



Computerized reconstruction of fragmentary skeletal remains



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ABSTRACT

This research presents a new software, “Fragmento”, for accurate analyses of fragmentary human skeletal remains and facilitation of three-dimensional (3D) fragmentary matching and full bone reconstruction. The framework utilizes the power of statistical bone atlases to create 3D templates for bone matching and to interpolate missing anatomy for full bone reconstruction. Developed tool has enhanced features allowing the user to visualize, review and scale all scanned skeletal remains within a 3D statistical template, merging accepted registered elements to provide a fully reconstructed bone. A three stage validation was performed on Fragmento: Stages I and II used simulated fragmentary data which was compared to full bones with an error less than 3 mm; Stage III compared output from geographic information system (GIS) software with comparable results. This validation process demonstrates the robustness and utility of Fragmento as tool for 3D fragmentary bone matching and full bone reconstruction.

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1. Introduction

In forensic contexts, a biological profile constructed from unidentified skeletal remains assists in the search for missing persons and is necessary for sorting commingled remains and identifying victims in mass graves. The reliability of information extracted from the skeletal remains is highly dependent on the degree of integrity and preservation of the specimens. In cases of sub-optimal conditions or partial bones, the missing elements may limit the amount of information that can be derived from the skeleton [1]. Commingling further complicates the task because not all fragments are easily reconstructed or designated to a single individual.

Commingled human remains present a logistical and methodological challenge. In cases where the material is highly fragmented, the challenge increases exponentially. Adams and Byrd [2] provide an extensive summary of methods that have been used to address commingled remains in forensic contexts. The Scientific Working Group for Forensic Anthropology (SWGANTH)

also provides guidelines for resolving commingled human remains [3]. The SWGANTH guidelines recommend scientific methods for determining the minimum number of individuals (MNI) and assessing the most likely number of individuals (MLNI or the Lincoln Index). These guidelines describe methods for element reconstruction, visual pair matching, osteometric evaluation, and taphonomic comparisons in the assessment of MNI and MLNI.

The three-dimensional (3D) approach to quantifying commingled remains is a logical extension of coding and two-dimensional methods developed in zooarcheology [4] and bioarcheology [5]. Herrmann and Bennett [6] quantified small fragmented remains into an Osteological Information System (OIS) using geographic information system (GIS) software to derive minimum number of elements (MNE) values and minimum number of individuals (MNI) estimates. However, utilization of these systems is time-consuming, and the observer must manually digitize each fragment into the OIS application. Further, these methods do not provide a tool for reconstructing the complete anatomy from partial information, which limits the use of the data for morphometric analyses.

Historically, stature estimation has received the most attention with respect to fragmentary remains [7,8]. Population-specific discriminant functions have been derived from numerous measurements and measurement combinations to facilitate analyses of

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incomplete elements. Several studies propose an indirect method of first reconstructing long bone length and then estimating stature [9,10]. Recent research has shown increased accuracy in estimating parameters of the biological profile using a 3D bone surface within a computational framework that permits the use of non-linear classifiers to explore morphological features of bone surfaces [11–14].

The usefulness of computer modeling for fossil reconstructions has been recognized as a mathematically rigorous process, and statistical bone atlases (SBA) have been used to reconstruct the AL288-1 (“Lucy”) femur [15–17]. A statistical bone atlas is an average mold (or template mesh) that captures the primary shape variation of a bone and allows for the comparison of global shape differences between populations, as well as for the rapid generation of automated computer measurements. Statistical bone atlases have been utilized to investigate and quantify sexual dimorphism in the femur [18], cranium [19], and patella [14], and to document directional asymmetry in the clavicle [12].

The research summarized in this paper expands the statistical atlas framework to the analysis of fragmentary and commingled remains. The bone atlas template was used to develop user-friendly software (Fragmento) that enables forensic anthropologists and archeologists to quantify and reconstruct fragmentary human skeletal remains from 3D surface files generated by computed-tomography, or 3D scanner such as laser or white light. The statistical atlas was used to create 3D templates for each of the four bones currently supported by the software (innominate, cranium, humerus, femur). The templates are used to group fragmentary elements and then to interpolate missing parts between the grouped elements to generate a full 3D bone model. The system also serves as an osteological case or scene management tool by facilitating the review and visualization of the skeletal remains within the application.

2. Methods

Fragmento analyzes fragments of the cranium and three post-cranial bones: innominate, humerus, and femur. In this work, “fragment” refers to a partial bone extracted from the scene, while “template” refers to the intact, averaged reference-population skeletal element used to guide fragment placement. The system serves as an osteological case or scene management tool where all scanned fragments are reviewed and labeled with unique identification numbers inside the application. The software enables the visualization of fragmentary bone elements, with the ability to reject or accept elements. This is followed by initial registration of fragmentary elements within a 3D statistical bone template for each bone. Fragmento is designed to merge accepted registered elements and provide a fully reconstructed bone which can then be exported to different software for 3D landmarking followed by measurements or geometric morphometric.

The framework utilizes statistical atlases for creation of 3D templates for bone matching and to interpolate missing anatomy for full bone reconstruction. To generate the template, 3D statistical bone atlases are constructed from large datasets of bones [11–14,20]. The atlases guarantee surface correspondence across the entire sample, which allows for an accurate calculation of the template (or average mold) that captures the global shape characteristics of the population.

The flowchart in Fig. 1 outlines the steps for analyzing fragmentary remains using Fragmento. The first step involves digitization of fragmentary elements using computed tomography (CT) scanning or laser scanning. In the case of CT scanning, a segmentation step is performed to generate the surface models. Generated surface models are then imported into Fragmento. Each element is automatically labeled by a uniquely generated identifier. An iterative matching process is then performed to best match

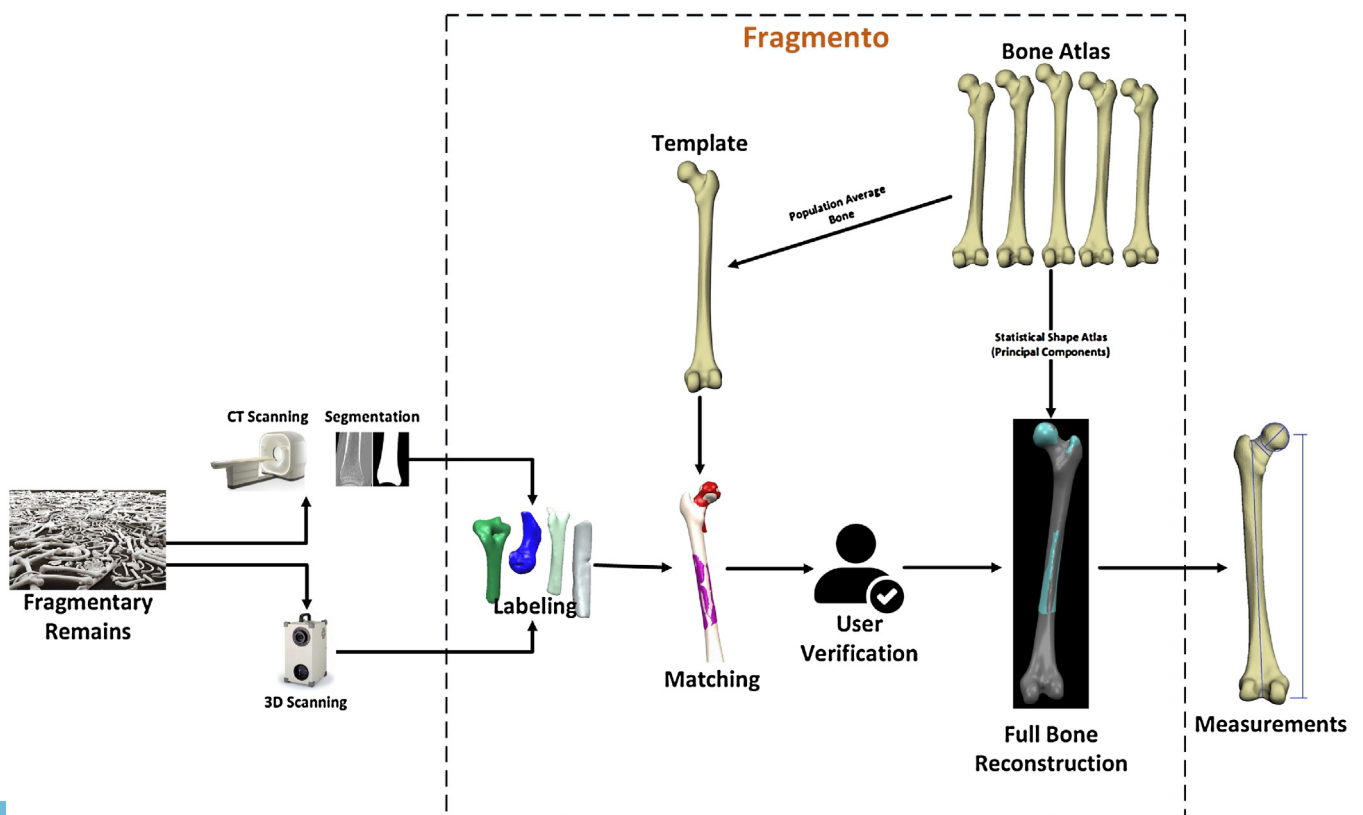


Fig 1. Overall system flowchart.

each fragment with the template corresponding to the specific bone.

2.1. Overview

The matching process is outlined in Fig. 2. First, features are extracted from each bone fragment by measuring surface roughness. Fragment surface points with roughness values between adaptively selected threshold values are considered feature points. A multi-stage technique is then used to identify the corresponding bone template for each fragment and register the fragment to that template. For each fragment, features are matched with the features of each bone template using an iterative closest point (ICP) algorithm [21]. The correct registration is guaranteed when the ICP algorithm converges to a local minimum, indicating that the root mean square (RMS) distance between the fragment and the template has been minimized in terms of both position and orientation. Final registration of a fragment to a bone template is based on the “best match score” in terms of RMS distance between

fragment features and template features. Fragmento embeds this method in a 3D virtual environment, enabling 3D visualization of the registration process of fragments to bone templates. This increases the control of fragment manipulation and allows for the fine-tuning of registration results. Matched fragments are then grouped into partial bones, which are then used to reconstruct the full bone.

2.2. Template creation

As described earlier template model is an average bone which capture population morphometric variation independent of bone size. Templates were created using previously developed method for creation of statistical bone atlas by generating dense correspondence across crania [19], femur [18].

2.3. Feature extraction

Feature extraction is the process of extracting unique singular points which, together, can be used to distinguish the shape. By

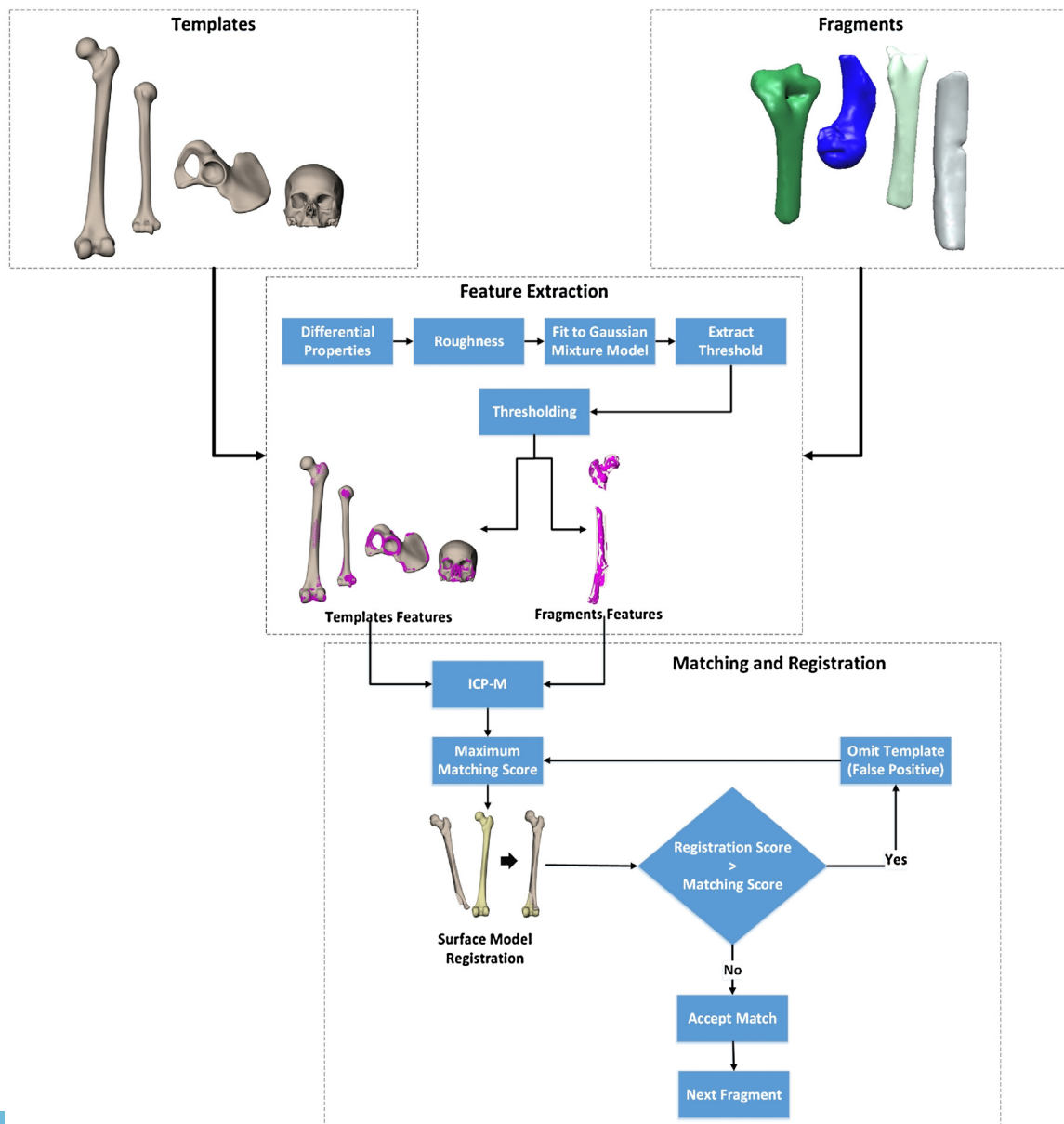


Fig. 2. Flowchart detailing process of matching fragmentary remains to specific bone template.

extracting features from fragment and template surface models, we ideally have two sets of points. One of them (fragment features) is a subset of the other (template features). Once this goal is achieved, the matching and registration processes are reduced to registering two unique set of points. This is more efficient (in terms

of time and memory) and less error-prone (singular points registration).

To extract features, we estimated local surface roughness, which describe the local shape around each point independent of scale. We assume that the roughness of fragment surface model

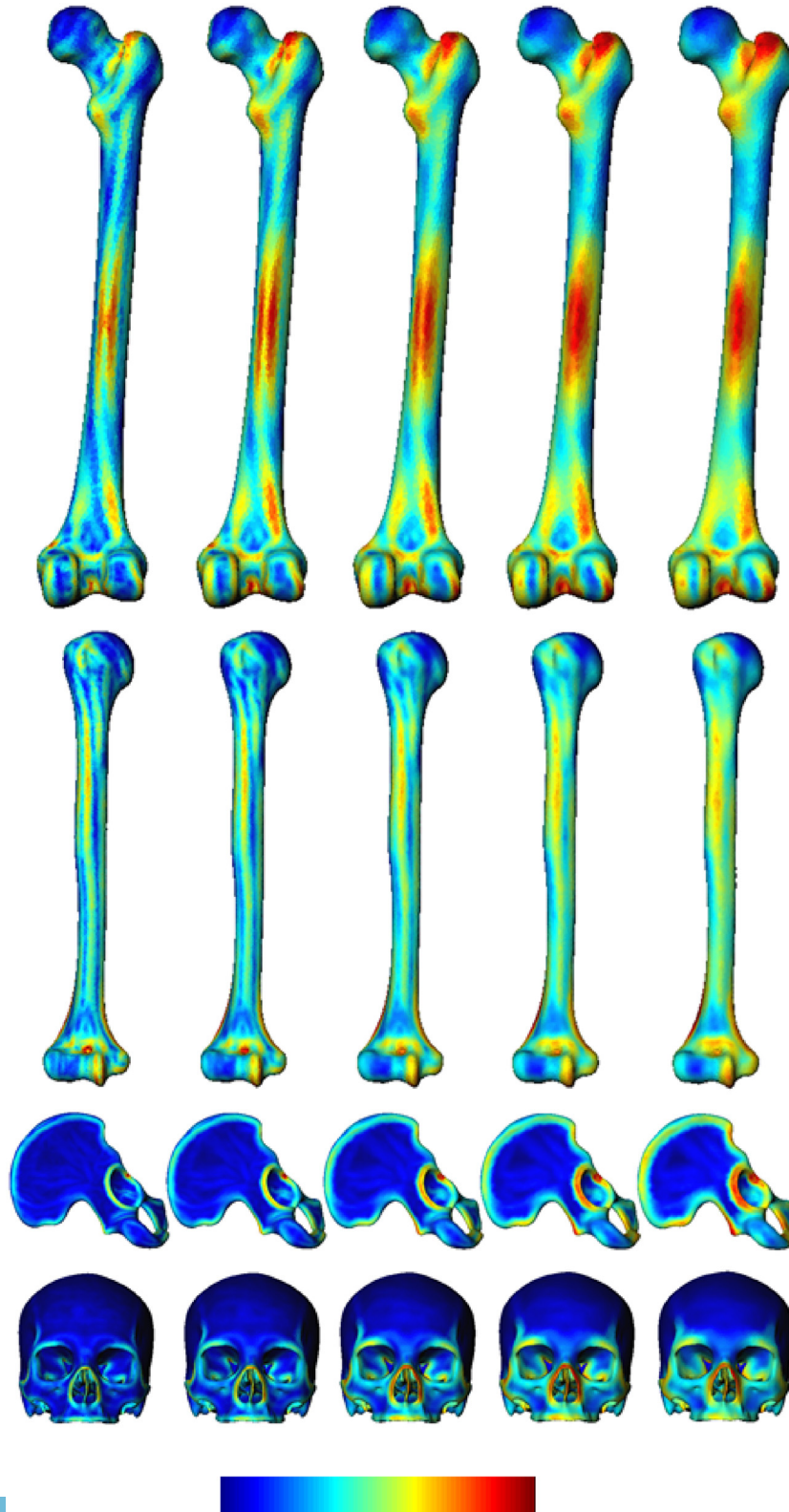


Fig. 3. Roughness maps of femur, humerus, innominate and skull templates at 1st, 2nd, 3rd, 4th and 5th neighborhood levels.

points follow a Gaussian mixture model (GMM), which ease features extraction process. Fig. 2 highlights the steps of the feature extraction process in the second block at the top middle part.

2.4. Differential properties approximation

Local surface shape variation is one of the useful shape surface properties. For estimating the local surface shape variation, large number of differential and integral methods were proposed. Although some of integral methods are robust, most of them are time-consuming. A valuable evaluation of local shape variation estimations was published by Surazhsky et al. [22], which showed that the Gauss–Bonnet scheme gives the best results for estimation of overall curvature, which is our objective here. Consequently, the Gauss–Bonnet scheme was chosen as the method for estimation of surface curvature.

2.5. Surface roughness

A different formula for representing surface curvature is proposed in Ref. [23] based on the principal curvatures. Curvedness measures the intensity of the surface curvature and describes how strongly curved the surface. For the present application, curvedness showed the best results for presenting local shape curvature. We propose a multi-scale surface roughness measure at a point based on weighting the variance of the point's neighbor's curvature, where the weight is defined as the ratio between the length of the edge between point i and j , to the total edge length of the edges between point i , and all its neighbors. This newly proposed measure is based on the curvedness, and point-to-neighbor's edge lengths.

The proposed measure can be computed at multiple scales by incorporating k -level neighborhood points as shown in Fig. 3. Incorporating small number of neighborhood levels means that the roughness is estimated in the very close neighborhood, which may not be accurate despite it is the highest resolution. This is because the fact that the model surface is not a continuous surface, instead it is digitized. So, that very high resolution is very sensitive to digitization or meshing and it is greatly dependent on the quality of the original models scanning method. On the other hand, incorporating large number of neighborhood levels means incorporating more points from the neighborhood. This will reduce sensitivity to digitization noise but will result in lower overall resolution. Neighborhood levels from 3 to 6 were found

empirically to be acceptable in terms of noise, resolution and computation time.

2.6. Gaussian mixture model

A Gaussian mixture model (GMM) is a parametric model used for clustering data in which analytic Gaussian density functions are fitted to the data, assuming the data were drawn from a number of Gaussian distributions. For application to matching and registration of bone fragments, is assumed that the calculated surface roughness of each template model is a mixture of two Gaussian distributions, representing distribution of surface points with low roughness values (smooth surface points) and high roughness values (feature points). Fig. 4 shows the histogram and the two Gaussian distributions of surface roughness of femur and skull template bone models calculated using the proposed roughness measure.

Based on the idea that fractured surfaces introduce higher values of roughness compared with native surfaces, the calculated surface roughness of each bone fragment can be represented as a mixture of three Gaussian distributions representing native surface smooth points, native surface features, and fracture surface points. Fig. 5(a) shows the surface roughness map of a sample femur fragment; Fig. 5(b) is the fragment bone model histogram and Gaussian distributions of surface roughness values. The features of the original bone can still be detected by the proposed surface roughness measure in the presence of high curvature, or high rough, at the edge of the fracture surface.

We have selected the mean of the second Gaussian distribution, from the GMM analysis as the threshold to filter out the features from the bone template surface models. To extract similar points from the fragment bone, we have selected the range between the second, and third means as the range of roughness that includes the features of the original bone. Fig. 6 shows the extracted features from the femur bone fragment and template models using GMM-extracted thresholds.

2.7. Matching and registration

This is a two-stage process that involves determining which template the bone fragment belongs to and what is the best recommended location for the bone fragment on the template. In Stage 1, the matching scores between feature points on the bone fragments and the feature points on the four templates are computed. Matching scores are computed by iteratively finding the best position that minimizes the root mean squared error (RMSE)

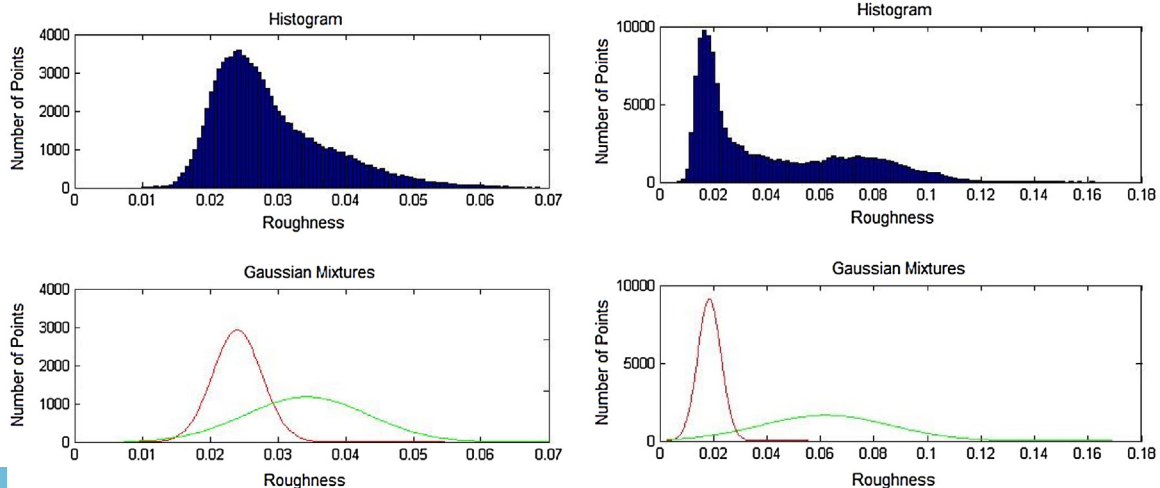


Fig. 4. Surface roughness of femur (left) and skull (right) template bone model: Histogram and distributions of Gaussian components.

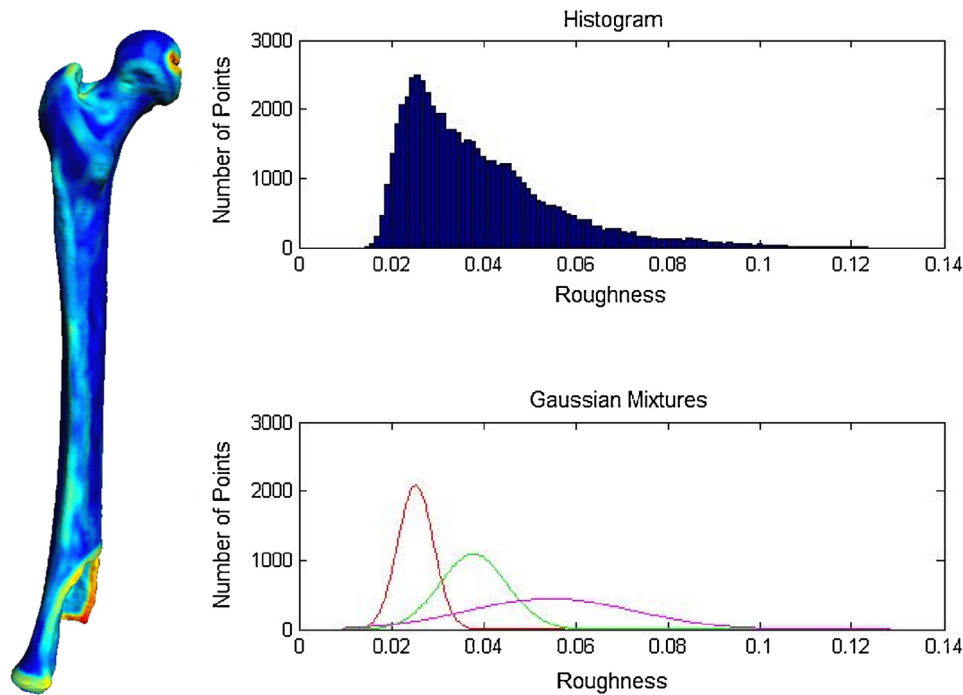


Fig. 5. Calculation of femoral fragment roughness, roughness Gaussian components and histogram (left), roughness surface map (right).

between the fragment feature points and the template feature points. In Stage 2, the registration score is computed by refining the position of the fragment relative to the template bone surface using ICP algorithm.

The matching and registration process is complete when the registration error is smaller than the feature matching error, indicating a rigorous identification. If the output error from the registration process is greater than the output error from the feature matching process, this indicates a false positive matching. To resolve this, the bone template model with the maximum feature matching score is discarded and the bone template model with the second-best feature matching score is used to register with the fragment.

2.8. Full bone reconstruction

Full bone reconstruction is enabled by the creation of the bone atlas, which captures variation in bone shape across sex and ancestry groups. Once anatomical correspondence is established, principal components are computed on the 3D bone surface of the entire population. The result of this operation allows the bone surface map to be represented by a more compact number of principal components which capture the variation of those surface points around the average bone surface model. Bone atlases were created using 400 individuals from the William Bass Donated Skeletal Collection (WBDSC) [24]. For the software to generate full bone from partial bone, a novel optimization algorithm was developed. The optimizer is initialized using the skeletal bone atlas identified by the algorithm as the closest bone in our database to the partial bone. The principal components are then modified to reconstruct a new bone model iteratively until convergence is achieved by minimizing fragments to full bone RMSE

2.9. Virtual environment

The Fragmento virtual 3D environment uses the Open Graphics Library (OpenGL) as the low-level 3D visualization engine [https://

www.opengl.org/] and QT as the graphical user interface (GUI) library. Fragmento enables the user to load scanned surface models in either stereolithography file format (*.stl) or open inventor file format (*.iv) generated using 3D surface reconstruction software. The GUI has the capability of loading one file or multiple files at once, each containing one or more surface models.

There are a number of versatile visualization options controlled by the user, through either the user controls or the interactive viewer. These include viewing options (rotate, pan, zoom, set the home view, view all loaded models, set parallel or perspective projection mode, change the lighting direction, change the model and background colors) and control options (assigning keys). There is also a transparency slider to set the desired surface model transparency. The user has the ability to apply transformations (translation, rotation and scaling) of the surface model for each selected model(s) and reset them individually. The interface enables the user to save modified models separately. Supplementary Appendix A [online] contains a detailed scenario using Fragmento.

After loading the fragment surface models to the viewer, surface roughness and features for each fragment surface model can be generated, reviewed and exported. The user has the ability to edit fragment surface model points to be used in the registration with the template surface; this gives the user the power to confirm feature matching points. Fragment surface models can be tested for registration against all four of the template surface models. Values for maximum iterations and minimum relative error of the ICP algorithm can be set by the user. Once registration is complete, the GUI displays the fragment surface models registered with the selected template surface model.

To evaluate the registration, two distance measures were calculated. The first distance measure is a global measure which sums the RMS distances between corresponding feature points on the fragment and template surface models. The global measure is displayed as text with zero value for best registration result and higher values for less registration quality. The second distance measure is a local measure which calculates the absolute distance



Fig. 6. Features detected on femur template (left) and femur fragment (right).

between corresponding feature points on the fragment and the template surface models. The local measure is displayed on the fragment bone surface model as a color-coded value with the darkest blue representing the closest to the template model and the darkest red representing the farthest from the template model.

Fragmento allows the user to merge non-overlapping fragment surface models that belong to the same template into one bigger fragment; the user also has the ability to split fragment surface models if they can not belong to the same bone. The final step is to reconstruct the complete bone surface model from the selected fragment surface model.

2.10. Validation

This novel software was validated using a three-stage validation: (I) validation of full bone reconstruction; (II) validation of simulated fragment data; and (III) GIS software quantification comparison.

2.10.1. System validation Stage I: validation of full bone reconstruction

To assess the ability of the statistical bone atlases to reconstruct missing information from existing fragments, a validation was performed using intact statistical bone atlases. Fragments of the innominate bone were deleted from 120 innominate bone atlas templates representing 10, 20 and 30% of the overall surface area. An additional validation was performed using fragments of the cranium deleted from 90 cranial bone atlas templates representing 30% of the overall surface area. A full bone was reconstructed from each sample using Fragmento. Reconstructed bones were then compared to original bones by computing overall surface RMSE.

2.10.2. System validation Stage II: simulated fragment data

To assess the overall system accuracy in matching and reconstruction, we analyzed a set of simulated fragmentary bones from the WBD Skeletal Collection. A subset of 10 innominate, 10 crania, 10 humeri, and 10 femora was randomly divided into four fragments. For each bone, two fragments were processed using Fragmento, thus generating a set of six partial bone combinations for each type of bone. Fragments were then matched and the reconstructed full bone was compared to the original bone model by calculating RMSE.

2.10.3. System validation Stage III: GIS software quantification comparison

To evaluate the system performance in matching fragmentary elements in real-life scenarios, a validation was performed comparing GIS software quantification against bone reconstruction results using Fragmento. The fragmentary skeletal remains

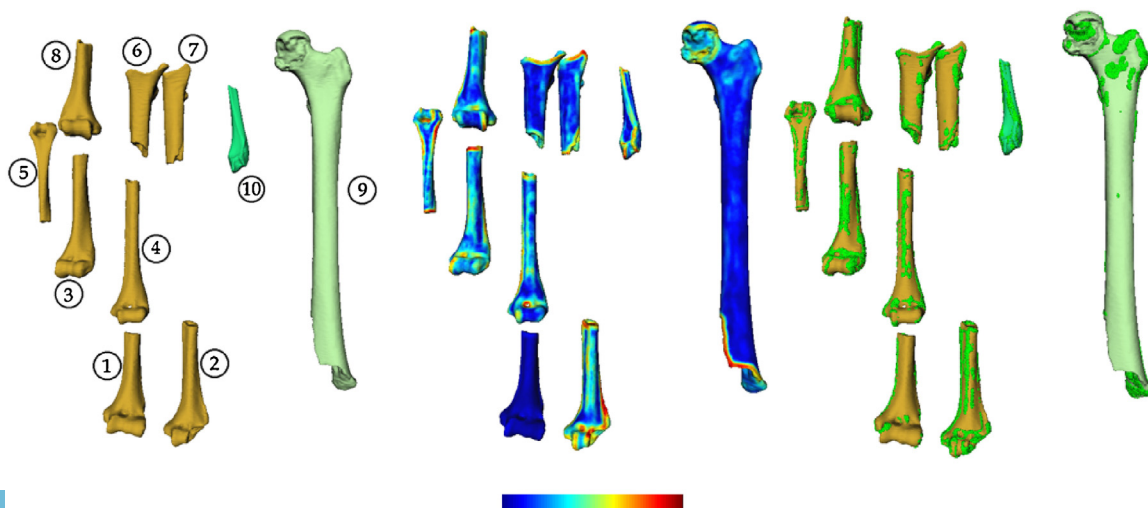


Fig. 7. Morton collection sample used for validating bone-matching algorithm.

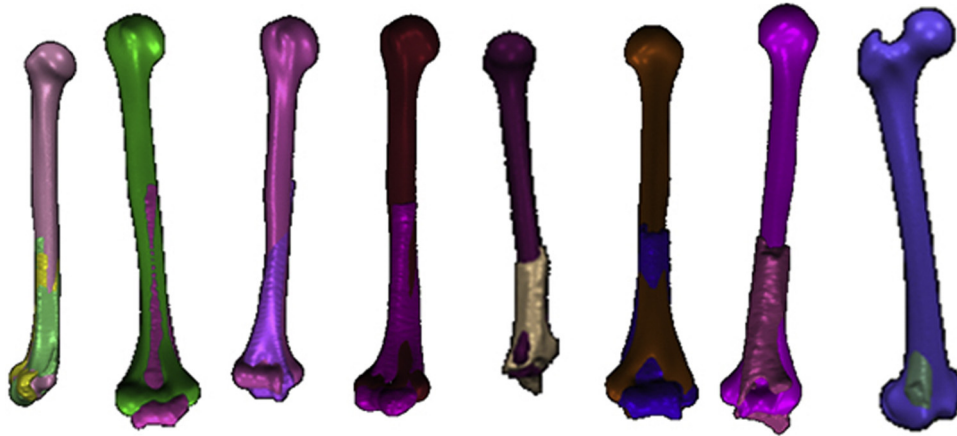


Fig. 8. Matching of fragmentary pieces from Morton collection using Fragmento.

Table 1
Results of full bone reconstruction Stage I validation for innominate.

% Missing (innominate)	RMSE (mm)	SD (mm)	MAX RMSE (mm)
10%	0.54	0.35	2.91
20%	0.60	0.40	3.20
30%	0.61	0.41	3.29

Table 2
Results of full bone reconstruction Stage I validation for crania.

% Missing (cranium)	RMSE (mm)	SD (mm)	MAX RMSE (mm)
30%	0.45	0.35	4.80

for this validation were part of the Morton collection [25], a collection of commingled human skeletal remains from the gulf coast of Louisiana. During this research, a total of 24,569 fragments were sorted from the Morton collection; 18,373 fragments were coded, 1232 fragments were digitized and 2061 fragments were scanned with computed tomography. A subset of the collection was chosen with fragments <0.2% of the full bone. Fig. 7 displays the features detected on the subset of Morton collection fragments. The validation compared the percent bone coverage when fragments were matched using both Fragmento (Fig. 8) and GIS software.

3. Results

Results for Stage I validation can be found in Table 1. Table 1 reports the RMSE, standard deviation (SD), and maximum RMSE (MAX RMSE) in surface distance for the Stage I validation reconstructions where fragments of 120 innominate bone atlas templates were deleted representing 10%, 20% and 30% of the overall surface area (% Missing).

Table 2 reports the RMSE, SD and MAX RMSE in surface distance for the Stage I reconstructions where fragments of 90 cranial bone atlas templates were deleted representing 30% of the overall surface area.

Fig. 9 illustrates the surface distance map using Fragmento in a reconstruction of the simulated fragmented cranium with mean RMSE error of 0.5 mm and maximum RMSE of 1.1 mm.

Table 3 reports the RMSE, SD, minimum RMSE (MIN RMSE) and MAX RMSE in surface distance for the Stage II validation of full bone reconstruction using simulated fragmentary bones from the WBD Skeletal Collection. Mean RMSE for all humeri used in this validation stage was 1.92, innominate mean RMSE was 1.99 mm, cranium and femur both had 2.15 mm mean RMSE.

Fig. 10 depicts the average overall surface RMSE map for 60 bones per bone type for the Stage II validation.

Fig. 11 shows the Stage III validation results employing Fragmento using Morton collection fragments. Each panel represents a different reconstruction completed from the whole

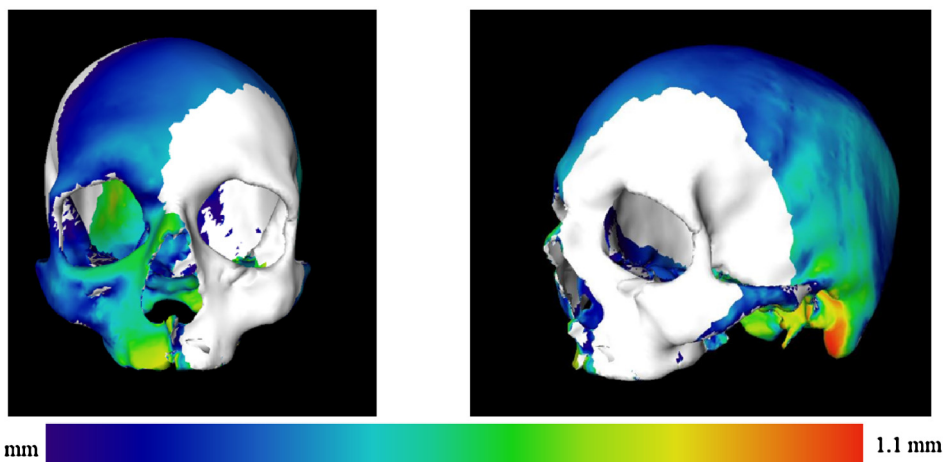


Fig. 9. Surface distance map of the RMSE in the reconstructed skull (simulated fragmentary skull).

Table 3
Results of full bone reconstruction Stage II validation for four bone types.

	RMSE (mm)	SD (mm)	MIN RMSE (mm)	MAX RMSE (mm)
Innominate	1.99	0.68	1.22	4.76
Cranium	2.15	1.07	1.04	5.63
Humerus	1.92	0.86	0.33	3.26
Femur	2.15	0.70	0.91	3.54

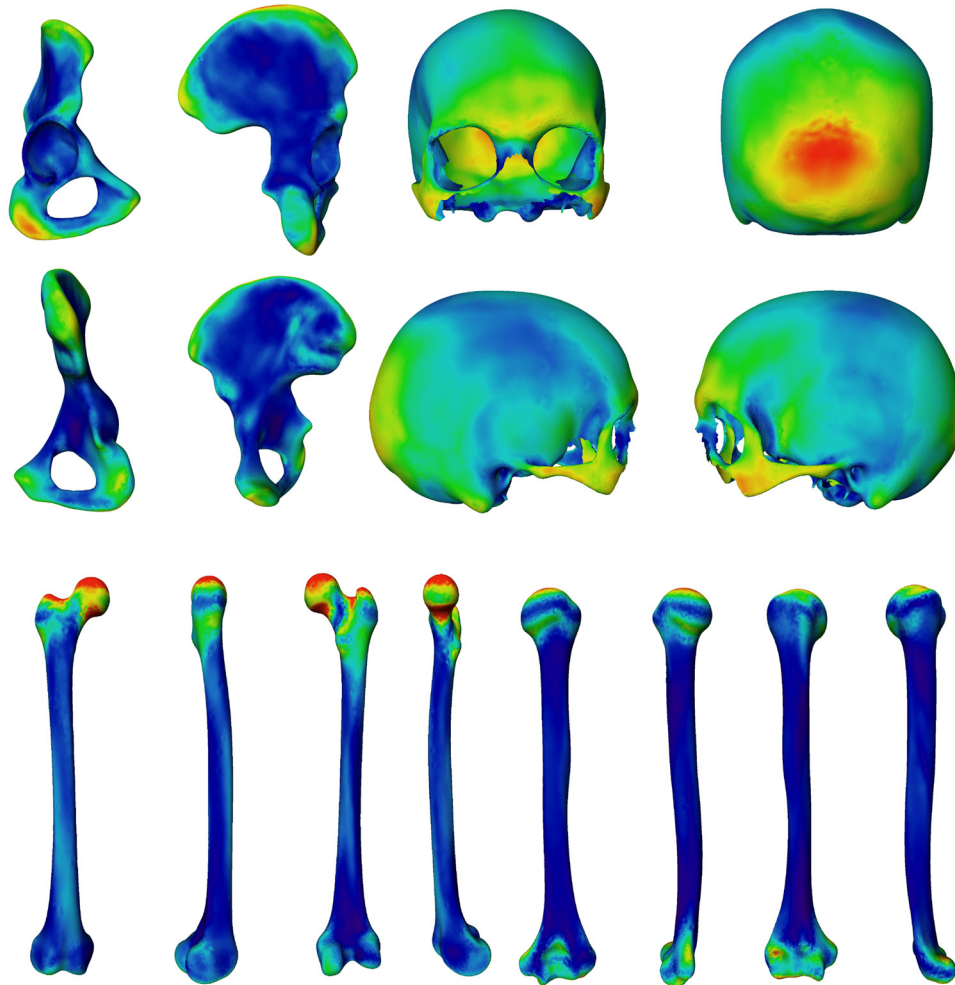


Fig. 10. Mean overall surface RMSE map for 60 innominate, crania, femora and humeri reconstructions for Stage II validation.

set of fragmentary bone pieces. Fragmento matching and reconstruction is depicted on the left; the average surface distance error map in millimeters between the reconstructed 3D model and the fragmentary pieces is depicted in the center; and the matched bone using GIS is depicted on the right. The percentage coverage employing both softwares for the samples used for side-by-side comparison is presented in Fig. 12.

4. Discussion

The use of computerized methods for fragmentary matching can save time and resources for processing large numbers of fragmentary commingled remains. Currently different groups utilize GIS [5] as a tool for matching by overlaying a 2D projection of fragments on 2D templates of the bone. This process is time consuming and does not provide information other than matching

of fragments, with no means for reconstructing the intact anatomy. This limits the use of geometric morphometric tools for predicting biological profile or the use of global non-linear methods on the entire bone surface [11–14,20]. While researchers have attempted 3D virtual reconstruction of bones, the process was manual and relied on mirroring of existing anatomy [1], which is not feasible with commingled remains and does not represent the true anatomy accurately given the asymmetry documented in skeletal elements [20].

Our team examined a sample of documented skeletal remains to construct statistical bone atlases (templates) and separate validation samples to test our new software program (Fragmento) for fragment matching and full bone reconstruction. Three validation stages were used to test Fragmento: Stage I tested the ability of Fragmento to reconstruct missing anatomy from statistical bone atlases of innominate bones and crania.

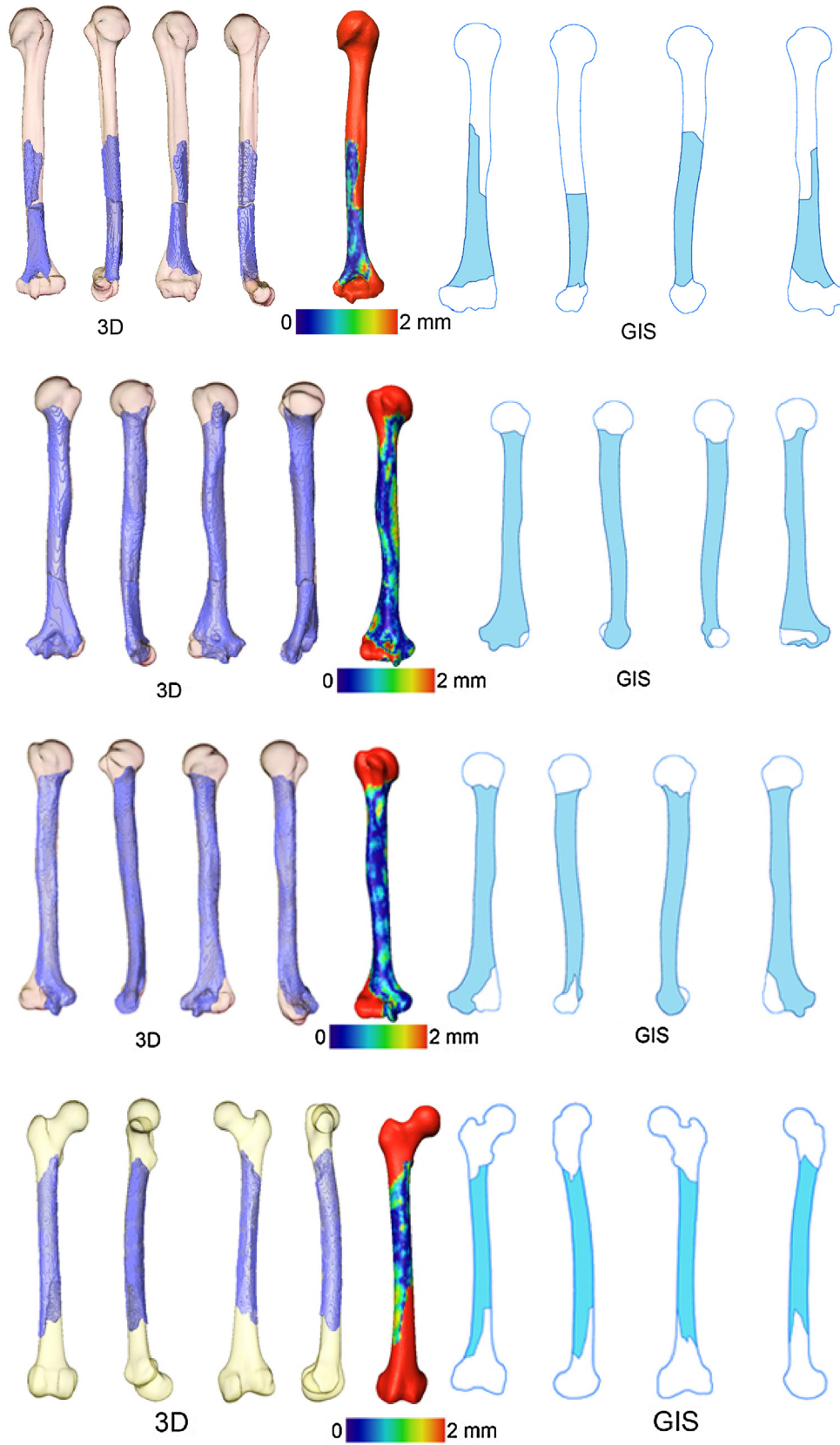


Fig. 11. Validation of reconstructed bone from Morton collection using Fragmento (left); surface distance map for reconstructed 3D model (center); and fragmentary pieces and GIS (right).

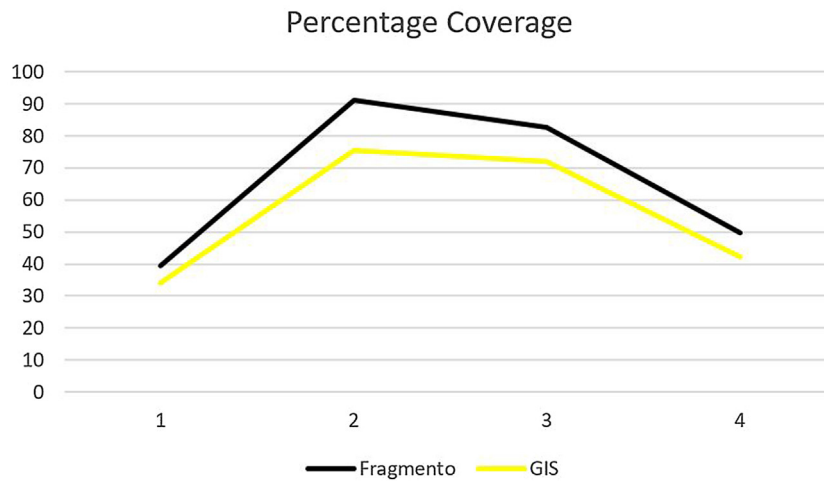


Fig. 12. Percentage coverage of fragments to full bone.

Results of this stage demonstrates Fragmento's ability to interpolate missing data within an accuracy less than 1 mm RMSE in global and local measures of surface distance between template features and fragments and totalling 30% of surface area. It is worth noting that the interpolation ability is bounded by the population used to create the particular bone atlas. However, Fragmento offers the ability to build new atlases to capture different population morphometrics. Stage II validation tested Fragmento analyzed simulated fragmentary data from the WBD Skeletal Collection. This stage demonstrates that Fragmento can match and reconstruct full anatomy with a RMSE less than 3 mm in RMS distance between fragment features and template features. Stage III validation compared Fragmento's performance in a quantifiable way to GIS using skeletal fragments from the Morton collection. Given the difference in the output of the two programs, we compared registration and matching performance by comparing identifications and placement of fragments on the template. The two-dimensional nature of the GIS framework prohibits any absolute comparison of percentage fragmentary coverage relative to the template; however, the parallel trends shown in Fig. 8 for the Stage III validation verify Fragmento's utility as compared to GIS with the added benefit that Fragmento embeds this method in a 3D virtual environment, enabling 3D visualization of the registration process of fragments to bone templates.

The developed software expands the usefulness of the statistical bone atlases into the analysis of fragmentary and commingled remains. It provides forensic anthropologists and archeologists with a means to quantify and reconstruct fragmentary remains, thereby enhancing analyses in challenging cases. The data management aspect of the application allows forensic anthropologists to digitally inventory complex commingled scenes; if geospatial data is integrated with each fragment, the refitting process can proceed geographically. Fragmento will be available for researchers to download and use freely at <http://mmahfouz.org>. It provides users with a platform for digitally labeling, sorting and archiving of fragments. This saves time compared to traditional methods of manual sorting and labeling. Further it creates a permanent record for the bone fragments, which minimizes damage to the actual bone collection. In addition to the added speed, flexibility, and accuracy of 3D matching compared to the 2D overlays and conventional manual methods, the developed software provides reconstruction of full bones from

fragmentary elements, which can be utilized for more accurate estimation of the biological profile or facial reconstruction in cases of cranial fragmentary reconstruction. Finally, the software will enhance collaboration between researchers and investigators by providing a platform where results can be shared during any stage of the matching process. This can result in time reduction, especially in the case of larger collections where collaboration between different teams might be necessary.

Current limitations of the software include the number of bones Fragmento can process: innominate, crania, humerus, and femur; future releases of the software with additional skeletal elements are planned. Improvements in the feature extraction process from one based on surface differential properties to one based on surface integral invariants will result in more robust feature extraction which can be computed at multiple scales by default. In addition, the fragment registration based on a variant of ICP algorithm in this software version is sensitive to the size of the fragments and the distinct geometrical features of the fragment. This enforced our limitation to only use fragments of 25% of element size in the automatic registration method; future releases will involve more robust registration methods relying on surface scale invariant properties. The current version of Fragmento does not estimate Minimum Number of [Skeletal] Elements (MNE) and Minimum Number of Individuals (MNI); future releases will include this functionality by providing candidate refit lists for imported fragments by incorporating different metrics such as "fragment proximity values". Finally, Fragmento's reconstruction abilities are limited to modern populations or populations with morphometric features similar to these populations; the software supports addition of new statistical bone atlases that can capture the geometric morphometric properties of any population of interest.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.forsciint.2017.03.017>.

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