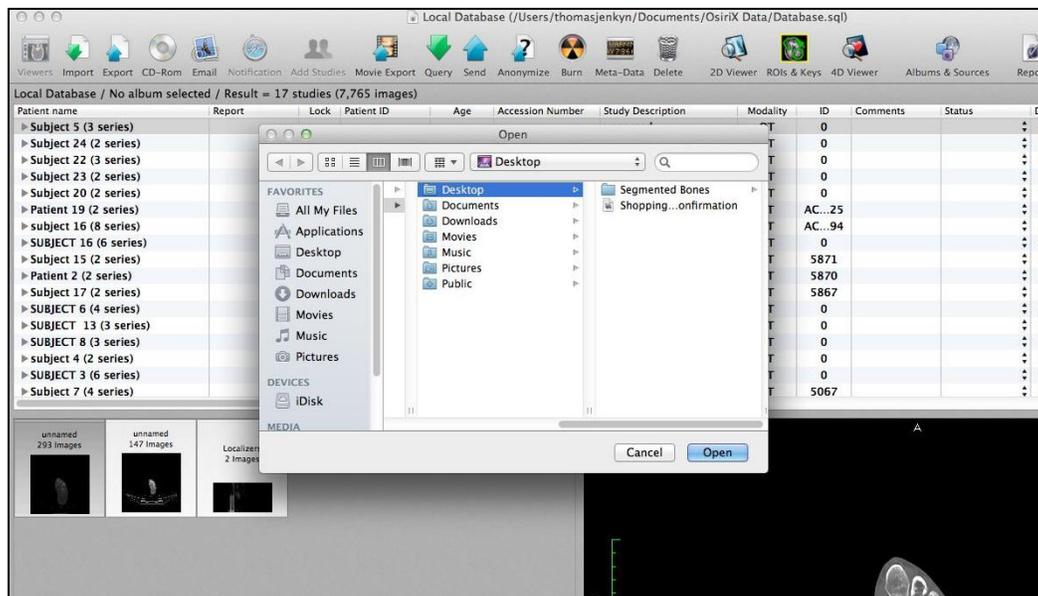


SEGMENTATION USING OSIRIX

Bone Segmentation Steps – OsiriX (Pixmeo, Geneva, Switzerland)

Note: **Do not** save any work throughout this unless this guide explicitly tells you to do so. Hitting save will result in losing data that you may need in order to proceed, and may result in an error message in the process.

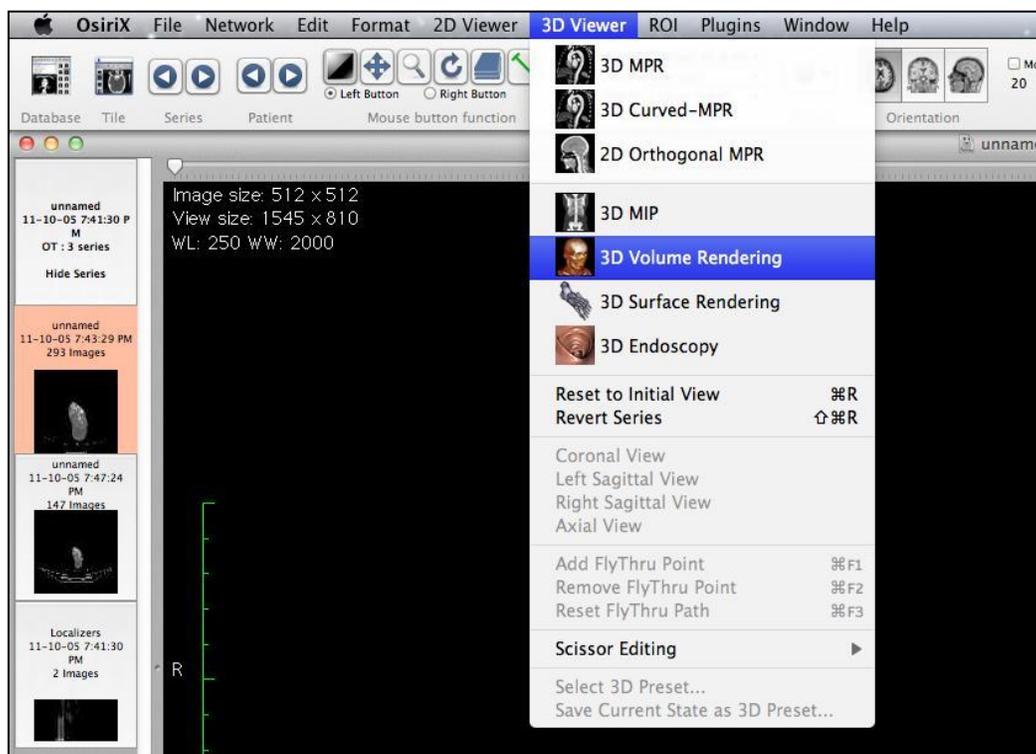
- 1) Open 'Finder' on the Desktop and in the Applications on the left menu bar, find OsiriX and double click to Open.
- 2) First, the CT scan files must be imported to the program and copied to the system before any manipulation can happen. Click on 'Import' at the top left and then select the series of CT files that you want to make into a 3D model.



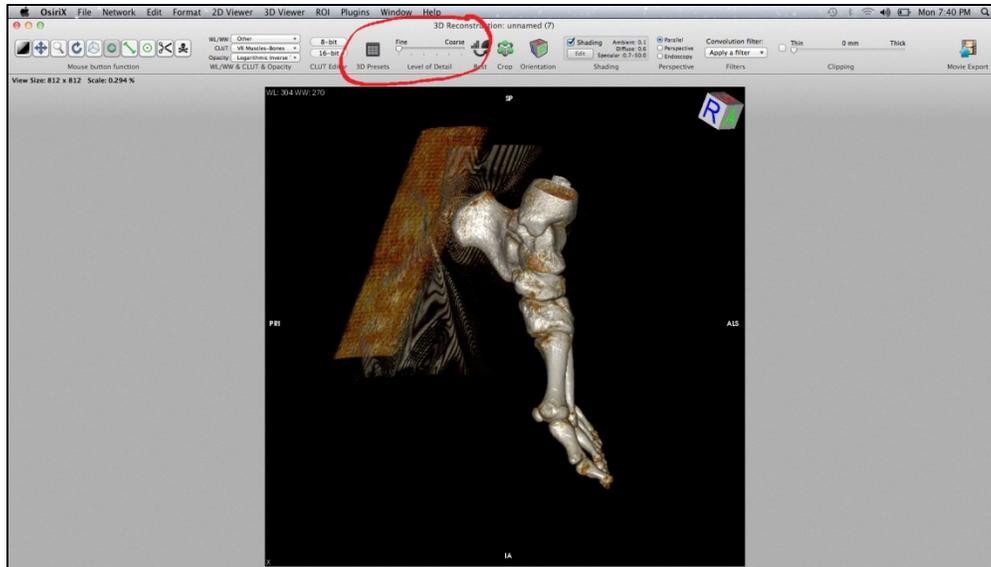
- 3) Once all the files have copied to the Local Database (above), double click the subject or patient CT whose bones you would like to segment.
- 4) The following screen will pop up > Click "I agree".



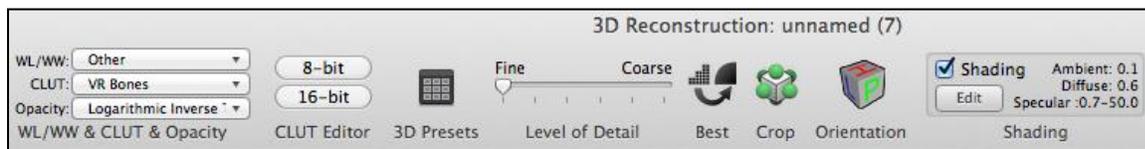
- 5) Choose the file to the left that has the most images or preview the one that appears most suitable (see highlighted pink area below). In this case, the one with the most images was the one chosen based on the slice thickness and CT properties.
- 6) Go to the top pull down menu under 3D Viewer and choose 3D Volume Rendering.



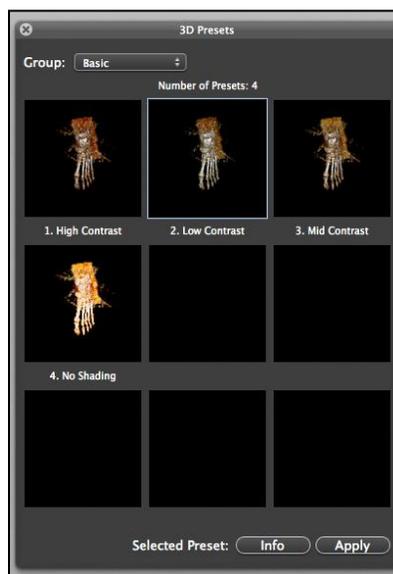
The 3D Volume Rendering window looks like the one below, with the tools in the second menu from the top.



- 7) On the second menu from the top (circled in red above), immediately change the level of detail to **FINE** (as far as it will go to the left).



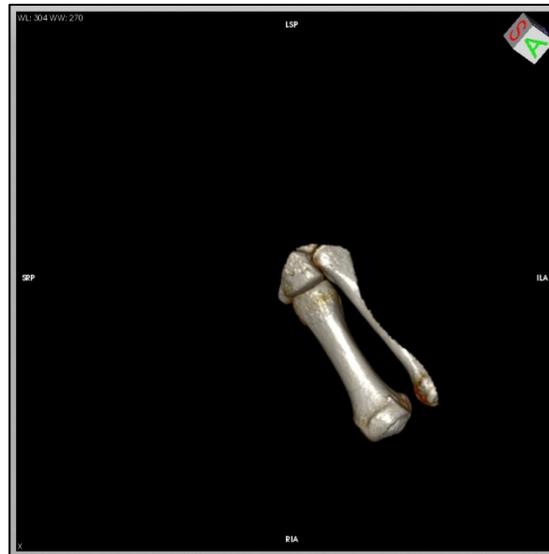
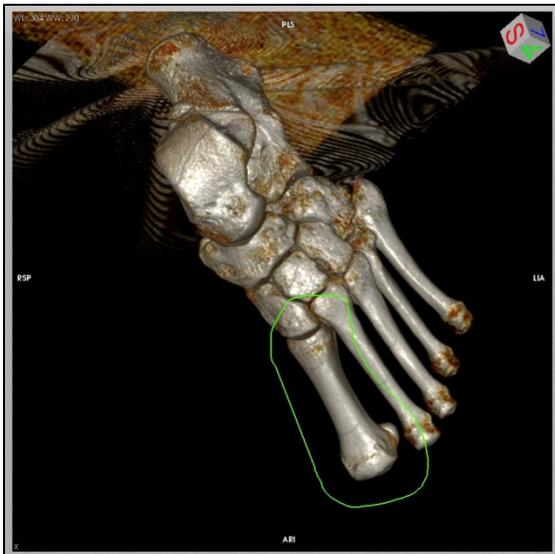
- 8) Click on the 3D presets menu to the left of that and choose the 'Basic' Group. Click on 'Low Contrast' and then click 'Apply'. This will allow for easier segmentation of the bones as there will be less visible noise and soft tissue surrounding the bone.



9) Description of tool functions (top left of the window in step 6):



- a. The **Poison sign** (far right) will get rid of an entire bone at once. This tool may be very useful, however, some bones may appear to be separate but in reality, there is some connection somewhere to another bone. If that's the case, this tool will remove two or more bones at one time.
- b. The **scissors** will allow you to select an area in bright green and then hitting 'Enter' once made your selection (below) will keep what you've selected, whereas the 'Delete' button will remove what you've selected.
 - i. It's easier to scissor around the bone you want right off the start, and press enter, and then use the delete button to eliminate the other bones that are near or touching afterwards.
 - ii. Note that the scissor function will cut everything in three dimensions from the plane you've chosen and protruding into the screen and bones behind the selection so be careful where you cut.



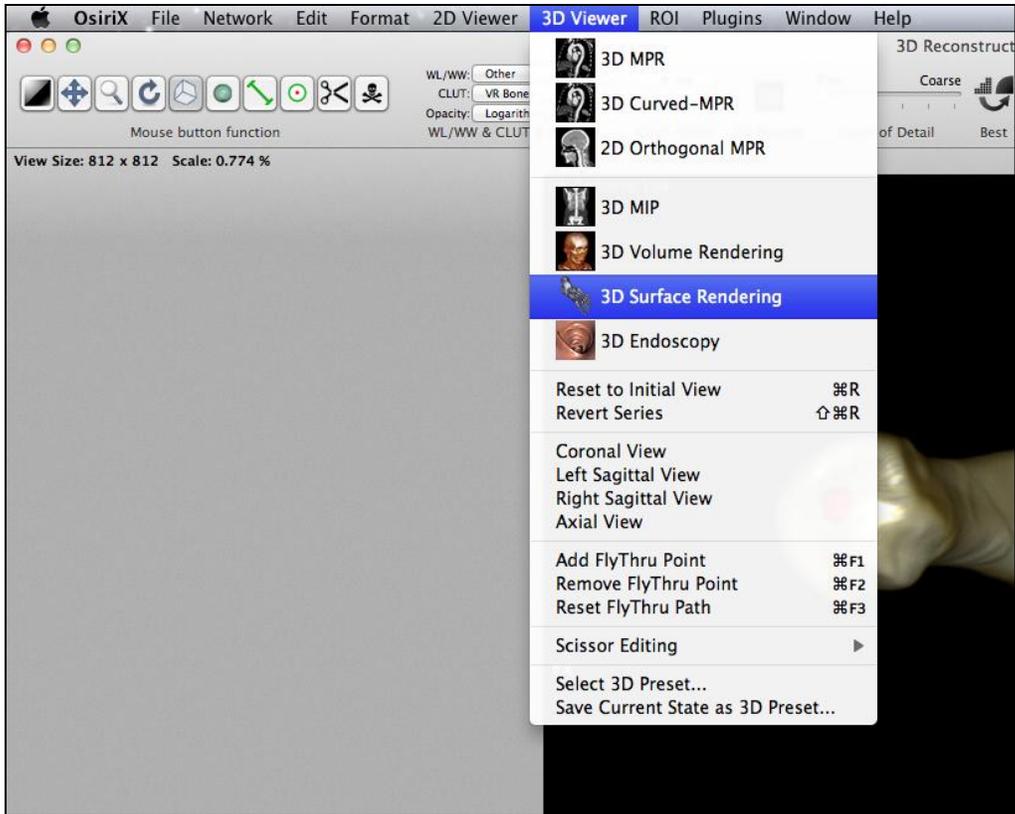
- c. The green circle with the red dot allows you to place a red sphere on the bone, marking any necessary landmarks. Try to do this as consistently as possible for each patient's CT scan, in order to compare the position of the same bony landmarks of the anatomy between subjects. These spheres will export as separate 'mesh' items, along with the single bone mesh.
 - i. You can choose to put the red points on the landmarks before or after segmentation, depending on how easily identifiable they are without the surrounding bone. For

segmenting the navicular in this study, the spheres were positioned before segmentation to mark the most medial point of the tuberosity as well as the most dorsal aspect.

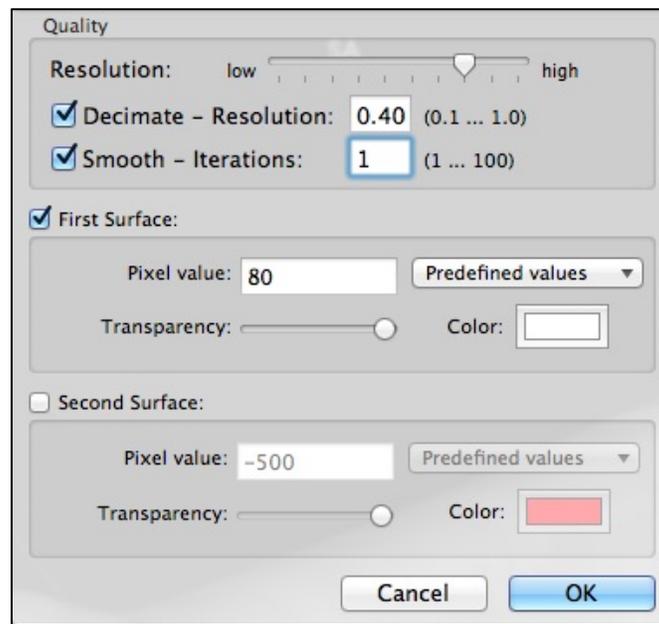
- d. The green line segment is a measurement tool if you want to determine the length of any two objects in two dimensions
- e. Greenish blue sphere – used to re-position the camera view, since you may be looking near the end of an extremity, the camera position may need to be changed to zoom in close on the right area.
- f. Box tool – used to rotate the model in three dimensions. The combination of these last two tools will allow you to zoom in and out and get the correct angle to use the scissor tool.
- g. Semi-circular arrow – rotates the object in the plane of view.
- h. Magnifying glass – used to zoom in and out (as well as the right click button at all times)
- i. Move function (four arrows) – left click will move the object within that plane of view. Used to reposition the object (similar to rotating the camera)
- j. Window level (black square far left) will adjust the window level and width – general CT settings. The 3D present chosen has default values for these parameters; therefore, this is not used for the purposes of this segmentation.

Note: Hold mouse over function to see what each does if you aren't sure. DO NOT hit the save button. This will create an error in the next step.

- 10) Only segment one bone at a time in the window – it is easier to crop a single bone without having to worry about what is behind it. Also, you want to export each bone separately to import into Rhinoceros.
- 11) Once the bone is segmented, the surface of the bone must be smoothed. Click on '3D Presents' similar to step 7 and in that window change the group type to: Bone CT. Select option 9 "Soft".
Note: This setting has specific presents that show the best balance between colour and density of the bone for this thesis. If you click on 'Info', the 3D Present parameters will be shown – window length/width, the colour look up table (CLUT) and the filter used for the CT scan. These are the best surface properties for exporting the bone model to the best of the author's knowledge.
- 12) At the top menu, select the 3D Viewer drop down menu again and select the 3D Surface Rendering option (below). This will create a mesh of the segmented bone by defining a surface around its known volume. The segmented bone model can only be exported from this 3D view.



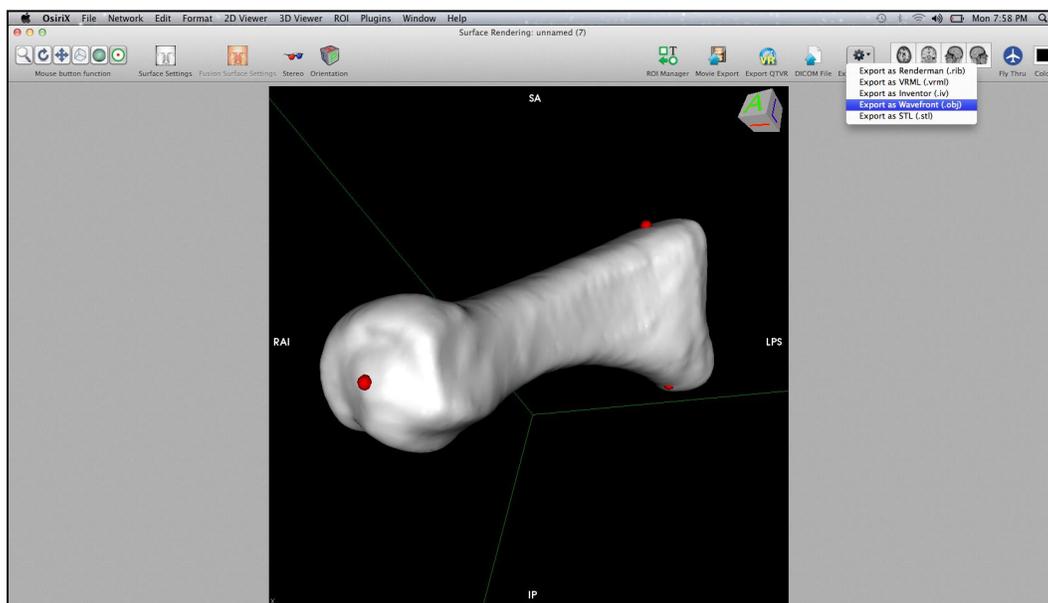
- 13) Once selected, the menu at the top of the window will pop up automatically for input regarding the desired surface settings (see below).



- a. The settings above will change depending on the patient, their bone density, as well as which bone you are working with.
- b. Move the 'Resolution' cursor to two notches to the left of high to start, and move to HIGH if that appears better.
- c. Initial settings should have 'Smooth – iterations' function to 1 (meaning less smoothing will occur at first).
- d. Initially, the Pixel Value should be set to 100 (instead of 300 by default). This setting represents the 'density' of the bone, for example, 50 for one patient made the bone too built up with sharp edges, whereas 100 created holes in the bone. The higher the pixel value, the less dense the bone – this value will need to be manipulated depending on the subject.
- e. You can also change the colour of the bone which may be a good idea to choose something that will work well in rhinoceros background.

Important: Once you set these values initially and they are too high (bone has holes and is not dense enough) then you cannot make it more dense by changing them in the 'surface settings' tab in the toolbar. You must close the window back to the 3D Rendering window and then start step 12 again. However, if the pixel value is started low, with a low 'Smooth' number as well, and the bone appears too dense, you can edit the surface settings by increasing the Iterations and Pixel Value gradually. I've found this to be the easiest way to get the bone looking the way you want. Start with low numbers and gradually increase them to the desired output.

- 14) The bone will now resemble the model below (example bone: first metatarsal of the left foot). From this point, the model can be exported as a 'Wavefront' or object file (.obj), which is found in the 'Export 3D-SR icon' on the Surface Rendering Menu to the right.
 - a. Select the folder you wish to save it in. The file can now be transferred to the PC of your choice so long as you have Rhinoceros on the machine for further analysis.



- 15) When closing any window, use the buttons on the top left, the red button. First, close the 3D Surface Rendering window, followed by the 3D reconstruction (volume) rendering. As long as you don't close the subject CT file (the 2D view at the beginning, that bone will remain segmented.
- 16) To start a **new** segmentation for another bone for the same patient, the last window must be closed and then the subject re-opened to start again.
Note: the red spheres will not ever disappear automatically from where they were placed, even when closing the subject CT files. So you have to manually use the tool function, click on them and hit delete before adding them to the next bone.
- 17) To quit OsiriX, you have to go to the top left and click Quit OsiriX, closing the last window will not do that for you

Taking screen shots with a MacBook Pro

1. **Apple (Command) Key +Shift+3**
Captures entire desktop to a file on the desktop as 'picture #'. This option lets you capture the whole screen.
2. **Apple (Command) Key +Shift+4**
Allows you to use your mouse to select a specific part of your desktop for capture. This will turn your mouse pointer into a cross, please hold down the mouse button and drag to select the part of the screen you want. When you release the button the screenshot will "snap" that part of the screen. Press 'Esc' to release.
3. **Apple (Command) Key +Shift+4 then press Spacebar**
Allows you to select which window to capture.