

Step by Step Instructions for Running Extension **Breast DCE-MRI Tumor Segment**

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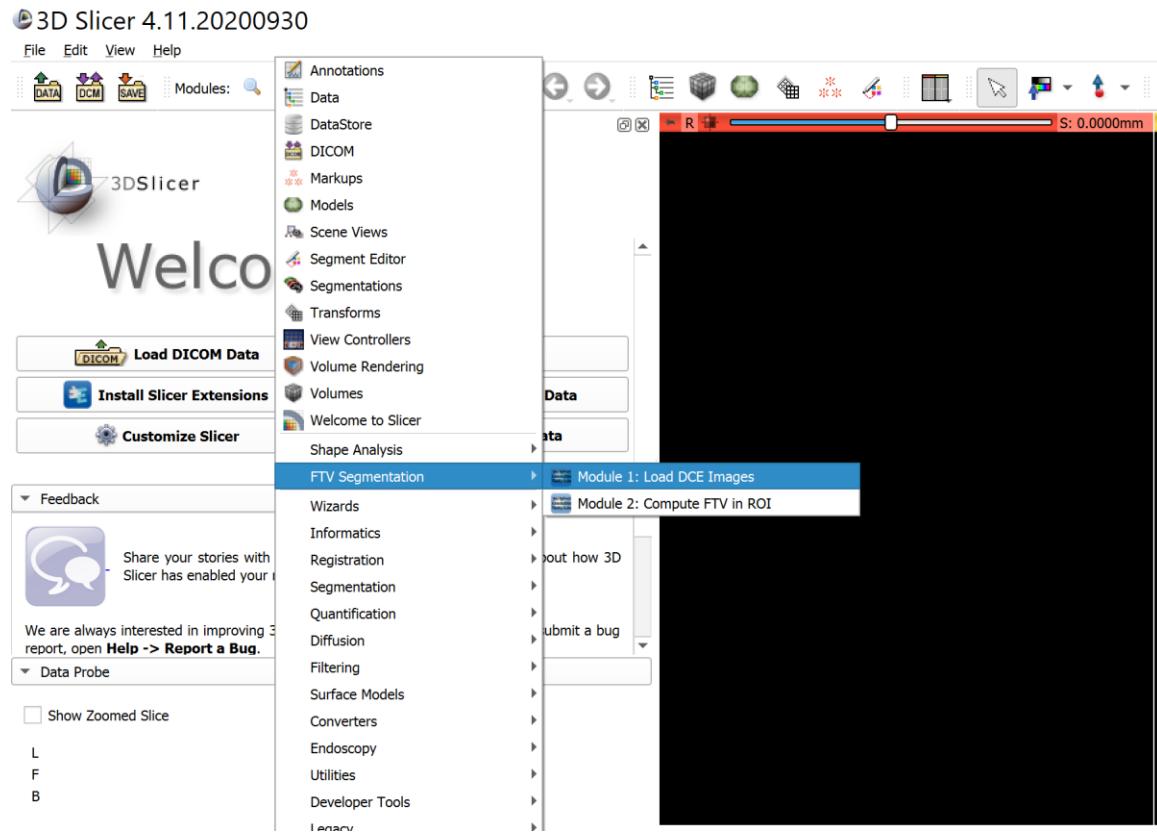
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Module 1: Load DCE Images

In this module, the user selects the MR exam to process, preferences for early and late phase timing, and method of DCE series identification (automatic or manual). The module will then load the pre-contrast, early post-contrast, and late post-contrast phases to the Slicer window.

Steps 1-5: Using Module 1

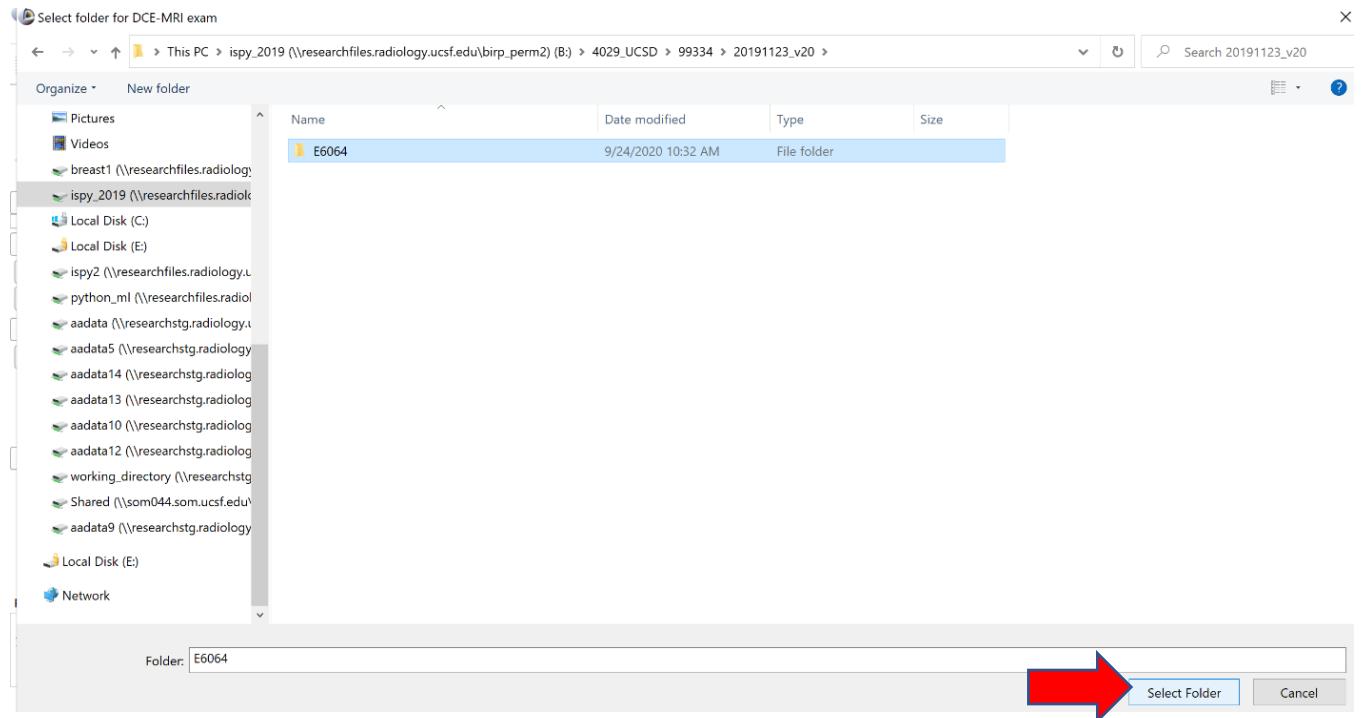
1. Open 3D Slicer and click on the button that says **Welcome to Slicer** to open the modules list. From this list, select **Module 1: Load DCE Images** from the **FTV Segmentation** category.



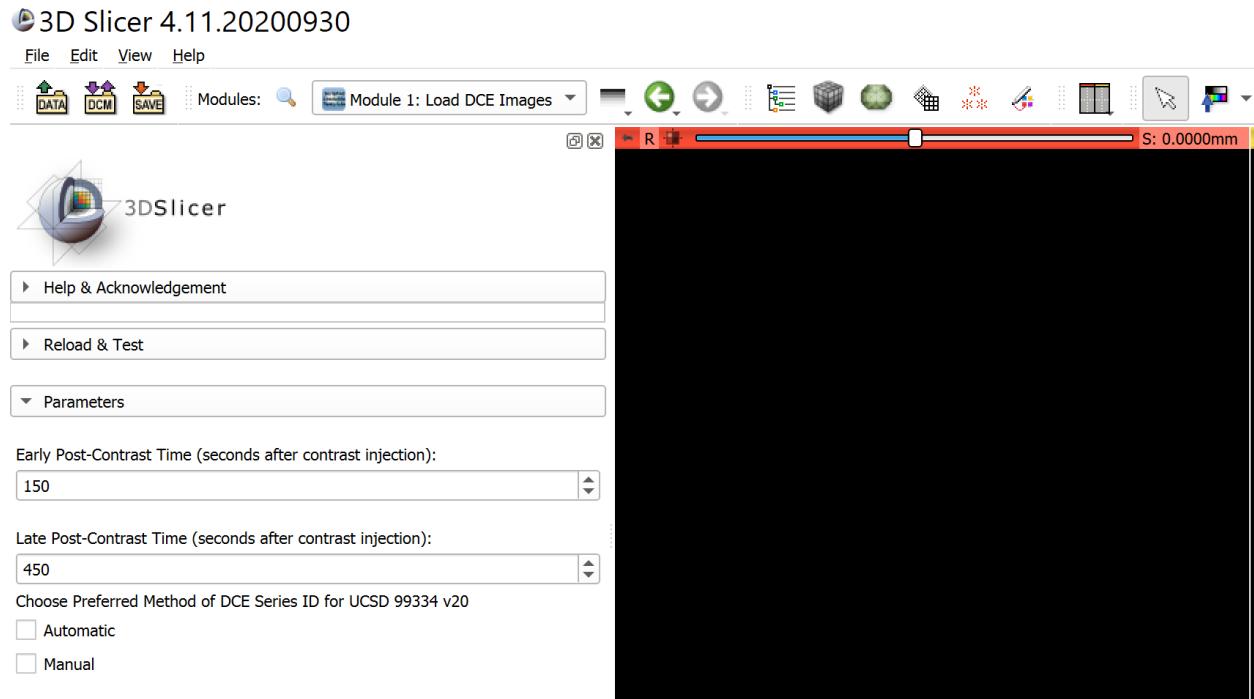
2. Immediately after you select the module, a popup menu will appear. Use this popup to choose folder of MR exam you want to run FTV segmentation on. The MR exam folder is the one the contains all of the DICOM series folders for a single visit.

Warning: This extension is only compatible with MR exams that use bilateral images with axial slices.

Single click on the exam folder to highlight it, and press the **Select Folder** button to choose that exam.

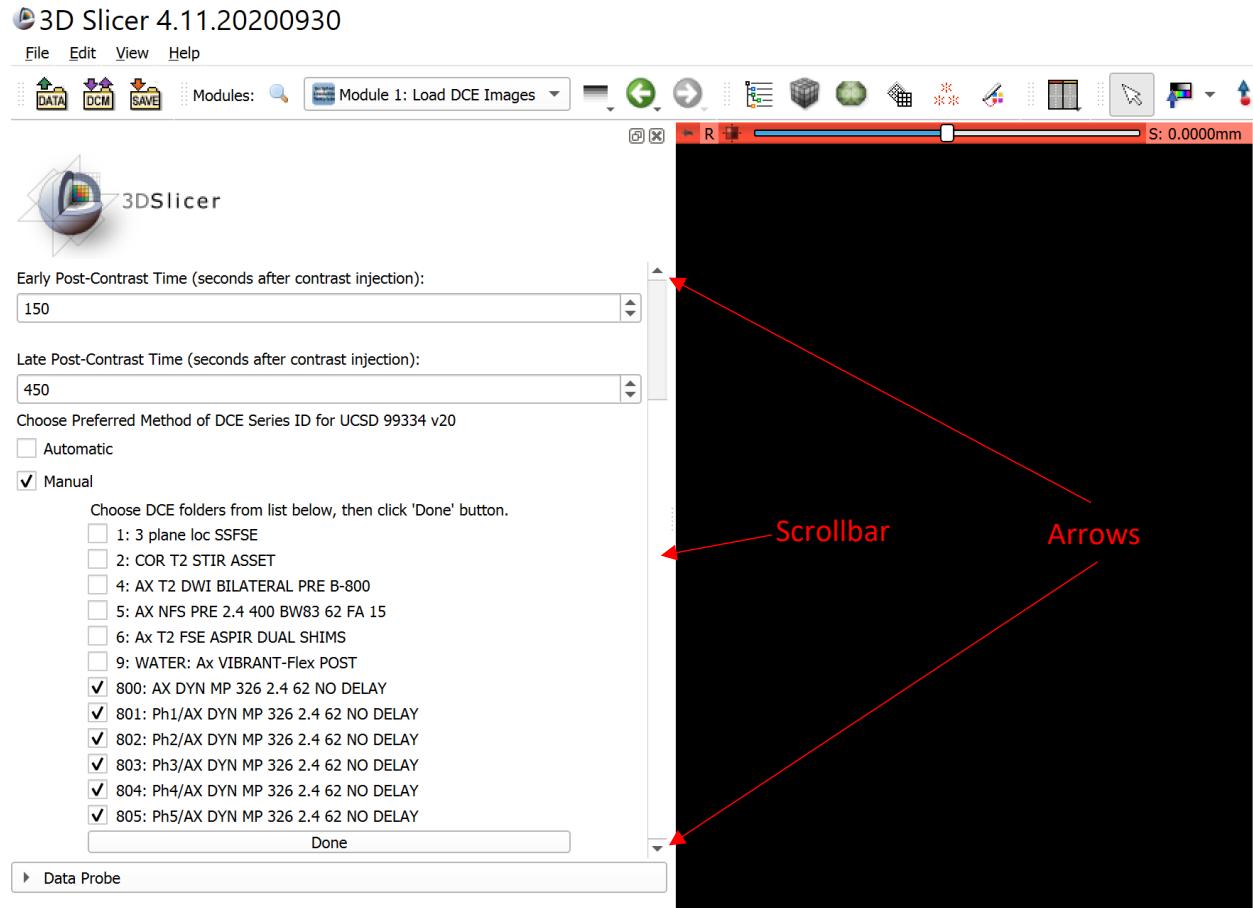


3. After you select the MR exam, you will see the module's widget under the **Parameters** tab on the left side of the Slicer window. By default, the module will use the early and late phase timings from the I-SPY2 TRIAL, in which the phase that occurs closest to 150 seconds after contrast injection is early post-contrast and the phase that occurs closest to 450 seconds after contrast injection is late post-contrast. However, you can change these timing settings by editing the corresponding text fields in the widget. The widget also asks you for your preferred method of DCE series identification. If you want the module to automatically identify the DCE series, check the box next to **Automatic**. If you want to manually specify which series the module should select as DCE, check the box next to **Manual**.



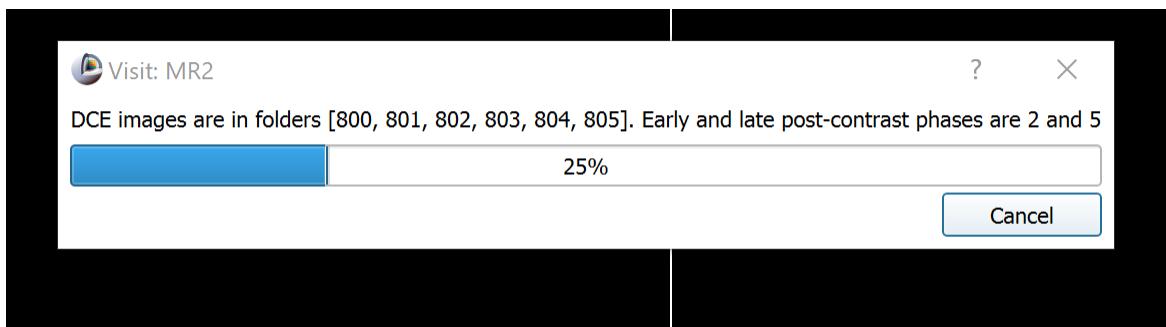
Step 4 is only for manual DCE series identification. If you selected the Automatic checkbox, skip to step 5

4. As soon as you check the **Manual** checkbox, a list of all image series folders for the chosen exam will appear. You may need to use the scrollbar or arrow buttons to see the entire list. Each item in the list contains a checkbox, series number, and series description. Check the box(es) next to the series that you want the module to select as DCE, then click the **Done** button when you have finished making all of your DCE series selections.



5. **Warning: Do not press the Automatic checkbox or the Done button for manual series ID more than once. Ignore “not responding” warnings, and do not worry if the progress bar takes a long time to update. Slicer should take roughly 2 to 4 minutes to complete step 5.**

If you chose automatic DCE series ID, the module will identify the DCE series at this step. Otherwise, it will use the DCE series you selected with manual DCE series ID. Using the DCE series and early and late target times, the module will then identify and load the pre-contrast, early post-contrast, and late post-contrast phases for the exam. The progress bar tells you which visit you're loading in the title. It also provides updates on which series folders were selected as DCE, early/late phase identification, and when each phase is loaded to the Slicer window. This progress bar disappears when all 3 phases have been loaded.



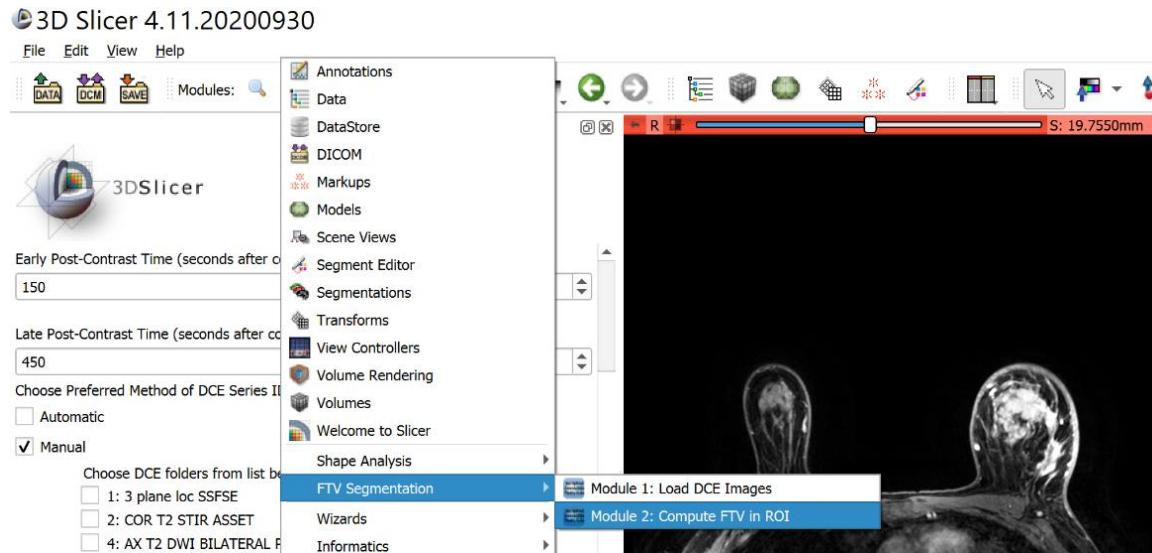
Module 2: Compute FTV in ROI

In this module, the user first selects the tumor region of interest (ROI) and also has the option to select regions within the ROI to exclude from the segmentation (omit regions). The phases loaded by Module 1 as well as subtraction images and MIPs derived from them may be used to guide selection of ROI and omit regions. Furthermore, the user has the option to either create ROI and omit regions by dragging bounding boxes to the appropriate position and size or import ROI and omit regions from an existing .xml file. If the user creates a new ROI and omit regions, they can be saved to an xml file for future use.

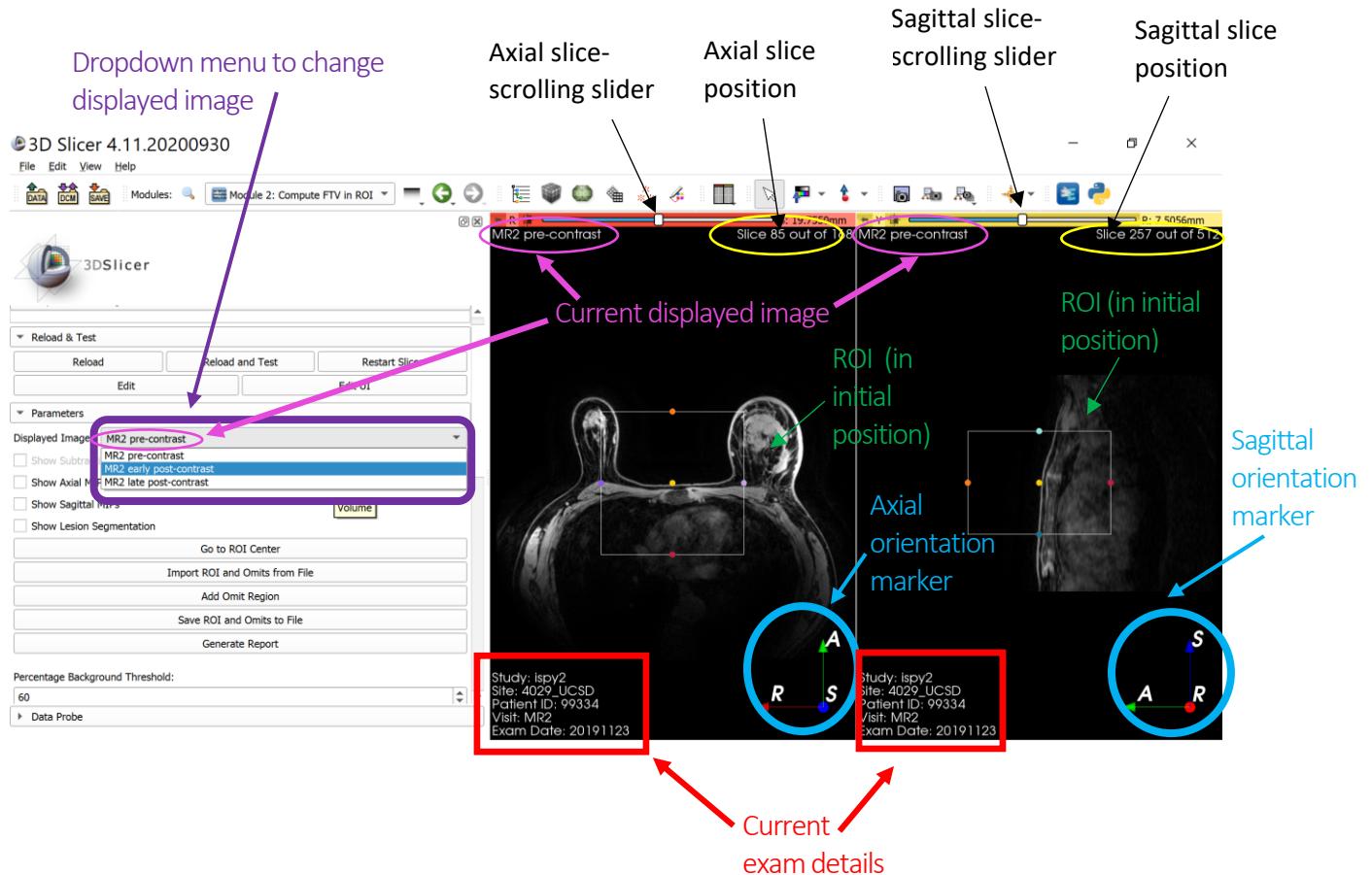
After ROI and omit region selections, the user can begin the segmentation process. If necessary, the user may change the segmentation thresholds from default values. The user can segment the lesion and overlay a tumor segmentation that is color-coded by signal enhancement ratio (SER) values onto the axial and sagittal views. In addition, the user may generate a report that includes several axial and sagittal images from the exam as well as relevant information such as FTV value, ROI boundaries, segmentation thresholds used, and details about the exam selected.

Steps 6-8: Startup and layout of Module 2

6. Select **Module 2: Compute FTV in ROI** from the **FTV Segmentation** section of the modules list.



7. The picture below shows what **Module 2** looks like immediately after it is done loading. The key features have been labeled for your convenience. For additional built-in Slicer functionalities that may be helpful while using **Module 2**, please see **Appendix**.



8. The contents of the widget for **Module 2**, which is located under the **Parameters** tab on the left side of the Slicer window, are shown below. There are 4 checkboxes, 4 buttons, and 3 boxes for entering numbers. The purpose of each of these is explained by its label. Additional important details to note are:

- Use scrollbar or arrows to access part of widget you need
- Must display post-contrast image to use **Show Subtraction** checkbox
- The 3 number value boxes just above **SER Color Ranges** image allow you to adjust segmentation thresholds for **Show Lesion Segmentation** and **Generate Report** functionalities
- The bottom of the widget contains the **SER Color Ranges** image that shows color coding used for the lesion segmentation.

Slicer



Parameters

Displayed Image: MR2 pre-contrast

Show Subtraction

Show Axial MIP

Show Sagittal MIPs

Show Lesion Segmentation

Go to ROI Center

Import ROI and Omits from File

Add Omit Region

Save ROI and Omits to File

Generate Report

Percentage Background Threshold:

60

Minimum Neighbor Count:

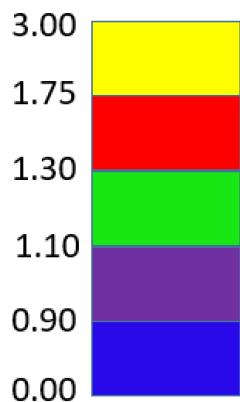
4

Peak Enhancement Threshold:

70

SER Color

Ranges



SER Color Distribution in Lesion

Yellow:

Red:

Green:

Purple:

Blue:

Total:



Scrollbar

Arrows

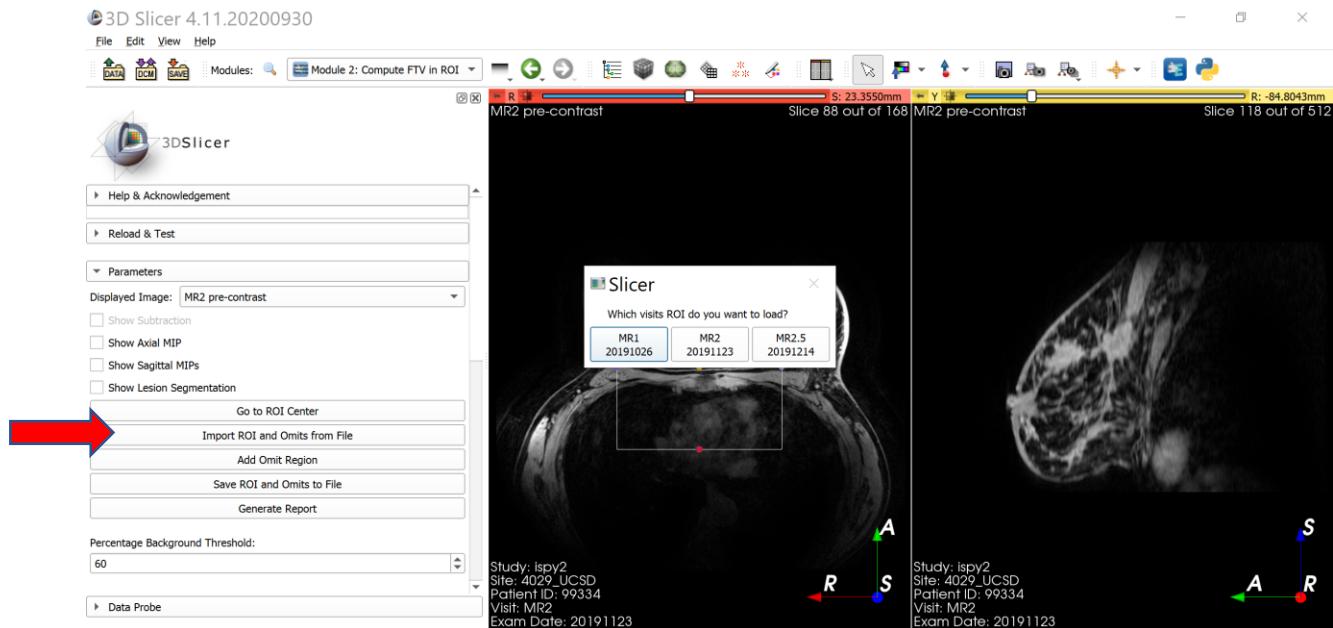
Steps 9-12: Defining and Saving ROI and Omit Regions

9. If the exam has ROI coordinates saved to an xml file, you can use this ROI by clicking the **Import ROI and Omits From File** button.

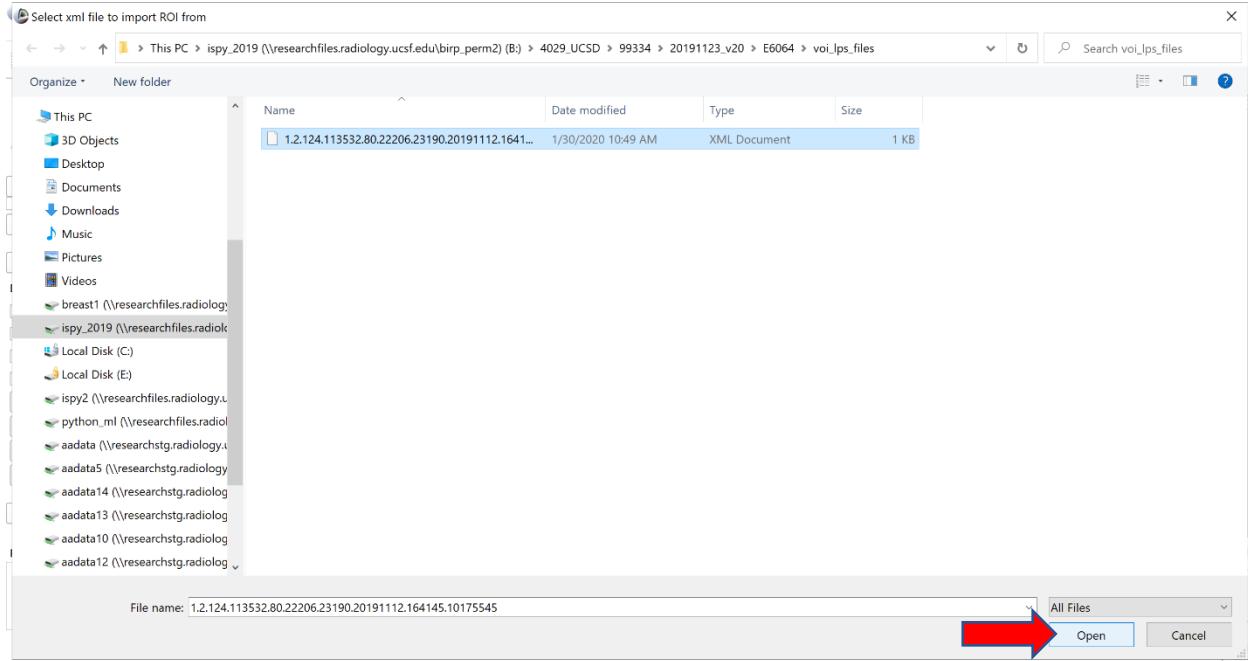
If the module finds **voi_lps_files** folders for multiple visits for this patient, a popup will ask you which visit's ROI and omits you want to load. Click on the button corresponding to the visit that has the ROI and omits you want.

If the module can only find a **voi_lps_files** folder for the current visit, the popup requesting visit selection will not appear, and the module will skip directly to the file selection menu with this **voi_lps_files** folder as the default directory.

If the module cannot find any **voi_lps_files** folders, the popup requesting visit selection will not appear, and the module will skip directly to the file selection menu with either the patient folder (assuming exam path goes like: **patient\visit\exam**) or the exam folder as the default directory.



If you saw the visit selection popup and chose a visit, the file selection menu will appear with the **voi_lps_files folder** for the visit you chose as the default directory. To choose an xml file, double click on it or single click on it and press the **Open** button.

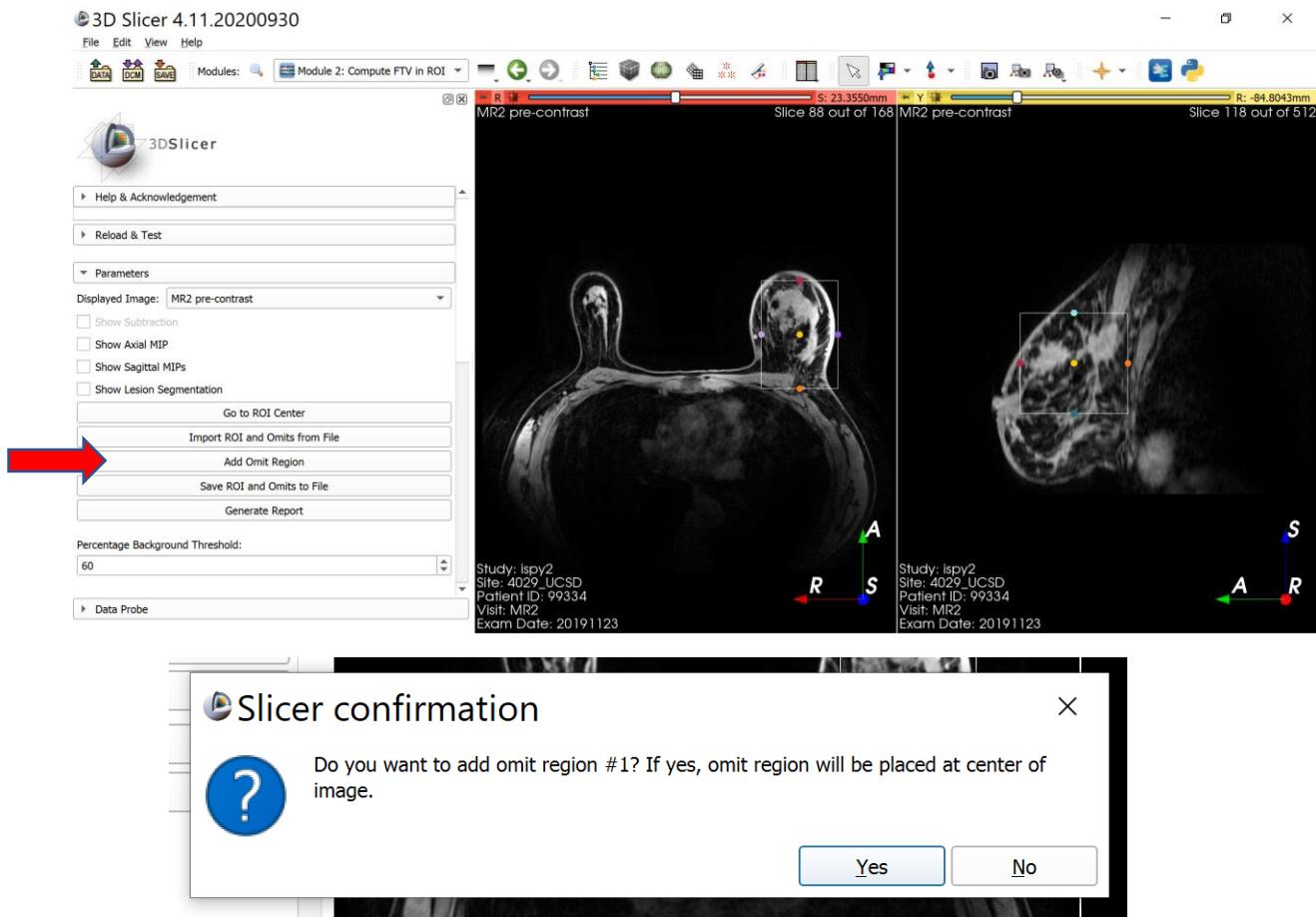


After you select the xml file, the ROI box will automatically move to the position specified in the xml file. The omit regions specified in the xml file will be created too, and any additional omit regions that were in the Slicer window before you loaded the xml file will be deleted.



If there is no xml file for the exam, you must choose the ROI by moving its box to the appropriate position and adjusting its boundaries in the x, y, and z directions. A left click and drag on the yellow circle in the center of the box adjusts the location of the ROI, while a left click and drag on any of the 6 circles on the edge of the box adjusts ROI boundaries.

10. If you would like to define your own omit region, click the **Add Omit Region** button. Since an omit region cannot be deleted once added to the scene, an additional yes/no popup like the one shown below appears to confirm that you want to add the omit region.

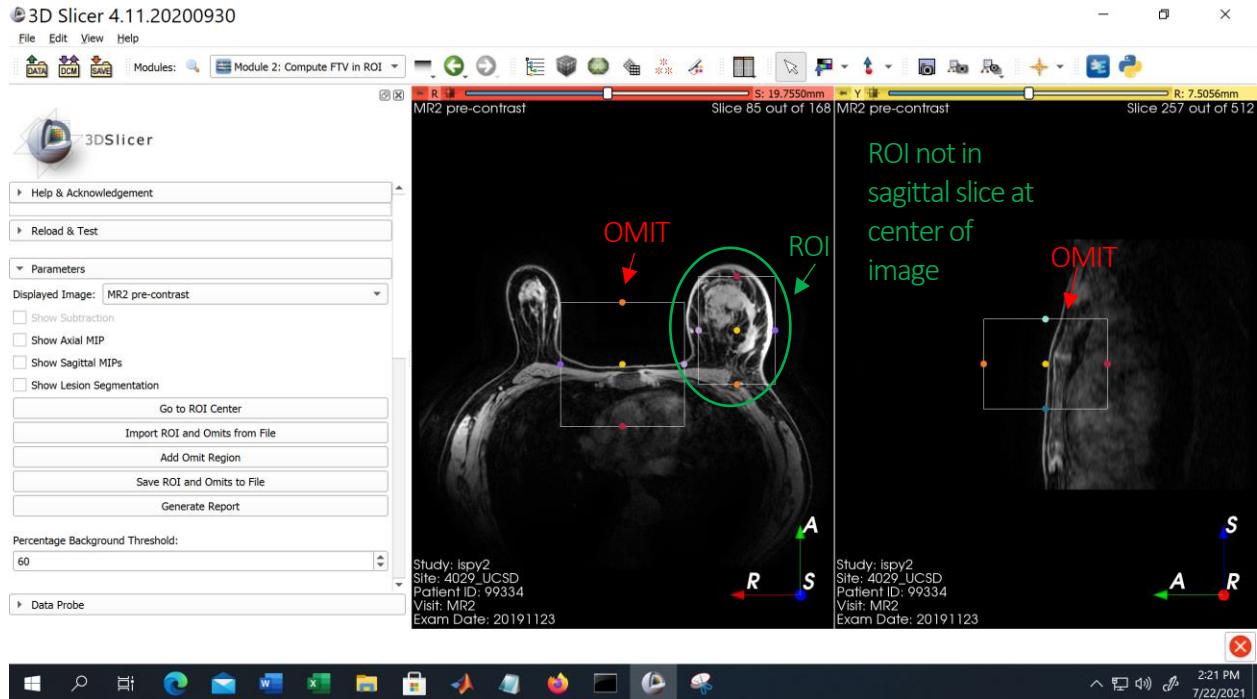


If you did not click the **Add Omit Region** button by mistake, select **Yes** and an omit region will be initialized in the center of the image. Otherwise, select **No** and the omit region will not be added.

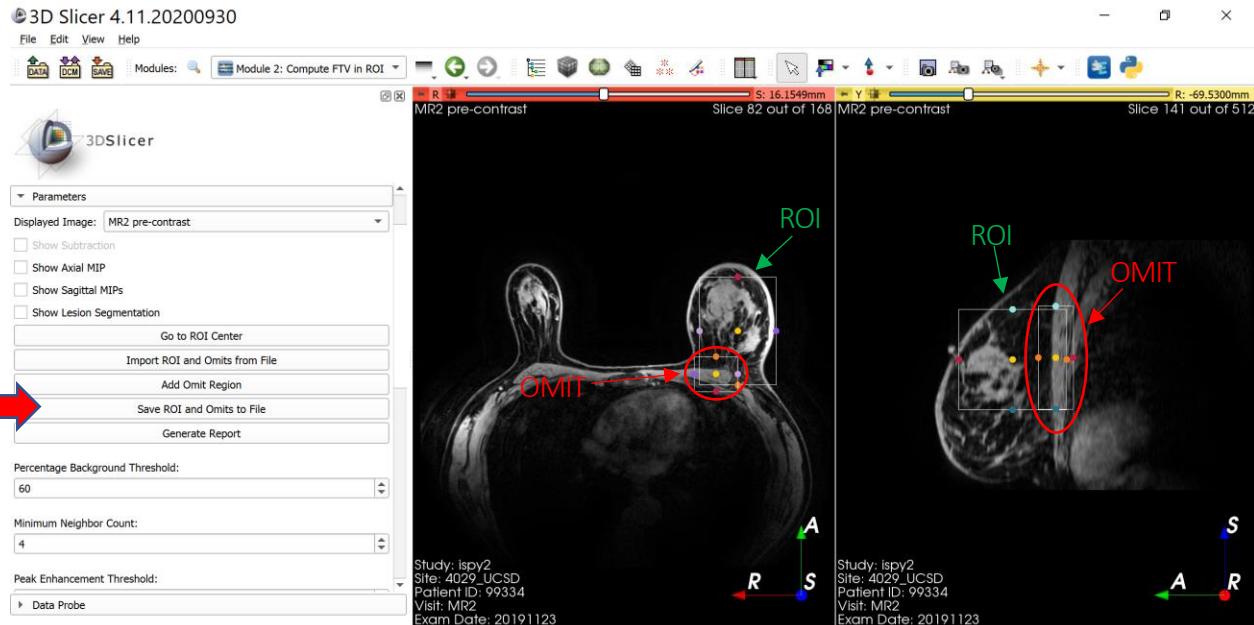
After you select **Yes**, a box corresponding to this omit region will be placed in the center of the image, and the module will display the axial and sagittal views at the center of the image.

Warning: If you add an omit region before moving the ROI from its initial position, please be aware that the larger box is the ROI and the smaller box is the omit region.

You can then define the boundaries of this omit region by adjusting the position and boundaries of this new box, as described in step 9. This module allows up to 5 omit regions to be in the scene.



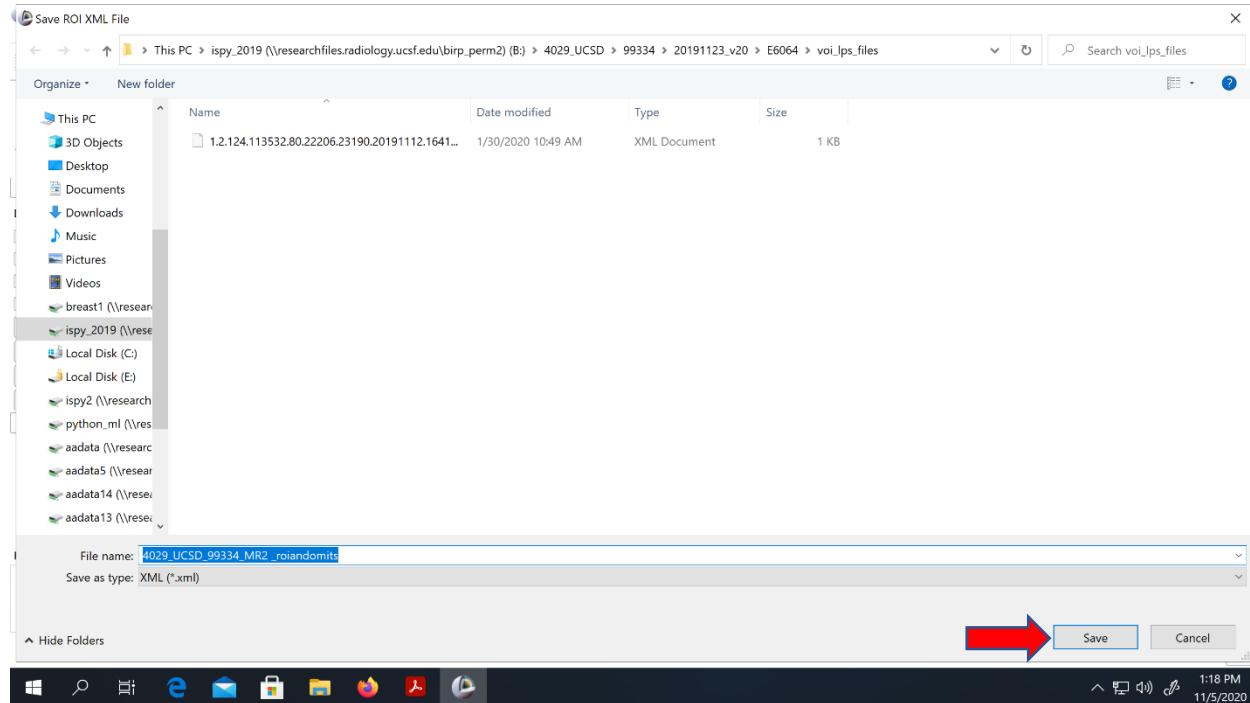
11. If you are finished with ROI and omit region(s) selection and would like to save the coordinates of these selections to an xml file, click the **Save ROI and Omits to File** button.



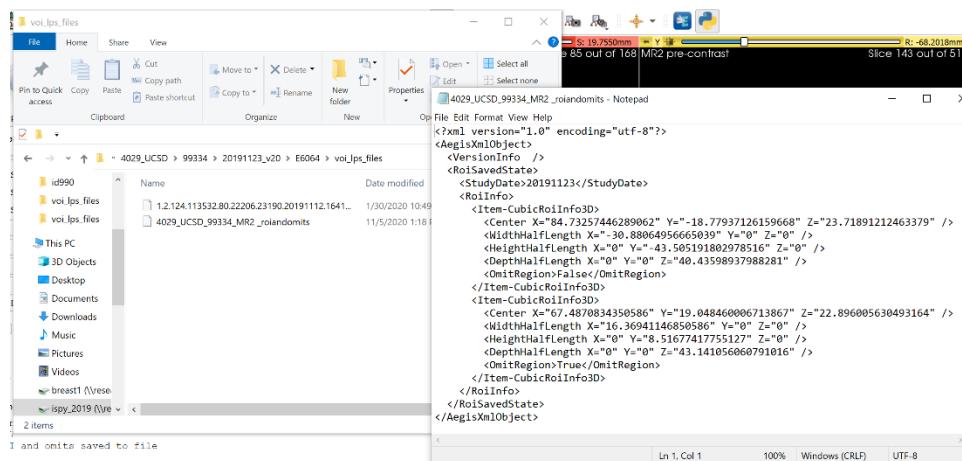
The file save menu will automatically navigate to the **voi_lps_files** folder for this exam, or create this folder and navigate to it if it didn't previously exist. You can type in the name that you prefer for this new xml file. By default, the name follows the format

<site name>_<Patient ID>_<visit>_roiandomits.xml

but you can edit the **File Name** field to give a different name. When you are finished naming this file, press **Enter** on your keyboard or click the **Save** button.

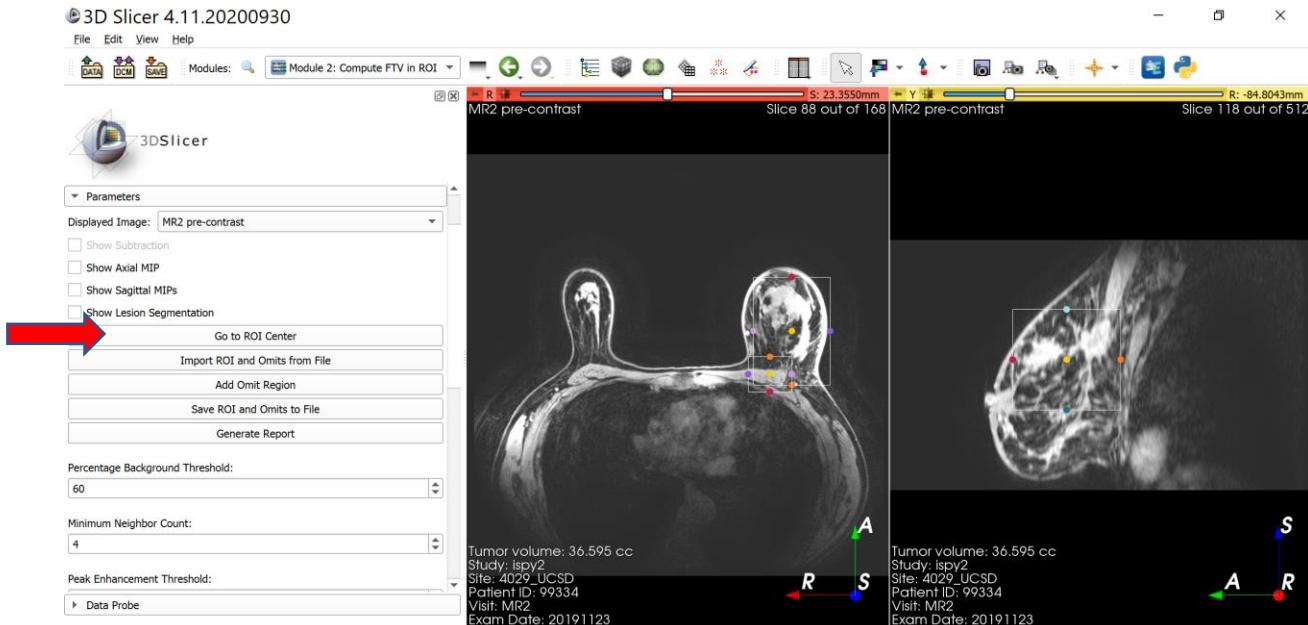


12. Then, you can go to the **voi_lps_files** folder for this exam and open the new xml file. In this file, the LPS coordinates of the ROI and omit region(s) are stored in Aegis xml format.



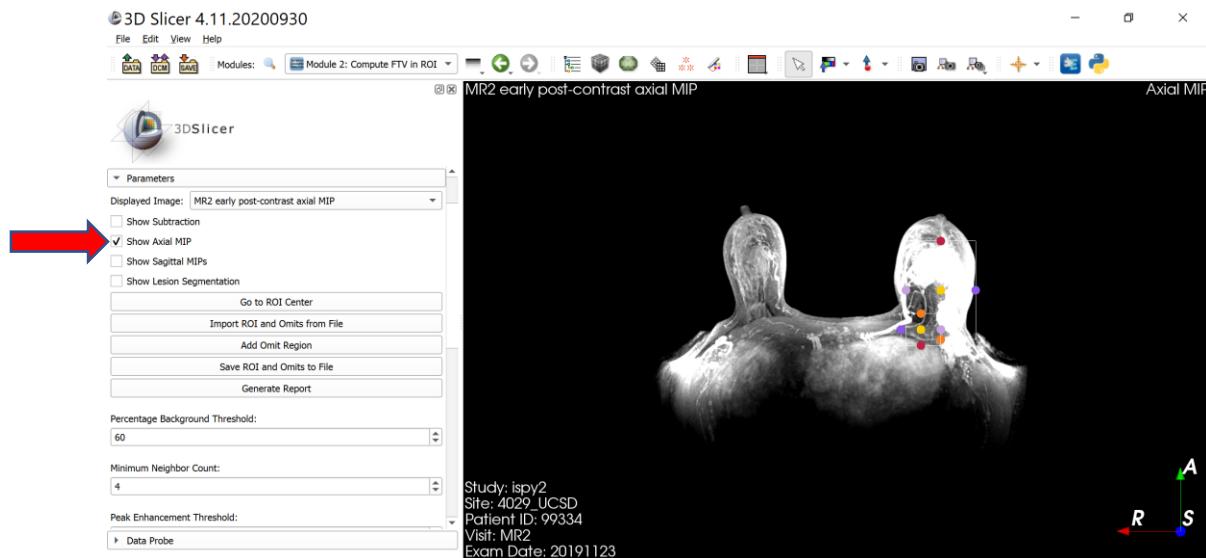
Step 13: Go to ROI Center

13. If you click on the Go to ROI Center button, the module will display the axial and sagittal slices at the center of the current ROI in the current displayed image. **This button is not useful when you are displaying a MIP.**



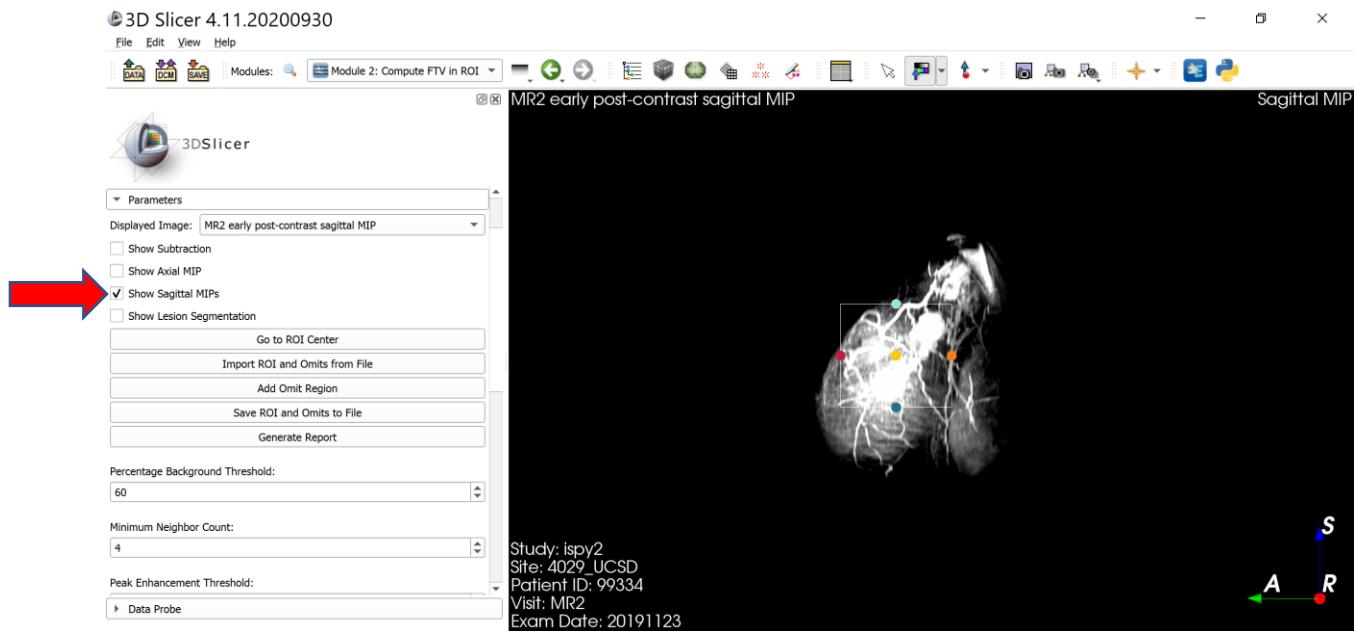
Steps 14-18: Viewing MIPs and Subtractions

14. To show an axial MIP of the image currently displayed in the dropdown menu, click on the checkbox next the words **Show Axial MIP**.



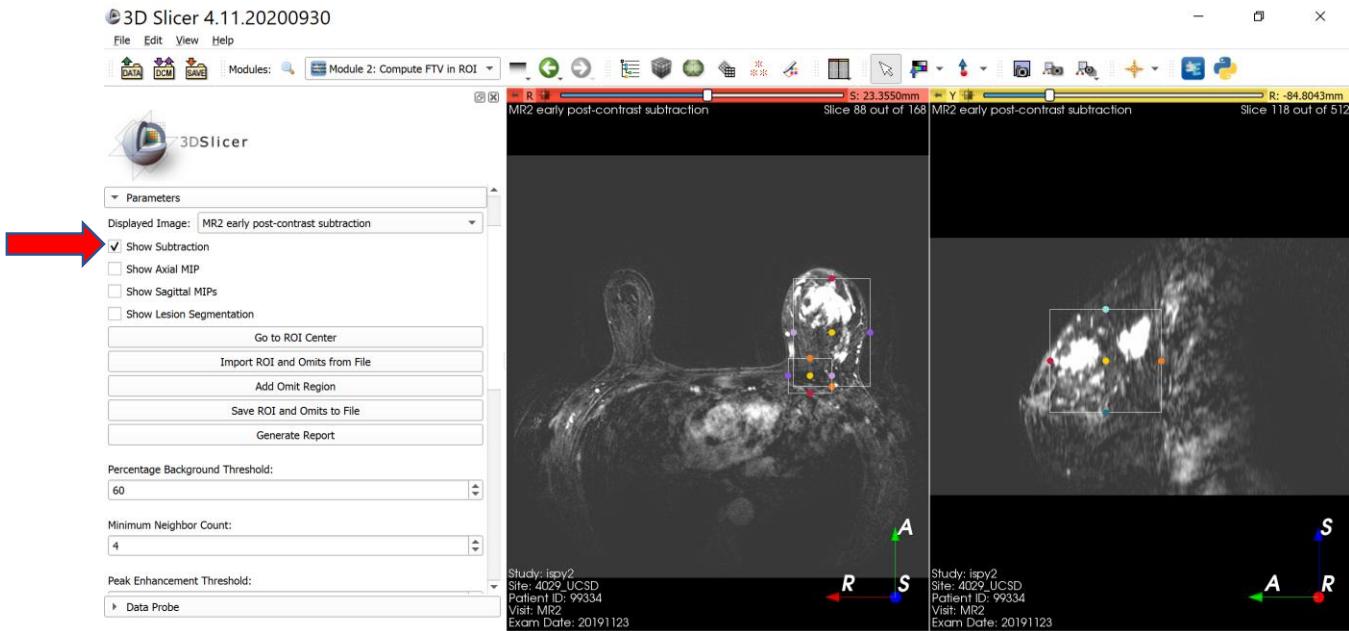
After you click on this checkbox, an axial MIP of the input image (in this case MR2 early post-contrast) is computed and displayed in real-time. To revert back to the input image, click on the checkbox again.

15. To show a sagittal MIP of the image currently displayed in the dropdown menu, click on the checkbox next the words **Show Sagittal MIPs**.



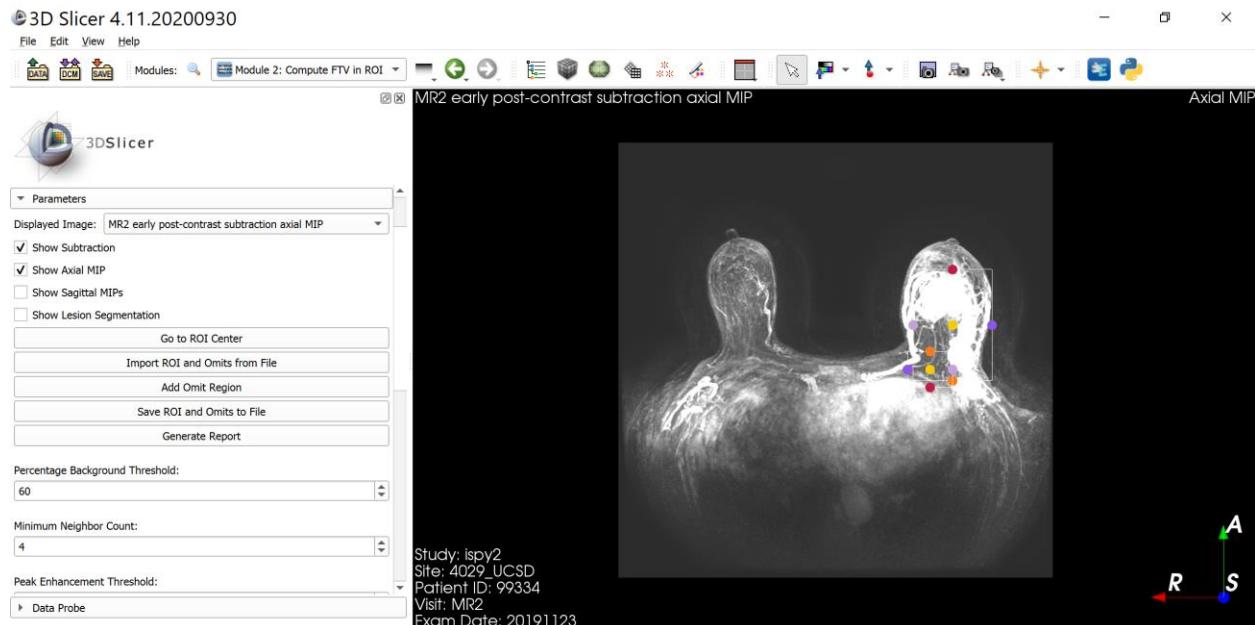
After you click on this checkbox, a sagittal MIP of the input image (in this case MR2 early post-contrast) is computed and displayed in real-time. Although this process creates 2 MIPs, one using sagittal slices from left half of image and the other using sagittal slices from the right half of the image, only the MIP that matches with the sagittal position of the ROI is displayed. To revert back to the input image, click on the checkbox again.

16. To show a subtraction image (input minus pre-contrast) of the image currently displayed in the dropdown menu, click on the checkbox next to the words **Show Subtraction**.



After you click on this checkbox, a subtraction of the input image (in this case MR2 early post-contrast) is computed and displayed in real-time. To revert back to the input image, click on the checkbox again.

17. You can also view a subtraction axial MIP or subtraction sagittal MIP by checking the **Show Subtraction** box and one of the MIP boxes. From there, you can revert back to the non-subtracted MIP by unchecking the **Show Subtraction** box, or revert back to the 3D subtraction image by unchecking the MIP box, or revert back to the original input image (in this case MR2 early post-contrast) by unchecking both boxes.

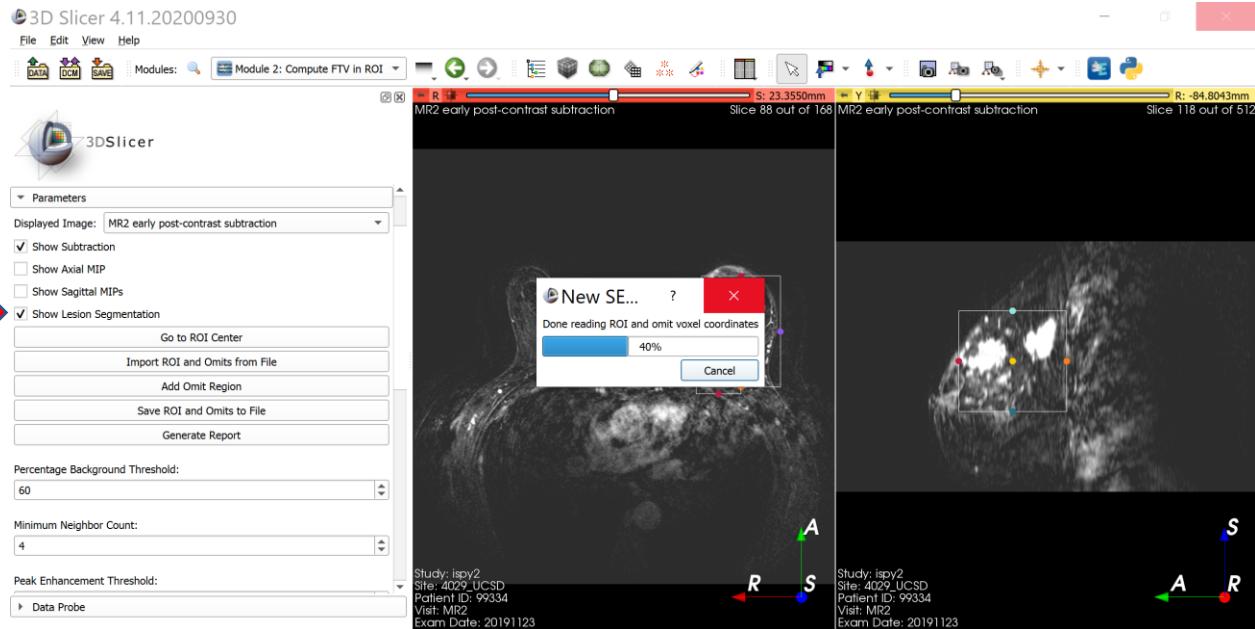


18. When you select another image from the dropdown menu while checkbox(es) are checked, the MIP, subtraction, or subtraction MIP of the new image will automatically be displayed. For example, if you are viewing the MR2 early post-contrast subtraction, and then select MR2 late post-contrast from the dropdown menu without first unchecking the **Show Subtraction** checkbox, the MR2 late post-contrast subtraction image will be displayed instead of the MR2 late post-contrast image. The only exception to this rule is when you have the **Show Subtraction** checkbox checked and switch to a pre-contrast image from the dropdown menu.

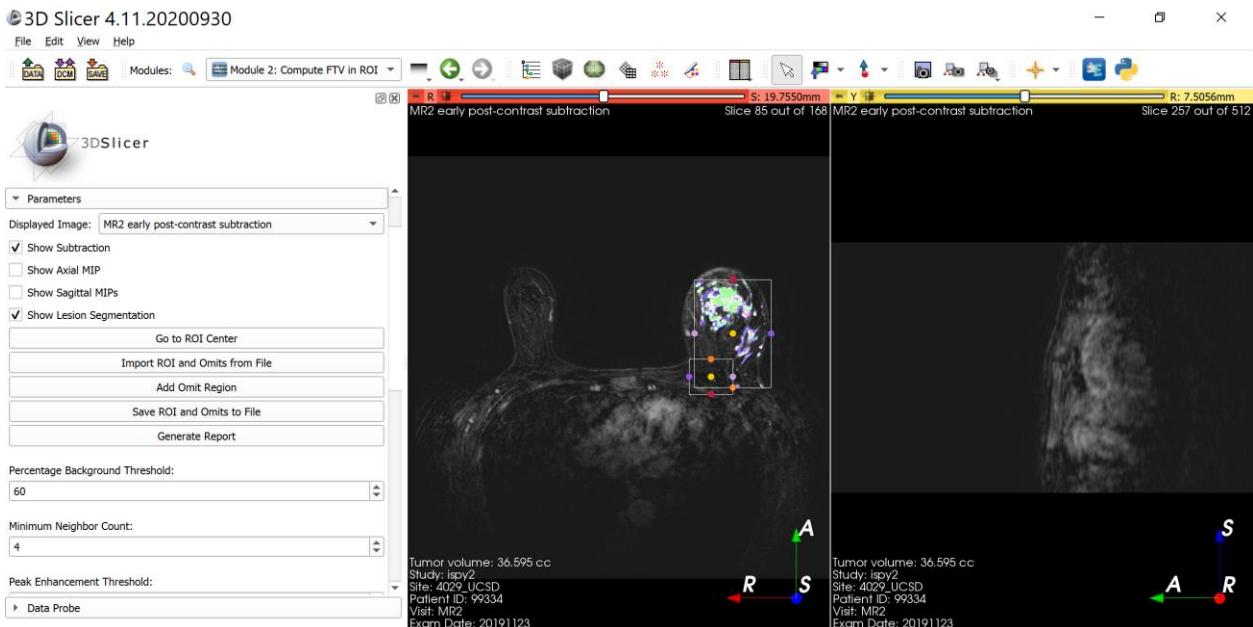
Step 19: Showing SER Colorized Lesion Segmentation

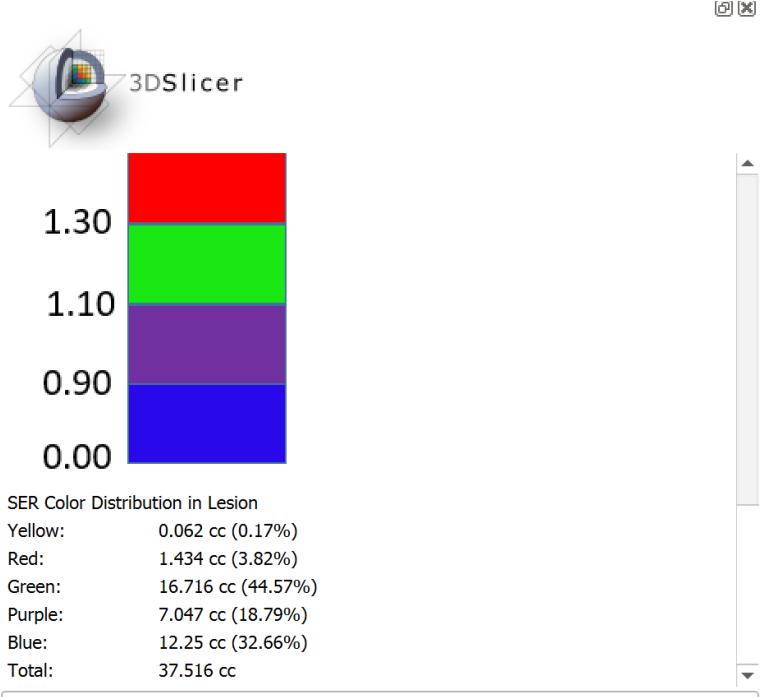
19. To overlay an SER colorized lesion segmentation onto the ROI, check the box next to the words **Show Lesion Segmentation**. Once the box is checked, a progress bar appears to provide updates on the progress of processing this request.

Warning: Do not press the Show Lesion Segmentation checkbox more than once. Ignore “not responding” warnings, and do not worry if the progress bar takes a long time to update (it will be stuck at 40% for most of the processing time). Slicer should take roughly 1.5 to 3 minutes to complete this step.



Once the progress bar disappears, the SER colorization will be superimposed on the displayed image. In addition, the FTV in cc will be added to the current exam details in the red and yellow slice views, and the distribution of tumor voxels by SER color will be added to the bottom of the module widget, underneath the **SER Color Ranges** image.

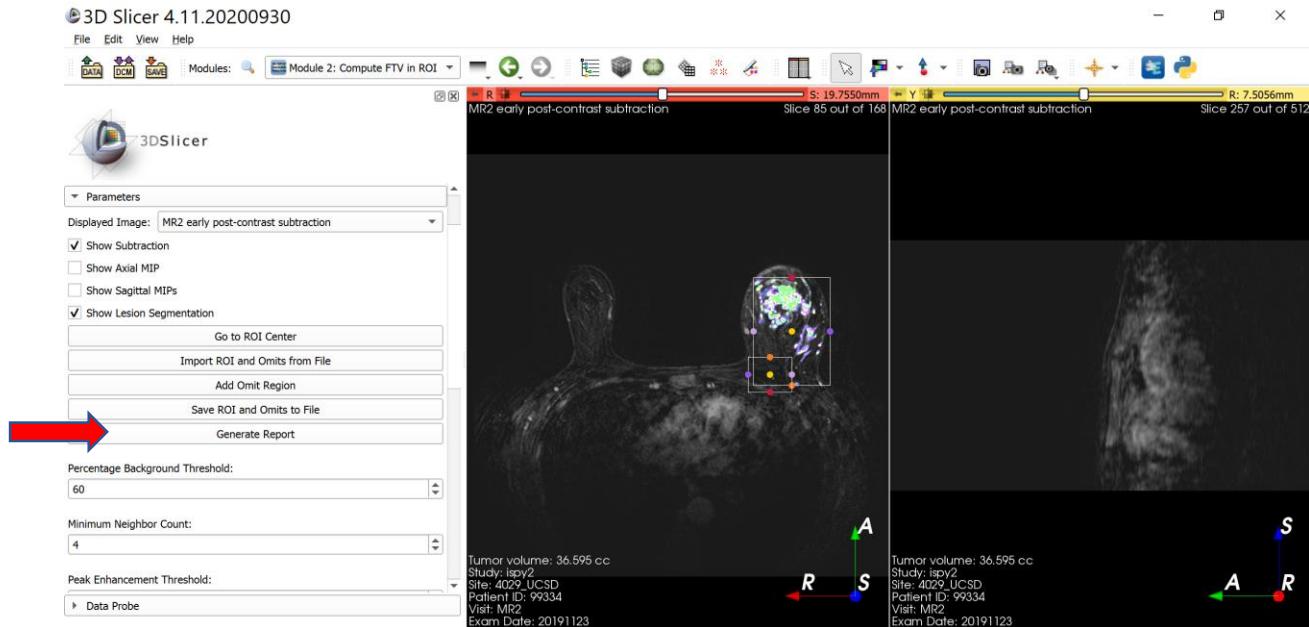




After the lesion segmentation has been computed and overlayed on the slice views, it can be easily and quickly be removed from/added back to the scene by checking/unchecking the **Show Lesion Segmentation** box, as long as ROI and omits and all 3 segmentation thresholds remain unchanged. However, if any of these are changed, a new lesion segmentation must be created the next time you check the box.

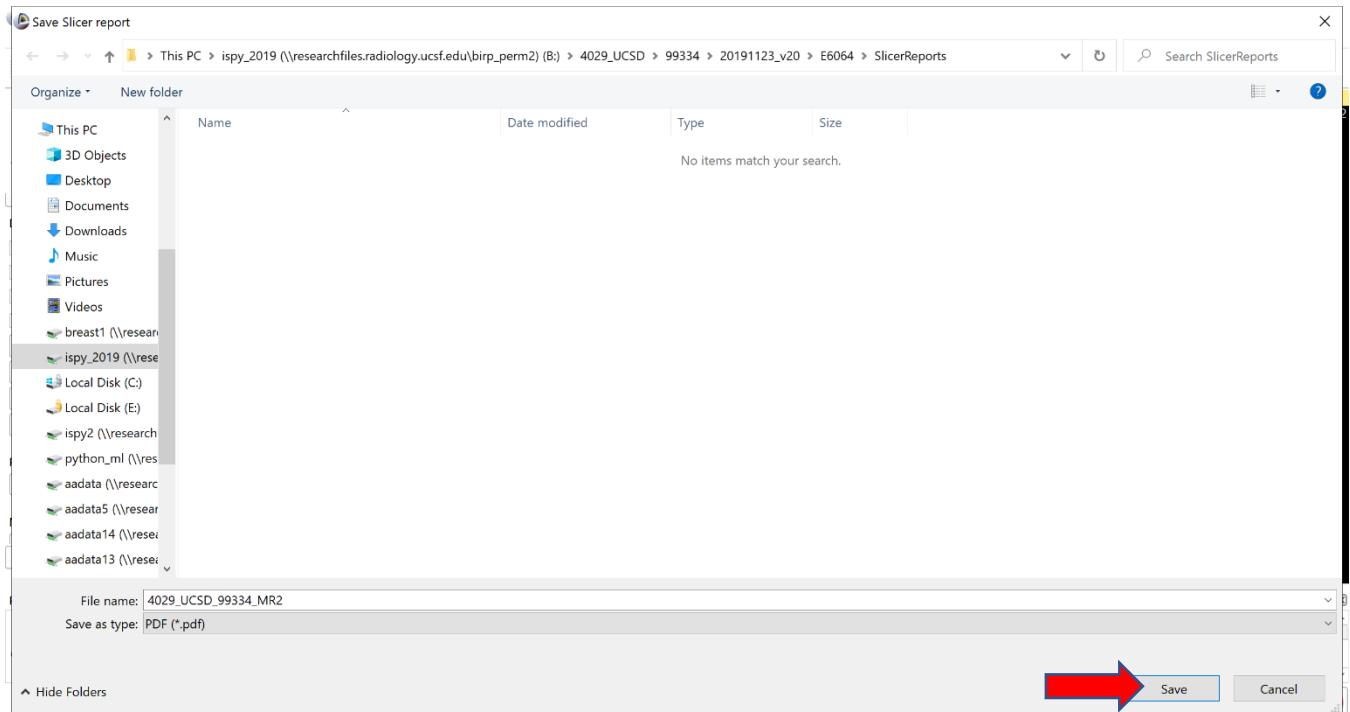
Steps 20-21: Generating Slicer Report

- 20.** To generate a pdf report like the one created by Aegis, click the **Generate Report** button. Once you do this, a progress bar will appear.



Warning: Do not press the Generate Report button more than once. Ignore “not responding” warnings. The progress bar will be stuck at 1%, then suddenly jump to 50% after about 1.5 to 2.5 minutes.

When the progress bar reaches 50%, a save menu appears. In this menu, the save location for the report is automatically set to a SlicerReports folder that is created inside the exam folder. By default the report's name is <site name>_<ISPY ID>_<visit>.pdf, but you can edit the “File Name” field to change this. Once you have finalized the file name, press “Enter” or click the “Save” button.

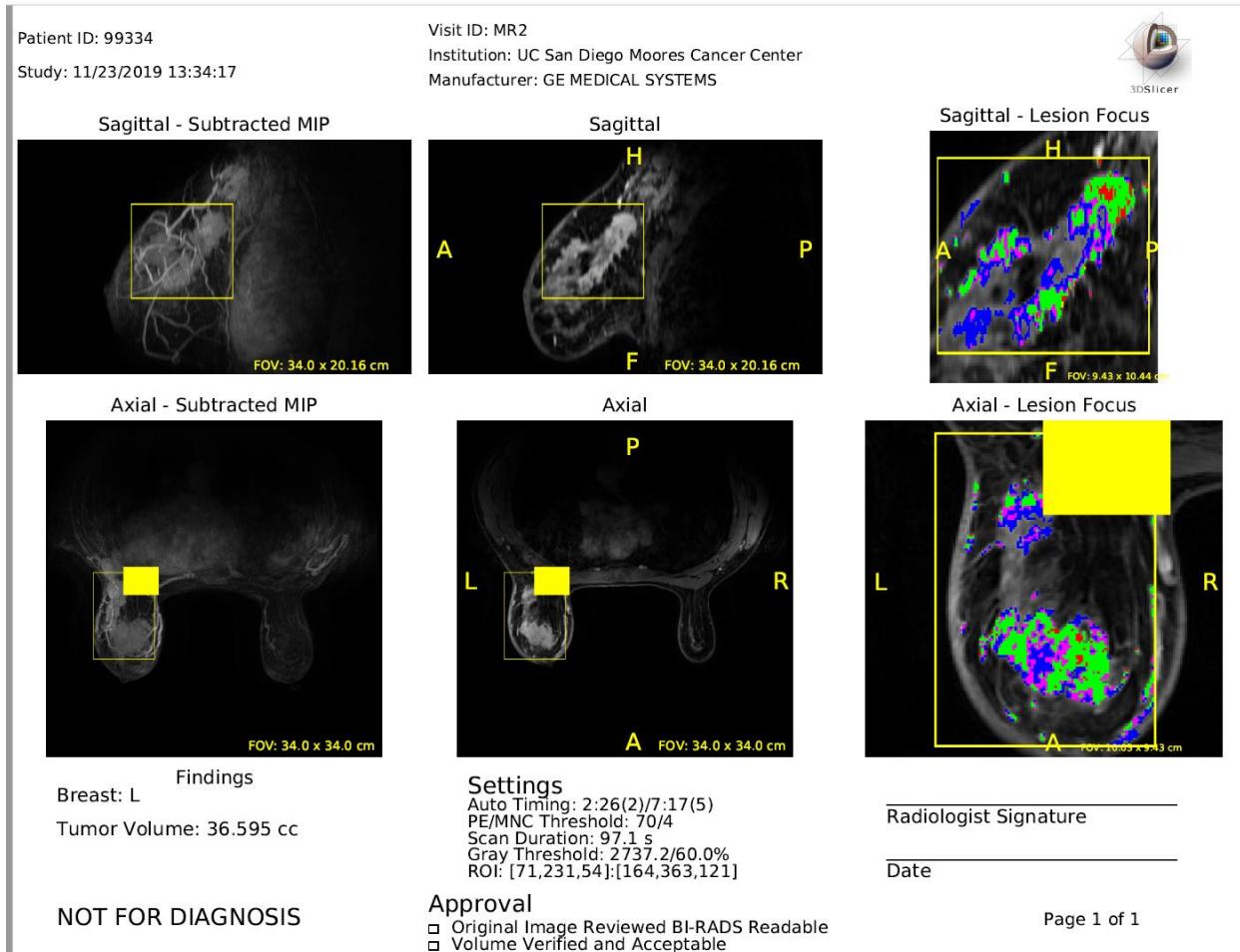


Warning: Progress bar will be stuck at 50% for a while, then suddenly jump to 99% after about 2.5 minutes.

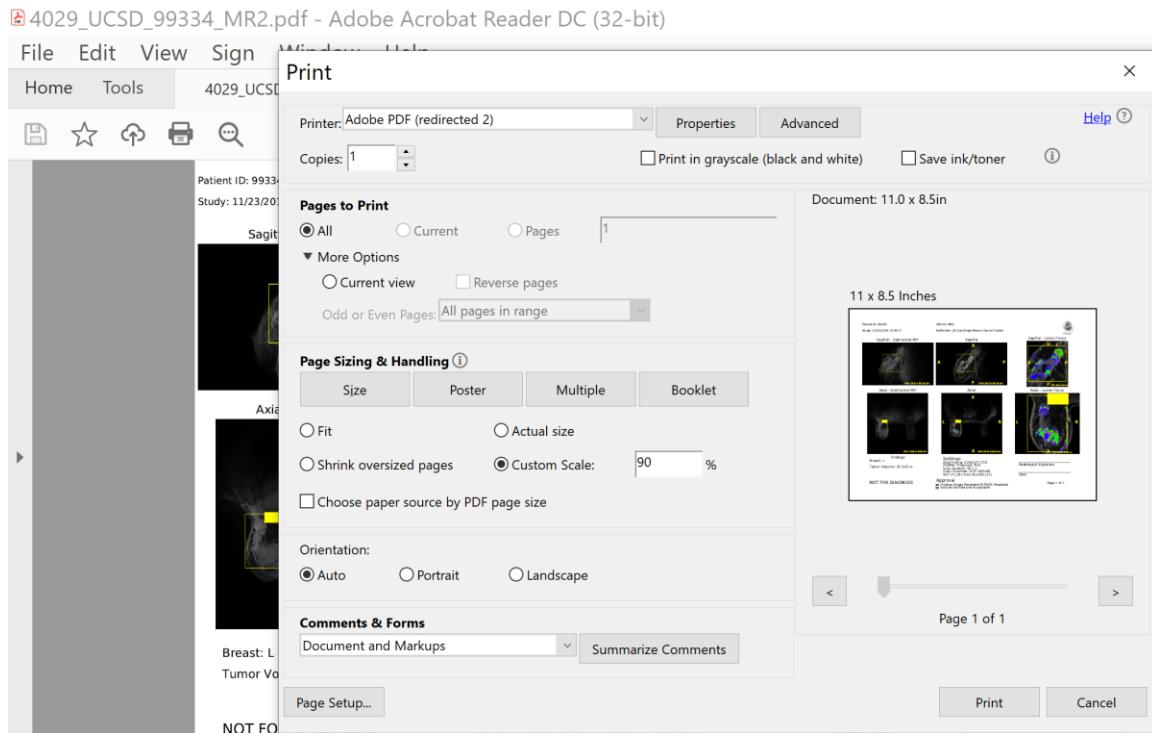
When the module has finished creating and saving the report, the progress bar will disappear and the words “Processing completed” will be printed to the Python Interactor.

To open the report, navigate to the SlicerReports folder for this exam. The report is saved as a pdf, jpeg and DICOM, which all have the name you gave the pdf. This report has all of the images (including ROI & omits) and text fields seen in the Aegis report.

An example of the Slicer report is shown below.

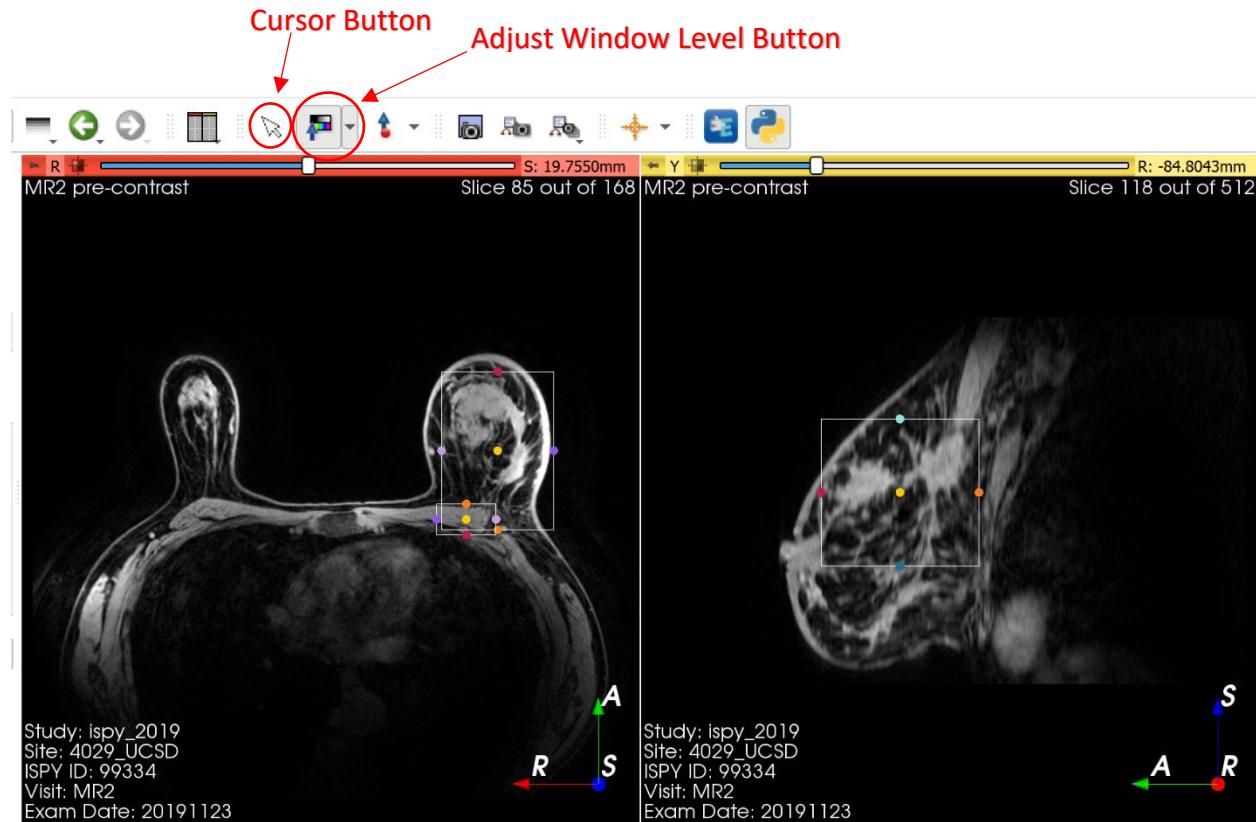


21. If you want to print the report, you will have to adjust its orientation and size so that its contents are not too close to the edges of the page. For example, in the picture below, the Orientation has been set to Auto and a Custom Scale of 90% is being used.



Appendix: Built-in Slicer Features to Use While Running Module 2

Window Level Adjustment

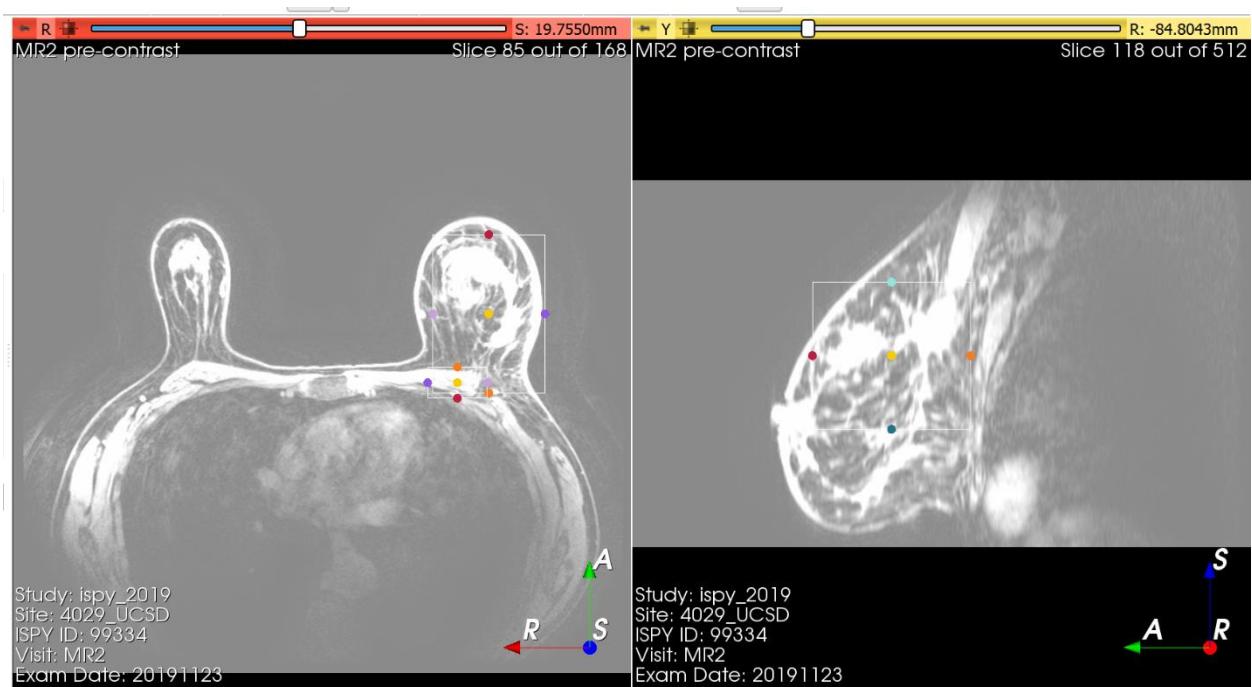


To adjust the window level, click on the **Adjust Window Level** button. Then, you can do any of the following:

Left click + drag up – makes all pixels more black



Left click + drag down – makes all pixels more white. This is the opposite effect from left click + drag up.



Left click + drag left – makes image look more black and white.



Left click + drag right – makes image look more uniform in intensity (all grey). This is the opposite effect from left click + drag left.



When you are done with these adjustments, click on the cursor button. Module 2 has been programmed so that the window level adjustments that the user makes with this tool are applied to all images that the user can display as well as the report.

Zoom

To adjust zoom in a particular view (eg red axial view)

Zoom out: Right click + drag up

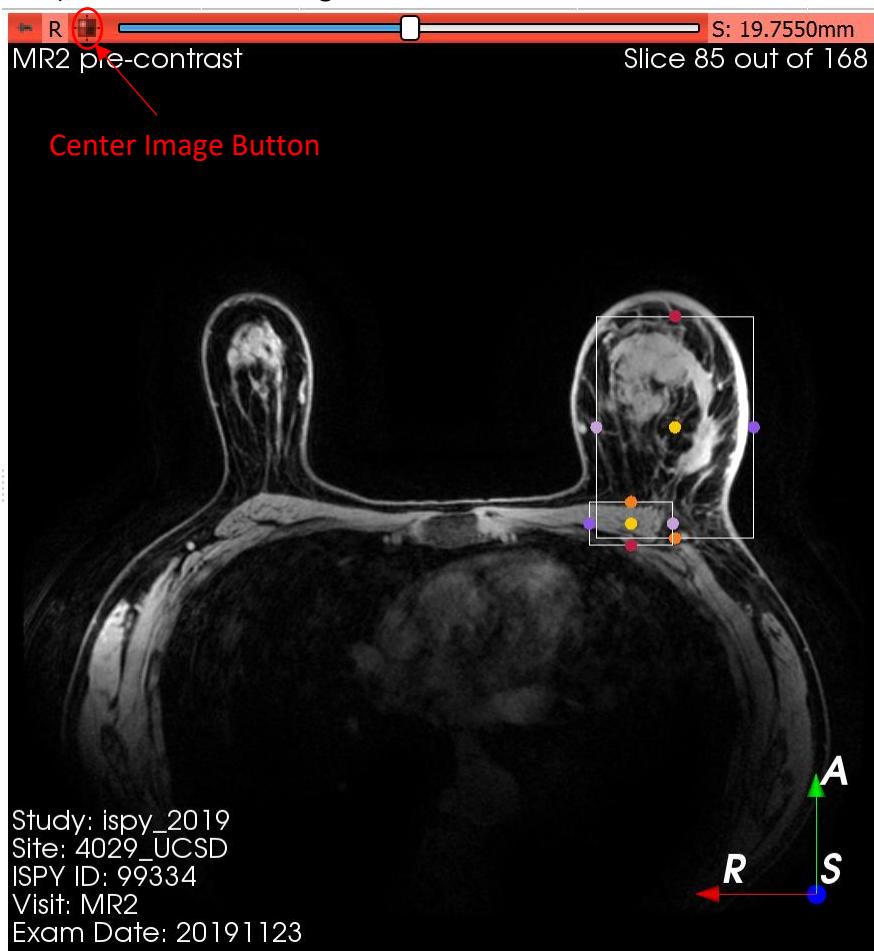
Zoom in: Right click + drag down

Shift Image

To shift the position of the image within a view (eg red axial view), do Shift + left click + drag up/down/left/right to shift the image up/down/left/right.

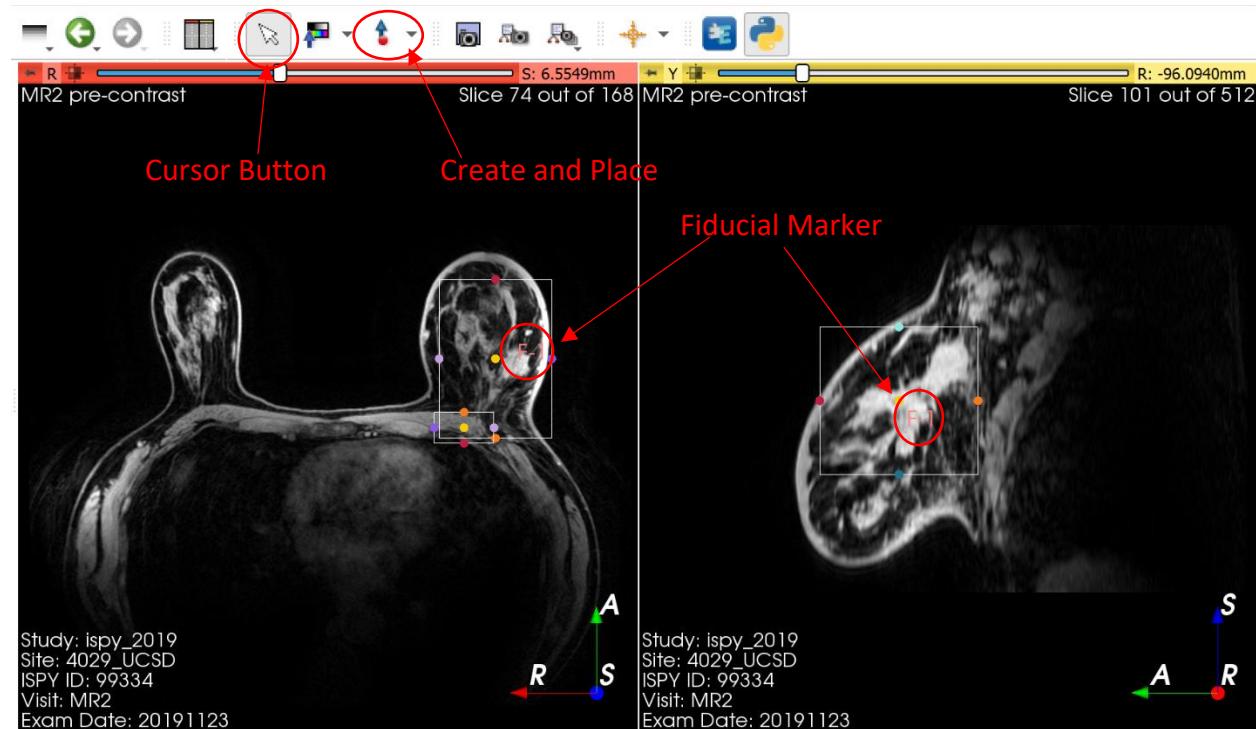
Center Image

To reset image zoom, shift, and slice slider back to their default positions within a view (eg red axial view), click the **Center Image** button.



Fiducials

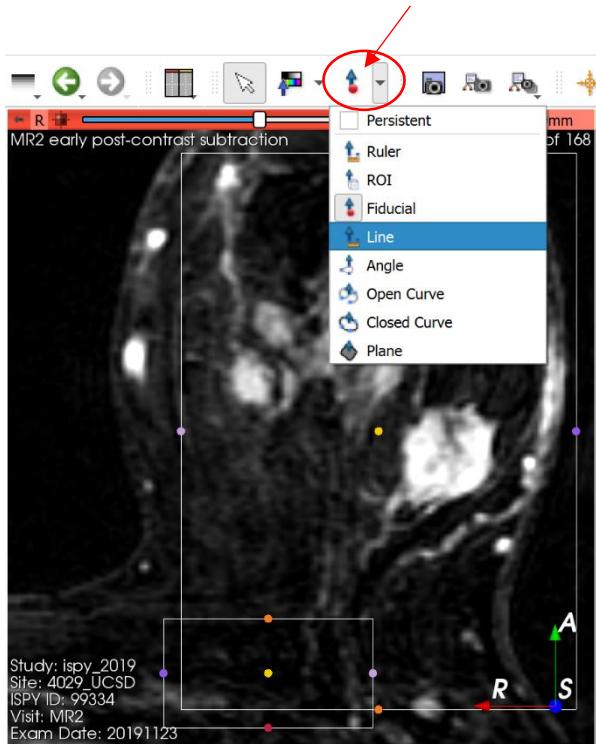
To place a fiducial marker on the image, select the **Fiducial** option from the **Create and Place** menu arrow. Then, in any of the slice views, click on the location where you want to place the fiducial marker. The 1st fiducial marker will show up as a dot with the text **F-1** written above it, the 2nd one will say **F-2**, and so on. The fiducial marker only occupies one voxel, so to find its exact position on the red or yellow view, use the left and right arrows to scroll through slices in that view. To stop placing fiducials and return to using the regular cursor, click on the **Cursor** button.



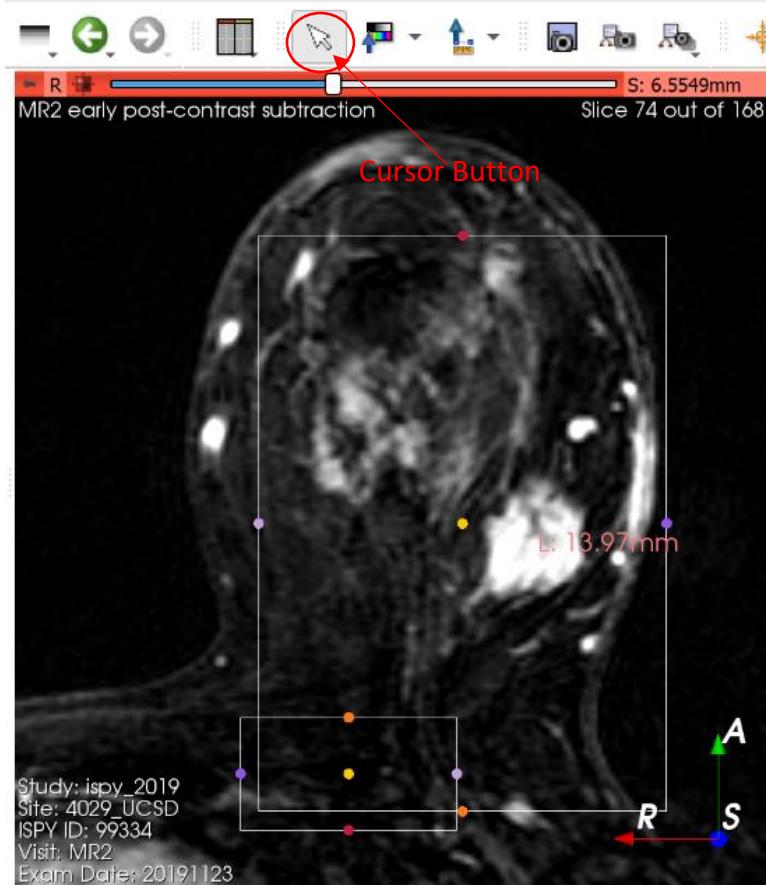
Measurement Line

To measure the diameter of a region of the image, such as the tumor, click on the **Create and Place** menu arrow, then select the **Line** option.

Create and Place

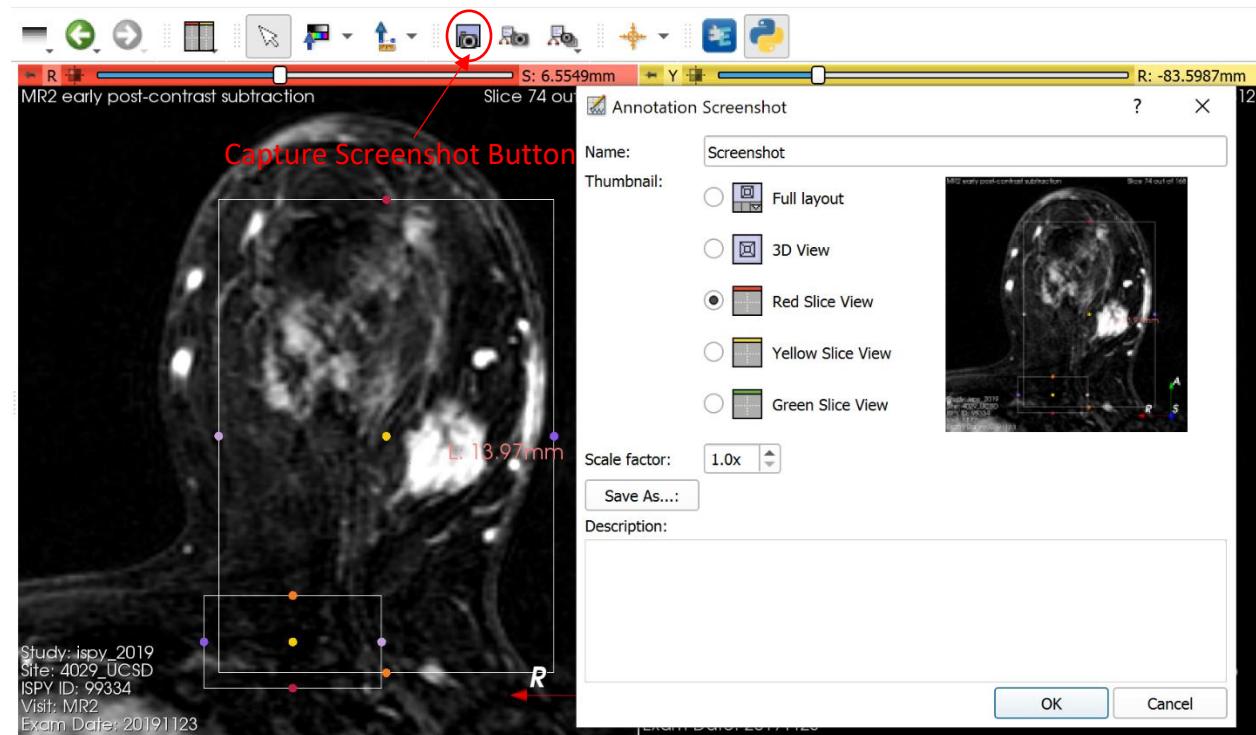


Once you have selected the **Line** tool, click one time where you want the start point of the line to be, then click a second time somewhere else to place the endpoint. The length in mm will be written directly above the line. When you are done placing the line, click the **Cursor** button to go back to using a normal mouse.



Capture Screenshot

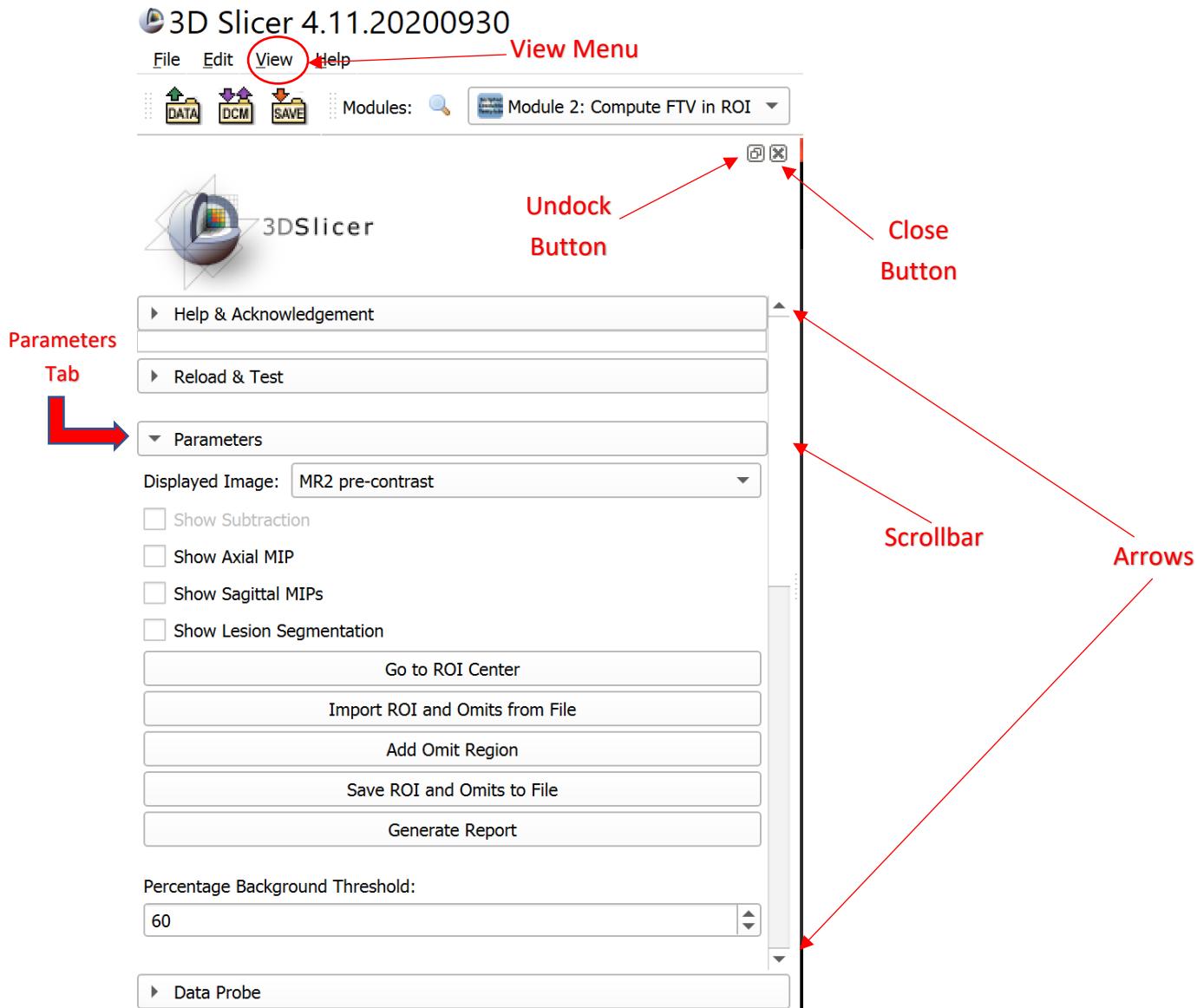
If you want to save this tumor measurement view to an image file, you can use built-in Slicer functionality to do so. Click on the **Capture Screenshot** button. In the Annotation Screenshot pop-up that appears after you click this button, you can choose which slice view(s) you want to save, click on the **Save As...** button to choose image location and save name, then press the **OK** button to confirm.



Undocking and Redocking Module Widget

By default, the module panel is located on the left side of the Slicer window, directly under the module selection menu. Here are the key features:

- Currently selected module's widget is located under the **Parameters** tab. Click on this tab to hide or show widget.
- To make module panel a separate window, click on the **Undock** button. Then, drag corners of module panel window to increase its height or width.
- Use scrollbar or arrows to move up/down to part of widget you need.
- Click **Close** button to remove module panel from view. To bring it back, select **Module Panel** from the **View** menu



To re-dock the module after it has been undocked, drag it to one of the edges of the main Slicer window until you see a blue highlighted region, then release the mouse.

