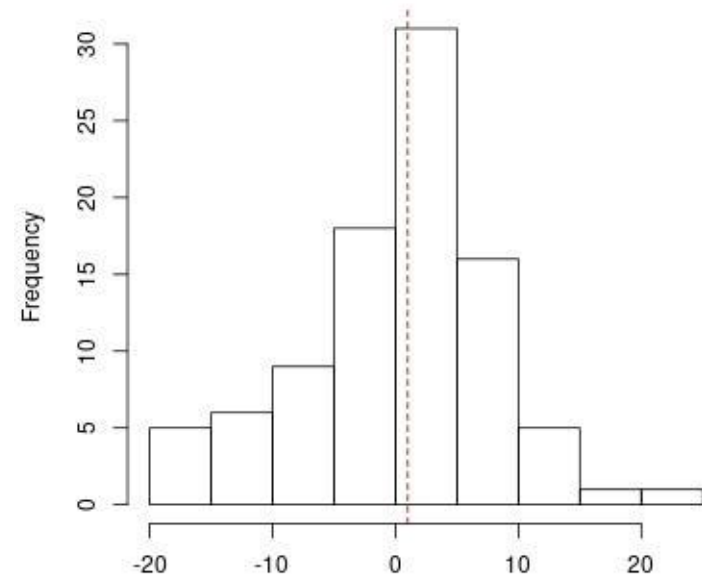
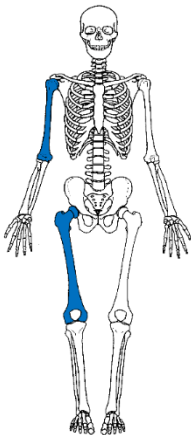


Figure 8. Articulation distribution with case comparison not excluded

Osteometric Sorting



Association:

- Correlated measurements
- t -distribution
- Null hypothesis: both elements are similar enough in size to have come from a single individual

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

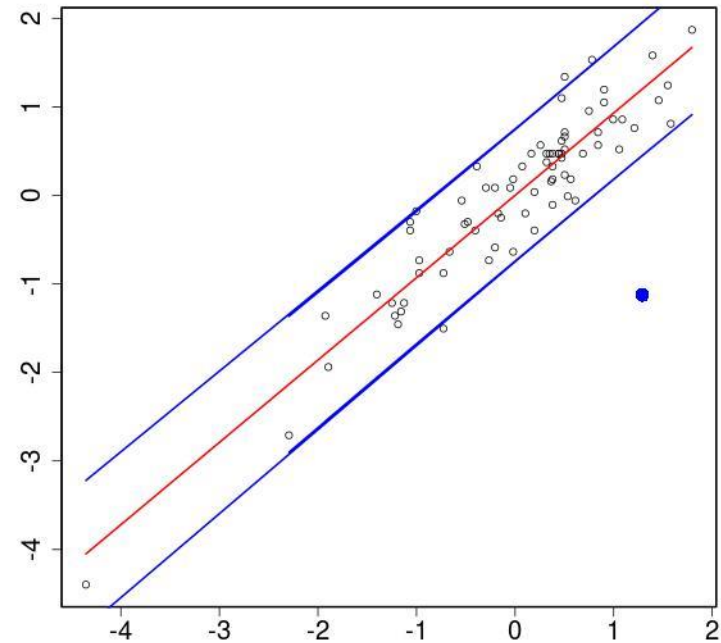
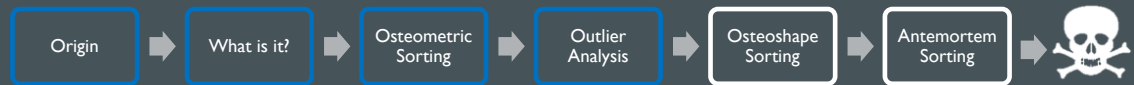


Figure 9. Association plot with case comparison excluded

Outlier Analysis



Outliers:

- Metric measurements
- Stature point estimates

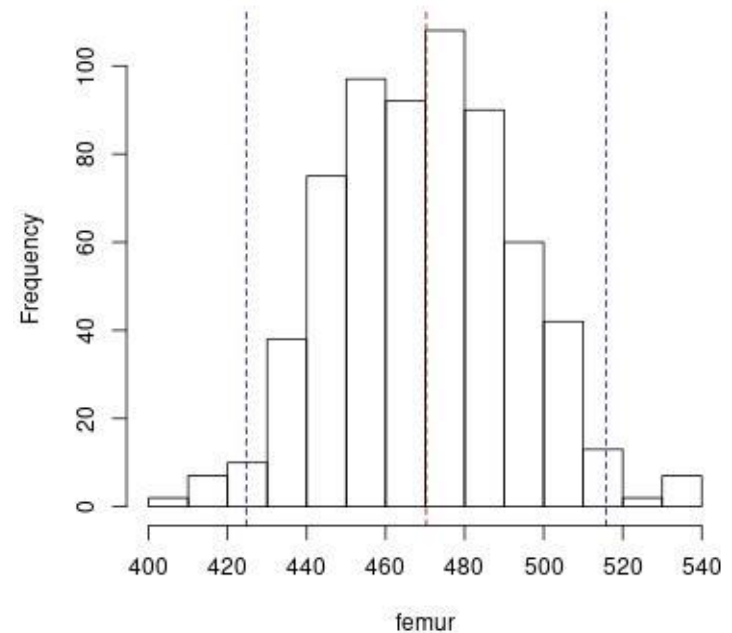
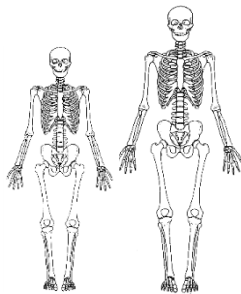
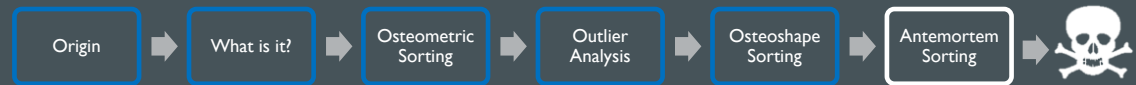


Figure 10. Stature plots with standard deviations

Osteoshape Sorting



Osteoshape:

- Pair-matching from photographs using form (shape-size) data
- Non-fragmented single form space
- Fragmented pairwise form spaces
- ~98% lowest Hausdorff distance = true-pair

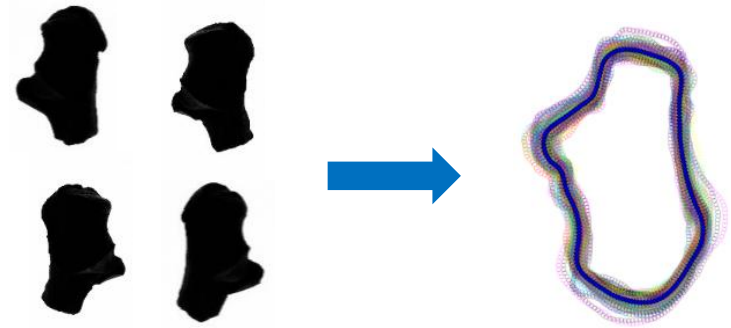


Figure 11. Single registration space

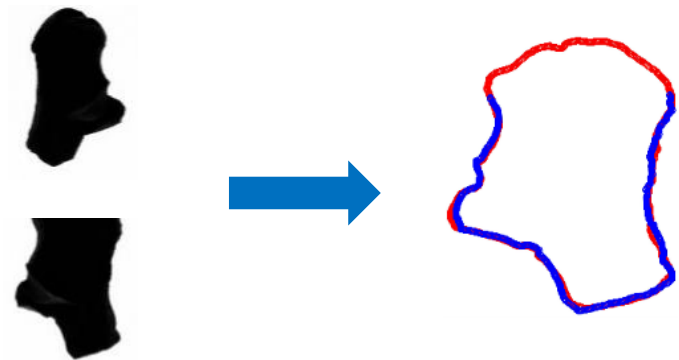
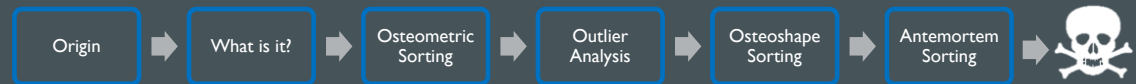


Figure 12. Pairwise registration space

Antemortem Sorting



Antemortem stature

- Closed assemblages
- Known antemortem statures
- Postmortem length measurements
- *t*-distribution
- Null hypothesis: The bone length is not too long or short to belong to an individual with a particular stature

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

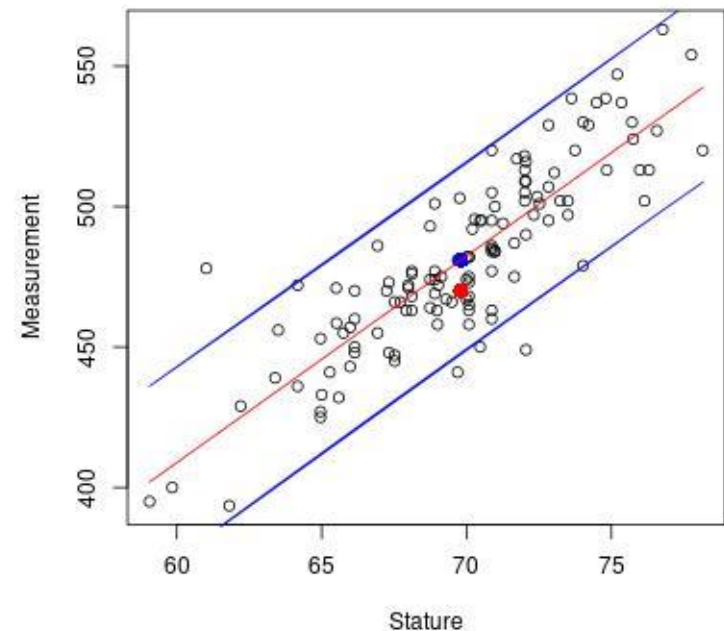


Figure 13. Stature graph with case comparison not excluded

OsteoSort



Demonstration

REFERENCES

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