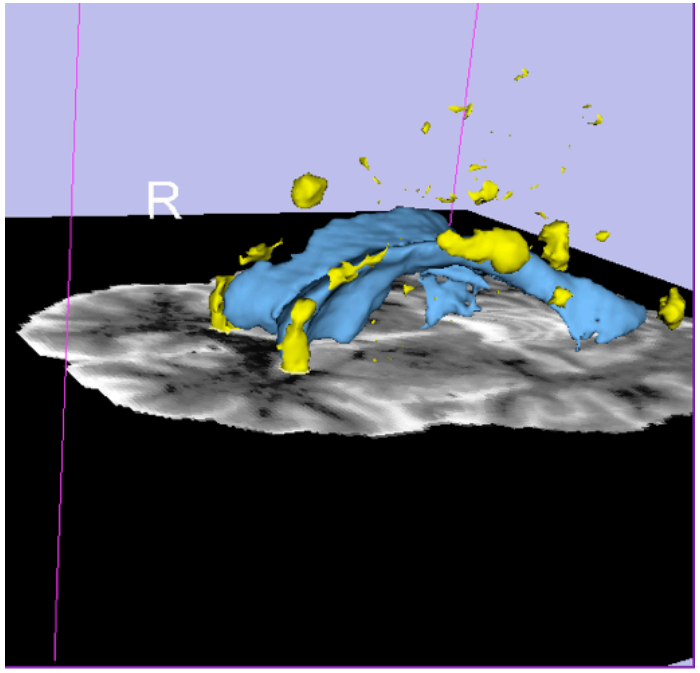
Detecting White Matter Lesions in Lupus



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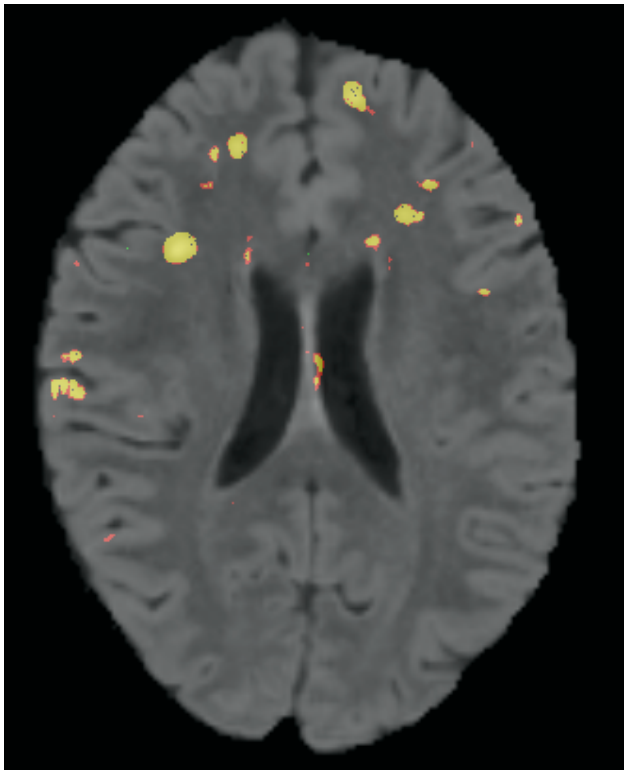
Mark Scully

Learning objective



This tutorial demonstrates an automated, multi-level method to segment *white matter brain lesions* in lupus.

Following this tutorial, you'll be able to load scans into Slicer3, and segment and measure the volume of white matter lesions on the provided data-set.

Prerequisites

This tutorial assumes that you have already completed the tutorial **Data Loading and Visualization**. Tutorials for **3DSlicer** are available at the following location:

http://www.na-mic.org/Wiki/index.php/Slicer3.2:Training

Material

This course requires the following installation:

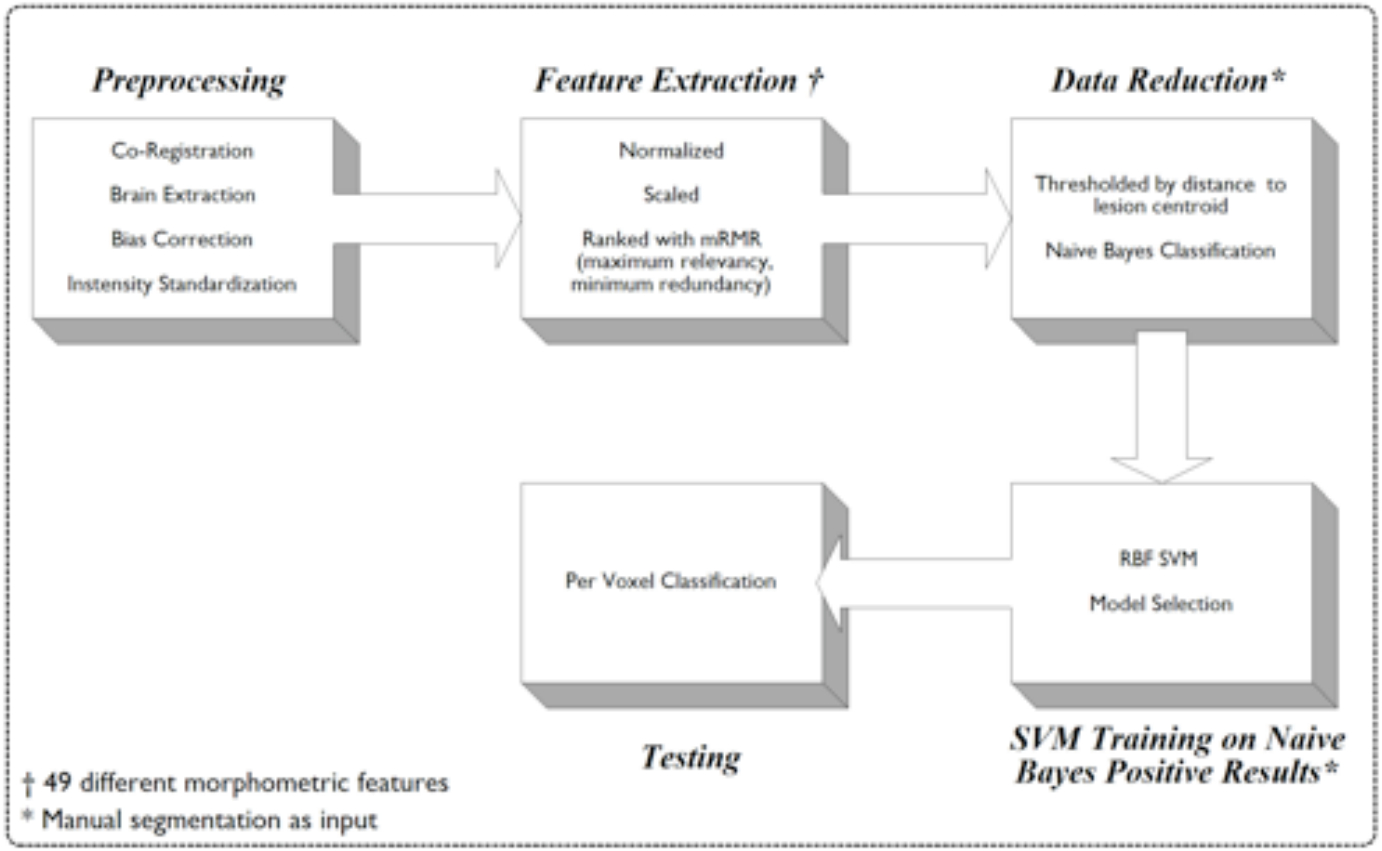
- The current stable version of 3DSlicer 3.4 Software which can be installed from:
  - http://slicer.org/pages/Special:SlicerDownloads
- The White Matter Lesion module extension to 3DSlicer
  - (see follow on instructions on slides 7-9 of this tutorial)
- The Lupus Lesion Tutorial Data, which can be downloaded from:
  - http://wiki.na-mic.org/Wiki/images/c/c8/LesionSegmentationTutorialData.tgz

- n.b., a reliable internet connection will be required for downloading the data

Disclaimer

It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules.

Methods



Flowchart summarizing the *training pipeline* for the white matter lesion classification procedure employed in this tutorial.

Methods

The method makes use of local morphometric features based on multiple MR sequences, including **T1-weighted**, **T2-weighted**, and **Fluid Attenuated Recovery** from ten subjects.

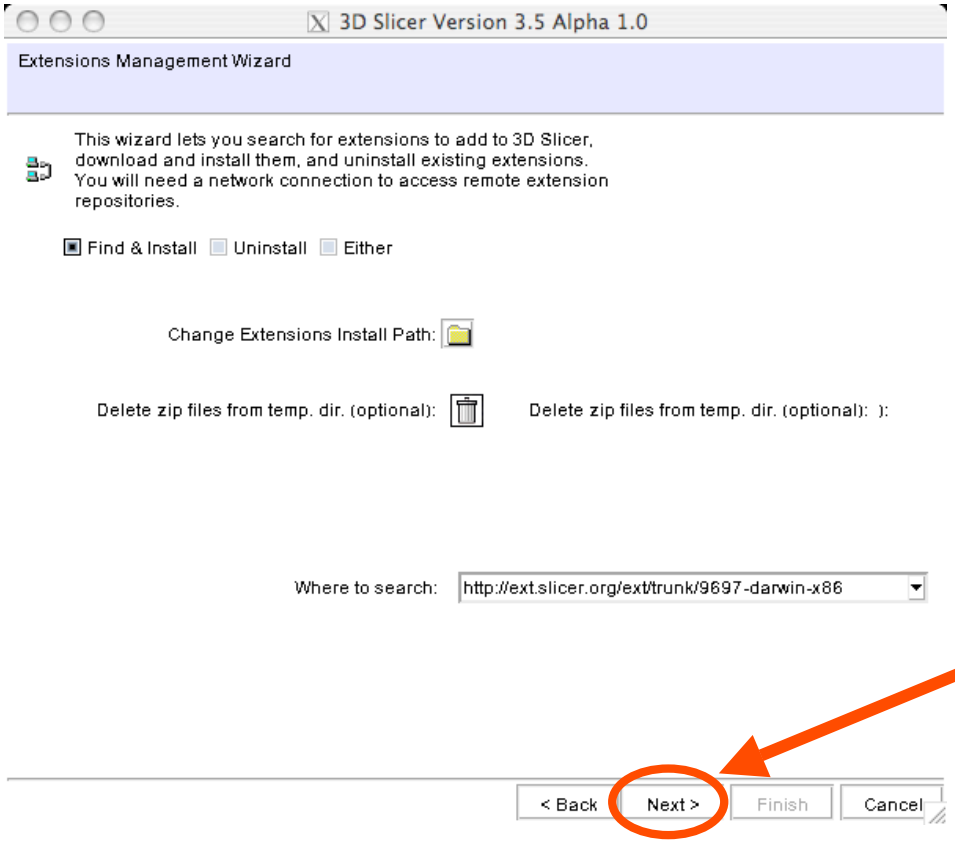
After preprocessing, including co-registration, brain extraction, bias correction, and intensity standardization, 49 features were calculated for each brain voxel based on local morphometry.

At each level of segmentation a supervised classifier takes advantage of a different subset of the features to conservatively segment lesion voxels, passing on more difficult voxels to the next classifier.

This multi-level approach allows for a fast lesion classification method with tunable trade-off between sensitivity and specificity, with accuracy comparable to a human rater.

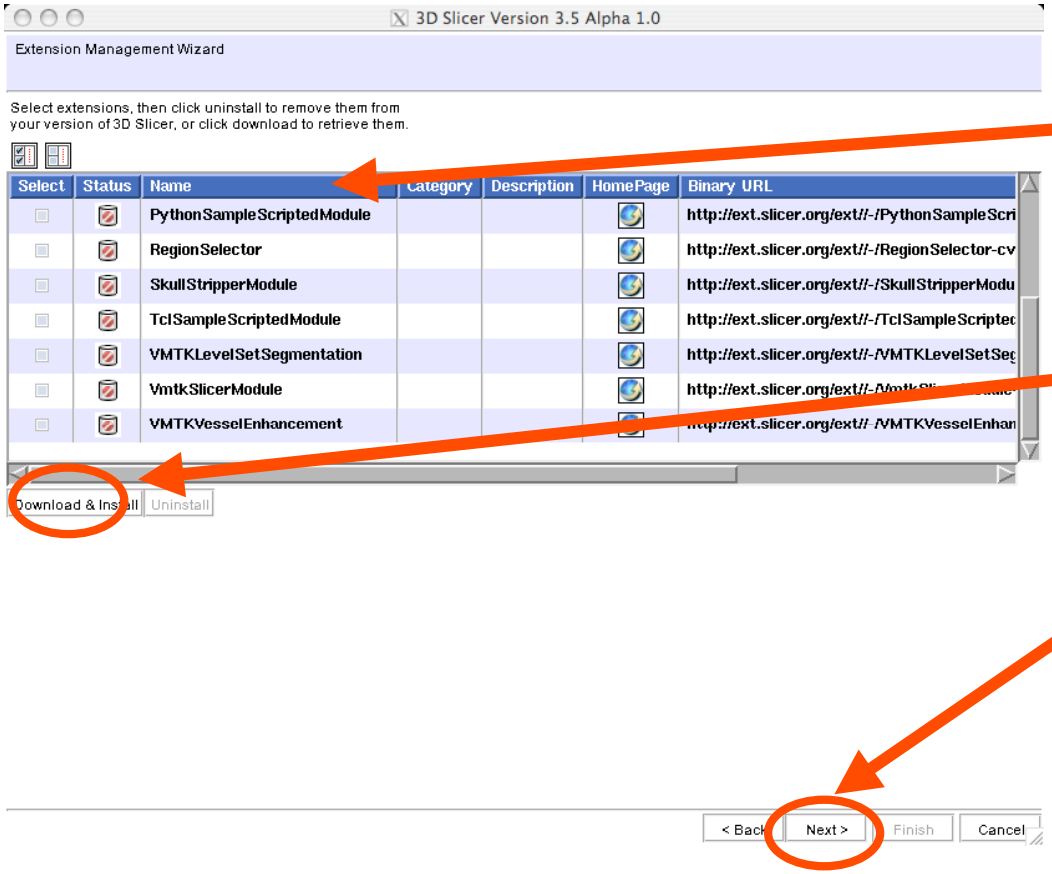
When applying the above classifier to novel data sets, such as the sample data in this tutorial, the user should follow 3 steps (described on slides 11-20) to apply the classifier to the data set they wish to predict lesions upon.

Finding the Module



- To add the external module, Select the **Extensions Management Wizard** from the **View** menu within 3DSlicer.
- Click **next** to search the external site for the appropriate module to install.

Installing the Module

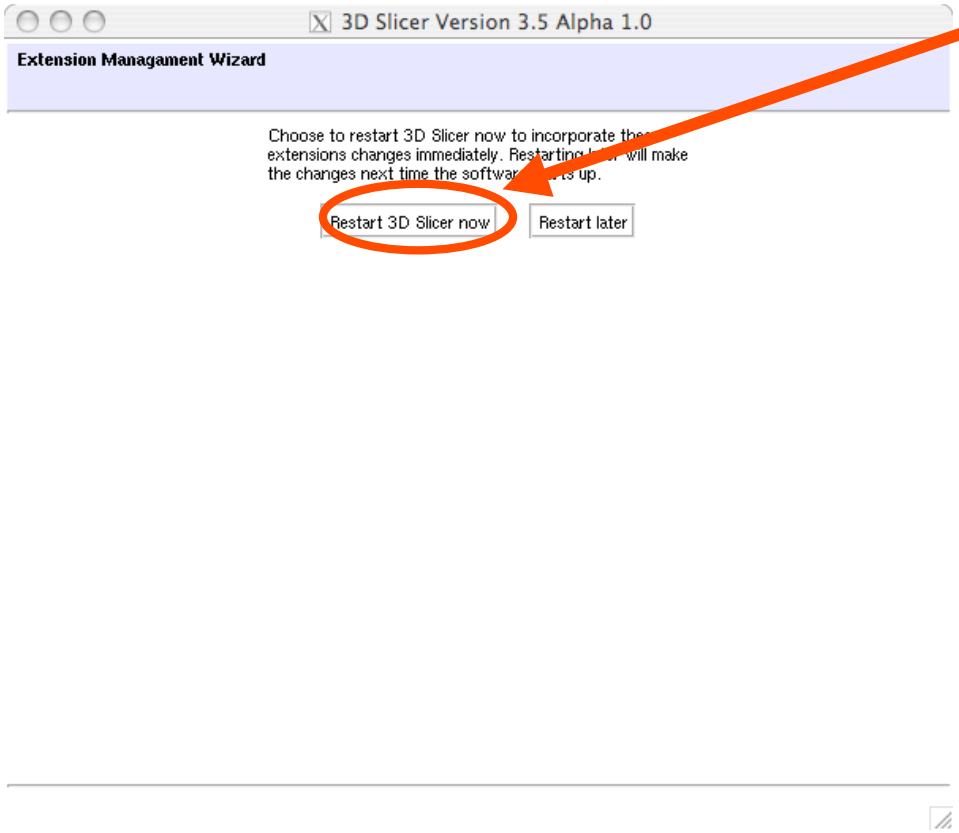


Select **LesionSegmentationApplications** from the list

Click **Download & Install**.

Click **Next** after the status turns green

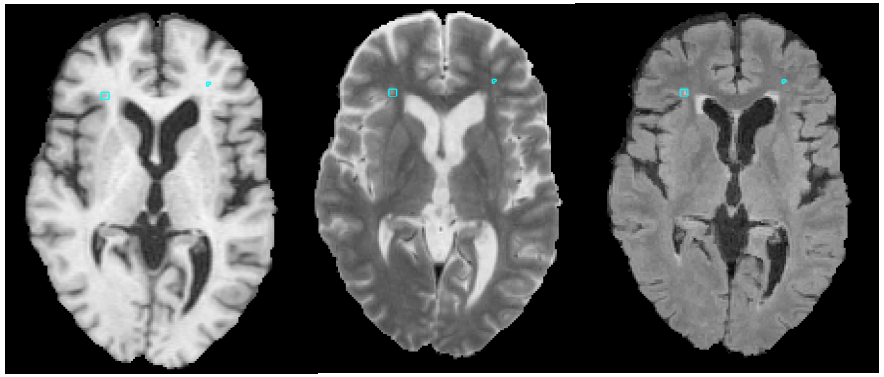
Finish Installing Module



Click **Restart 3D Slicer** now once you have installed the module

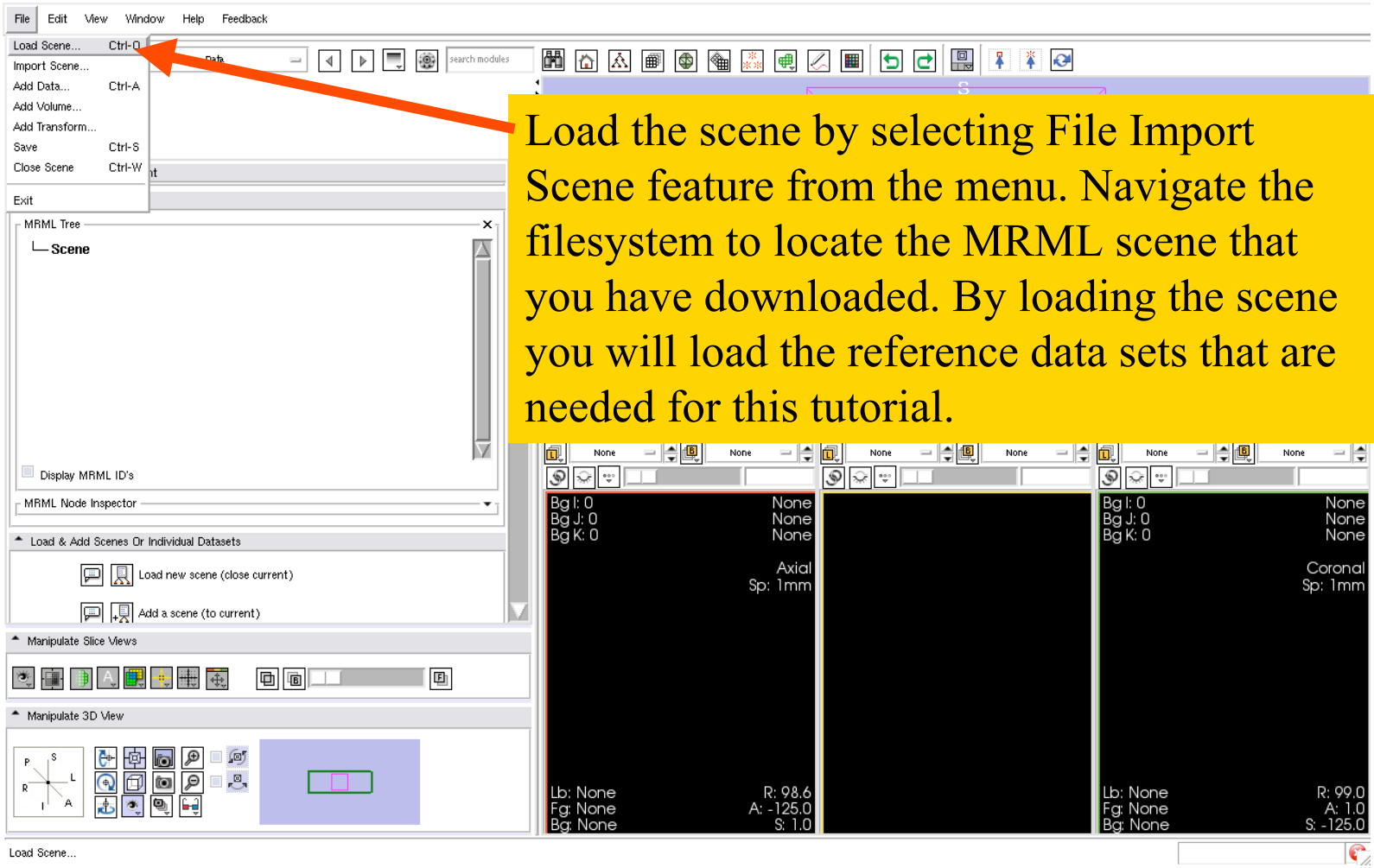
Tutorial Data

This course is built upon two scans of patients with lupus that have **T1**, **T2**, and **FLAIR** images. These images have been co-registered and brain extracted outside of the scope of this tutorial. Also, the tutorial data contains model files that support the module introduced in this tutorial. Finally, results files from one subject are included in the tutorial data. The following summary shows the contents of the **LesionSegmentationTutorial** archive once downloaded and uncompressed to your filesystem.



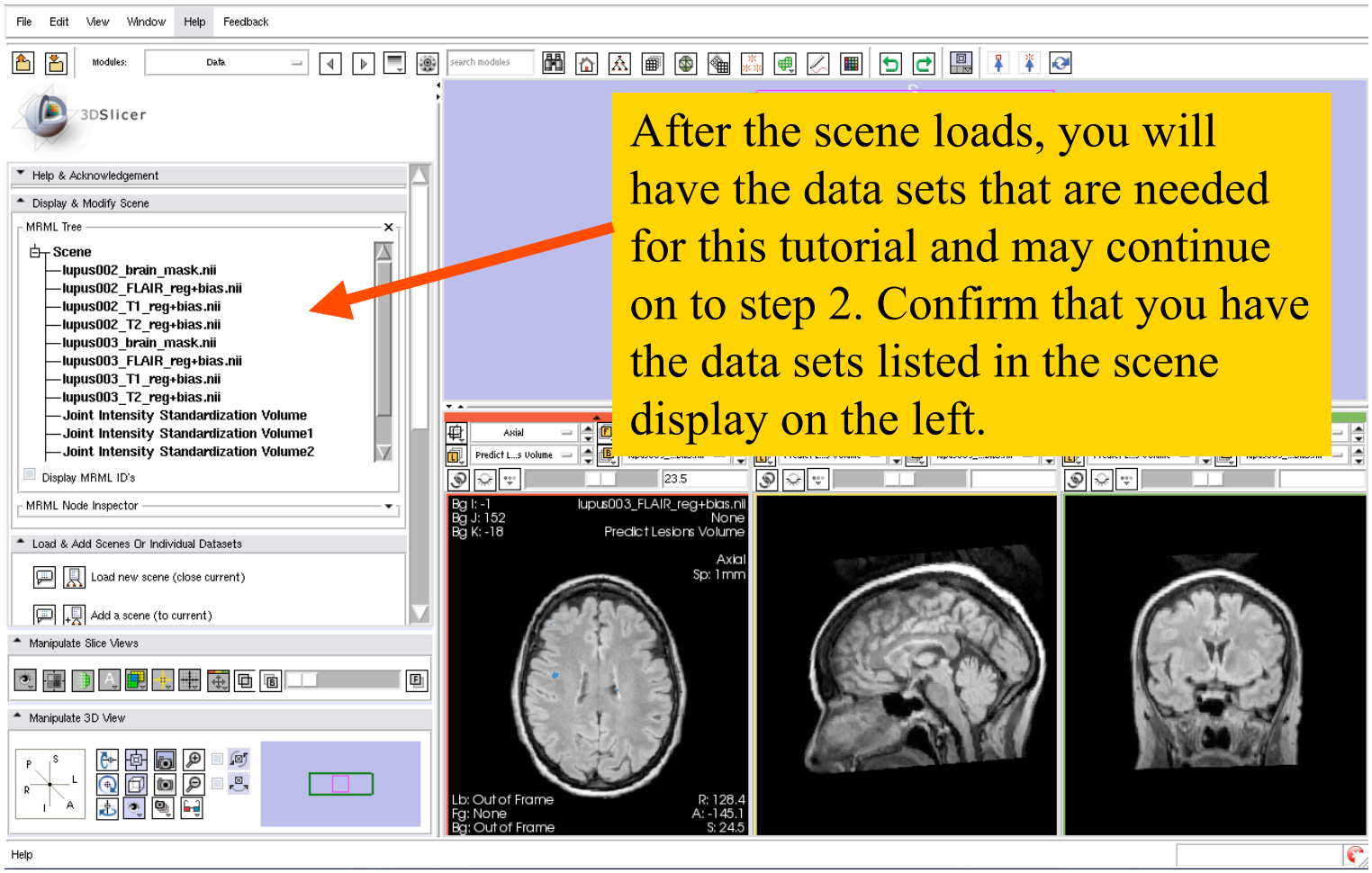
Joint Intensity Standardization Volume.nhdr
Joint Intensity Standardization Volume.raw.gz
Joint Intensity Standardization Volume1.nhdr
Joint Intensity Standardization Volume1.raw.gz
Joint Intensity Standardization Volume2.nhdr
Joint Intensity Standardization Volume2.raw.gz
LesionSegmentTutorial.mrml
Predict Lesions Volume.nhdr
Predict Lesions Volume.raw
Predict Lesions Volume1.nhdr
Predict Lesions Volume1.raw
lesionSegmentation.model
lupus002_FLAIR_reg+bias.nii.gz
lupus002_T1_reg+bias.nii.gz
lupus002_T2_reg+bias.nii.gz
lupus002_brain_mask.nii.gz
lupus003_FLAIR_reg+bias.nii.gz
lupus003_T1_reg+bias.nii.gz
lupus003_T2_reg+bias.nii.gz
lupus003_brain_mask.nii.gz
svm.model

Module Step1: Setup



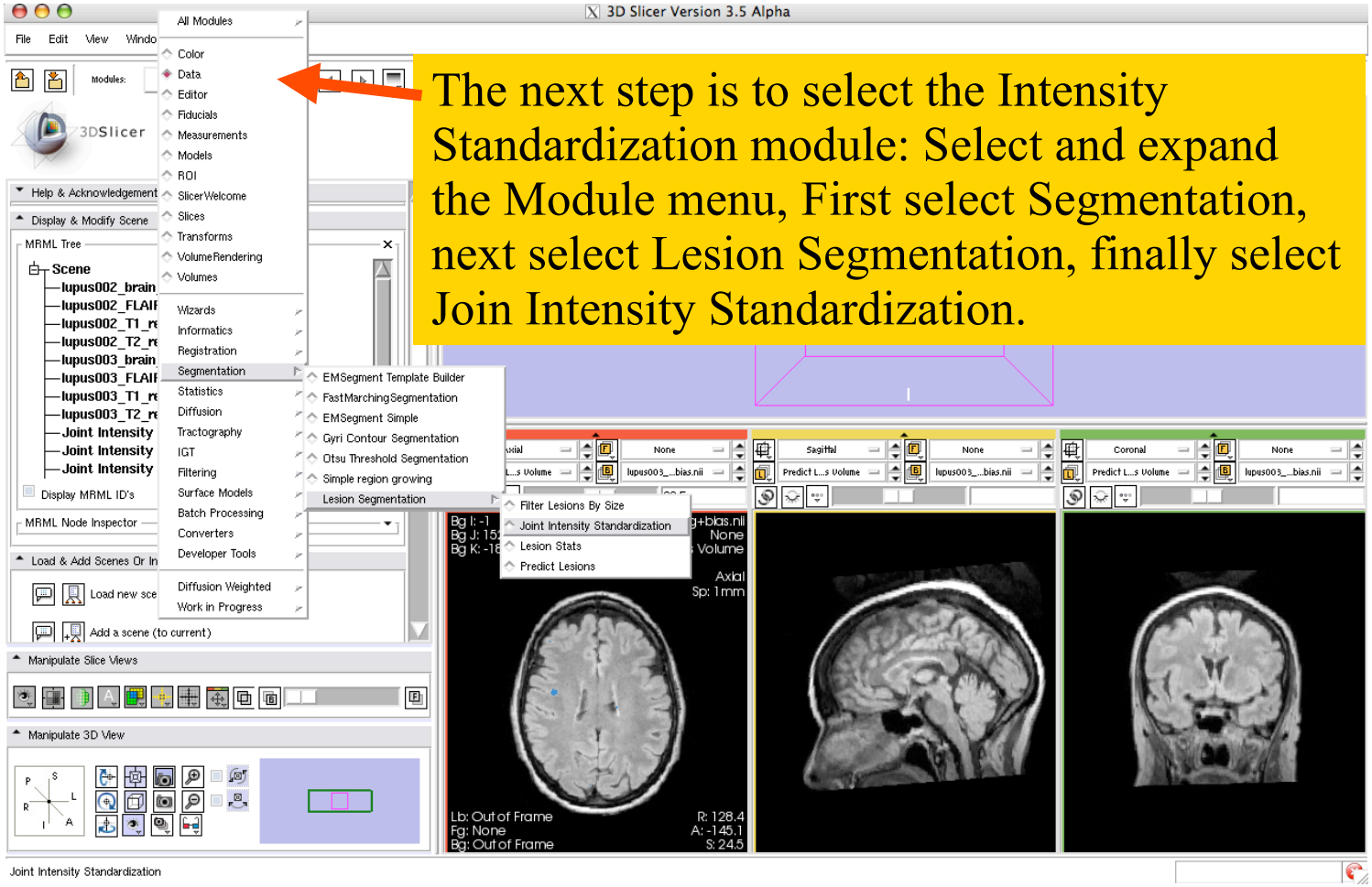
Load the scene by selecting File Import Scene feature from the menu. Navigate the filesystem to locate the MRML scene that you have downloaded. By loading the scene you will load the reference data sets that are needed for this tutorial.

Module Step 1: Results



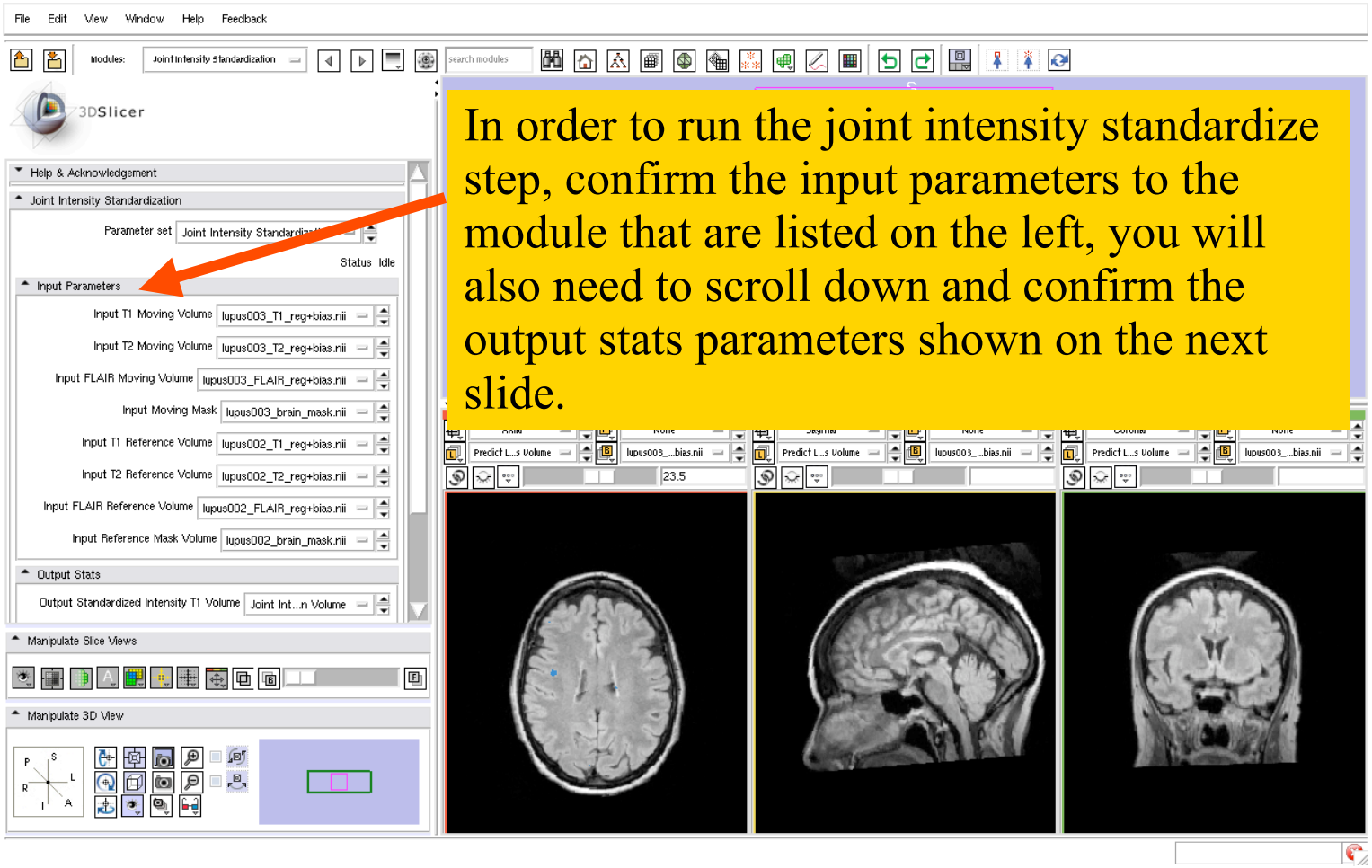
After the scene loads, you will have the data sets that are needed for this tutorial and may continue on to step 2. Confirm that you have the data sets listed in the scene display on the left.

Module Step 2: Setup

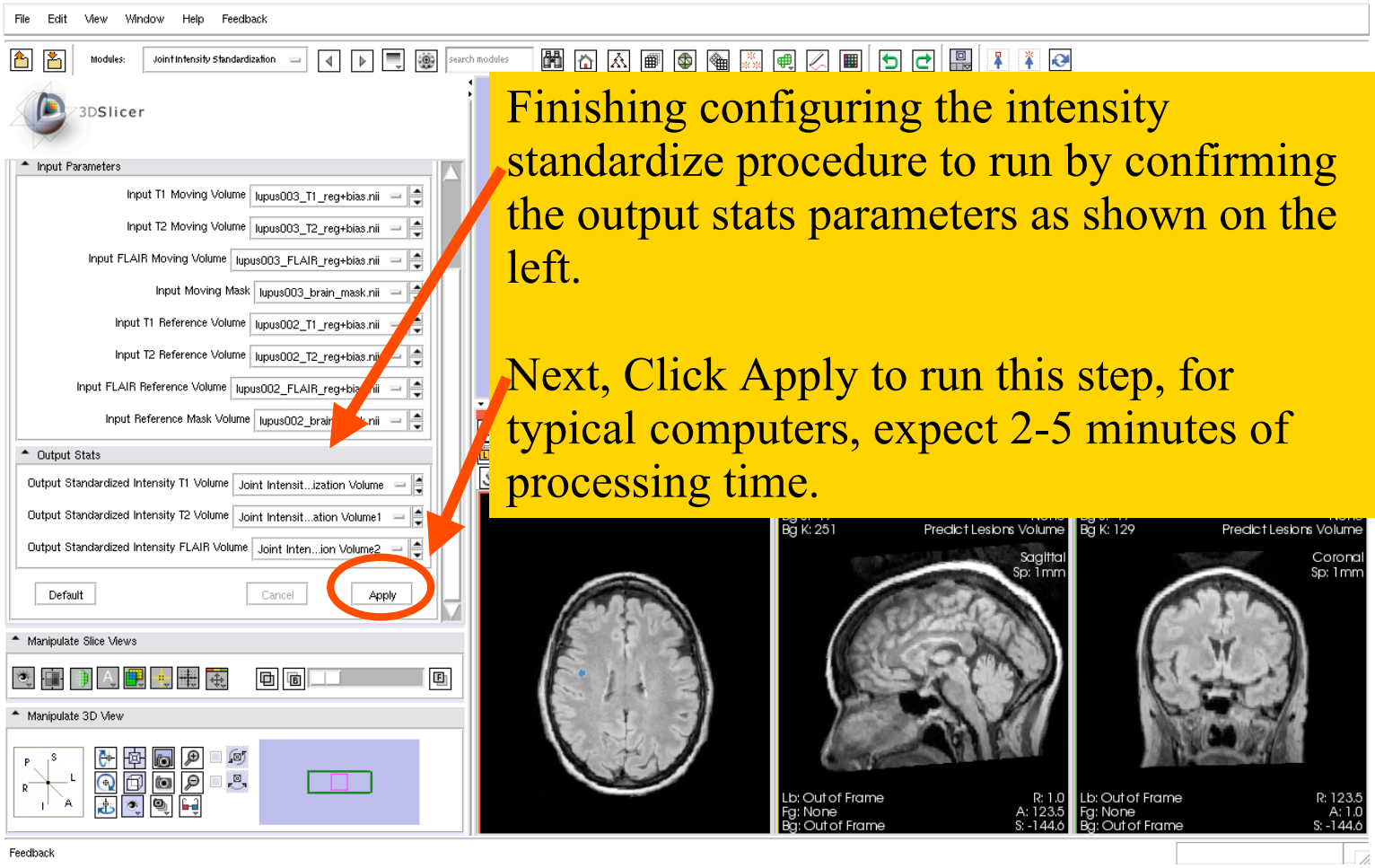


The next step is to select the Intensity Standardization module: Select and expand the Module menu, First select Segmentation, next select Lesion Segmentation, finally select Join Intensity Standardization.

Module Step 2: Setup



Module Step 2: Running



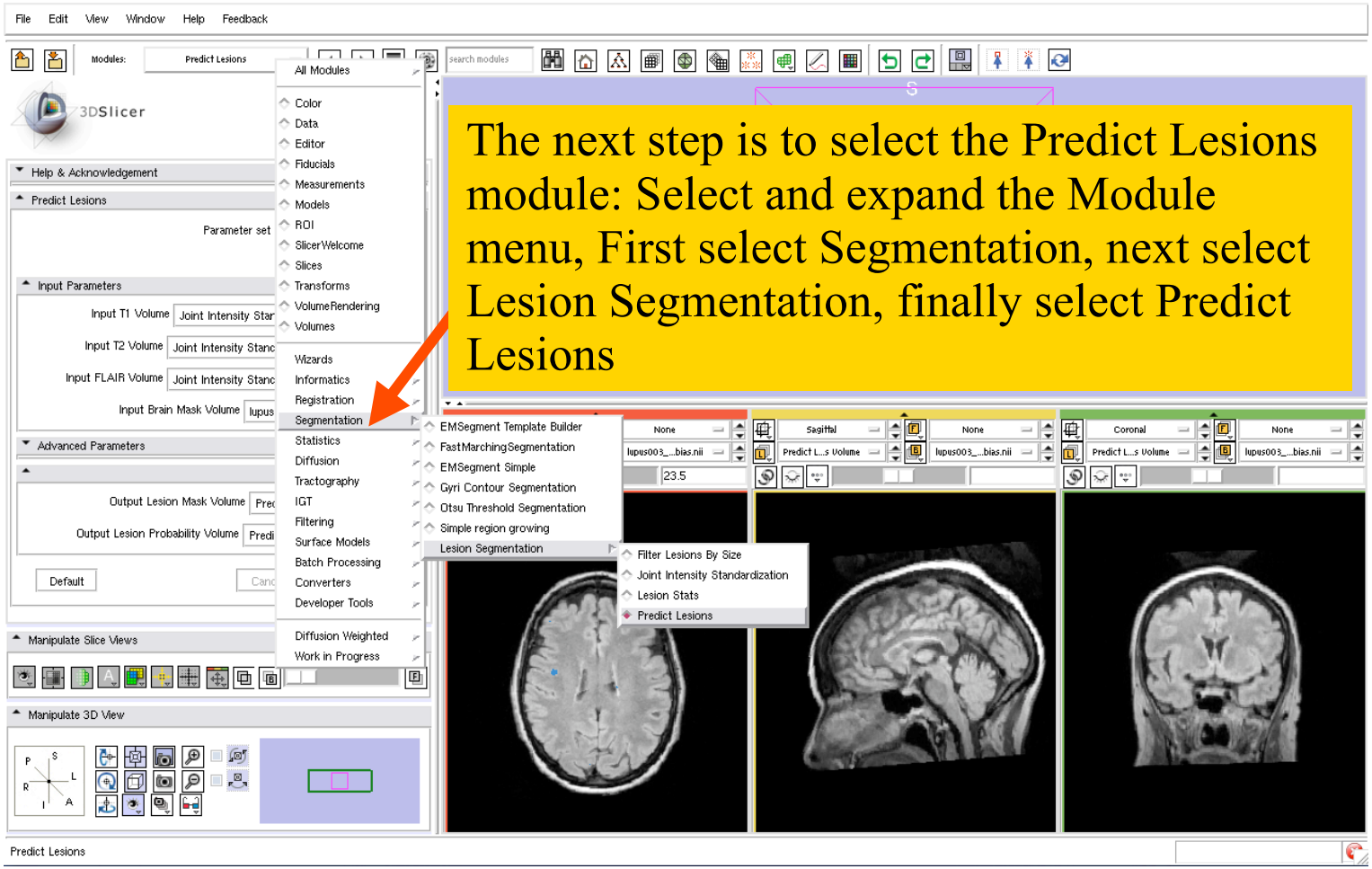
Finishing configuring the intensity standardize procedure to run by confirming the output stats parameters as shown on the left.

Next, Click Apply to run this step, for typical computers, expect 2-5 minutes of processing time.

Importance of Intensity Standardization

- At this stage, intensity standardization is now complete. This preprocessing is needed because the scale and range of intensities within each of the **T1**, **T2**, and **FLAIR** sequences vary across individuals, the intensity standardization attempts to normalize the intensities within each sequence. The normalized intensity values are the input for the next phase, step 3 which classifies the input images from step 2 to predict where white matter lesions are present in the given data set.

Module Step 3: Setup



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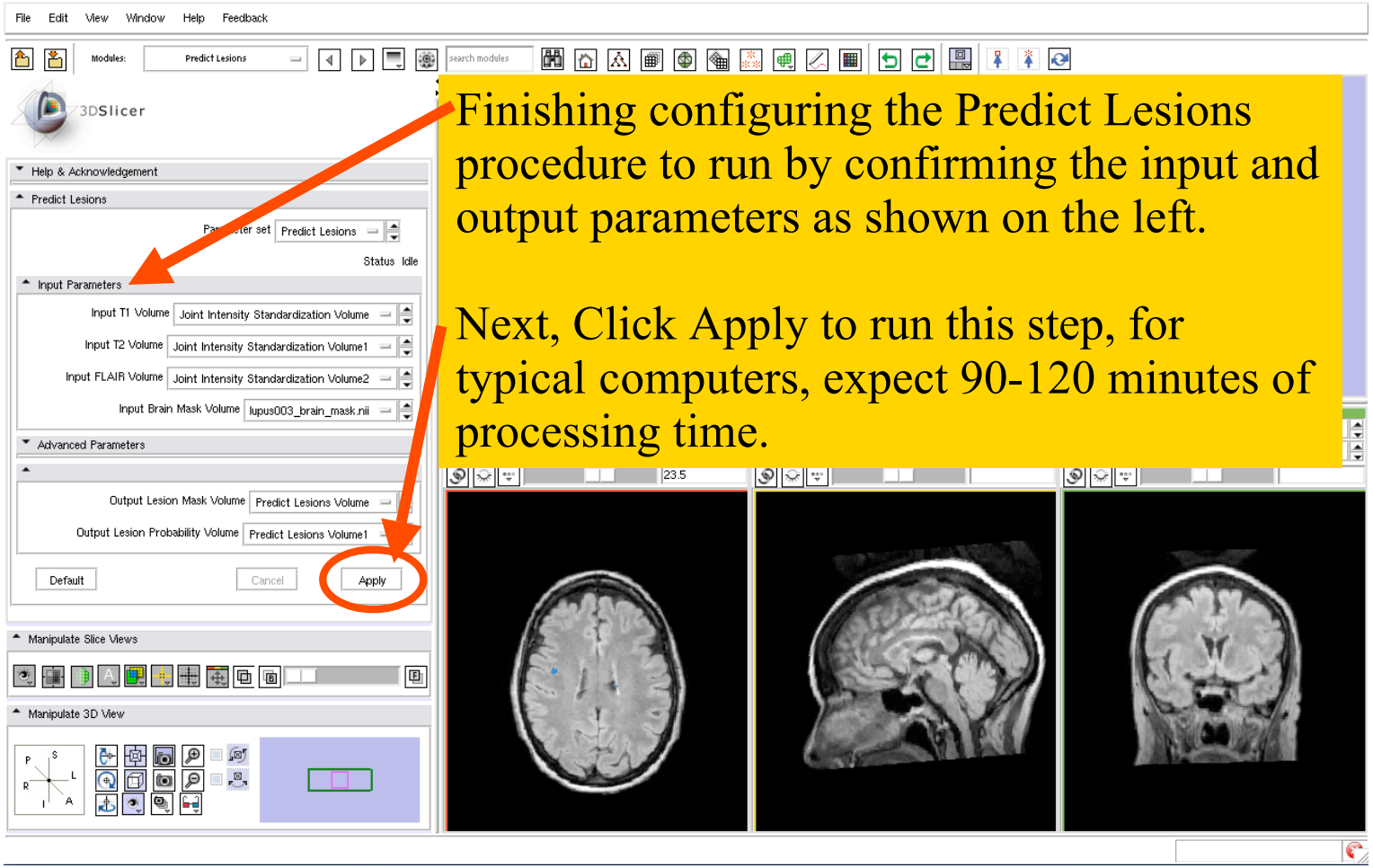
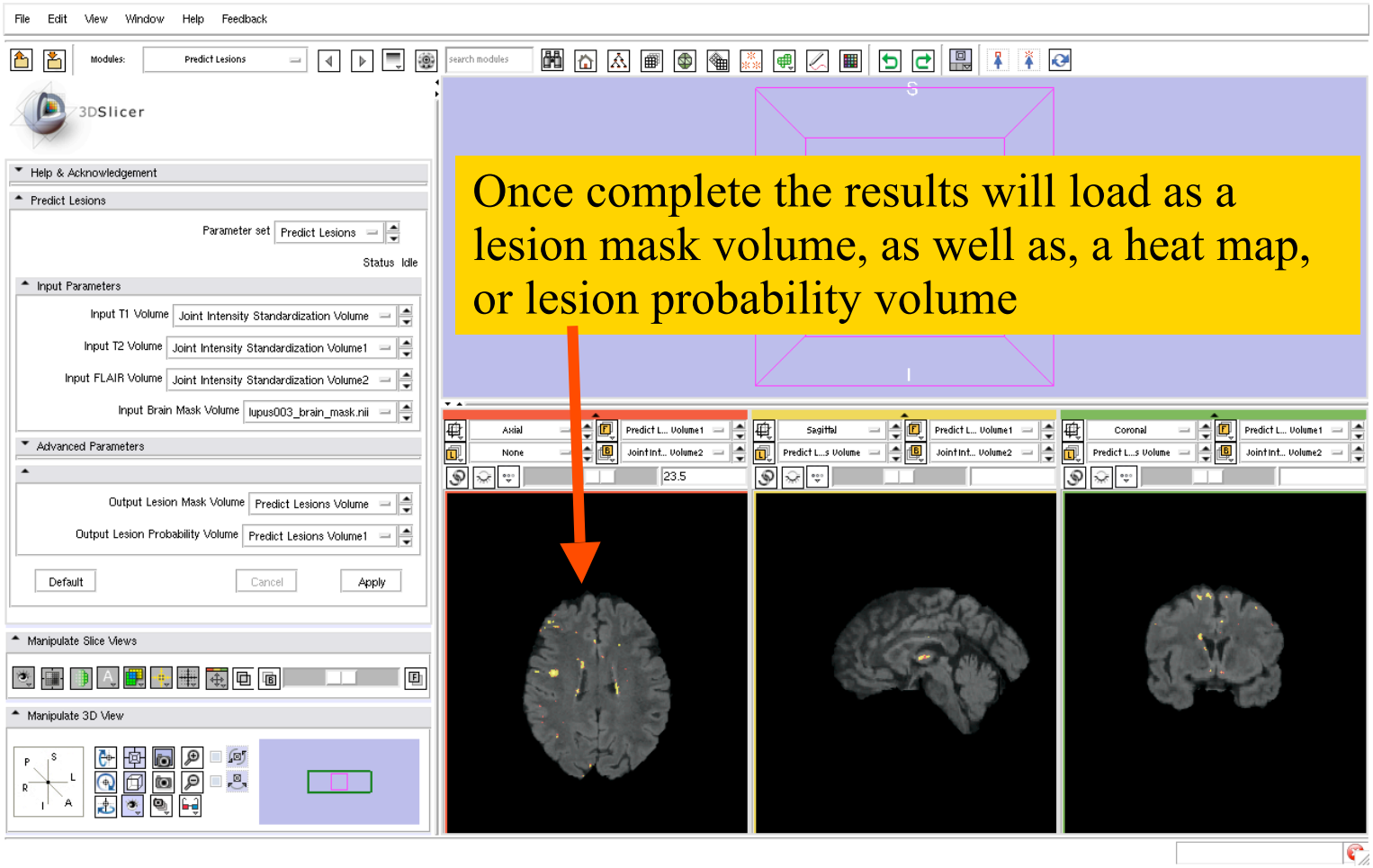
Module Step 3: Running



Finishing configuring the Predict Lesions procedure to run by confirming the input and output parameters as shown on the left.

Next, Click Apply to run this step, for typical computers, expect 90-120 minutes of processing time.

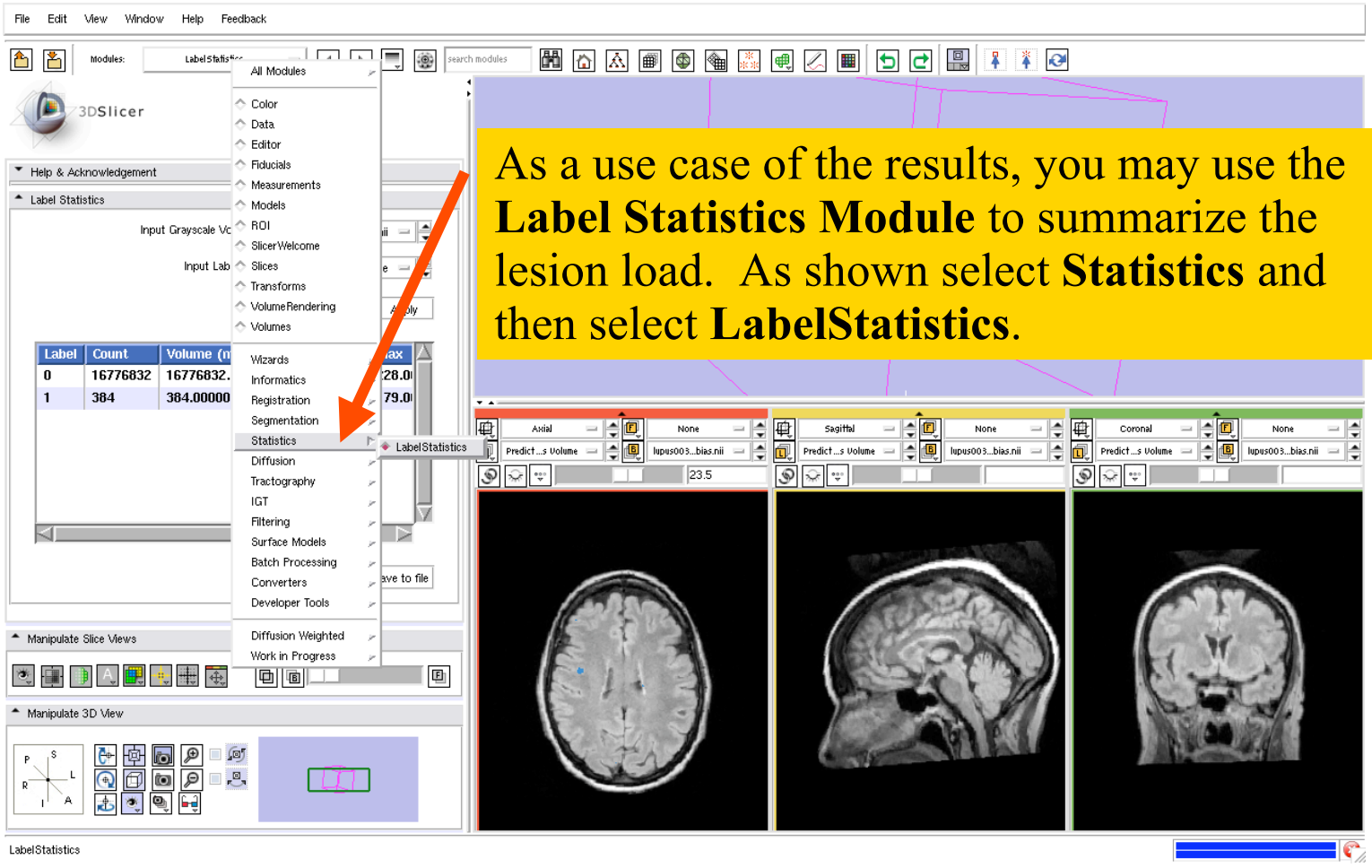
Module Step 3: Results



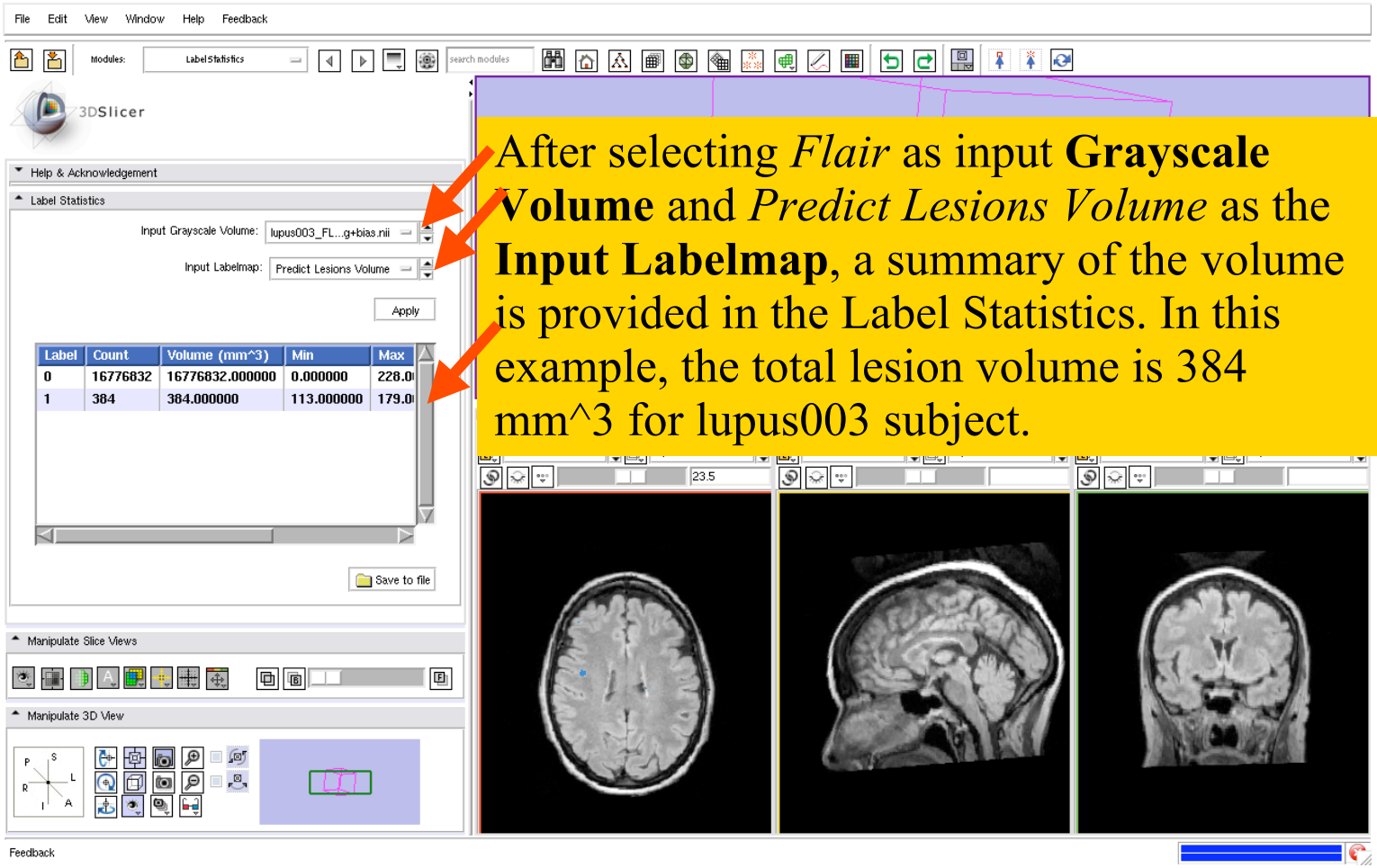
Predicted Lesions

Following Stage 3, you now have both volumes and probability images that represent where white matter lesions are predicted for the given data set. The remainder of this tutorial will show you first how you may use the volume data to measure the lesion load, and also how the data can be rendered to visualize the location and extent of lesions for the given data set.

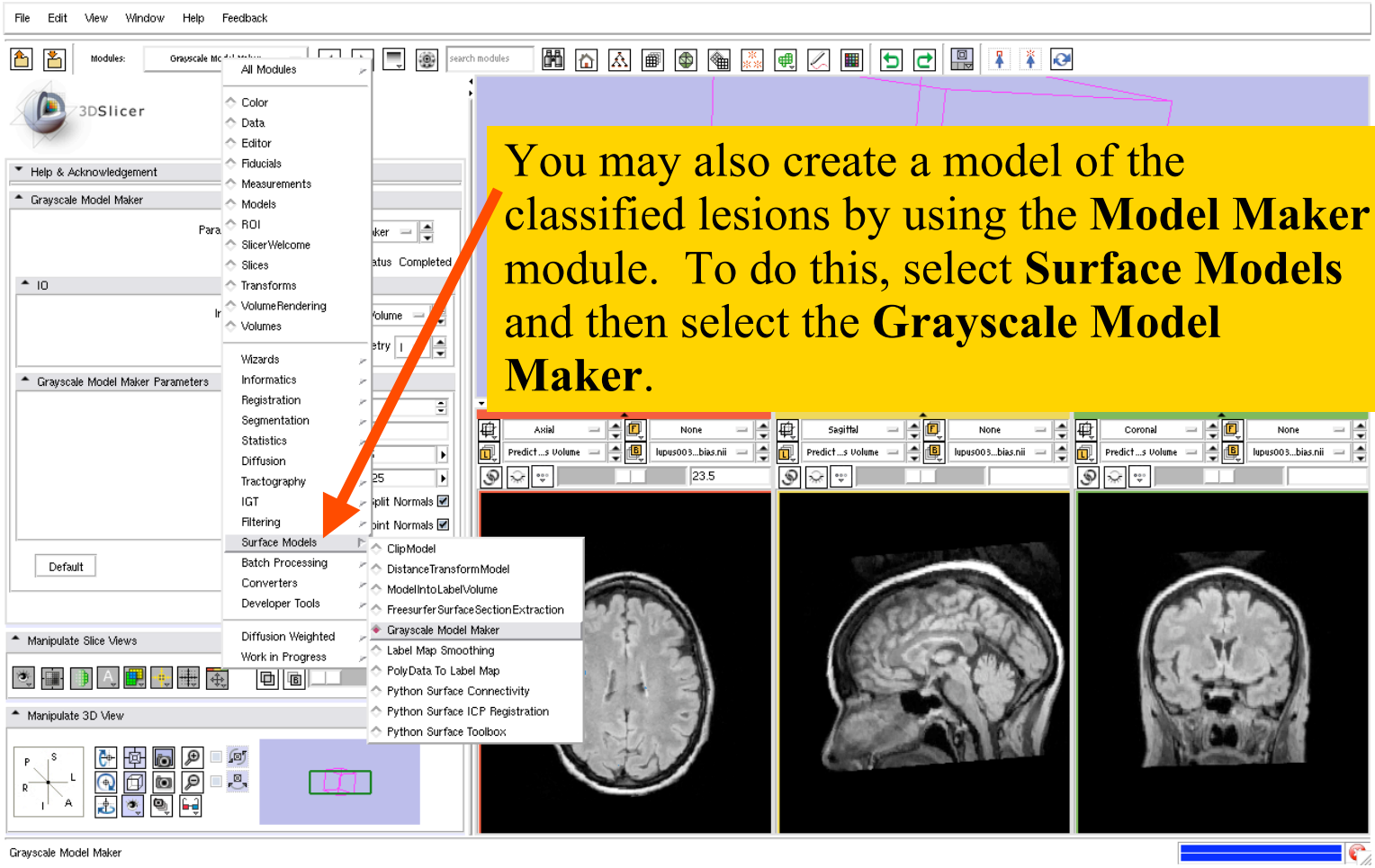
Example Measurement



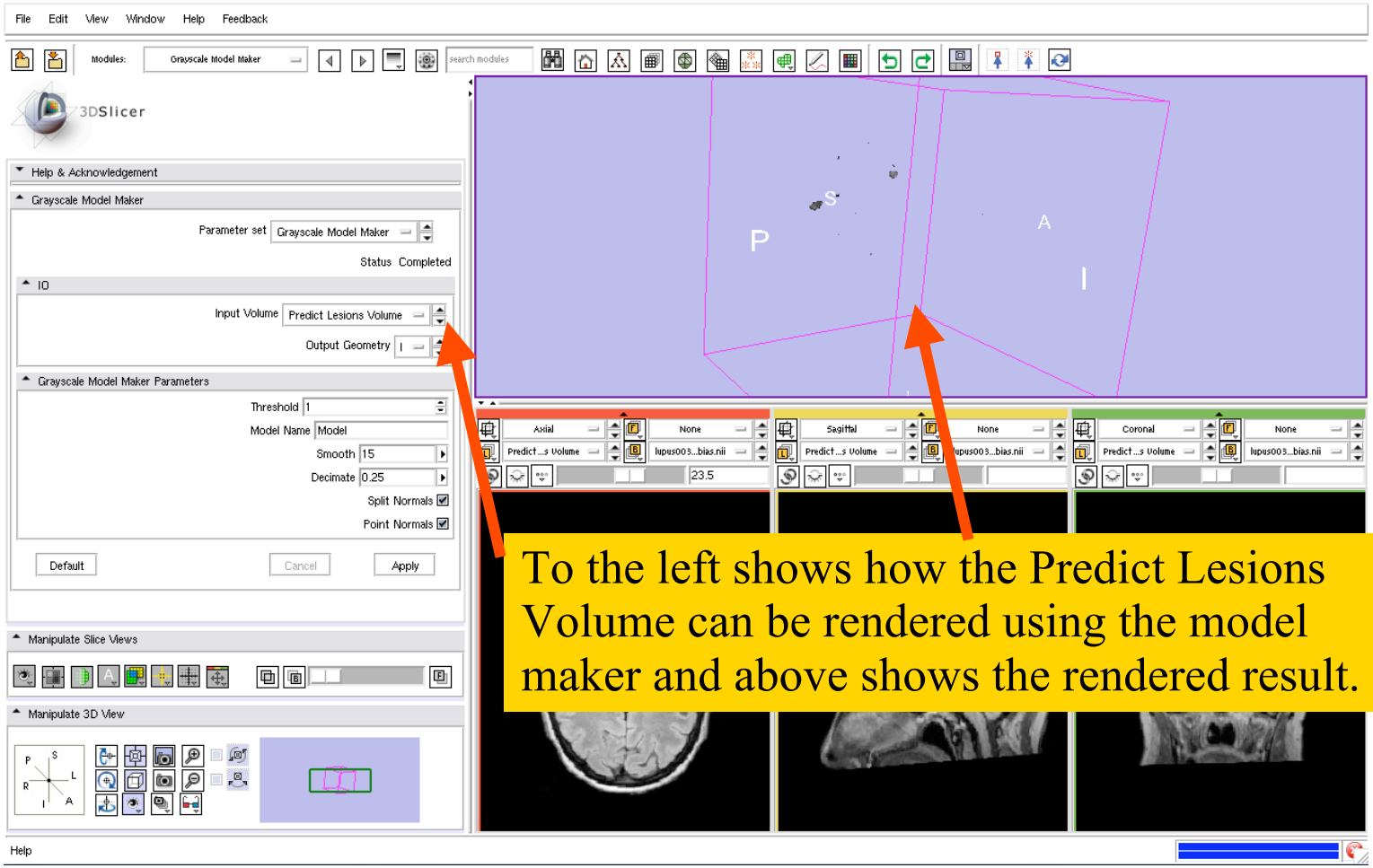
Example Measurement



Setup Example Model



Results Example Model

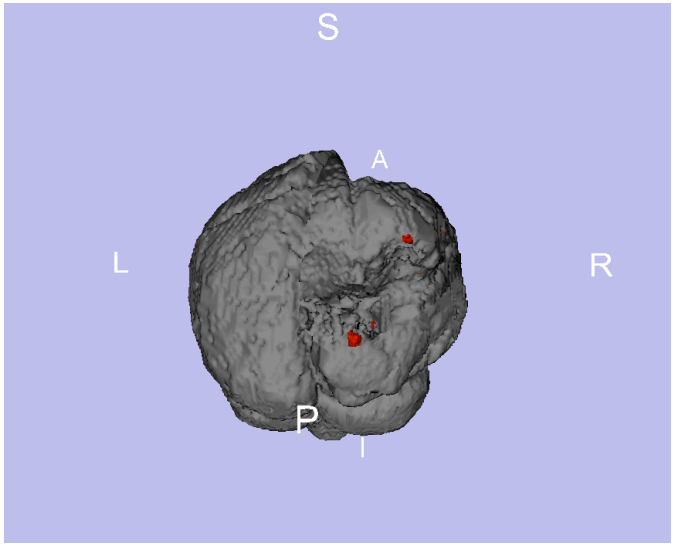


Discussion

- This concludes the objective of the tutorial; however, since the tool has produced a label map, as shown in the example, you may now measure the volumes of the automatically labeled lesion tissue or summarize the anatomical location of lesions for other cases in the tutorial data set. Since, the lesion load is associated with symptom severity and can be used to guide treatment and care.
- You may use the lesion label maps as input to the change tracker capability in Slicer to assess time course of the illness (change in lesion size, number over time).
- You may use the label maps to assess either perfusion or diffusion deficits through co-registration of the lesion maps with pMR, ASL, or DTI.

Conclusion

- This capability provides an intuitive graphical user interface to interact with the data
- The tool has been built in an open-source environment and is readily available to the scientific community



For More Information

- Register as a user of this 3dSlicer Module using the NITRC resource to keep updated on any changes or additions to either the capability or tutorial
  - http://www.nitrc.org/projects/lupuslesion/
- You may also send e-mail message with any questions or concerns to Jeremy Bockholt (jbockholt@mrn.org)

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