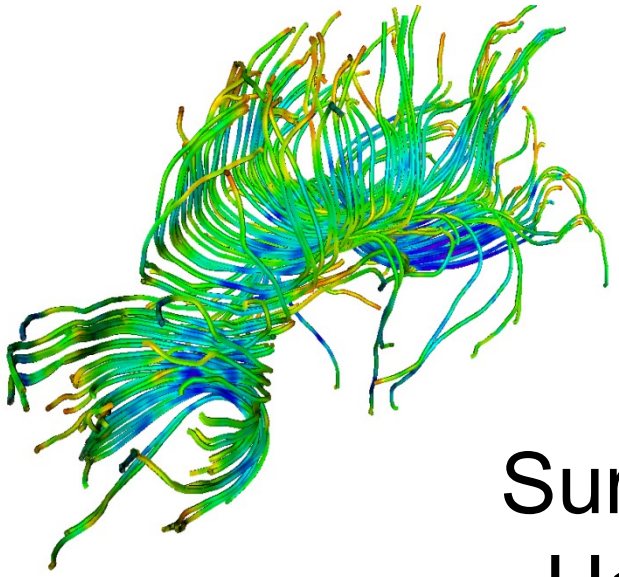
NA-MIC
National Alliance for Medical Image Computing
http://www.na-mic.org

Diffusion Tensor Imaging Tutorial



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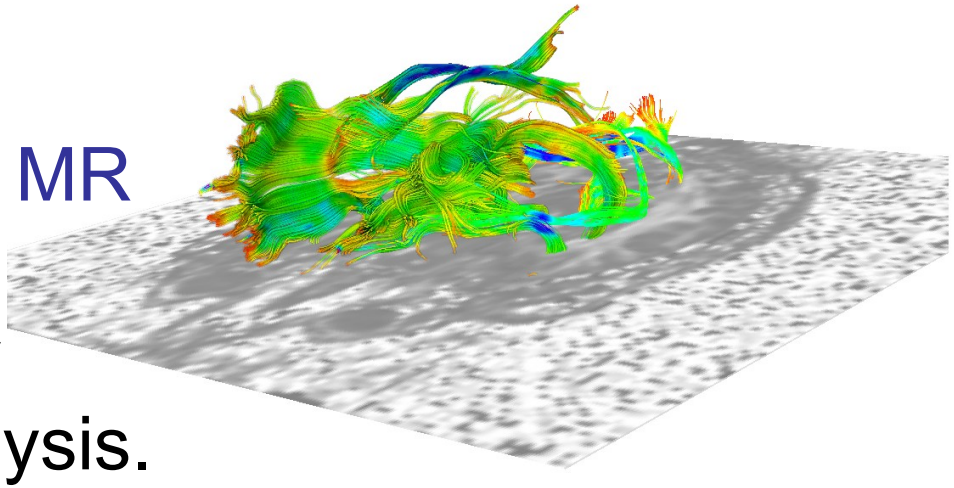
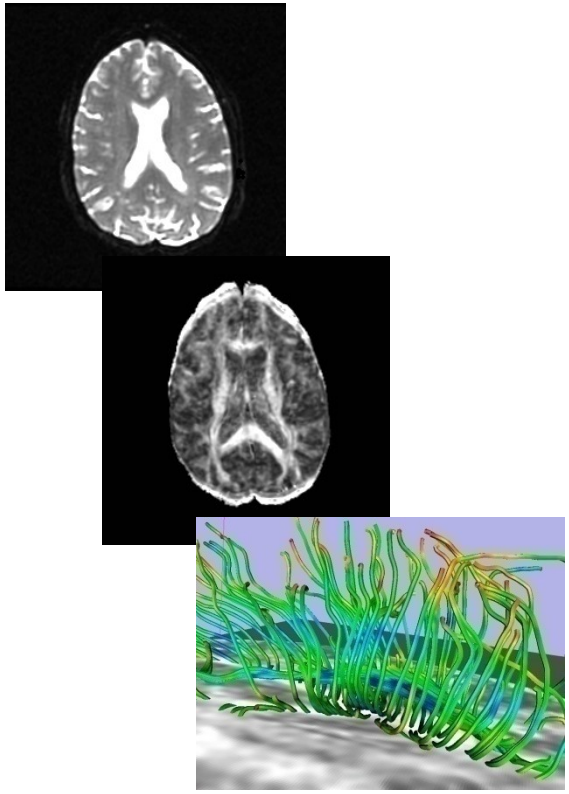
DTI tutorial

This tutorial is an introduction to the advanced Diffusion MR capabilities of the Slicer3 software for medical image analysis.

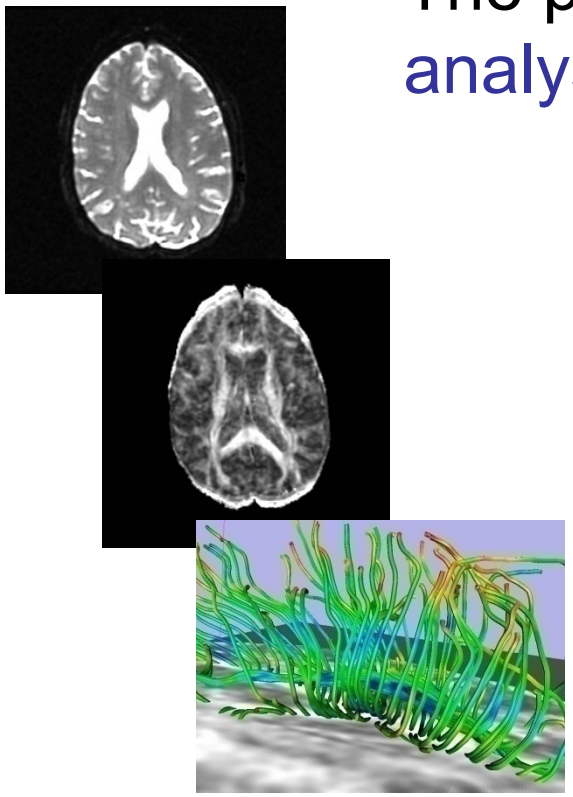


Outline



This tutorial guides you through the process of loading diffusion MR data, estimating diffusion tensors, and performing tractography of white matter bundles.

Outline

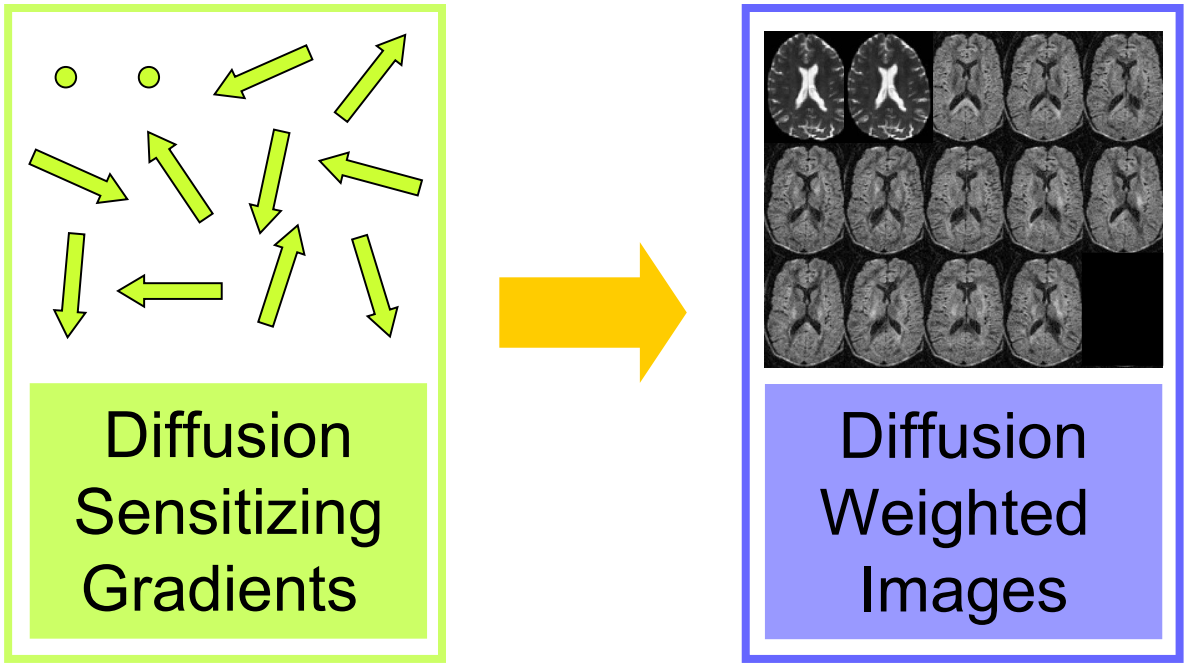


The processing pipeline uses 9 image analysis modules of Slicer3.6

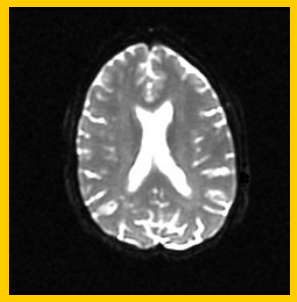
1. Data
2. Volumes
3. Diffusion Tensor Estimation
4. Diffusion Tensor Scalar Measurements
5. Editor
6. LabelMap Seeding
7. Fiber Bundles
8. Fiducials
9. Fiducial Seeding

Tutorial Dataset

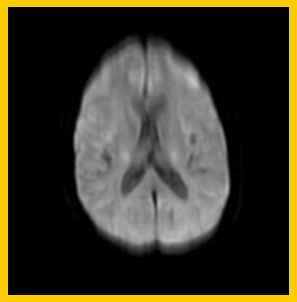
The Diffusion MR tutorial dataset is composed of a Diffusion Weighted MR scan of the brain acquired with 12 gradient directions and 2 baseline.



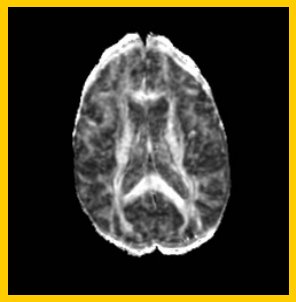
DTI Processing Pipeline



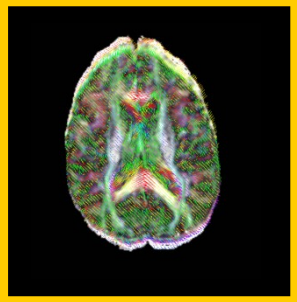
DWI Acquisition



Tensor Calculation

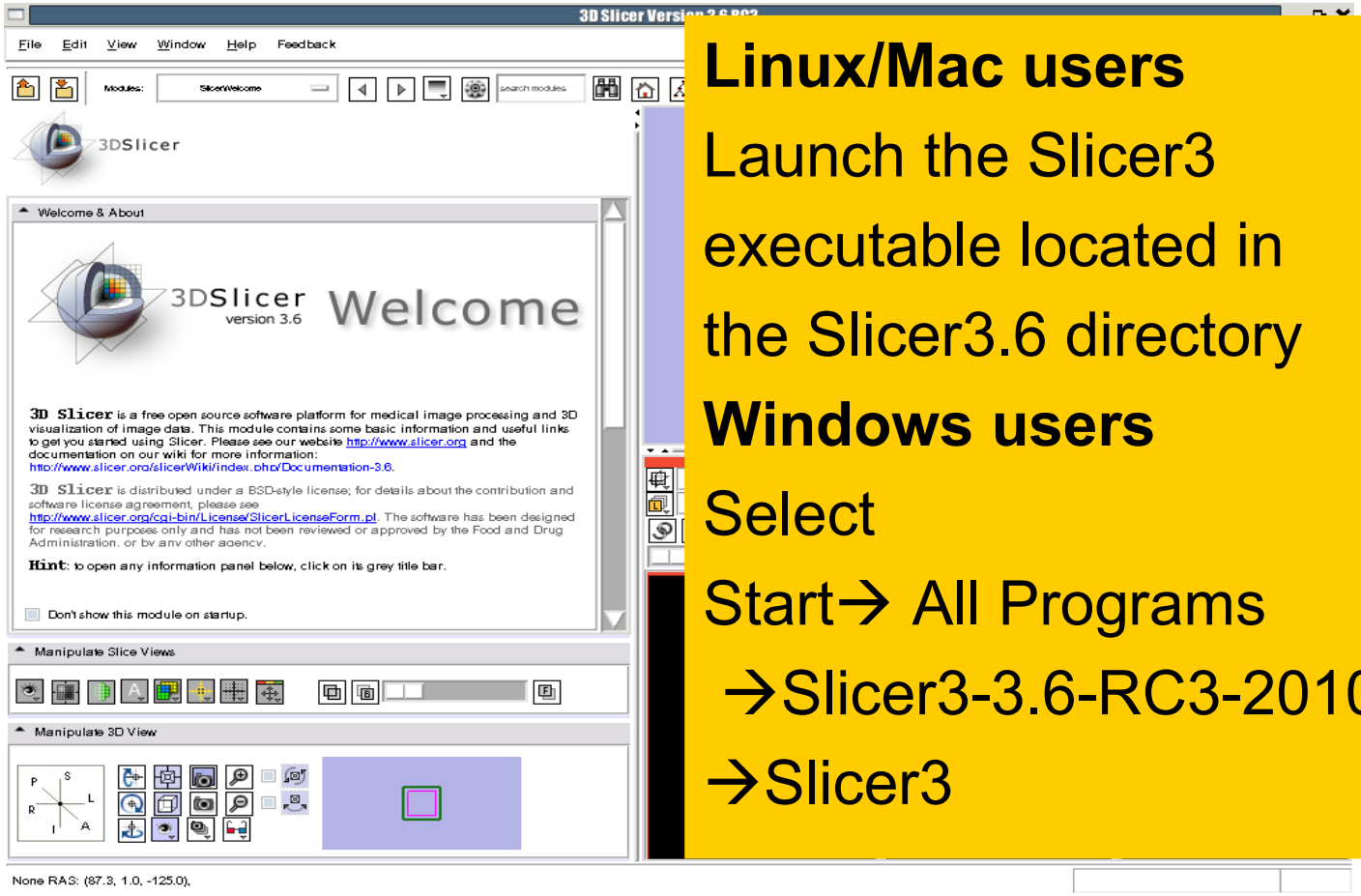


Scalar Maps



3D Visualization

Start Slicer3



Linux/Mac users

Launch the Slicer3 executable located in the Slicer3.6 directory

Windows users

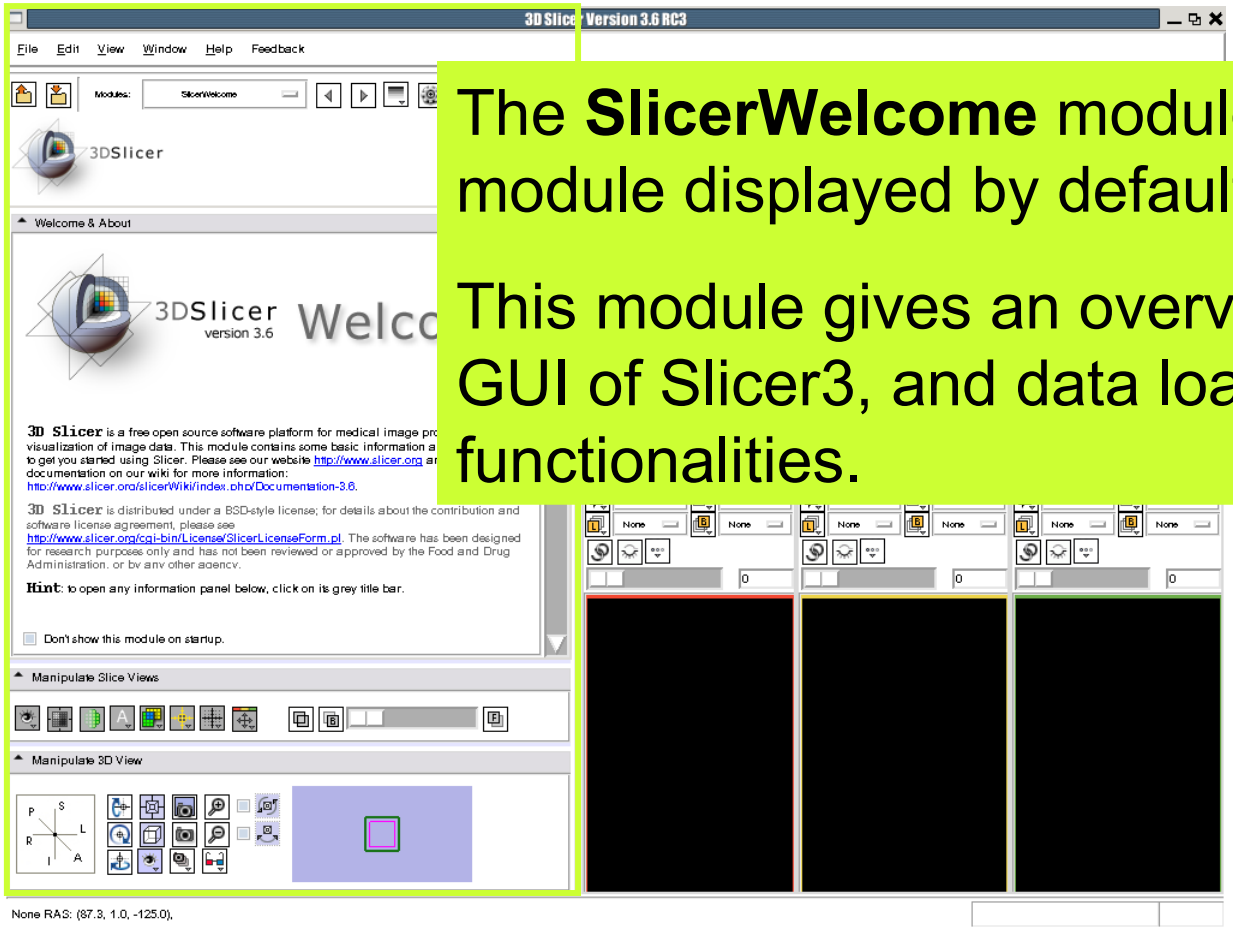
Select

Start→ All Programs

→Slicer3-3.6-RC3-2010-06-04

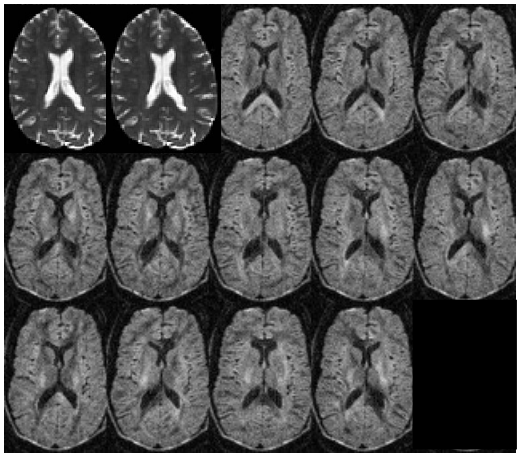
→Slicer3

Slicer Welcome



The **SlicerWelcome** module is the module displayed by default.

This module gives an overview of the GUI of Slicer3, and data loading & saving functionalities.

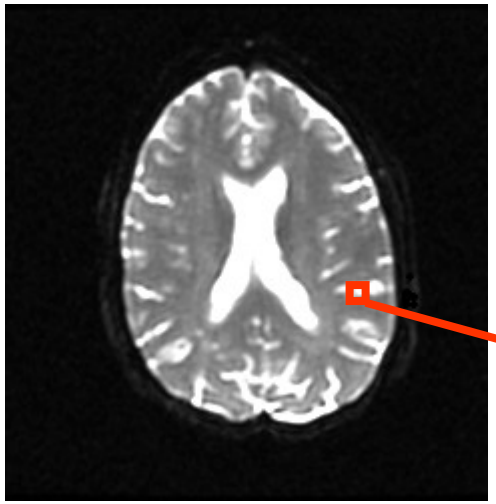


Part 1:

Diffusion data loading and tensor estimation

Diffusion Tensor

Stejskal-Tanner



$$S_i = S_0 e^{-b\hat{g}i^T \underline{D} \hat{g}_i}$$

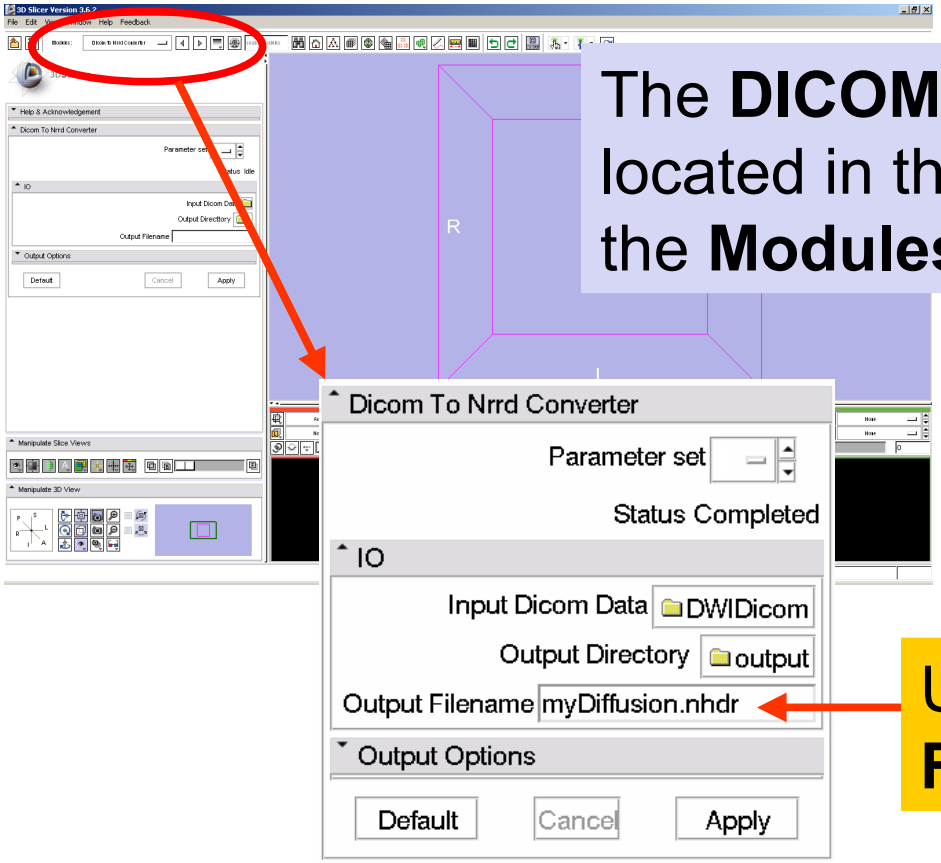
$$\underline{\mathbf{D}} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix}$$

Tutorial Dataset

The dataset used in this tutorial is in **the Nrrd file format**, which is part of the NA-MIC kit.

To convert your own Dicom data to Nrrd, use the **DicomToNrrdConverter** module in Slicer.

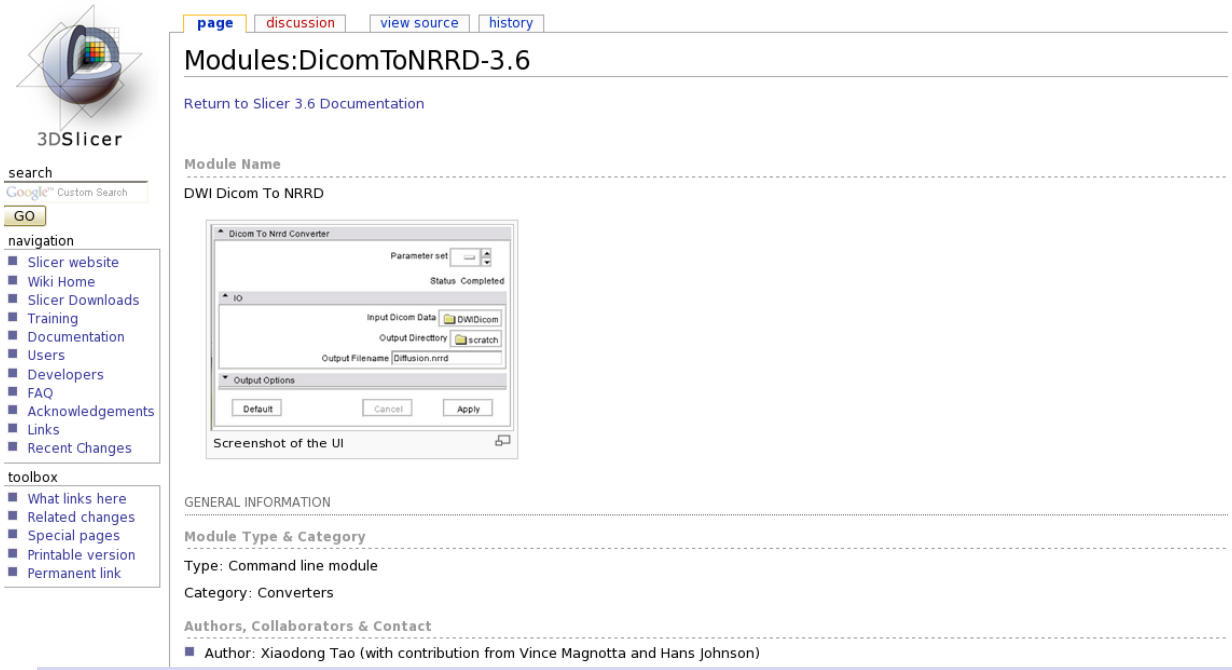
DicomToNrrd converter



The **DICOMToNrrdConverter** is located in the **Converters** category in the **Modules** menu

Use .nhdr for **Output Filename** extension

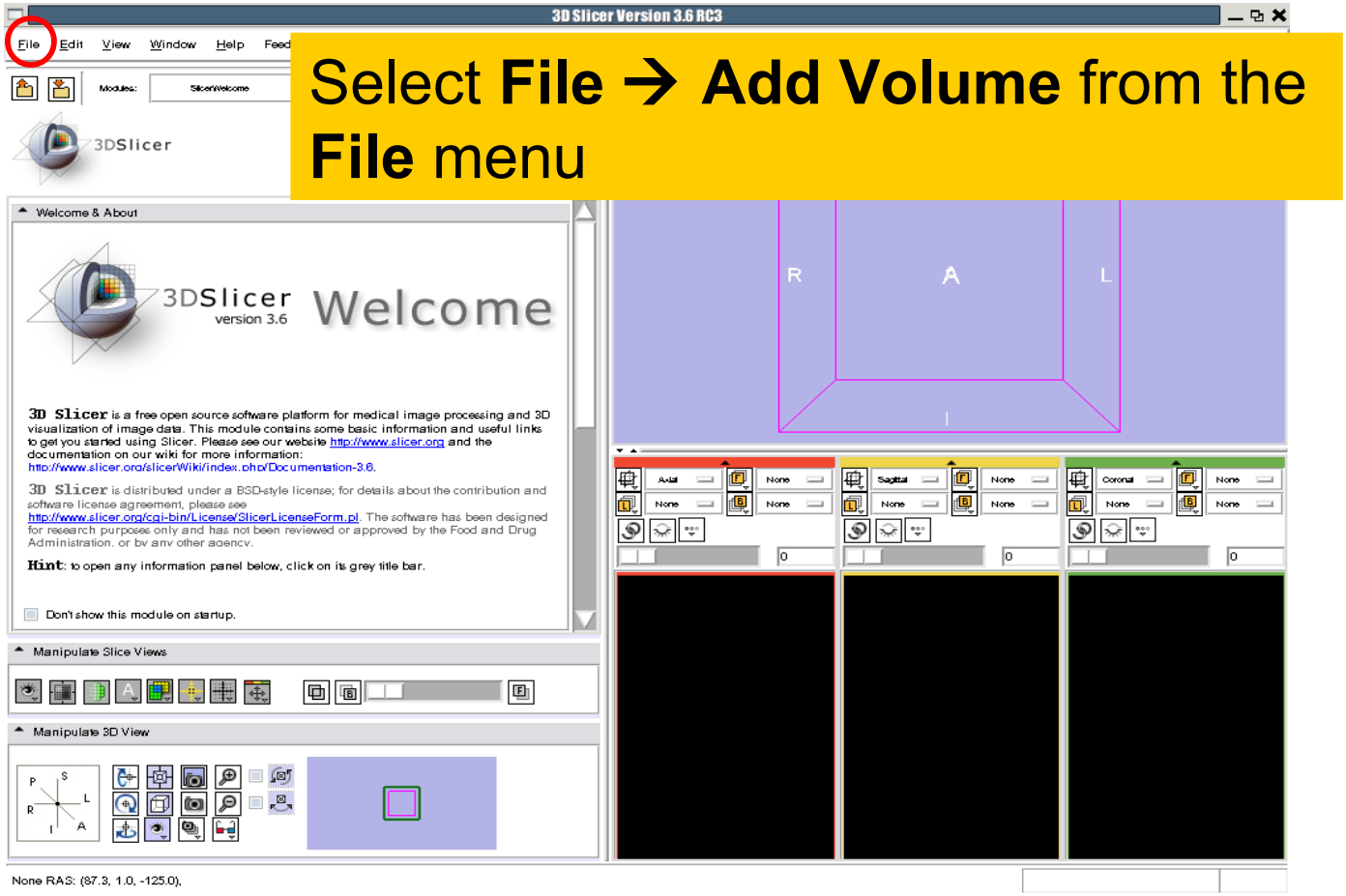
DicomToNrrd converter



A list of supported DWI formats can be found on the documentation page of the **DicomToNrrdconverter:**

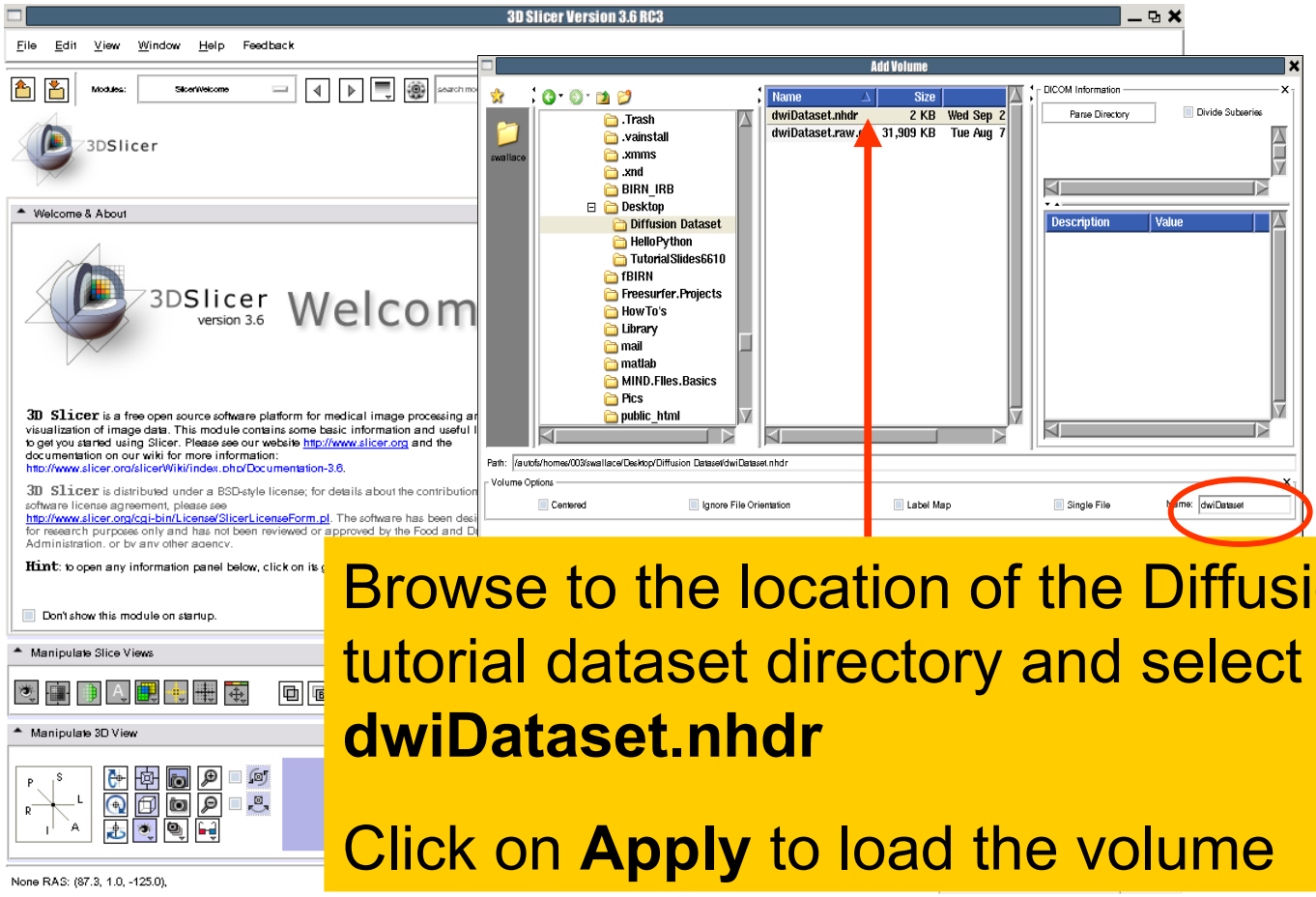
http://www.slicer.org/slicerWiki/index.php/Modules:DicomToNRRD-3.6

Loading the DWI Volume



Select **File → Add Volume** from the **File** menu

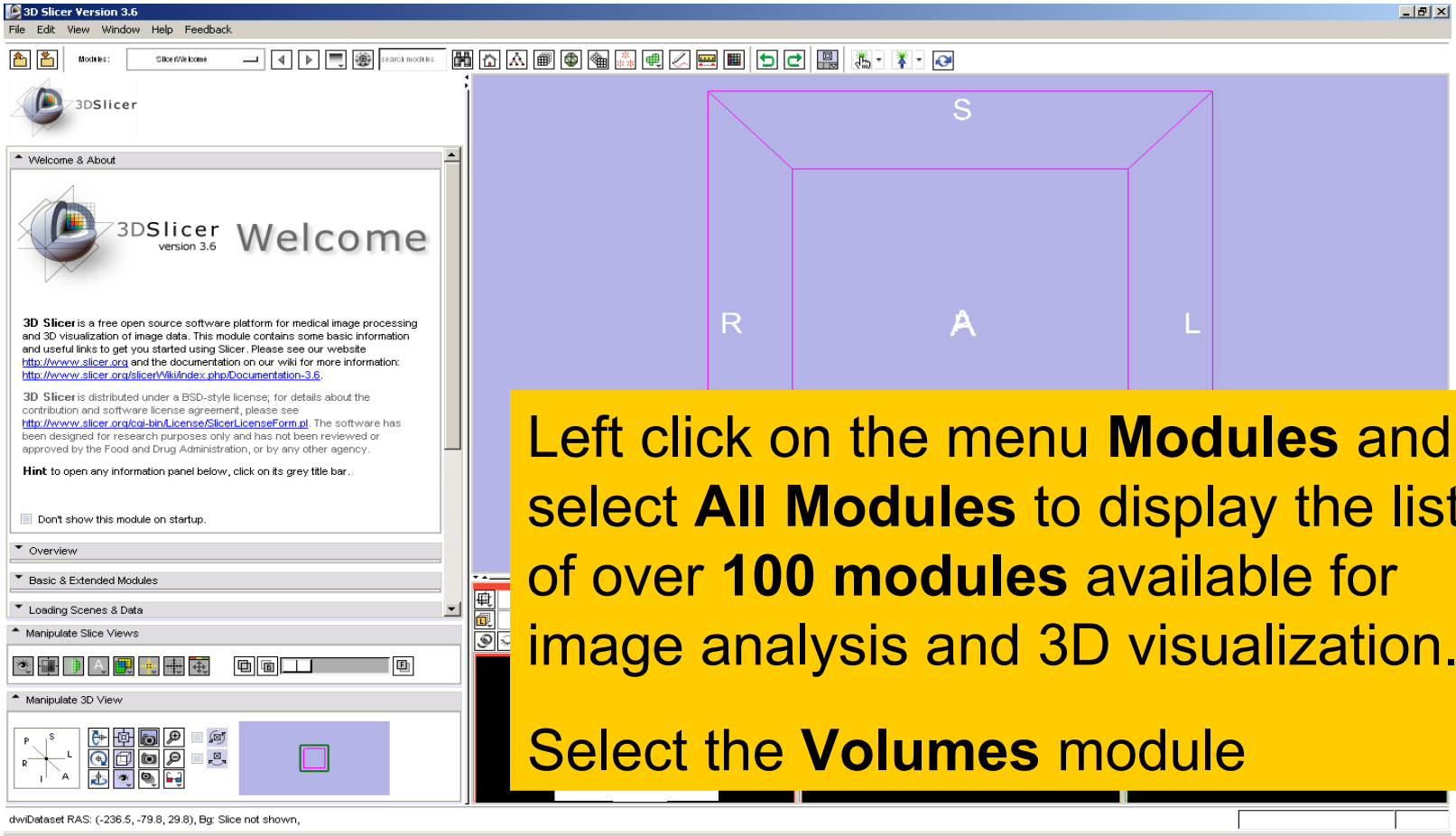
Loading the DWI Volume



Browse to the location of the Diffusion tutorial dataset directory and select the file **dwiDataset.nhdr**

Click on **Apply** to load the volume

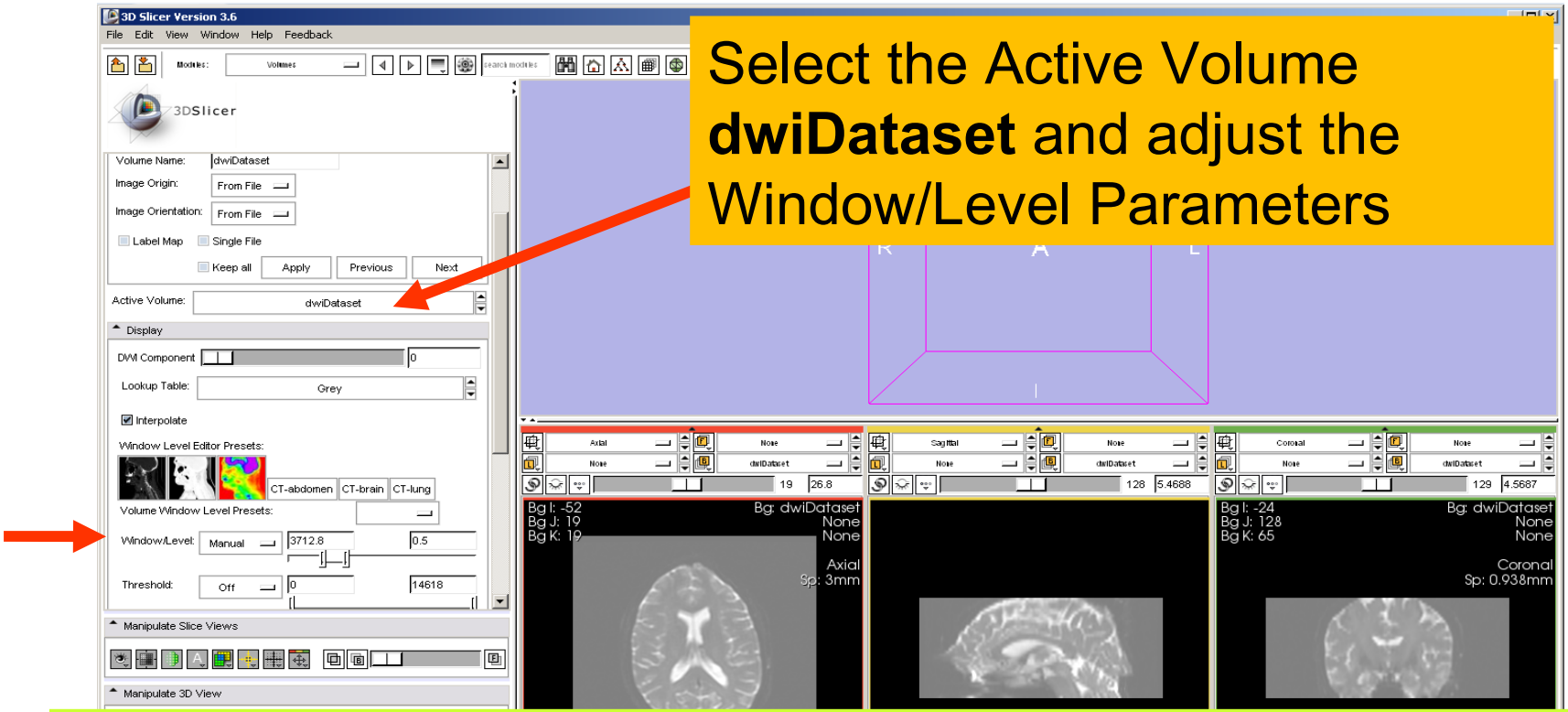
Loading the DWI Volume



Left click on the menu **Modules** and select **All Modules** to display the list of over **100 modules** available for image analysis and 3D visualization.

Select the **Volumes** module

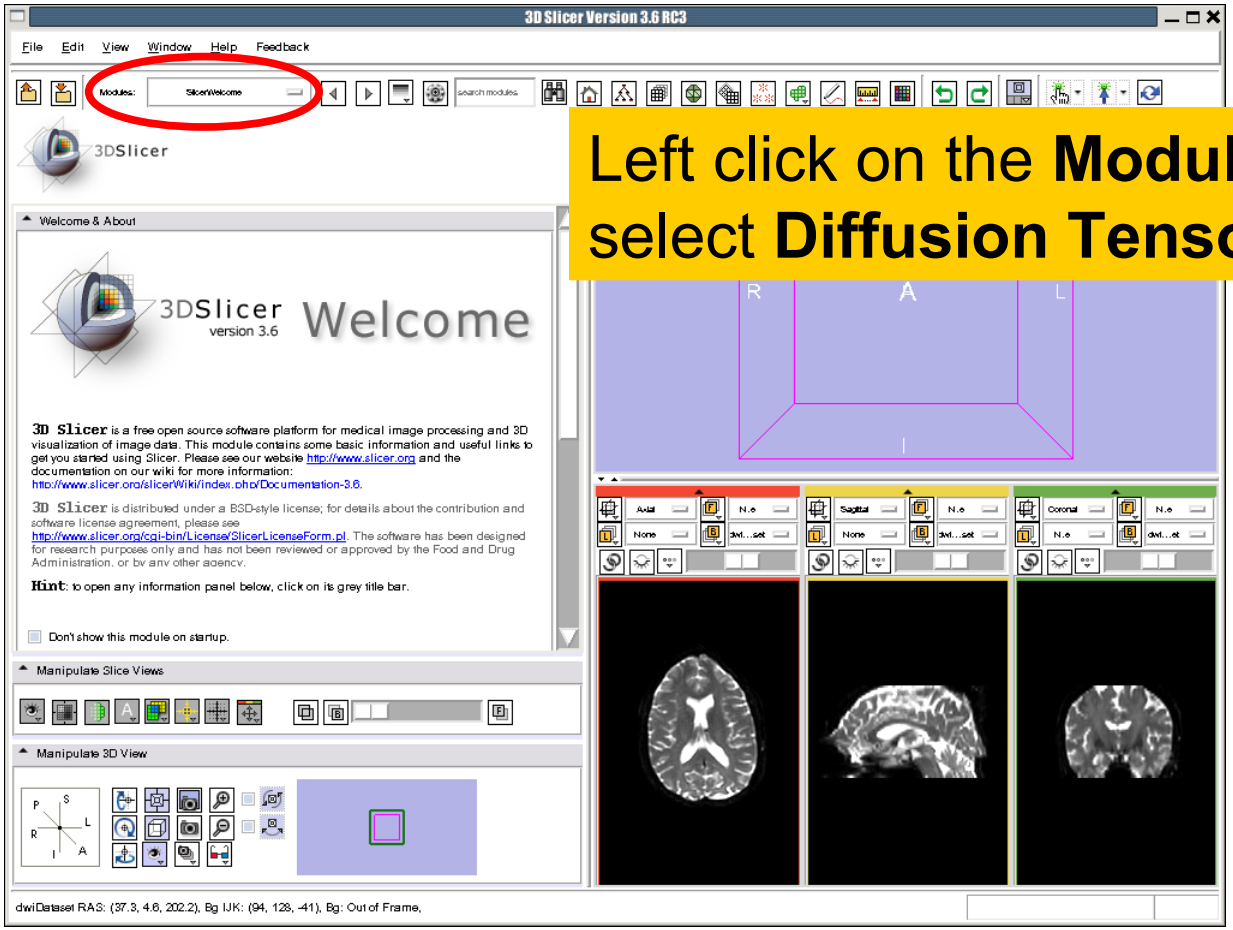
Loading the DWI Volume



Select the Active Volume **dwiDataset** and adjust the Window/Level Parameters

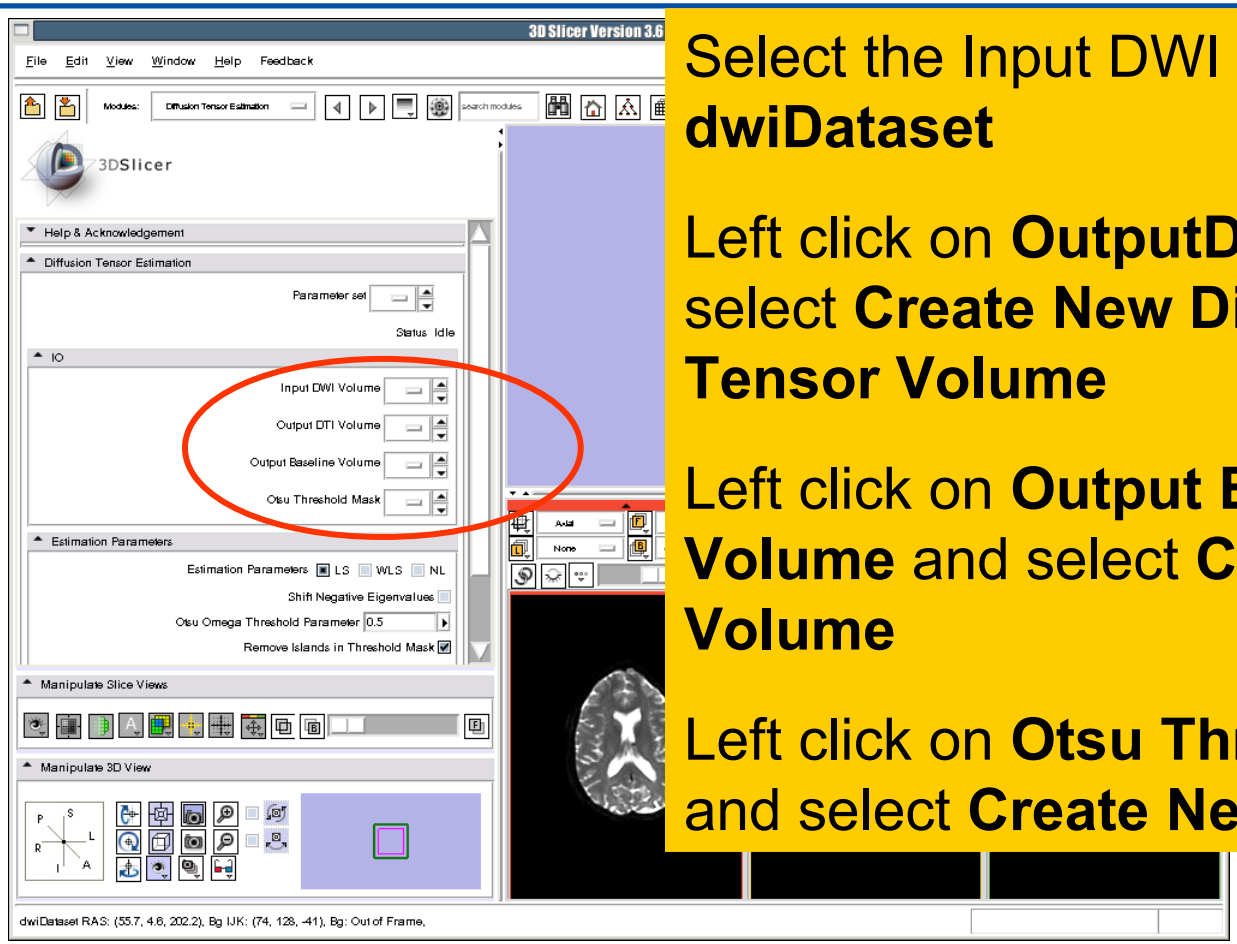
Slicer displays the anatomical views of the baseline volume of the diffusion dataset in the 2D Slice Viewer.

Tensor Estimation



Left click on the **Modules** menu and select **Diffusion Tensor Estimation**.

Tensor Estimation



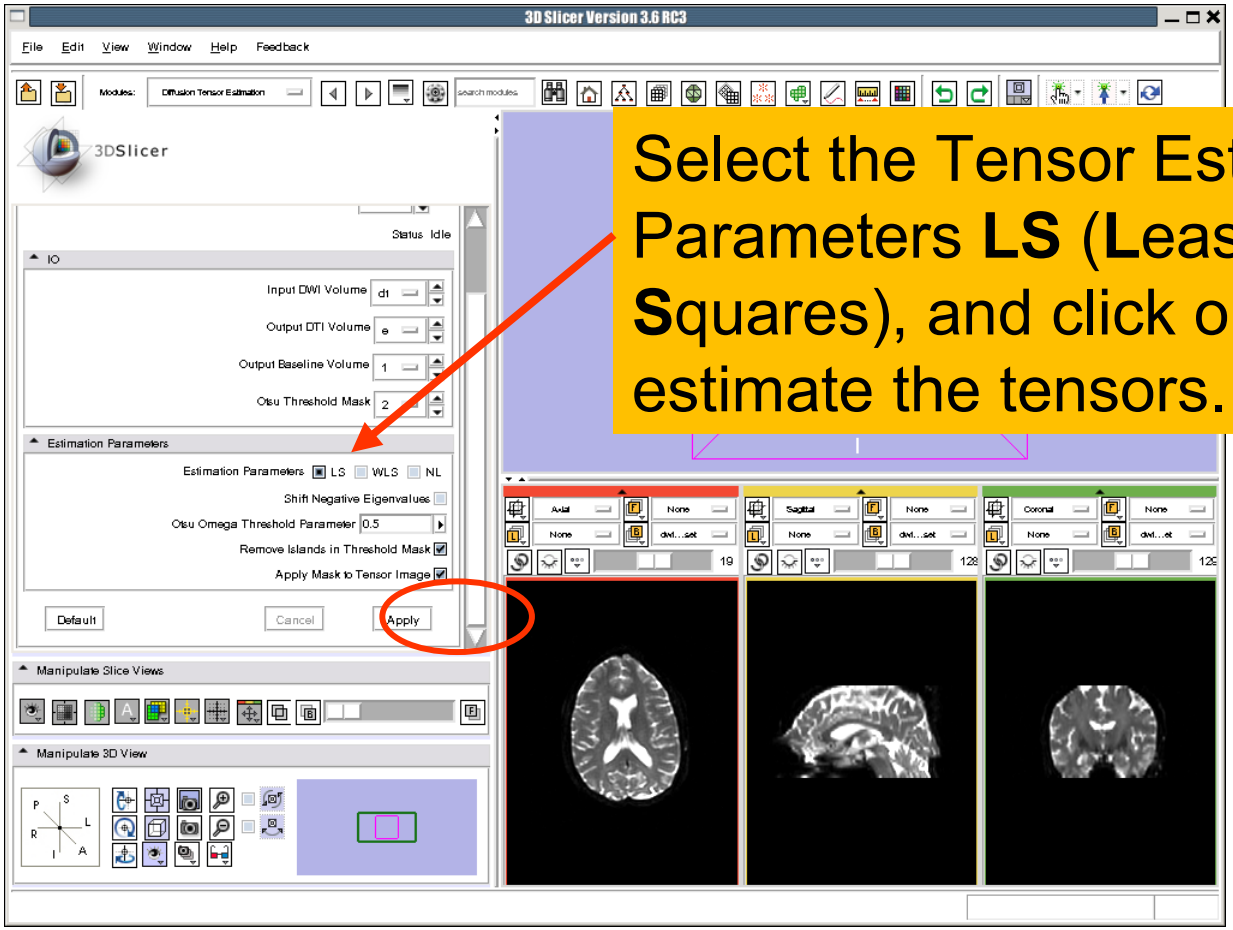
Select the Input DWI Volume **dwiDataset**

Left click on **OutputDTIVolume** and select **Create New Diffusion Tensor Volume**

Left click on **Output Baseline Volume** and select **Create New Volume**

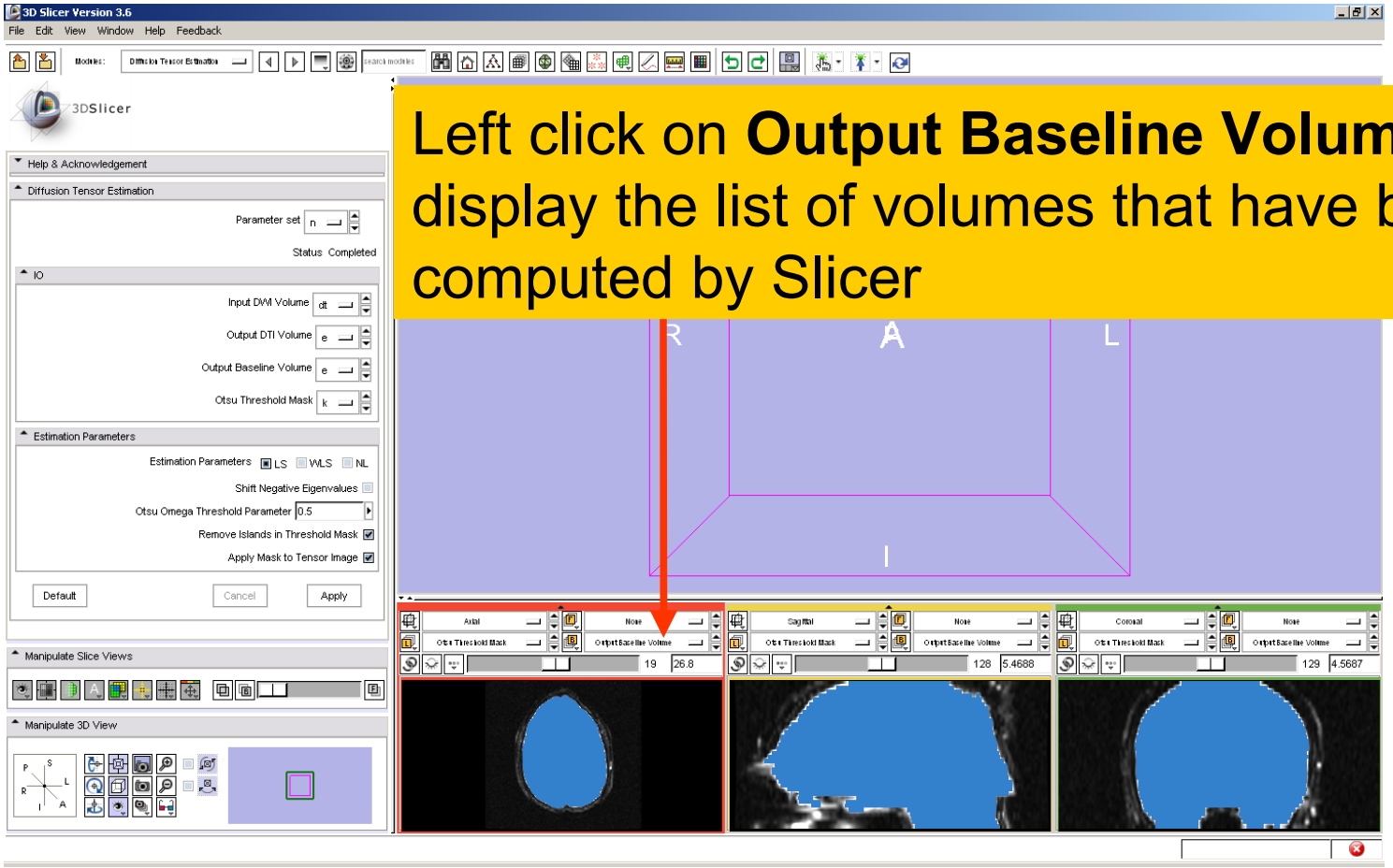
Left click on **Otsu Threshold Mask** and select **Create New Volume**

Tensor Estimation



Select the Tensor Estimation Parameters **LS** (**L**east **S**quares), and click on **Apply** to estimate the tensors.

Tensor Estimation



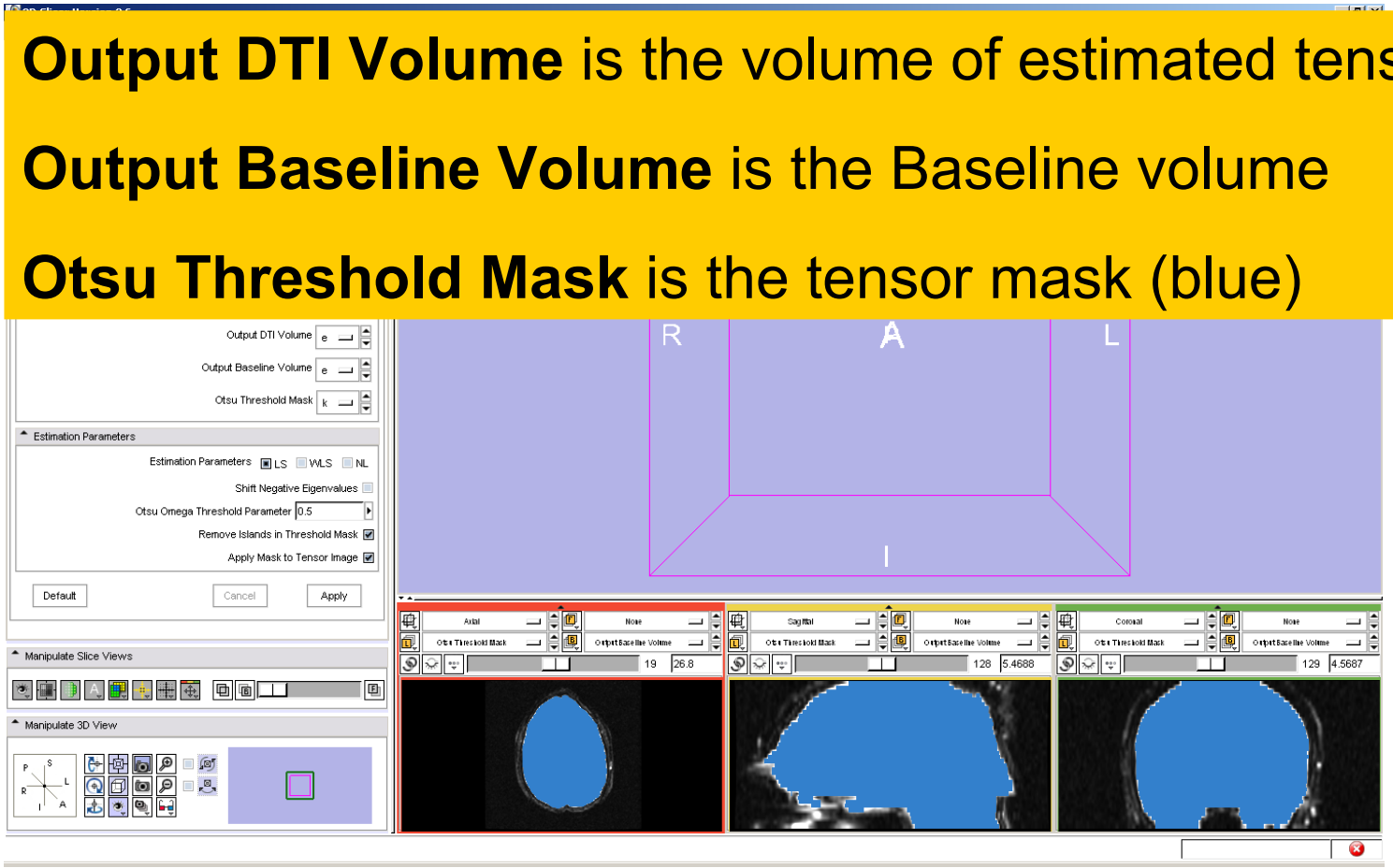
Left click on **Output Baseline Volume** to display the list of volumes that have been computed by Slicer

Tensor Estimation

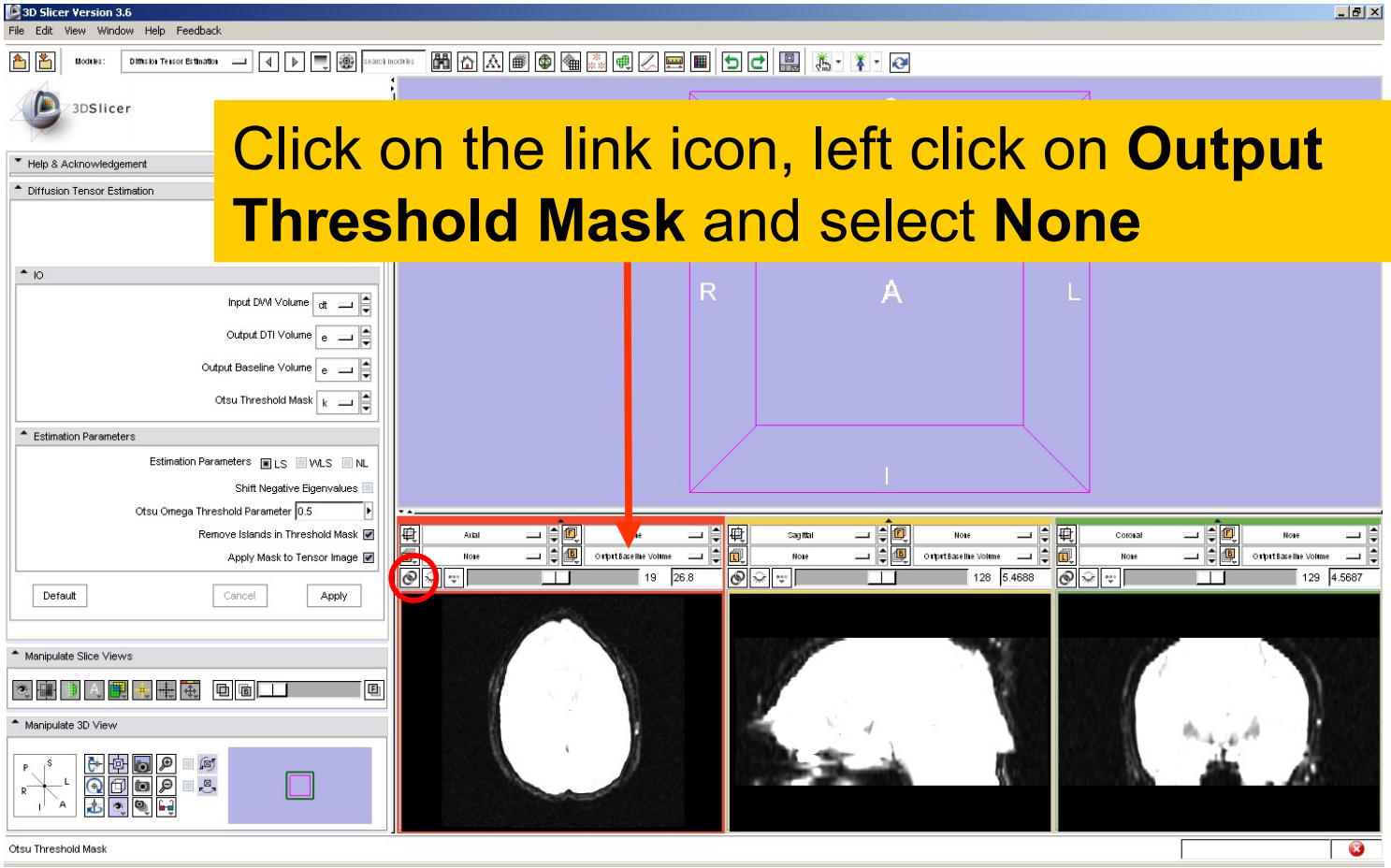
Output DTI Volume is the volume of estimated tensors

Output Baseline Volume is the Baseline volume

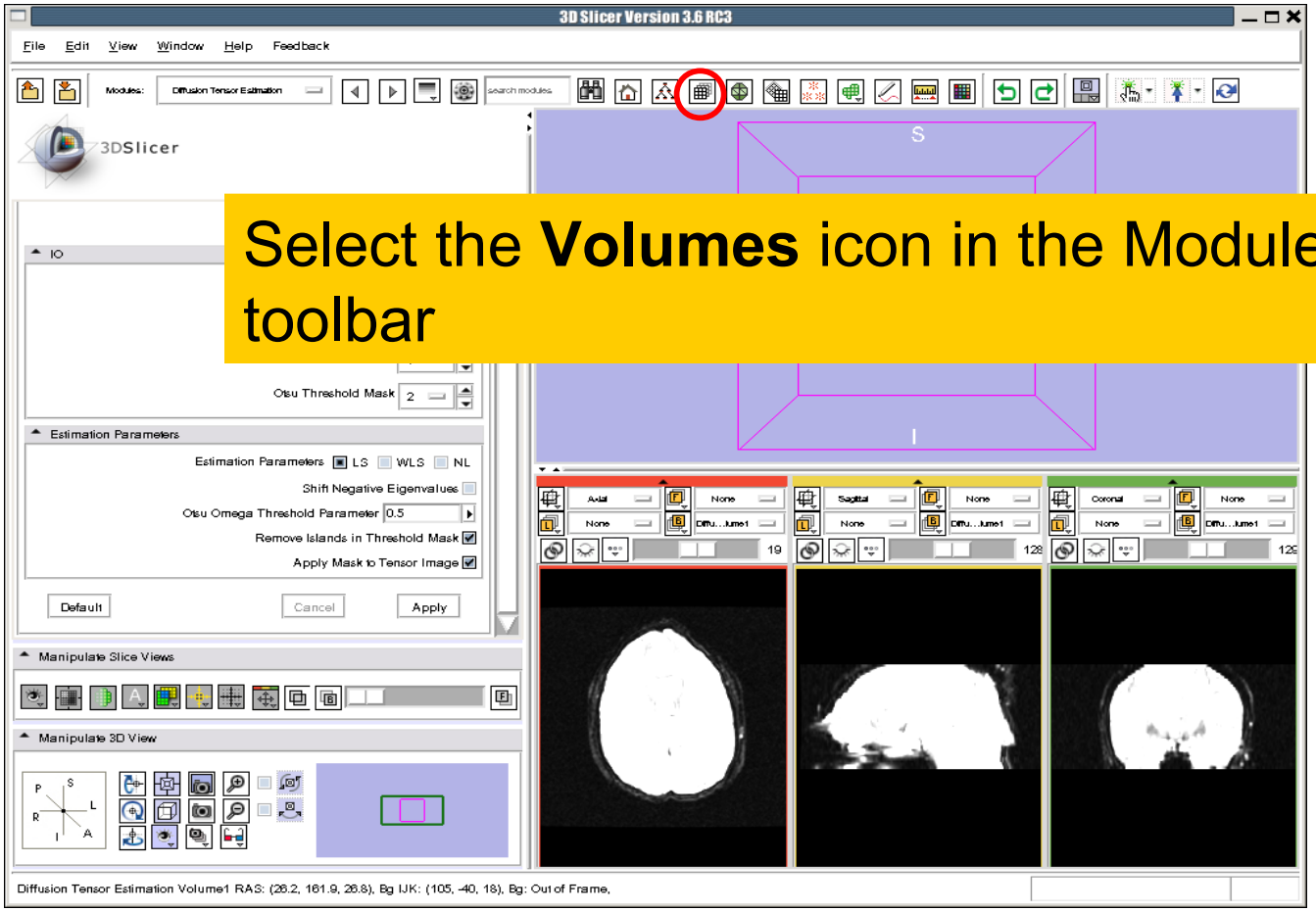
Otsu Threshold Mask is the tensor mask (blue)



Tensor Estimation

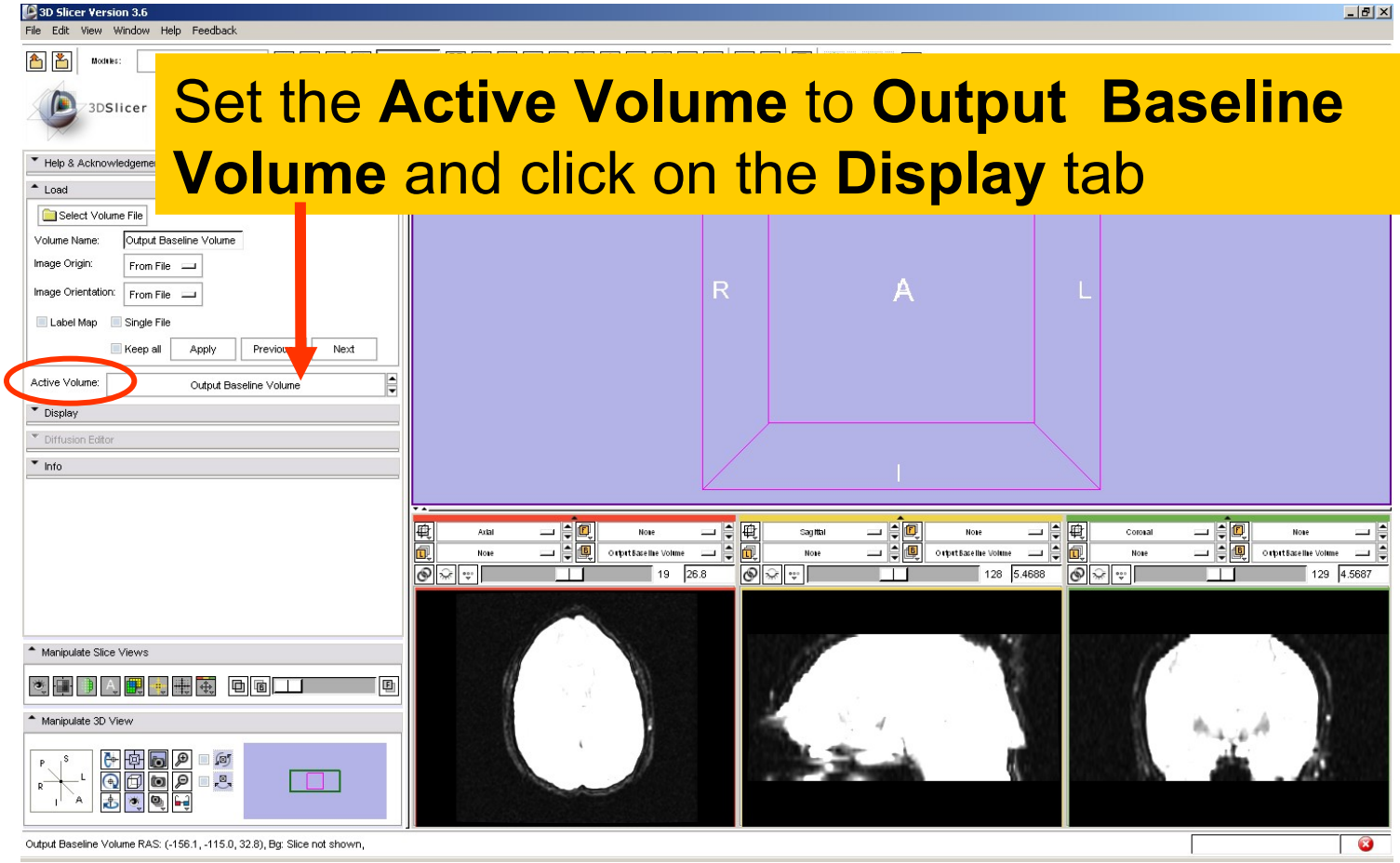


Tensor Estimation

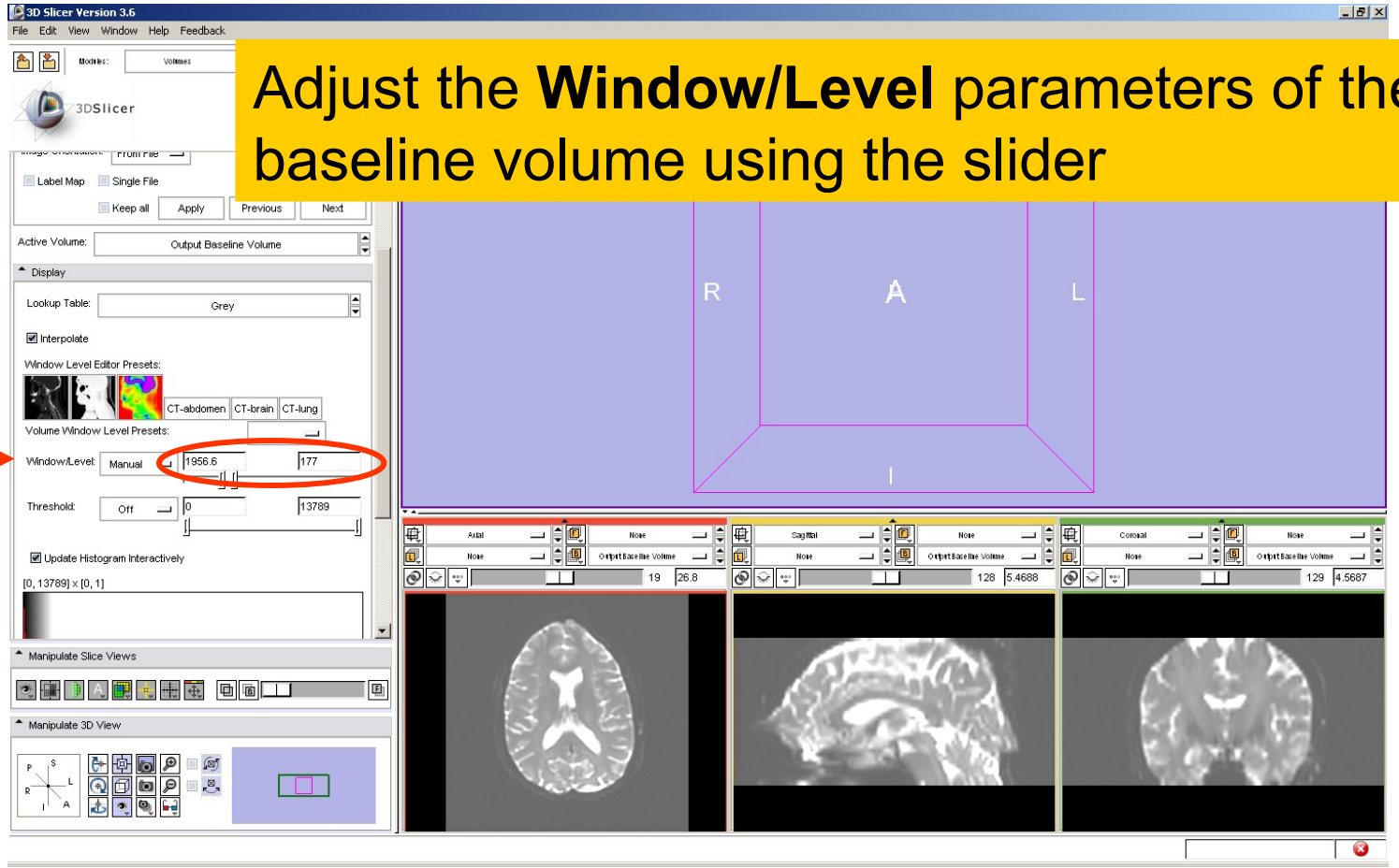


Select the **Volumes** icon in the Modules toolbar

Tensor Estimation

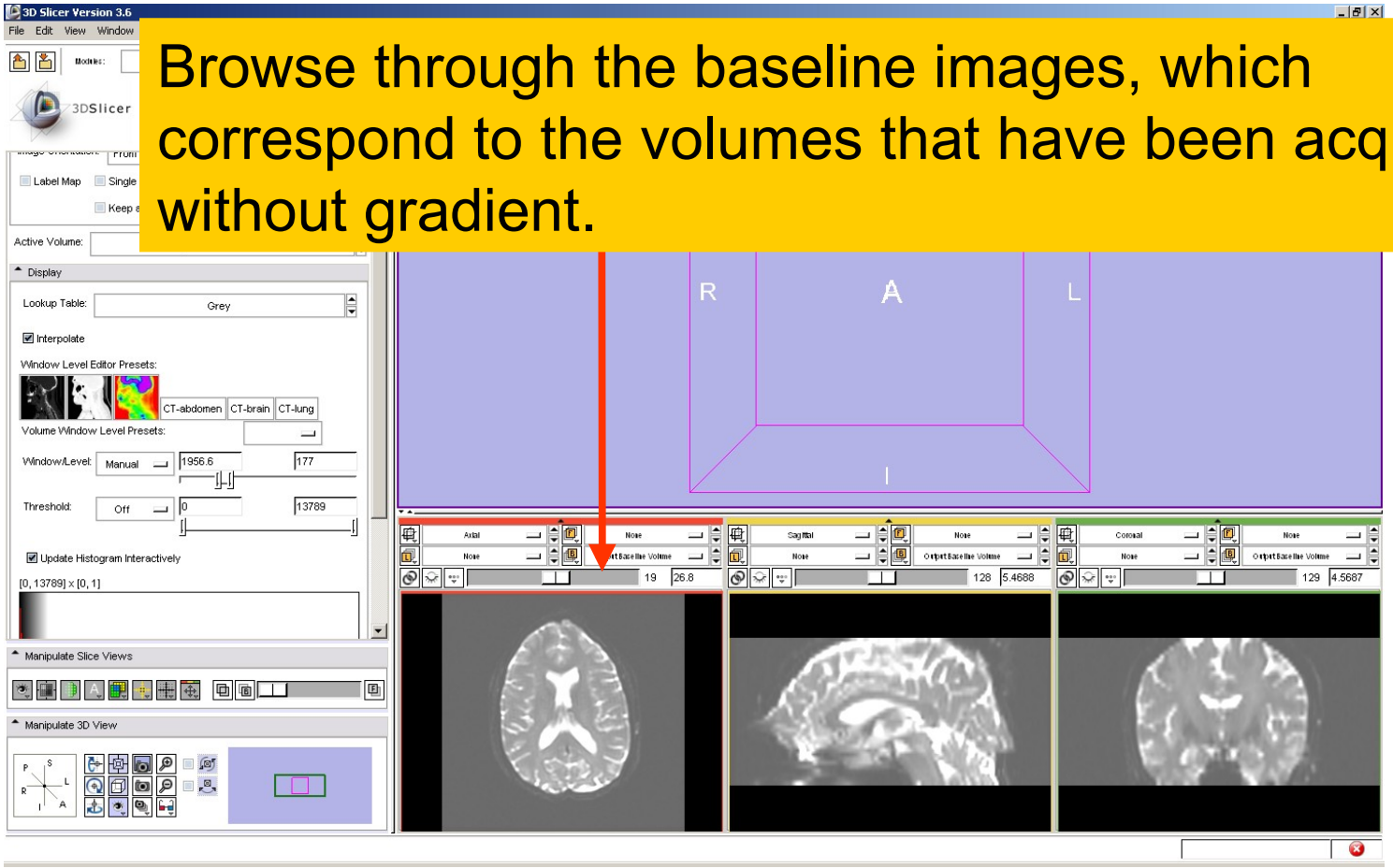


Tensor Estimation

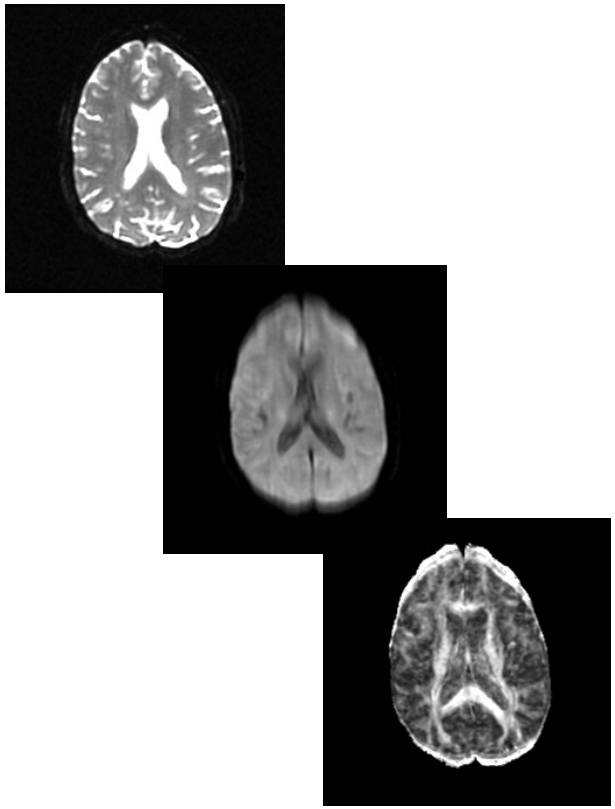


Adjust the **Window/Level** parameters of the baseline volume using the slider

Tensor Estimation



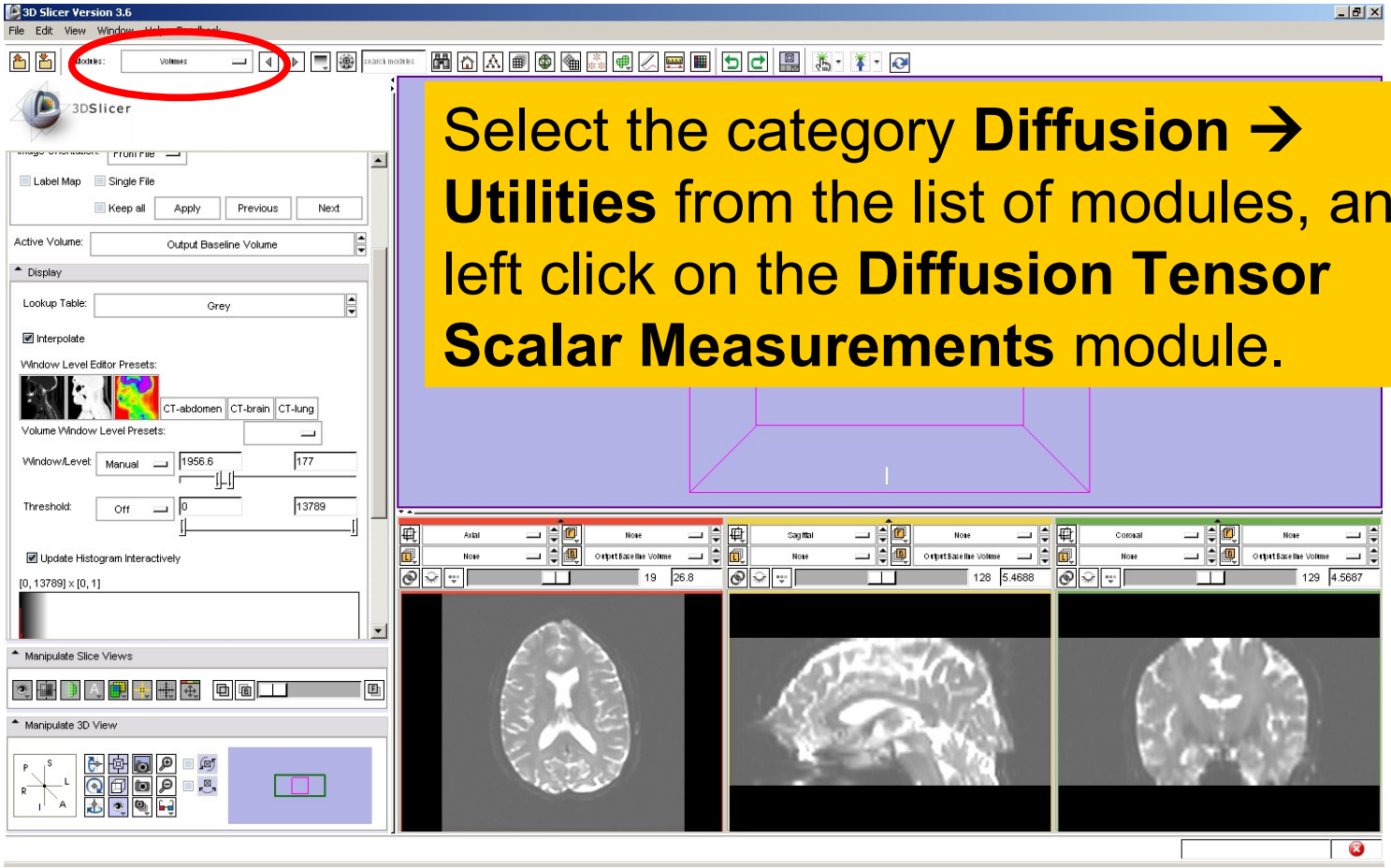
Browse through the baseline images, which correspond to the volumes that have been acquired without gradient.



Part 2:

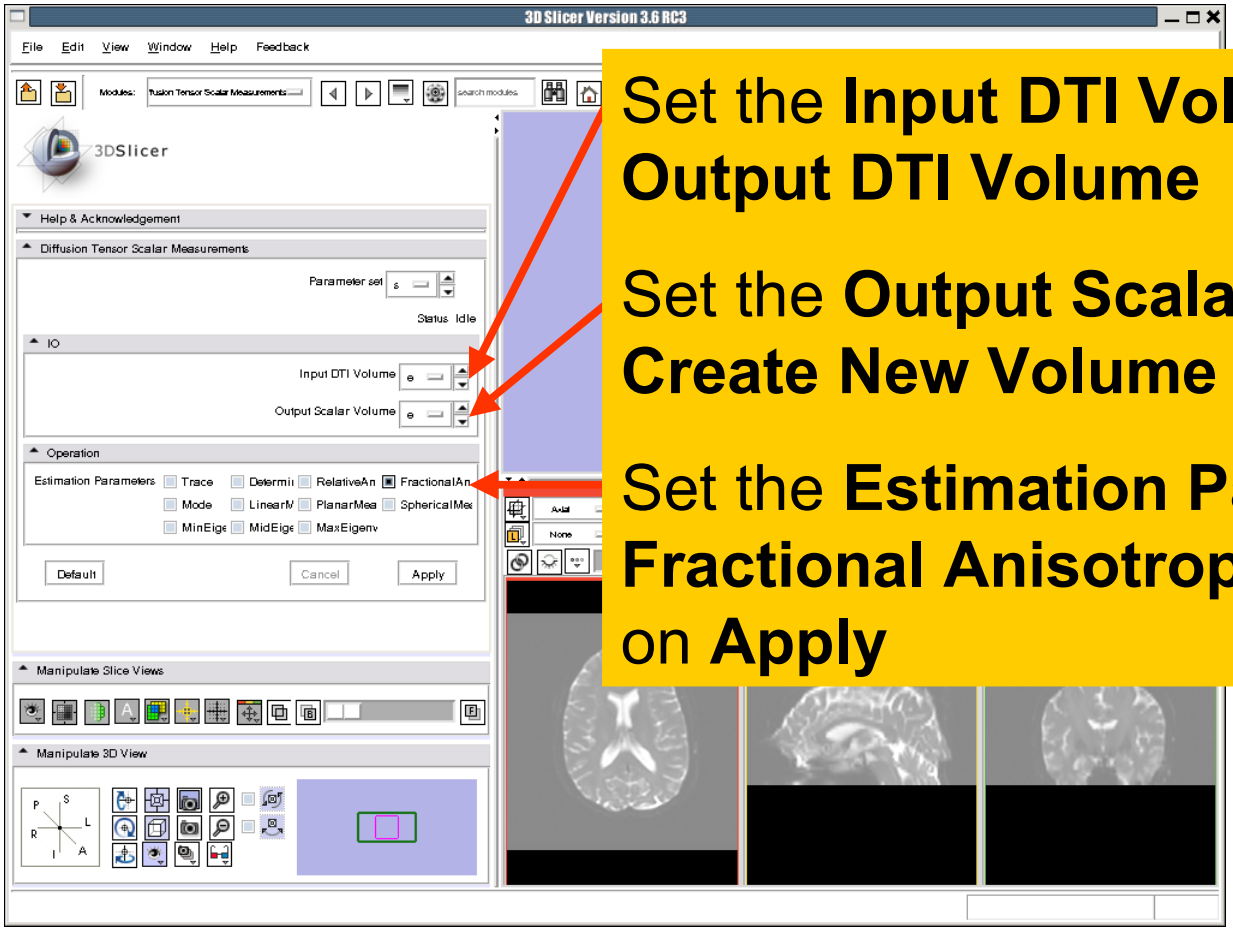
Scalar Measurements

Scalar Measurements



Select the category **Diffusion → Utilities** from the list of modules, and left click on the **Diffusion Tensor Scalar Measurements** module.

Scalar Measurements

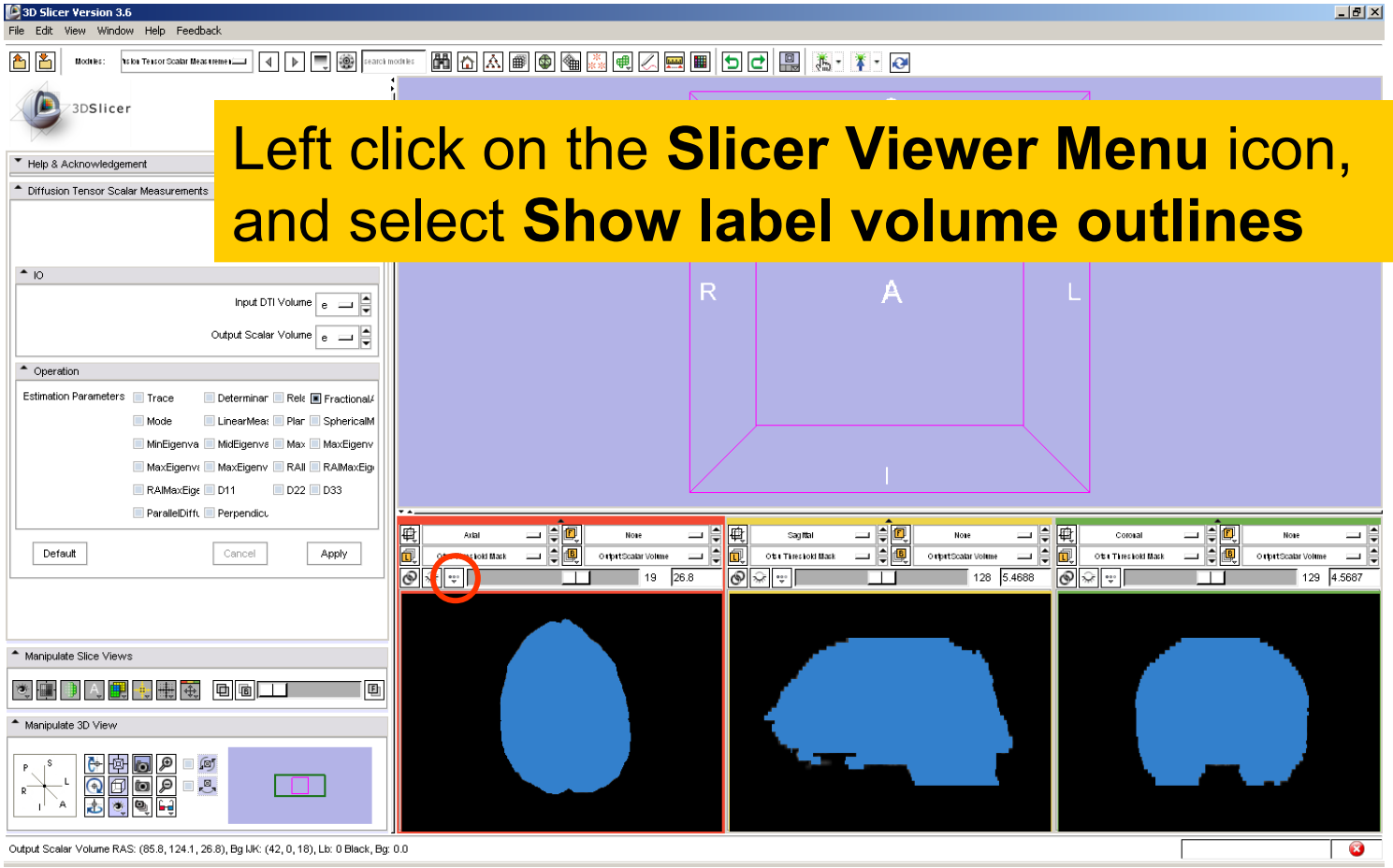


Set the **Input DTI Volume** to **Output DTI Volume**

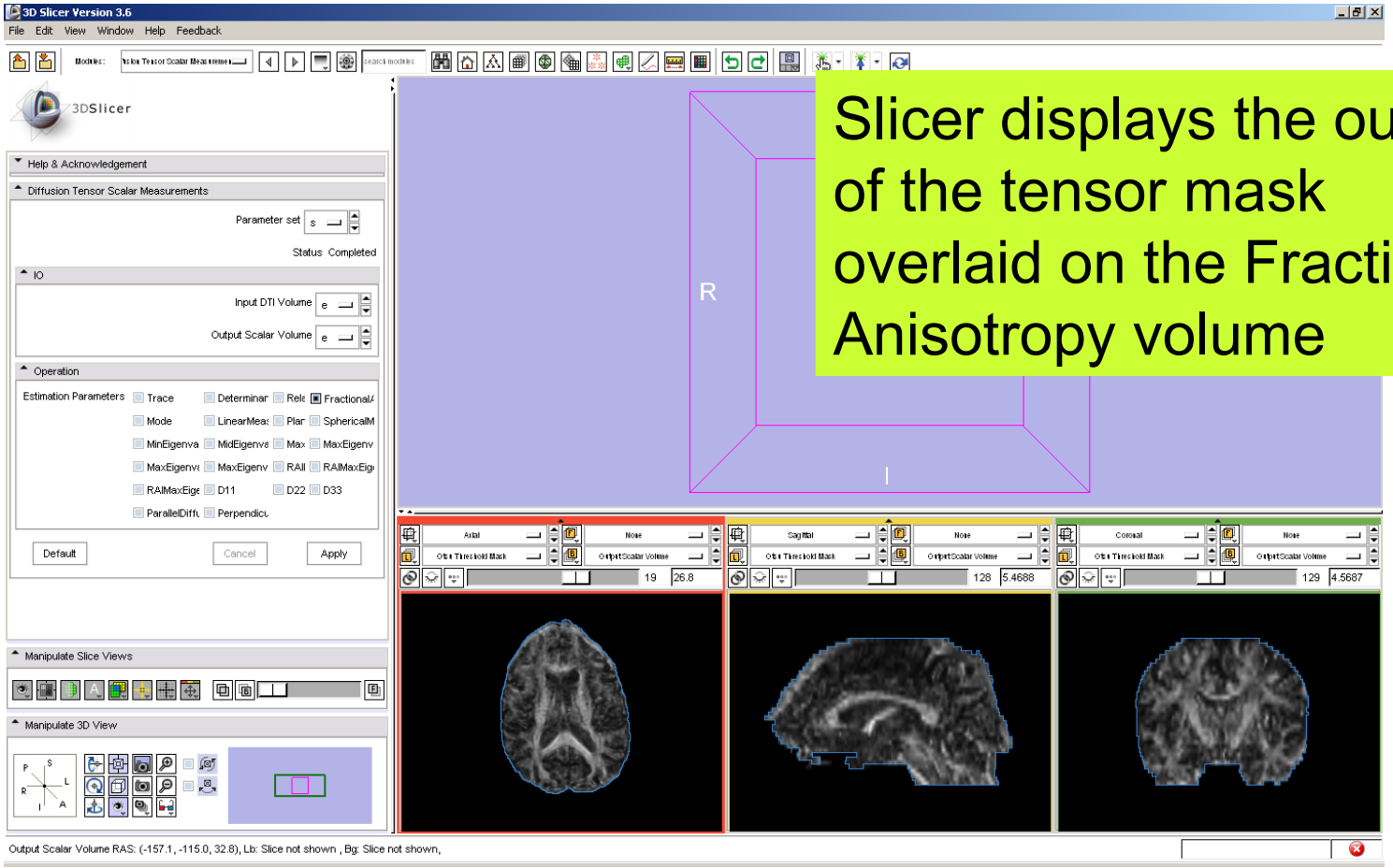
Set the **Output Scalar Volume** to **Create New Volume**

Set the **Estimation Parameters** to **Fractional Anisotropy,** and click on **Apply**

Fractional Anisotropy Volume

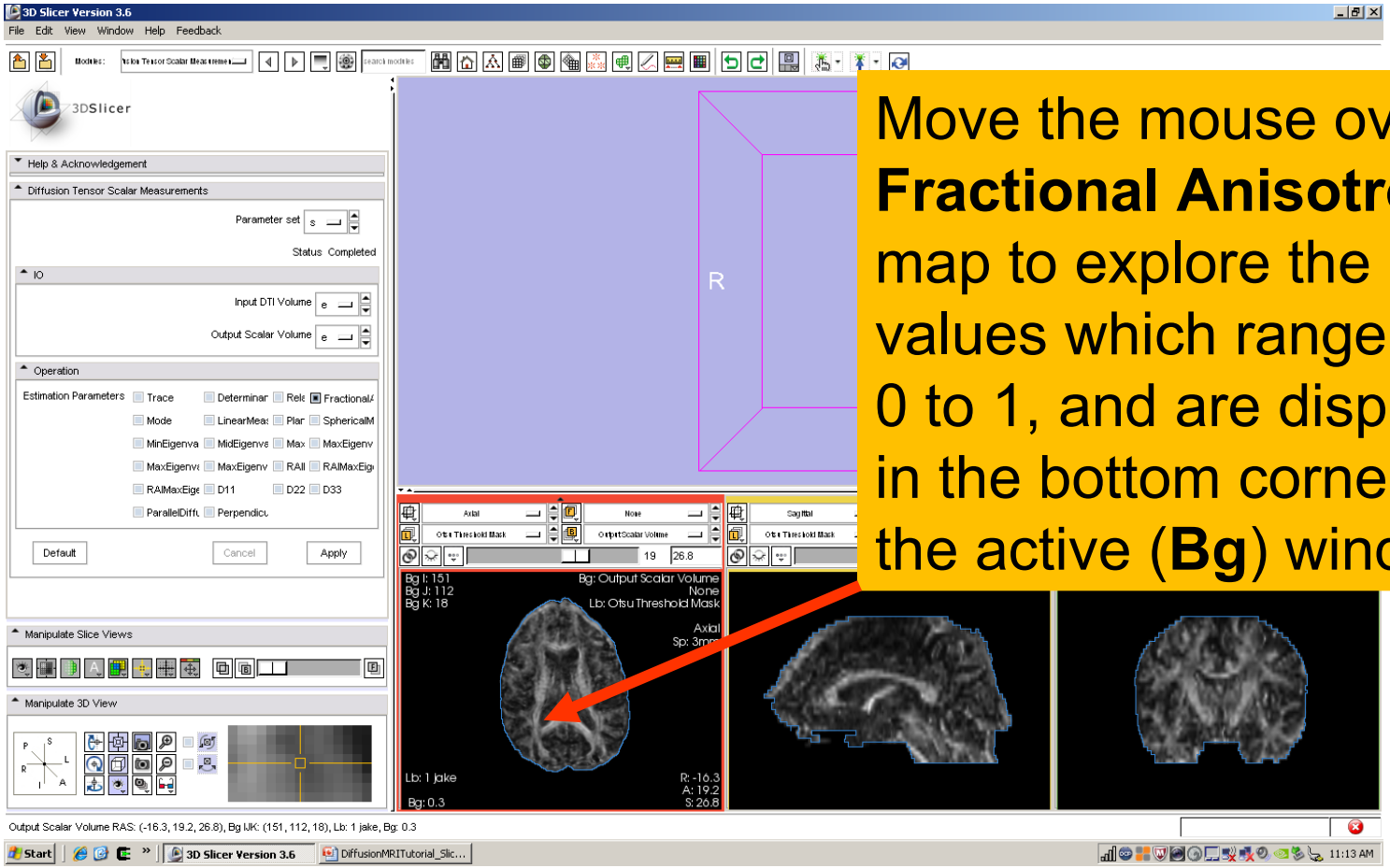


Fractional Anisotropy Volume

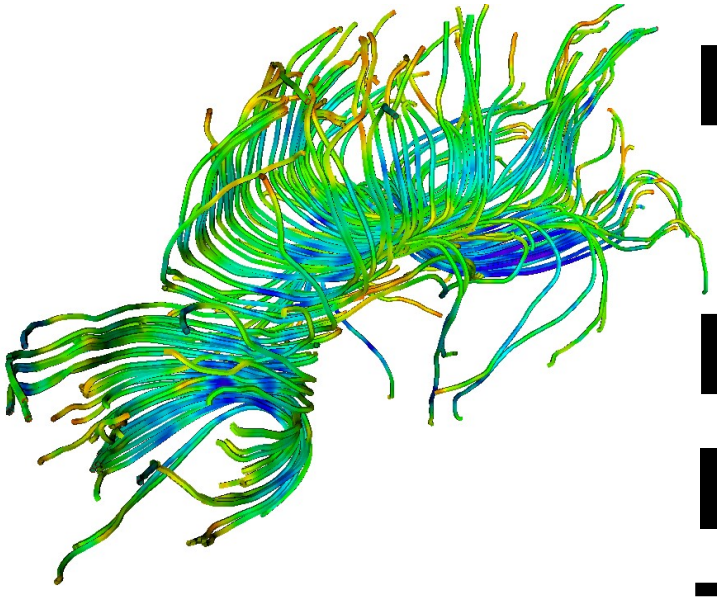


Slicer displays the outline of the tensor mask overlaid on the Fractional Anisotropy volume

Fractional Anisotropy Volume



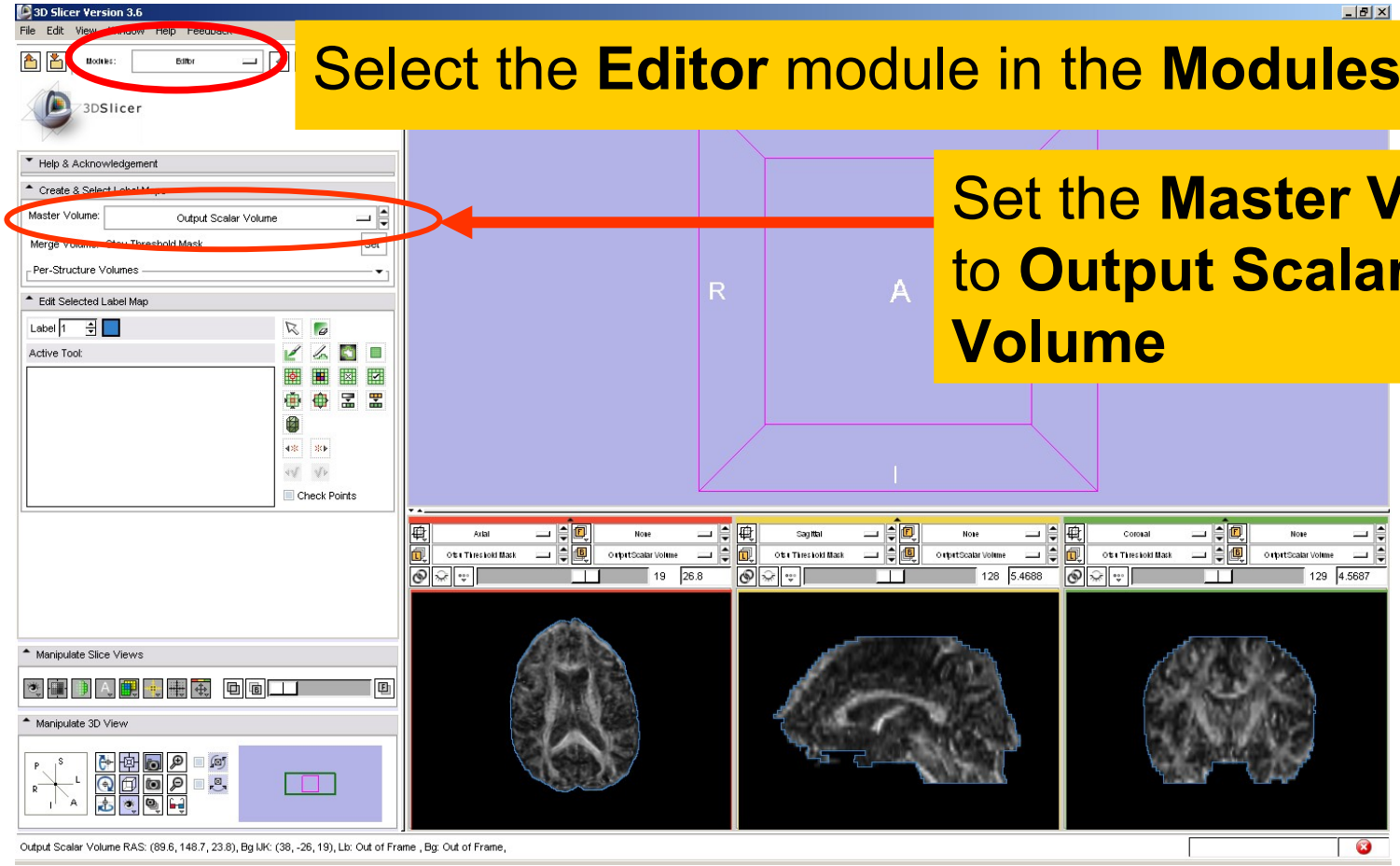
Move the mouse over the **Fractional Anisotropy** map to explore the FA values which range from 0 to 1, and are displayed in the bottom corner of the active (**Bg**) window.



Part 3:

Region of Interest Based Tractography

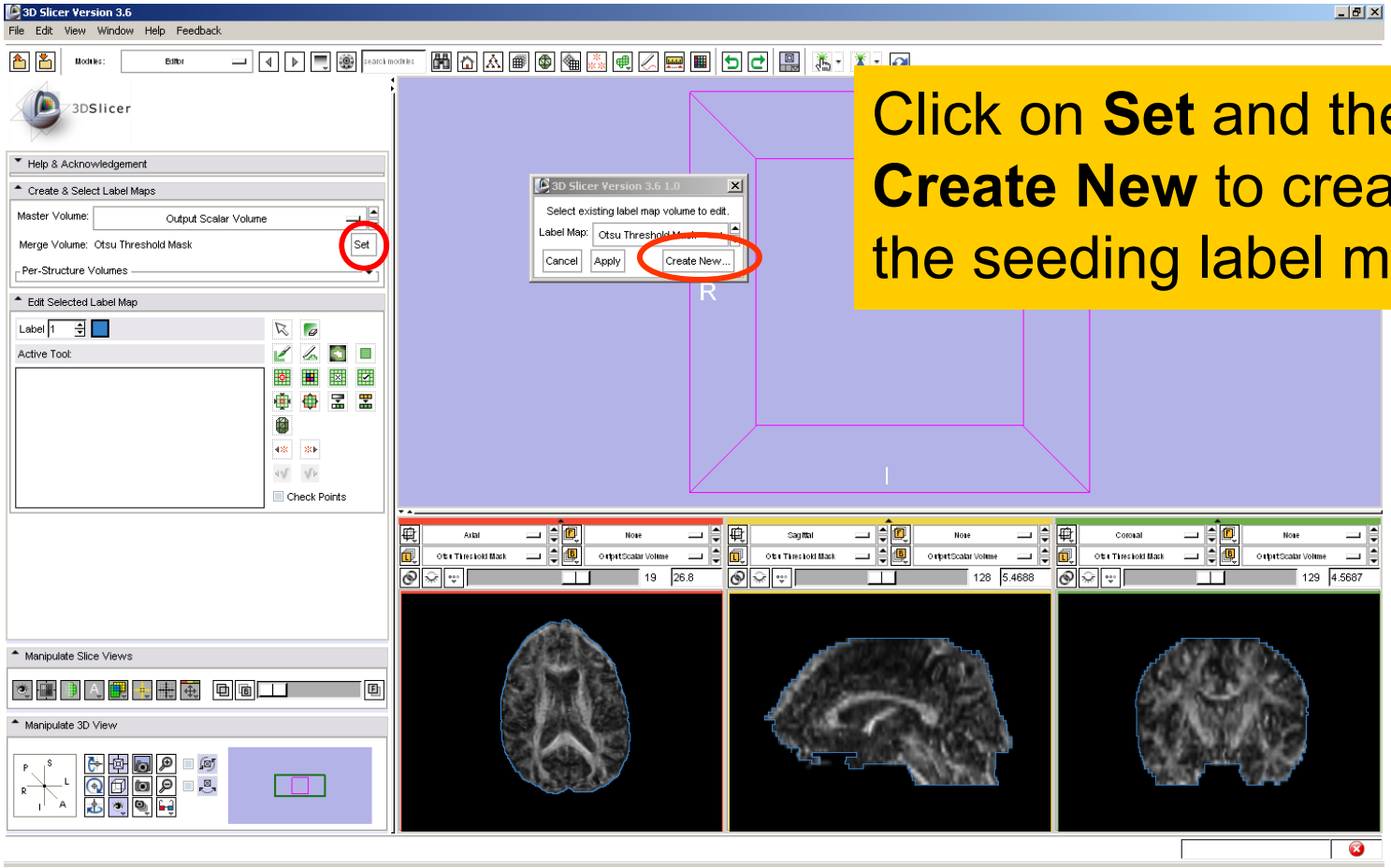
LabelMap Generation



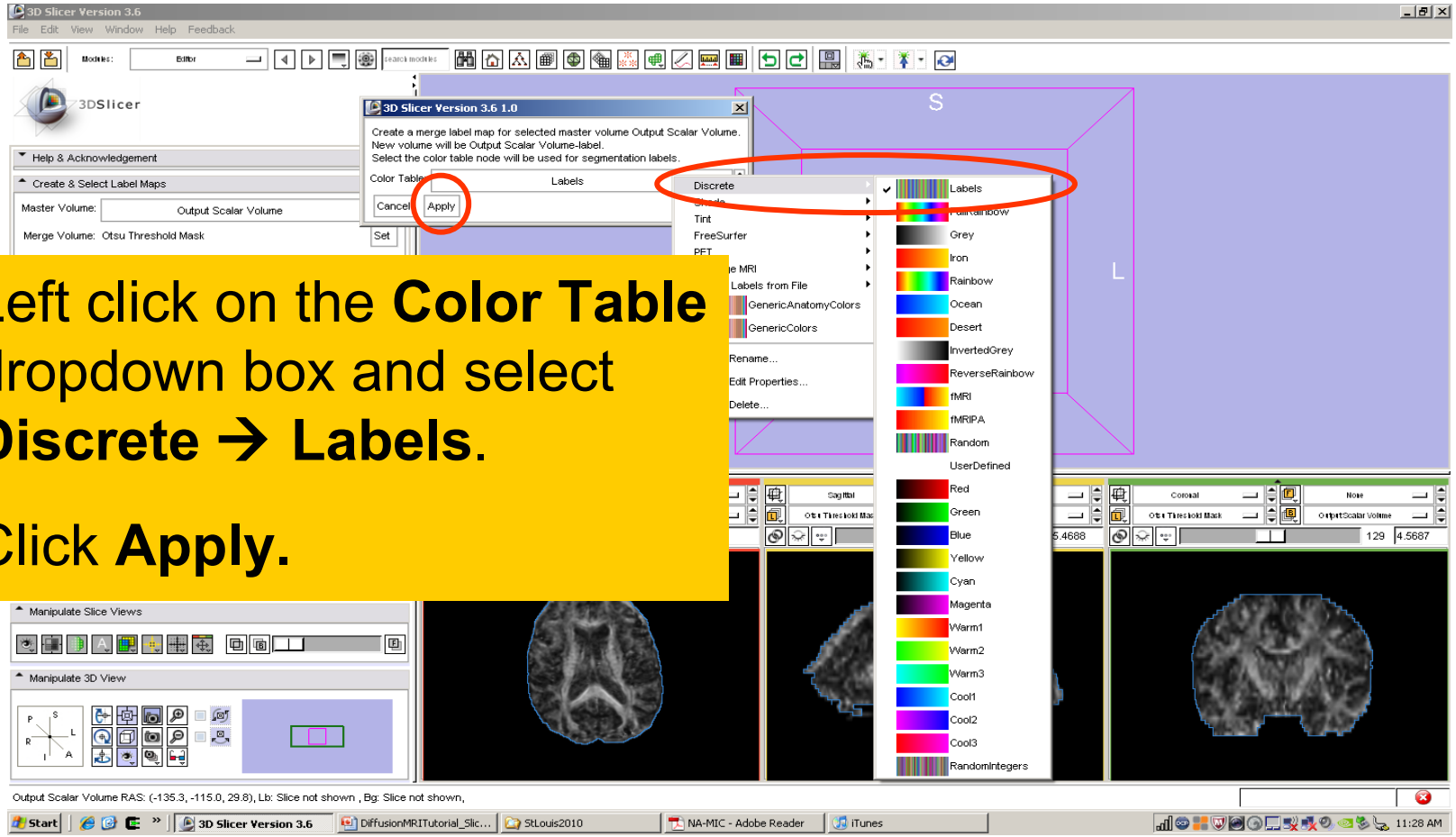
Select the **Editor** module in the **Modules** menu.

Set the **Master Volume** to **Output Scalar Volume**

LabelMap Generation



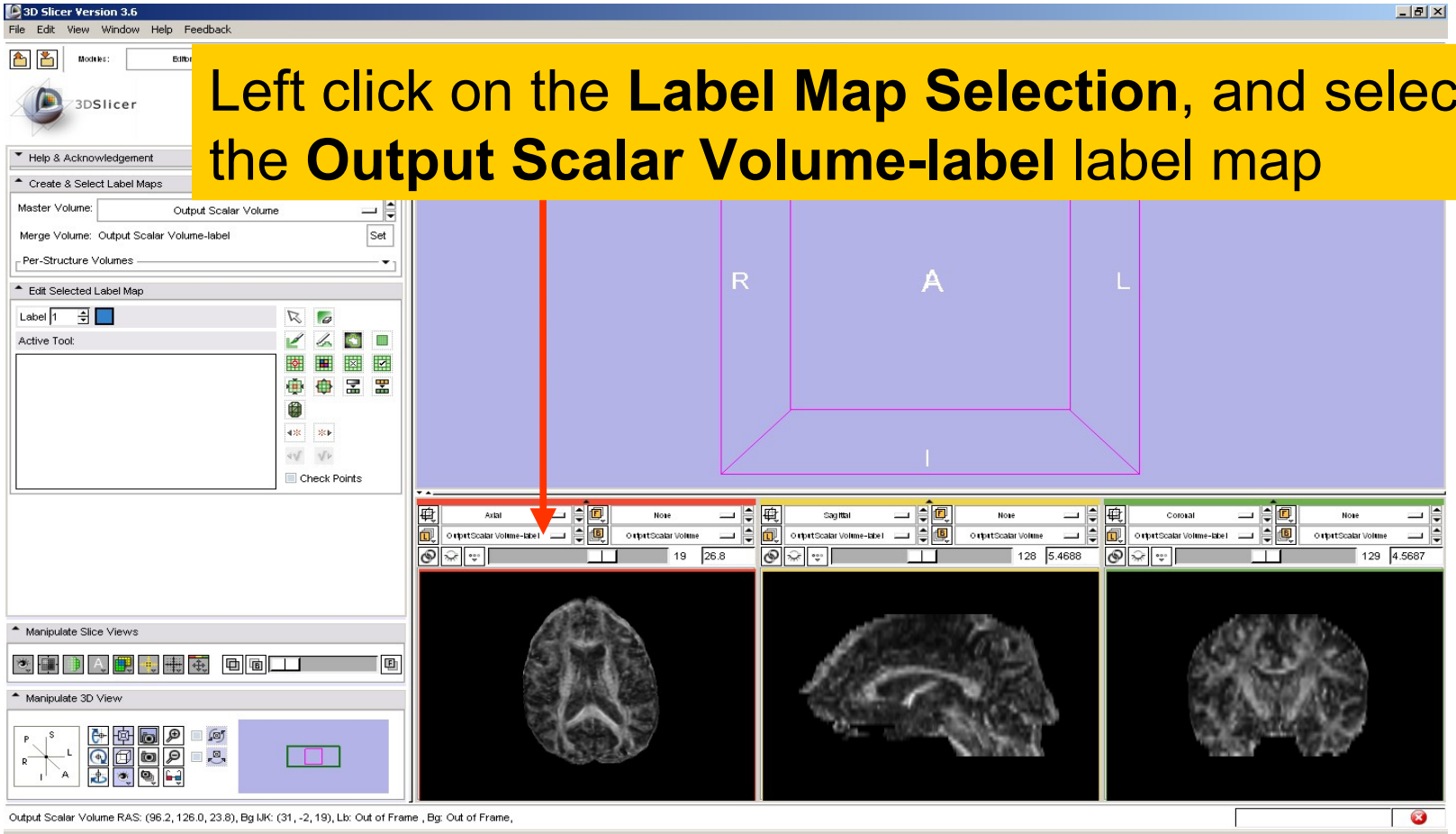
LabelMap Generation



Left click on the **Color Table** dropdown box and select **Discrete → Labels.**

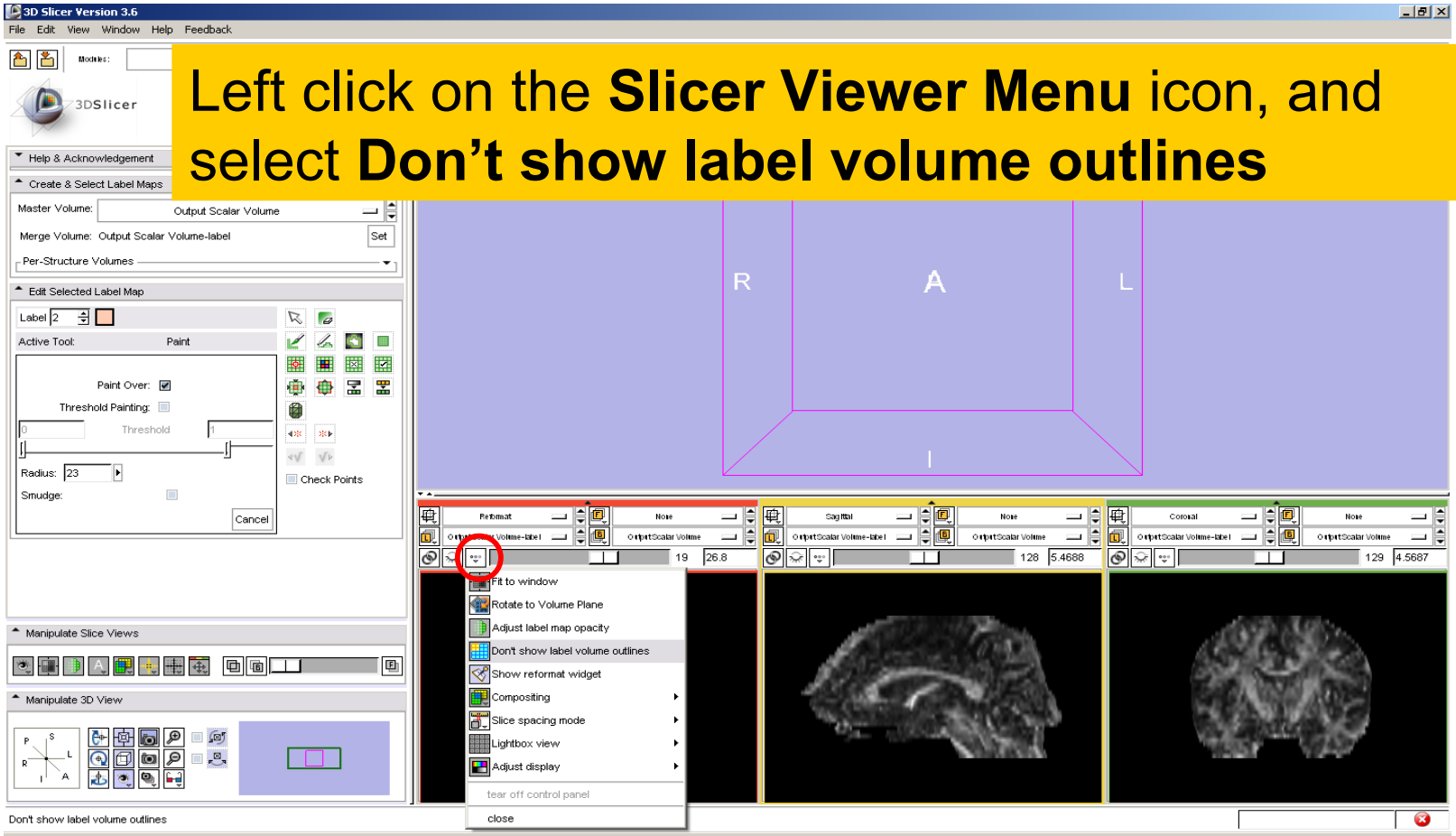
Click **Apply.**

LabelMap Generation



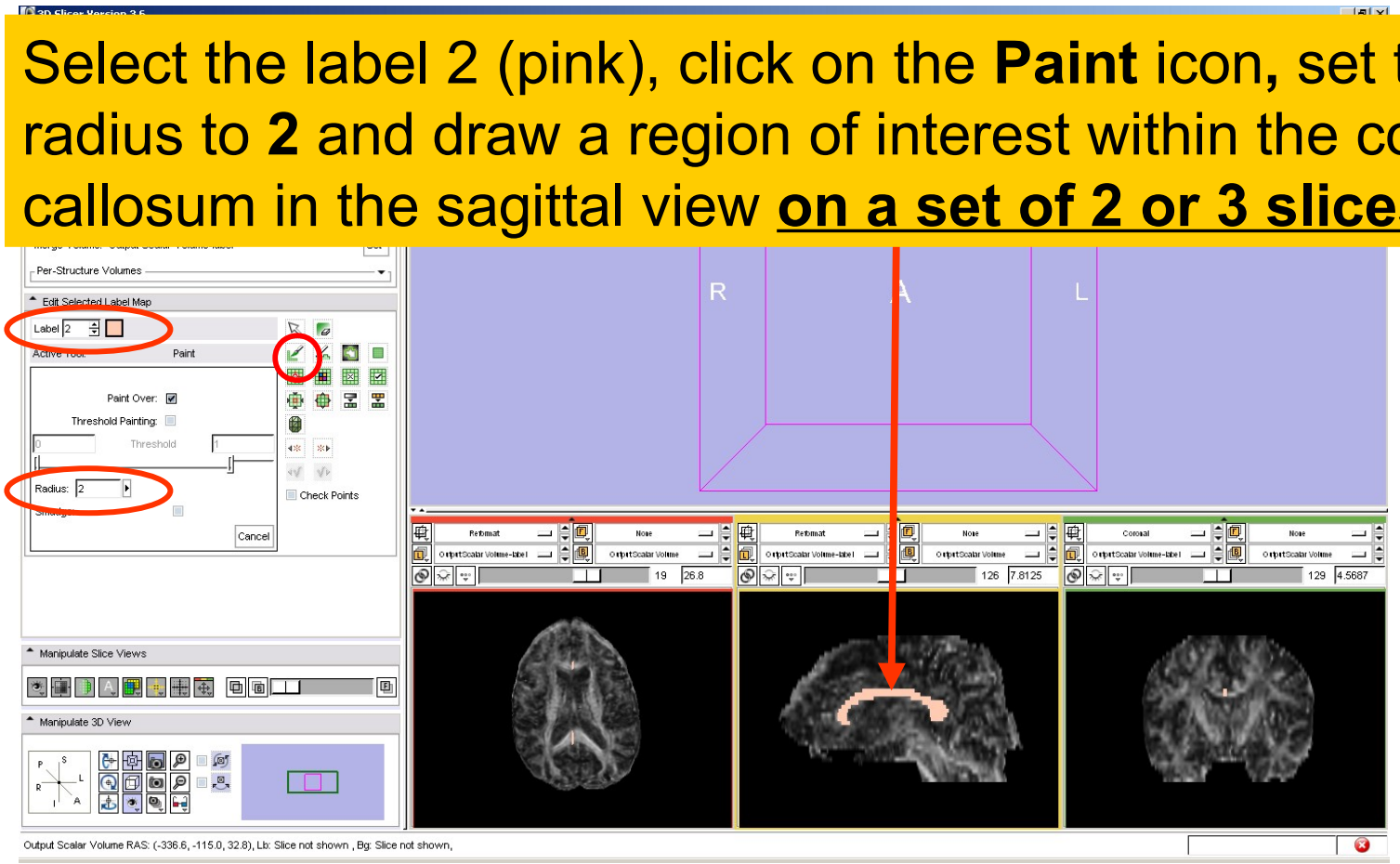
Left click on the **Label Map Selection**, and select the **Output Scalar Volume-label** label map

LabelMap Generation

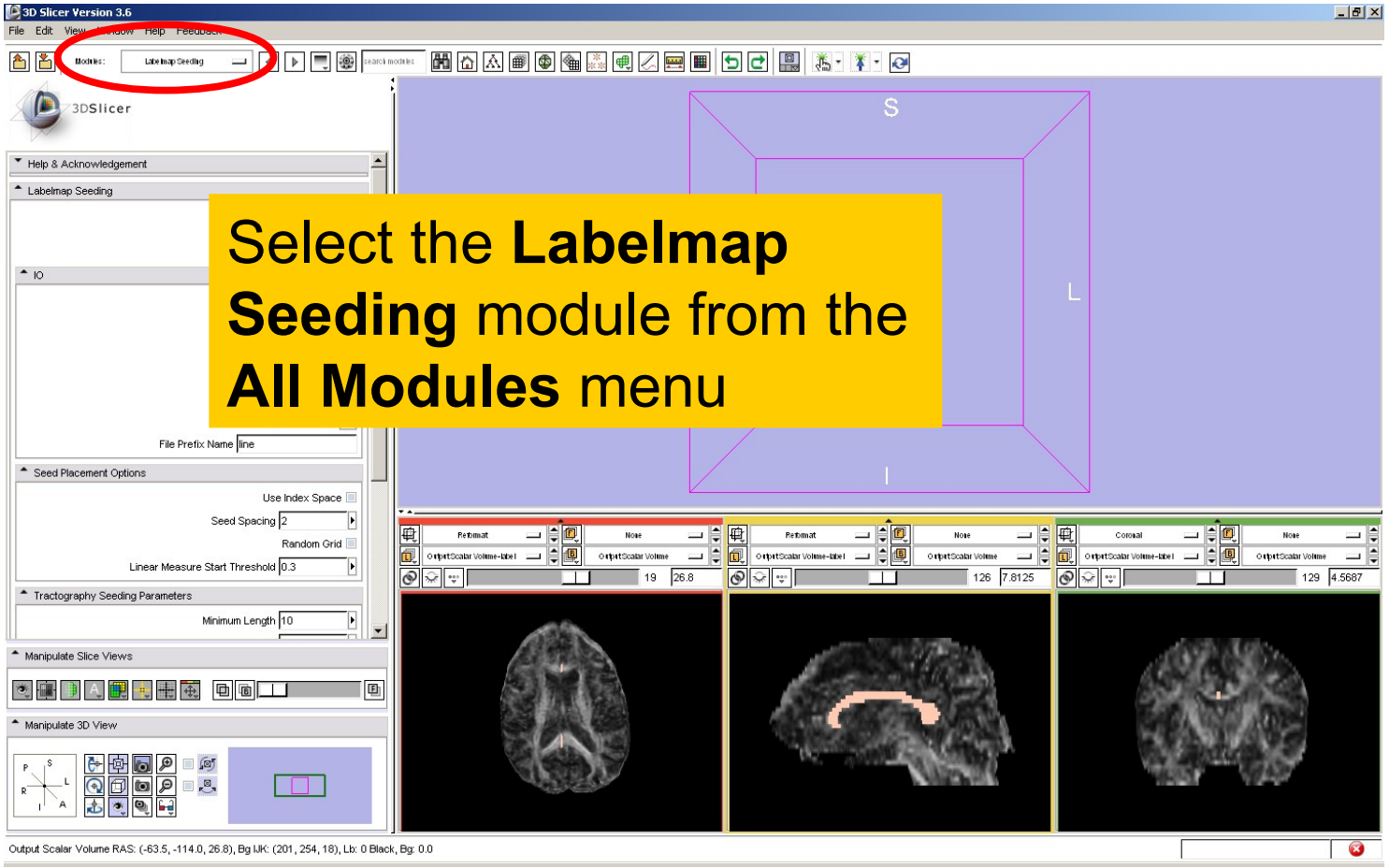


LabelMap Generation

Select the label 2 (pink), click on the **Paint** icon, set the radius to **2** and draw a region of interest within the corpus callosum in the sagittal view **<u>on a set of 2 or 3 slices</u>**

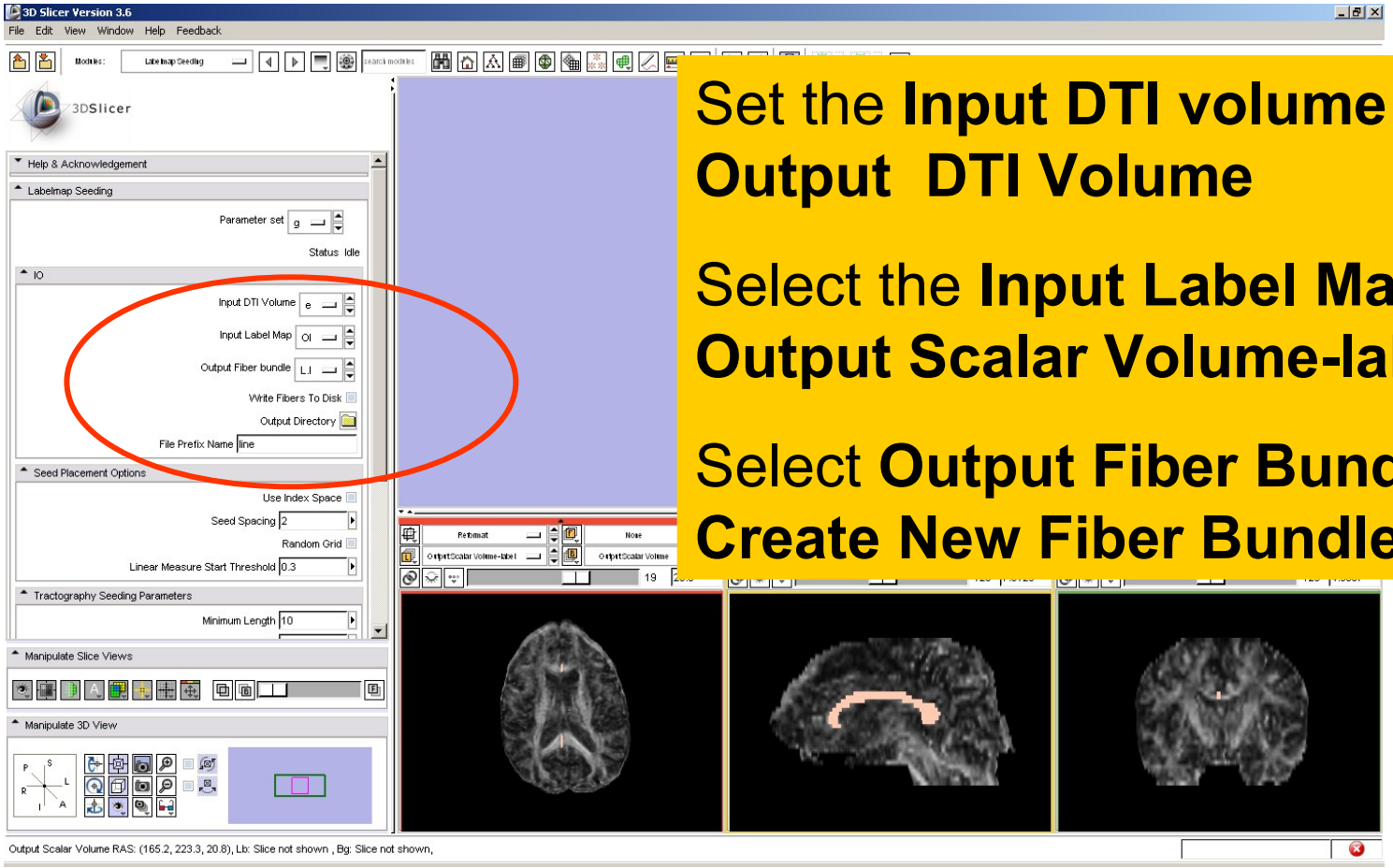


LabelMap Seeding



Select the **LabelMap Seeding** module from the **All Modules** menu

LabelMap Seeding

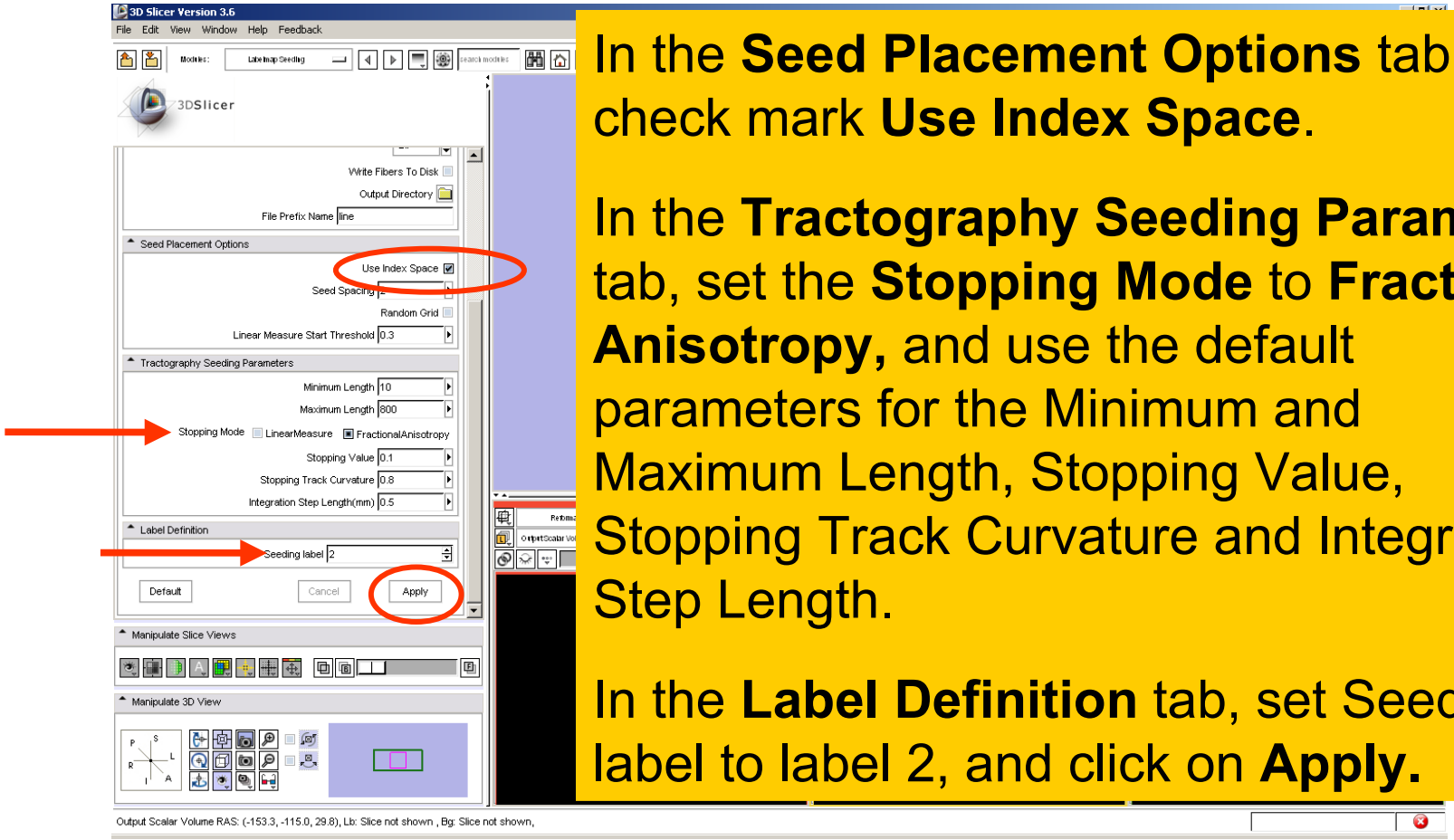


Set the **Input DTI volume**
Output DTI Volume

Select the **Input Label Map**
Output Scalar Volume-label

Select **Output Fiber Bundle**
Create New Fiber Bundle

LabelMap Seeding



In the **Seed Placement Options** tab, check mark **Use Index Space**.

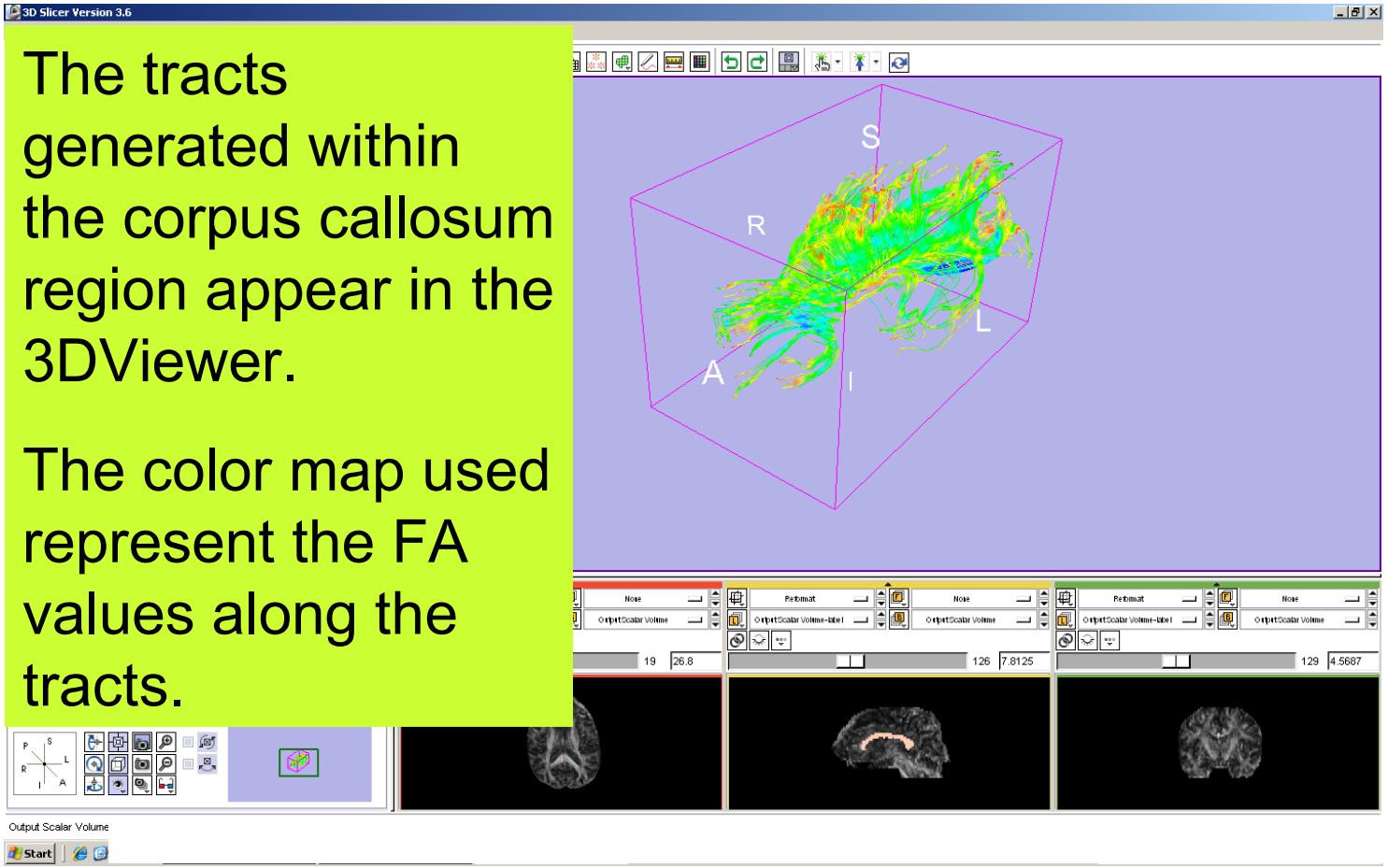
In the **Tractography Seeding Parameters** tab, set the **Stopping Mode** to **Fractional Anisotropy,** and use the default parameters for the Minimum and Maximum Length, Stopping Value, Stopping Track Curvature and Integration Step Length.

In the **Label Definition** tab, set Seeding label to label 2, and click on **Apply.**

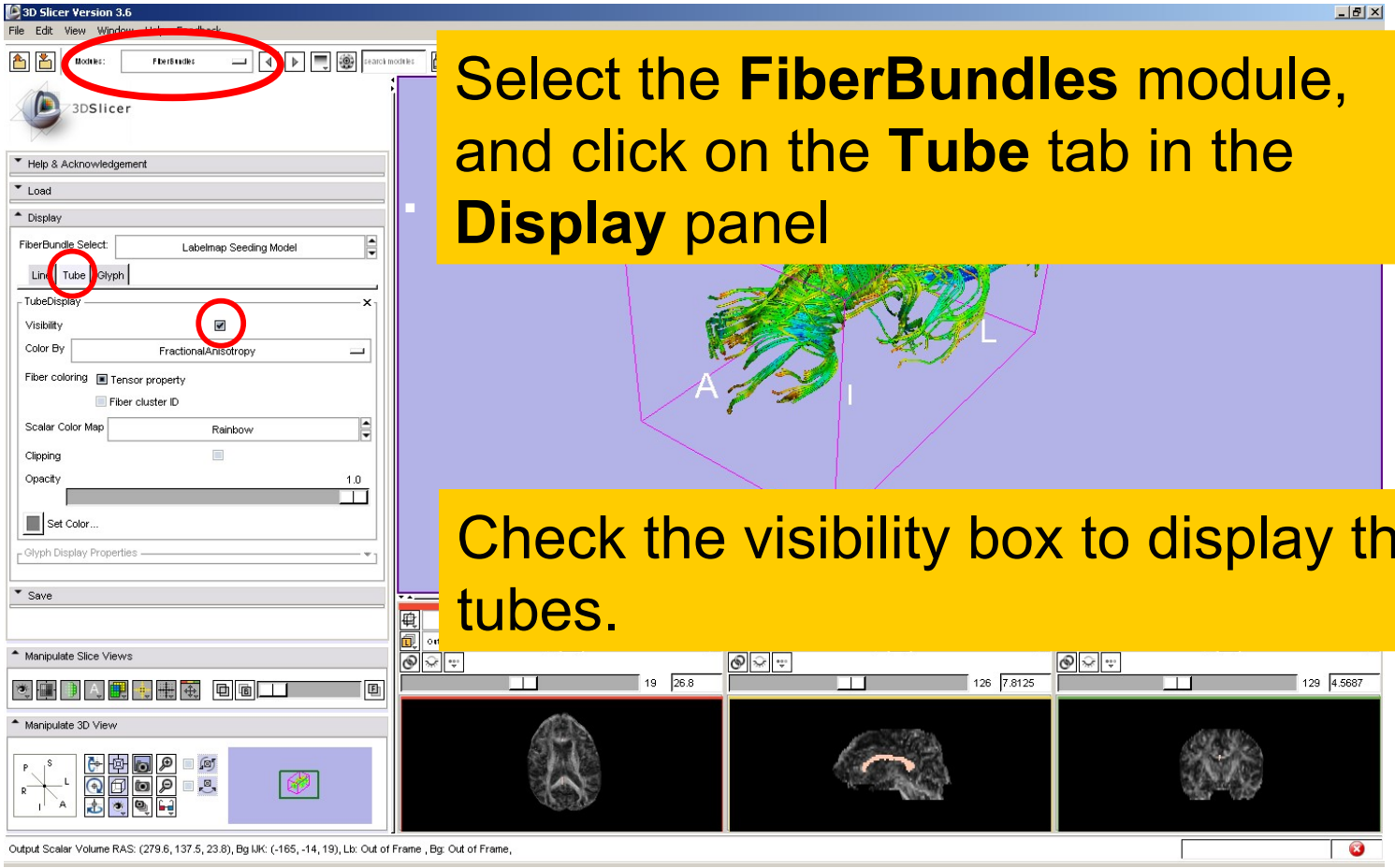
LabelMap Seeding

The tracts generated within the corpus callosum region appear in the 3DViewer.

The color map used represent the FA values along the tracts.



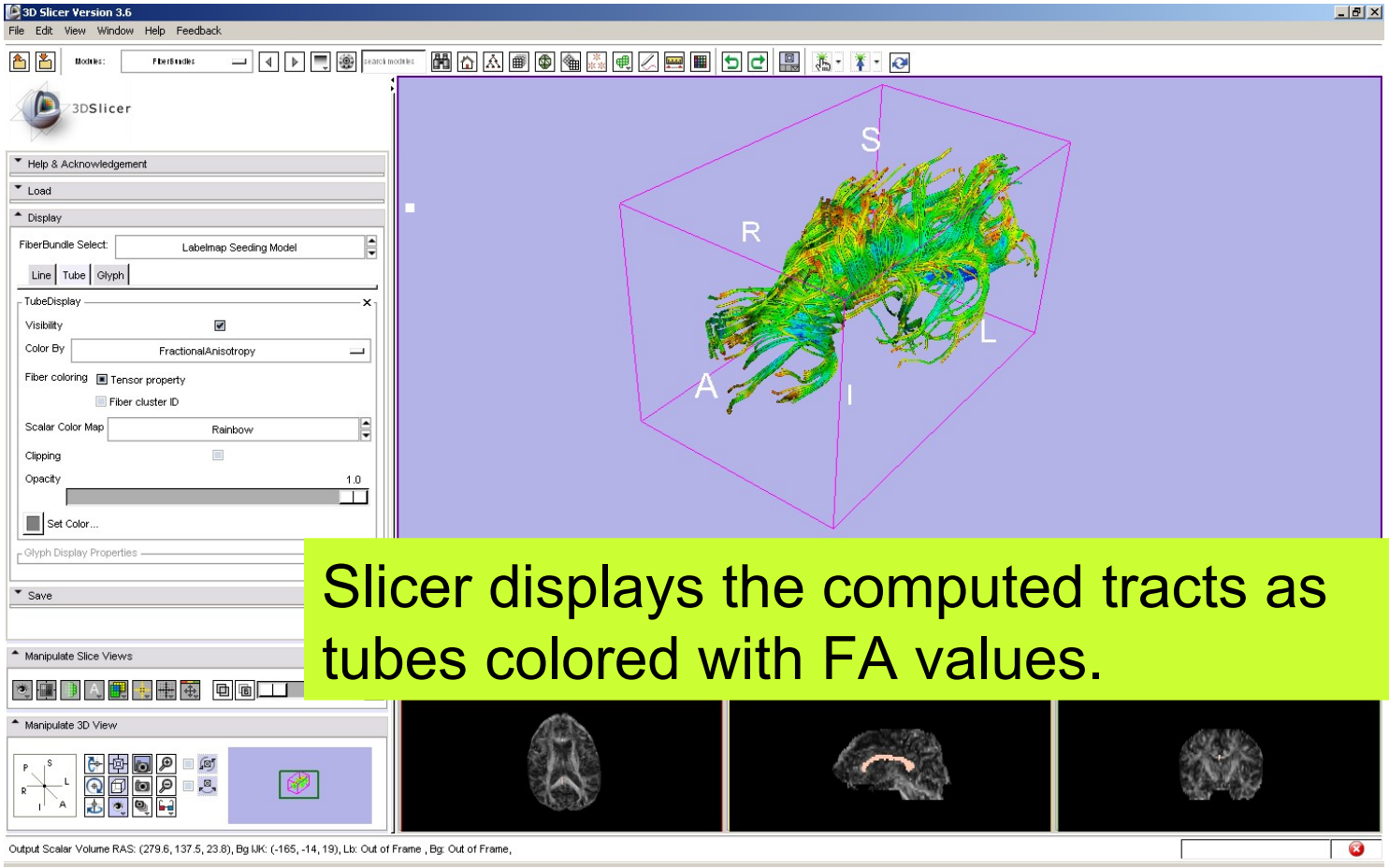
LabelMap Seeding



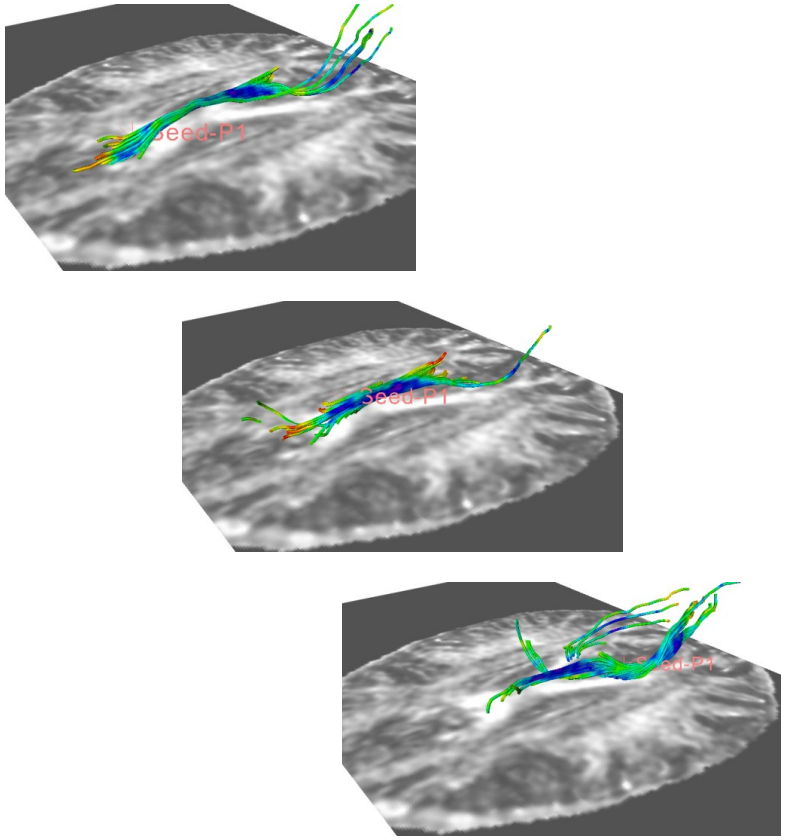
Select the **FiberBundles** module, and click on the **Tube** tab in the **Display** panel

Check the visibility box to display the tubes.

LabelMap Seeding



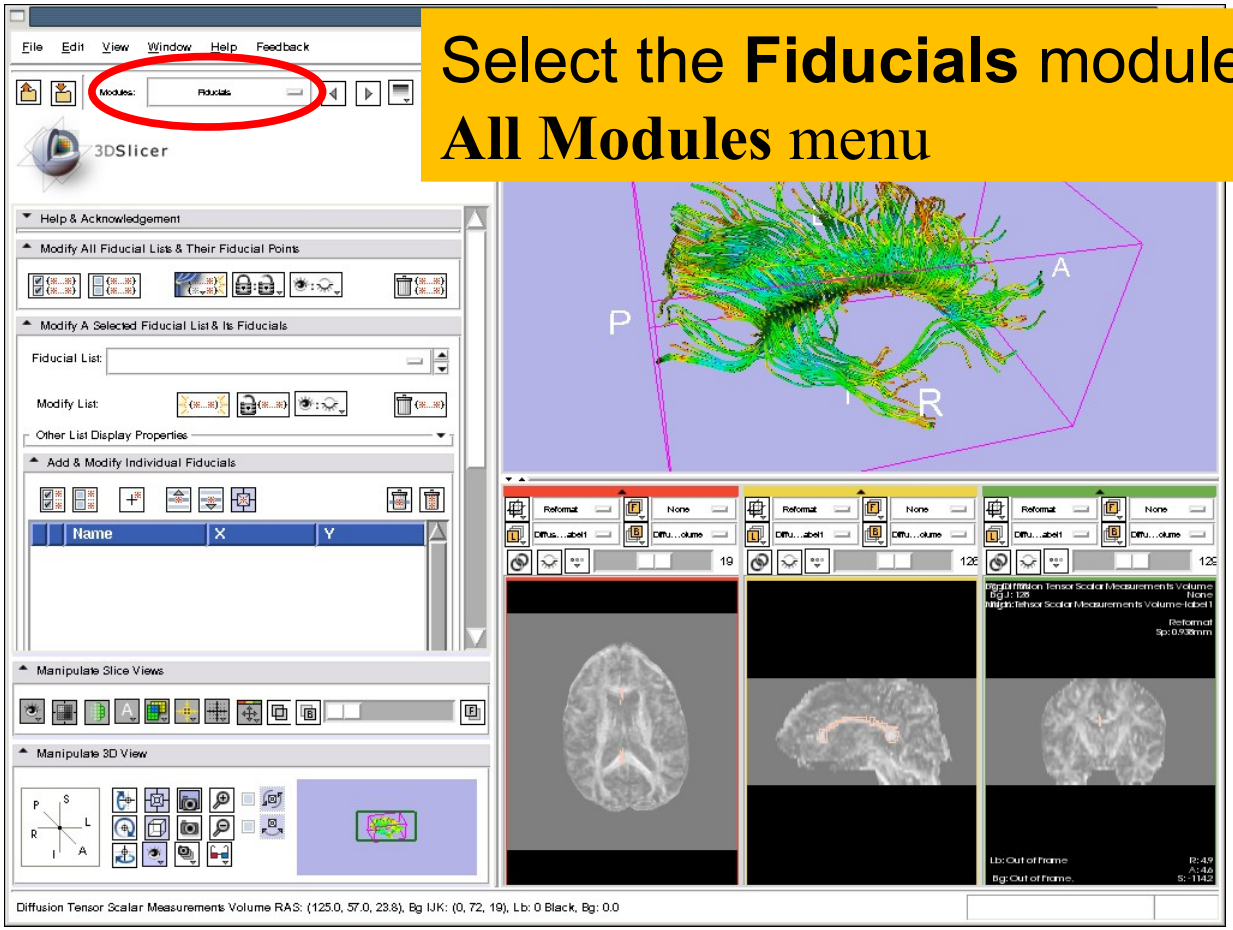
Slicer displays the computed tracts as tubes colored with FA values.



Part 4:

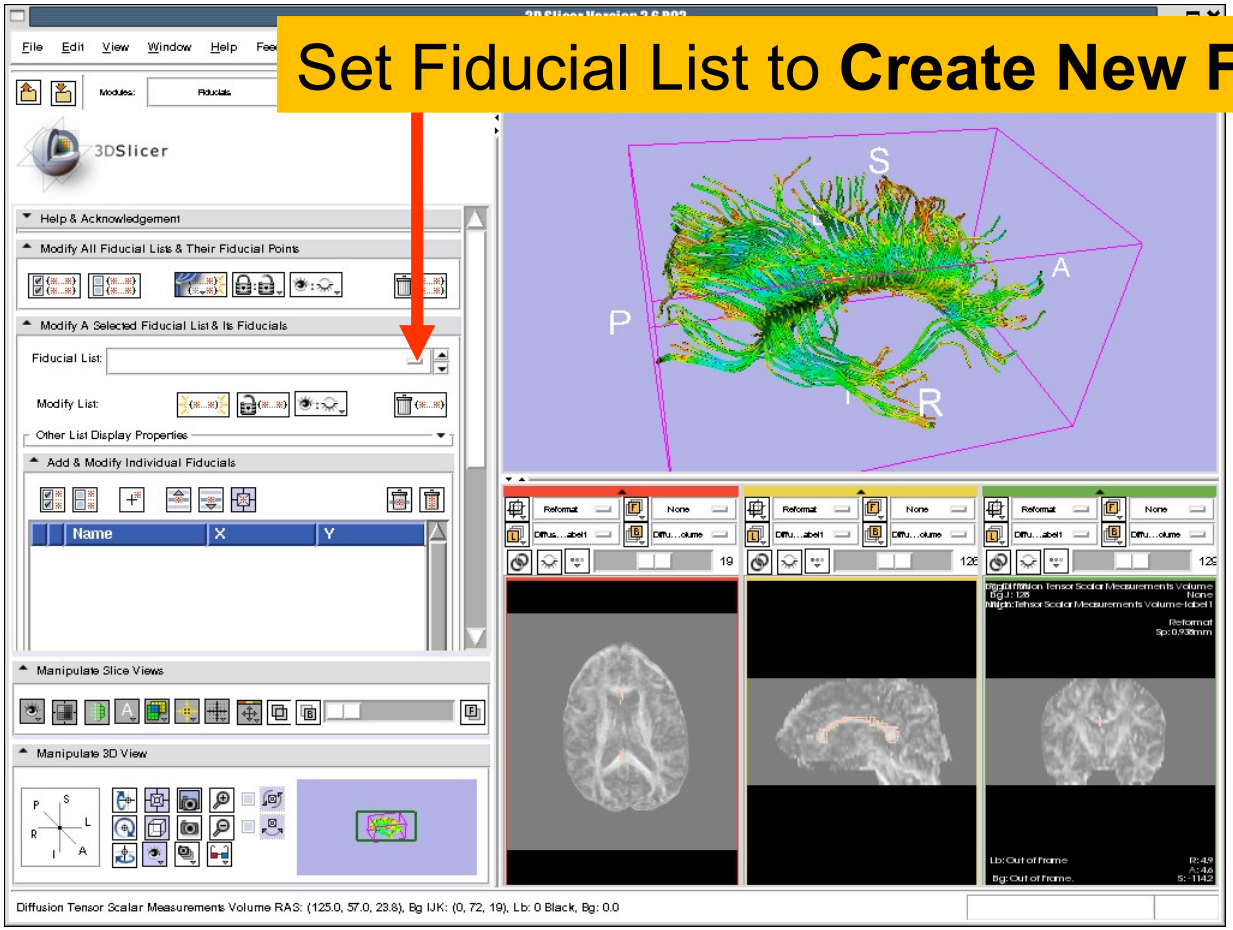
Tractography on-the-fly

Fiducial Seeding

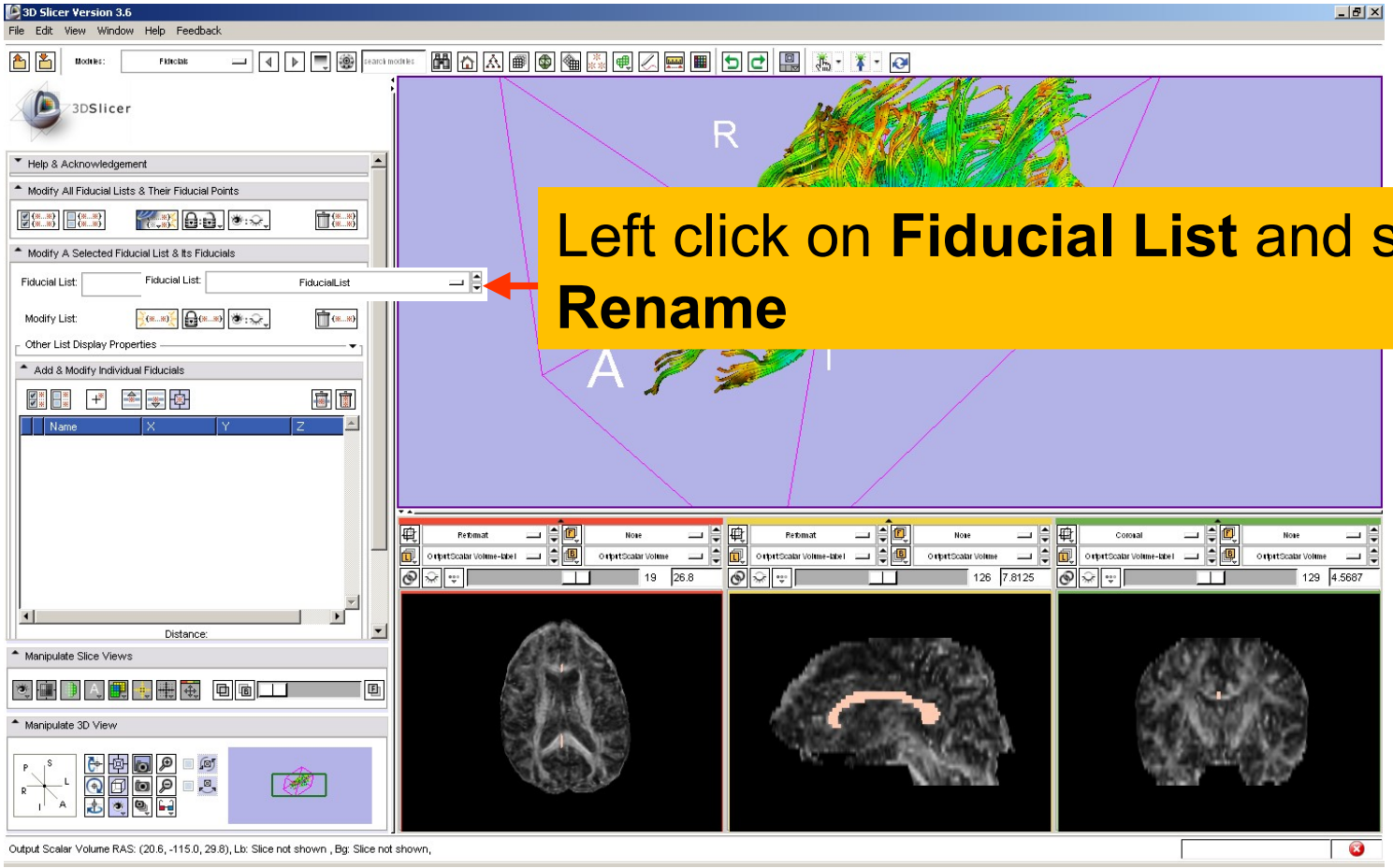


Select the **Fiducials** module in the **All Modules** menu

Fiducial Seeding

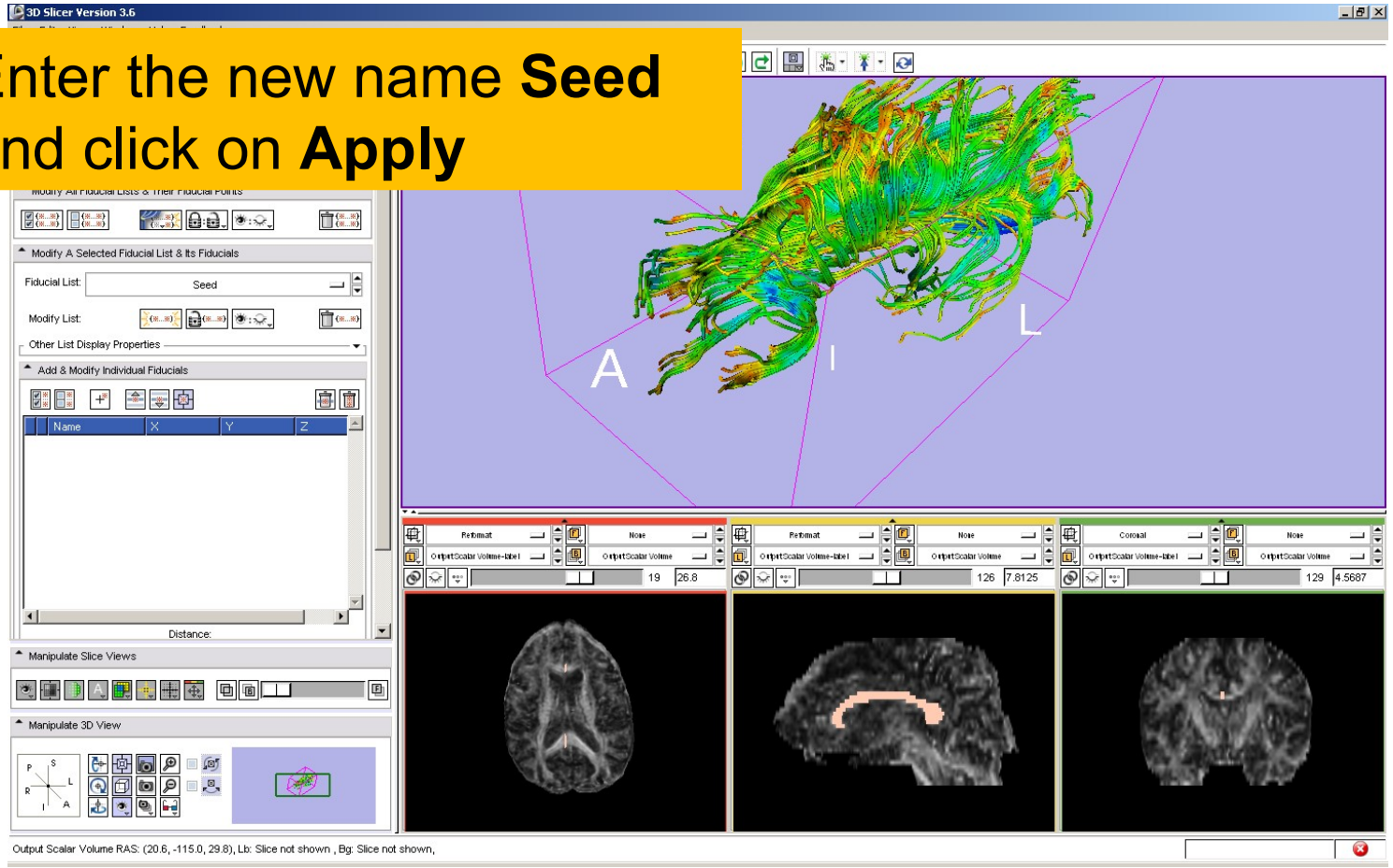


Fiducial Seeding

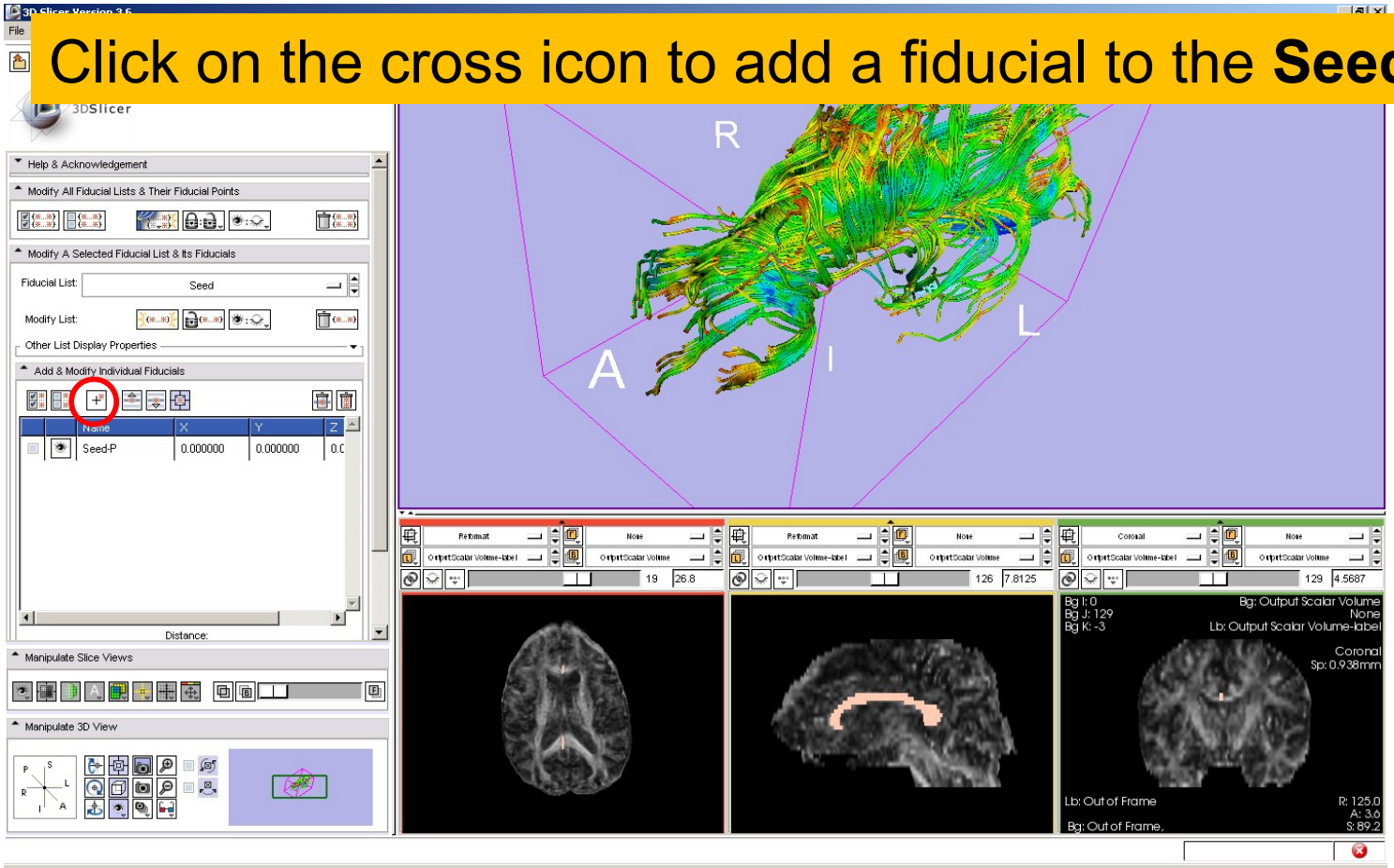


Fiducial Seeding

Enter the new name **Seed** and click on **Apply**

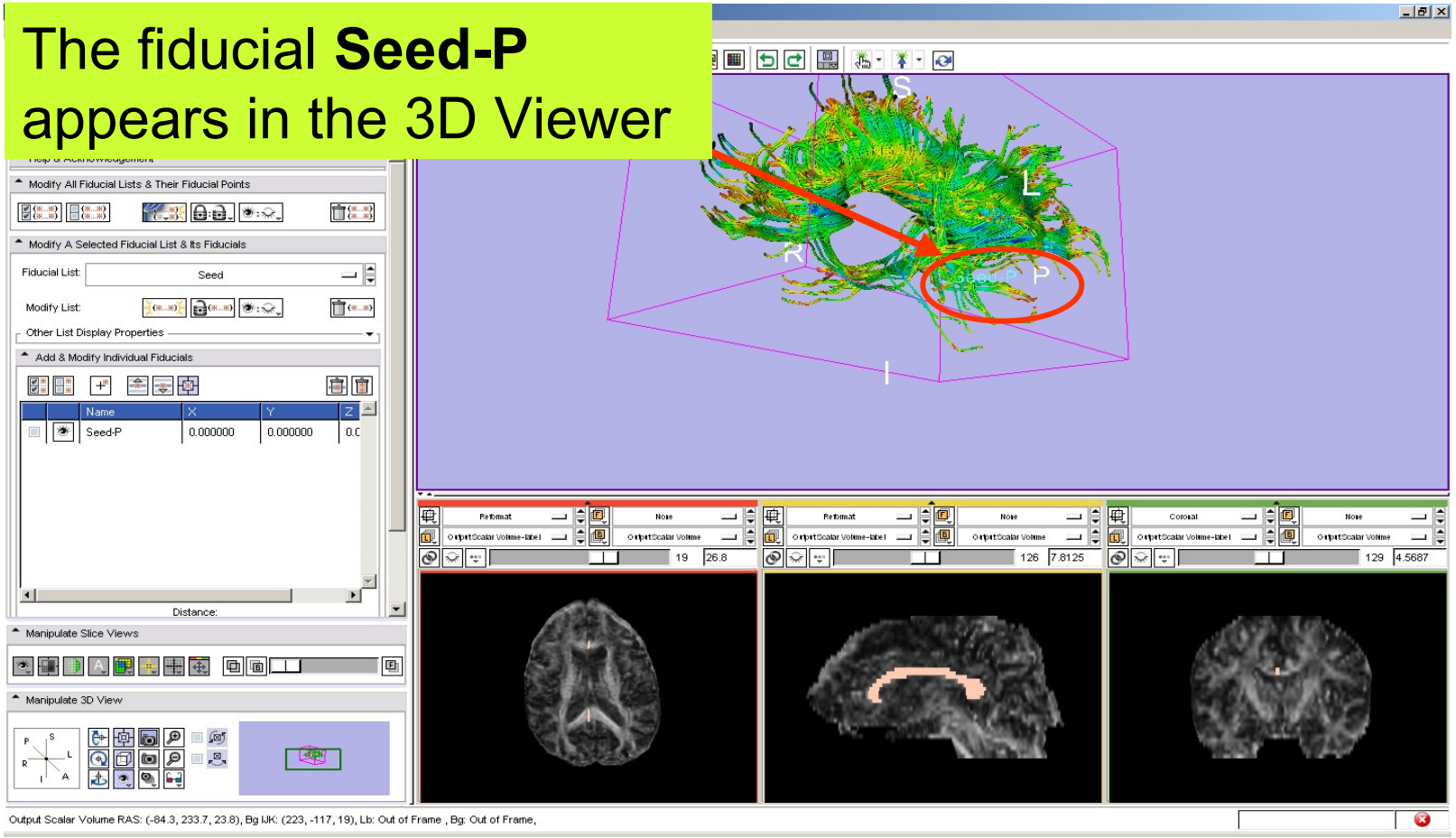


Fiducial Seeding



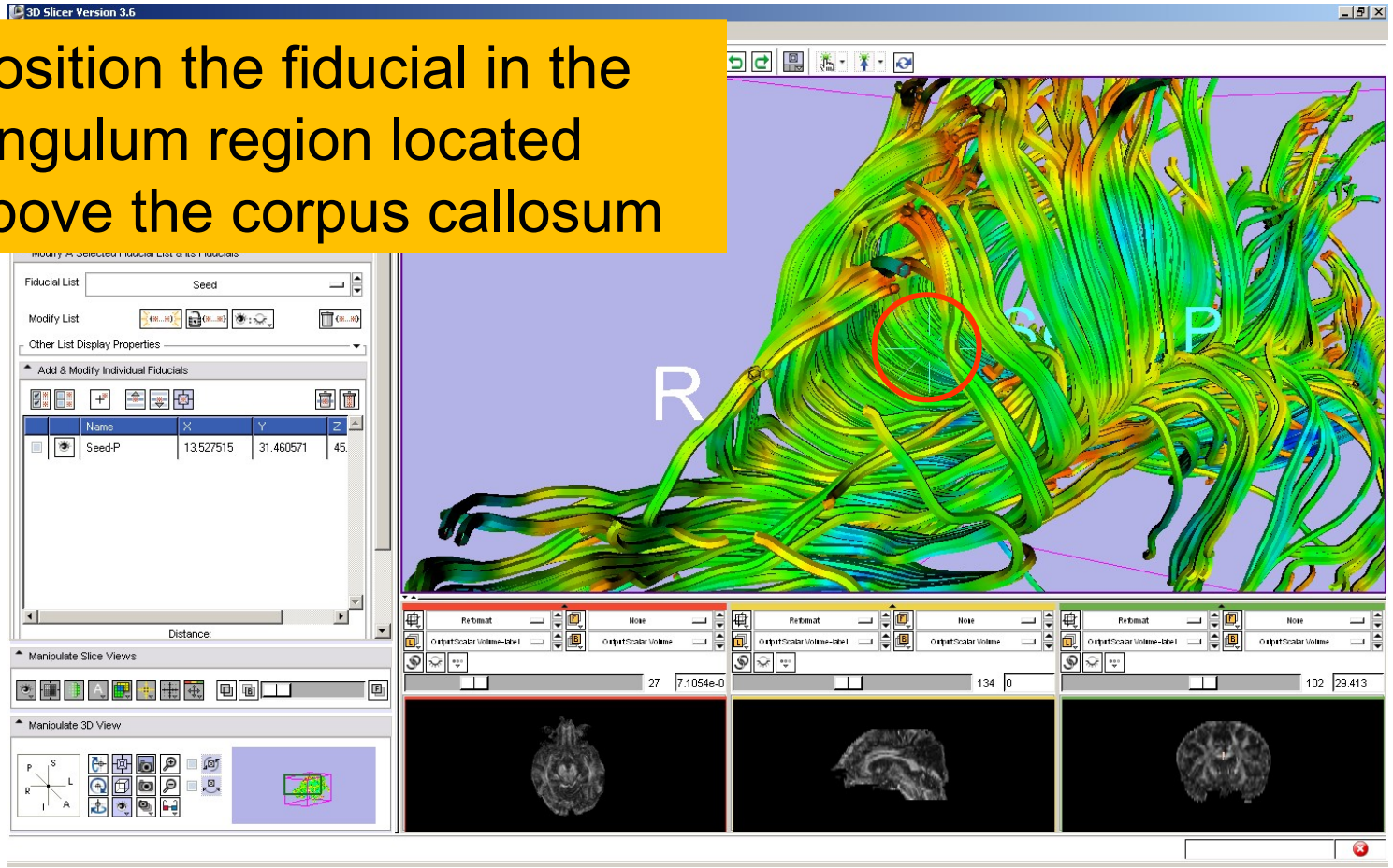
Fiducial Seeding

The fiducial **Seed-P** appears in the 3D Viewer



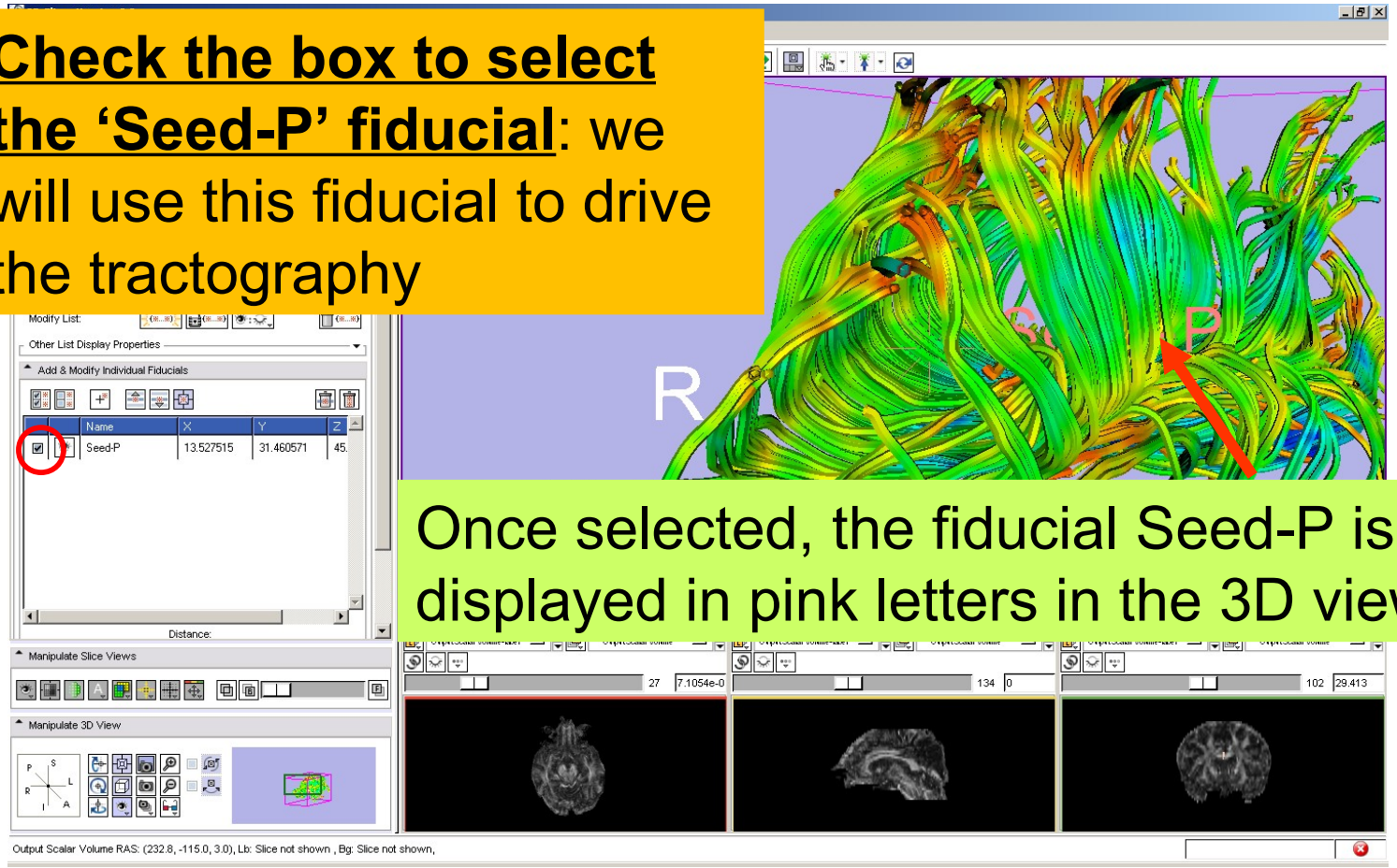
Fiducial Seeding

Position the fiducial in the cingulum region located above the corpus callosum



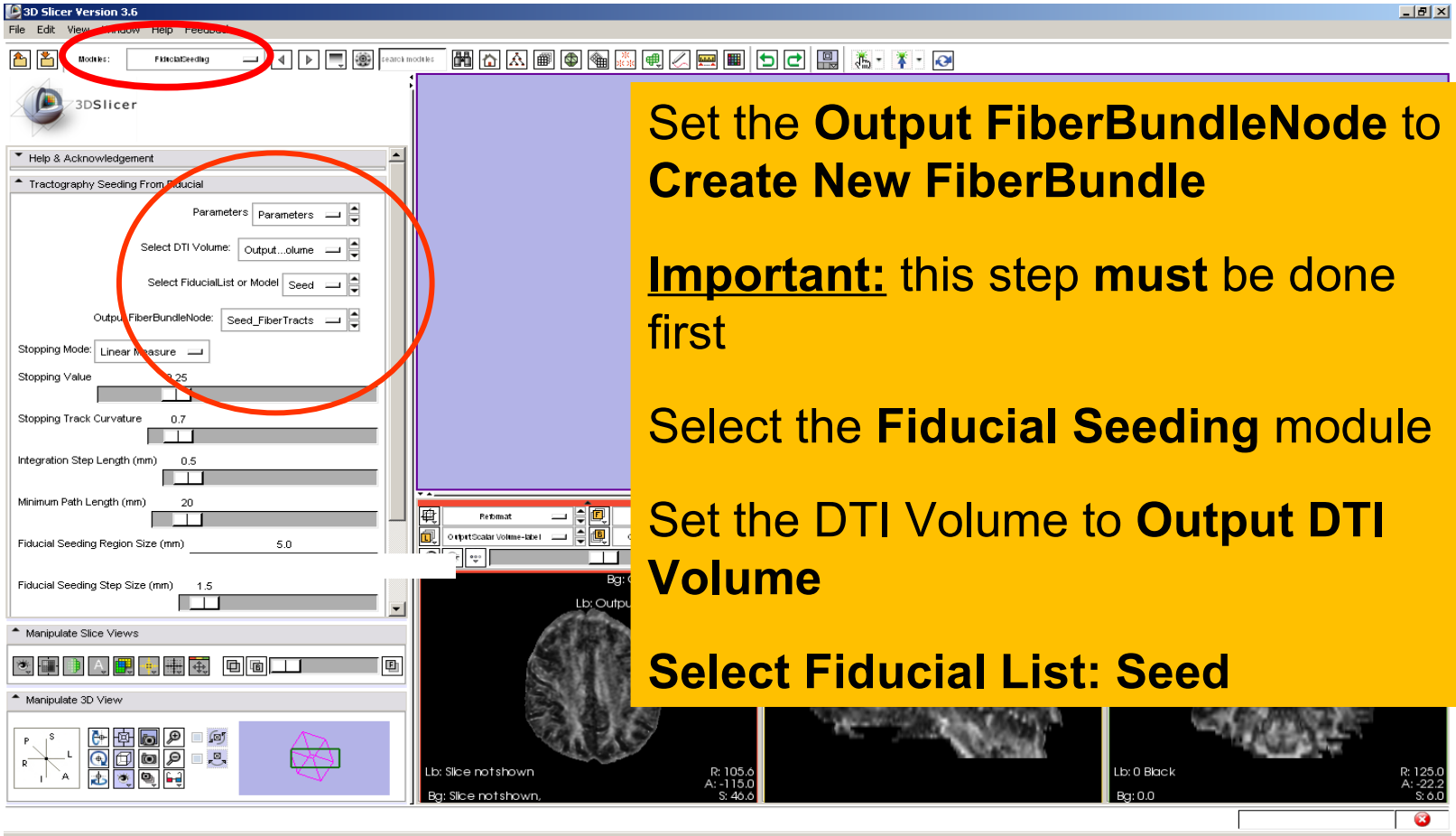
Fiducial Seeding

Check the box to select the 'Seed-P' fiducial: we will use this fiducial to drive the tractography



Once selected, the fiducial Seed-P is displayed in pink letters in the 3D viewer.

Fiducial Seeding



Set the **Output FiberBundleNode** to **Create New FiberBundle**

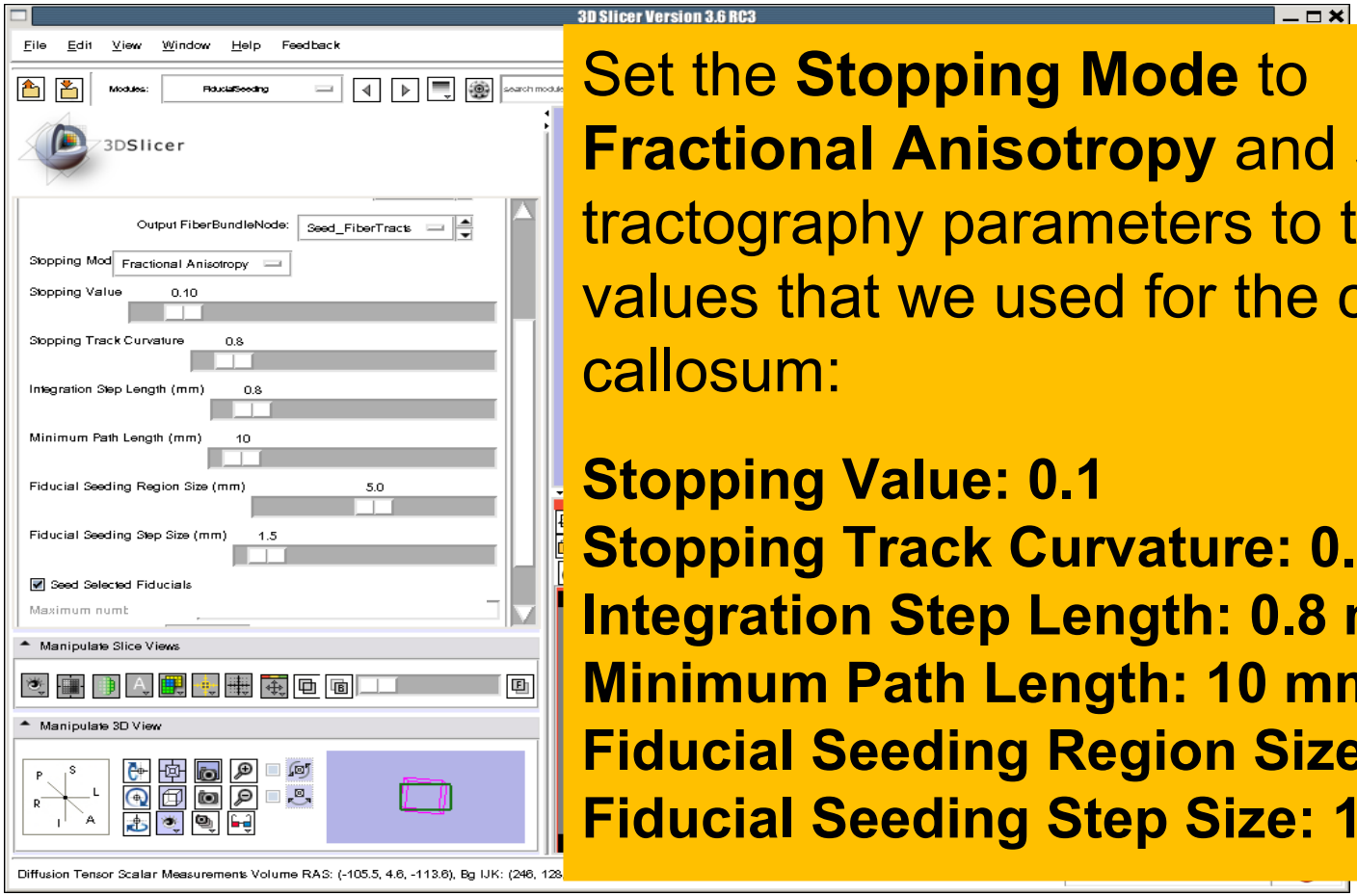
<u>Important:</u> this step **must** be done first

Select the **Fiducial Seeding** module

Set the DTI Volume to **Output DTI Volume**

Select Fiducial List: Seed

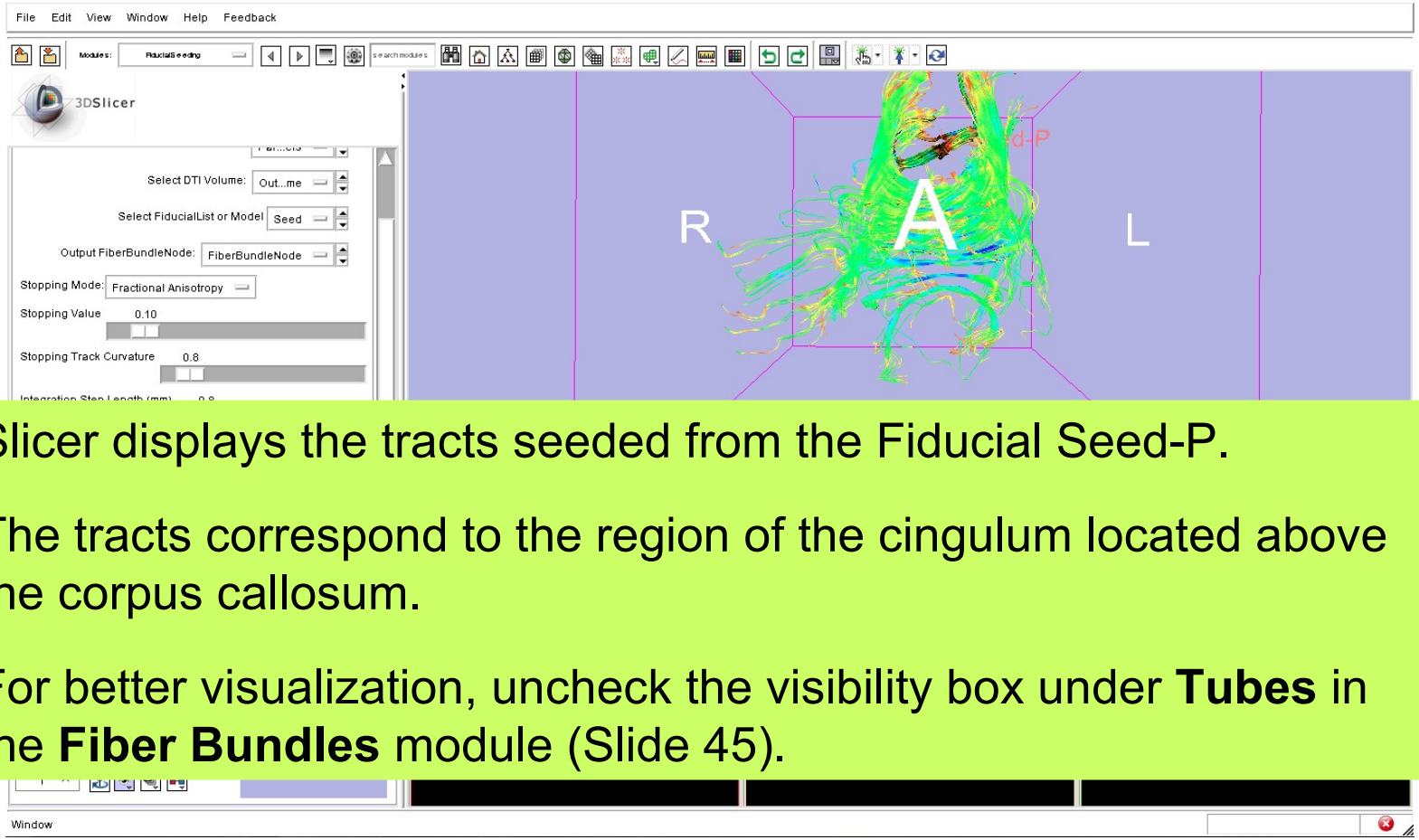
Fiducial Seeding



Set the **Stopping Mode** to **Fractional Anisotropy** and set the tractography parameters to the values that we used for the corpus callosum:

Stopping Value: 0.1
Stopping Track Curvature: 0.8
Integration Step Length: 0.8 mm
Minimum Path Length: 10 mm
Fiducial Seeding Region Size: 5 mm
Fiducial Seeding Step Size: 1.5 mm

Fiducial Seeding

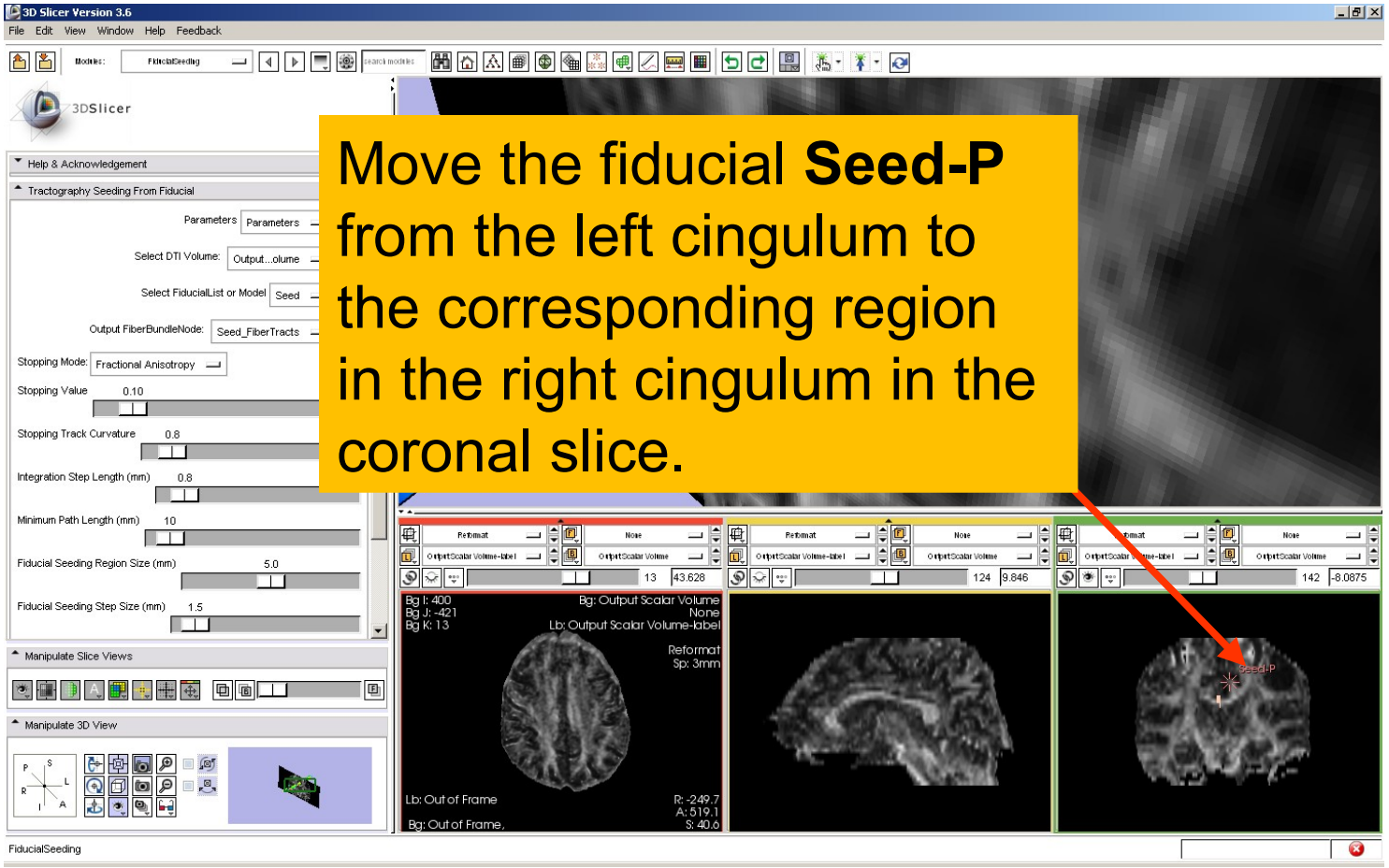


Slicer displays the tracts seeded from the Fiducial Seed-P.

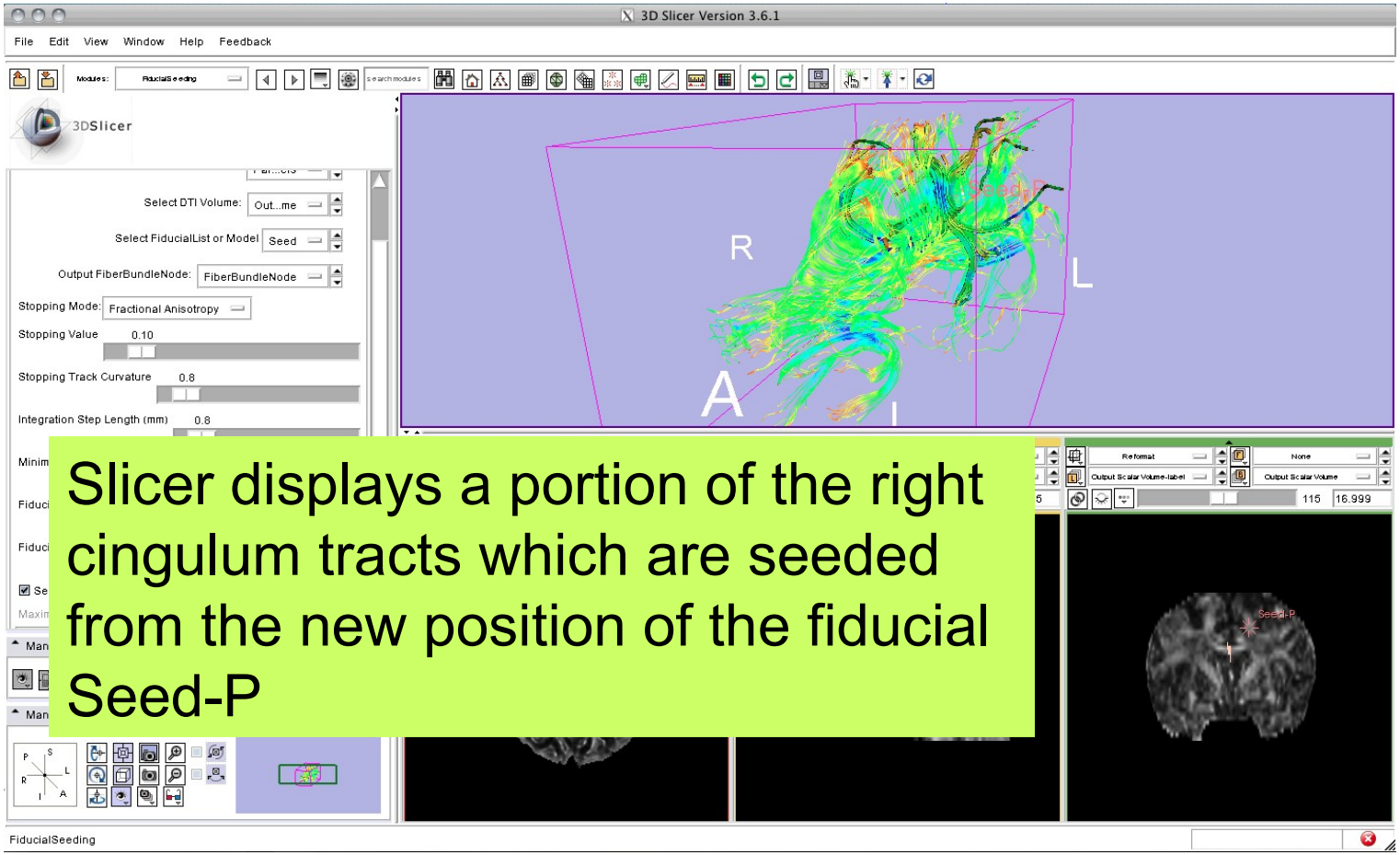
The tracts correspond to the region of the cingulum located above the corpus callosum.

For better visualization, uncheck the visibility box under **Tubes** in the **Fiber Bundles** module (Slide 45).

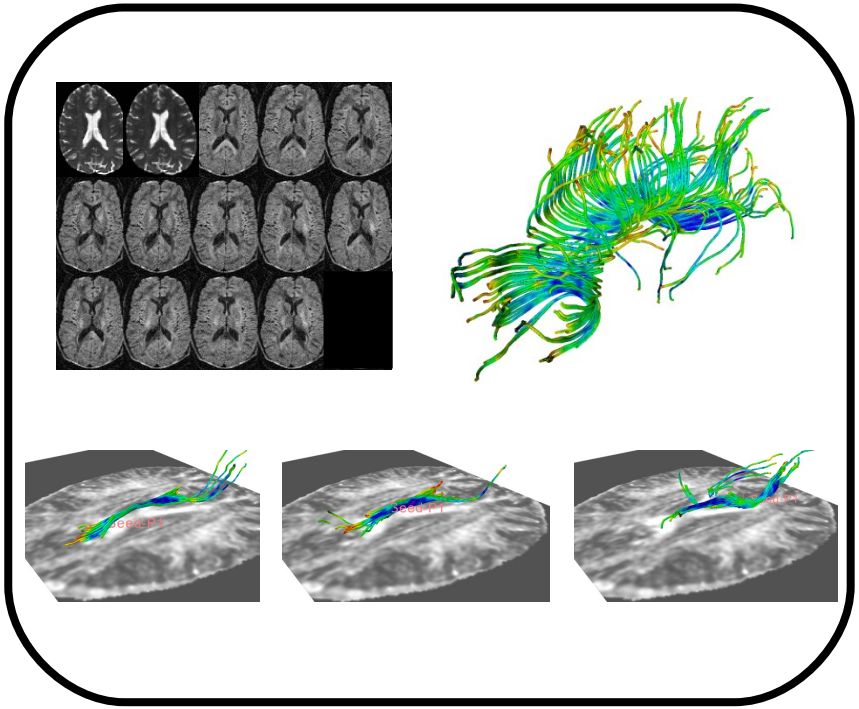
Fiducial Seeding



Fiducial Seeding



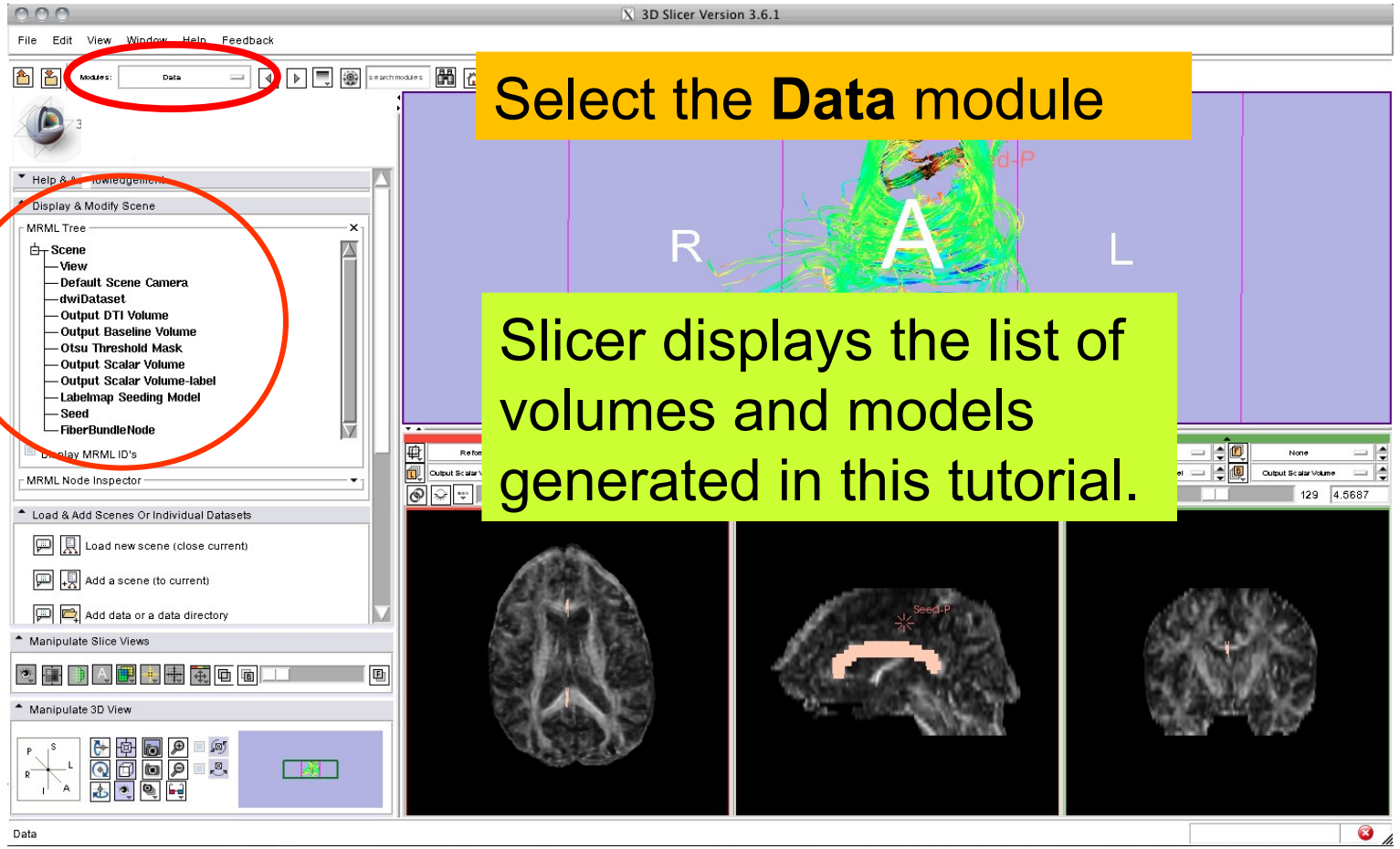
Slicer displays a portion of the right cingulum tracts which are seeded from the new position of the fiducial Seed-P



Part 5:

Saving a DTI Scene

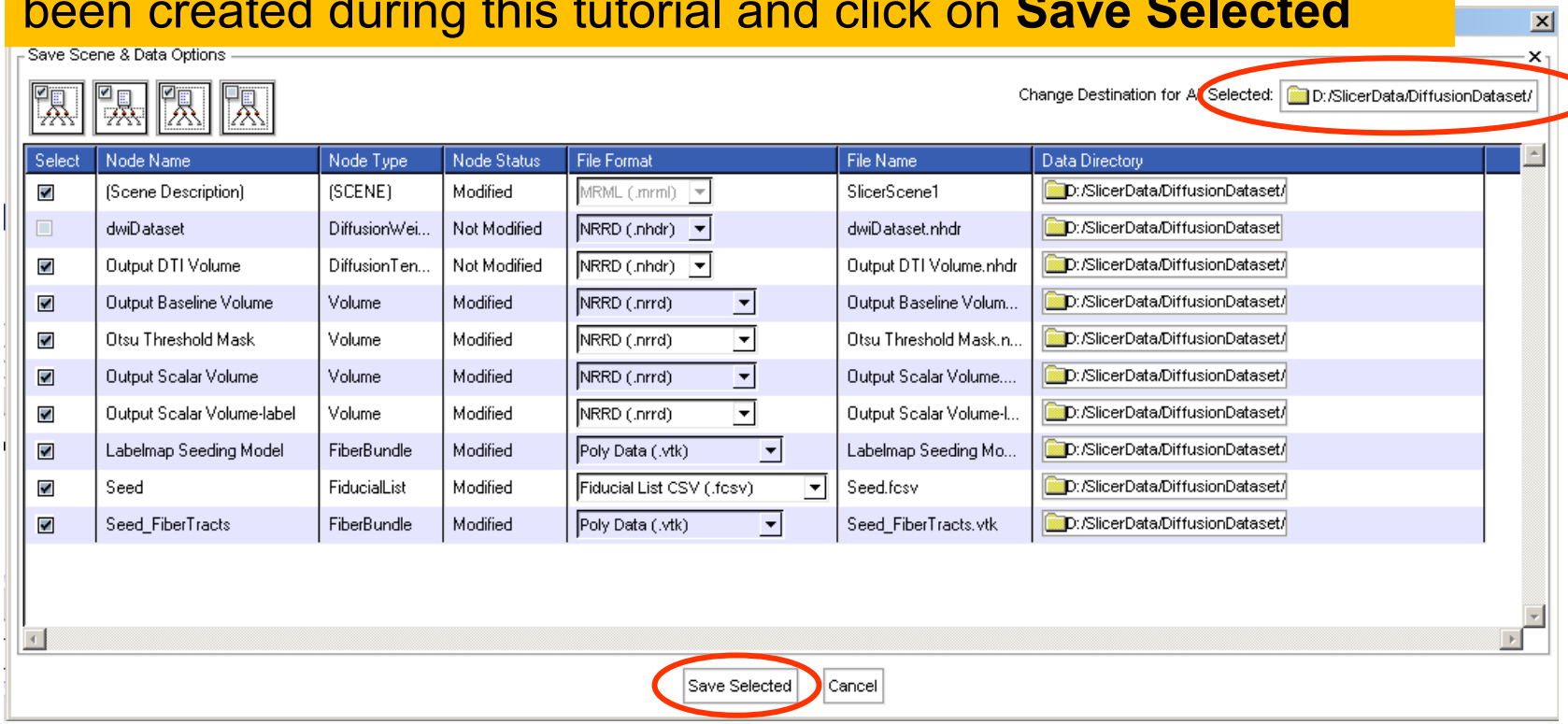
DTI Scene



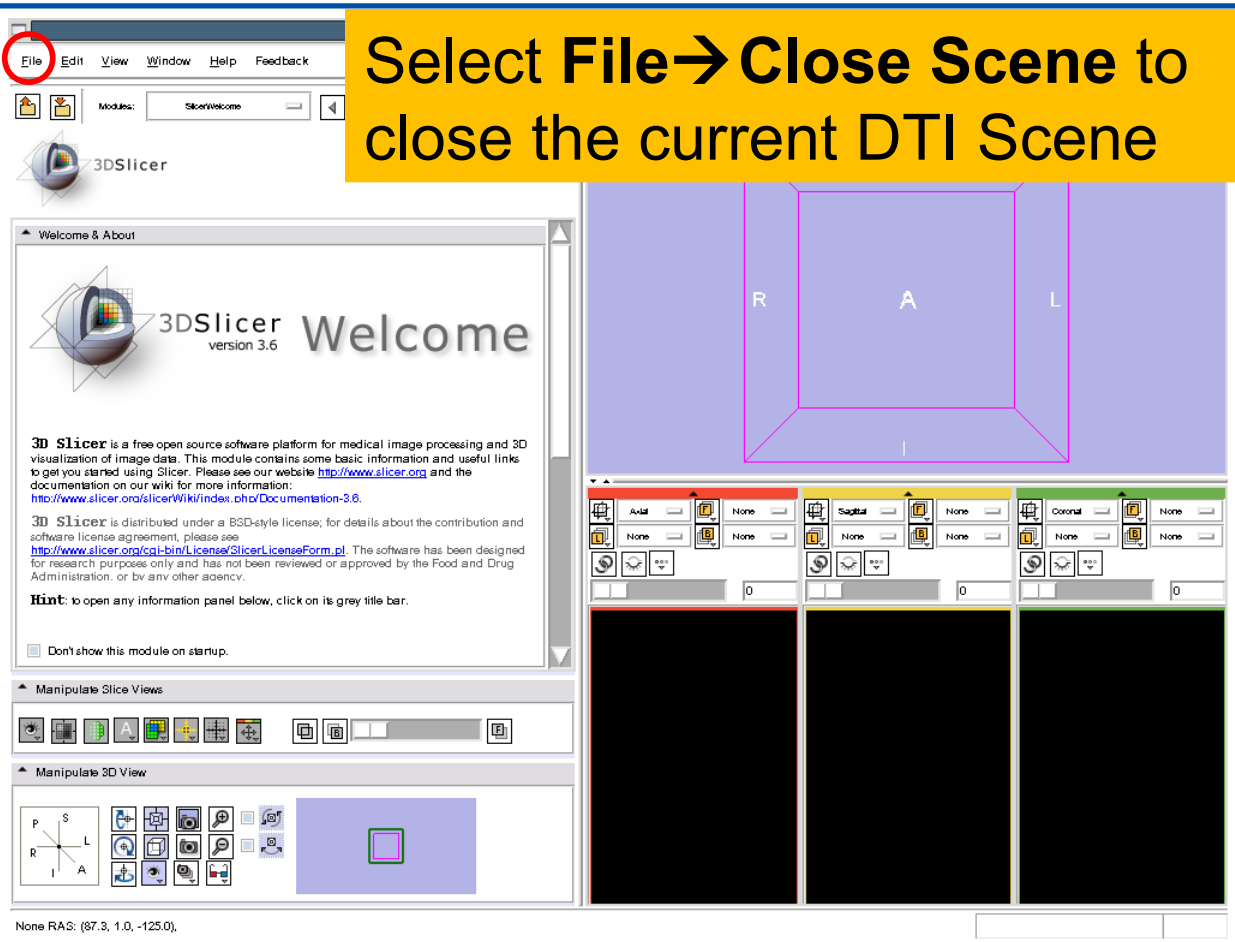
Saving a DTI Scene

Saving a DTI Scene

Browse to a directory where you would like to save the data. Once you have selected a directory, select all the files that have been created during this tutorial and click on **Save Selected**

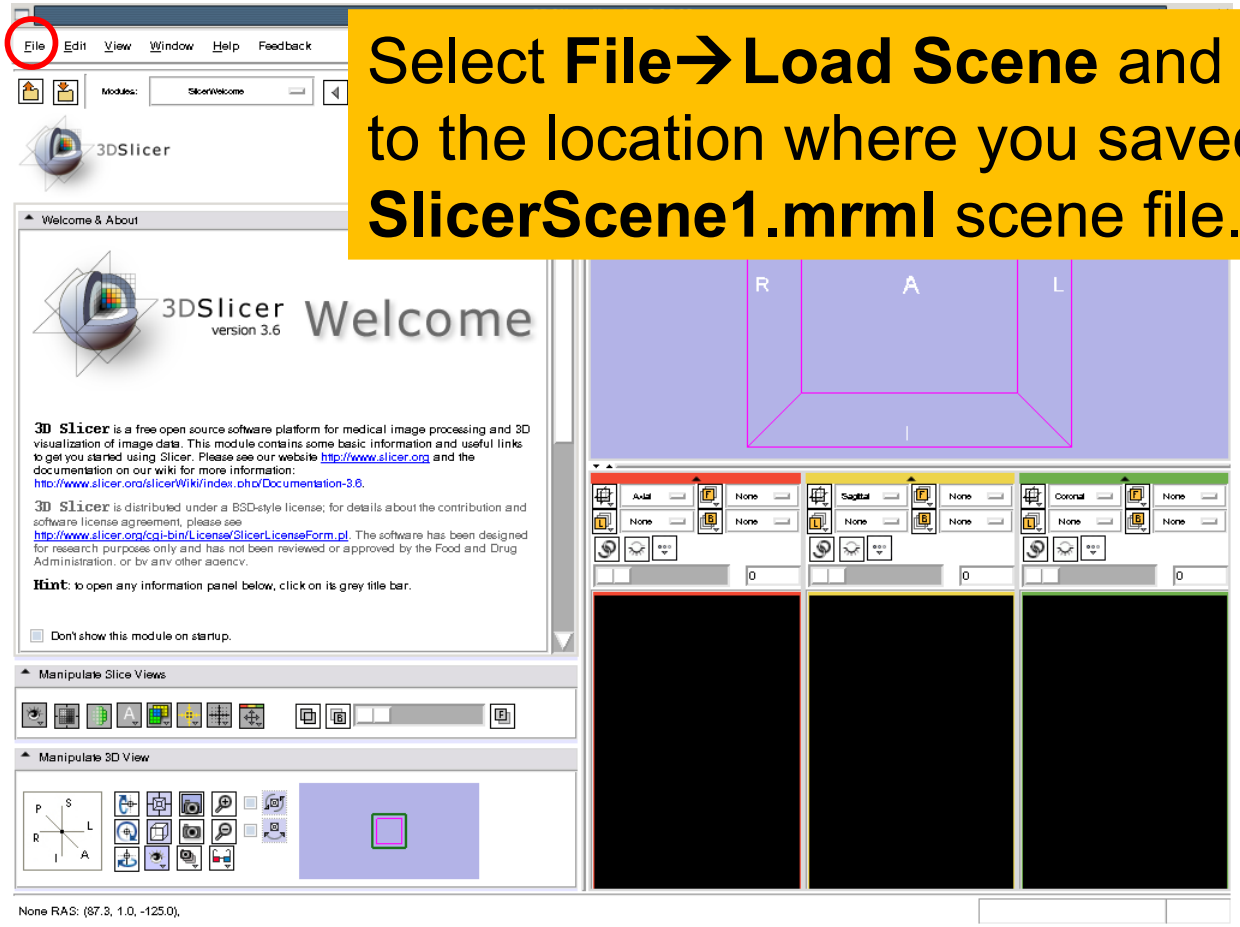


Saving a DTI Scene



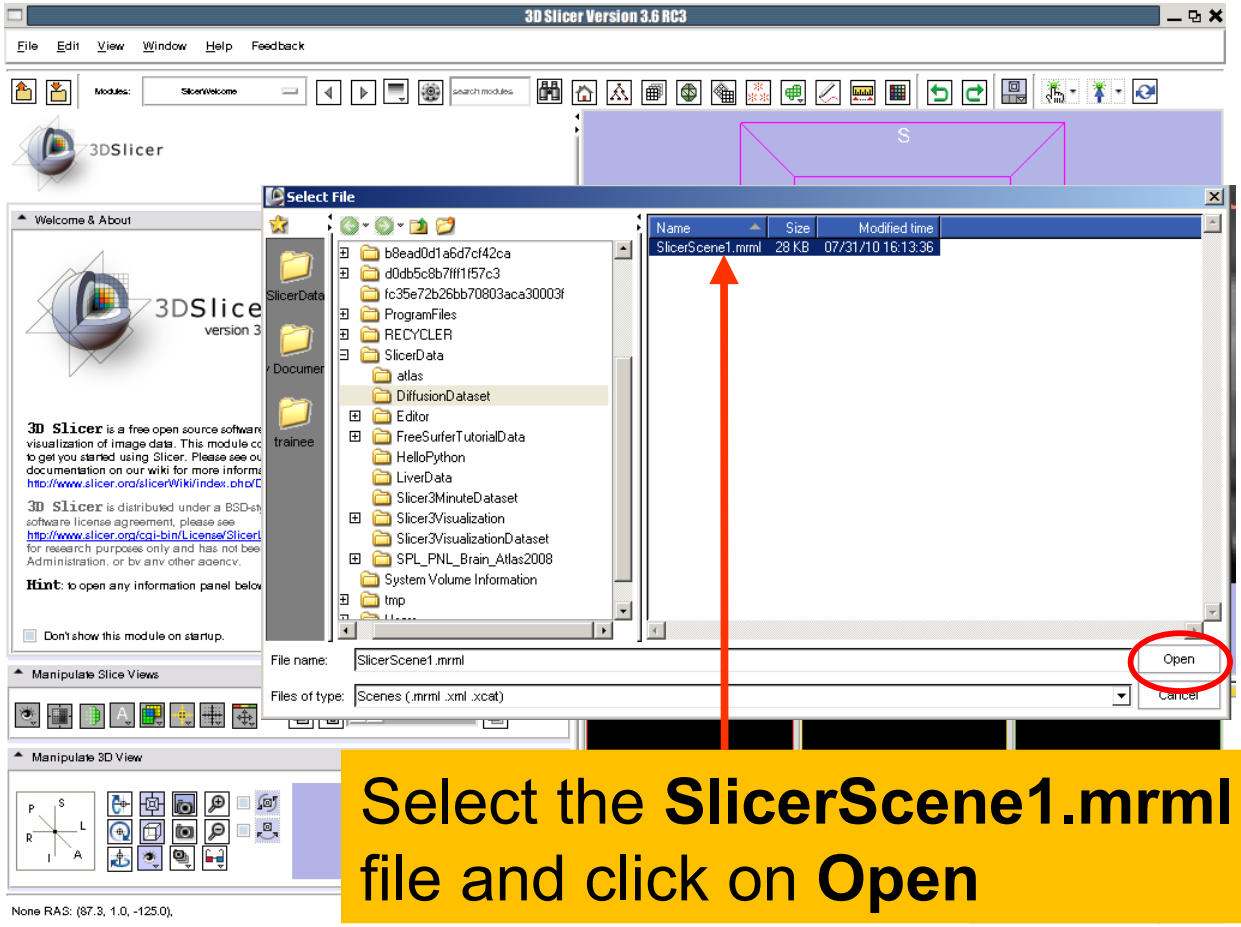
Select **File→Close Scene** to close the current DTI Scene

Loading a DTI Scene



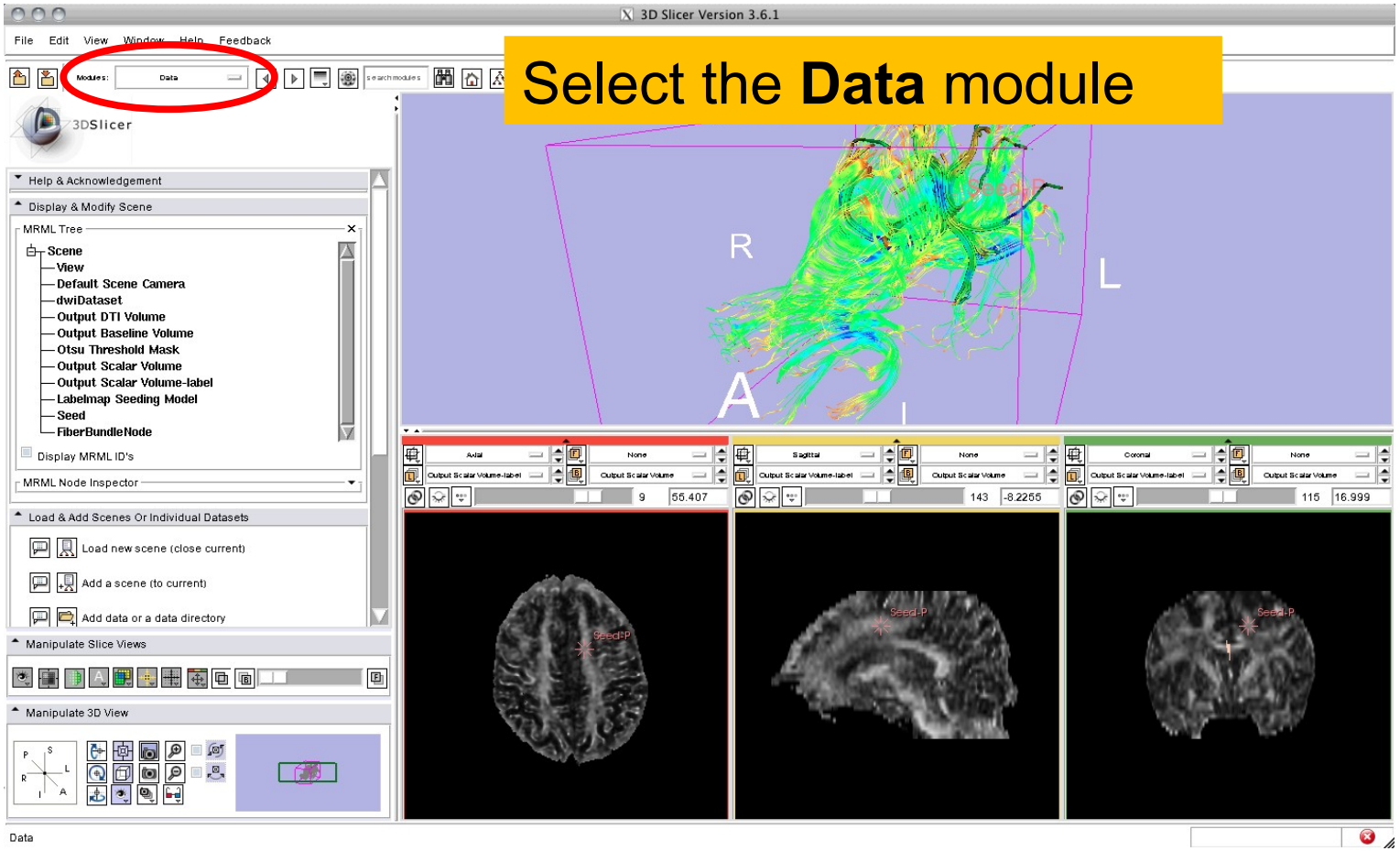
Select **File→Load Scene** and browse to the location where you saved the **SlicerScene1.mrml** scene file.

Loading a DTI Scene



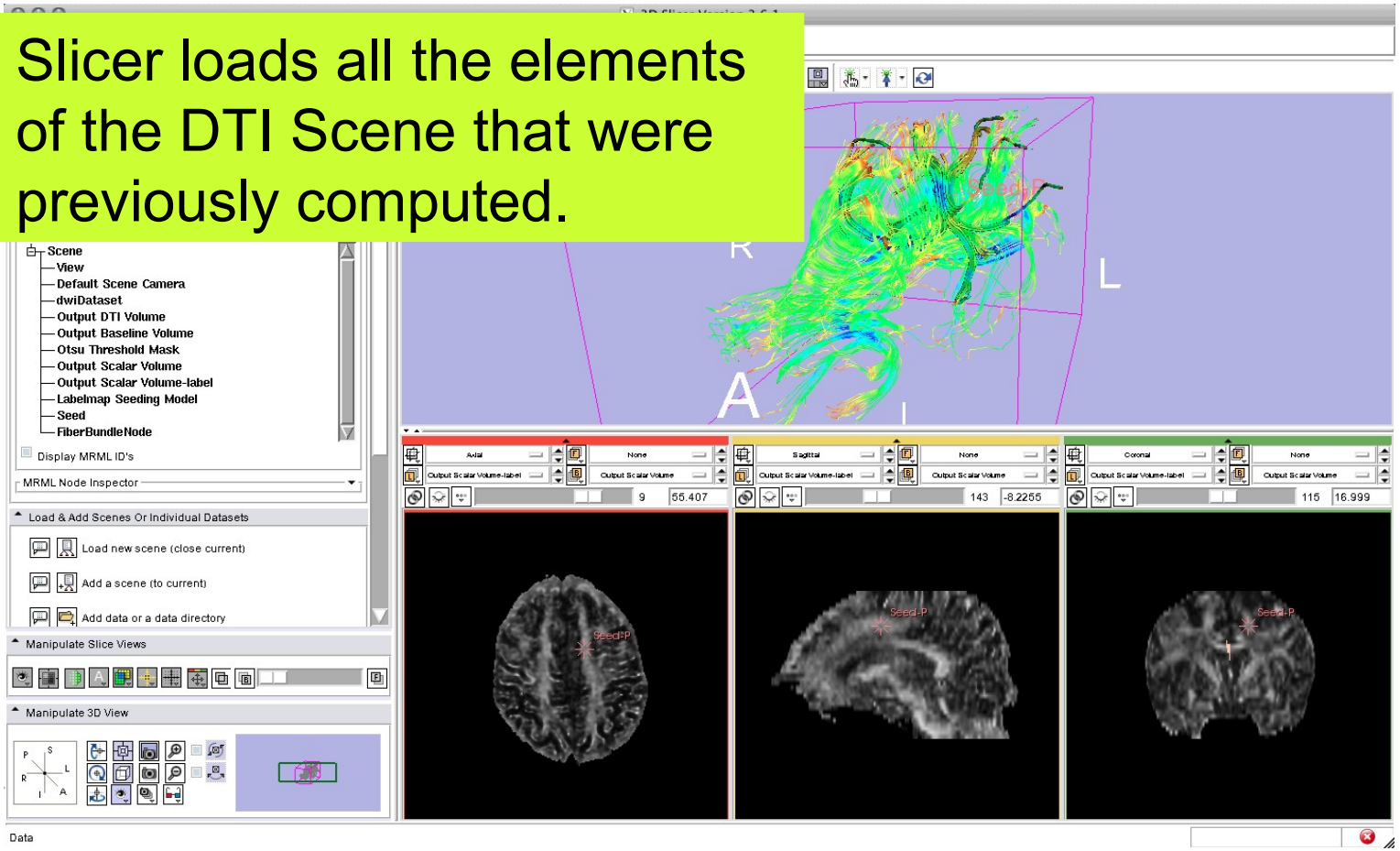
Select the **SlicerScene1.mrml** scene file and click on **Open**

Loading a DTI Scene

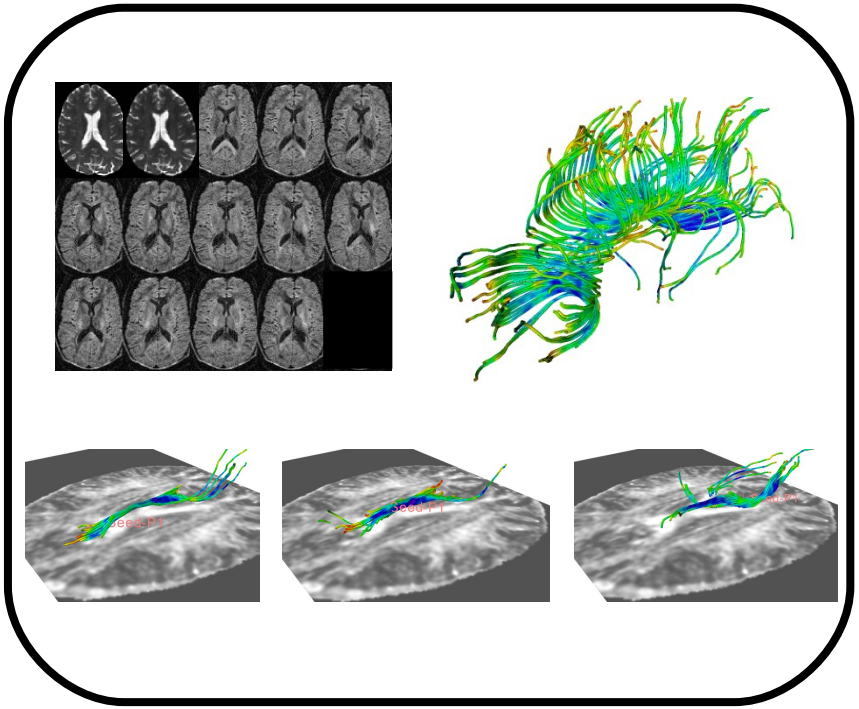


Loading a DTI Scene

Slicer loads all the elements of the DTI Scene that were previously computed.



Conclusion



This tutorial guided you through some of the Diffusion MR capabilities of the Slicer3 software for studying the brain white matter pathways.

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Acknowledgments

National Alliance for Medical Image Computing
NIH U54EB005149

Neuroimage Analysis Center
NIH P41RR13218