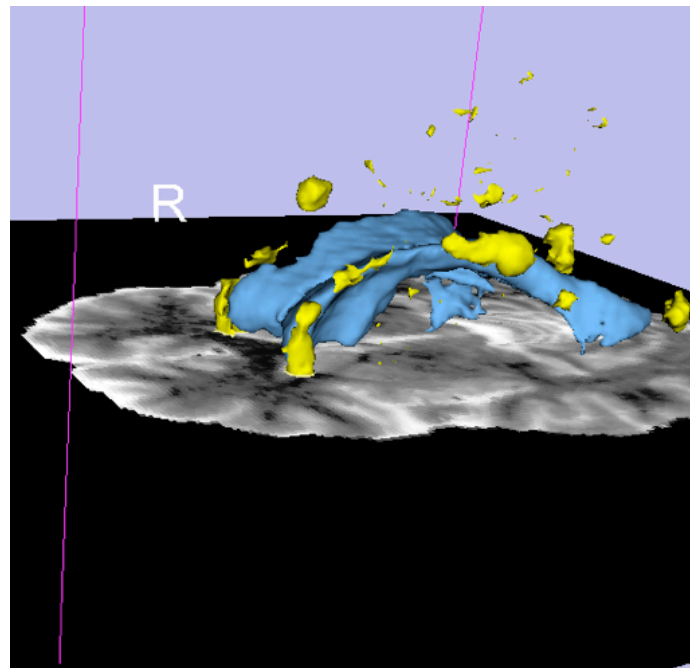


# Detecting White Matter Lesions in Lupus

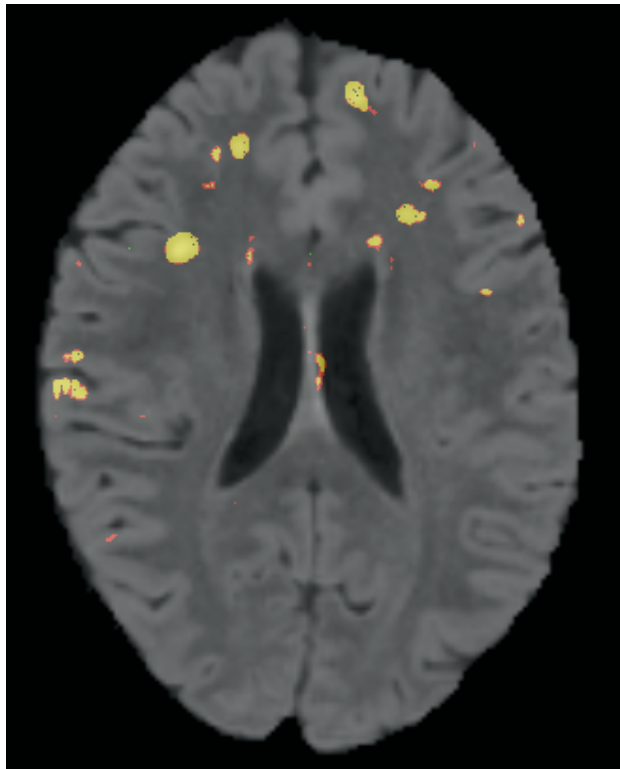


Version 2.1  
6/25/2009

H. Jeremy Bockholt  
Mark Scully

# *Learning objective*

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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*

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This tutorial assumes that you have already completed the tutorial **Data Loading and Visualization**. Tutorials for **Slicer3** are available at the following location:

- **Slicer3** tutorials

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



# Material

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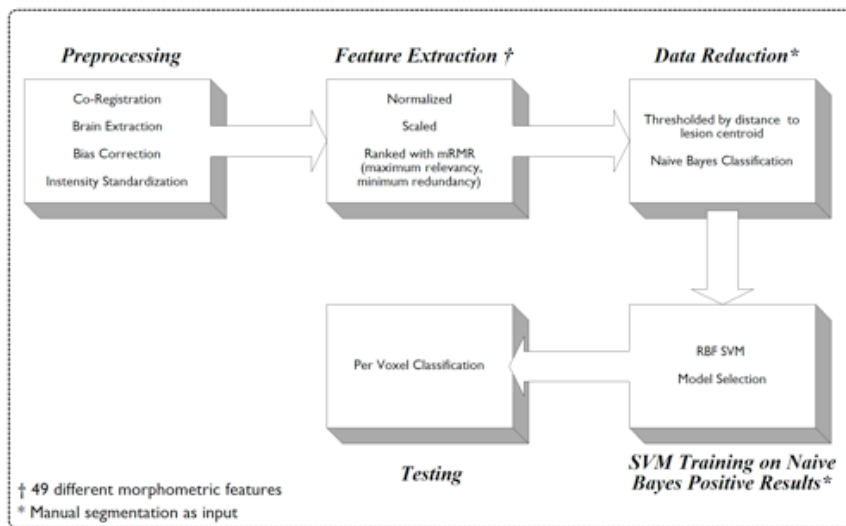
This course requires the following installation:

- The current version of Slicer 3.5.x Software which can be installed from:
  - <http://www.slicer.org/pages/Downloads>
- The White Matter Lesion module extension to Slicer 3
- The Lupus Lesion Tutorial Data, which can be downloaded from:
  - <http://www.nitrc.org/frs/download.php/569/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.*

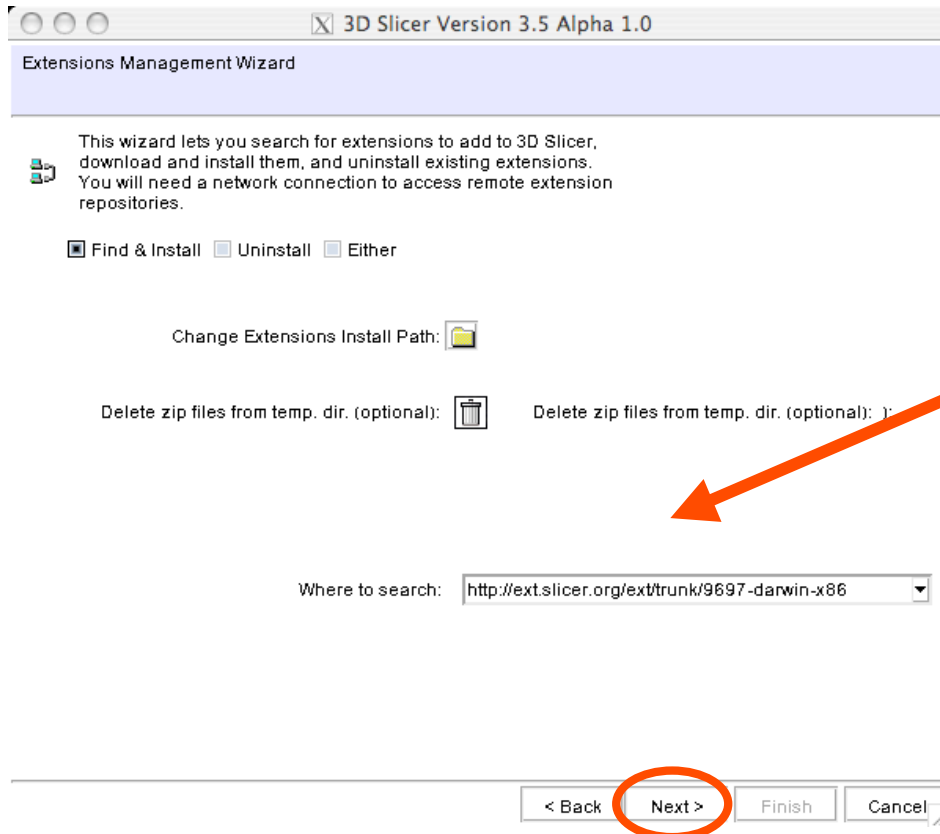
# Methods



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.

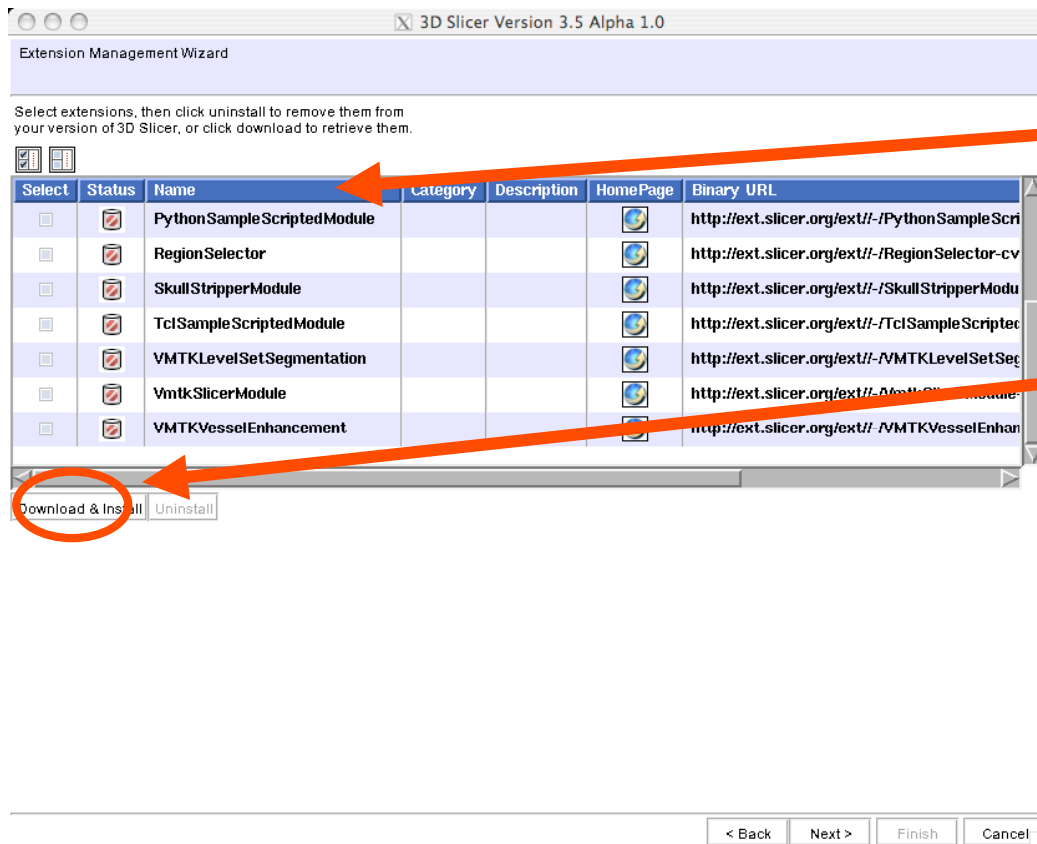


# Getting the Module



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

# Installing the Module



Select  
**LesionSegmentati  
onApplications**  
from the list

Click **Download &  
Install.**

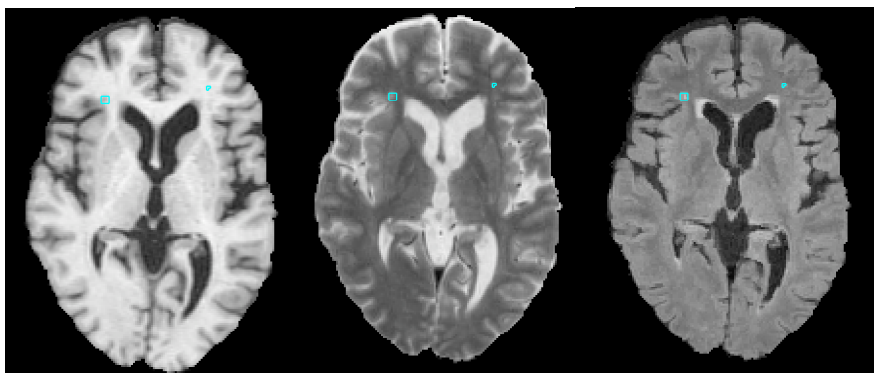
Click **Finish** when  
download  
completes and  
restart Slicer to use  
the external module



# 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.

The following summary shows the contents of the `data/LesionSegmentationTutorial` directory once download and uncompressed



```
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
```

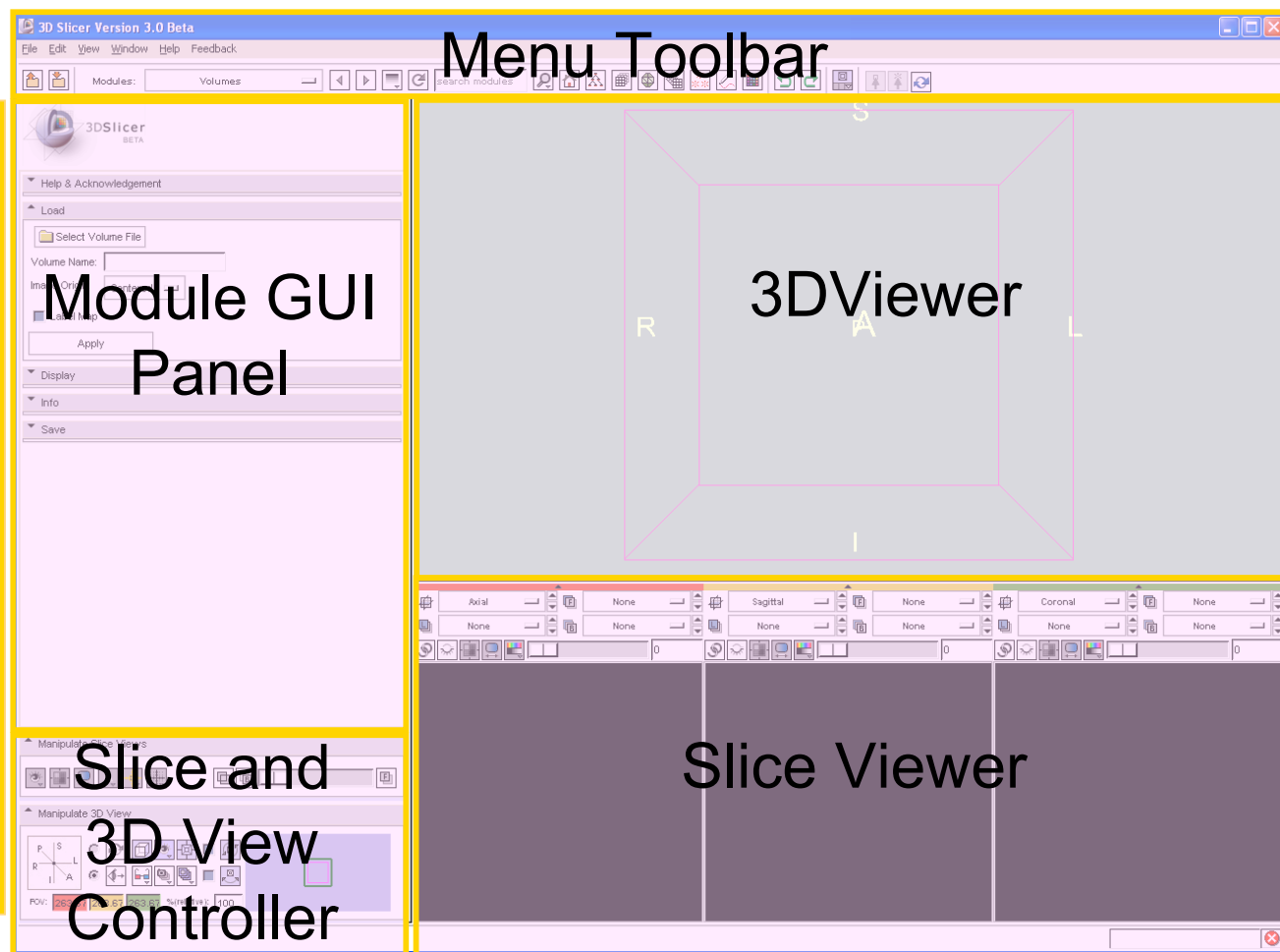




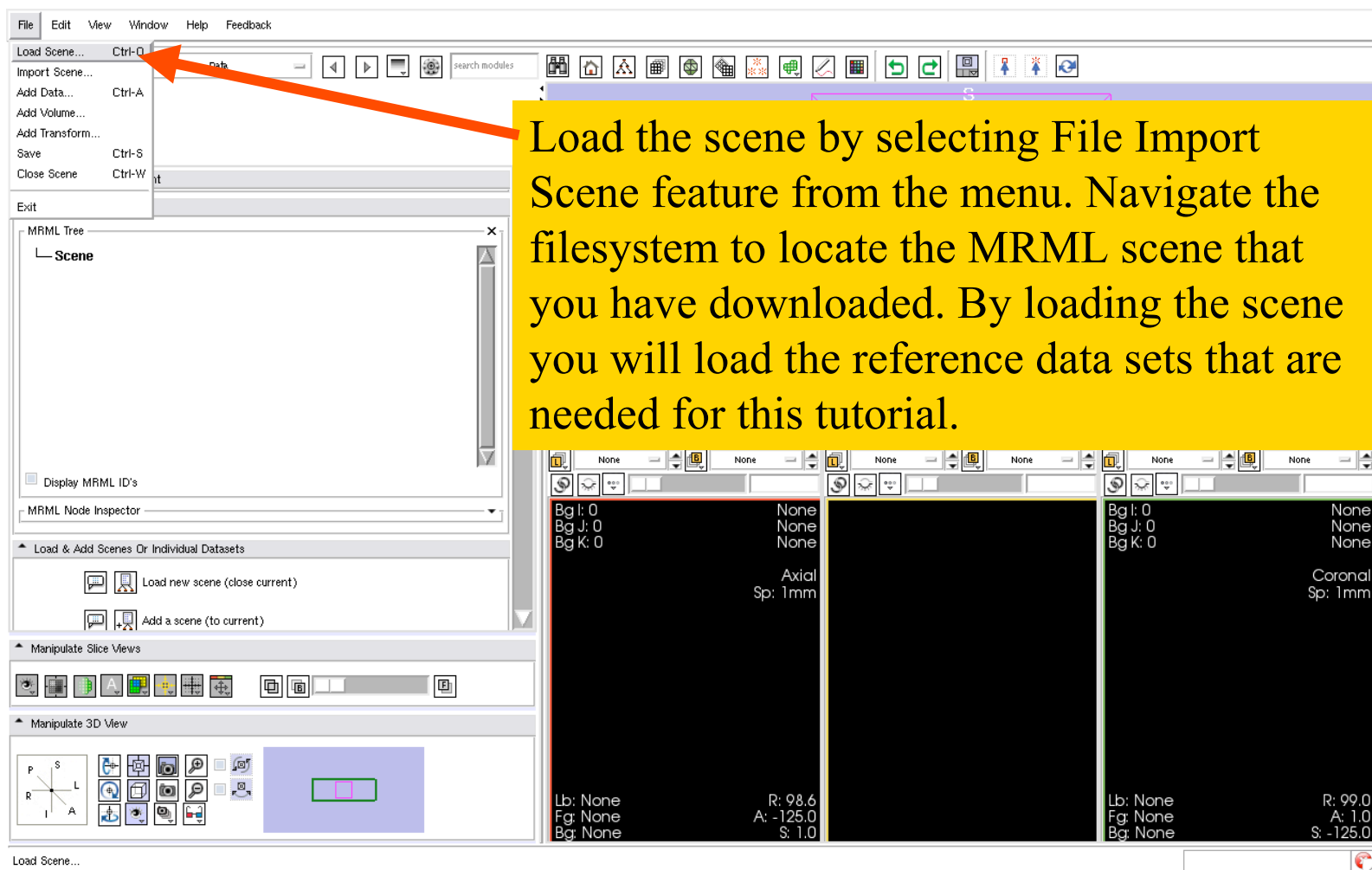
# Slicer3 GUI

The Graphical User Interface (GUI) of Slicer3 integrates five components:

- the Menu Toolbar
- the Module GUI Panel
- the 3D Viewer
- the Slice Viewer
- the Slice and 3D View Controller



# Step 1: Setup

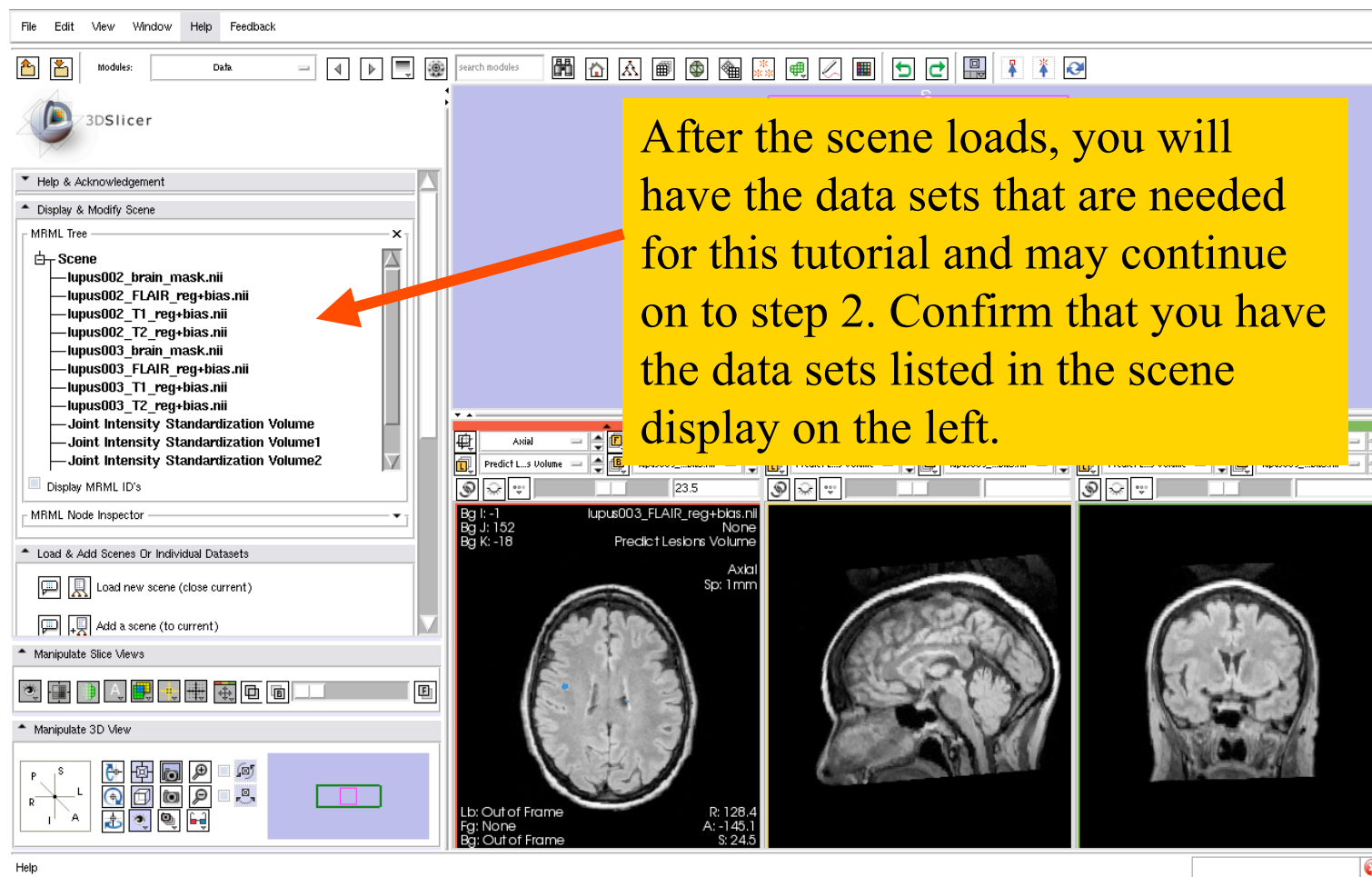


The screenshot shows the 3DSlicer application window. The 'File' menu is open, and the 'Load Scene...' option is highlighted with a red arrow. A yellow callout box contains the following text:

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.

The interface includes a menu bar (File, Edit, View, Window, Help, Feedback), a toolbar, and several panels: MRML Tree (showing 'Scene'), MRML Node Inspector, Load & Add Scenes Or Individual Datasets (with 'Load new scene (close current)' and 'Add a scene (to current)' buttons), Manipulate Slice Views, and Manipulate 3D View. The main display area shows three orthogonal views: Axial, Coronal, and a 3D perspective view. The Axial view shows a slice with parameters: Bg I: 0, Bg J: 0, Bg K: 0, Axial Sp: 1mm, and rotation values (R: 98.6, A: -125.0, S: 1.0). The Coronal view shows a slice with parameters: Bg I: 0, Bg J: 0, Bg K: 0, Coronal Sp: 1mm, and rotation values (R: 99.0, A: 1.0, S: -125.0).

# Step 1: Results

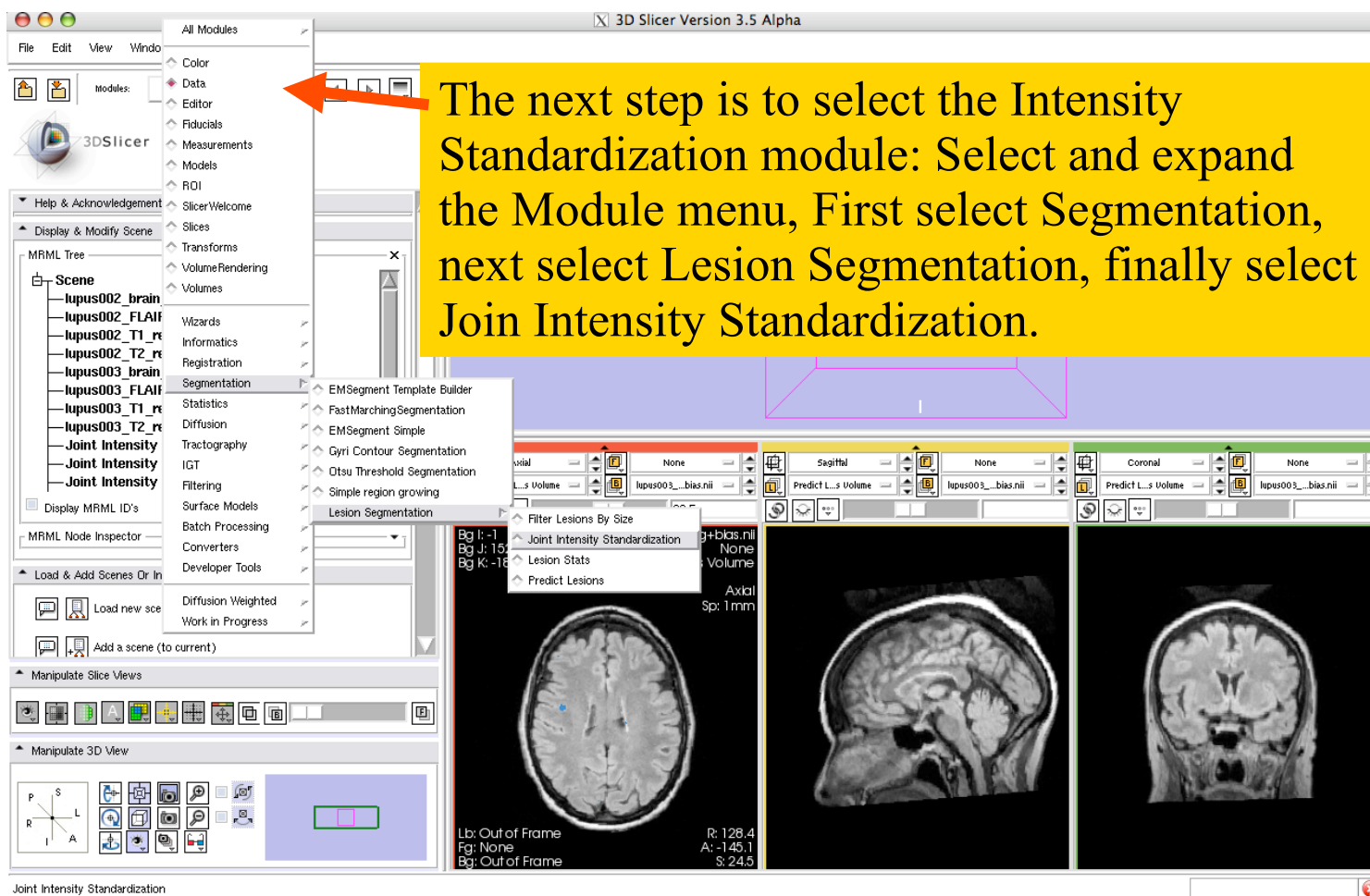


After the scene loads, you will have the data sets that are needed for this tutorial and may continue on to step 2. Confirm that you have the data sets listed in the scene display on the left.

The screenshot shows the 3DSlicer interface with the following components:

- MRML Tree (Left Panel):** Lists the loaded data sets:
  - Scene
    - lupus002\_brain\_mask.nii
    - lupus002\_FLAIR\_reg+bias.nii
    - lupus002\_T1\_reg+bias.nii
    - lupus002\_T2\_reg+bias.nii
    - lupus003\_brain\_mask.nii
    - lupus003\_FLAIR\_reg+bias.nii
    - lupus003\_T1\_reg+bias.nii
    - lupus003\_T2\_reg+bias.nii
    - Joint Intensity Standardization Volume
    - Joint Intensity Standardization Volume1
    - Joint Intensity Standardization Volume2
- MRML Node Inspector (Below MRML Tree):** Shows the selected node and its properties.
- Load & Add Scenes Or Individual Datasets (Below MRML Node Inspector):** Includes buttons for "Load new scene (close current)" and "Add a scene (to current)".
- Manipulate Slice Views (Below Load & Add Scenes):** Contains icons for navigating between different slice views.
- Manipulate 3D View (Below Manipulate Slice Views):** Contains icons for manipulating the 3D view, including a 3D orientation diagram.
- 3D View (Right Panel):** Displays three MRI slice views: Axial, Sagittal, and Coronal. The Axial view is selected, showing a brain slice with a blue dot. The Sagittal and Coronal views show the brain in different orientations.

# Step 2: Setup

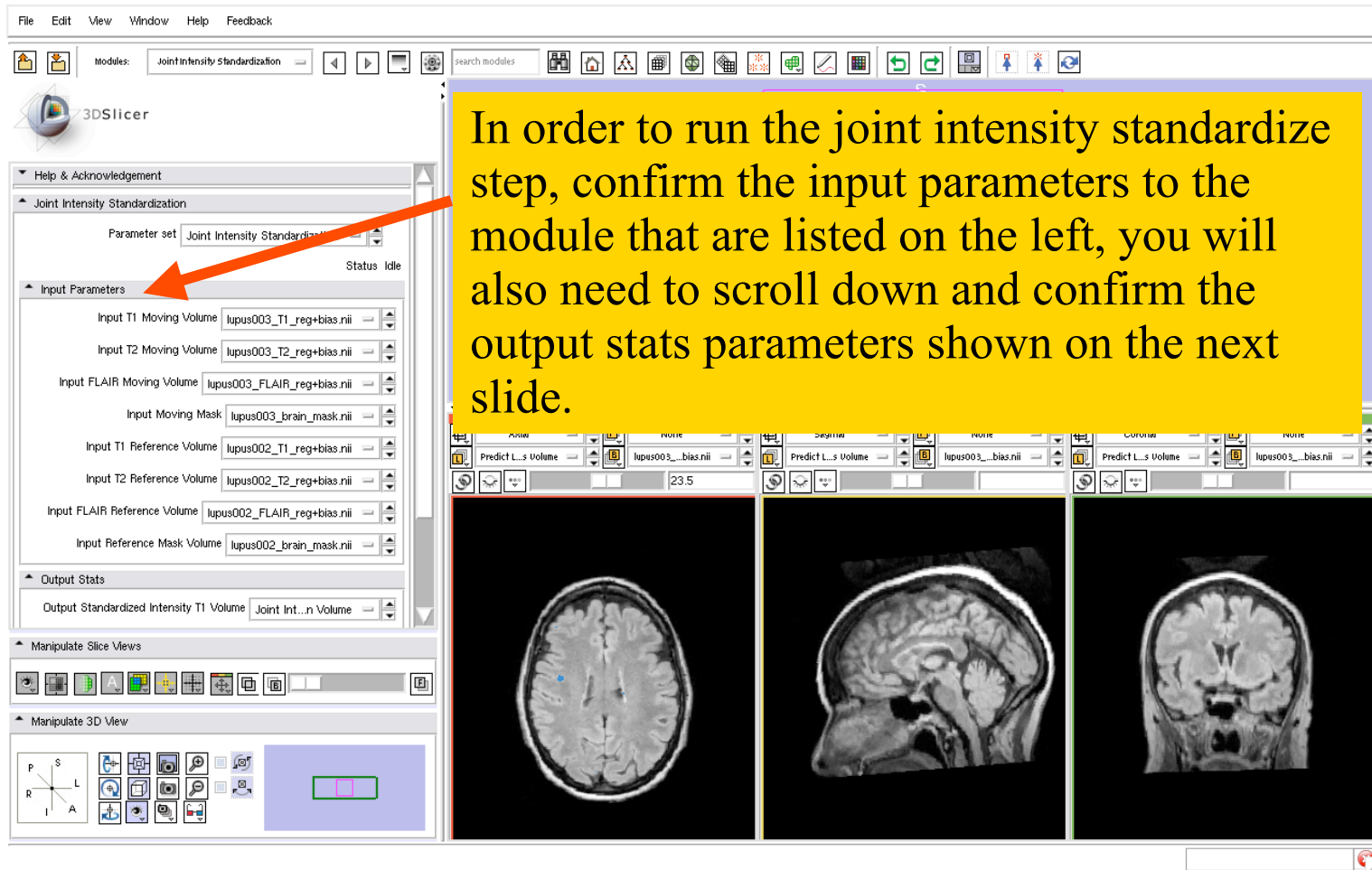


The screenshot shows the 3D Slicer Version 3.5 Alpha interface. A yellow callout box with a red arrow pointing to the 'Segmentation' menu item contains the following text:

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 Joint Intensity Standardization.

The interface shows the MRML Tree on the left with a 'Scene' containing several volumes. The 'Segmentation' menu is open, showing options like 'EMSegment Template Builder', 'FastMarchingSegmentation', 'EMSegment Simple', 'Gyri Contour Segmentation', 'Otsu Threshold Segmentation', 'Simple region growing', and 'Lesion Segmentation'. The 'Lesion Segmentation' sub-menu is also open, showing 'Filter Lesions By Size', 'Joint Intensity Standardization', 'Lesion Stats', and 'Predict Lesions'. The 'Joint Intensity Standardization' option is highlighted. The main view shows three orthogonal slices (Axial, Sagittal, Coronal) of a brain MRI volume.

# Step 2: Setup



In order to run the joint intensity standardize step, confirm the input parameters to the module that are listed on the left, you will also need to scroll down and confirm the output stats parameters shown on the next slide.

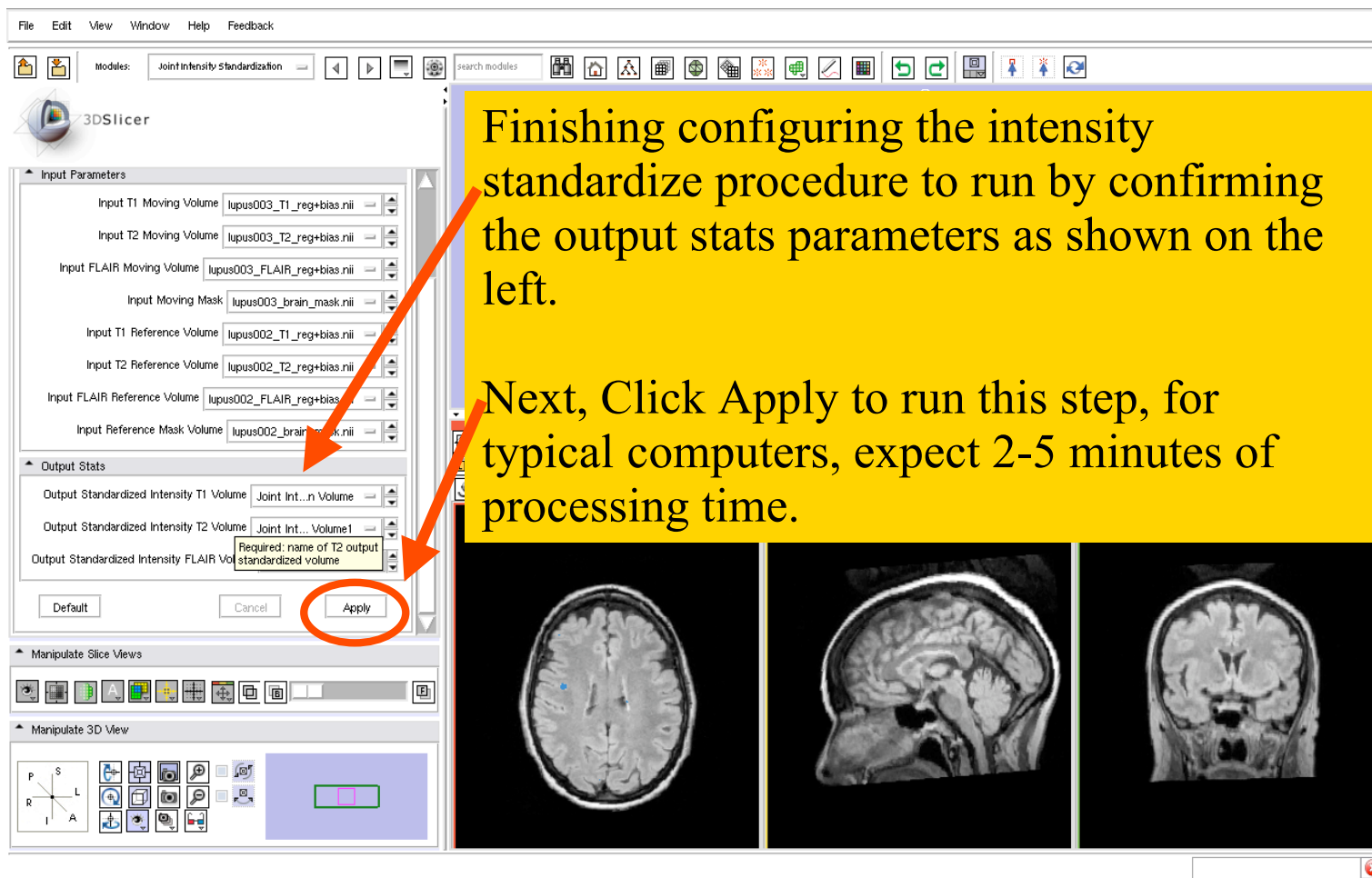
The screenshot shows the 3DSlicer interface with the 'Joint Intensity Standardization' module selected. The 'Input Parameters' section is highlighted in yellow, and an orange arrow points to it. The parameters listed are:

- Input T1 Moving Volume: lupus003\_T1\_reg+bias.nii
- Input T2 Moving Volume: lupus003\_T2\_reg+bias.nii
- Input FLAIR Moving Volume: lupus003\_FLAIR\_reg+bias.nii
- Input Moving Mask: lupus003\_brain\_mask.nii
- Input T1 Reference Volume: lupus002\_T1\_reg+bias.nii
- Input T2 Reference Volume: lupus002\_T2\_reg+bias.nii
- Input FLAIR Reference Volume: lupus002\_FLAIR\_reg+bias.nii
- Input Reference Mask Volume: lupus002\_brain\_mask.nii

The 'Output Stats' section shows the 'Output Standardized Intensity T1 Volume' set to 'Joint Int...n Volume'.

The 3D view area shows three MRI slices: an axial slice, a sagittal slice, and a coronal slice.

## Step 2: Running



File Edit View Window Help Feedback

Modules: Joint Intensity Standardization

Input Parameters

- Input T1 Moving Volume: lupus003\_T1\_reg+bias.nii
- Input T2 Moving Volume: lupus003\_T2\_reg+bias.nii
- Input FLAIR Moving Volume: lupus003\_FLAIR\_reg+bias.nii
- Input Moving Mask: lupus003\_brain\_mask.nii
- Input T1 Reference Volume: lupus002\_T1\_reg+bias.nii
- Input T2 Reference Volume: lupus002\_T2\_reg+bias.nii
- Input FLAIR Reference Volume: lupus002\_FLAIR\_reg+bias.nii
- Input Reference Mask Volume: lupus002\_brain\_mask.nii

Output Stats

- Output Standardized Intensity T1 Volume: Joint Int...n Volume
- Output Standardized Intensity T2 Volume: Joint Int... Volume1
- Output Standardized Intensity FLAIR Volume: Required: name of T2 output standardized volume

Default Cancel **Apply**

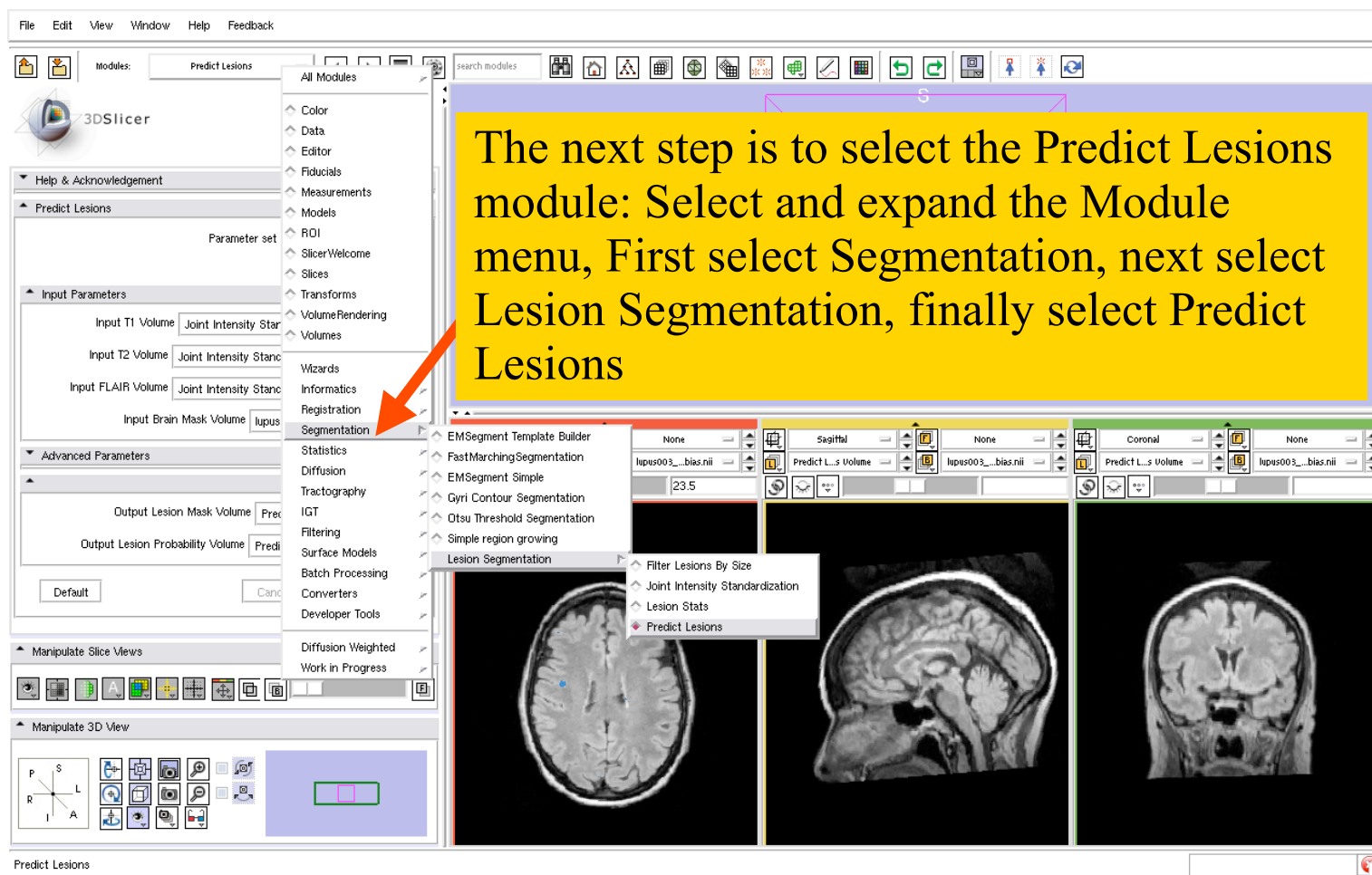
Manipulate Slice Views

Manipulate 3D View

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.

# Step 3: Setup



The next step is to select the Predict Lesions module: Select and expand the Module menu, First select Segmentation, next select Lesion Segmentation, finally select Predict Lesions

File Edit View Window Help Feedback

Modules: Predict Lesions

3DSlicer

Help & Acknowledgement

Predict Lesions

Parameter set

Input Parameters

Input T1 Volume Joint Intensity Star

Input T2 Volume Joint Intensity Stanc

Input FLAIR Volume Joint Intensity Stanc

Input Brain Mask Volume lupus

Advanced Parameters

Output Lesion Mask Volume Prec

Output Lesion Probability Volume Predi

Default Cancel

Manipulate Slice Views

Manipulate 3D View

Predict Lesions

search modules

All Modules

- Color
- Data
- Editor
- Fiducials
- Measurements
- Models
- ROI
- SlicerWelcome
- Slices
- Transforms
- VolumeRendering
- Volumes
- Wizards
- Informatics
- Registration
- Segmentation
  - EMSegment Template Builder
  - FastMarchingSegmentation
  - EMSegment Simple
  - Gyri Contour Segmentation
  - Otsu Threshold Segmentation
  - Simple region growing
  - Lesion Segmentation
    - Filter Lesions By Size
    - Joint Intensity Standardization
    - Lesion Stats
    - Predict Lesions
- Statistics
- Diffusion
- Tractography
- IGT
- Filtering
- Surface Models
- Batch Processing
- Converters
- Developer Tools
- Diffusion Weighted
- Work in Progress

None Sagittal None Coronal None

lupus003...bias.nii Predict L...s Volume lupus003...bias.nii

23.5

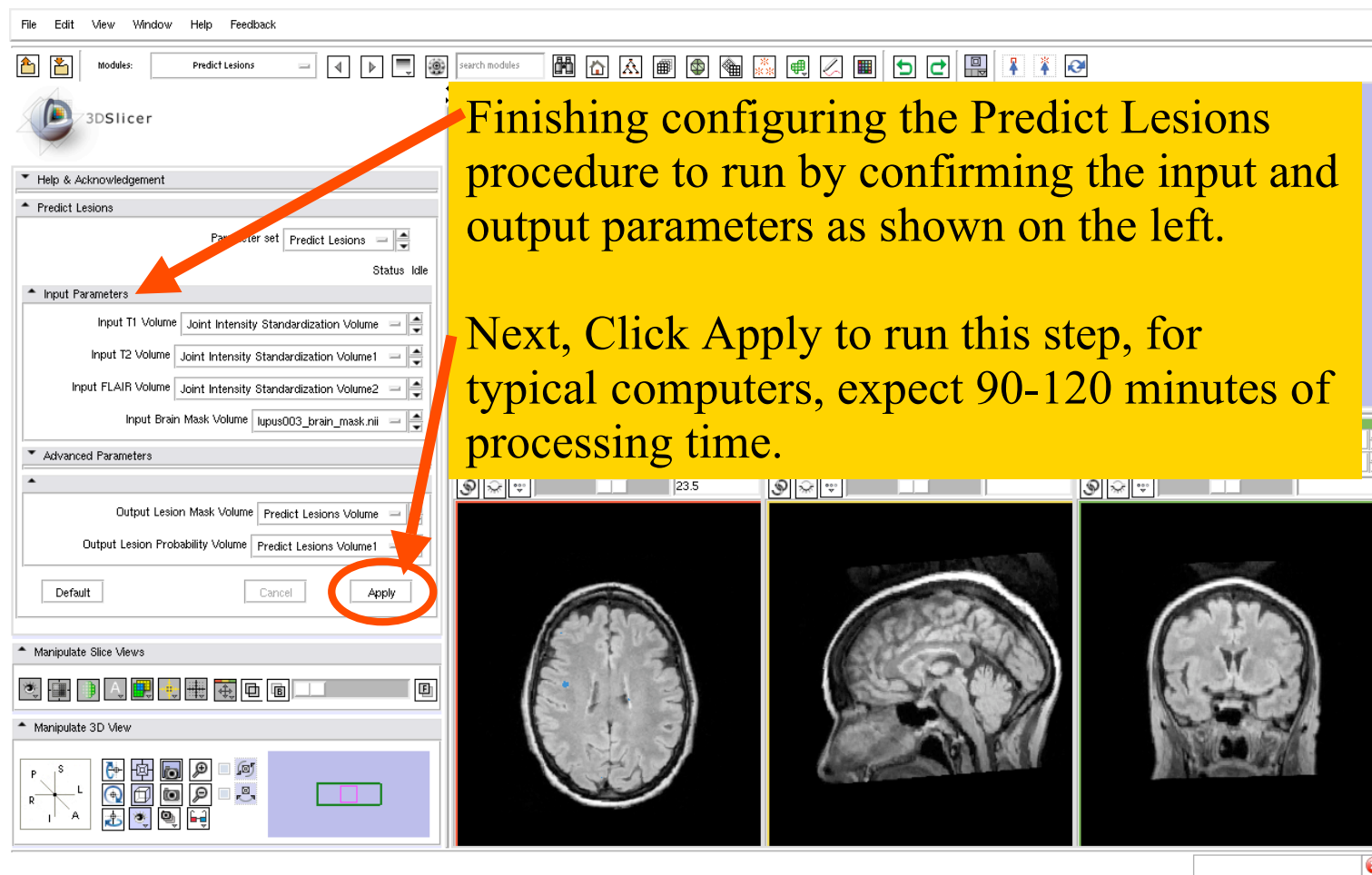
Filter Lesions By Size

Joint Intensity Standardization

Lesion Stats

Predict Lesions

# Step 3: Running



File Edit View Window Help Feedback

Modules: Predict Lesions

3DSlicer

Help & Acknowledgement

Predict Lesions

Parameter set: Predict Lesions

Status: Idle

Input Parameters

Input T1 Volume: Joint Intensity Standardization Volume

Input T2 Volume: Joint Intensity Standardization Volume1

Input FLAIR Volume: Joint Intensity Standardization Volume2

Input Brain Mask Volume: lupus003\_brain\_mask.nii

Advanced Parameters

Output Lesion Mask Volume: Predict Lesions Volume

Output Lesion Probability Volume: Predict Lesions Volume1

Default Cancel **Apply**

Manipulate Slice Views

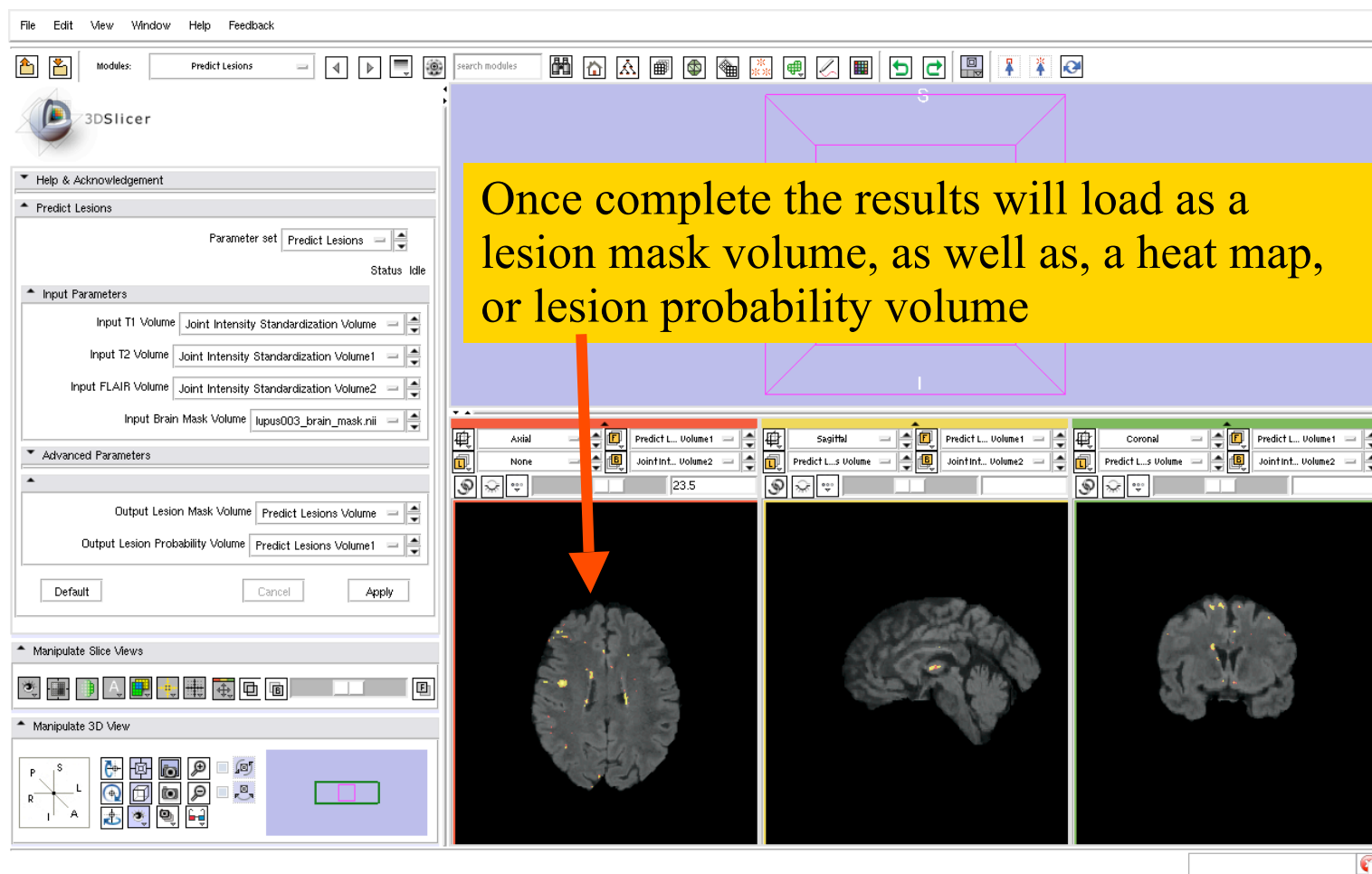
Manipulate 3D View

23.5

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



# Step 3: Results



File Edit View Window Help Feedback

Modules: Predict Lesions

3DSlicer

Help & Acknowledgement

Predict Lesions

Parameter set: Predict Lesions Status: Idle

Input Parameters

Input T1 Volume: Joint Intensity Standardization Volume

Input T2 Volume: Joint Intensity Standardization Volume1

Input FLAIR Volume: Joint Intensity Standardization Volume2

Input Brain Mask Volume: lupus003\_brain\_mask.nii

Advanced Parameters

Output Lesion Mask Volume: Predict Lesions Volume

Output Lesion Probability Volume: Predict Lesions Volume1

Default Cancel Apply

Manipulate Slice Views

Manipulate 3D View

Predict Lesions Volume1

Joint Int. Volume2

Predict Lesions Volume1

Joint Int. Volume2

Predict Lesions Volume1

Joint Int. Volume2

23.5

Once complete the results will load as a lesion mask volume, as well as, a heat map, or lesion probability volume



# *Discussion*

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- Since the tool has produced a label map, you may now measure the volumes of the automatically labeled lesion tissue or summarize the anatomical location of lesions. 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*

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- 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*

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- 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](mailto:jbockholt@mrn.org))



# *Acknowledgments*

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NIH U54EB005149

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NIH U24-RR021992

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*H. Jeremy Bockholt and Mark Scully  
National Alliance for Medical Image Computing*