The Application of NextEngine Scanning Technology to Commingled Skeletal Analysis at the Milwaukee County Poor Farm Cemetery: A Replicable Method for Restoring Individuality

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Abstract: The analysis and subsequent disentanglement of human skeletal elements from commingled or mixed burial contexts is an essential step in creating individual identifications of those individuals represented in these burials. This work is integral to the overall goal of using methodologically robust techniques to contextualize and represent individuals recovered in archaeological or forensic settings. A suite of commingled burial analysis methods are currently used to achieve this goal. These methods are essential to the field, but can still introduce error. To provide additional lines of evidence to support these analyses, this study investigates the efficacy of a three-dimensional pair-matching technique, using a NextEngine™ scanner and both open source and proprietary software to test two methods of mesh-to-mesh value comparison for reliability and replicability.

Keywords: Commingled Analysis, Pair Matching, Three-Dimensional Scanning, NextEngine

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Introduction

The disentanglement and subsequent analysis of human skeletal elements from commingled burial contexts is essential to the process of identifying and representing, as equally as possible, all individuals within a burial context. Not only are commingled burials, or burials in which the bones of two or more individual human skeletons have become intermixed, some of the most complex to excavate and analyze; (Osterholtz et al. 2014, Adams and Byrd 2014). Because of these challenges, many experts in commingled burial analysis (Adams and Byrd 2014, Osterholz et al. 2014, Ubelaker 2002) place an emphasis on optimizing methods within these contexts, since identification of individuals is not possible without the most accurate reassociation of skeletal elements (Adams and Byrd 2014). One primary method currently used to accomplish this goal is pair-matching right and left skeletal elements (Adams and Byrd 2014, Ubelaker 2002). Figure 1 illustrates different commingled analysis methods.

Though commingled analysis faces anatomical challenges including bilateral asymmetry, healed fractures, and osteologically manifested illness, some of these issues can be alleviated through methods that make use of tech-

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nology such as three-dimensional scanning. To contribute to the current methods of pair-matching analysis, this study tests a new three-dimensional pair-matching method put forth by Karell et al (2016). Keeping in mind the various professional venues for conducting commingled analysis, which include research institutions, cultural resource management firms, and educational institutions, the replicability of these methods is also tested and evaluated. For the greatest amount of transparency, applicability, and scientific integrity, the use of open-source and non cost-prohibitive methods is encouraged.

Figure 1. An example of morphological pair matching. Adapted from open source educational materials: Smithsonian Written in Bone (2009).

Background

A suite of thorough techniques has been created by bioarchaeologists, physical anthropologists, and forensic anthropologists to approach commingled burials. These include visual pair-matching (Adams and Byrd 2006), which entails comparing a series of landmarks on right and left elements to determine a match, osteometric Comparison (Byrd 2008), joint articulation of close-fitting joints (Ubelaker 2002), and even Morphometric Comparison (Garrido-Varas 2015). Figure 2 illustrates Morphometric Comparison.

Each of these analyses contribute an increased level of accuracy and sensitivity to the process of creating associations between commingled skeletal elements, especially when used in concert with one another. However, these techniques are not without limitations. Many of these techniques are visually based, and can therefore be subjective. For instance, visual pair matching relies upon visual assessments of mirrored physiological landmarks in juxtaposition with each other on paired elements, such as right and left humerii (Adams and Byrd 2016). With these visually based techniques, there is room for error or a lack of surety even with the most experienced observers.

The careful and skilled work of trained osteological analysts in both archaeological and forensic settings cannot be replaced, but will be strengthened by the support of the statistically significant findings possible with three-dimensional scanning analysis. Karell et al., (2016) propose a solution to the

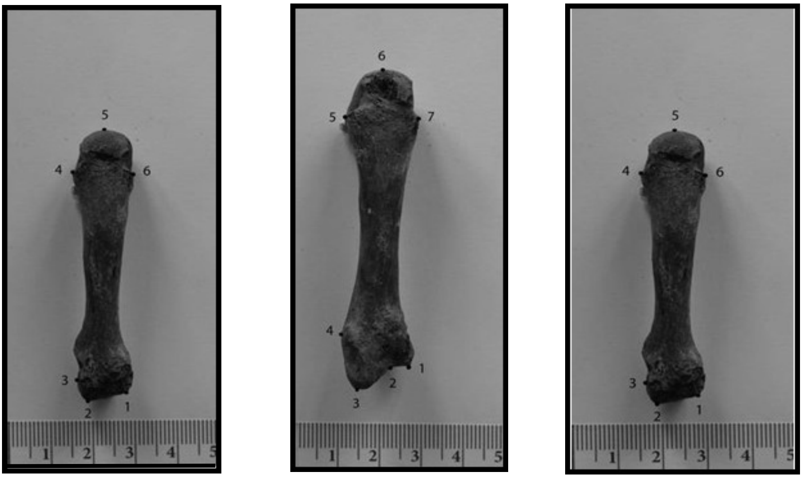

Figure 2. Morphometric Comparison. Adapted and reproduced with permission from Garrido-Varas 2015:120.

problems specifically inherent in visual pair-matching in the form of three-dimensional pair-matching that uses point-to-point comparisons of three-dimensional scans of bone. To do this, Karell et al. attempt a manual Mesh Value Comparison (MVC) and an automatic MVC. The manual MVC uses the software Flexscan 3D to manually superimpose and compare scanned elements while the automated MVC method uses Lightbox 3D, a medical imaging software, to run comparison of scans automatically. Both methods produce a statistical output of the degree of match found in each scan comparison.

This pilot project tests this method and proposes an open-source alternative to one of Karell et al.'s suggested methods. In addition, this paper outlines specific future applications of three- dimensional scanning in commingled analysis.

Materials and Methods

Every analysis of commingled human remains, from modern forensic contexts to the recovery of early hominin species, requires the utmost attention to detail and caution. Many North American historic institutional commingled burial contexts carry with them not only the complications of a multi-individual burial, but also the evidence of marginalization, loss of identity, and objectification. Individuals recovered from commingled contexts at the Milwaukee Poor Farm Cemetery (MCPFC) in particular, reveal evidence of these cultural intersections in the form of postmortem medical investigation and anatomization (Richards et al. 2017:251-254). The subjects of these activities were most often poor and disenfranchised individuals. The anatomization of these individuals further exposed an already vulnerable group of people. The burial program at the MCPFC illustrates the “marginal status of the individuals likely in life and certainly in death” (Richards 1997). For this reason, the highest level of care and sensitivity has been undertaken when working with these individuals.

Study Individuals

Eight adult (age > 20) individuals from the MCPFC were selected based on good preservation for this pilot study. Only one female was present within the initial study group due to an overall larger ratio of males recovered from the cemetery. A more equal ratio of females to males will be included in the expanded study. For each individual, the left and right radii and the left and right ulnae were selected to be three dimensionally surface scanned, due to the representation of these skeletal elements in commingled contexts. Known individuals were selected for this study to test the applicability of the method before applying it to a truly commingled context. To maintain provenience and to avoid commingling, each individual underwent osteological profile analysis and scanning with associated tracking forms and cards for each step of the process. As a further precaution, only one individual per day was scanned. As a blind, randomized numbers were assigned to a second file of the scans once they were completed. This allowed for the testing to proceed in a simulated commingled setting. Table 1 illustrates the sample group, including Lot Number, Randomized Number, age, sex, and element completeness.

Scanning Protocol

Three-dimensional surface scans were completed on all elements using a NextEngine™ 3D scanner. Each element was scanned with a 360-degree positioning, 7 scan divisions, in a 25” range, with a point density of High Standard Definition, or 850 points/in2. Each element was processed in ScanStudio™, the proprietary software associated with the NextEngine™ for noise reduction and trimming. Elements were then exported as .obj files for analysis.

Table 1. List of individuals including age, sex, and completeness.
The scale of element completeness is represented in a scoring system where 1= fully complete, 2= limited fragmentation, and 3= heavy fragmentation.

Original Lot Number	Randomized Number	Age Category	Sex	Element Completeness
91-049-5014	8	Middle Adult	Male	1
91-049-5128	7	Old Adult	Female	1
91-049-5145	5	Young Adult	Male	1
91-049-5146	1	Middle Adult	Male	2
91-049-5209	4	Old Adult	Male	1
91-049-5210	6	Middle Adult	Male	1
91-049-8113	2	Young Adult	Male	1
91-049-8136	3	Middle Adult	Male	1

Mesh-to-Mesh Value Comparison Method—Manual

All methods set forth by Karell et al. 2016 test the mesh value comparison (MVC) of two meshes, which are digital point clouds that represent thousands of data points taken by the scanner when scanning the bones. The Karell et al. (2016) Manual mesh-to-mesh value comparison (Manual MVC) uses LMI Technologies Flexscan 3D to compare the scans of elements. Illustrated in Figure 3, this software provides a thorough analysis and visual representation according to Karell et al. (2016). This software, while highly sophisticated and of quality, is not openly accessible (licensing cost: $1499.00). Due the licensing costs, this technique could not be tested and the overall inaccessibility of the method limits its replicability.

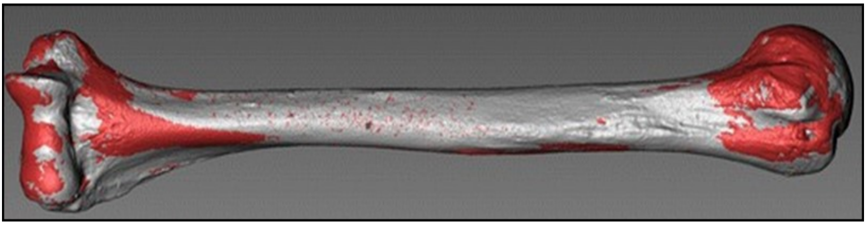

Figure 3. Fine alignment tool in FlexScan 3D. This software is not open-source (licensing cost $1499), so this method was unable to be tested. Image reproduced with permission from Karell et al 2016.

Mesh-to-Mesh Value Comparison Method—Automated

To test this method, all software employed by Karell et al 2016 were used. Viewbox 4, a medical software most often used for comparing MRIs, while not technically open source, can be utilized at no cost with a registration lag-time screen.

First, mirrored scans of all right skeletal elements were created in Netfab Basic so they could be compared against the left elements. Then they were entered into Viewbox 4. The automated MVC method Karell et al 2016 used included an estimated overlap for the scans of 100 %, with an initial position for rough alignment set at 20 and a nearest neighbor search “Approximate (fast)” with a point sampling of 1 %. This means that the program was given parameters for a very loose starting point for scan analysis and a less accurate sampling strategy that would yield results more quickly. The quick turnaround sacrifices the amount of points that are compared against each other for their closest matching point. These parameters did not yield satisfactory results so “Exact (Slow)” was used with a point sampling of 100%. This matched the scans point to point, with one hundred iterations, meaning that more exact starting points and comparisons were selected for, with a larger sample size of three-dimensional points, enabling a much more thorough comparison.

Viewbox 4 then generated the Mesh-to-Mesh MVC values, which are statistical values representing the similarity between two scans. These were then logged into Microsoft Excel to be analyzed. The pool for comparison was narrowed by side: a right radius cannot be matched with a right radius. All right elements were compared against left elements, using the mirroring capabilities in Netfab Basic, which, in creating mirrored scans of the right elements, enabled them to be directly compared with the left elements. A mesh-to-mesh MVC value was recorded for each. A low value of distance between two scans was an indicator of a strong match. Figure 5, below, illustrates a positive pair match and a negative one.

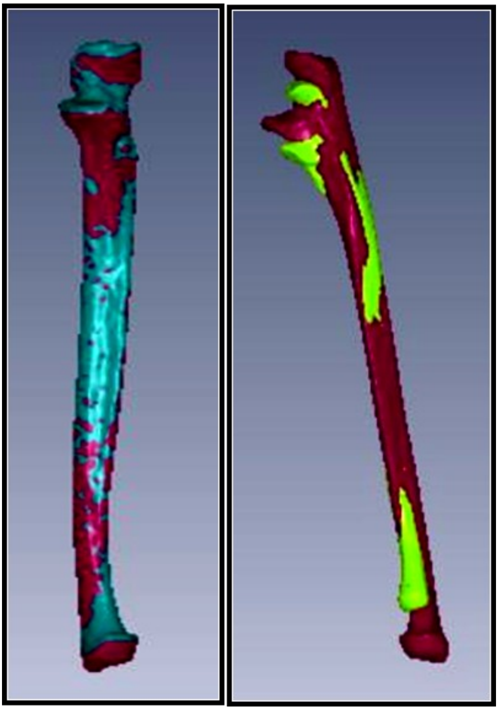

Figure 5. Scans of Ulnae illustrating automated MVC. Example of a true match (Left). Each separately scanned ulna is represented by a different color allowing for a visual representation of the statistical match value. Note stippling, or the interspersed colors of each bone in the diaphyseal area of the true match scan, which indicates many areas of statistical overlap. A Poor match (Right) is indicated by no interspersal of colors and protrusions where the two bones do not align.

The three lowest values were cross-referenced by running all scans through the automated MVC in reverse order to ensure true matches: that left and right agreed. Then the blind was removed and the results were compared to the known pair-matches. The standard deviations of mesh-to-mesh values from true pair matches were calculated to inform a possible cutoff threshold for positive pair matches. Though this was not a truly automated process to the non-registered Viewbox 4 user, it was still a very simple process: the controls of the program and the data readouts were accessible to most users.

Results

To analyze the MVC comparison results, a specificity and sensitivity were determined using Microsoft Excel, as was done by Karell et al. 2016. Specificity and sensitivity testing determines the number of true and false positives and negatives, determining the percentage of accuracy over precision. For the automated MVC method for ulnae, the sensitivity was 85.71% and the specificity was 88.89 %. This resulted from one false positive and one false negative and is comparable with the Karell et al. (2016) values. This sample included an ulna that was shortened due to a healed fracture (lot 5014) which was incorrectly matched with two smaller ulnae (Table 2).

Table 2. Sensitivity and Specificity for Ulnae

Sensitivity and Specificity for Ulnae	
True Positives	6
False Negatives	1
False Positives	1
True Negatives	8
Sensitivity	85.71%
Specificity	88.89 %

For the radii, the sensitivity was 87.50% with one false negative, and specificity was 100.00% (Table 3). This was also related to a healed fracture. The factors of healed fractures and bilateral asymmetry will be further tested in future research, but there is precedent (Garrido-Varas 2015) for quantifying and controlling for these issues.

Table 3. Sensitivity and Specificity for Radii.

Sensitivity and Specificity for Radii	
True Positives	8
False Negatives	1
False Positives	0
True Negatives	7
Sensitivity	87.50%
Specificity	100.00 %

Discussion and Conclusions

The results indicate that both a high level of specificity and a high level of sensitivity, meaning that the results can be both very specific and very accurate, can be achieved when testing pair match designations using three-dimensional scanning and even using an automated testing technique. The speed, accuracy, and low-impact of this method may prove it to be a highly useful tool for bolstering pair matches. This MVC method was tested to determine whether sophisticated technology and analysis can be made replicable and accessible as well. Though the results are not the 100% accuracy of the Manual MVC comparison done by Karell et al 2016, the high rate of sensitivity and specificity coupled with the high replicability of using open-source or open availability software are promising. These factors illustrate that this type of analysis has the potential to be highly useful to skeletal analysts at all levels.

This analysis did, however, raise the issue of taphonomic condition. Some scans were unable to be used due to taphonomic damage to the bone, specifically fragmentation. This reduced the number of individuals available for this study, but did not affect the data in any other way. It did, however, inspire future aims for this research that will now include ways to refit taphonomically damaged fragments in a program such as MeshLab so that these elements can be analyzed just as effectively as whole bone. Additional future research will include an expansion of this study with larger sample size, as well as two specific related studies. The first would test a novel method similar to the manual MVC test proposed by Karell et al. 2016. The proposed method would utilize the Hausdorff distance feature in MeshLab to test the compatibility of compared scans, similarly to the manual MVC method. The benefit of this method is that Meshlab is a software program that is freely accessible to all, and thus much more easily replicated and utilized. The second area of future research will combine the techniques of bioarchaeology with those of kinesiology.

Because not all skeletal elements are standardized, even beyond the differences of bilateral asymmetry, there are many times a joint articulation is needed to contribute to a pair match, or to create connections to axial elements through joints. To provide a solution for these quandaries, future research will test the hypothesis that if skeletal elements belong to a joint, they will react normally to a force simulation that would be applied to that joint in life, whereas if they do not refit to the joint properly, their reaction to a normal applied force would be atypical. OpenSim, a clinical biomechanical software that is openly available, tests joint reaction force, though most often in MRI scans of already articulated elements. This software will be modified to best fit the commingled analysis application. Once these methods have been tested on a larger scale, they will be actively applied in concert with other commingled analyses.

This research illustrates that the MVC method put forth by Karell et al (2016) is a highly useful and replicable tool for commingled skeletal analysis. Also highlighted are the problems that arise when using software that is not accessible to all. If other institutions cannot access software, such as the highly useful but expensive FlexScan3D, as illustrated in figure 3, then results using this software technically cannot be replicated, and without replicability, the accuracy and usefulness of the method cannot be ascertained. It is clear that with these and other methods available to institutions, even more highly accurate and sensitive analyses and identifications of individuals recovered from commingled contexts can take place.

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