

## MANUAL STEPS DESCRIPTION

In this document, the manual steps performed in the project are explained. Following the pipeline described in the READ\_ME.txt provided, steps 1, 3 and 4 are manual and performed in 3D-Slicer. 3D Slicer is an open-source software available online: <https://download.slicer.org/>.

### **STEP 1: Visual inspection of images**

All the images were inspected to decide the pre-processing steps:

#### **A. CONTROL IMAGES**

- All control images did not have information about pixel spacing. Need to solve that by changing the header.
- All control images contained correctly the ROI (see Figure 1), Except Control4a image (see Figure 2).



Figure 1: Control1a image



Figure 2: Control4a image

#### **B. SCOLIOTIC IMAGES PREOP**

- See that most of the images contained noise (see Figure 3). Need a denoising filter. Moreover, pixel spacing and ROI are the similar for all of them.



Figure 3: 1preop image

### C. SCOLIOTIC POSTOP

- Also contained noise. The pixel scaping was correct and the ROI was similar for all of them.
- See some artifacts near the screws. They gave some problems when doing the segmentation using the thresholding tool in matlab (see Figure 4)



Figure 4: Ipostop image

From the inspection we could conclude that there were three things needed to be corrected before doing the segmentations:

- Cropping of ROI in Control image 4
- Change pixel spacing of all control images
- Denoising in scoliotic images

Also, an affine registration between the control, preop and postop CTs was made to make sure that the patients were aligned and fair comparisons could be drawn.

### STEP 2: Pre-processing code presented

### STEP 3: Manual segmentations

All the steps for the segmentation were performed using 3D slicer. 3D slicer was used because it is a free open-source image computing software focused on clinical and biomedical applications. It contains numerous modules and extensions providing a vast number of different applications, including DICOM import and export of images, AI, spatial registration, or image segmentation. The specific modules used are explained below.

The segmentations were performed using the results obtained from the pre-processing steps. Specifically, the results.0.nii of each patient folder, which are the results for the registrations.

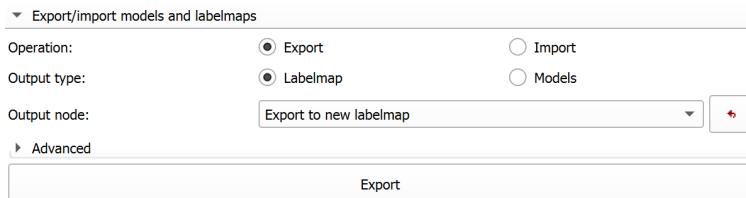
### A. BONE SEGMENTATION

1. Segment editor → Advanced segmentation → Yen Threshold. Modify lower bound for each image as needed.
2. 3D view to see how that was done. Some images needed some post-processing after the threshold was applied.
3. Remove small islands. Default one → 1000 voxels.
4. Scissors to eliminate the bed.
5. Closing. Default one.
6. Gaussian smoothing 1mm. (if needed)

## B. LUNGS SEGMENTATION

The lungs were segmented individually using the extension module from 3D Slicer called Chest Imaging Platform → Lung Ct segmenter. Download it using the Extension manager. The steps followed were the following:

1. Choose the Airway segmentation button. If not, parts of the trachea will be segmented together with the right and left lungs. Also click on medium detail.
2. Click on Start and follow instructions for locating the fiducials.
3. When finished, see the approximate 3D visualization. If seen correctly, click on apply and wait.
4. Check that the airway has been segmented in a separate label.
5. Go to the segmentations module.
6. Remove the airways segment (by selecting that segmentation and clicking on remove selected)
7. If needed, use the scissors tool to remove unwanted parts.
8. Click on Export/Import models and labelmaps with these settings and click on export.



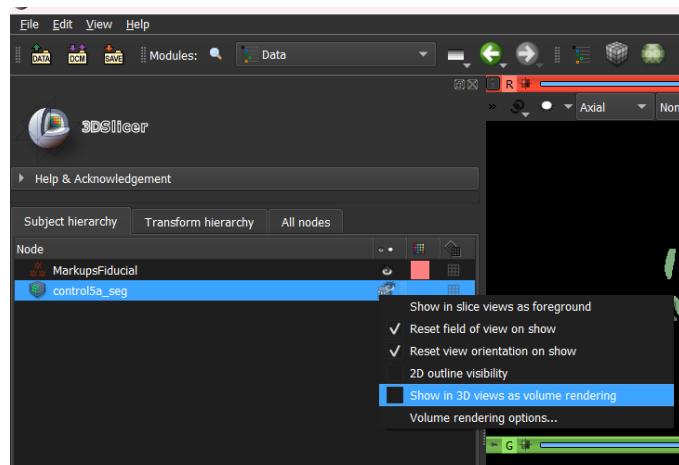
9. Lastly, scroll down to Export Files, select on Reference volume the label map you just exported (it will be called Lung segmentation-label), and click on Export to download the segmentation.

### **STEP 4: Skeletonization code presented**

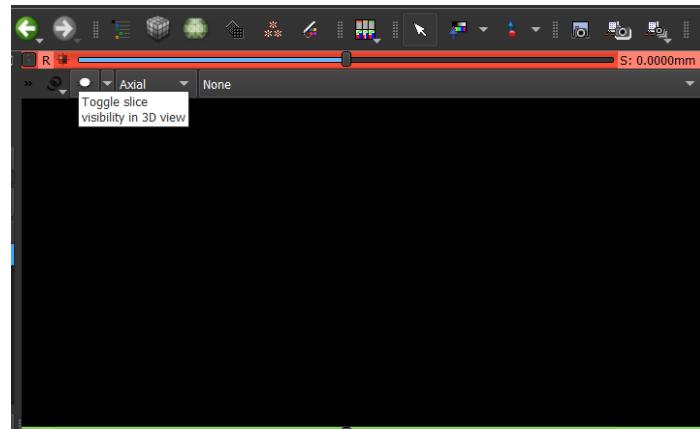
### **STEP 5: Locating landmarks**

Locating the landmarks will be done in 3D Slicer. Follow steps explained below:

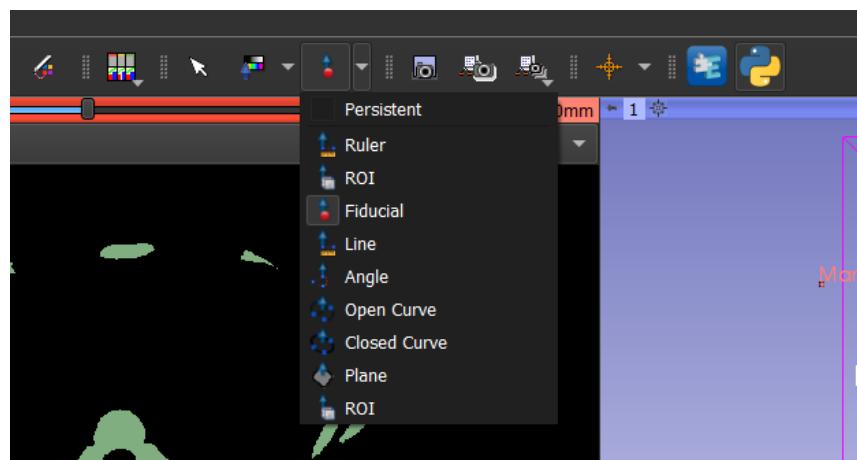
1. The first step is to load the data. For this you should open both the segmentation and skeletonization files.
2. On the 'Data' section, right click on each of them and select view as 3D, to make them visible in the 3D viewer that is in slicer.



3. In the red box, so axial view, Toggle slice visibility in 3D view. So now you can see in the 3D view where in the skeletonization and segmentation you are.

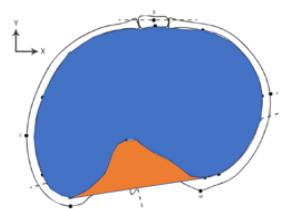
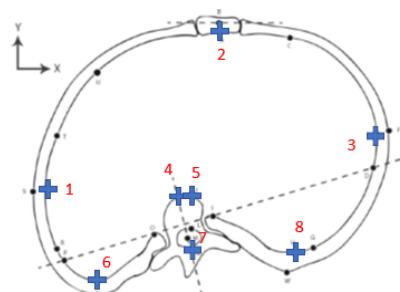


4. Next, go to 'Markups' section and create a new fiducial markup, we will have one fiducial markup per each rib. And name them in an understandable way
5. Select the first landmark on the skeletonization in the red/axial view(see figure below, with the locations of the landmarks). After that continue with the second landmark and place all 8 of them in an ascending order, by clicking on the Fiducial symbol as shown here:

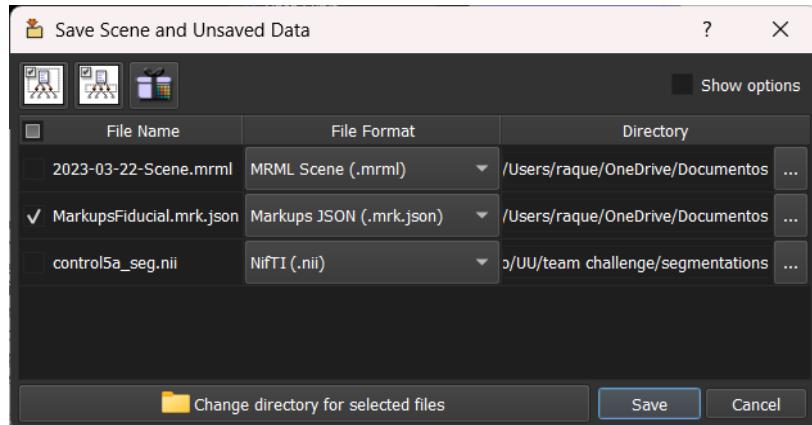


The Landmarks are organized as follows and should be placed in the order that is shown below:

1 = lateral most point on convexity  
 2= posterior midpoint of sternum  
 3=lateral most point of concavity  
 4=true Anterior of vertebral body (along vertebral axis)  
 5= most anterior point of vertebral body  
 6= posterior convex rib  
 7=posterior spinal canal  
 8=most posterior concave rib  
  
 surface1=surface lungs and mediastinum  
 surface2=surface spine



- Last step is saving the Fiducials when all landmarks are placed correctly. This can be done by going to File → Save and select only the fiducials file. This file contains all the landmark coordinates that will be used in further processing of the data



## **STEP 6: Metrics**

Once all the landmarks are located and downloaded as json files, they are used to calculate several metrics.