

PATIENT-SPECIFIC BONE QUALITY EVALUATION FROM CT IMAGES

by

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Certification of Authorship

- The icon of the software application is under the "Flaticon license" downloaded from [flaticon](#).
- 3D volume reconstruction modified from [Howard Chen's Post](#).

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Abstract

DXA scans are the standard for assessing the quality of a patient's bone in terms of their BMD. However, CT scans are a more prevalent subset of medical imaging that do not have an established method through which a patient's bone quality is evaluated through their BMD. This project's main objective is to propose a software tool by which image processing techniques can be applied using Python in order to extract BMD information about a vertebrae bone sample from a CT scan. Along with developing the software, another objective was to segment multiple vertebrae from a CT scan and validate the information that the tool can provide by using finite element analysis (FEA) to perform a pedicle-screw pullout test across multiple vertebrae. The relationship between the BMD and CT scan could then be used to assess the tool's capability. The software tool, *VertScan* [1], was successfully developed and is able to extract BMD values of the vertebrae. However, the FEA implementation was not completed due to issues in implementation of the design, and as such, cannot definitively validate the capabilities of this software. The methodology by which FEA analysis can be conducted is included in the report, and may be replicated at a future time to determine the accuracy of a CT-based tool such as *VertScan*. At the current stage of this project, it is inconclusive as to how accurately the software tool can perform analysis of bone quality, and rather, the detailed methodologies by which a CT-based software application can be made for such a purpose are outlined in this report.

Introduction & Background

Osteoporosis is a disease that can affect a wide range of individuals. Statistics indicate that over 200 million individuals worldwide are afflicted with osteoporosis - with 50% of women being affected and 20% of men affected by osteoporosis. Treating osteoporosis is initiated by early diagnosis of the condition - which can also prevent serious fractures [2]. As such, it is important to investigate all avenues by which such a disease may be diagnosed. In investigating the possibility of other techniques/methods, from an engineering point-of-view, there is the possibility for refinement of an existing solution or the creation of a new solution which potentially performs better than the standardized previous solution. In doing so, there is the opportunity to create a positive impact in the medical community as Osteoporosis can be detected more precisely early on.

DXA scans are currently the standard in evaluating bone mineral density. However, CT scans do not have a standardized procedure by which such a measurement can be performed. However, the topic has had studies performed, with one such study detailing the success of screening Osteoporosis using machine learning [3]. Another study noted that DXA scans were able to only detect Osteoporosis in 17.1% of individuals while the QCT scan was able to detect the ailment in up to 46.4% of the patients [4]. From the aforementioned studies along with the various other ones conducted, the ability to draw upon CT images and CT attenuation to obtain BMD is not out of the question, and can be performed with positive results.

Objectives

The undertaking of this project is to ultimately develop a software tool that is able to detect osteoporosis and thereby provide an assessment on the quality of the bone using image processing techniques. However, this main goal can be divided into 3 major components.

The first component is the development of the image processing software tool that can assess bone quality by extracting BMD. The software application must feature a graphical user interface (GUI) that a user can interact with to upload DICOM images of the CT scan, which can then be analyzed to output the bone mineral density of each vertebrae.

The second component is the finite element analysis of the bone. Using a 3D model of the vertebra, two pedicle screws are inserted into the vertebra, and a series of pull out tests are conducted across different vertebrae to establish whether there is a correlation between the BMD results of the former image processing component. This component is separated from the software application as it does not functionally provide any output that is particularly useful to the application. Rather, its objective is to determine how well the image processing algorithm is at extracting an accurate BMD assessment.

The final major component is the segmentation of the vertebrae. The segmentation component is responsible for segmenting the bone directly from the CT scan from other components such as soft tissue. This segmentation is what is able to drive the software application with the segmented dataframe, as well as provide the FEA component with the 3D model of the vertebrae to perform the analysis.

The three separately established objectives work in conjunction to service the main goal of having a tool that can accurately predict bone quality using image processing techniques.

Theory

Segmentation

In order to extract the orthotropic mechanical properties of the vertebral bone, one slice of the axial view of the spine from a CT scan must be selected and the vertebral bone must be segmented from the surrounding soft tissue. Fig. 1 shows the axial view of the selected slice of the CT scan, and Fig 2 displays the corresponding segmentation of the vertebrae in the slice shown in Fig 1. The segmentation can be performed using a combination of image processing techniques such as thresholding, dilation and erosion, and contour detection.

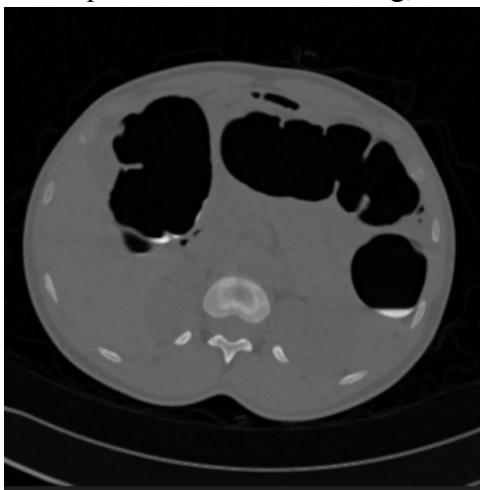


Fig. 1. Grayscale CT scan axial view

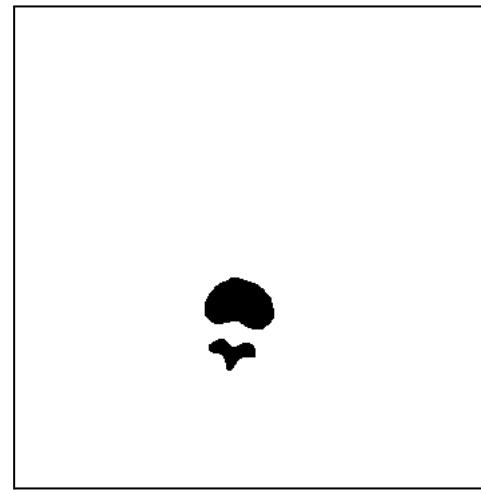


Fig. 2. Segmented vertebrae from CT scan in Fig.1.

Thresholding

Thresholding is a simple image segmentation technique where each pixel in a grayscale image is replaced with a white pixel if the image intensity I_{ij} is less than the set thresholding value T [5]. Fig. 3. shows a histogram of an image with the threshold point, where all intensity values to the left of the red line would be removed from the image. Thresholding can be applied to the axial view of the grayscale CT scan above, as the area that represents the bone is a lighter pixel intensity than the area that represents soft tissue. Using a histogram of the CT image, a reasonable threshold value can be selected to threshold out the soft tissue, therefore segmenting the spine.

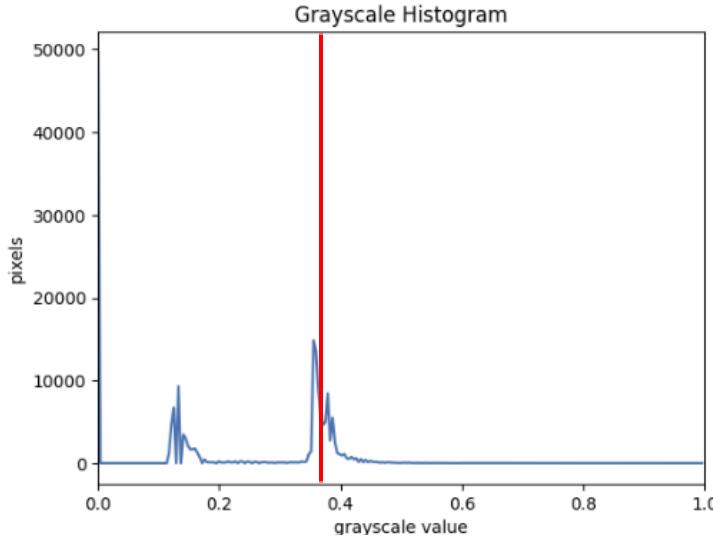


Fig. 3. Grayscale histogram of CT scan from Fig. x1 with its threshold point

Contour Detection

The contours of a binary image are curves joining all of the continuous points that share the same color or intensity [6]. The result of finding all of the contours of a binary image can result in a mask of a segmented area, which can then be applied back to the original image. An example of this process is shown below in Fig. 5. After applying a threshold to an image, some of the weaker lines on regions of interest can form holes, which will impact the contour detection. Performing dilation and erosion on the binary image can help solve the problem of poor contour detection [7].

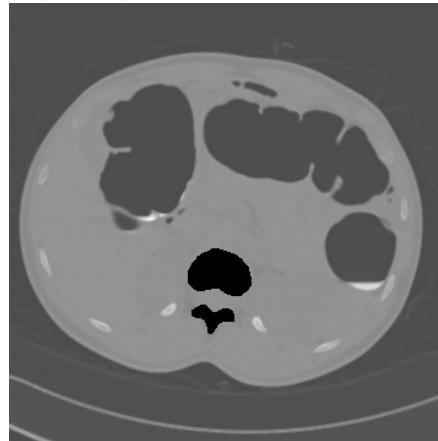


Fig 4. Contour mask of spine applied to the CT scan in Fig. 1.

Dilation and Erosion

Dilation and erosion are morphological operations, which are image processing operations that process images based on shapes [7]. Dilation is used to fill in small holes in objects, where erosion is used to remove floating pixels and thin lines in objects [7]. The effects of erosion and dilation can be seen below in Fig. 6. Dilation and erosion can be combined to perform morphological opening and closing operations. Applying erosion first and then dilation results in morphological opening, which can be used to remove small objects from an image.

without interfering with the shape and size of the larger objects in the image . Applying dilation first and then erosion results in morphological closing, which can be used to fill in small holes in an image without interfering with the shape and size of the larger objects in the image [7]. Examples of morphological opening and closing can also be seen below in Fig. 6. Applying dilation and morphological opening to the image above before detecting the contours would help improve the poorly segmented vertebrae.

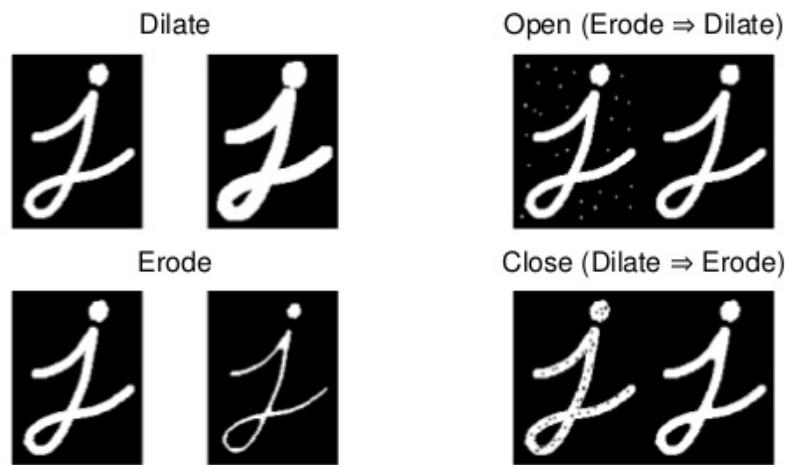


Fig. 5. Examples of dilation and erosion [7]

Orthotropic Mechanical Properties

Bone Dimensions Calculation

- **Approximation of vertebral height**

When analyzing medical imaging data such as CT scans, it is often necessary to measure the height of specific vertebrae in order to diagnose certain conditions or monitor the progression of a disease. One commonly used method for calculating vertebrae height involves multiplying the thickness of each DICOM slice by the number of slices that cover the height of the vertebrae.

DICOM, or Digital Imaging and Communications in Medicine, is a standard format used for storing and transmitting medical images. Each DICOM slice corresponds to a specific cross-section of the body, and the thickness of each slice is typically measured in millimeters.

To calculate the height of a vertebrae using this method, one would first identify the range of slices that contain the vertebrae of interest. Then, the thickness of each slice in that range is multiplied by the number of slices, and the resulting values are summed to obtain the total height of the vertebrae.

It is important to note that this method assumes that the vertebrae are evenly spaced and that the slice thickness is consistent throughout the scan. In reality, the actual height of the vertebrae may vary slightly due to differences in spinal curvature or compression, and the slice thickness may also vary depending on the imaging protocol used. Therefore, this method should be used with caution and in conjunction with other diagnostic tools to ensure accurate measurements.

- **Vertebral axial area**

Each DICOM image is made up of a grid of pixels, with each pixel representing a small area of tissue. The pixel spacing refers to the distance between adjacent pixels, typically measured in millimeters. The contour of the vertebral body is traced using OpenCV, a real-time optimized Computer Vision library, then returns the contour area in terms of number of pixels.

Finally, the contour area is multiplied by the pixel spacing provided in the DICOM files to obtain the vertebral axial area in square millimeters. This accounts for the fact that each pixel represents a specific area of tissue and allows for more accurate measurements.

- **Vertebral volume estimation**

To estimate the vertebral volume, one would first calculate the axial area of the vertebral body and the height as described above. Then, the vertebral height is multiplied by the axial area to obtain the vertebral volume in cubic millimeters.

Bone Mass Density (BMD) Calculation

Bone mineral density (BMD) is frequently used to diagnose osteoporosis, determine which individuals are at risk for therapy, and track how each patient responds to that medication. In clinical studies of osteoporosis treatments, it is frequently employed as a substitute for an actual measure of effectiveness. Consequently, a method for measuring bone mass density (BMD) on the CT images is proposed in this stage.

Bone mineral density (*BMD*) in medicine is measured in g/cm^2 is the mineral mass of the bone per unit image area. However, it is assumed in this study that the *BMD* on each pixel represents the image's intensity. Then each intensity value is adjusted to fall within a point range of constants $\{a, b, c, d, e\}$ in order to compute the *BMD* on the CT image. The measurement of Bone mineral density (*BMD*) is defined as equation

$$\rho = BMD = \frac{BMC}{Area}$$

Where

BMD: bone mineral density in g/cm^2

BMC: sum of pixel (or Hounsfield units) intensity in the image

Area: sum of intensity in each vertebral poses

Criteria for change the intensity in the image to point of *BMC* is defined as equation

$$BMC(x) = \begin{cases} a & \text{if } 1 \leq x \leq 50 \\ b & \text{if } 51 \leq x \leq 100 \\ c & \text{if } 101 \leq x \leq 150 \\ d & \text{if } 151 \leq x \leq 200 \\ e & \text{if } 201 \leq x \leq 255 \end{cases}$$

Where x is intensity of image and a, b, c, d, e, f are constants (experimentally derived parameters).

Alternatively, various studies have found that the voxel-specific CT attenuation values is linearly proportional to the apparent density given by the general equation

$$\rho_{app} = \alpha HU + \beta$$

Where

ρ_{app} : bone density in g/cm^3

HU : CT attenuation values

α, β : experimentally derived parameters

Elastic Modulus Calculation

The biomechanical behavior of bone structures is extensively studied using the finite element (FE) method. While computed tomography (CT) scanning is frequently used to get material and morphological data about bone samples. Therefore, providing CT images, numerous studies have proposed various density-elasticity relationships in order to estimate the bone elastic constants, assuming that the density and elasticity of bone are correlated. In general form, the elastic modulus is found using the power equation

$$E = \alpha \rho_{app}^{\beta}$$

Where

E : elastic modulus

ρ : bone density

α, β : experimentally derived parameters

Since the apparent density is found linearly related to the CT attenuation values, the equation calculating elastic modulus can be written as

$$E = \alpha(HU)^{\beta}$$

FEM Validation

The purpose of FEM validation is to observe the response of a system to various physical conditions as opposed to computing direct values of a specific property. In the case of this validation, the FEM analysis will study the response of the system to a pedicle screw pull-out as well as a load-displacement test. The peak of the load-displacement curve can yield the pull-out strength of the bone. The pull-out force is defined as the point at which force decreases with increasing displacement [8].

Any finite element analysis will require 2 major components. The first component is the 3D model of the subject (bone model and segmentation covered above) and the second is the mesh. Meshing is performed in order to transform a model into a refined amalgamation of tiny components that are individually analyzed to obtain the force or displacement where one of the two variables are known. The relation is given in Fig.8 below.

$$K_{ij}u_j = f_i \quad \text{or} \quad \mathbf{Ku} = \mathbf{f}$$

$$\begin{bmatrix} K_{11} & K_{12} & \cdots & K_{1n} \\ K_{21} & K_{22} & \cdots & K_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ K_{n1} & K_{n2} & \cdots & K_{nn} \end{bmatrix} \begin{Bmatrix} u_1 \\ u_2 \\ \vdots \\ u_n \end{Bmatrix} = \begin{Bmatrix} f_1 \\ f_2 \\ \vdots \\ f_n \end{Bmatrix}$$

Fig.6. The nonlinear algebraic equation that FEA attempts to solve. Where f is the force applied to node i , u is the displacement with the force f and k is the stiffness matrix

In other words, meshing divides an object into numerous elements, with each node of the element having the force applied with the material properties defined by the stiffness matrix in order to obtain the displacement.. Due to the complex geometry of the pedicle screw, the pedicle screw is meshed into 10-node tetrahedral elements. However, the material-mapped meshing of the bone will be done through a software known as Bonemat as per another study [9] in order to obtain an accurate mesh with mapped material properties. Bonemat will require the density-elasticity relationship and a simple input mesh in order to map properties across the tetrahedral mesh.

The material properties of the bone are obtained based on literature that established Density-Elasticity based relations for the vertebral bone (which is needed by Bonemat to create the mesh) . These relations are given in Fig. 8 below [9].

$$\rho_{QCT} = \rho_{Ash} = \rho_{App} \times 0.6 \left(\frac{g}{cm^3} \right).$$

$$E_{bone} = 4730 \rho_{APP}^{1.56}$$

Fig. 7. A list of the mapping relations for the various material properties.

The pullout test shall adopt a procedure in which the inferior surface of the vertebrae is fixed, and a force perpendicular is applied to the head of the screw to measure pullout strength. The loading and boundary conditions utilized in a pull out test study to determine spinal screw loosening is given in Fig. 9, and the same conditions are adopted for this design as well - a fixed inferior surface with axial pullout.

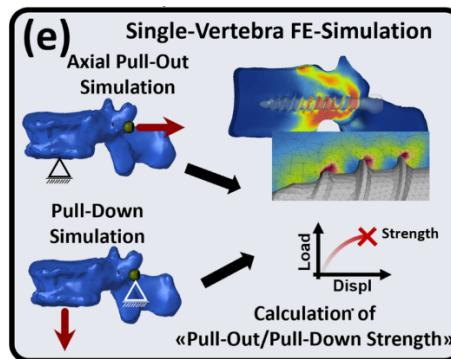


Fig. 8. : The pull out boundary and loading conditions adopted for this design from a different study [10].

Design

Overall Application Design

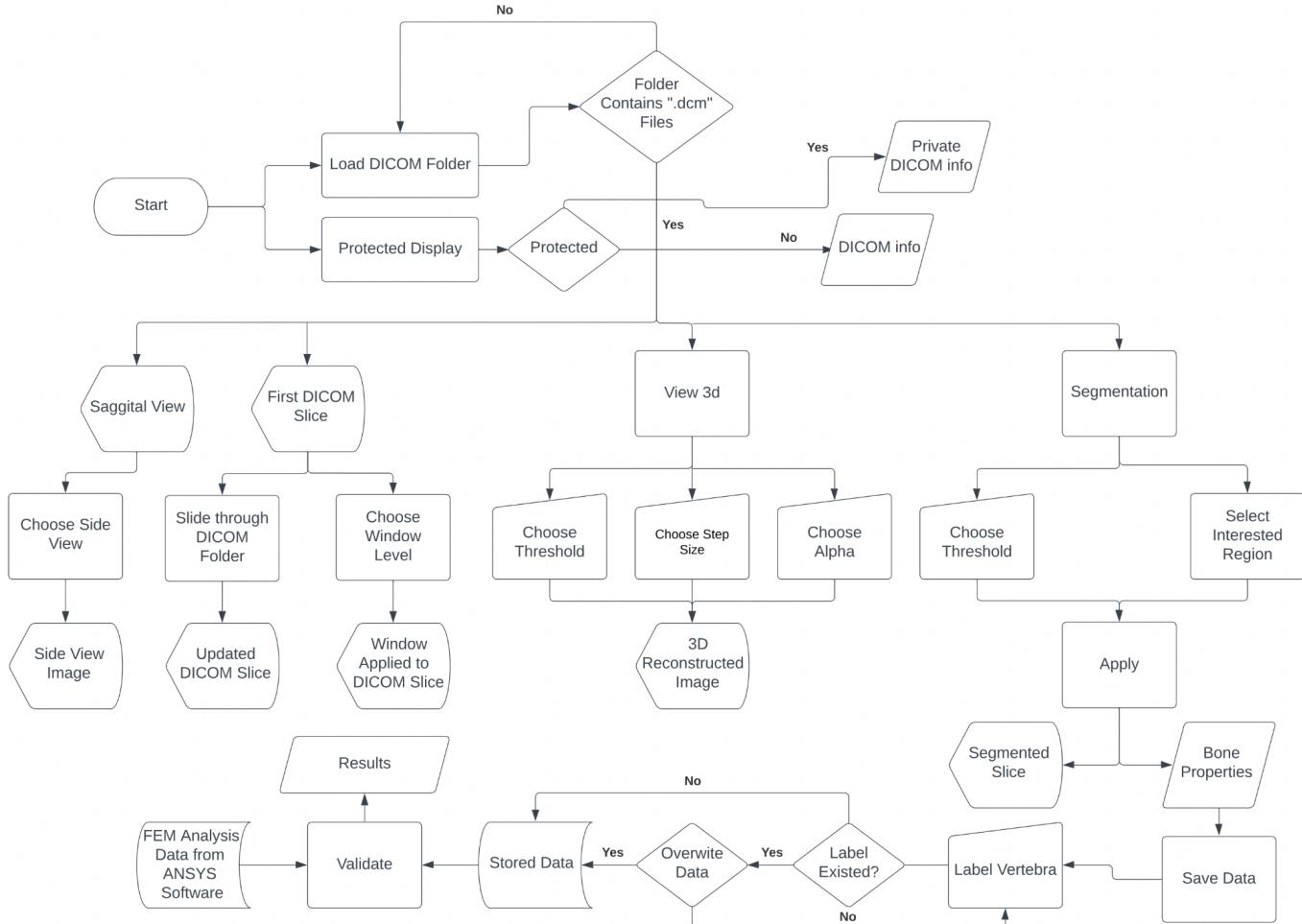


Fig.9. A flowchart of the software application's sequence

The full application design flow chart is shown above in Fig. 10. Each of the individual subsystems will be integrated through a user interface. When a user starts the application, they will be prompted to load a folder with DICOM files, and if the files are valid, information about the DICOM scan and a preview of the scan will appear. If a user wishes to hide personal information associated with a DICOM scan, they can check the 'Protected Display' option, which will load the DICOM scan without displaying private information associated with the scan. Once the system processes the DICOM folder, two windows will appear, one displaying the sagittal view of the scan, and the other displaying the first slice of the scan from the axial view. A slider will be present underneath the preview, which will allow the user to view each slice. Additionally, the user will have the option to filter out bone or soft tissue in the preview, to help them find the optimal slice to use for the BMD analysis. Once a slice has been selected, the user can select the 'Segmentation' option, where they will be able to select the region of the scan they wish to segment, as well as select a threshold value which best fits their image. Applying the

selected region of interest and threshold value will yield a segmented slice as well as the bone properties of the segment. The obtained bone properties are then saved and the vertebrae is labeled. The bone properties are then correlated with the FEM analysis results to validate the precision of the computation of the properties.

Segmentation

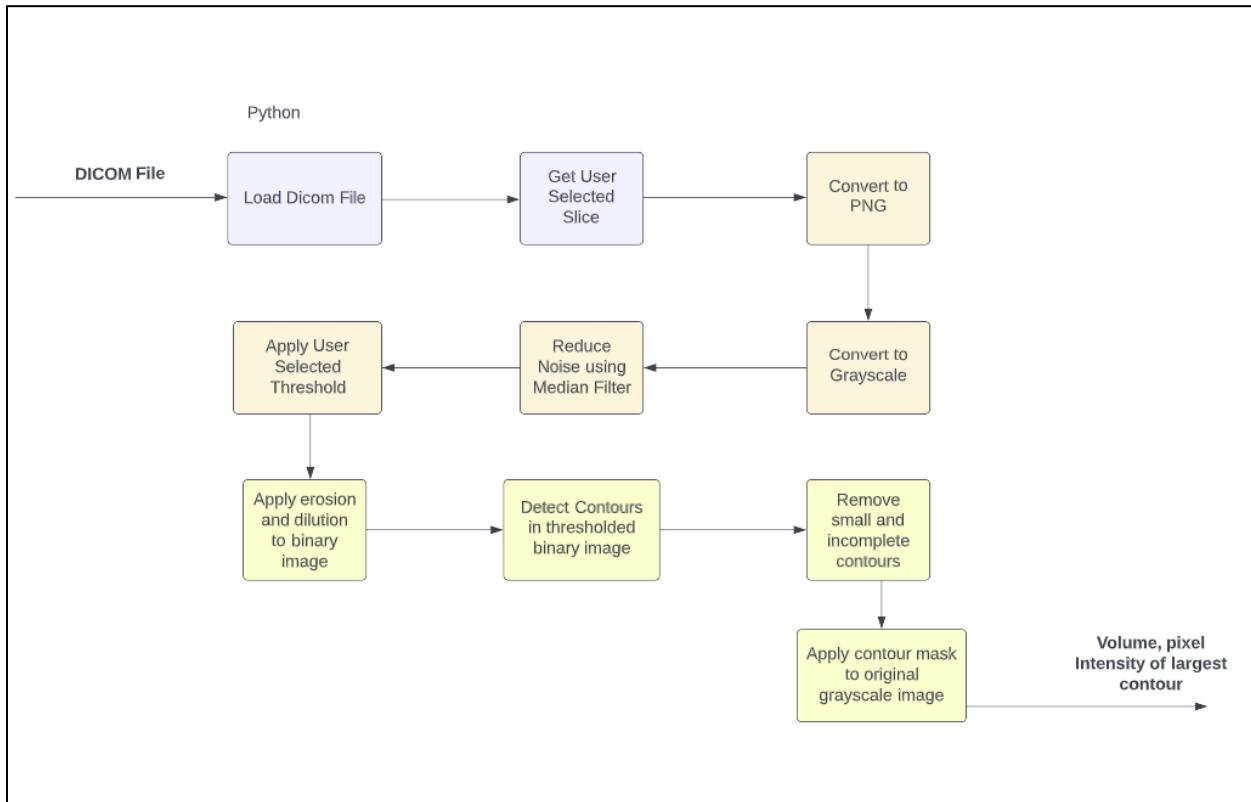


Fig.10. The block diagram of the segmentation subsystem.

With the segmentation subsystem being the first subsystem to run in the application, it must be responsible for extracting the data stored in the DICOM file, and prepare it for further processing and manipulation in future subsystems. CT images of a patient's body are stored in DICOM files, which consist of multiple slices on the axial plane, captured from top to bottom [11]. The DICOM file is loaded into the system using the Pydicom library and the desired slice is selected through a user interface. The selected slice is then converted to a PNG image in order for it to be compatible with the OpenCV Python library. OpenCV functions will be used for all of the necessary image-processing operations.

Thresholding will be used on the axial view PNG image to segment the vertebrae from the soft tissue, but before the threshold can be applied, the image must be converted to grayscale and noise must be reduced. Converting the image to grayscale before thresholding is necessary to rank the pixel intensities from strongest to lightest [5]. A median filter will be applied to the image to remove any noise, which will result in a cleaner segmentation [12]. A median filter was chosen instead of a gaussian filter due to the prominence of salt and pepper noise in various test images.

Thresholding is then applied to the grayscale image to segment the vertebrae from the soft tissue. The threshold value used is a critical factor in determining the accuracy of the segmentation results. In the past, a constant threshold value was obtained through trial and error using a test image. However, this method did not always produce the optimal segmentation, as each DICOM slice has its own optimal threshold value. To address this, the subsystem is now integrated with a user interface where the user can select the appropriate slice and threshold value to use for the segmentation process.

Once the threshold value has been selected, erosion and dilation are applied to refine the edges of the image, contours in the image are detected, unwanted contours are removed, and a mask of the contours are applied to the original grayscale image of the scan. The morphological closing method is used to fill in small holes on the edges of the vertebrae using the skimage library [7]. Contours are detected using OpenCV. Unwanted contours are removed by deleting any contours that do not have four sides or are smaller than a specified threshold [6]. The remaining contours are drawn over the original grayscale image, which acts as a mask of the segmented vertebrae. The regions of interest are added to a list, and the area and average pixel intensity of the largest region of interest is extracted.

Bone Properties Extraction Subsystem Design

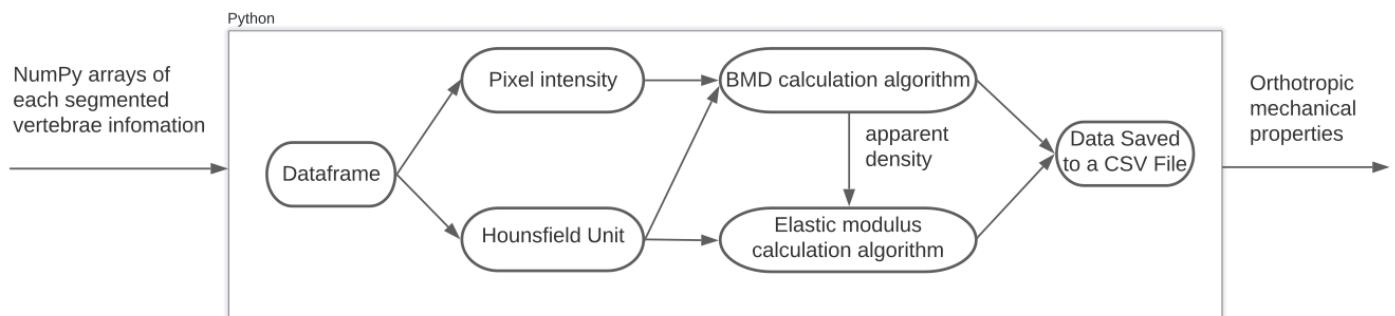


Fig.11. The block diagram of the bone property extraction subsystem.

After vertebrae are segmented and their information is converted into NumPy arrays, they are stored in a Pandas dataframe with labels (i.e. L1-L5 for lumbar vertebrae) for the simplicity of accessing data. Taking advantage of dataframe, the required data (i.e. pixel intensity, CT attenuation values, volume) can be easily organized and fed into the algorithms for bone properties calculations. For example, to obtain the L1 mechanical properties, L1 information is extracted from the dataframe by calling its label as inputs of algorithms. Additionally, those calculated values can be appended to the created dataframe and saved to a CSV file (data file). As the results, the data is stored on a local computer for future utilization as well as validation by comparing the mechanical values with the FEM validation subsystem.

FEM Validation

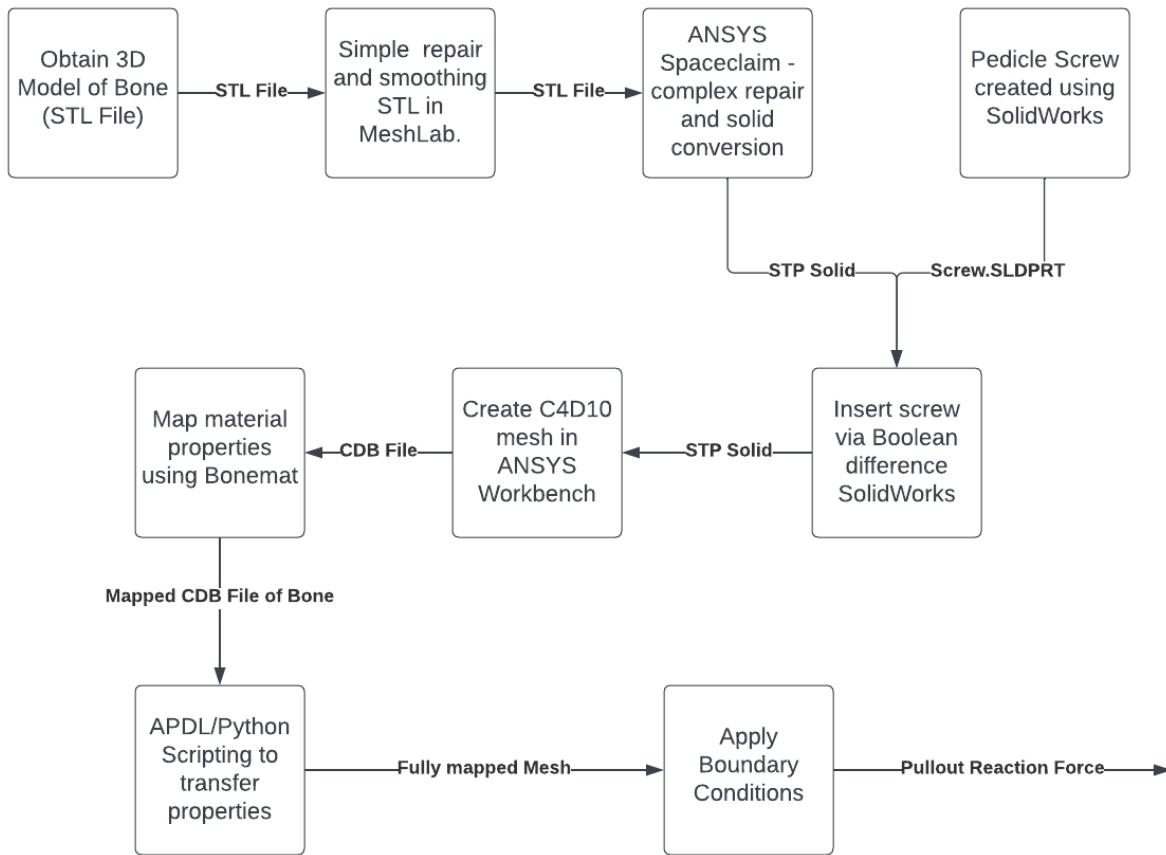


Fig.12. The block diagram of the FEM validation subsystem.

Shown above in Fig. 12. is a block diagram of the FEM validation subsystem. The process is initiated with the STL file being imported from the segmentation subsystem output created through 3D Slicer. The STL file first goes through MeshLab, where duplicated vertices and edges are first deleted, and then a laplacian smoothing with 20 steps is applied to smooth the surface [9]. This smoothed STL file is then imported into ANSYS SpaceClaim, where sharp edges, multiple STL pieces and other general STL errors are fixed. However, this process must be carefully done so as to maintain the integrity of the geometry of the vertebrae. After repairing the STL, the auto-skin feature is used to convert the STL to a solid model. Once the solid model has been constructed, it can be exported as a STP file, and then into a SolidWorks part.

For the pedicle screw pullout test, a pedicle screw will need to be constructed and ultimately inserted in SolidWorks. When selecting the size for the screw, there are normally considerations made for anatomical reasons such as proximity to the thoracic aorta at the T12 level of the vertebra. However, as the design in this project has segmented bone and does not directly assess placement, there is no particular need for such a consideration. The pedicle screw will need to be inserted into the 3D model in SolidWorks and then fixed. The insertion itself occurs using a boolean difference operation (using the assembly cavity feature in SolidWorks)

and then concentrically mating the screw with the cavity. The dimensions selected for the pedicle screw follow a study in which pullout tests were conducted with pedicle screws in order to test which sort of connections (bonded or contact) are better in increasing pullout strength (and thereby better serve the purpose of the pedicle screw). From the implementation of the mentioned study, Fig. 14 displays a general model of the screw. The simple dimensions are a 6.5mm outer diameter with a 45mm length. Better screw dimensions can be seen in **Appendix A**. Studies that are more patient specific such as the screw loosening study often provide a better screw selection as they are personalized. However, as mentioned earlier, this project is more for the validation of the image-processing tool and performing a correlation. As the same screw model is used across all tests to benchmark the force, there is little importance on screw dimension.



Fig. 13. The complete model of the screw utilized [13]

The bone model (with the screw) must then be converted into a mesh for further analysis. Due to the shape that bones naturally are, the mesh selected is a 10-node quadratic tetrahedral mesh to give more refined results. The standard procedure at this stage is to take the simplified mesh and convert it into a mesh with mapped material properties utilizing density-elasticity relationships to map the material properties. The standard tool used is Mimics [14], however, as Mimics is not a freeware piece of software, Bonemat is used. This general workflow is depicted in Fig. 15. The section of the mesh that is created in ANSYS Workbench which contains only the bone is exported as a .cdb file, and then imported and manually positioned using the transform operation in Bonemat to place the mesh model onto the DICOM CT scan. It is important to note that due to computing resource limitations, Bonemat used a gap value of 250. A gap value translates into limiting the number of different material properties created. Suppose two elements A and B have a difference in their Young's Modulus by a value of 250, Bonemat will simply ignore one, and treat them as having the same material property. In an ideal scenario where higher computational power is available, a gap value of 0-50 would be used for more accurate results [15].

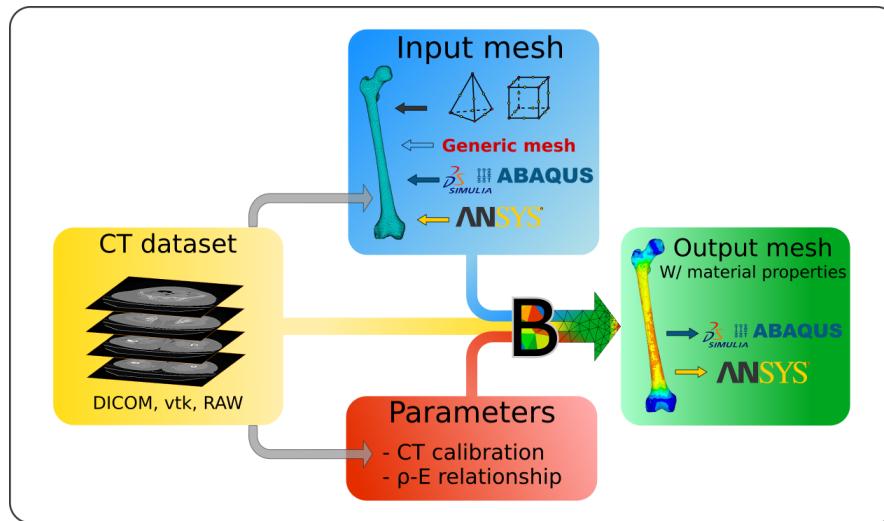


Fig.14. A diagram of the Bonemat workflow [15]

At this stage we have the meshed, material-property mapped pedicle screw inserted vertebrae model. However, due to the fact that there are screws in the original mesh, the Python script shown in **Appendix B** is utilized to create an APDL script that will take the mapped elements of the bone-only mesh, and apply them onto the mesh of the entire bone-screw mesh. This model will undergo a finite element analysis - specifically a structural analysis with a force displacement analysis. The FEM solver selected in this instance is ANSYS - which is an unorthodox selection as compared to other studies that used ABAQUS for FEM Analysis [14]. ANSYS was instead chosen for this implementation due to the wide range of tutorials available and the beginner friendly interface. With the mesh and model inputs being completed, the FEA can be conducted. As per the partial specifications, a pullout test on the pedicle screw will be conducted in order to evaluate the quality of the bone based on the pull-out strength that is obtained. These pull-out tests can then be correlated with the BMD values in order to validate the accuracy of the BMD calculation through the image processing stage. If there is a high correlation, then the image processing analysis can be deemed as a valid method of evaluation of bone quality.

Alternative Designs

Segmentation

One alternative design approach for segmenting the bone from soft tissue is region-based segmentation, which involves growing regions in the DICOM image based on intensity values, and selecting the regions with pixel intensities that correspond to bone [16]. Region-based segmentation can also be implemented using the OpenCV Python library.

Region-based segmentation is less sensitive to noise than threshold-based segmentation and results in a cleaner segmentation when there is a significant difference in the pixel intensity values of each region, so it could result in a better segmentation depending on the quality of the CT scan [16].

However, using region-based segmentation can potentially result in a less accurate segmentation compared to threshold-based methods, since the pixel intensity levels of soft tissue and bone can overlap in some DICOM images, in which the regions would merge both the bone and soft tissue sections [16]. In the threshold-based method used, the user is able to choose their own threshold value, eliminating the possibility of merging regions.

Orthotropic Properties

One potential approach for extracting orthotropic properties from bone structures is to use a convolutional neural network (CNN) model, which is a powerful deep learning technique for pattern recognition and feature extraction. CT scans provide detailed images of the bone structure that enable the CNN to learn the patterns and relationships in these images and make accurate predictions of bone mineral density (BMD).

However, using deep learning for BMD prediction comes with certain challenges. One of the main challenges is the need for large amounts of labeled data, as deep learning algorithms require extensive datasets to learn patterns and generalize well to new data. Collecting and annotating a large dataset of CT scans with BMD measurements can be time-consuming and resource-intensive.

Additionally, the interpretability of deep learning models can be a challenge. It can be difficult to understand how a deep learning model arrives at a particular prediction, which is crucial for clinical decision-making.

Therefore, while deep learning is a promising approach for extracting orthotropic properties, it is important to consider the challenges associated with data availability and model interpretability. Balancing the benefits of using deep learning for accurate BMD prediction with the challenges of data collection and model interpretability is important for successful application in clinical settings.

Finite Element Analysis

In terms of procedure, there are few other methods that may be used. A large problem is in attempting to have various file formats work together. In theory, the easiest way to do things is through skipping the entire STL workflow. 3D Slicer can instead directly create a mesh of the model, and this can be exported as a .vtk file [17]. The issue with .vtk files is their lack of support. It is hard to get programs such as BoneMat or commercial FEA solvers such as ANSYS

to work with .vtk files. The only viable option for .vtk file based FEA is another FEA solver known as FEBio [18]. FEBio is an option that can work for regular biomechanical analysis of a sole bone model. However, for this project's use case of utilizing pedicle screws, it becomes difficult and involves using unorthodox contact methods such as elastic-tied contact (which is incorrect for a pedicle screw). If the project had instead involved a compression test as seen in [14], then the mentioned workflow would have been viable. However, there are little to no literary reviews on usage of FEBio, and as such, it was not fully explored. A variety of other literary sources indicate a design process similar to the one described in the *Design* section of this project [9][19].

Aside from procedural differences, there are different pieces of software that can be used. SolidWorks can be substituted by Fusion360, AutoDesk and any other major solid CAD software in order to perform the boolean operation between the bone model and the screw(s). Various studies also adopt ABAQUS as the FEA solver, as well as a different software used for the actual material mapping of the properties [9]. Mimics and Simpleware ScanIP are two pieces of software that are commercial solutions to material property mapping. Adopting these pieces of software may have been easier to work with as they are commercial solutions, however, they are not freeware software as BoneMat is.

Overall, there were a wide range of options for alternative solutions that were considered for the purpose of this project. However, many of the design choices implemented in this project were chosen for a particular reason with careful engineering analysis.

Material/Component list

This project was able to leverage . Any commercial-license software used such as Solidworks and ANSYS were provided by the Toronto Metropolitan University's Mechanical and Industrial Engineering department. Therefore, there was no overall cost incurred in the completion of this project.

| Software |
|------------------|
| 3DSlicer |
| SolidWorks |
| ANSYS SpaceClaim |
| ANSYS WorkBench |
| ANSYS Mechanical |
| BoneMat v3.2 |
| MeshLab |

The final software product (VertScan) is a Python-based software application that typically requires a set of components and materials to function correctly. Here is a list of some essential components and materials used in this project:

1. Python interpreter: Python version 3.x.
2. Integrated Development Environment (IDE): Visual Studio Code (VScode)
3. Libraries and Modules:
 - numpy==1.24.1
 - matplotlib==3.6.3
 - opencv-python==4.7.0.68
 - pydicom==2.3.1
 - pillow==9.4.0
 - imutils==0.5.4
 - scipy==1.10.0
 - scikit-image==0.19.3
 - glob2==0.7
4. Version Control System (VCS): Git was used for managing source code, tracking changes, and collaborating with others.

Measurement and Testing Procedures

As the software tool itself does not implement any network based operations such as utilizing HTTP requests or cloud based services, the performance of the software does not have much to consider in terms of scalability. As it is a desktop application, an executable simply can be created and distributed to users. Furthermore, since it is a Python-native application, the program is able to execute on both MacOS systems as well as Windows. Therefore, for testing *VertScan* for software functionality, simple manual testing was conducted on the GUI to ensure that the application performs as expected.

As mentioned, the FEM analysis is what is responsible for validating the information produced by *VertScan*. This analysis in itself is a testing procedure. For each vertebrae, it is expected that two values are produced. A left screw pullout strength value as well as a right screw pullout strength value (in Newtons). By taking the strength values of each respective side, a correlation between the BMD value and the pullout strength can be determined. The basic principle is that if a higher BMD value is produced by *VertScan*, then the pullout strength should be a relatively larger force. Conversely, if the BMD value is a lower value, then the pullout strength should be a relatively smaller force. If the results are strongly correlated, then it indicates that the tool works as expected. Another methodology through which the results can be quantitatively verified is through referencing literature. The table below depicts some of the pullout strength values that may be used as a benchmark [20].

| | Overall | Normal BMD | Osteoporotic | P† |
|-------------|-------------|-------------|--------------|------|
| Control | 742 ± 320 N | 781 ± 378 N | 719 ± 291 N | 0.65 |
| Reinsertion | 732 ± 307 N | 793 ± 336 N | 698 ± 293 N | 0.44 |
| P* | 0.78 | 0.85 | 0.61 | |

Fig. 15. A list of pullout strengths across different bone [20]

Performance Measurement Results

- **DICOM preview**

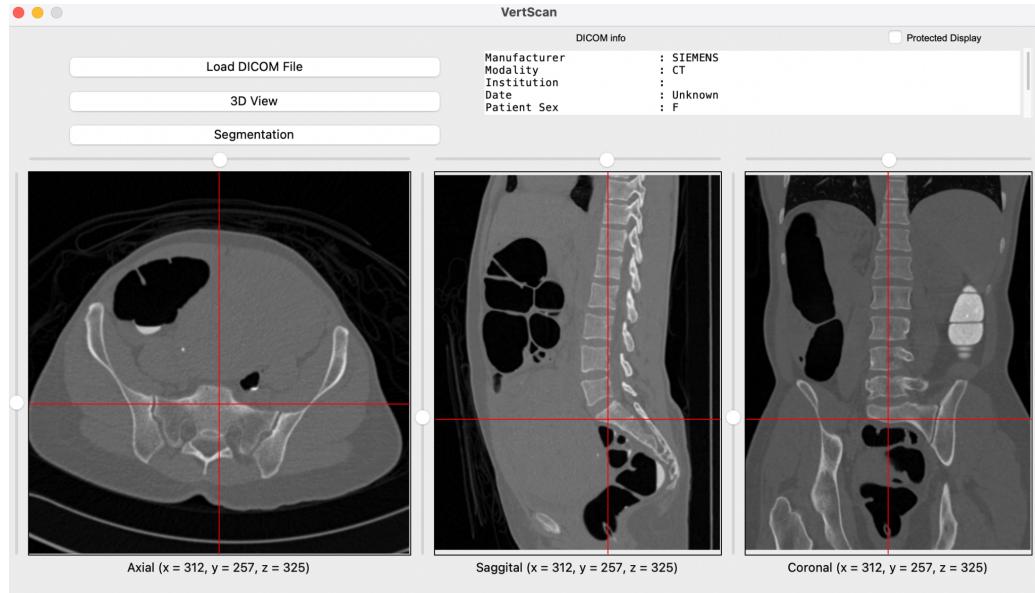


Fig. 16. Preview DICOM slices in different planes

The *VertScan* software provides an intuitive user interface that enables users to load DICOM files, view DICOM information, and display DICOM slices in the axial, sagittal, and coronal planes. The preview simulation also allows users to slide through the entire DICOM slices simultaneously in different planes and show the coordinates (x, y and z) of the current images to gain a comprehensive understanding of the anatomy and pathology being studied.

- **3D view**

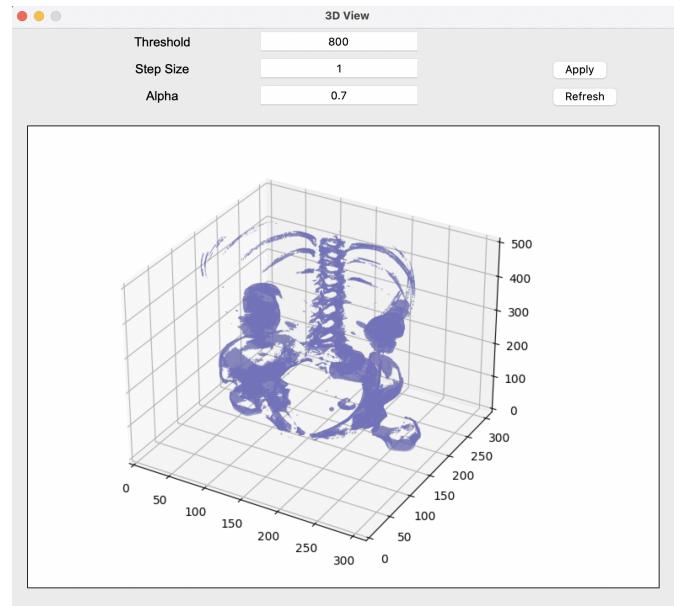


Fig. 17. 3D reconstruction from DICOM slices

The 3D view tool in the software application supports the creation of a three-dimensional model of an object or anatomy using medical images in the DICOM file format. The process involves extracting information from a series of 2D images, usually obtained through CT scans, and reconstructing them into a 3D model. This technique allows medical professionals to visualize internal structures and organs in a more comprehensive and accurate manner.

- **Segmentation and properties extraction**

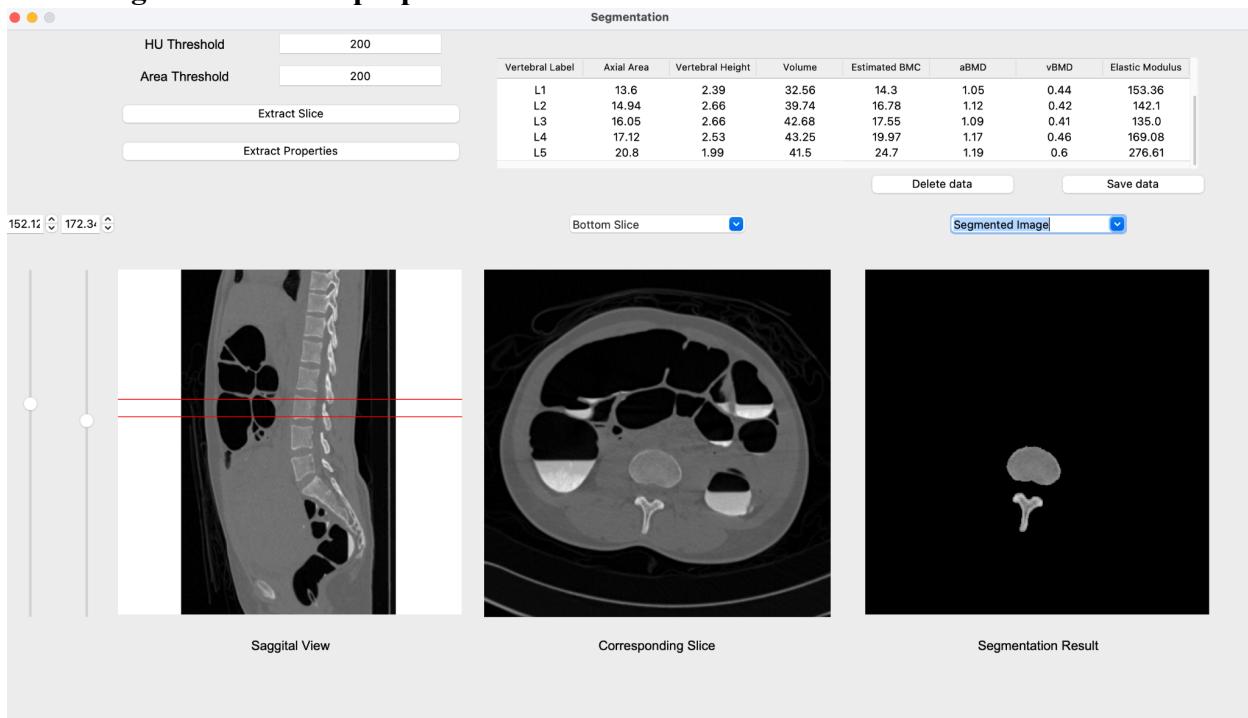


Fig. 18. Segmentation and properties extraction

The segmentation and properties extraction features are the backbone of our innovative software application that provides valuable insights to surgeons on the severity of osteoporosis in each vertebra of the spine. These features offer a comprehensive analysis of the vertebral body, enabling clinicians to make informed decisions for their patients. Specifically, users can easily select specific vertebrae on a sagittal image and extract the corresponding slice for segmenting the vertebral body. This process is fast, accurate, and significantly reduces the time required for manual segmentation. Furthermore, our software employs state-of-the-art algorithms that guarantee high precision in obtaining the properties of the vertebrae.

- CAD Modelling

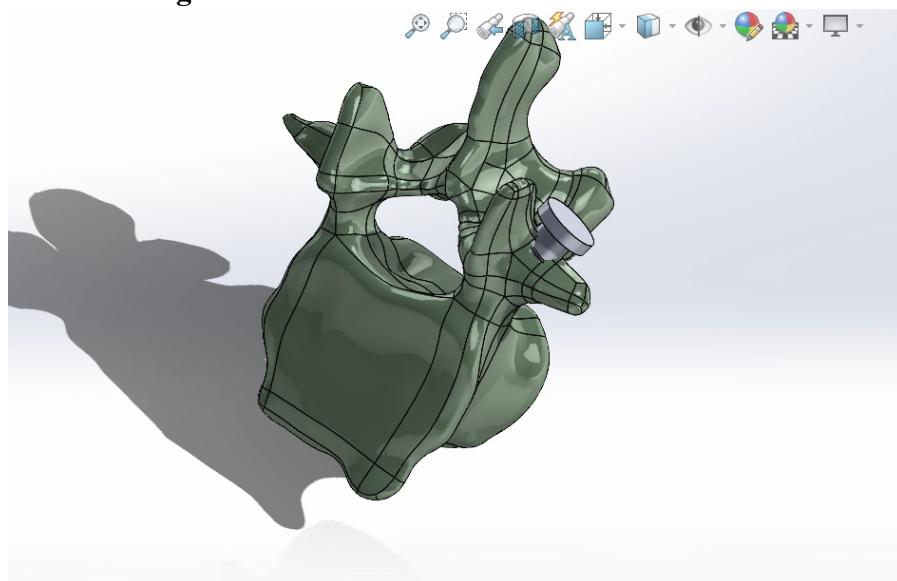


Fig. 19. A depiction of the CAD model of the pedicle screw inserted vertebrae

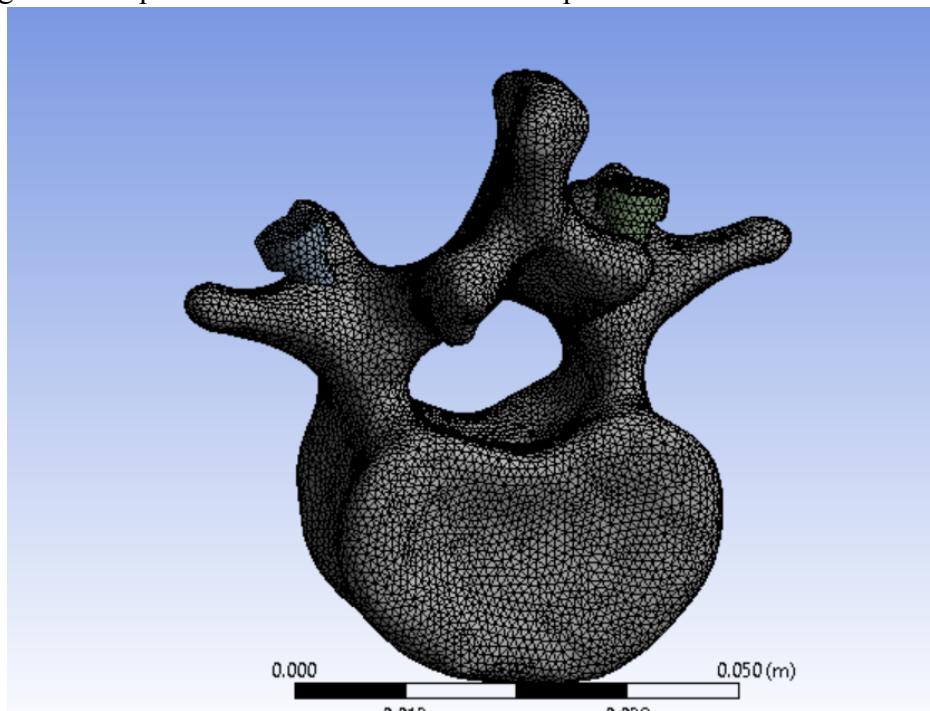


Fig. 20. The overall meshed model - where each element used a meshing size of 0.001m and quadratic tetrahedral elements

The image shown above is that of the STL repaired bone model (using SpaceClaim's auto-skin feature). This bone model is then meshed in ANSYS Workbench as shown in Fig.20 and exported as a .cdb file.

- Material Property Mapping

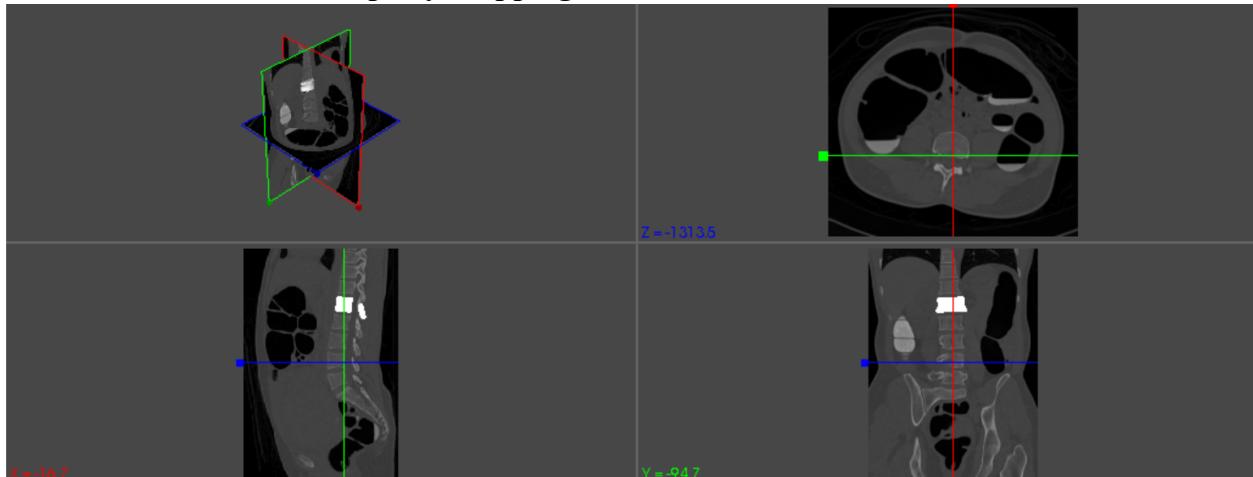


Fig.21. Bonemat's detection of the finite element model on the CT rectilinear grid

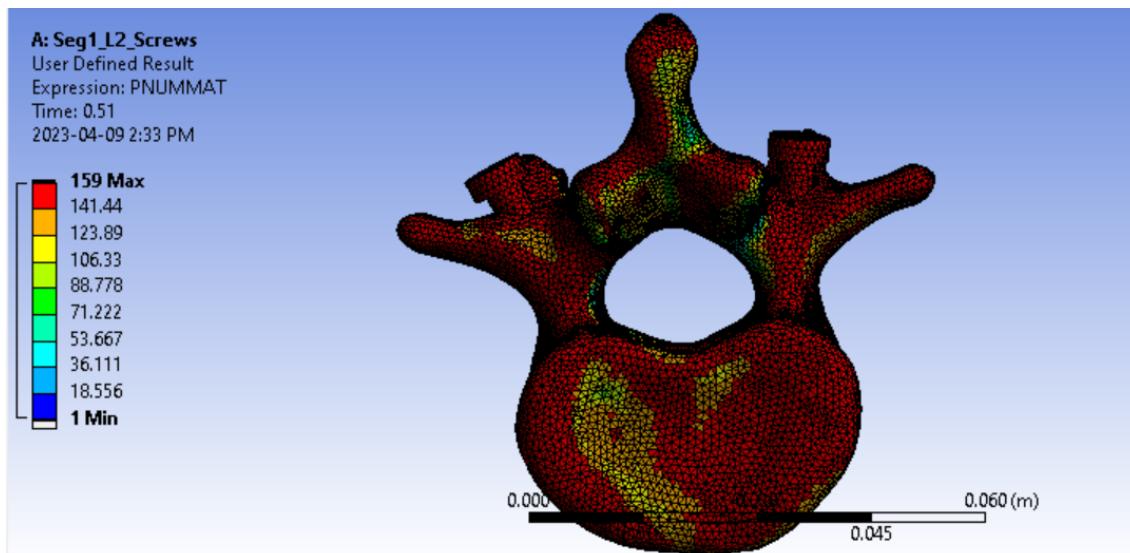


Fig.22. Bonemat mapped 159 different materials based on a gap value of 250

Bonemat produces the material-mapped mesh as shown above in Fig.22 after the application of the Bonemat operation seen in Fig.21. This mapping leads to 159 different materials. The mapping from Bonemat is applied back onto the Bone using the Python script shown in **Appendix B**. At this stage, it is ready for applying the FEA conditions.

- Finite element analysis

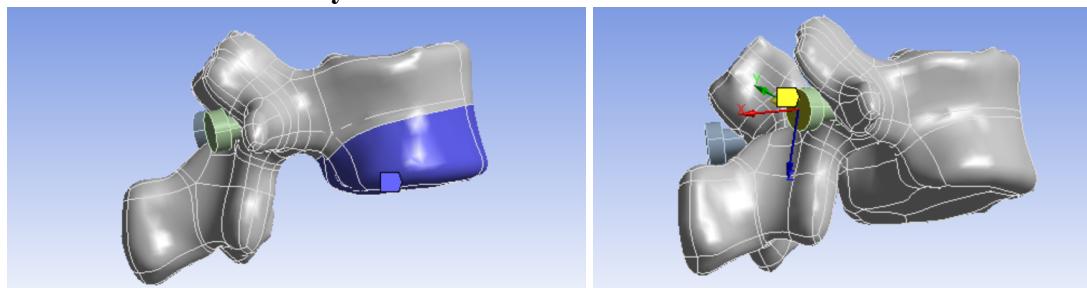


Fig.23. The boundary and load conditions exercised for the analysis

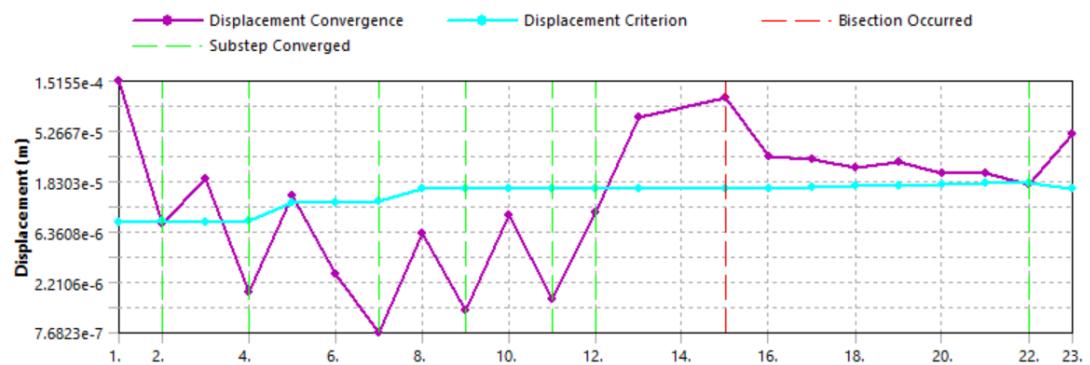


Fig.24. The displacement convergence graph which depicts the pullout.

The boundary conditions are shown in the left image in Fig.23 while the loading condition is shown in the right image in Fig.23. It can be seen that the boundary condition is a fixing of the inferior surface, while the load is a displacement load of 3mm applied to the head of the screw.

A depiction of the displacement progress graph is shown above in Fig.24. Unfortunately, the simulation did not converge, and as a result, quantitative data could not be obtained that would be able to provide verification. The purple line shown above should fall beneath the blue line, and there should be a point at which the values coincide, and the displacement intended should occur. As this process could not be completed, the FEM process failed to yield pullout strength data.

Analysis of Performance

| Vertebral Label | Axial Area | Vertebral Height | Volume | Estimated BMC | aBMD | vBMD | Elastic Modulus |
|-----------------|------------|------------------|--------|---------------|------|------|-----------------|
| T10 | 11.1 | 1.99 | 22.14 | 14.29 | 1.29 | 0.65 | 323.87 |
| T11 | 12.03 | 2.13 | 25.6 | 14.85 | 1.23 | 0.58 | 263.0 |
| T12 | 12.4 | 2.26 | 28.04 | 14.49 | 1.17 | 0.52 | 210.3 |
| L1 | 13.6 | 2.39 | 32.56 | 14.3 | 1.05 | 0.44 | 153.36 |
| L2 | 14.94 | 2.66 | 39.74 | 16.78 | 1.12 | 0.42 | 142.1 |
| L3 | 16.05 | 2.66 | 42.68 | 17.55 | 1.09 | 0.41 | 135.0 |
| L4 | 17.12 | 2.53 | 43.25 | 19.97 | 1.17 | 0.46 | 169.08 |
| L5 | 20.8 | 1.99 | 41.5 | 24.7 | 1.19 | 0.6 | 276.61 |

Table. 1. Vertebral properties obtained from the software

The table presents a set of measurements for various vertebral segments, including T10 to L5. We can perform statistical analysis on the data to explore patterns, relationships, and differences among the variables.

Variable pairs correlation coefficient are

- Axial Area - Volume = 0.94
- Axial Area - Estimated BMC = 0.82
- Axial Area - vBMD = 0.46
- Estimated BMC - aBMD = 0.89
- Estimated BMC - Elastic Modulus = 0.82

These results suggest strong positive correlations between Axial Area and Volume, Estimated BMC, and aBMD, indicating that larger vertebral segments tend to have more bone mineral content and density. There is a moderate positive correlation between Axial Area and vBMD, indicating that larger segments tend to have higher volumetric bone mineral density. Finally, there is a strong positive correlation between Estimated BMC and Elastic Modulus, indicating that segments with more bone mineral content tend to be stiffer.

We can compare the means of the variables between different vertebral segments to test for significant differences. For example, we can use an ANOVA or t-test to compare the means of Elastic Modulus between the thoracic (T10-T12) and lumbar (L1-L5) segments. The result shows a significant difference in Elastic Modulus between the two groups ($F(1, 5) = 13.28, p = 0.013$), with the lumbar segments having a higher mean Elastic Modulus than the thoracic segments. This suggests that the lumbar segments may be more resistant to compression and shear forces than the thoracic segments.

Overall, the table provides a detailed quantitative analysis of the geometrical and biomechanical properties of the vertebral segments, which can be useful for understanding the factors that contribute to vertebral health and stability. The measurements provide insight values

to predict the risk of fractures or to evaluate the efficacy of interventions to prevent or treat osteoporosis.

Conclusions

Overall, the undertaking of this project has led to the development of a software image processing tool that has the potential to obtain information on properties such as the BMD and elastic modulus with an intuitive user interface. This project employed the usage of segmentation of the vertebral bone, image processing in Python and finite element methods. In terms of initial objectives for the software tool's capabilities, there aren't any deviations from the initial objectives.

There were some difficulties in the initial design as the specifics of the implementation for this project were not easily understood or available. There was a large amount of research and prototyping in the design process to create the final end product that has been produced.

As aforementioned in the report, the FEM portion was inconclusive in producing quantitative results. This is largely due to a large amount of time being spent on unfamiliar topics such as CAD modeling, using STL repair tools, usage of highly niche software such as Bonemat and overall, working with a topic that is in a different domain. Had more time been available, the final step of getting results to converge would have been completed as the load settings could have been optimized. It is important to note that the finite element modeled here takes roughly 2-3 hours per iteration. Therefore, having greater computing resources would be a factor that would allow for much faster and efficient testing. Regardless, a sound methodology has been proposed in great detail that could be replicated to obtain results that can provide a conclusive output.

Aside from completing the FEM aspect, the application in the future can benefit from deployment to a platform that is more accessible such as a cloud platform. Additionally, the tool can be extended to allow for real-time visualization and interaction with the segmented 3D model, providing the user with more control and flexibility. Finally, the software can be integrated with electronic health records to enable easy tracking of changes in bone health over time, as well as to facilitate data sharing and collaboration among healthcare professionals and researchers. These future extensions can enhance the capabilities of the software image processing tool, making it an even more valuable resource for assessing bone health and improving patient care.

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Appendices

*Citation 21 provides the source of the Dicom images that are used in this study

Appendix A: Derived parameters

- Mapping between pixel intensities in the image to bone mineral content (BMC)

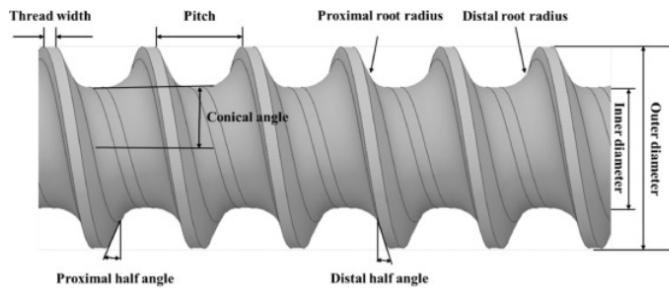
$$BMC(x) = \begin{cases} 0.0026 & \text{if } 1 \leq x \leq 50 \\ 0.0048 & \text{if } 51 \leq x \leq 100 \\ 0.0061 & \text{if } 101 \leq x \leq 150 \\ 0.0076 & \text{if } 151 \leq x \leq 200 \\ 0.0093 & \text{if } 201 \leq x \leq 255 \end{cases}$$

- Elastic modulus equation

$$E = 757\rho_{app}^{1.94}$$

Appendix B : Screw Dimensions

| | |
|----------------------------|-----------|
| Thread-shank junction | Deep step |
| Pitch (mm) | 2.8 |
| Proximal root radius (mm) | 0.8 |
| Distal root radius (mm) | 1.2 |
| Proximal half angle (deg.) | 14 |
| Distal half angle (deg.) | 25 |
| Thread width (mm) | 0.2 |



[10104399Citation]

Appendix C : Python Script for Material Mapping

```
import os
#create new file with materials and ADPL material change commands
materialsTxt = open('MaterialDataAPDLInput.txt', 'w+')
#Bonemat CDB File
inputCDB = open('MappedSeg1L2Gap150.cdb', 'r')

#parse lines for the material data (first loop) & the mapping of elements (second loop)
lines = inputCDB.readlines()
EBLOCKlines = []
EBLOCKflag = False

for line in lines:
    if 'MPTEMP' in line or 'MPDATA' in line:
        materialsTxt.write(line)
        continue
    elif 'EBLOCK' in line:
        EBLOCKflag = True
        continue
    elif EBLOCKflag:
        EBLOCKline = line.split()
        if(len(EBLOCKline) == 19):
            EBLOCKlines.append('mpchg,' + EBLOCKline[0] + ',' + EBLOCKline[10])
            #termination for EBLOCK line is -1
        if('-1' in EBLOCKline):
            EBLOCKflag == False

materialsTxt.write('\n')

for mappingLine in EBLOCKlines:
    materialsTxt.write(mappingLine + '\n')
```