Document Title:	**Computerized Reconstruction of Fragmentary Skeletal Remains for Purposes of Extracting Osteometric Measurements and Estimating MNI**
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Title: Computerized Reconstruction of Fragmentary Skeletal Remains for Purposes of Extracting Osteometric Measurements and Estimating MNI

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1. Abstract

The purpose of this research grant is to improve forensic anthropology practice and policy by facilitating more complete and accurate analyses of fragmentary human skeletal remains. Through the term of this grant we developed a user-friendly software that enables forensic anthropologists to quantify and reconstruct fragmentary human skeletal remains (crania, pelves, humeri, and femora) from three-dimensional surface files generated by computed-tomography or laser scans. First, the system serves as an osteological case or scene management tool. All scanned skeletal remains from each scene can be reviewed within the application. The software allows the user ability to visualize fragmentary elements, reject or accept elements. This is then followed by initial alignment of fragmentary elements with three dimensional statistical template for each bone. Upon accepting the alignment of the elements, the software merges the elements and provides a fully reconstructed bone; measurements can then be conducted by the user to apply to regression equations, discriminant functions, or to use with software such as Fordisc 3.0.

During the course of this grant, a total of 24,569 fragments were sorted from the Morton Shell Mound from the gulf coast of Louisiana, 18,373 fragments were coded, 1232 fragments were was digitized and 2061 fragments were CT Scanned. . The developed software was validated using both simulated data, and real data from Morton collection. Software was compared to GIS, same fragment ID's were matched using both systems and fragments was placed in comparable location on the template. The reconstruction results on simulated data was less than 2 mm mean RMS error for pelvis, skull, humerus and femur. The developed system generated similar results when compared to GIS looking at both the ID of matched fragments and location of matched fragments on the template.

2. Introduction

Within the larger medicolegal system, forensic anthropologists perform the essential task of creating a biological profile to aid law enforcement in identifying unknown human remains--an important first step in the criminal apprehension and conviction process. The four primary components of the biological profile are age, sex, ancestry, and stature. The proposed project focuses on the number of individuals, sex and ancestry estimation, and measurement extraction for use in stature estimation. The parameters of the biological profile are intricately interwoven in that, frequently, one component is necessary in order to make precise determinations about other component(s). In cases of mass disasters or commingled remains, the determination of individual biological profile parameters is complicated by the presence of multiple unassociated elements. The ability to make biological profile assessments on isolated bones or bone fragments is critical. The proposed application provides a system to perform such analyses and to manage complex mass disaster or commingled bone cases.

Commingled human remains represent a logistical and methodological challenge to forensic anthropologists. In cases where the material is highly fragmented the challenge increases exponentially. Recent work on commingled human remains by Adams and Byrd (2008)[1] attempts to provide a series of cases examples and studies of methods to address commingled remains in forensic contexts. In 2011, the Scientific Working Group for Forensic Anthropology (SWGANTH) approved draft guidelines for resolving commingled human remains (http://swganth.startlogic.com/Commingling%20Rev0.pdf). Key points of the SWGANTH guidelines target the determination of the minimum number of individuals (MNI), the assessment of the most likely number of individuals (MLNI or the Lincoln Index), and the use of

scientific methods to achieve these goals. The guidelines recommend element reconstruction, visual pair matching, osteometric evaluation, and taphonomic comparisons in the assessment of MNI and MLNI. The application and method proposed in this project would address all these points and provide a systematic and quantifiable evaluation of each bone fragment.

Although developed independently, the three-dimensional approach to the quantification of commingled remains is a logical extension of coding and two-dimensional methods developed in zooarchaeology [2] and bioarchaeology [3][4]. Recent work by Herrmann and Devlin (2008)[4] quantify small fragmented remains into an Osteological Information System (OIS) using Geographic Information System (GIS) software to derive minimum number of elements (MNE) values and MNI estimates. These systems are time consuming and are dependent on the observer to manually digitize each fragment into the OIS application. The resulting image provides an MNE estimate for the element under investigation.
By and large, stature estimation is the only element of the biological profile that has been given due attention with respect to fragmentary remains [5][6][7]. Most of these studies developed population-specific discriminant functions from a series of long bone measurements. However, some studies used an indirect method of first reconstructing long bone length and then estimating stature [5][8][9]. In paleoanthropology, however, the usefulness of computer modeling for fossil reconstructions has been recognized as a mathematically rigorous process [10][11][12]. Reconstructions of the AL288-1 ("Lucy") femur by members of our research team proved to be close approximations of original reconstructions (Sylvester et al. 2008)[12]. Furthermore, validation tests on femora of known length from the William Bass Donated Skeletal Collection (WBDSC) resulted in reconstructions with errors of less than 1mm (Sylvester et al. 2008)[12]. These reconstructions were done using previously developed statistical bone atlases to reconstruct the fragmentary remains [13][14][15].

3. Methods

The purpose of this research is designed to work on fragments of four skeletal elements, femur, humerus, pelvis and skull bones. The first step involves generation of surfaces models for the fragmentary elements. This can be done using CT or laser scanner. In the case of CT scanning, a segmentation step is performed to generate the surface models. Upon creation of the fragmentary elements models, the next step is to extract features from each bone fragment by measuring surface roughness. Surfaces points with roughness above certain specified threshold values are denoted as feature points. A multi-stage technique is then used to identify, match and register these bone fragments to their corresponding template bone model. For each bone fragment, the features are used to be matched with template bone features using iterative closest point (ICP) algorithm. As long as it has been proven that ICP algorithm converge to a local minimum with respect to the mean-square distance metric, which means that it guarantees the correct registration given that the two shapes are somehow close in terms of position and orientation, we used different combinations of position and orientation of bone fragment relative to the template bone. For each combination, we applied ICP to try to match and register each fragment features with the four template bone's features. The best match score, in terms of minimum root-mean-square error, is used along with the position/orientation and transformation to register the bone fragment with the corresponding template model.

We refer to template model here as an average mold that captures the primary shape information of a skeletal element. Three dimensional statistical bone atlases are constructed from large datasets of bones [13][14][15]. The atlas guarantees point-to-point and surface correspondence across the entire sample, which allows for an accurate calculation of an average template. This template bone captures the

global shape characteristics for each bone across an entire population which can then be used to guide the placement of the fragmentary pieces into anatomically correct space and to estimate missing fragments.

The presented work is embedded in a 3D virtual environment where the user loads surface models, starts the procedure and views the final results. The user can accept or reject the matching and registration results after running the procedure, as well as she/he can manipulate each model separately either by hand or through GUI controls and start the procedure again.

Figure 1 highlights the proposed framework where fragmentary pieces are first CT scanned and segmented to generate surface models. The resultant surface models are then used to extract fragmentary bones features, followed by matching and registration. The visual feedback block presents user interactions through developed 3D virtual environment.

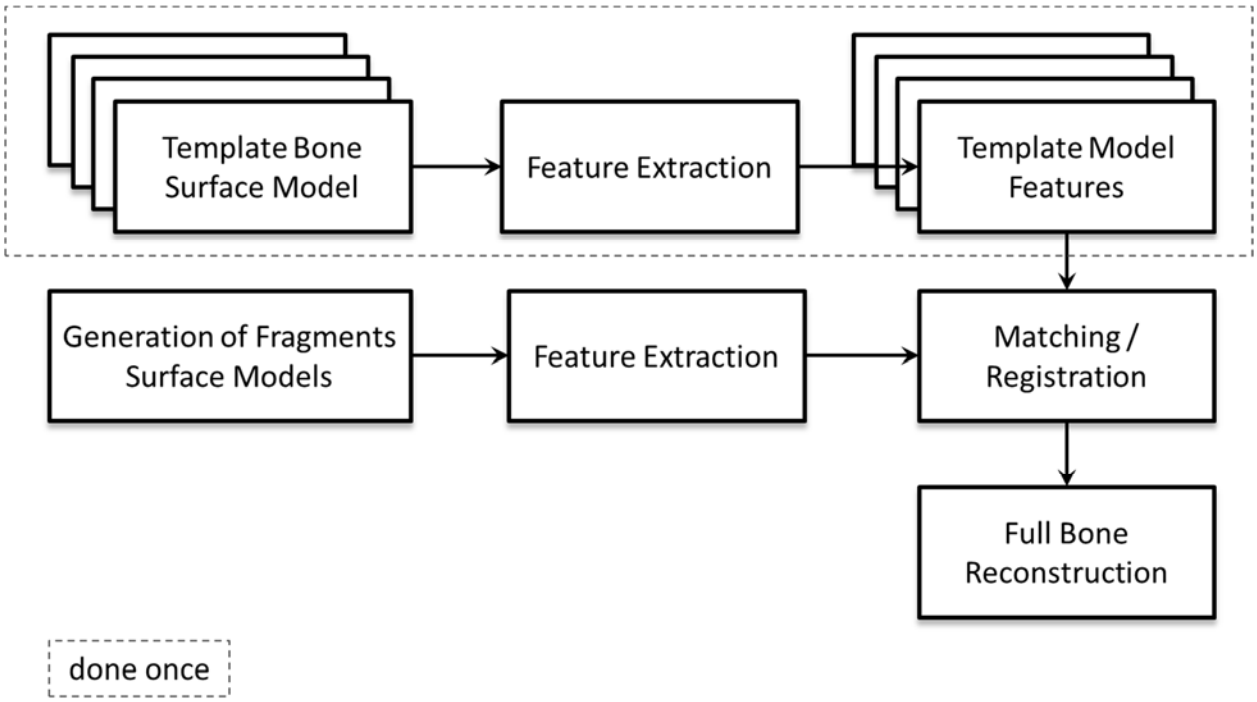

Figure 1 Software framework

3.1. Template Model

A statistical shape atlas, SSA, is an average mold, or a template mesh, that captures the primary shape variation of a bone (**Figure 2**) [13], along with its statistical modes of variations. A proposed method for creating a SSA and generating dense correspondence across populations for complex anatomical structures was developed in [13]. Figure 3 shows the process of adding a new bone to the statistical atlas. In the present study, we used femur, humerus, pelvis, and skull template bone surface models.

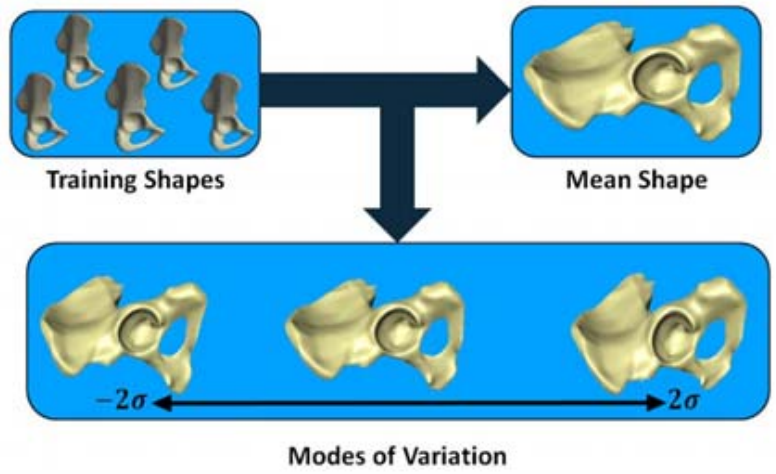

Figure 2 Pelvis statistical shape atlas

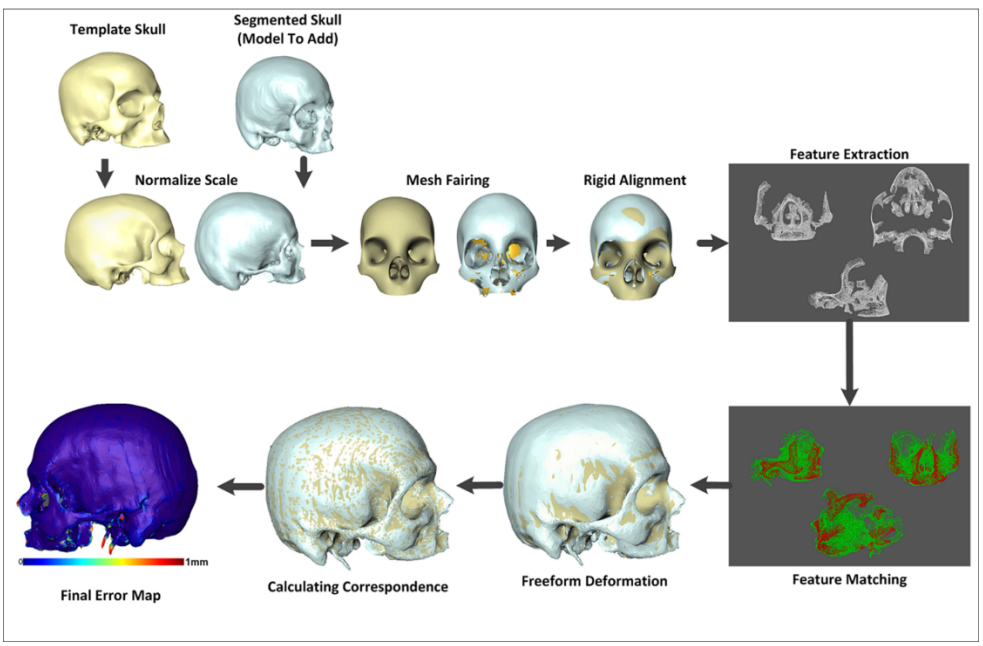

Figure 3 Process of adding a new bone to statistical atlas

3.2. Surface Model Generation

Figure 4 shows the generation process of bones surface models. The bone fragments are first CT scanned using $0.625 \times 0.625 \times 0.625\ mm^3$ voxel resolution. The DICOM images acquired from the CT scans are then manually segmented, and surface models are generated though 3D reconstruction. **Figure 5** shows an example of the surface models generation process, where the CT image is segmented to create a binary region of inside /outside the bone, which is used for generating the 3D surface model.

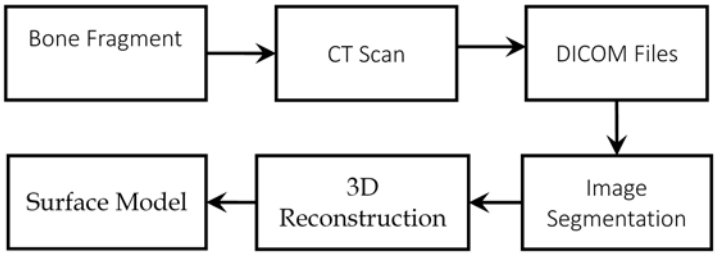

Figure 4 Surface models generation process

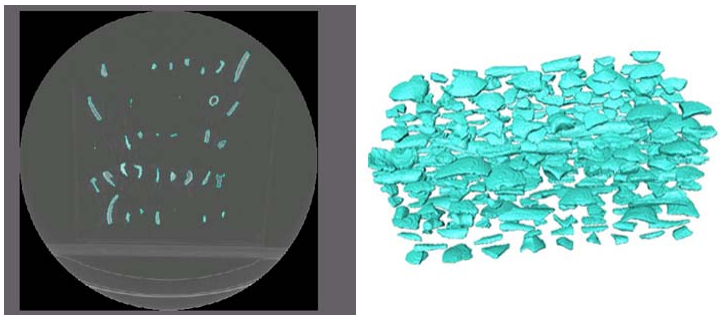

Figure 5 Example of surface models generation process

3.3. Feature Extraction

Figure 6 highlights the steps of feature extraction process.

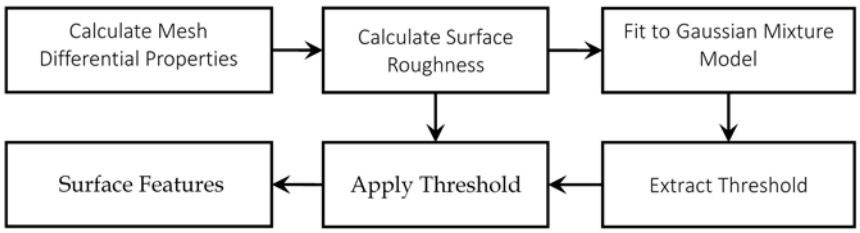

Figure 6 Feature extraction process

3.3.1. Mesh Differential Properties

Different methods were proposed for approximation of the surface differential properties. A valuable evaluation of different curvature estimation can be found in [16]. The evaluation showed that the Gauss-Bonett scheme gives the best results for estimation of overall curvature. Consequently, Gauss-Bonett scheme was chosen as the method for estimation of surface differential properties. Below are the details of the calculation of differentials properties using a discrete Gauss-Bonett scheme. **Figure 7** shows the neighborhood notation used in Gauss-Bonett scheme.

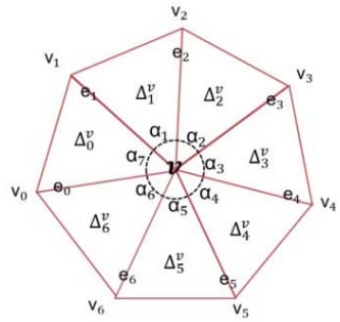

Figure 7 Neighborhood notation of Gauss-Bonett scheme

The following steps are used for calculating mesh differential properties using Gauss-Bonett scheme.

1. Face normal, Eq. 1.
2. Weighted vertex normal, Eq. 2.
3. Gaussian and mean curvature, Eq. 3, Eq. 4.
4. Maximum and minimum curvature, Eq. 5, Eq. 6.

$$n_f = e_i \times e_{i+1} \qquad \text{Eq. 1}$$

$$n_v = \sum_{f=0}^{n} n_f \,.\, \alpha_f \qquad n_v = \frac{n_v}{|n_v|} \qquad \text{Eq. 2}$$

$$K = \frac{2\pi - \sum_{i=0}^{n-1} \alpha_i}{A/3}, \qquad A = \sum_{i=0}^{n-1} a_i\,, \qquad a_i = \frac{\|e_i \times e_{i+1}\|}{2} \qquad \text{Eq. 3}$$

$$H = \frac{0.25 \sum_{i=0}^{n-1} \|e_i\| \beta_i}{A/3} \qquad \text{Eq. 4}$$

$$k_1 = H + \sqrt{\max(0, H^2 - K)} \qquad \text{Eq. 5}$$

$$k_1 = H - \sqrt{\max(0, H^2 - K)} \qquad \text{Eq. 6}$$

where β_i is the deviation of normal i.

3.3.2. Surface Roughness

For the present application, curvedness showed the best results for presenting local shape variations. We have proposed a different multi-scale surface roughness measure based on weighting the variance of the point's neighbors curvature. The newly proposed measure, Eq. 7, is based on the curvedness, and it forms the weights based on the point-to-neighbors edge lengths.

$$R_i = \frac{1}{|N_i|} \sum_{j \in N_i} \left| C_j - \overline{C_i} \right| * \frac{E_{ij}}{E_n} \qquad \text{Eq. 7}$$

$$\bar{C}_i = \frac{1}{|N_i|}\sum_{j \in N_i} C_j, \qquad E_n = \sum_{j \in N_i} E_{ij} \qquad \text{Eq. 8}$$

Where

R_i	Roughness at point i
$\bar{C}_i$	Average curvedness of the neighbors of point i
C_j	Curvedness at neighbor $j \in N_i$
E_{ij}	the length of the edge between i , j
E_n	total edge length which is the summation of the edge lengths of the point i's neighbors

The proposed measure can be computed at multiple scales by incorporating k-level neighborhood points in the equation, $k = 1,2,\ldots$ **Figure 8** - **Figure 12** show roughness maps of femur, humerus, pelvis and skull template bones computed at 1st, 2nd, 3rd, 4th and 5th neighborhood levels.

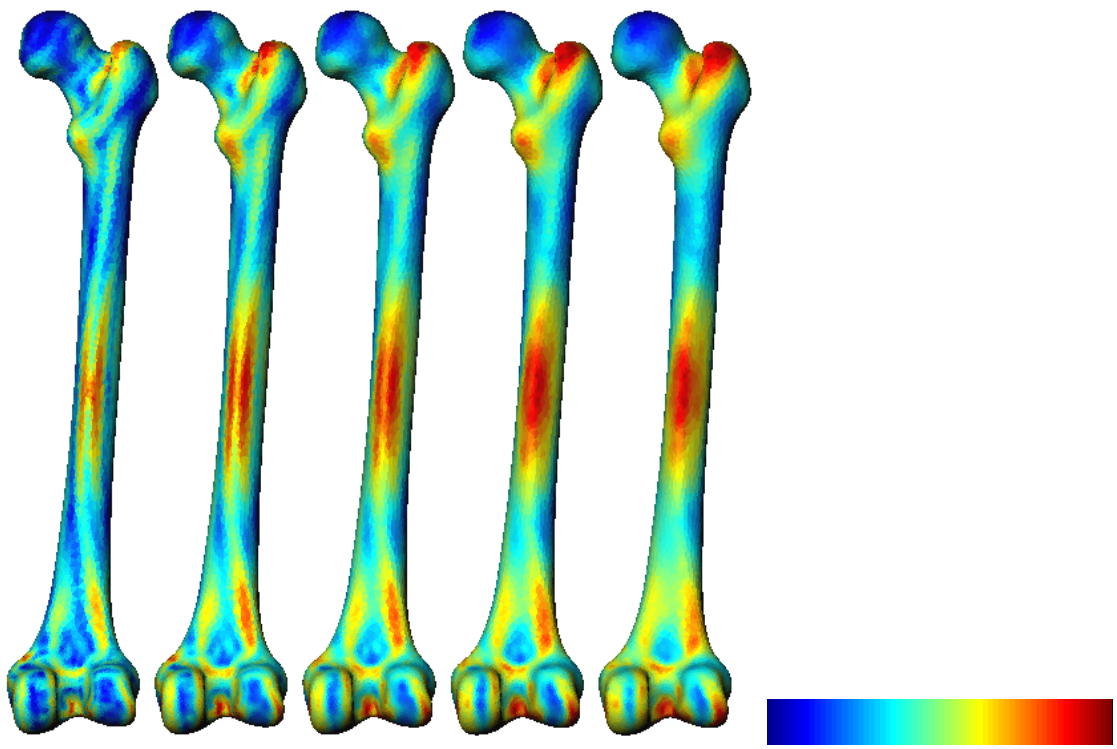

Figure 8 Roughness maps of femur template bone at 1st , 2nd , 3rd , 4th and 5th neighborhood levels

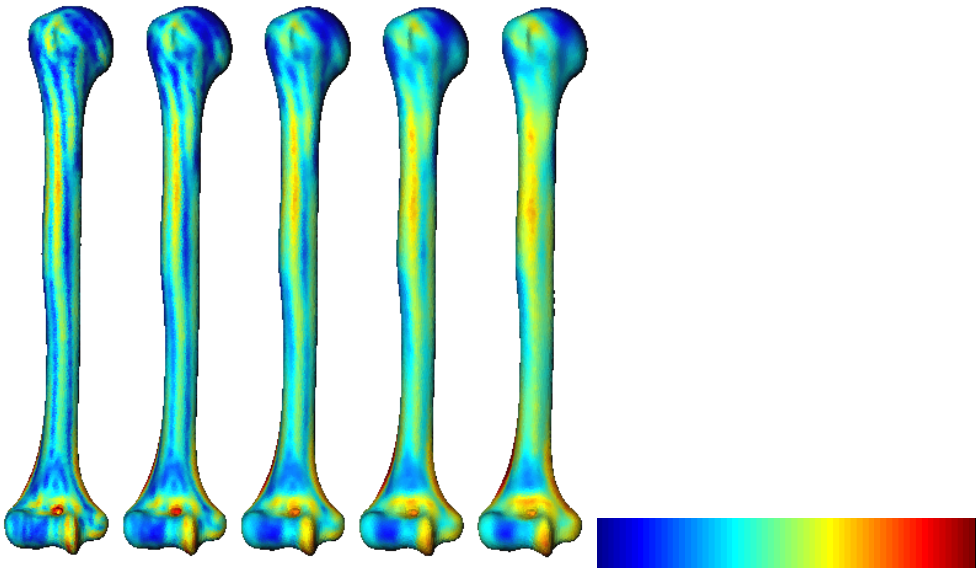

Figure 9 Roughness maps of humerus template bone at 1st , 2nd , 3rd , 4th and 5th neighborhood levels

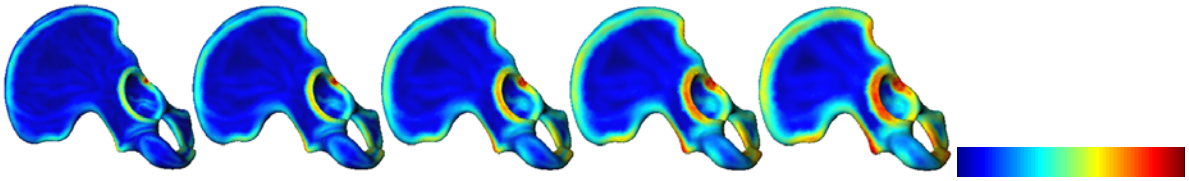

Figure 10 Roughness maps of pelvis template bone at 1st , 2nd , 3rd , 4th and 5th neighborhood levels

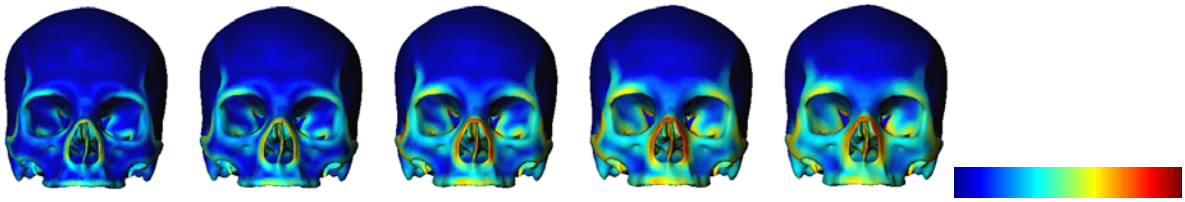

Figure 11 : Roughness maps of skull template bone at 1st , 2nd , 3rd , 4th and 5th neighborhood levels

3.3.3. Gaussian Mixture Model

Gaussian mixture model 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 the problem in hand, we're assuming the calculated surface roughness of each template model is a mixture of two Gaussian distributions, that represents distribution of surface points with low roughness values (smooth surface points) and high roughness values (feature points). **Figure 12** show the histogram

and the two distributions of Gaussian components of femur and skull template bone models surface roughness calculated using the proposed roughness measure, Eq. 7, Eq. 8.

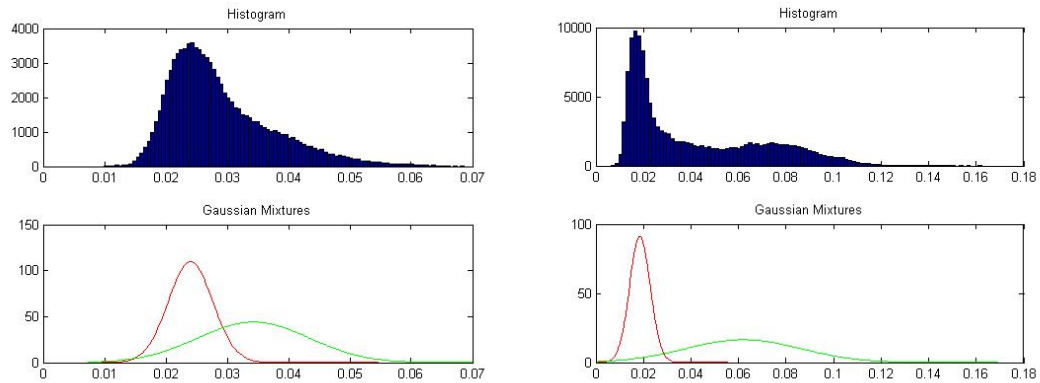

Figure 12 Surface roughness of femur (left), skull (right) template bone model, histogram and distributions of Gaussian components

Based on the idea that fractured surfaces introduce higher values of roughness, compared with native surfaces, we assumed that the calculated surface roughness of each bone fragment is a mixture of three Gaussian distributions, representing native surface smooth points, native surface features and fracture surfaces points. **Figure 13** shows the surface roughness of femur fragment bone model histogram and distributions of Gaussian components of its surface roughness values. It is worth to note here that the features of the original bone still can be detected by the proposed surface roughness measure, in the presence of high curvature, or high rough, points at the edge of the fracture surface.

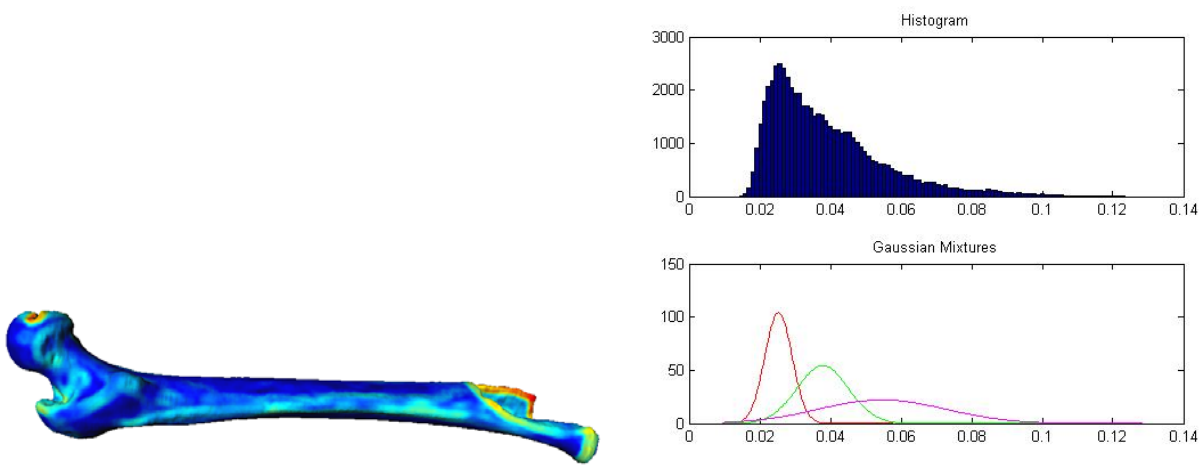

Figure 13 Surface roughness of femur fragment bone model

We've selected the mean of the second Gaussian distribution μ_2, resulting from GMM analysis as the threshold that filter out the features from template bone surface models. To extract similar points from the fragment bone, we've selected the range between the second, μ_2, and the third, μ_3, means as the range of roughness that include the features of the original bone. **Figure 14** show the extracted features from template and fragment femur bone models using GMM extracted thresholds.

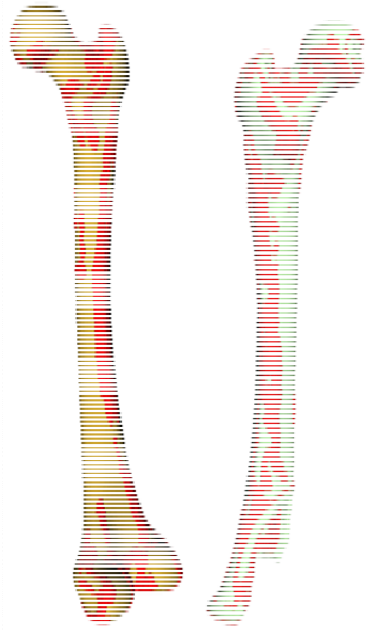

Figure 14 Features detected on femur template model (left) and femur fragment (right)

3.3.4. Matching and Registration

The process of matching and registration is highlighted in **Figure 15** and **Figure 16**. Basically the process is divided into two stages. The first stage involves matching of the extracted fragment features with the features of the four template models (B_i). Fragment features are positioned at different locations (t_j) with respect to the bounding box of the template model, and at each position, they are rotated around different coordinate system axes, (R_k). For each position and orientation, fragment features are matched with template features using iterative closest point (ICP).

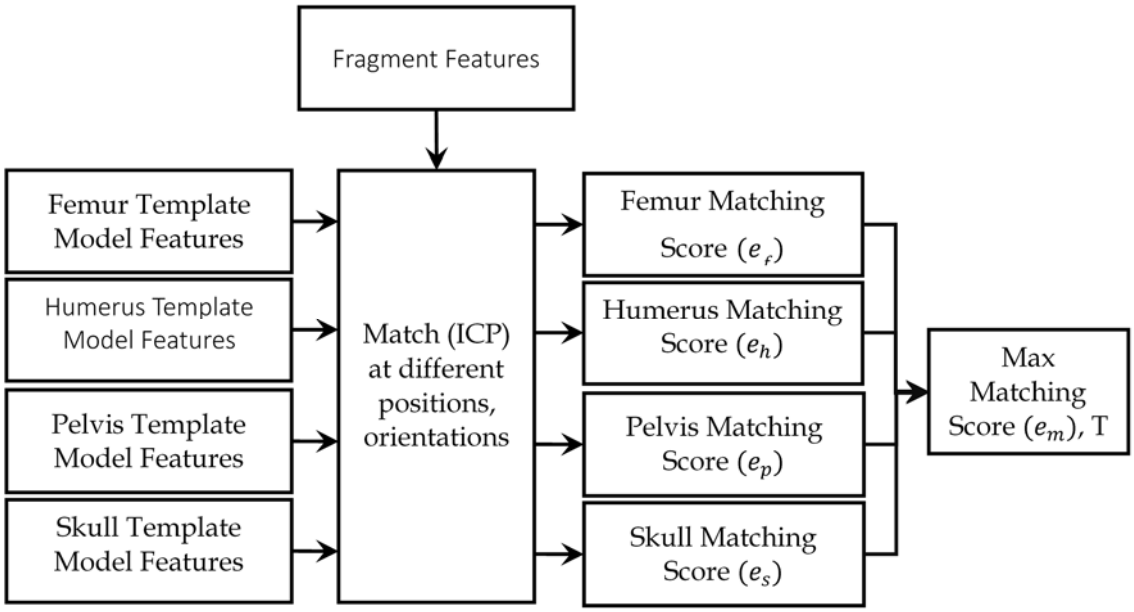

Figure 15 Matching and registration process – A

From all matchings, we select the best matching score (B_m, t_n, R_l) based on the minimum root-mean-square error, RMS_{ijk} and extract its rigid transformation, T. The second stage involves registration of the fragment surface model with the template surface model based on the best matching score from the first stage. The fragment model is first positioned and oriented using (t_n, R_l), transformed by T and then registered with the template model B_m using ICP. If the output error from the registration process (e_r) is greater than the output error from the feature matching process (e_m), then we are facing a false positive matching. To solve this issue, we discard the template model with the max feature matching from the matching process and used the second best feature matching score template model to register with the fragment. If the registration error is smaller than the feature matching error, then we are done with the matching, registration and identification too.

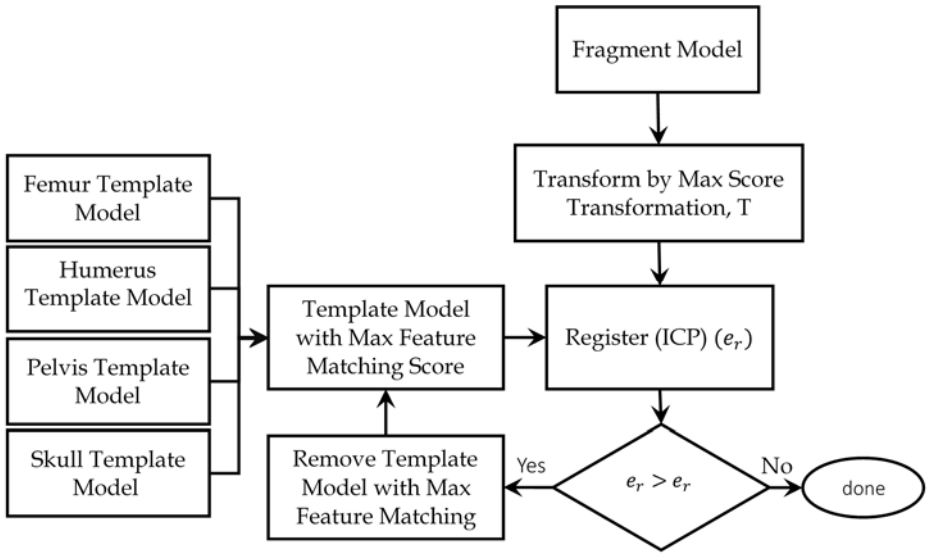

Figure 16 Matching and registration process – B

3.3.5. Virtual Environment

A major component of this grant was to develop a virtual 3D environment based on Open Graphics Library (OpenGL) 3D visualization library [https://www.opengl.org/] and QT graphical user interface library. The virtual enviroment encapsulate both the automatic alignment functionalities and the manual registration and manipulation functionalities. The developed environment enables the user, through graphical user interface (GUI), to load scanned models in either surface model file format (*.surf) or open inventor file format (*.iv). The GUI has the capability of loading one or multiple files at once each containing one or more models. Once the models loaded to the scene viewer, the user has the ability to:

1. Do rotation, panning and zooming through interactive viewer widget as well as wheel controls.
2. Return to the home view, set the home view, view all the loaded models.
3. Switch between parallel and perspective projection modes.
4. Change the lighting direction.
5. Change background color.
6. Select specific model for further operation.

The loaded models are assigned random keys as well as random colors which can be updated through material editboxes. The user has the ability to apply transformation (translation, rotation and scaling) through user controls as well as interactive viewer. The transformations can be applied, reset or confirmed for the selected model(s). The interface enables the user to save the modified models separately. **Figure 17** and **Figure 18** show examples of two screens from the virtual enviroment, Appendix A contains a more in depth scenario of using the developed application.

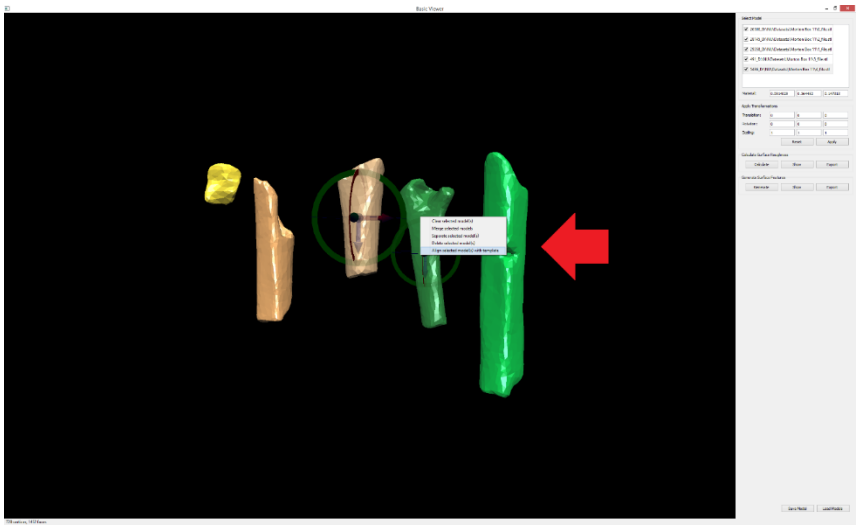

Figure 17 Fragment models loaded in the developed virtual environment

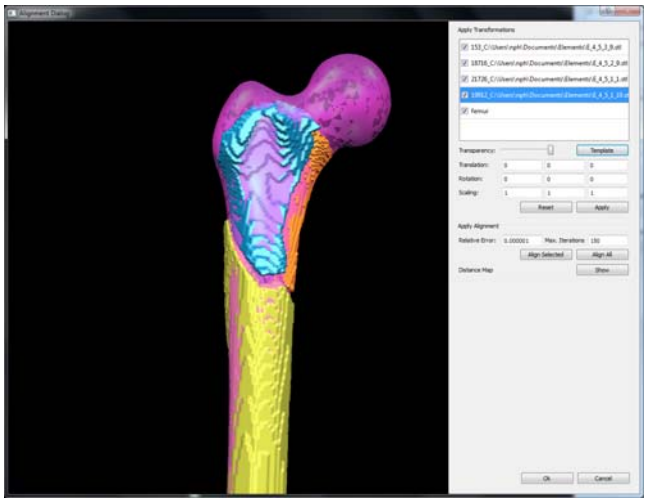

Figure 18 Align fragments with template model

The GUI also provides the user the control to generate and export surface roughness values for the selected model(s) as well as all loaded models using variable neighborhood size, different local curvature measures (mean curvature, shape index, curvedness and signed curvedness) and different scale-space calculation scheme (difference-based, variance-based, edge weighted-based). For our application, after loading the fragment models in the scene to the viewer, the user can select different fragments through select tool, right click and select “align selected models with template”. This will pop-up a small dialog to choose which template model to align with, or the user can check “All” to test alignment with all template bones. Once accepted, a separate alignment dialog will appear showing the selected fragments and the template model(s) loaded.

In the alignment dialog, the user has the ability to apply any transformation to the loaded fragment models as well as to the template model before starting the algorithm. Default values for maximum iterations and minimum relative error of ICP algorithm are loaded and can be changed by the user. The dialog enables the user to either start the matching/registration procedure for the selected model(s) or for all. Once done, the GUI will display the fragment models registered with the proper template bone.

The user can accept/reject matching(s)/alignment(s) by right clicking at the fragment and selecting accept/reject for selected or all fragments. If the alignment has been accepted, it will be reflected to the fragment model in the main viewer, and it will be neglected if rejected. Again, the user can apply transformations to the fragment(s) of rejected matching(s)/ alignment (s) and start the procedure again.

4. Results

Results of the feature detection on template models for the four bones is shown in **Figure 19**. A subset of Morton collection fragments as well as a subset of simulated fragments were used to verify the developed matching algorithm as shown in **Figure 20** and **Figure 21**. For each fragment, matching scores against all the template bones at different positions and orientations, were listed, based on the root mean square error, where the root mean square error is calculated in centimeters as the average of distances between corresponding points. The template bone with the minimum non-false-positive root mean square error was considered the best match, and the fragment was identified as being part of it.

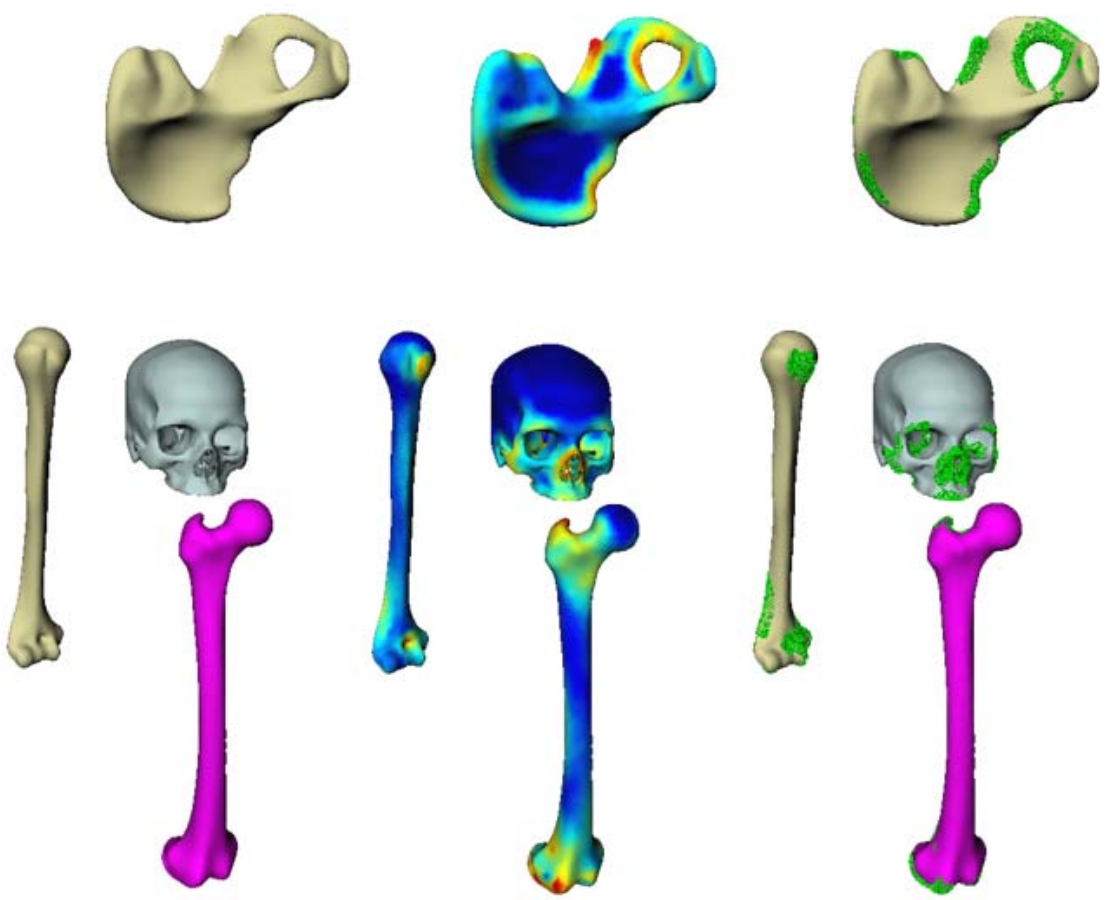

Figure 19 Template models, their roughness maps and detected features

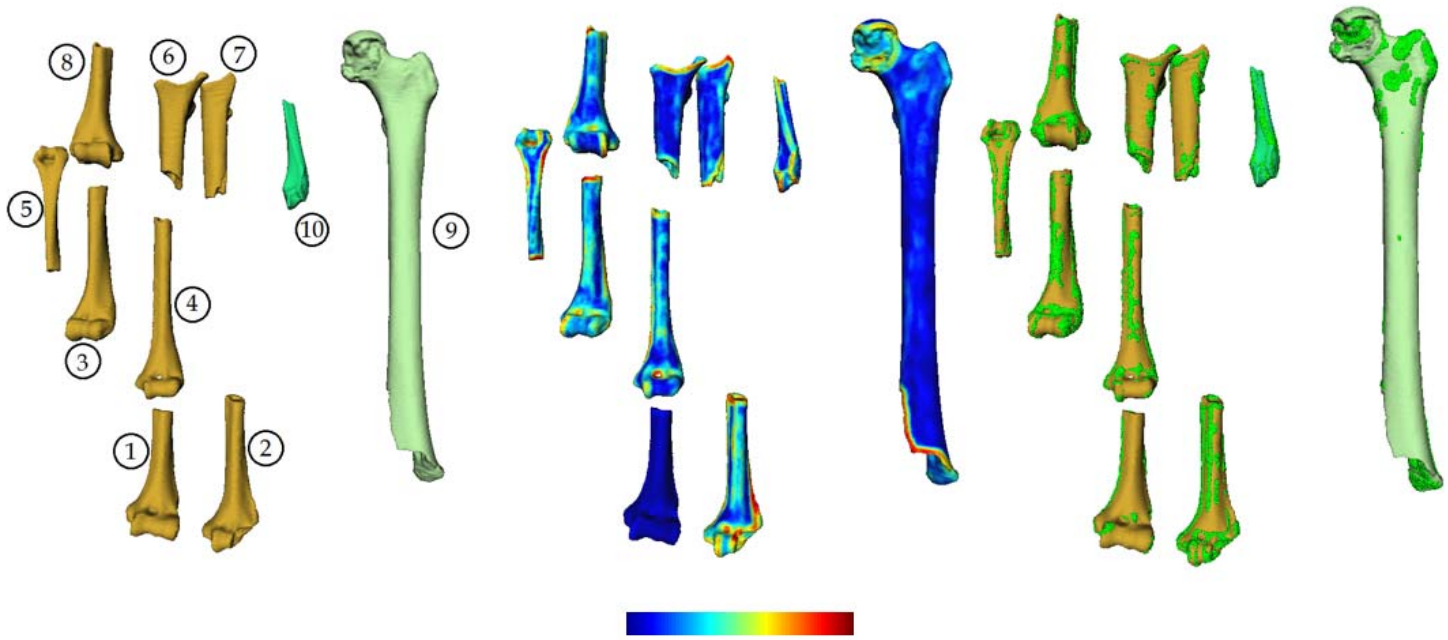

Figure 20 Morton collection sample used for validating bone matching algorithm

Figure 21 Example of simulated partial fragments used for validating bone matching algorithm

Table 1 shows the matching and registration root mean square errors (RMSE) with each template model at different orientations and positions and the automatically matched bone. Red colors highlight false positive matching's which are detected by comparing feature matching errors and registration errors. Green colors highlight correct true positive matching's which are verified by comparing feature matching errors and registration errors. **Figure 22** shows results of matching fragmentary pieces from Morton collection using developed software.

Table 1 Matching algorithm validation and minimum RMSE (cm) green color highlights a correct matching, while red color highlights an incorrect matching

Fragment	Femur	Humerus	Pelvis	Skull	Matched Bone
1	*0.73328*	*0.514663*	*0.699231*	*0.385311*	*Humerus*
2	*0.667225*	*0.557928*	*0.783834*	*0.455202*	*Humerus*
3	*0.850877*	*0.640472*	*0.898699*	*0.698427*	*Humerus*
4	*0.634426*	*0.664907*	*0.699361*	*0.753343*	*Humerus*
5	*0.653042*	*0.563865*	*0.781884*	*0.840516*	*Humerus*
6	*0.733875*	*0.619259*	*0.776236*	*0.519864*	*Femur*
7	*0.79863*	*0.608945*	*0.823335*	*0.625949*	*Femur*
8	*0.716187*	*0.573982*	*0.829414*	*0.549071*	*Humerus*
9	*0.845232*	*1.296698*	*4.058093*	*2.949372*	*Femur*
10	*0.932372*	*1.024249*	*1.250394*	*0.883769*	*Femur*
11	*0.486868*	*0.499618*	*0.602452*	*0.472178*	*Femur*
12	*0.739734*	*0.755775*	*0.954680*	*0.414900*	*Femur*

Figure 22 Matching of fragmentary pieces from Morton collection using developed software

Validation of the bone reconstruction was conducted on simulated data to assess the ability of statistical atlas to reconstruct missing information from existing fragments. Using correspondence of statistical atlases, different fragments of the pelvis were deleted from 120 samples representing 10, 20 and 30% of the overall surface area. For each sample the statistical shape model (SSM) was constructed using the leave-one-out method. For each output model from the atlas, this model was excluded from the training set and the remaining bones were used to create the SSM. **Figure 23** shows the simulated fragments and the average surface distance error map of reconstruction for the 120 pelvis bones. **Table 2** show the mean, standard deviation and maximum RMS error for the reconstruction for the 120 pelvis. **Figure 24** shows the average distance error of reconstruction for 90 skulls using "leave-one-out" experiment, **Table 3** shows the mean, standard deviation and maximum RMS error for the reconstruction using leave on out experiment for 90 skull.

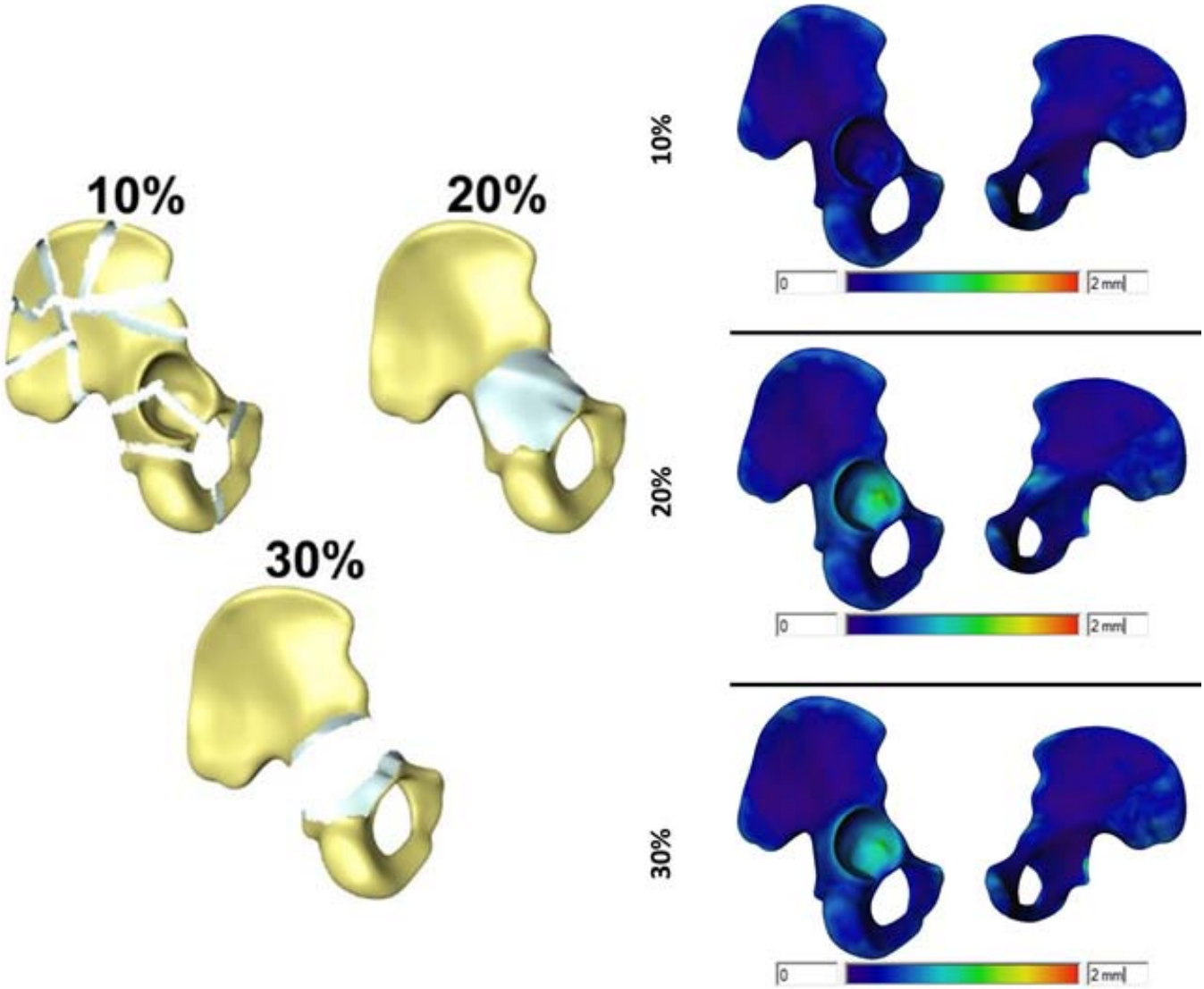

Figure 23 Full bone reconstruction validation for pelvis

Table 2 Results of full bone reconstruction validation for pelvis

% Missing	RMS (mm)	STD (mm)	Max (mm)
10%	0.54	0.35	2.91
20%	0.6	0.4	3.2
30%	0.61	0.41	3.29

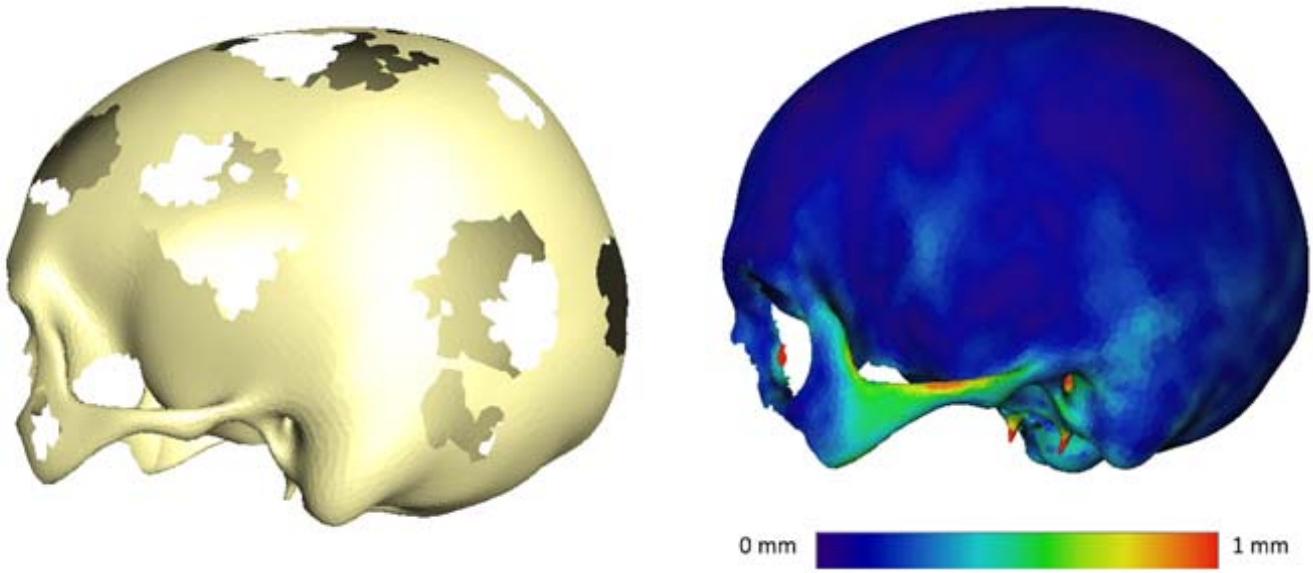

Figure 24 Full bone reconstruction validation for skull

Table 3 Results for full bone reconstruction validation for skull

% Missing	RMS (mm)	STD (mm)	Max (mm)
30%	0.45	0.35	4.8

Figure 25 shows the results of reconstruction of simulated skull fragment using developed software with mean RMS error of 0.5 mm and maximum error of 1.1 mm. **Figure 26** to **Figure 29** show the results of comparison of fragments matching and full bone reconstruction using developed software and GIS system.

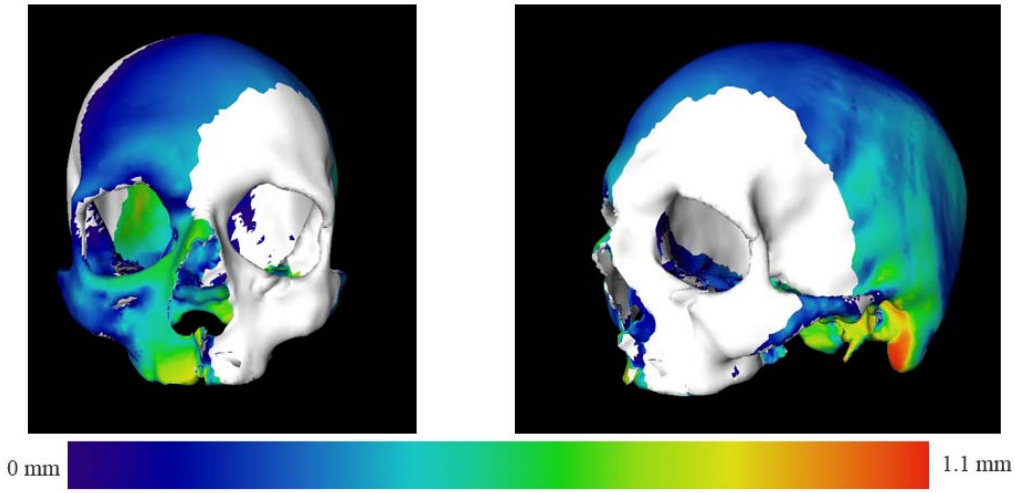

Figure 25 Distance map of the error in the reconstructed skull using the software (simulated fragmentary skull)

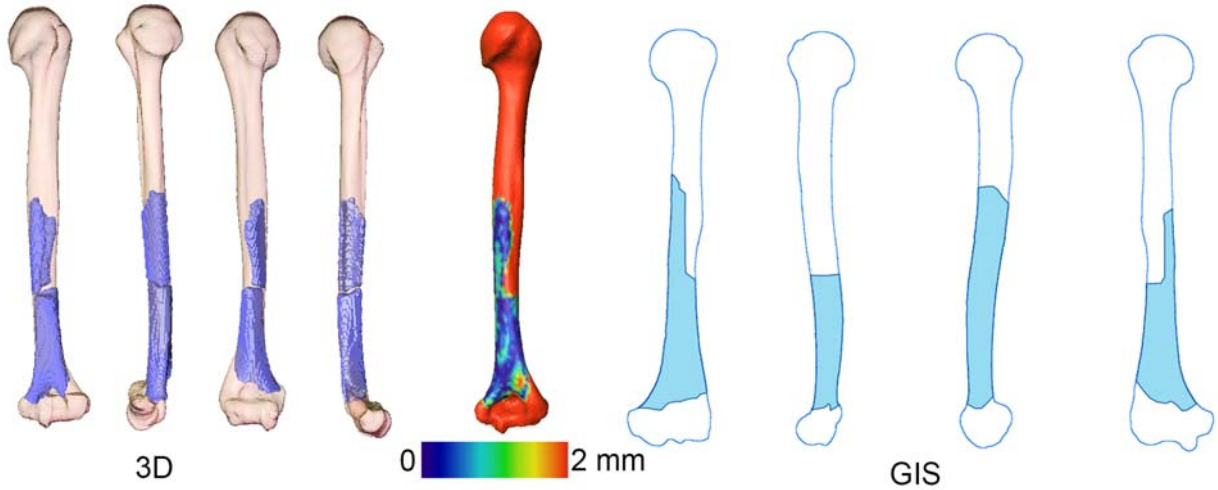

Figure 26 Validation of reconstructed bone from Morton collection using developed software (left), distance map between reconstructed 3D model and fragmentary pieces and GIS (right)

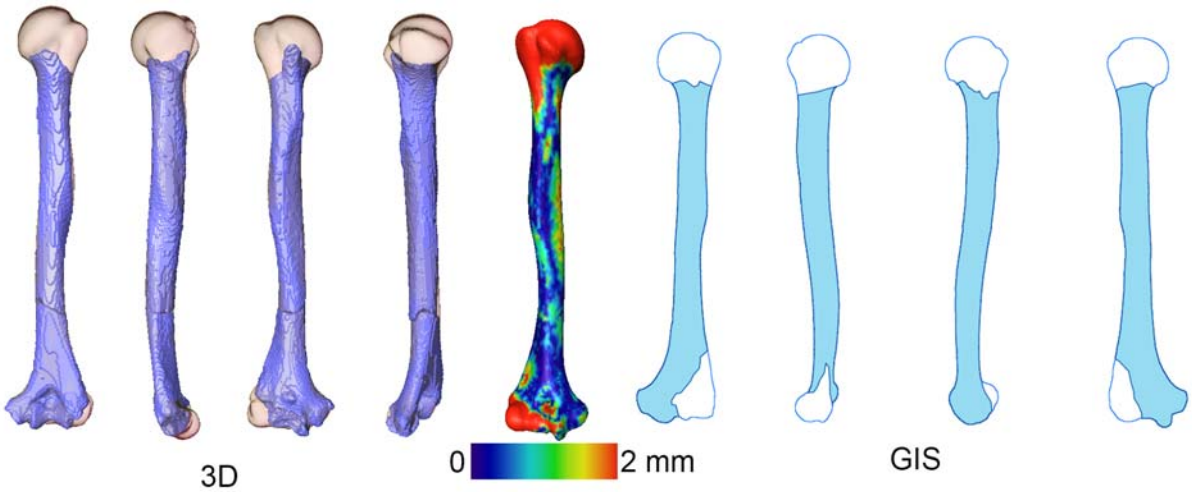

Figure 27 Validation of reconstructed bone from Morton collection using developed software (left), distance map between reconstructed 3D model and fragmentary pieces and GIS (right)

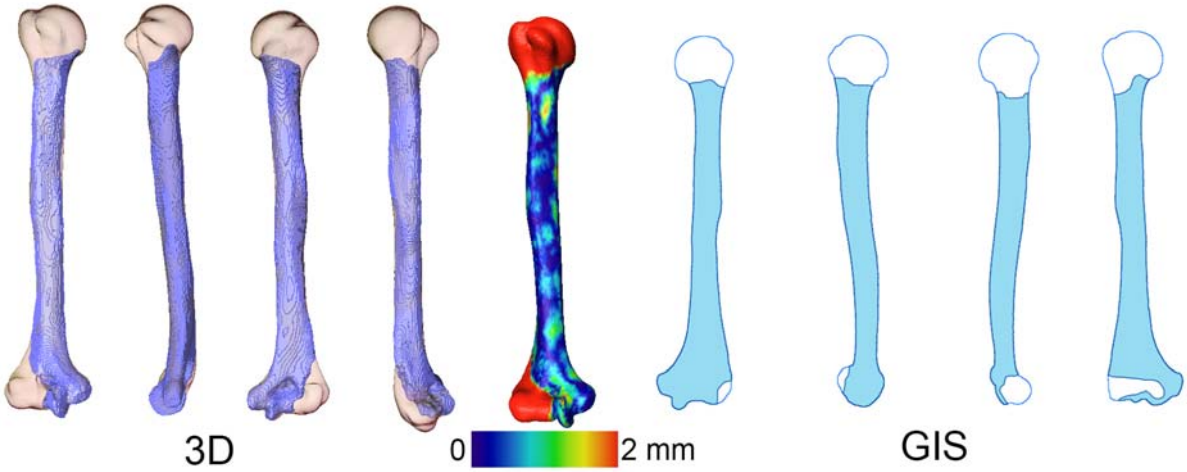

Figure 28 Validation of reconstructed bone from Morton collection using developed software (left), distance map between reconstructed 3D model and fragmentary pieces and GIS (right)

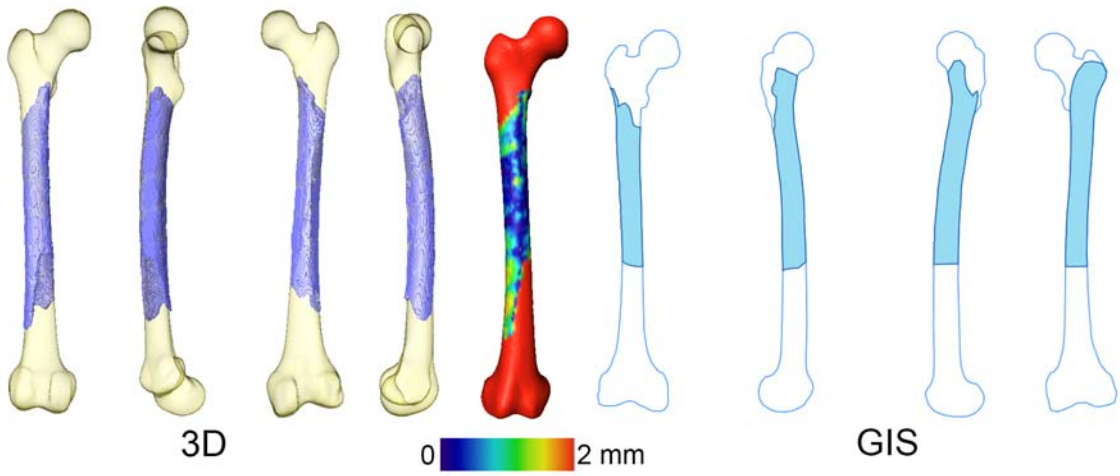

Figure 29 Validation of reconstructed bone from Morton collection using developed software (left), distance map between reconstructed 3D model and fragmentary pieces and GIS (right)

Table 4 shows percentage coverage of Morton collection elements used in the validation study. **Table 5** shows the number of fragments sorted, coded, digitized and CT scanned from the Morton collection during the course of the grant.

Table 4 Elements reconstructed from Morton collection in the validation experiment and their element coverage % value

FEM	0.442519627
FEM	0.369916495
FEM	0.199869862
FEM	0.421780743
FEM	0.037546688
FEM	0.173381003
FEM	0.078867841
FEM	0.337983823
FEM	0.250040714
FEM	0.218311589
HUM	0.340868503
HUM	0.140539778
HUM	0.719475515
HUM	0.268089708
HUM	0.119372121
HUM	0.251810742
HUM	0.43019809
HUM	0.753070155
HUM	0.160353832
HUM	0.048746059

Table 5 Number of Morton collection fragments sorted, coded, digitized and scanned during the course of the grant

Fragment Sorted	24,569
Fragments Coded	18,373
Fragments Digitized	1232
Fragments CT scanned	2061

5. Conclusion

During the course of this grant, user-friendly software was developed that enable forensic anthropologists to quantify and reconstruct fragmentary human skeletal remains (crania, pelvis, humeri, and femora are the focus of the initial platform; additional elements will be added with subsequent releases of the software) from three-dimensional surface files generated by computed-tomography or laser scans. First, the system serves as an osteological case or scene management tool. All scanned skeletal remains from each scene will be reviewable within the application. The software allows the user ability to visualize fragmentary elements and reject or accept elements. This is then followed by initial alignment of fragmentary elements with three dimensional statistical templates for each bone. Upon accepting the alignment of the elements, the software merges the elements and provides a fully reconstructed bone. Measurements can then be conducted by the user to apply to regression equations, discriminant functions, or to use with software such as Fordisc 3.0. The developed software was validated using both simulated data, and real data from Morton collection. Software was compared to GIS, same fragment ID's were matched using both systems and fragments was placed in comparable location on the template. It is worth noting that GIS doesn't provide a reconstructed bone or three dimensional distance map between matched fragments and template and thus no quantitative numbers were generated for the comparison.

The developed project expands the usefulness of the statistical atlases into the analysis of fragmentary and commingled remains. In addition, forensic anthropologists are provided with a means to quantify and reconstruct remains that are damaged or fragmentary, thereby enhancing analyses in challenging cases. The data management aspect of the application will allow forensic anthropologists to digitally inventory complex commingled scenes; if geospatial data is integrated with each fragment then the refitting process can proceed geographically. Therefore, the developed application will significantly impact forensic anthropologists and crime scene investigators ability to reconstruct mass disasters, commingled mass graves, and highly fragmentary individual burials or surface scatters.

In addition during the course of the grant the research team has CT scanned, sorted, coded and digitized large percentage of Morton collection.

6. Future Work

With the Beta release of the software and its use by the community, support will be provided for bug fixes and user interface enhancements based on user's feedback.

7. References

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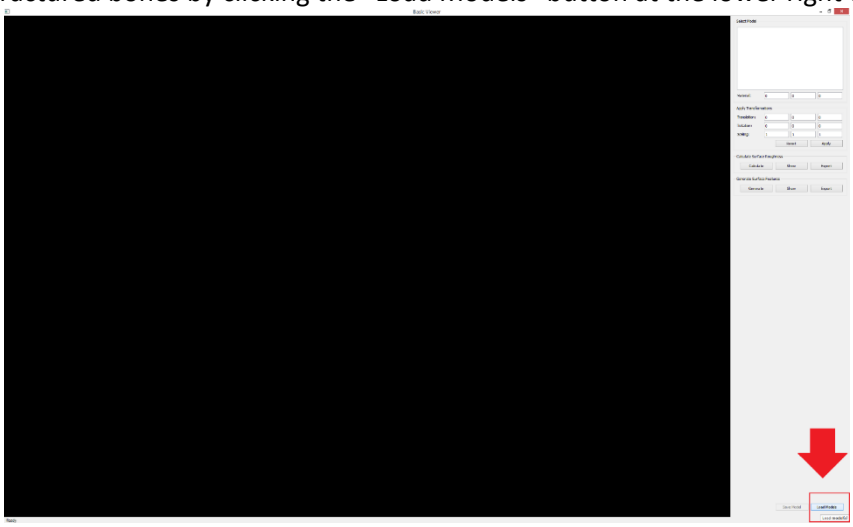
8. Appendix A (software usage example)

I. Installation and Start Up

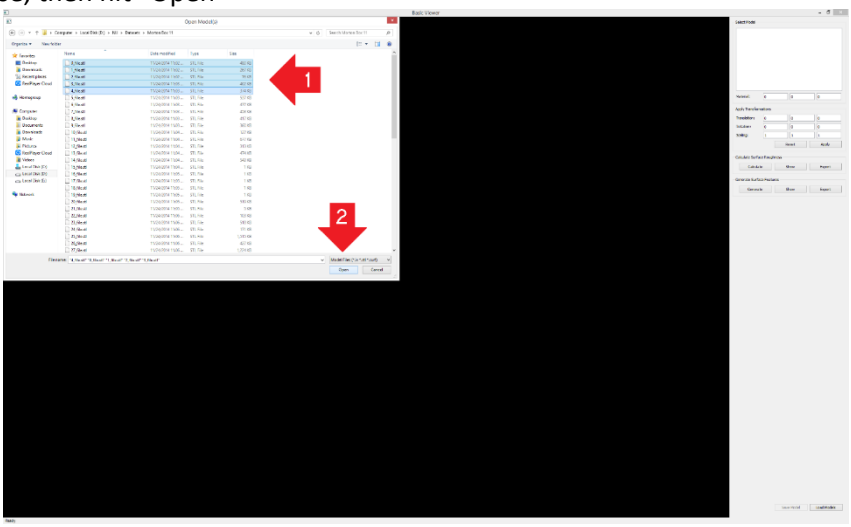
1. Double click BoneMatchSetup.exe.
2. When prompted by the User Account Control window, select Yes (Windows Vista, 7, or 8 only).
3. When prompted to choose an install location, you may choose the default (C:\Program Files (x86)\BoneMatch) or select Browse to choose another folder. Select Install to begin installing the application.
4. The installation pop up window will display "Installation Complete" when Setup has completed successfully. Select Close to close the installer.
5. To launch the software, double click the new BoneMatch icon located on your desktop.

II. Using the Application

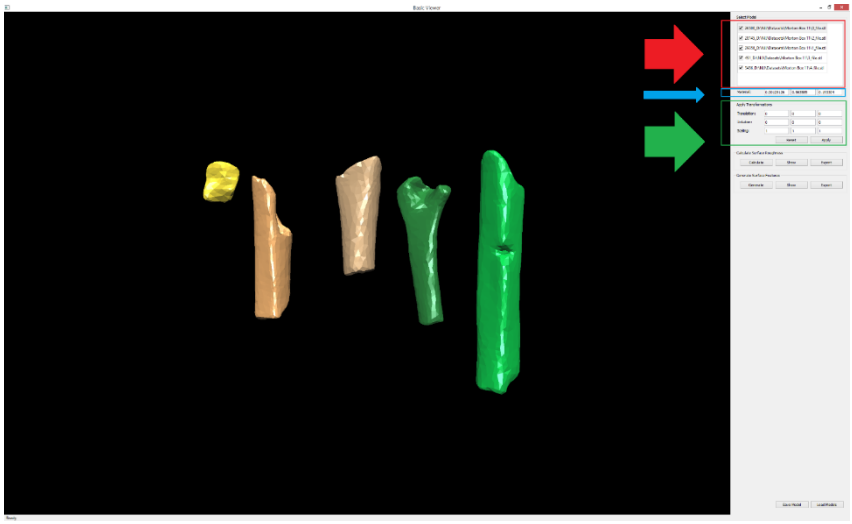
1. Load fractured bones by clicking the "Load Models" button at the lower right corner



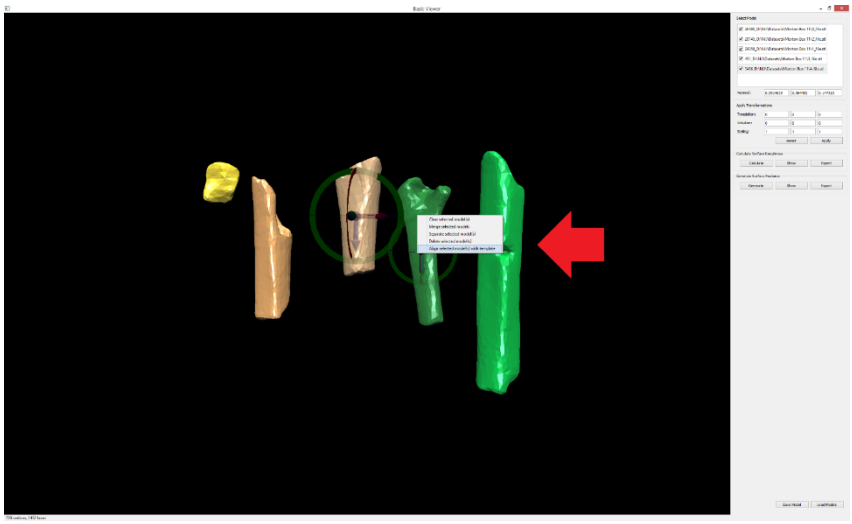
2. In the "Open Model(s)" dialog, select multiple models using SHIFT/CTRL keys on your keyboard or using mouse, then hit "Open"



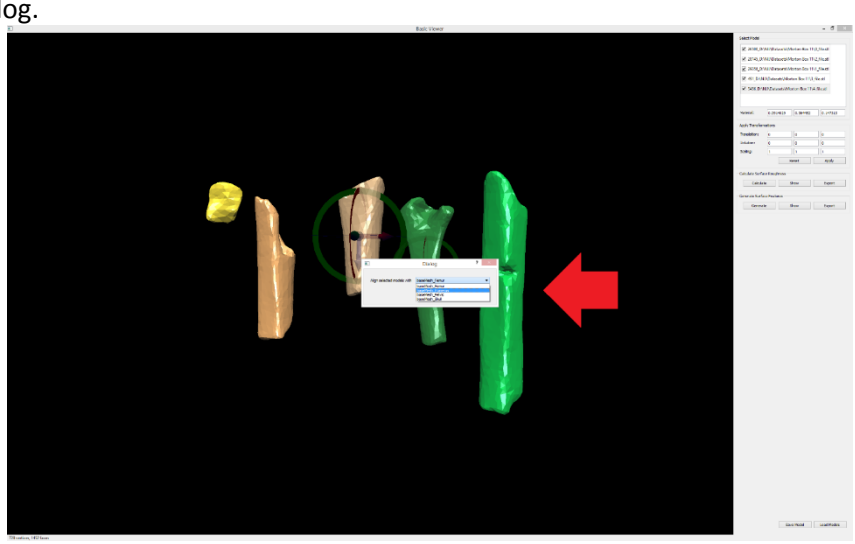
3. You can show/hide the loaded models from the corresponding checkboxes in the “Select Model” box (red highlighted). Also, you can update the model material (color) by selecting the model and updating the material values (blue highlighted). You can do some transformations on each model by selecting model, changing translation/rotation/scaling values (green highlighted). Note that you need to hit apply so that the non-reversible transformation applies.



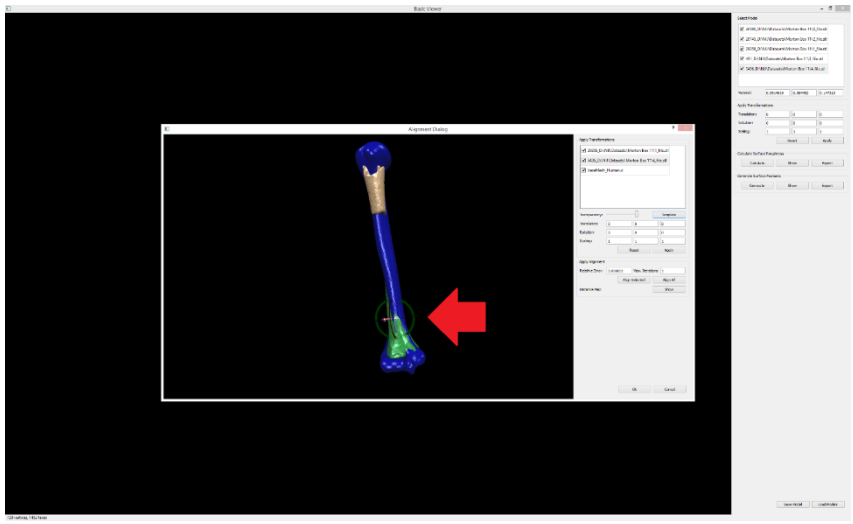
4. In the viewer, you can use the ESC key on your keyboard to switch between navigating and selecting modes. In navigation mode, if there are selected models then you can manipulate them (by dragging model’s manipulator). If there is no model selected in navigation model then you can rotate (left mouse button + move), pan (middle mouse button + move) and zoom (mouse wheel) the whole view. You can clear selection by right clicking, then selecting “Clear selected model(s)”. In selection mode, you can select multiple models using SHIFT/CTRL keys. Selected models have manipulators around them, as shown in the next figure. You can select multiple models (fragments), right click with mouse and select “Align selected model(s) with template”



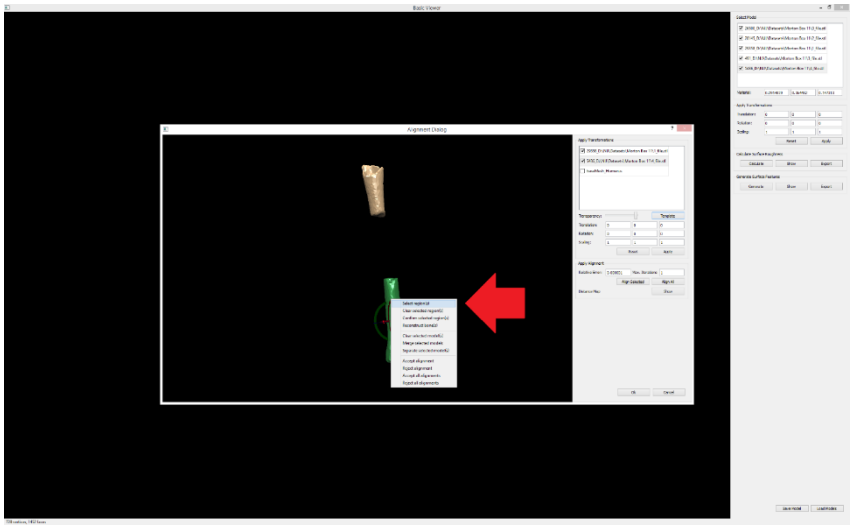
5. You can select which template you are willing to align the selected models (fragments) with, from the next dialog.



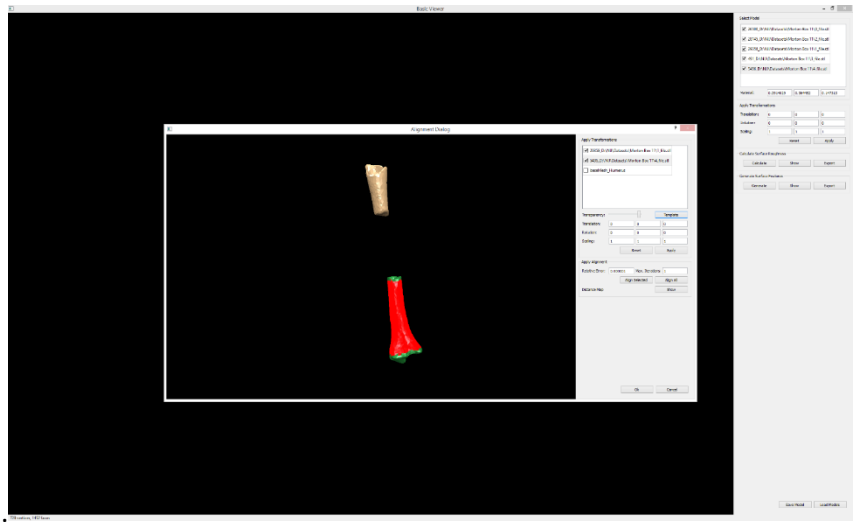
6. In the next (alignment) dialog, you can switch to selecting mode (ESC key), dragging the model with mouse by hitting the small white sphere at the center of the manipulator, or you can rotate the model using the three rings (rotation around three major axes).



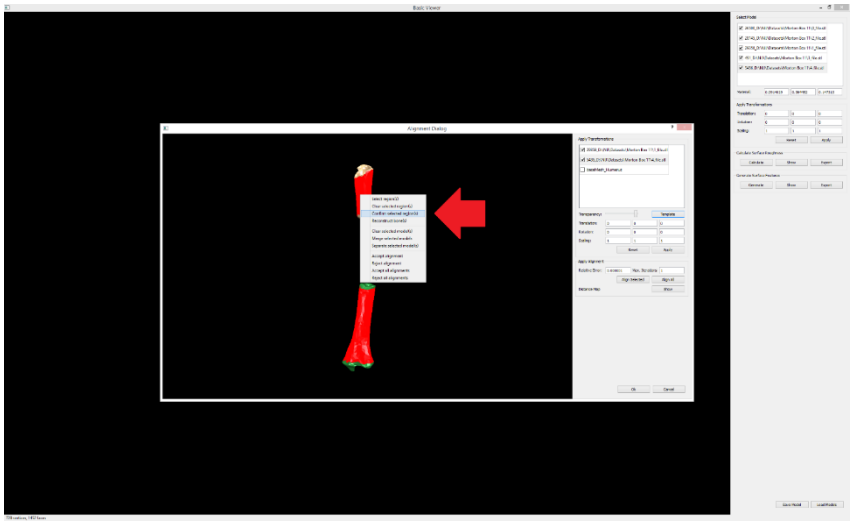
7. By selecting model, right clicking and htting “Select region(s)” from the pop-up meu, you can start selecting points belonging to the original non-fractured bone.



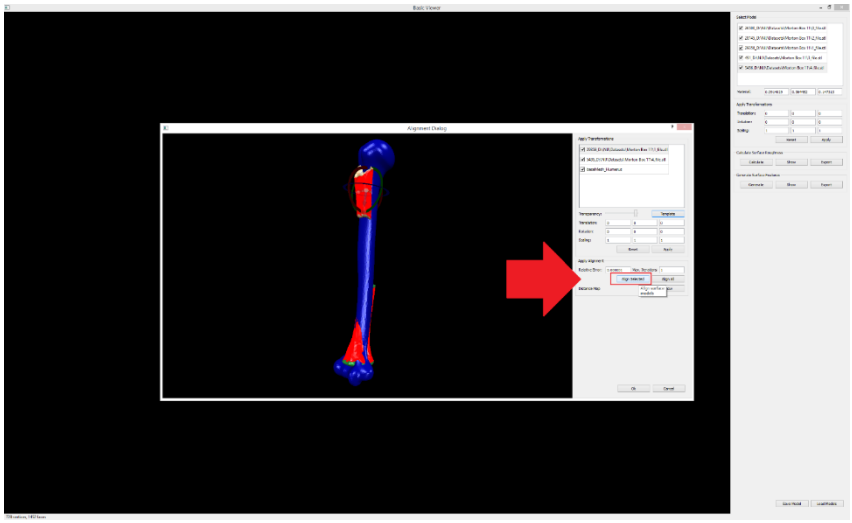
8. You can draw polygon on the screen that will be intersected with the models and extract the selected points



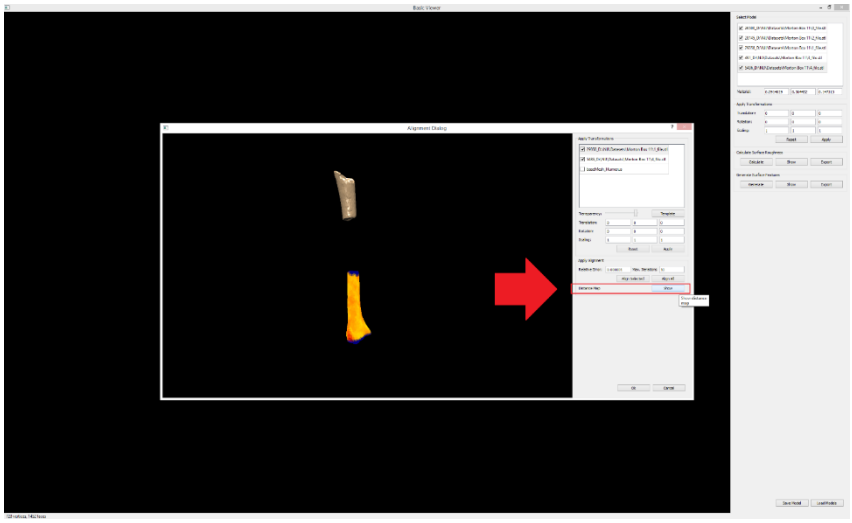
9. After being done with point's selection, you need to right click and confirm your selection by clicking "Confirm selected region(s)". You can also clear the selection by clicking "Clear selected region(s)" and start over again.



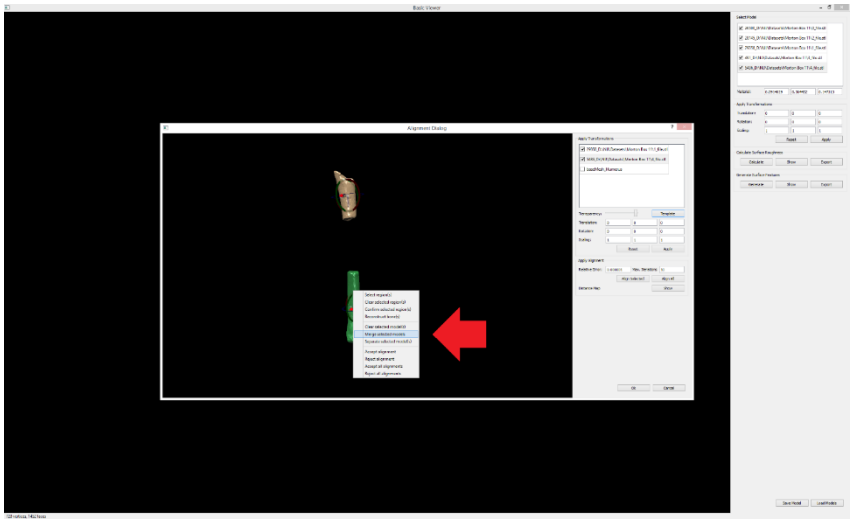
10. For better results, you can select models and align them to the template model using “Align Selected” button. You can change alignment parameters (number of alignment iterations, minimum error distance). You also can change model’s transparency by selecting the model and changing the transparency slider.

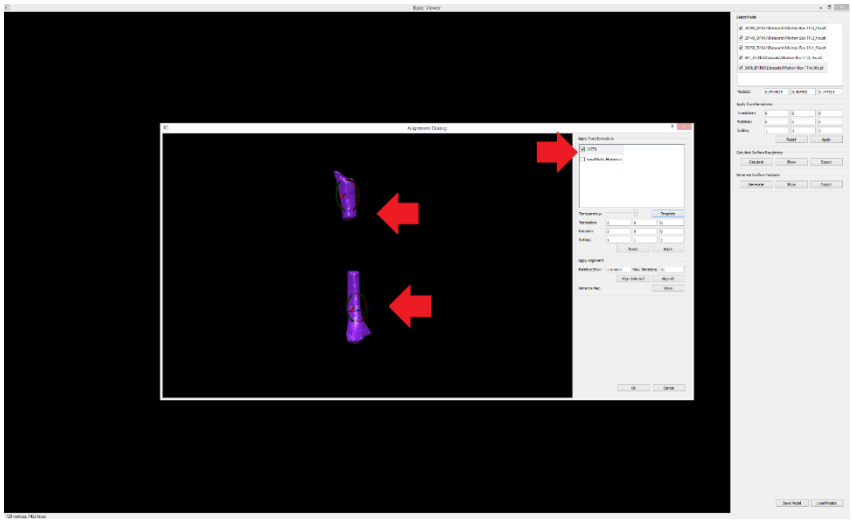


11. You can see the distance map between fragment and template points after alignment, by selecting model and clicking “Show” button besides “Distance Map” label.

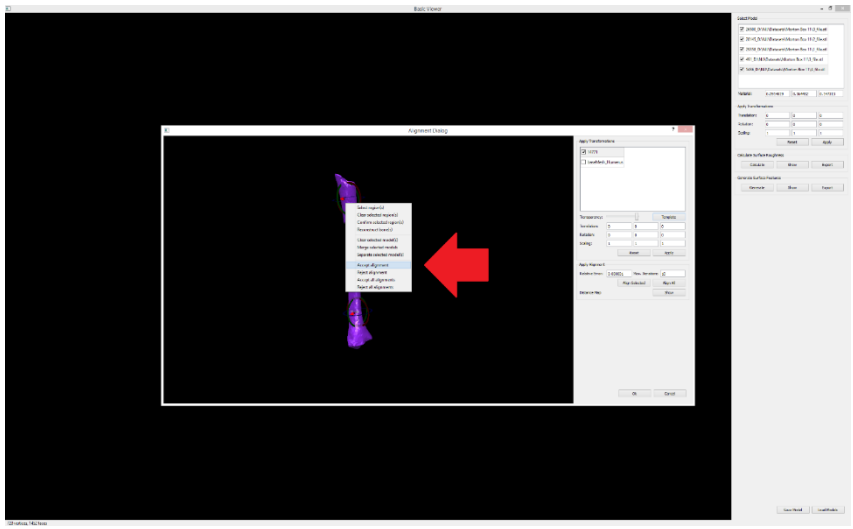


12. If you believe that multiple fragments belong to one element (two fractures of the same bone for the same person), then you can merge them, by selecting the fragments, right clicking and hitting “Merge selected models”. You can go back and separate them if you changed your mind. After merging multiple fractures, they should appear as one object (one color).

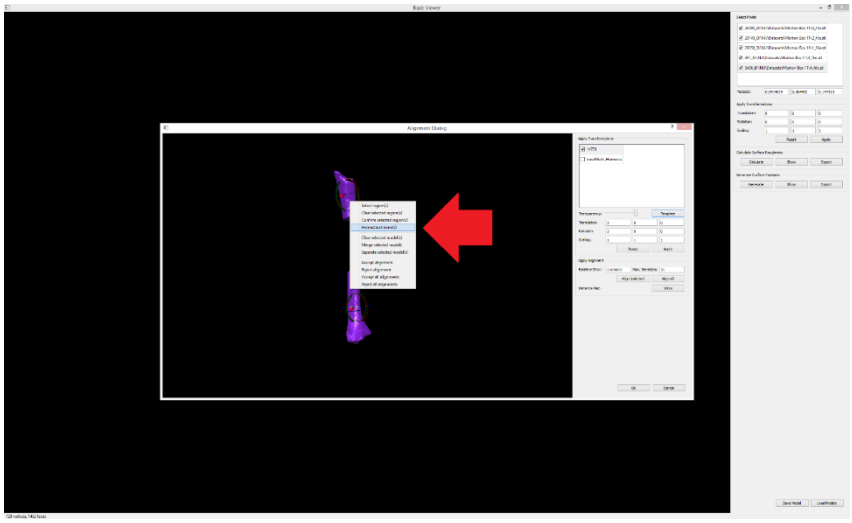




13. You need then to accept alignment by selecting the models, right clicking and hitting “Accept alignment”. Any time before accepting alignment, you can change the template by selecting “Template” button.



14. You can reconstruct the complete bone for the fractured models by selecting the models, right clicking and hitting “Reconstruct bone(s)”. It takes some time to reconstruct the complete bone.



15. You can hit “Ok” to accept the alignment and morphing. You can see the morphed model in the main application window. You also can save the morphed model to the computer’s HDD by selecting the morphed model, clicking “Save Model” button at the lower right corner of the screen, and select folder to save the model at.