



NAC



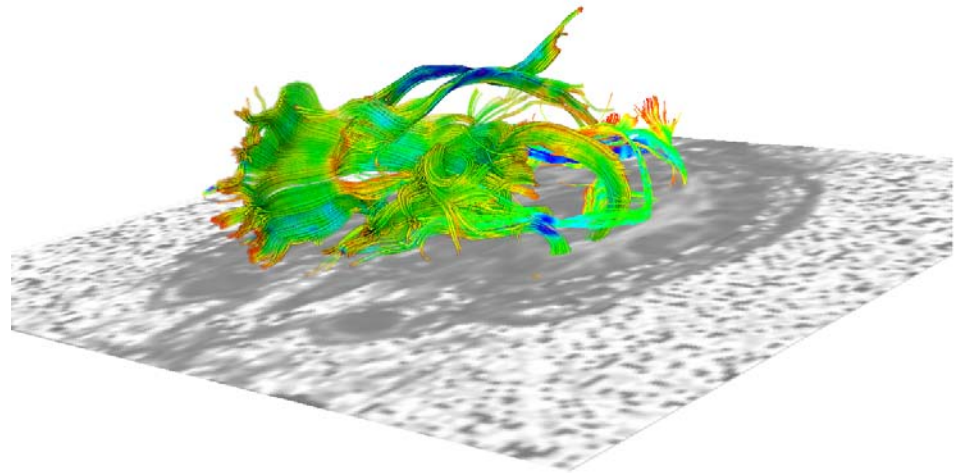
Diffusion Tensor Imaging tutorial

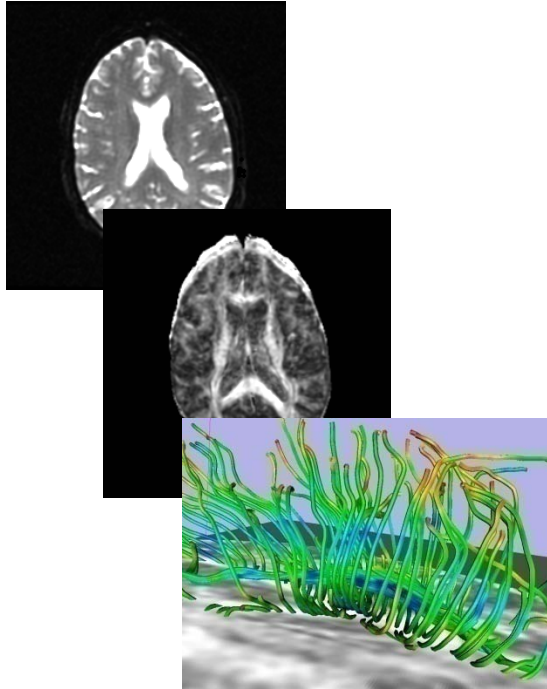
Sonia Pujol, Ph.D.

Surgical Planning Laboratory
Harvard University



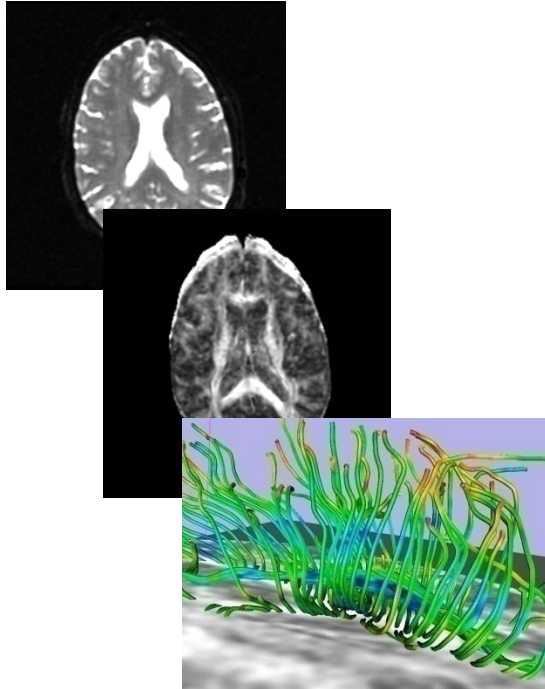
This tutorial is an introduction to the advanced **Diffusion MR** capabilities of the **Slicer3** software for medical image analysis.





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

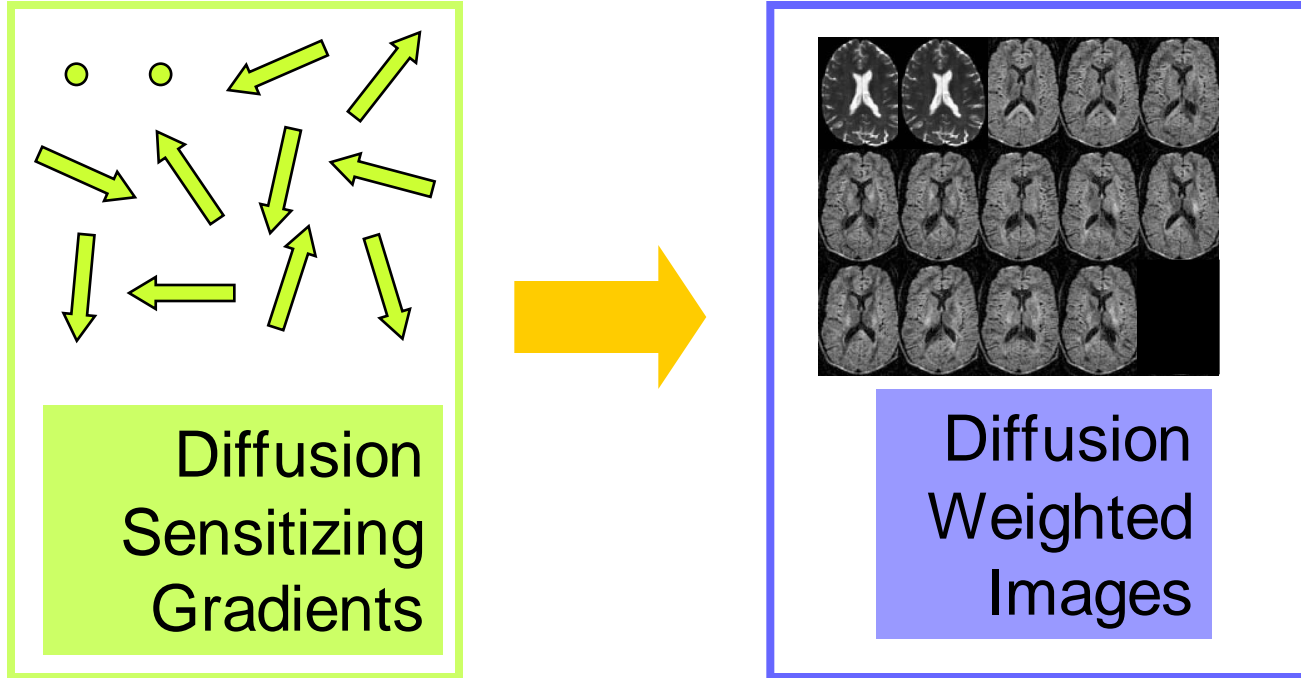
The processing pipeline uses **9 image analysis modules** of Slicer3.4



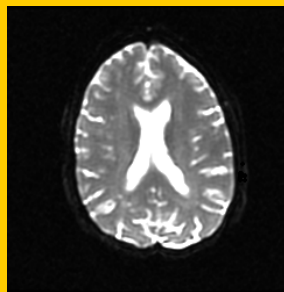
1. Data
2. Volumes
3. Diffusion Tensor Estimation
4. Diffusion Tensor Scalar Measurements
5. Editor
6. LabelMap Seeding
7. Fiber Bundles
8. Fiducials
9. Fiducial Seeding

Tutorial Dataset

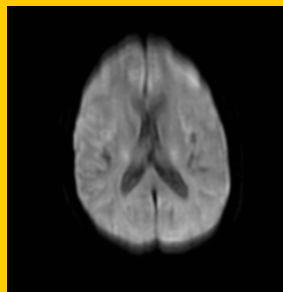
The Diffusion MR tutorial dataset is composed of a **Diffusion Weighted MR scan** of the brain acquired with 12 gradient directions and 2 baseline.



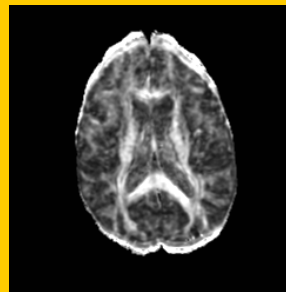
DTI Processing Pipeline



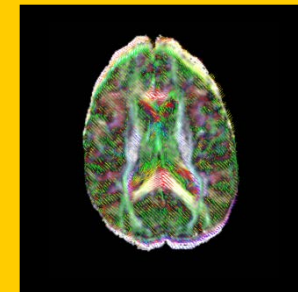
DWI
Acquisition



Tensor
Calculation



Scalar
Maps



3D
Visualization

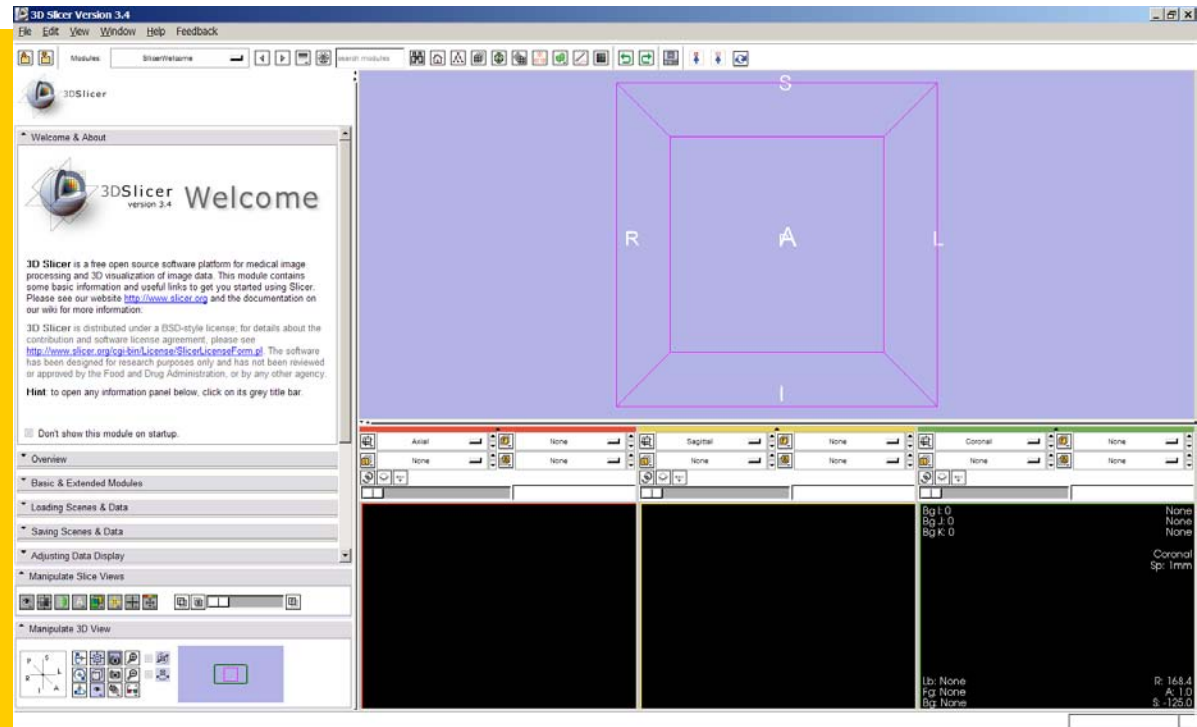
Linux/Mac users
Launch the Slicer3
executable located in
the Slicer3.4 directory

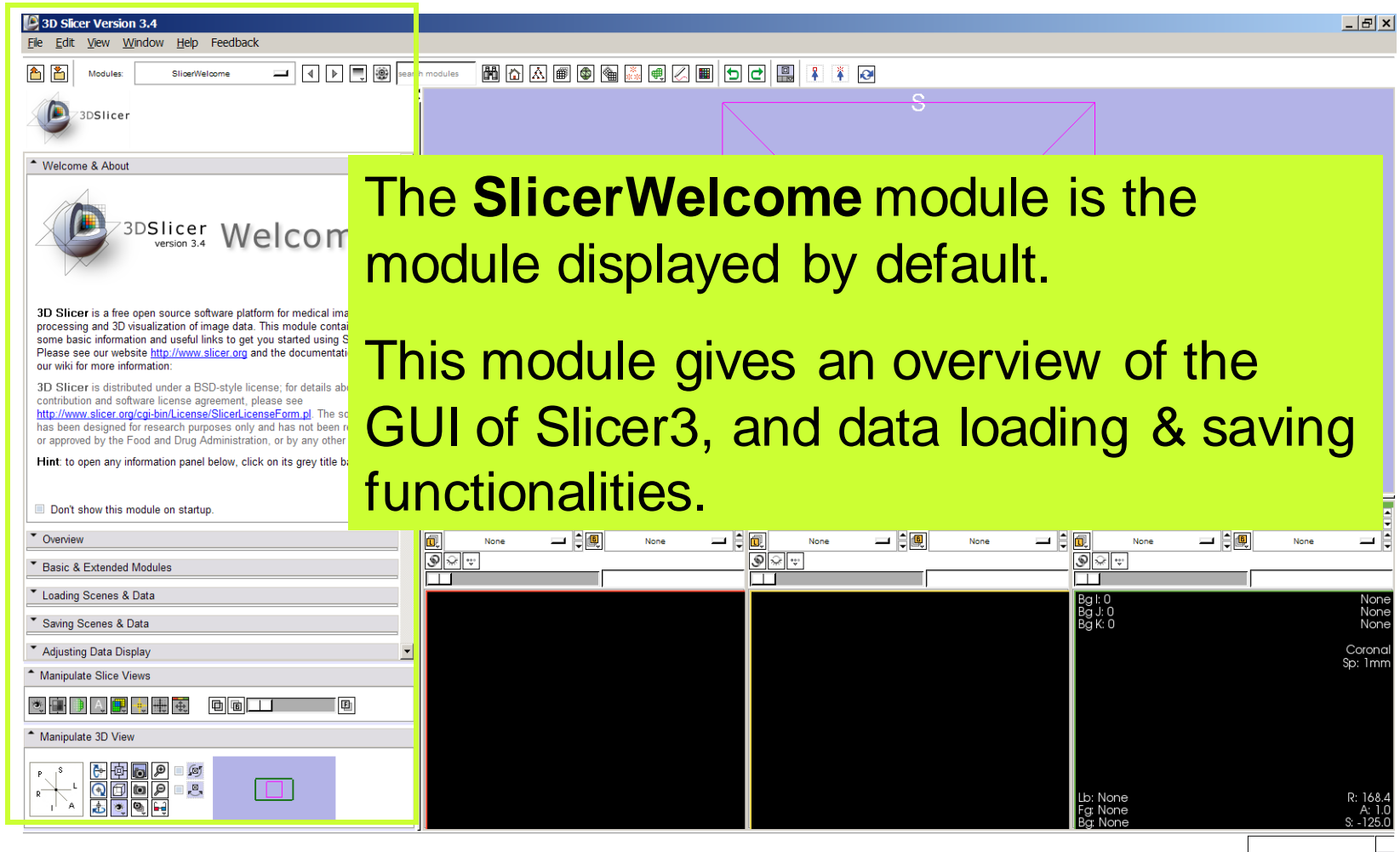
Windows users

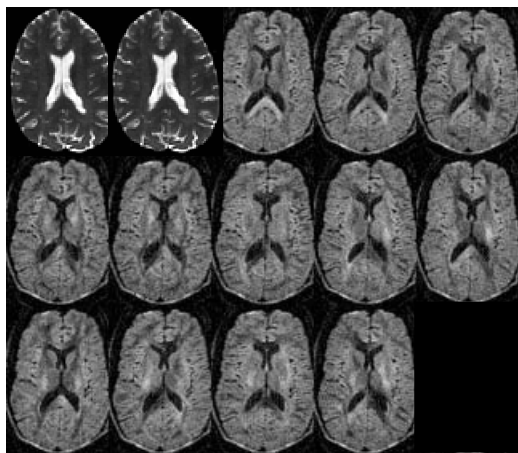
Select

Start → All Programs

→ Slicer3 3.4 2009-05-21 → Slicer3







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

Part 1:

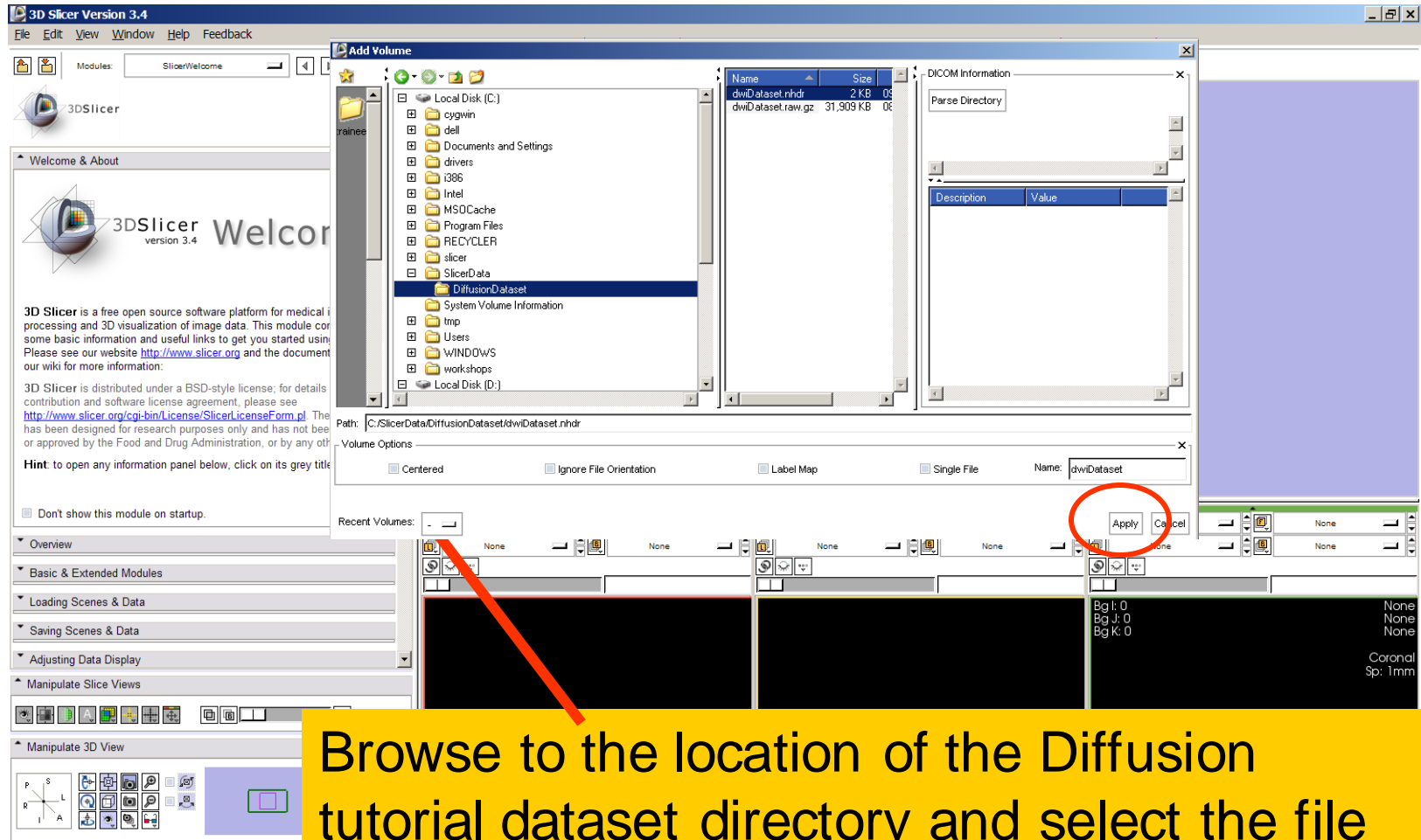
*Diffusion data
loading and
tensor estimation*



Loading the DWI volume

The screenshot shows the 3DSlicer Version 3.4 interface. The 'File' menu is circled in red. A yellow callout box with the text 'Select File → Add Volume from the File menu' is overlaid on the main 3D view. A red arrow points from the callout box to the 'File' menu. The interface includes a menu bar (File, Edit, View, Window, Help, Feedback), a toolbar, a 'Modules' panel, a 'Welcome & About' panel, and a 3D view area with three orthogonal slice views (Axial, Sagittal, Coronal) and a 3D view of a volume.

Loading the DWI volume

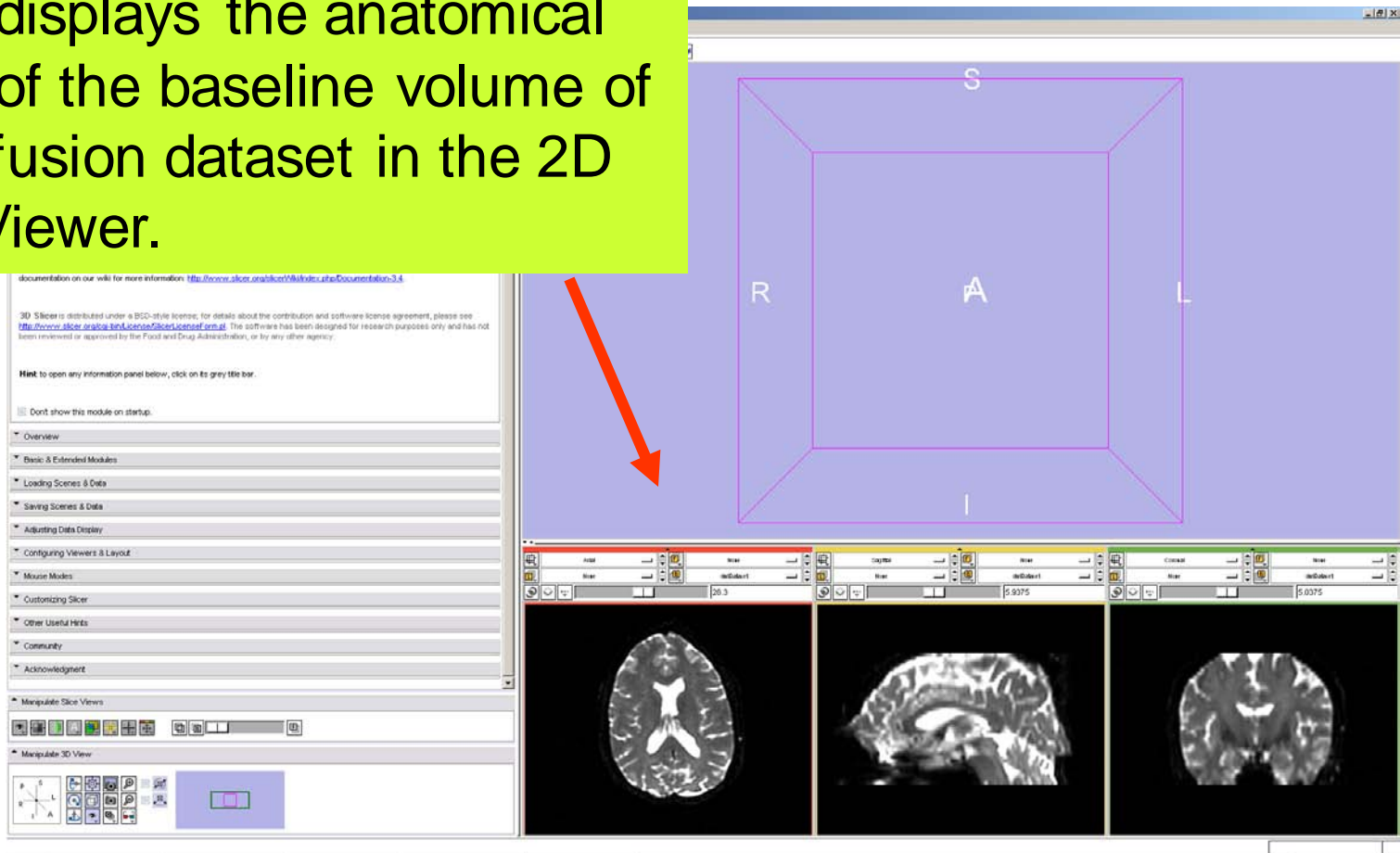


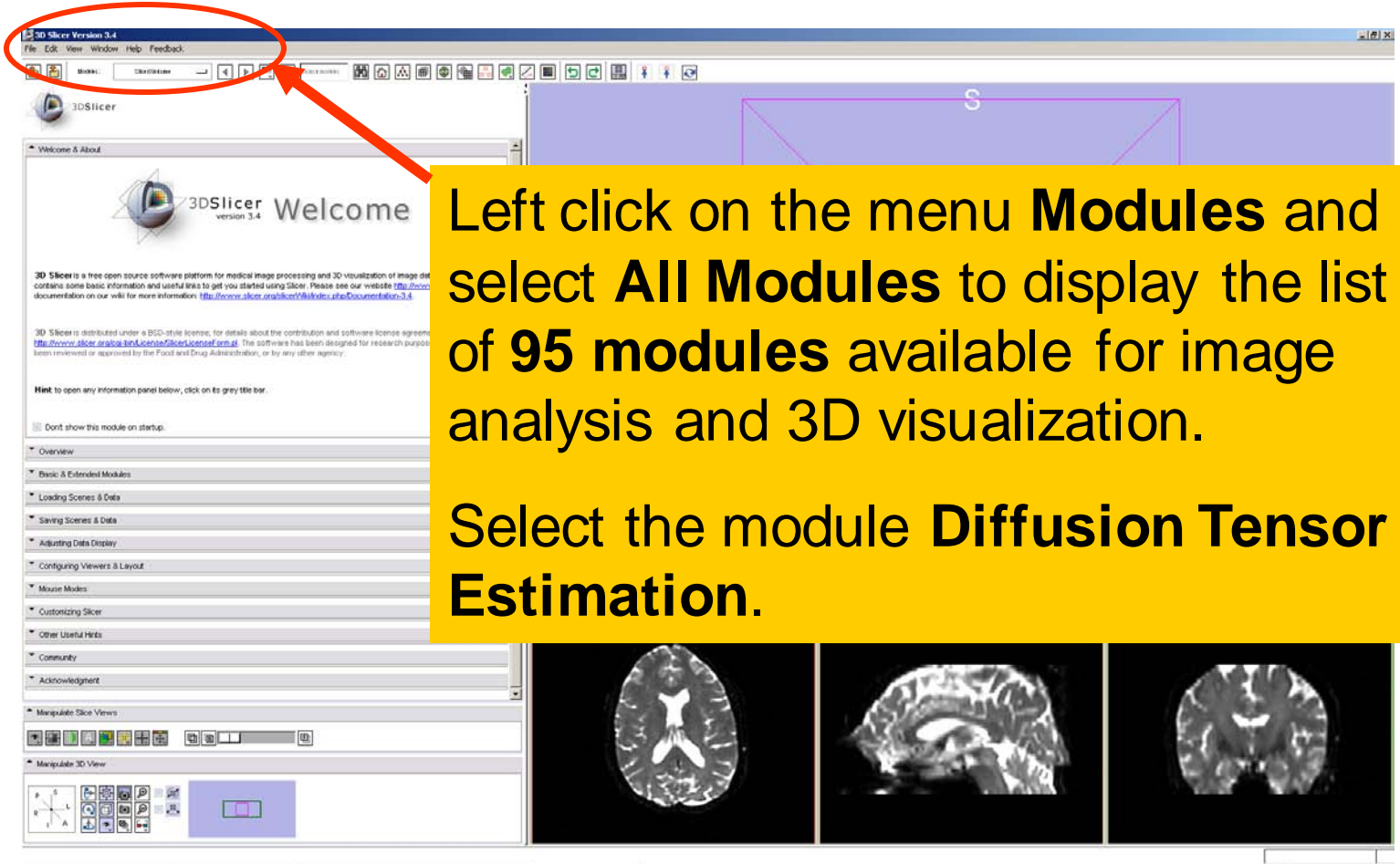
Browse to the location of the Diffusion tutorial dataset directory and select the file **dwiDataset.nhdr**

Click on **Apply** to load the volume

Loading the DWI volume

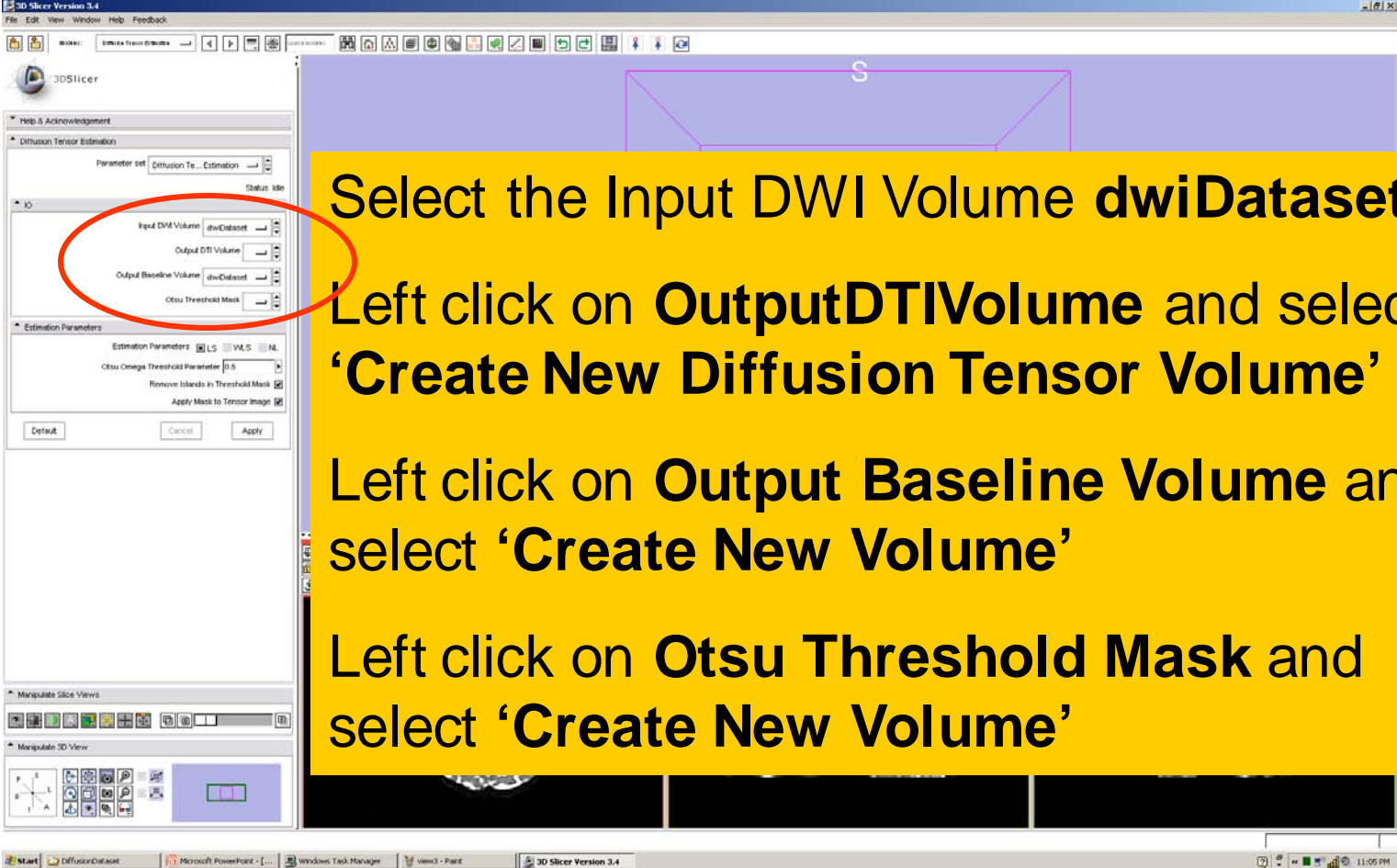
Slicer displays the anatomical views of the baseline volume of the diffusion dataset in the 2D Slice Viewer.





Left click on the menu **Modules** and select **All Modules** to display the list of **95 modules** available for image analysis and 3D visualization.

Select the module **Diffusion Tensor Estimation**.



The screenshot shows the 3D Slicer 3.4 interface with the Diffusion Tensor Estimation panel open. The 'IO' section is circled in red, highlighting the 'Input DWI Volume' (set to 'dwiDataset'), 'Output DTI Volume', 'Output Baseline Volume', and 'Otsu Threshold Mask' dropdown menus. The 'Estimation Parameters' section shows 'Estimation Parameters' set to 'LS', 'Otsu Omega Threshold Parameter' set to '0.5', and 'Apply Mask to Tensor Image' checked. The 'Manipulate Slice Views' and 'Manipulate 3D View' sections are also visible.

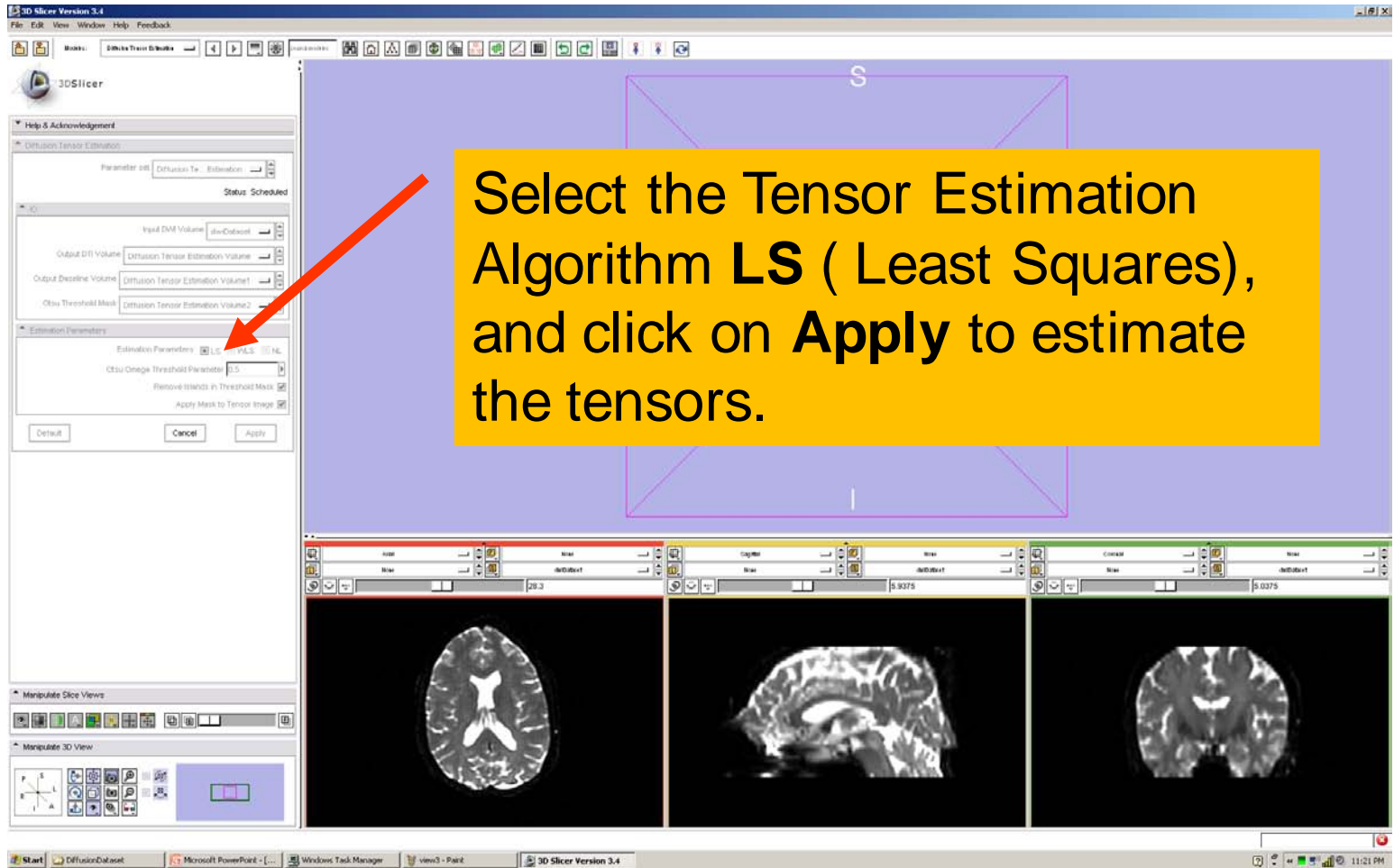
Select the Input DWI Volume **dwiDataset**

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

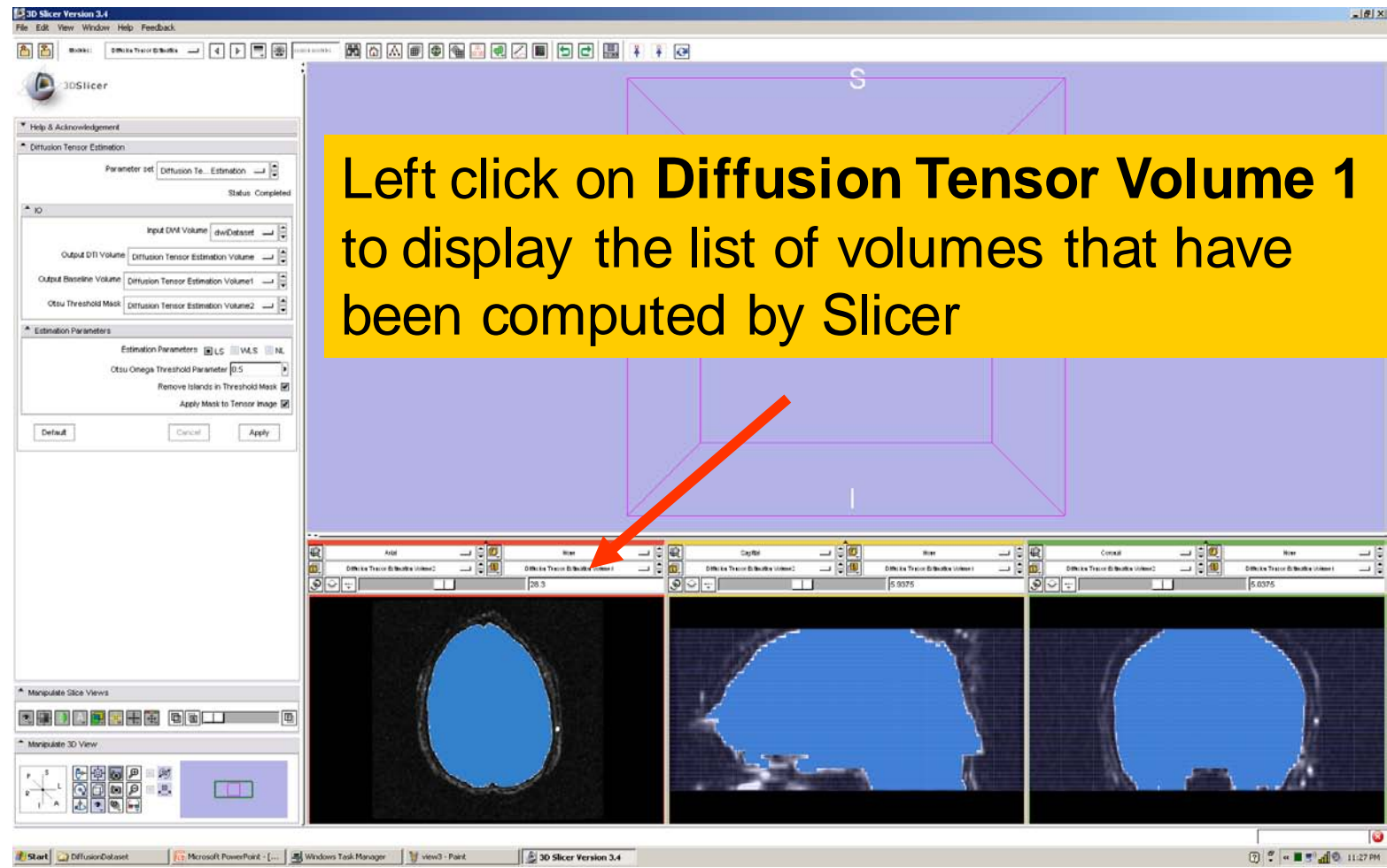
Left click on **Output Baseline Volume** and select **‘Create New Volume’**

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

Tensor Estimation



Tensor Estimation

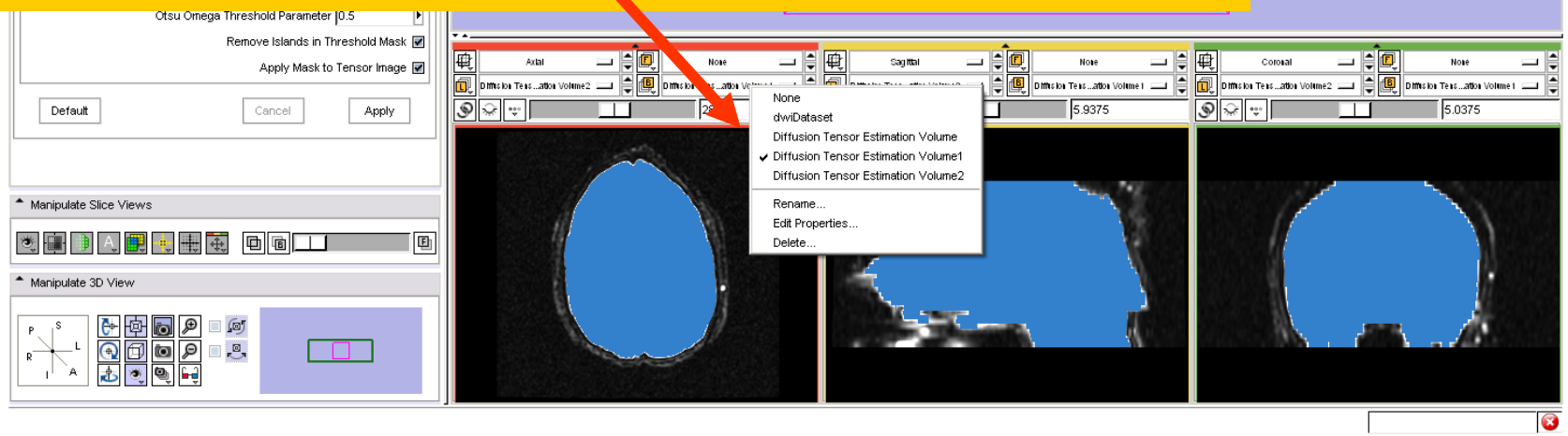


Tensor Estimation

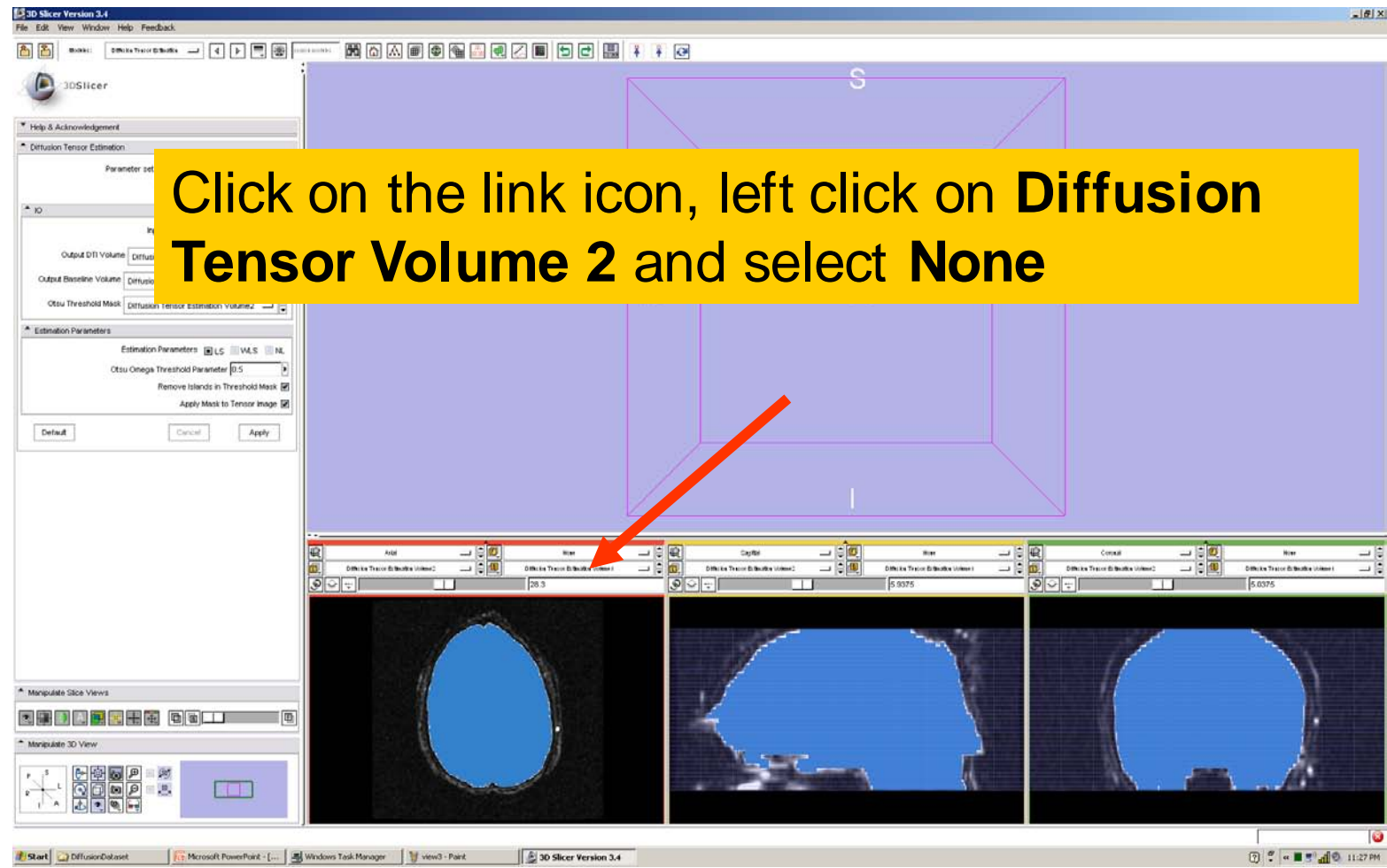
Diffusion Tensor Estimation Volume is the volume of estimated tensors

Diffusion Tensor Estimation Volume 1 is the Baseline volume

Diffusion Tensor Estimation Volume 2 is the tensor mask (blue)

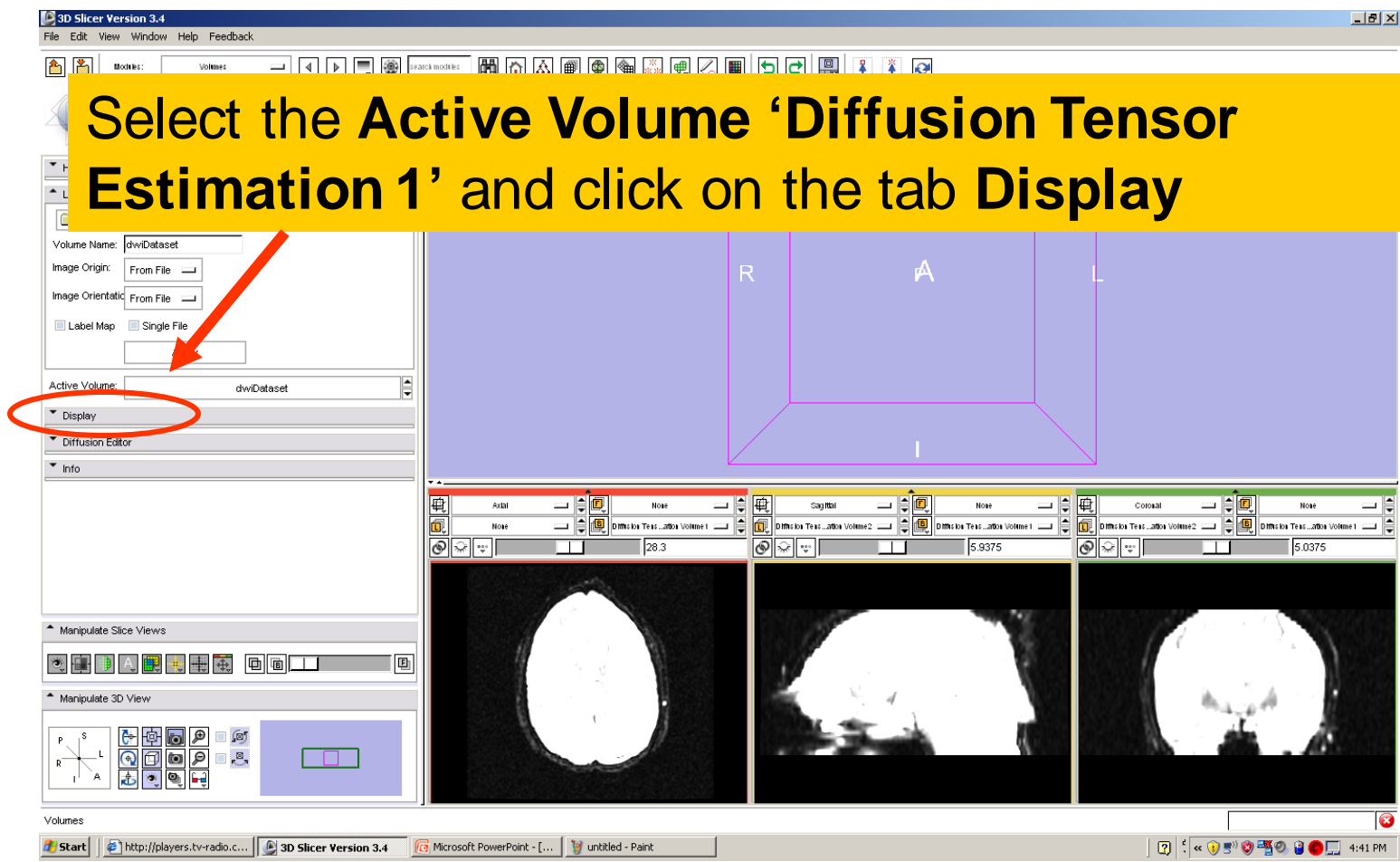


Tensor Estimation



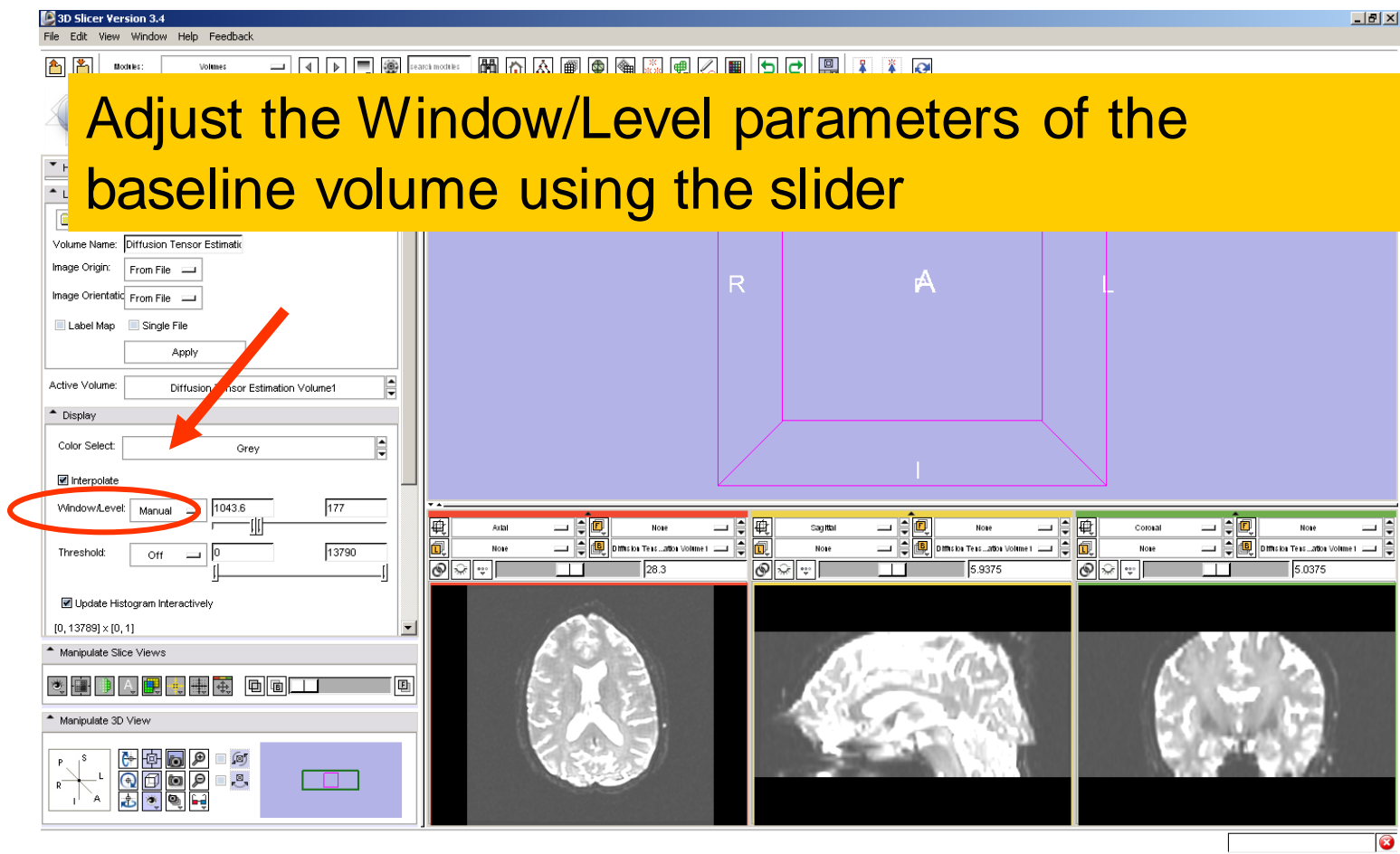
Tensor Estimation

Select the Active Volume 'Diffusion Tensor Estimation 1' and click on the tab Display



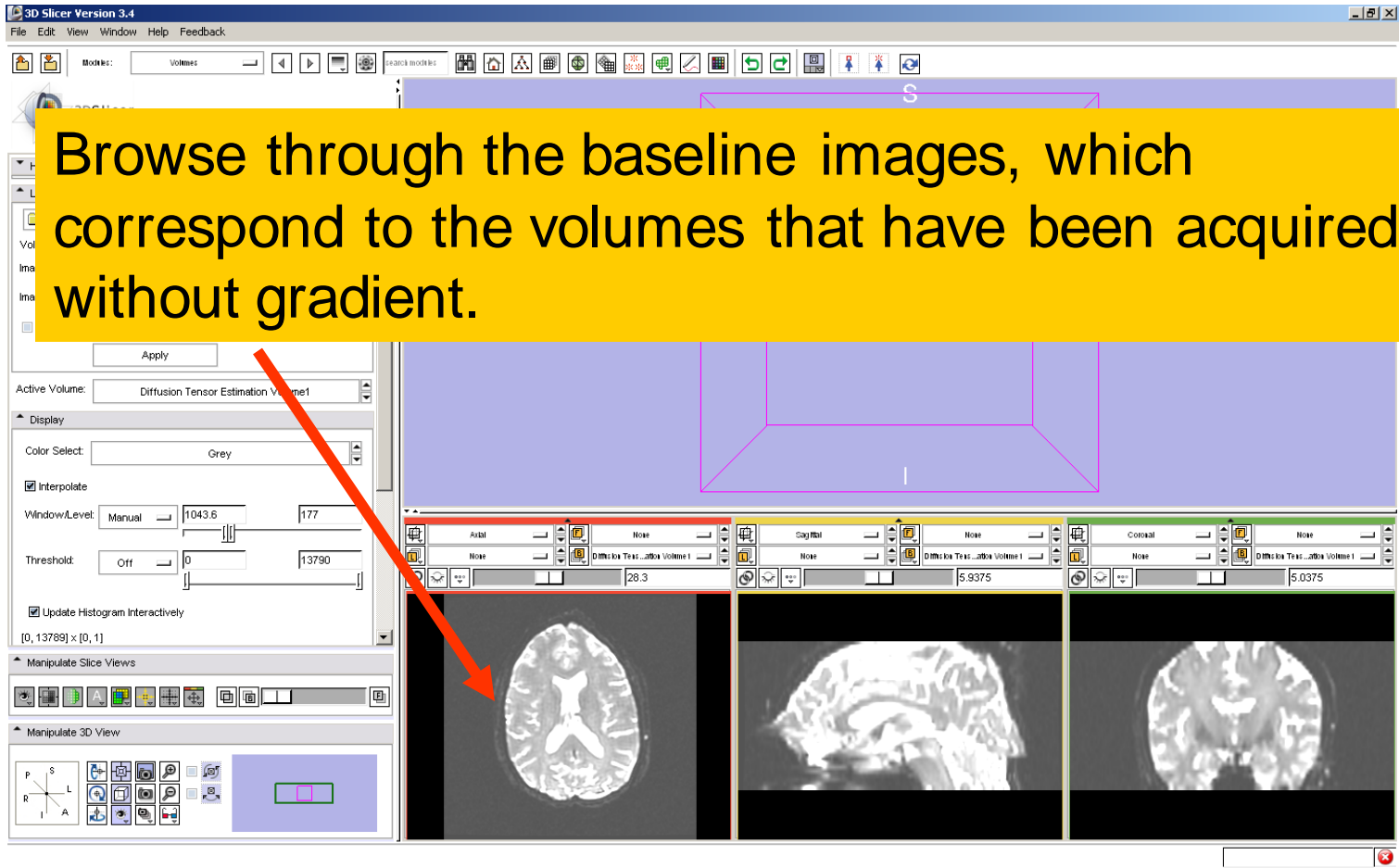
Tensor Estimation

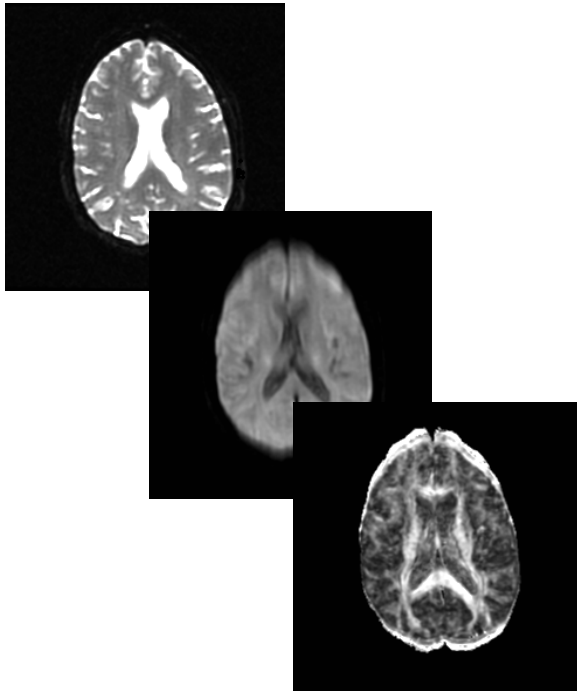
Adjust the Window/Level parameters of the baseline volume using the slider



Tensor Estimation

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





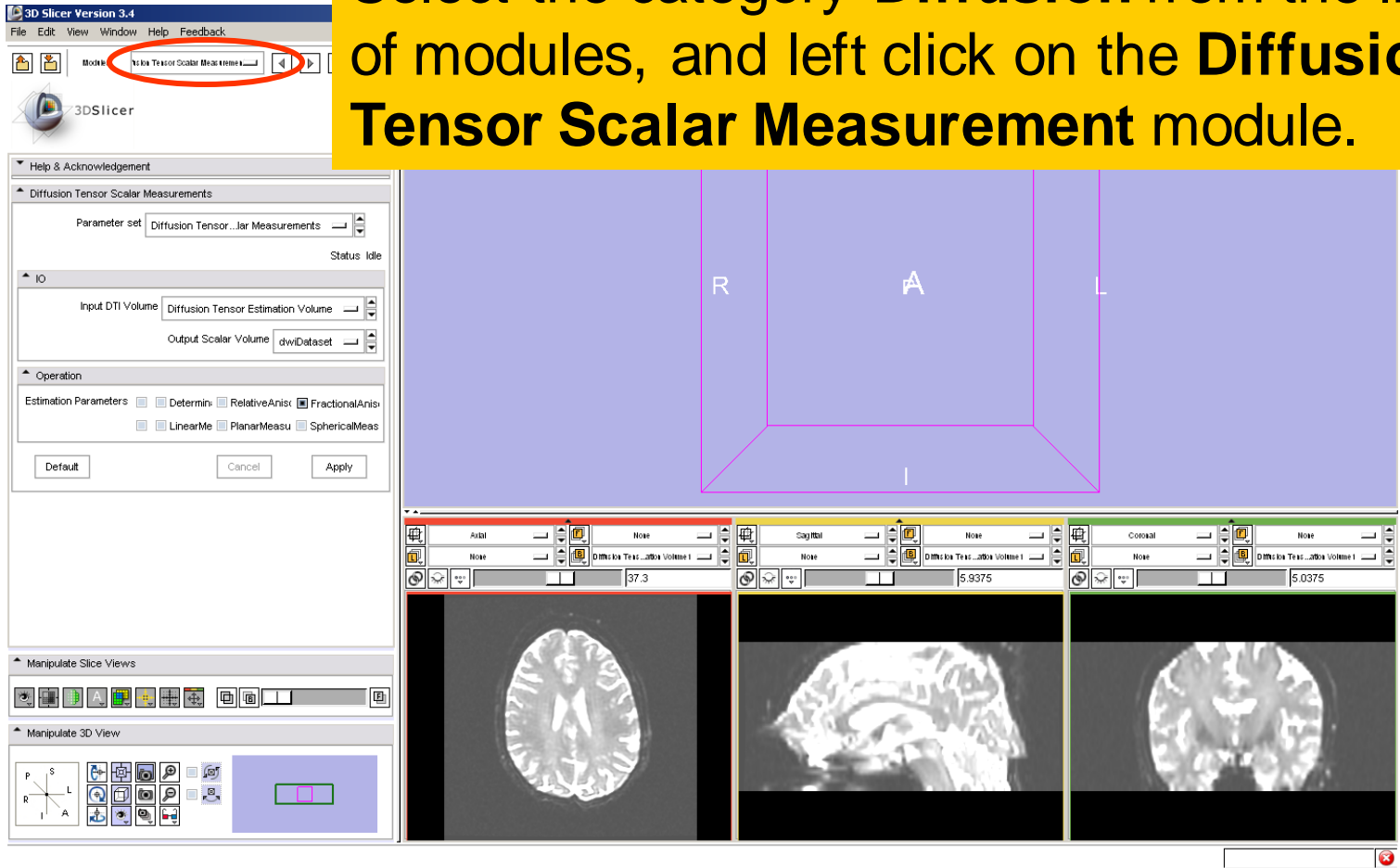
Part2:

Scalar

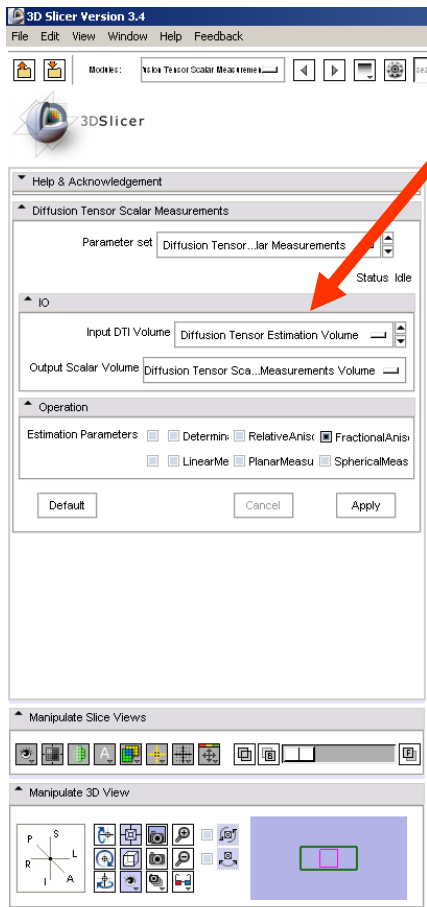
Measurements

Scalar Measurements

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



Scalar Measurements



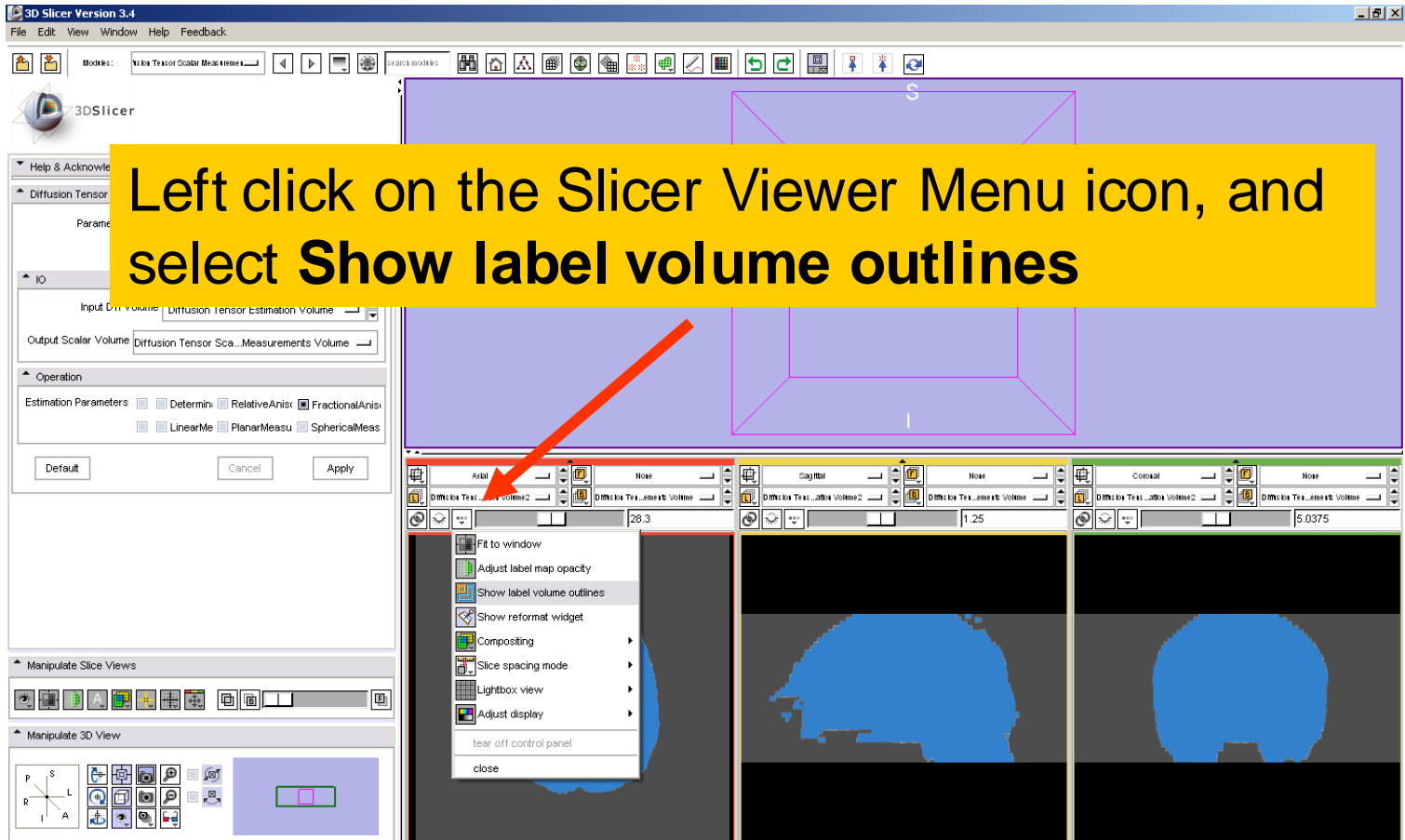
Select the Input DTI Volume **Diffusion Tensor Estimation Volume**

Select the Output Scalar Volume **'Create New Volume'**

Select the Operation **Fractional Anisotropy**, and click on **Apply**



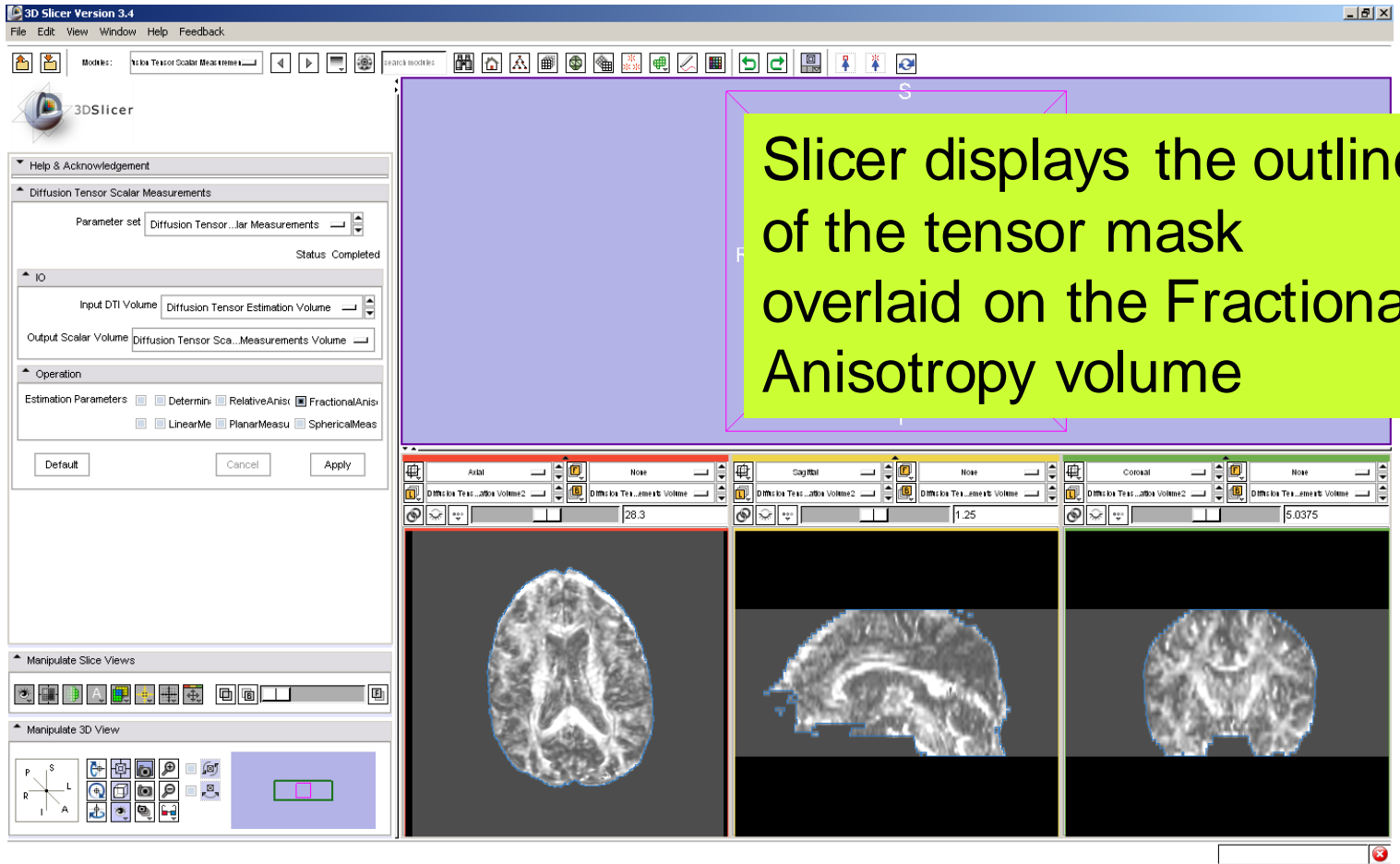
Fractional Anisotropy Volume



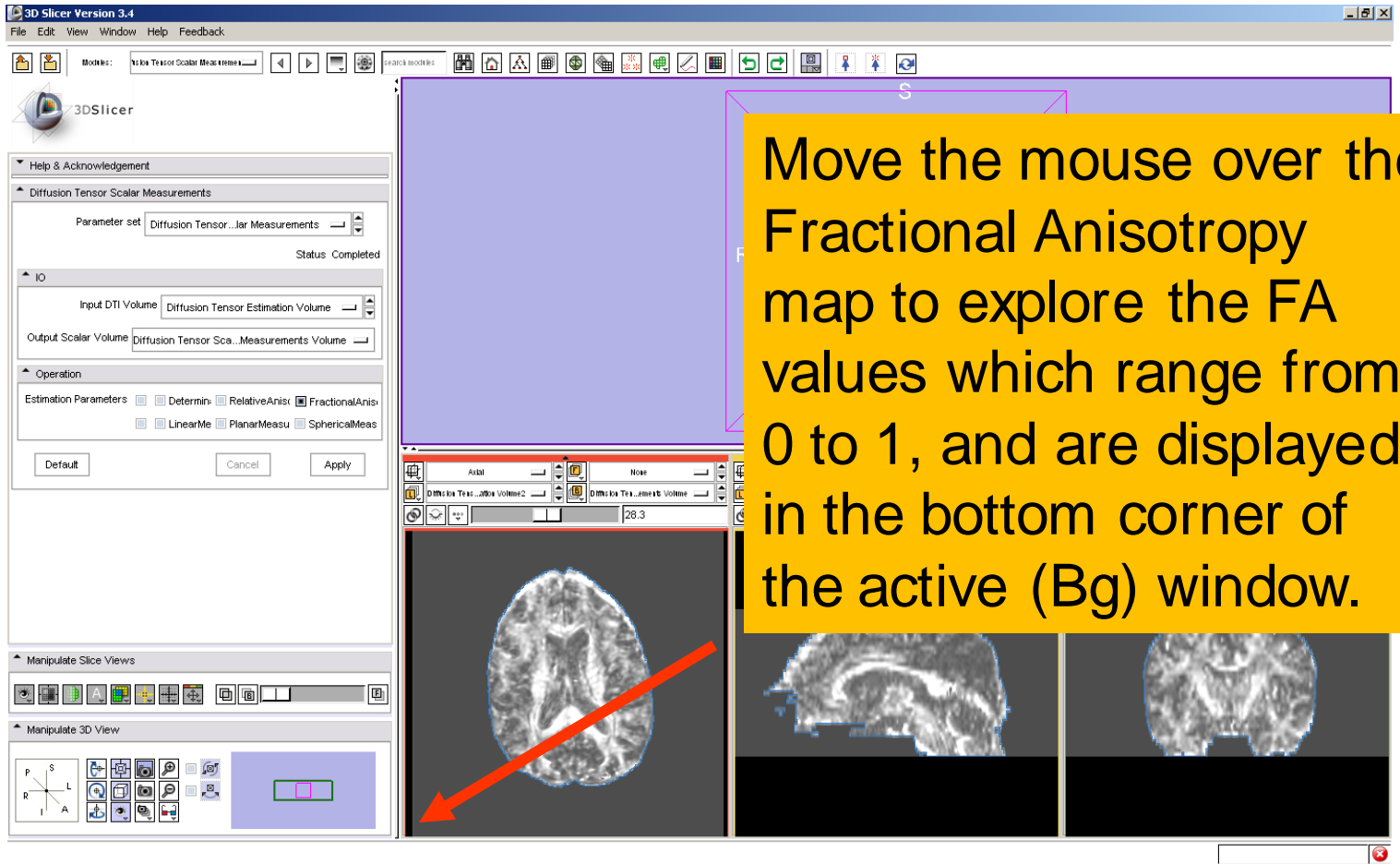
Left click on the Slicer Viewer Menu icon, and select **Show label volume outlines**

The screenshot shows the 3D Slicer 3.4 interface. The main window displays a 3D view of a brain slice with a purple wireframe box. The left sidebar contains the Diffusion Tensor Estimation Volume panel, which is currently set to Fractional Anisotropy. The bottom right corner shows the Slicer Viewer Menu, which is open and displays the 'Show label volume outlines' option. A red arrow points to the Slicer Viewer Menu icon in the bottom left corner of the 3D view.

Fractional Anisotropy Volume



Fractional Anisotropy Volume

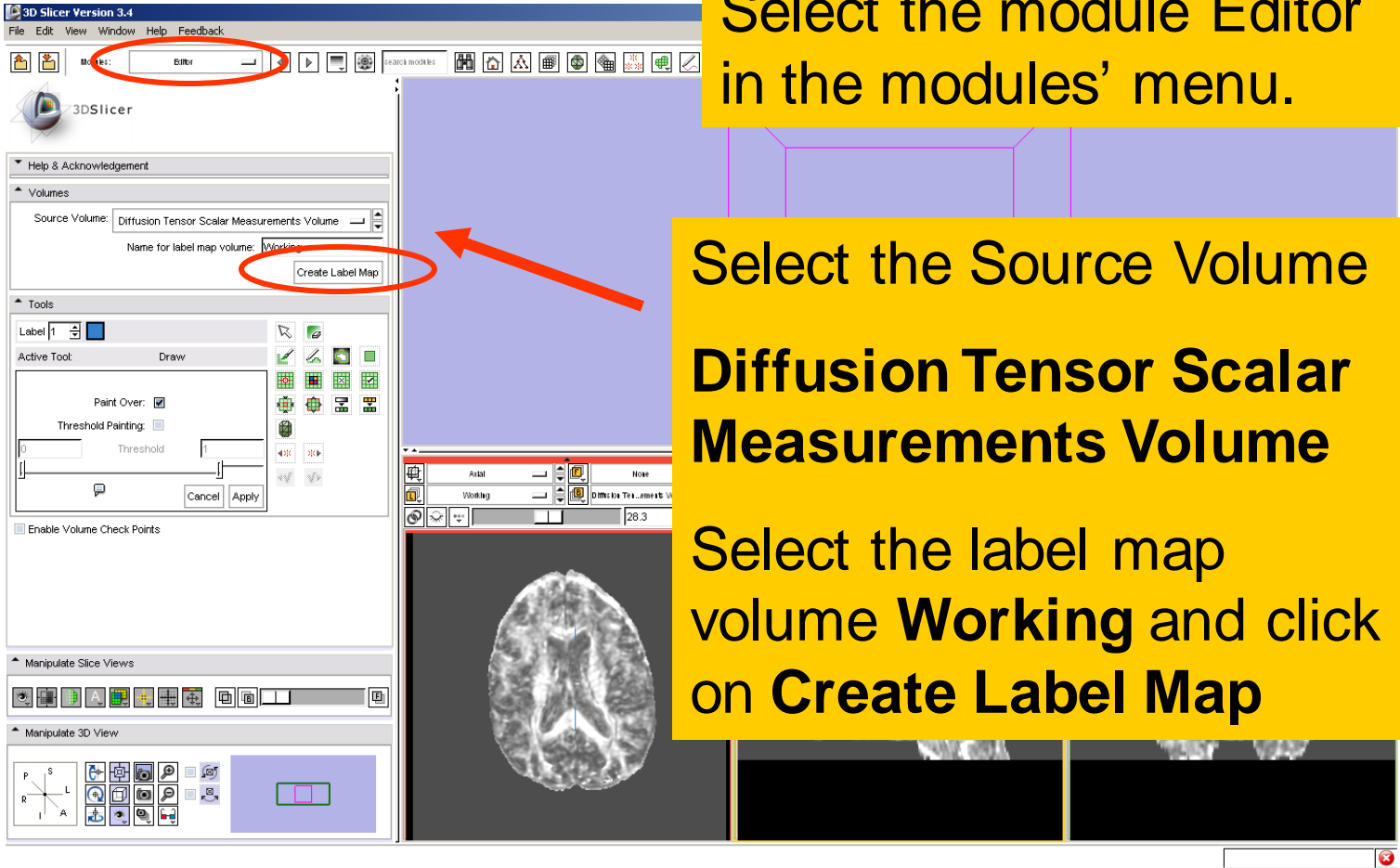




Part 3:

*Region of Interest
based
Tractography*

LabelMap Generation

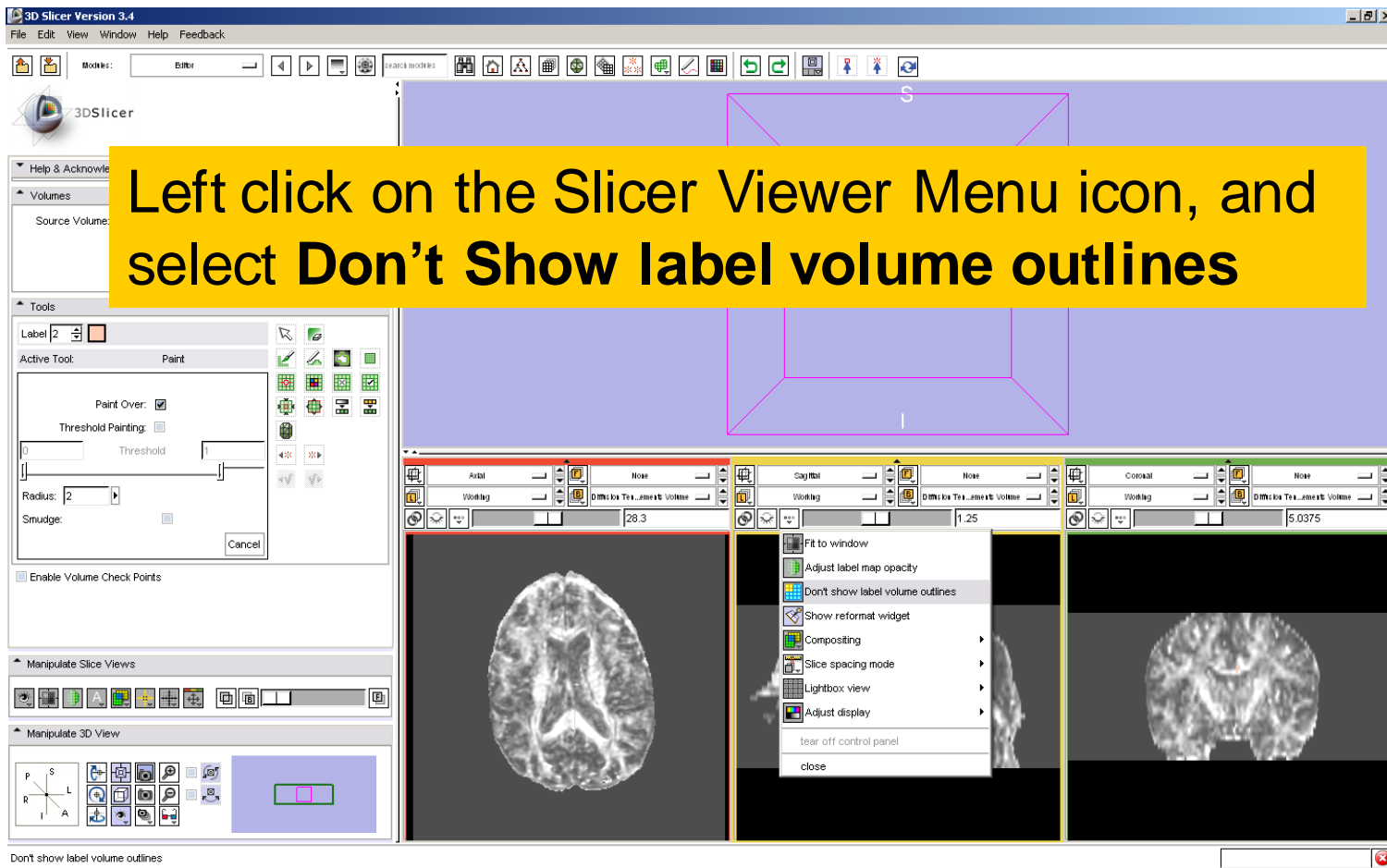


Select the module Editor in the modules' menu.

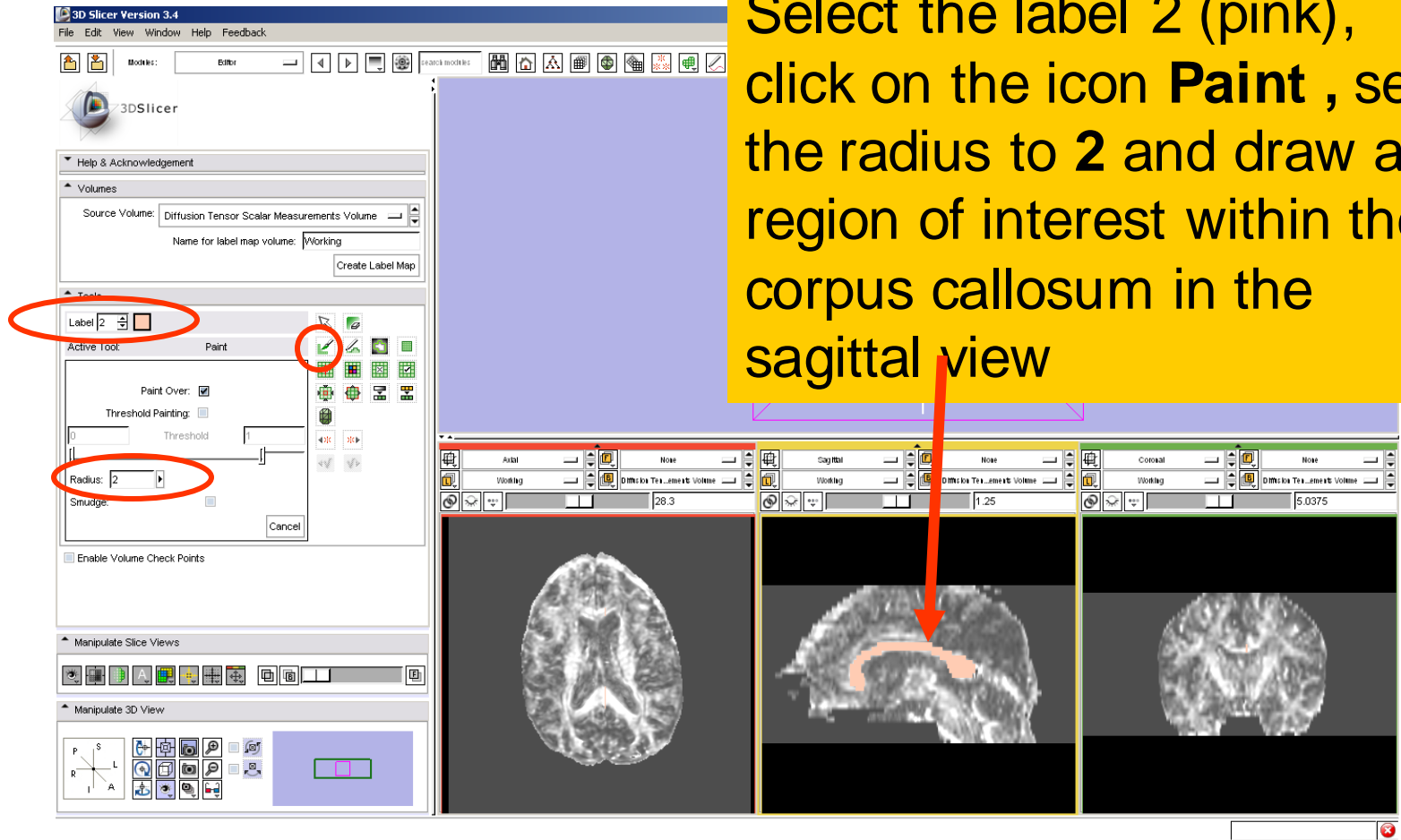
Select the Source Volume **Diffusion Tensor Scalar Measurements Volume**

Select the label map volume **Working** and click on **Create Label Map**

LabelMap Generation



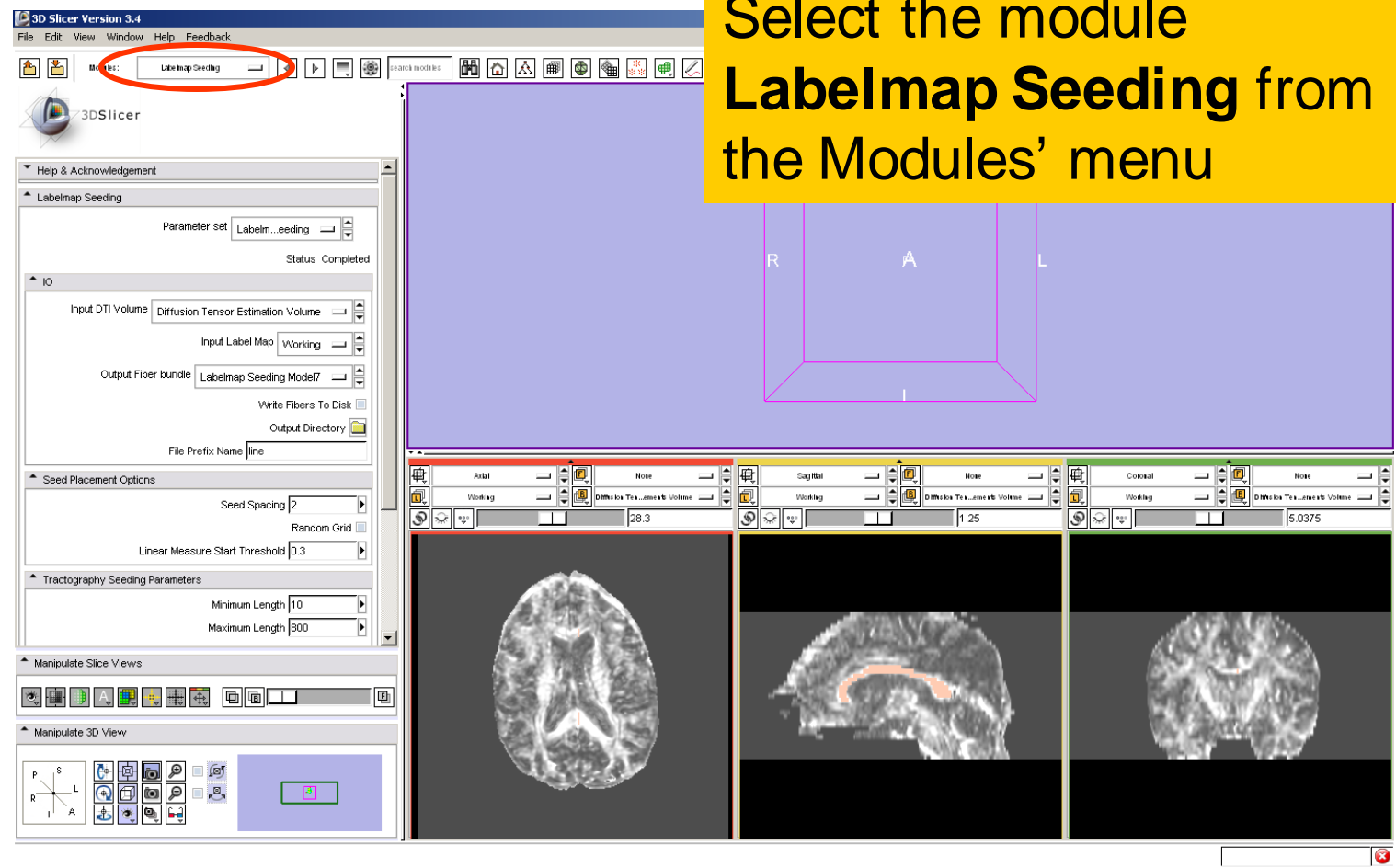
LabelMap Generation



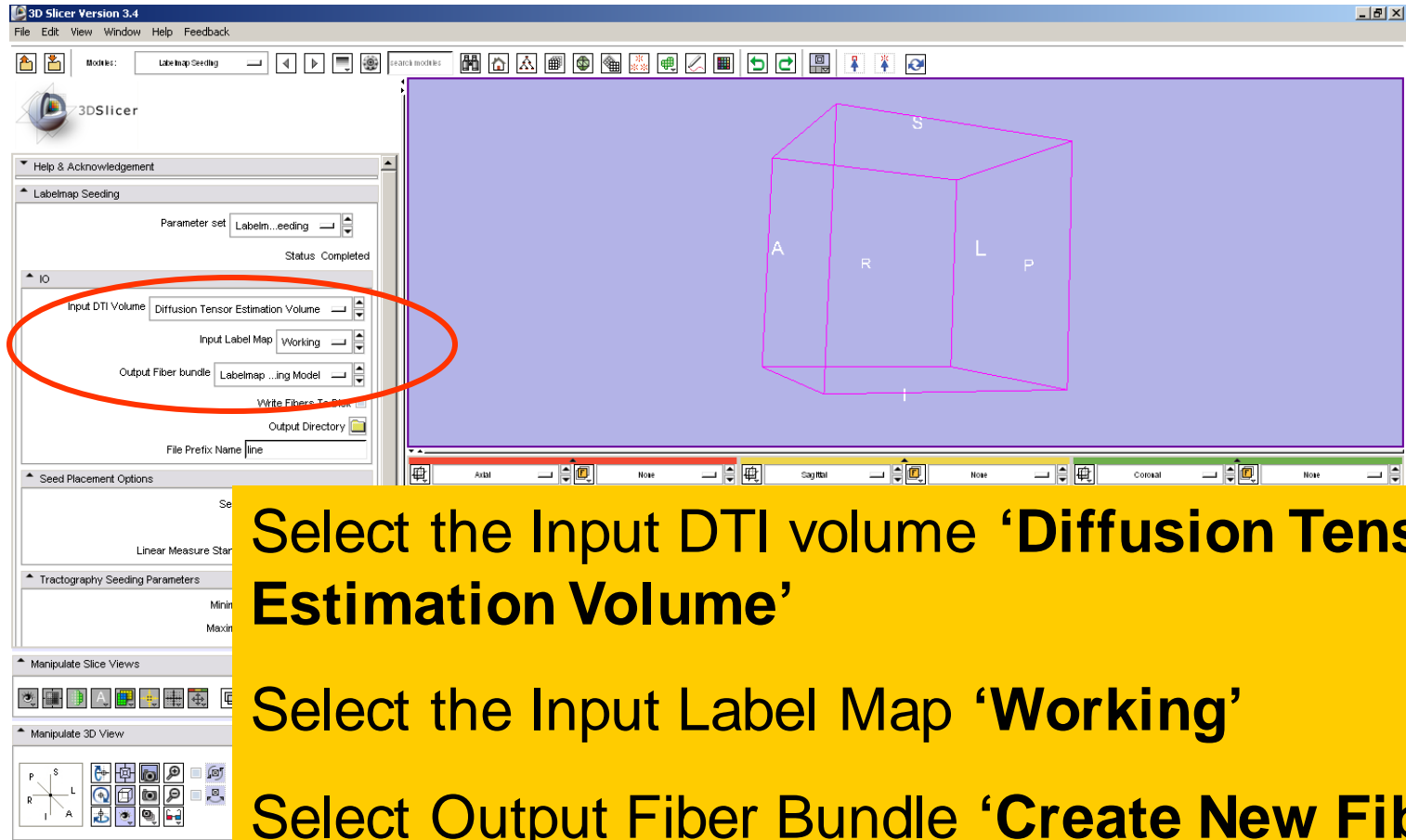
Select the label 2 (pink), click on the icon **Paint**, set the radius to 2 and draw a region of interest within the corpus callosum in the sagittal view

LabelMap Seeding

Select the module
Labelmap Seeding from
the Modules' menu



LabelMap Seeding

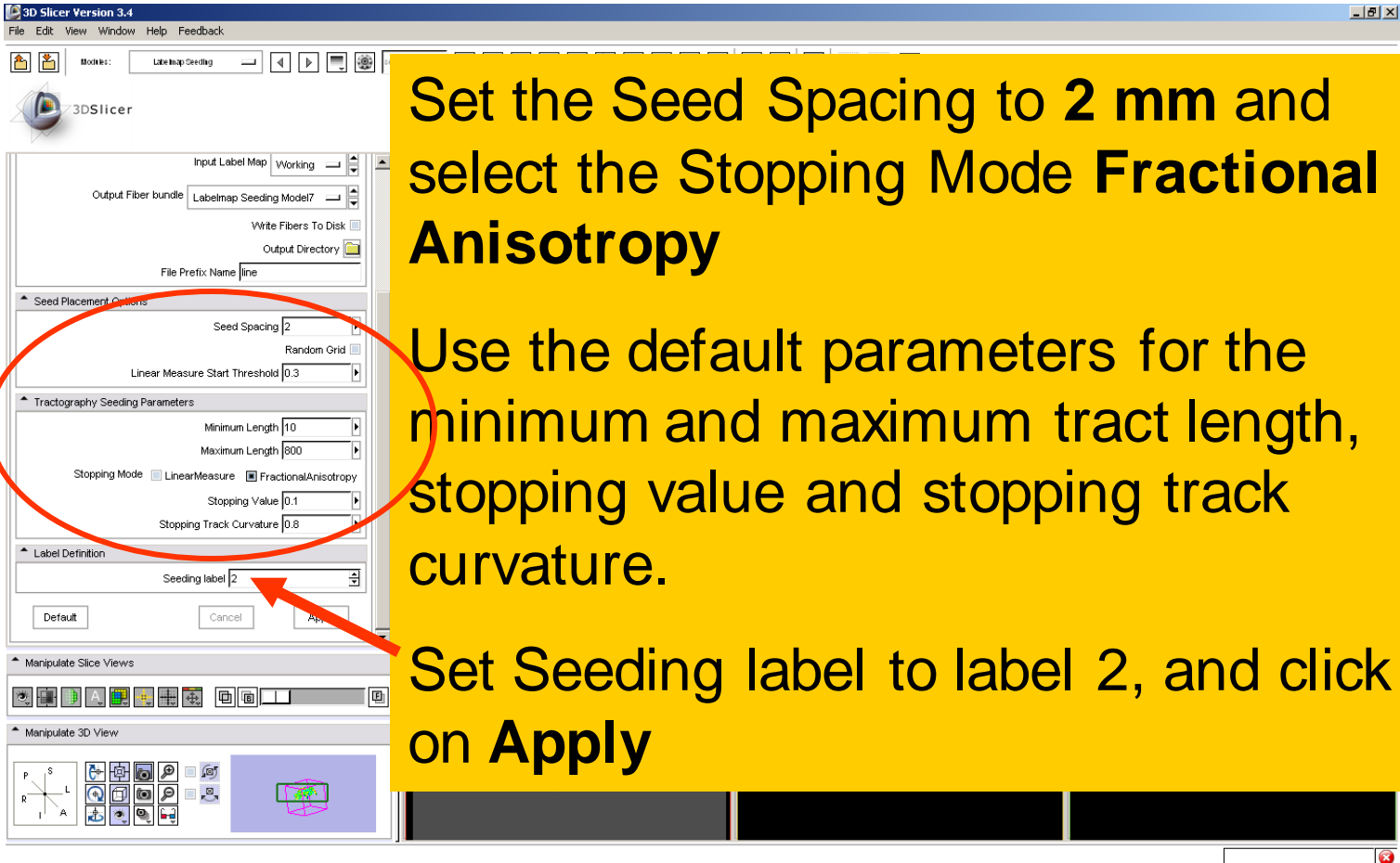


Select the Input DTI volume '**Diffusion Tensor Estimation Volume**'

Select the Input Label Map '**Working**'

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

LabelMap Seeding



The screenshot shows the 'LabelMap Seeding' dialog box in 3D Slicer 3.4. The 'Seed Placement Options' section has 'Seed Spacing' set to 2. The 'Tractography Seeding Parameters' section has 'Minimum Length' at 10, 'Maximum Length' at 800, 'Stopping Mode' set to 'Fractional Anisotropy', 'Stopping Value' at 0.1, and 'Stopping Track Curvature' at 0.8. The 'Label Definition' section has 'Seeding label' set to 2. A red circle highlights the 'Tractography Seeding Parameters' section, and a red arrow points to the 'Seeding label' field. The 'Apply' button is visible at the bottom right of the dialog.

Set the Seed Spacing to 2 mm and select the Stopping Mode **Fractional Anisotropy**

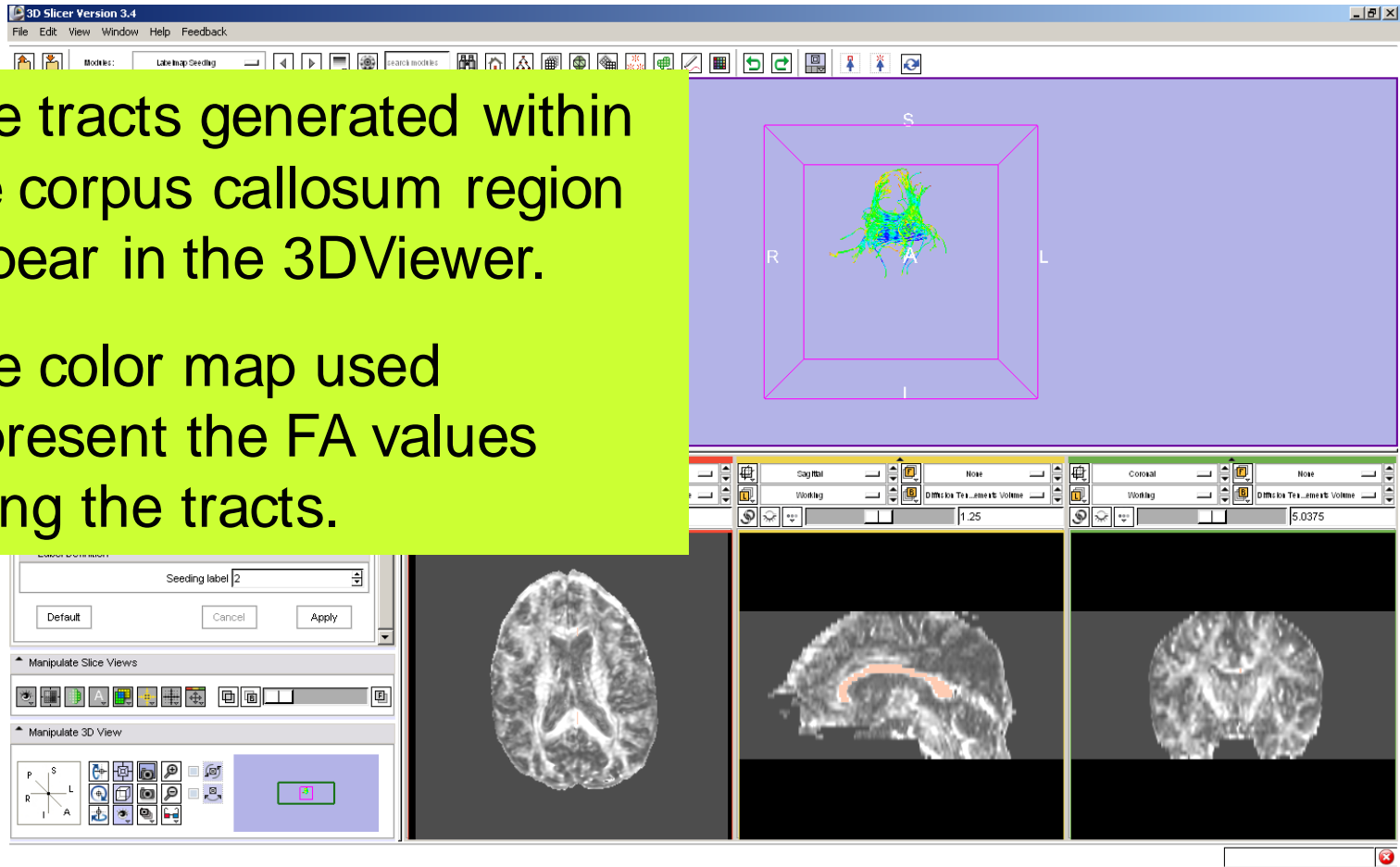
Use the default parameters for the minimum and maximum tract length, stopping value and stopping track curvature.

Set Seeding label to label 2, and click on **Apply**

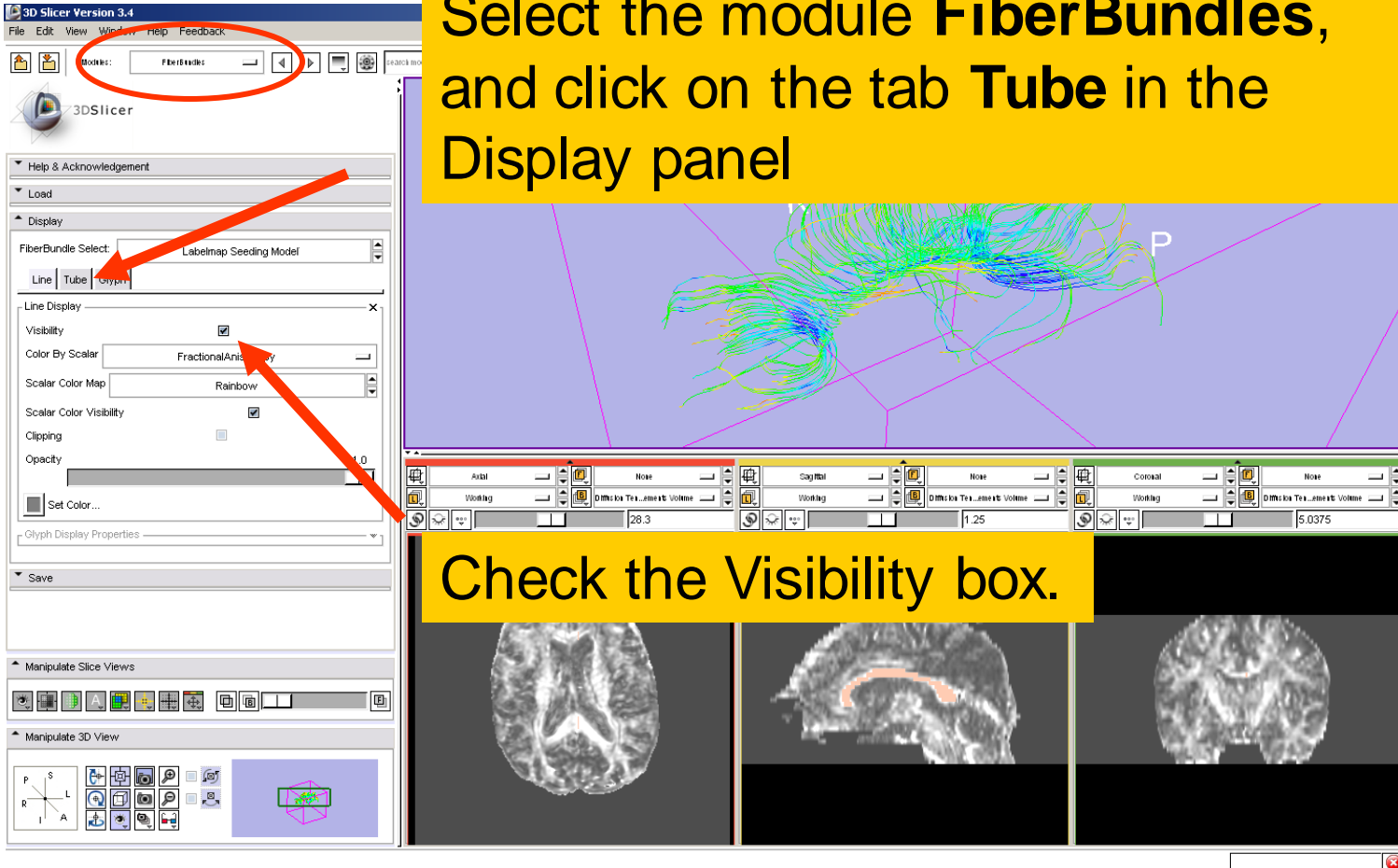
LabelMap Seeding

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

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

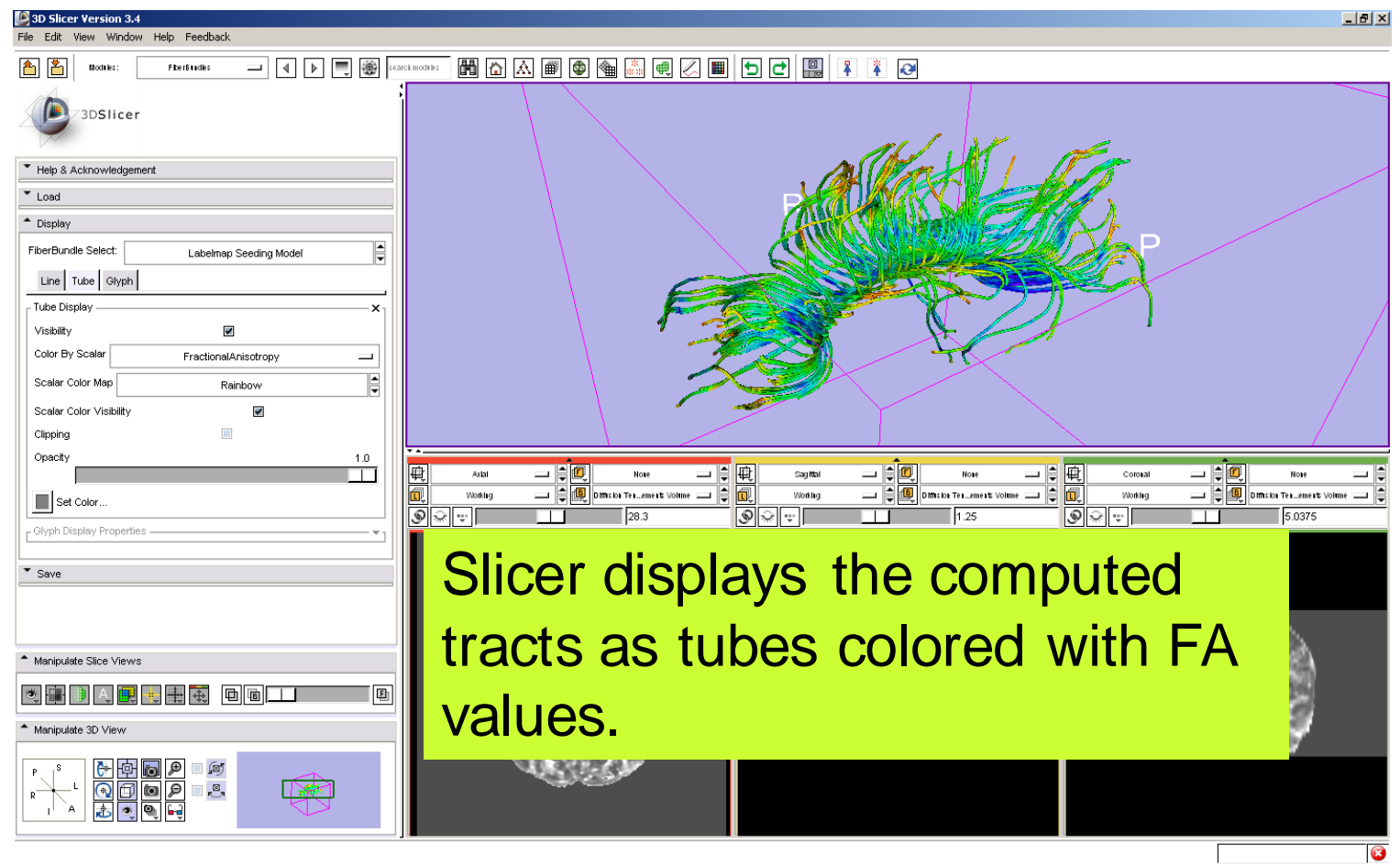


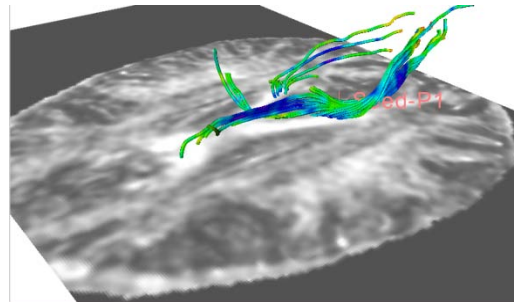
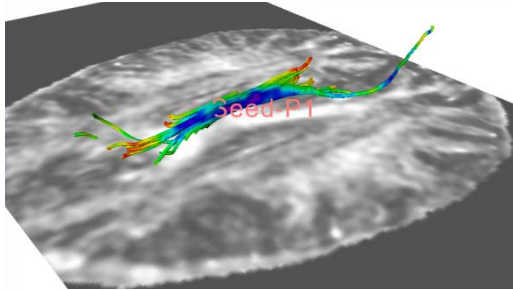
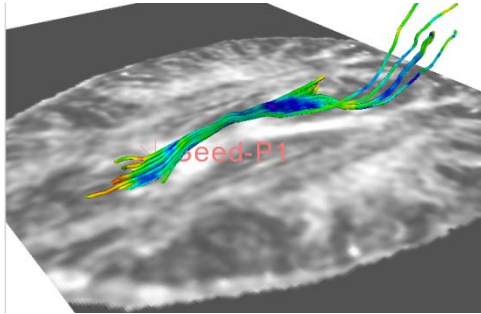
LabelMap Seeding



The screenshot shows the 3D Slicer Version 3.4 interface. The 'Modules' dropdown menu is circled in red and set to 'FiberBundles'. In the 'Display' panel, the 'FiberBundle Select' dropdown is set to 'Labelmap Seeding Model'. The 'Line | Tube | Glyph' tabs are visible, with 'Tube' selected. The 'Line Display' panel has the 'Visibility' checkbox checked. The main 3D view shows a brain with fiber bundles. Below the 3D view are three slice views: Axial, Sagittal, and Coronal. A yellow text box at the top right of the screenshot reads: 'Select the module **FiberBundles**, and click on the tab **Tube** in the Display panel'. A yellow text box at the bottom right of the screenshot reads: 'Check the Visibility box.' Red arrows point from these text boxes to the 'FiberBundles' module and the 'Tube' tab respectively.

LabelMap Seeding



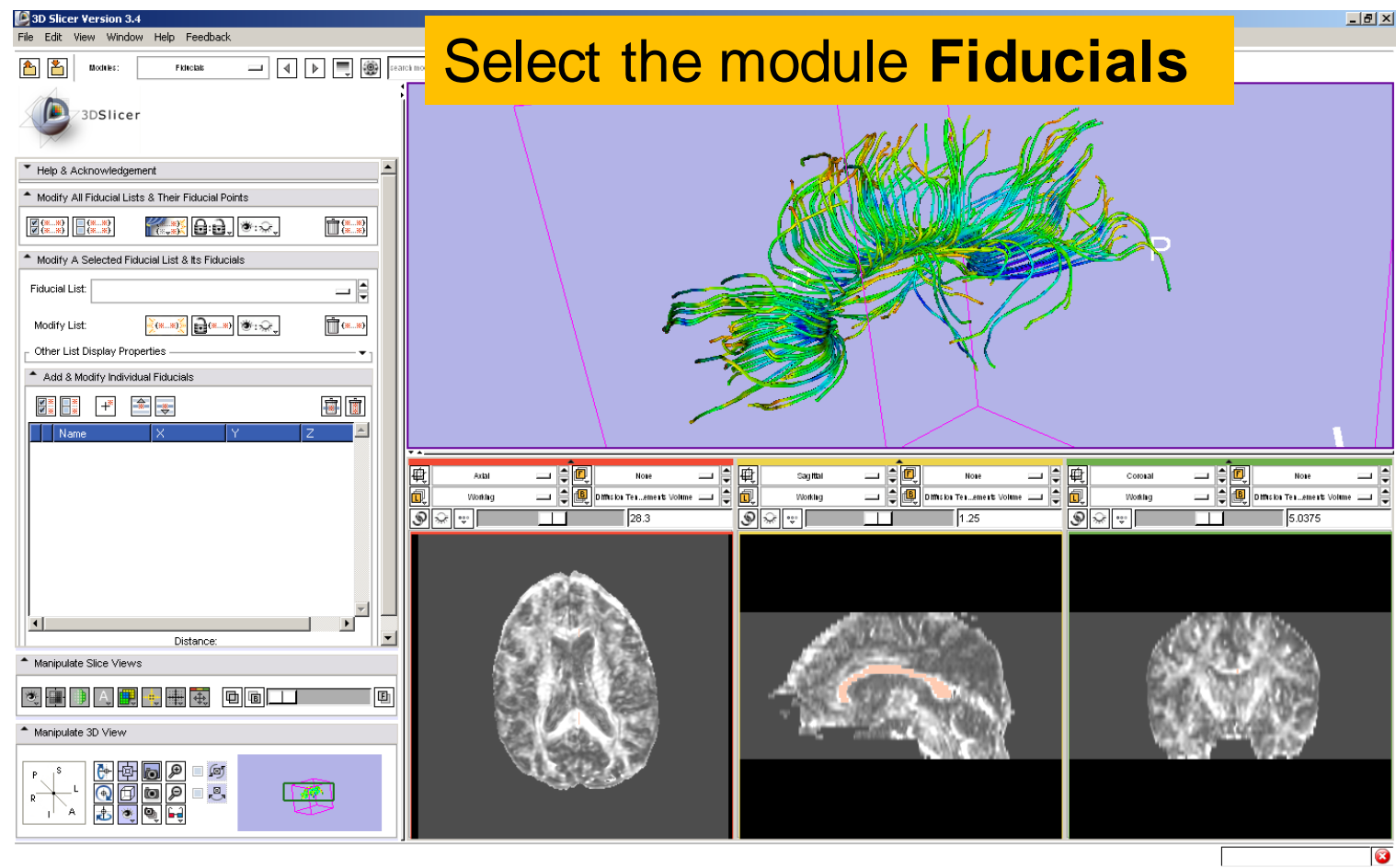


Part 4:

Tractography

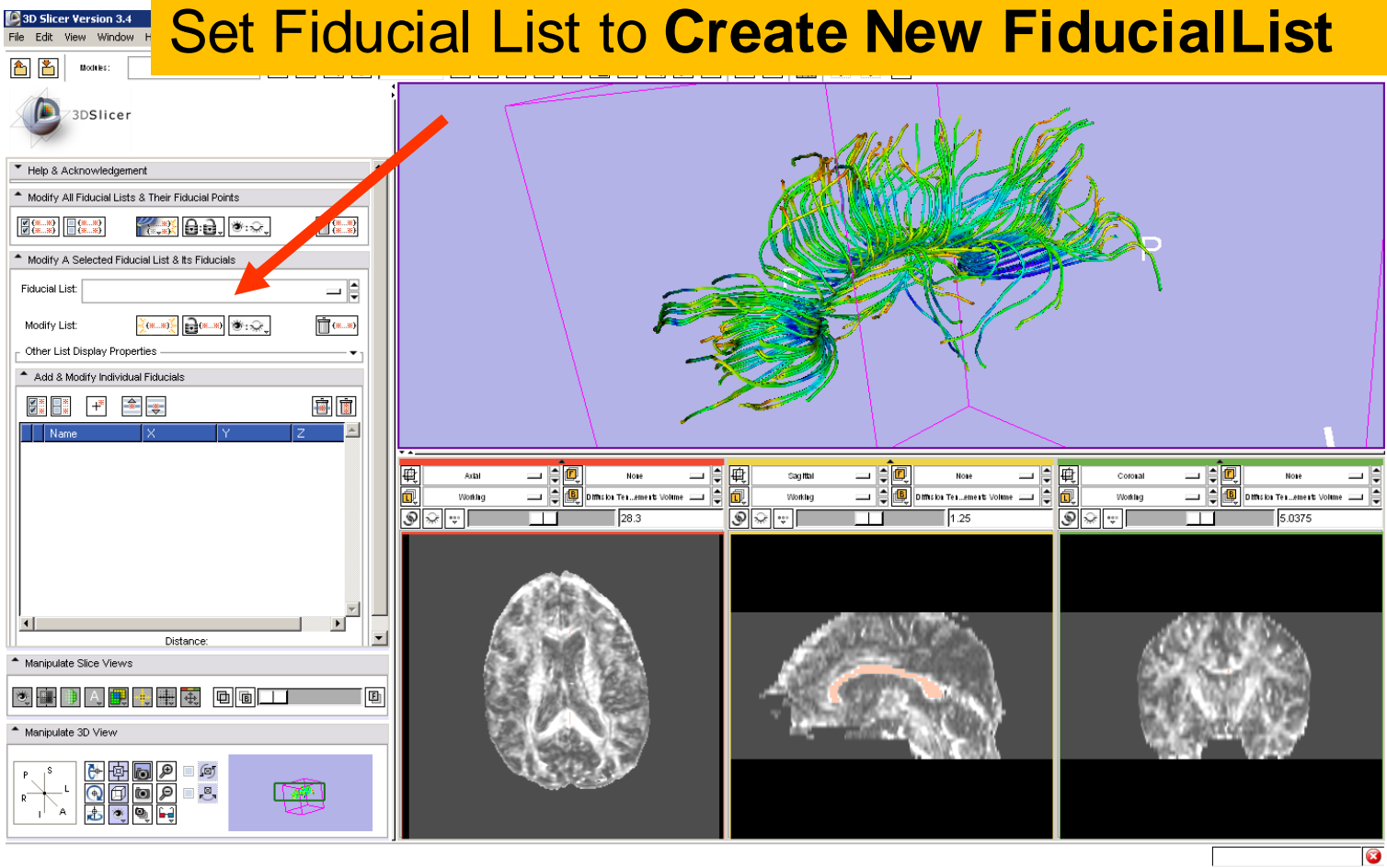
on-the-fly

Fiducial Seeding

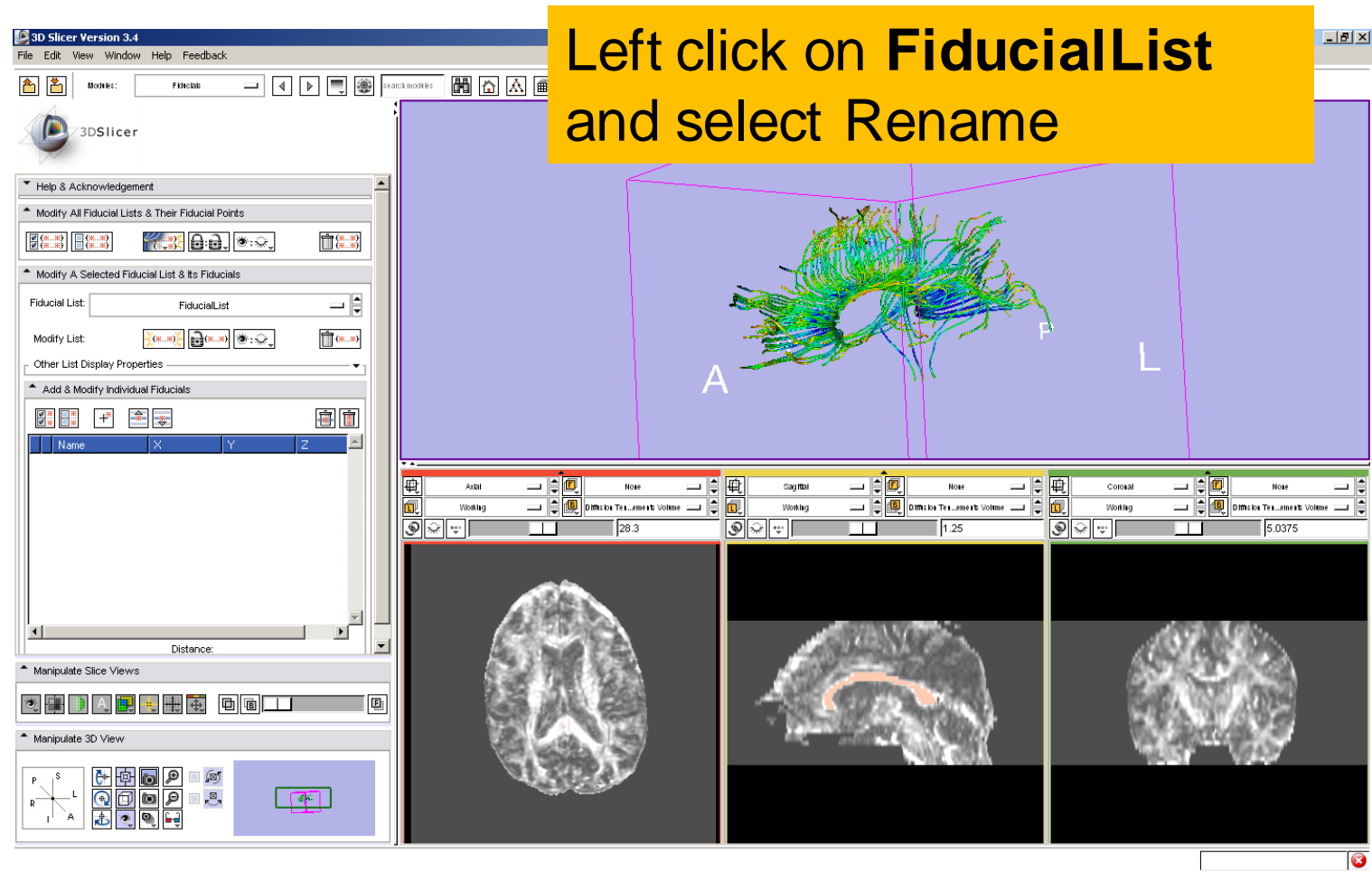


Fiducial Seeding

Set Fiducial List to Create New FiducialList

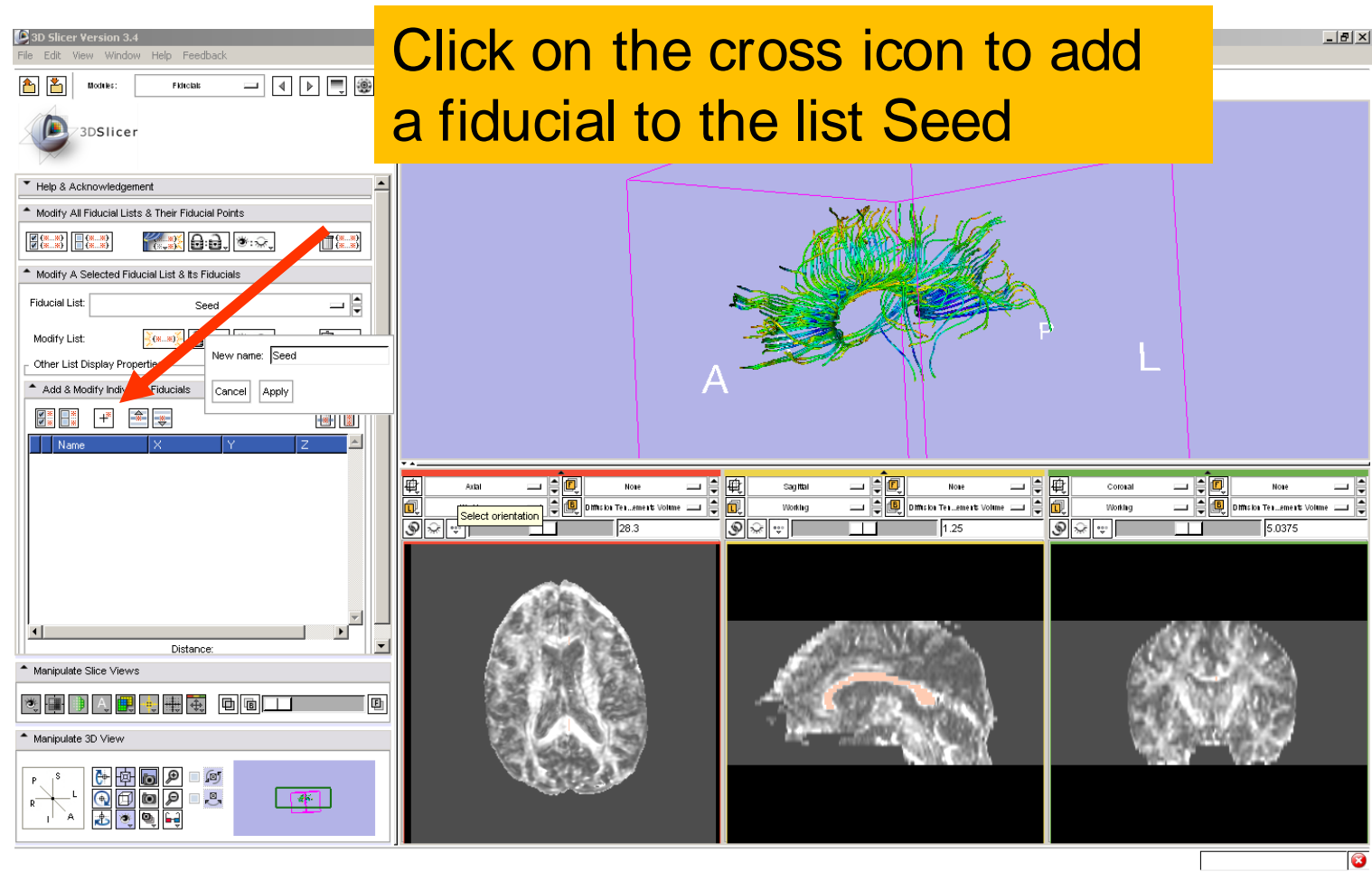


Fiducial Seeding



Fiducial Seeding

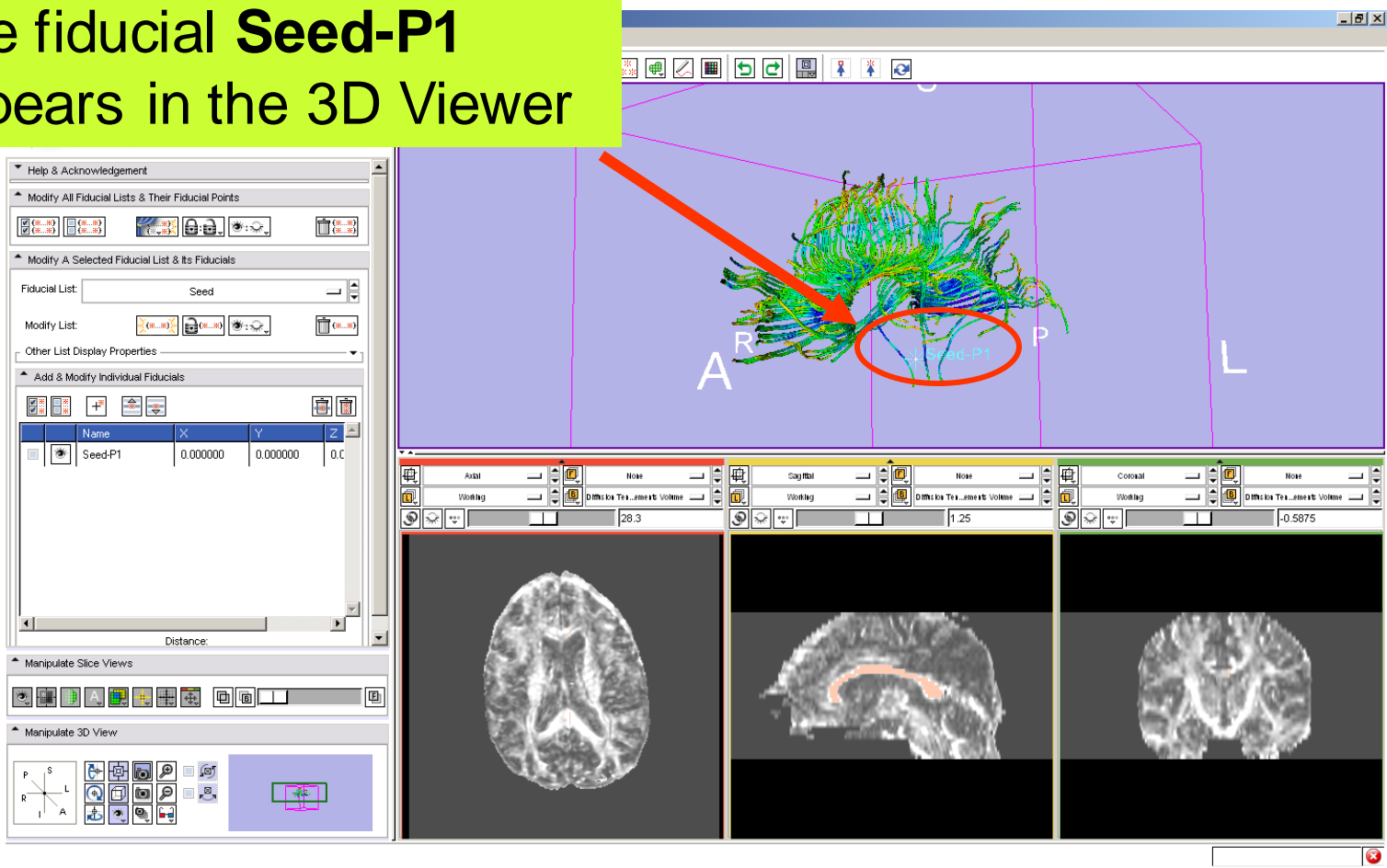
Click on the cross icon to add a fiducial to the list Seed



The screenshot displays the 3D Slicer interface. On the left, the 'Fiducial List' panel is open, showing a table with columns for Name, X, Y, and Z. A red arrow points to the cross icon in the 'Add & Modify Individual Fiducials' section. The main 3D view shows a brain with streamlines and a crosshair. The bottom panel shows three orthogonal slice views: Axial, Sagittal, and Coronal.

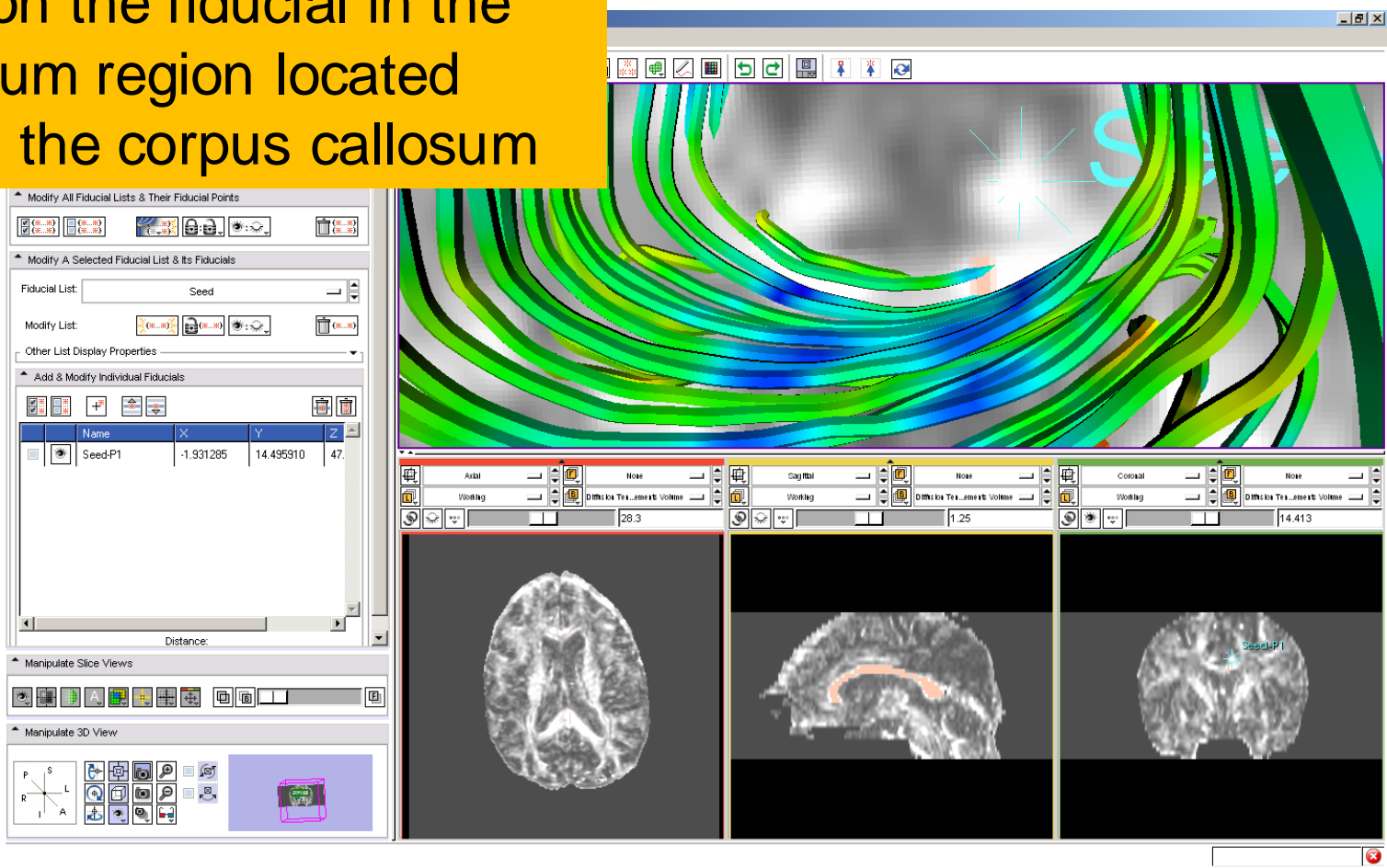
Fiducial Seeding

The fiducial **Seed-P1** appears in the 3D Viewer



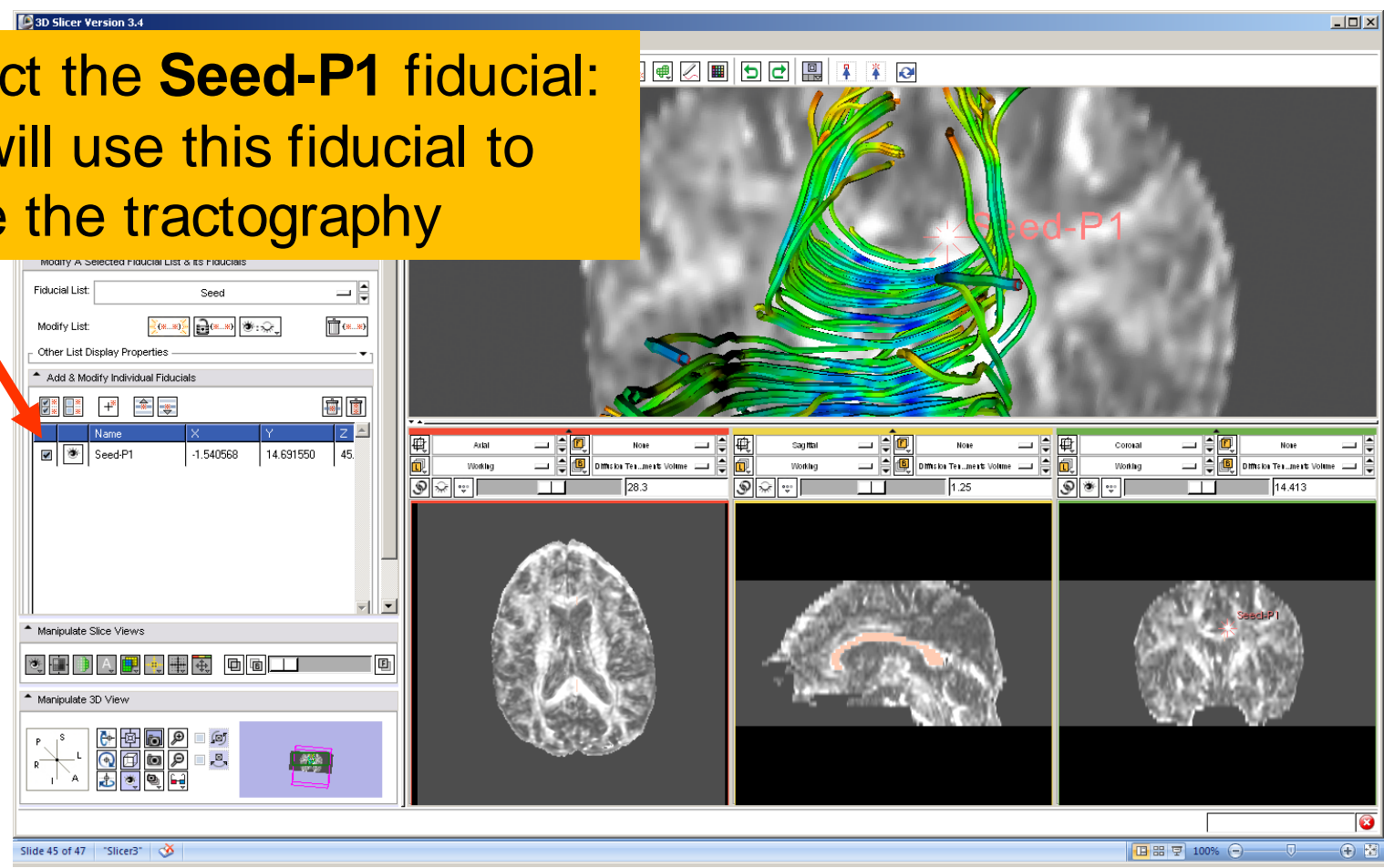
Fiducial Seeding

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



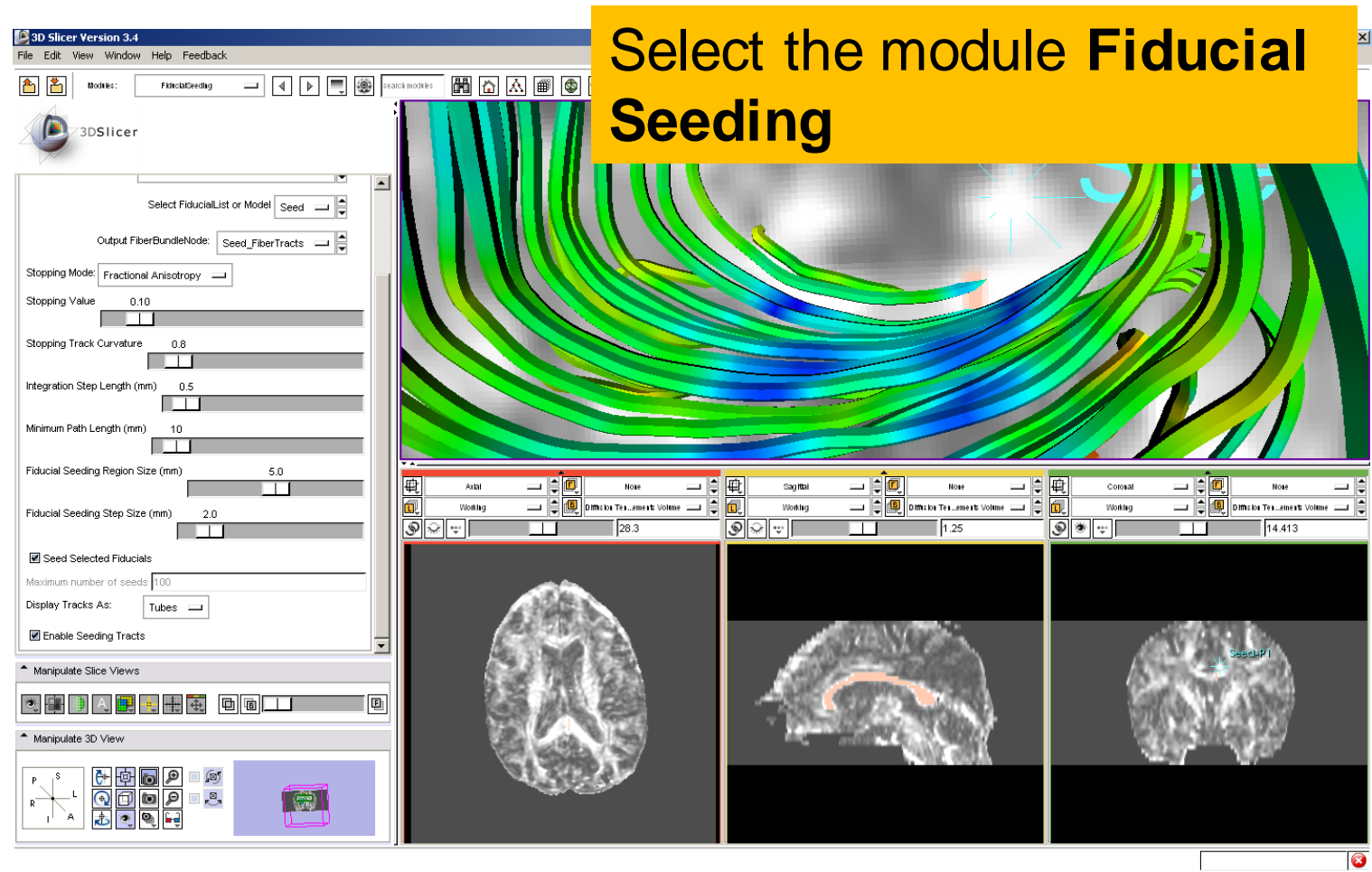
Fiducial Seeding

Select the **Seed-P1** fiducial:
we will use this fiducial to
drive the tractography



Fiducial Seeding

Select the module **Fiducial Seeding**

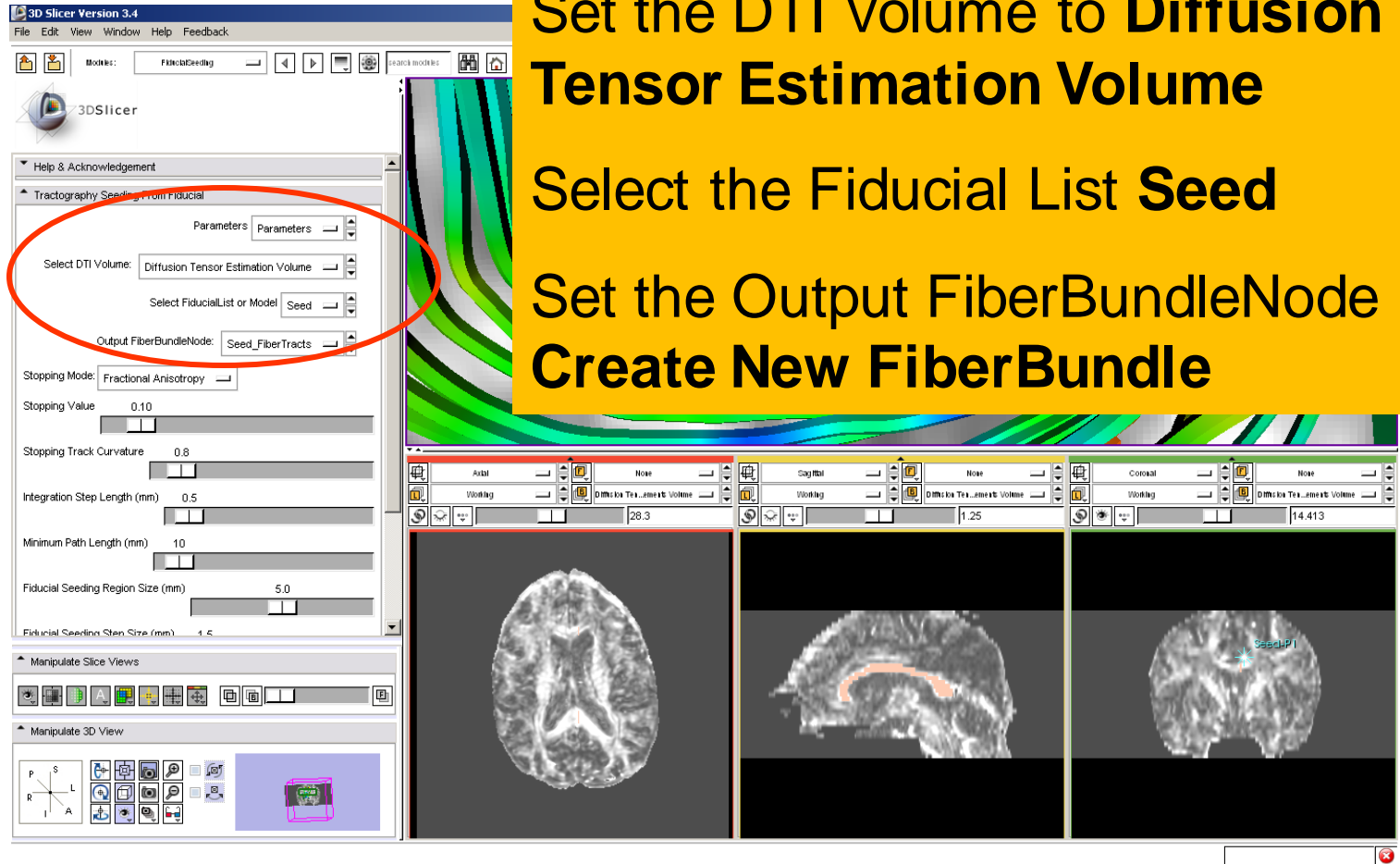


The screenshot displays the 3D Slicer Version 3.4 interface. The 'Fiducial Seeding' module is selected in the top toolbar. The left sidebar shows the module's configuration panel with the following settings:

- Select FiducialList or Model: Seed
- Output FiberBundleNode: Seed_FiberTracts
- Stopping Mode: Fractional Anisotropy
- Stopping Value: 0.10
- Stopping Track Curvature: 0.8
- Integration Step Length (mm): 0.5
- Minimum Path Length (mm): 10
- Fiducial Seeding Region Size (mm): 5.0
- Fiducial Seeding Step Size (mm): 2.0
- Seed Selected Fiducials
- Maximum number of seeds: 100
- Display Tracks As: Tubes
- Enable Seeding Tracks

The main 3D view shows a brain slice with green and blue fiber tracts. Below the 3D view are three smaller windows showing axial, sagittal, and coronal slices of the brain with a red curved line indicating the seeding region. The bottom status bar shows coordinates: 28.3, 1.25, and 14.413.

Fiducial Seeding

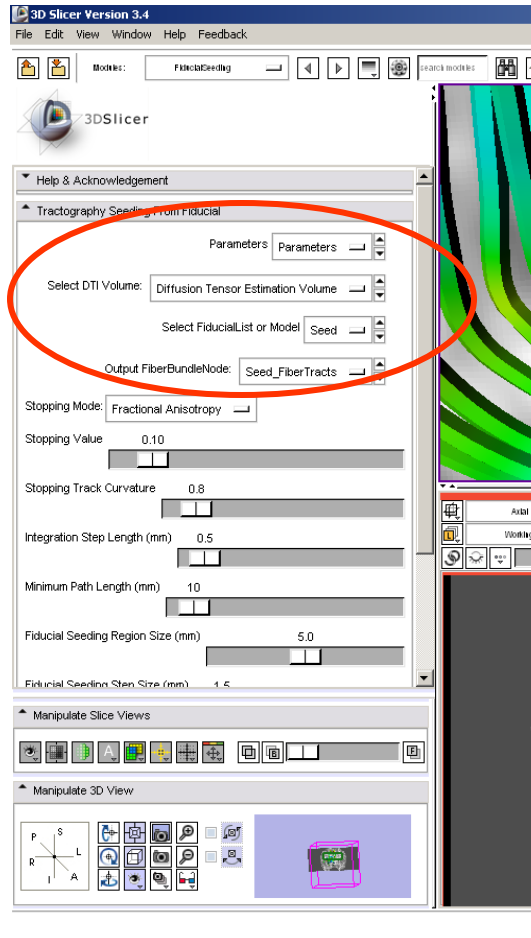


Set the DTI Volume to Diffusion Tensor Estimation Volume

Select the Fiducial List Seed

Set the Output FiberBundleNode to Create New FiberBundle

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

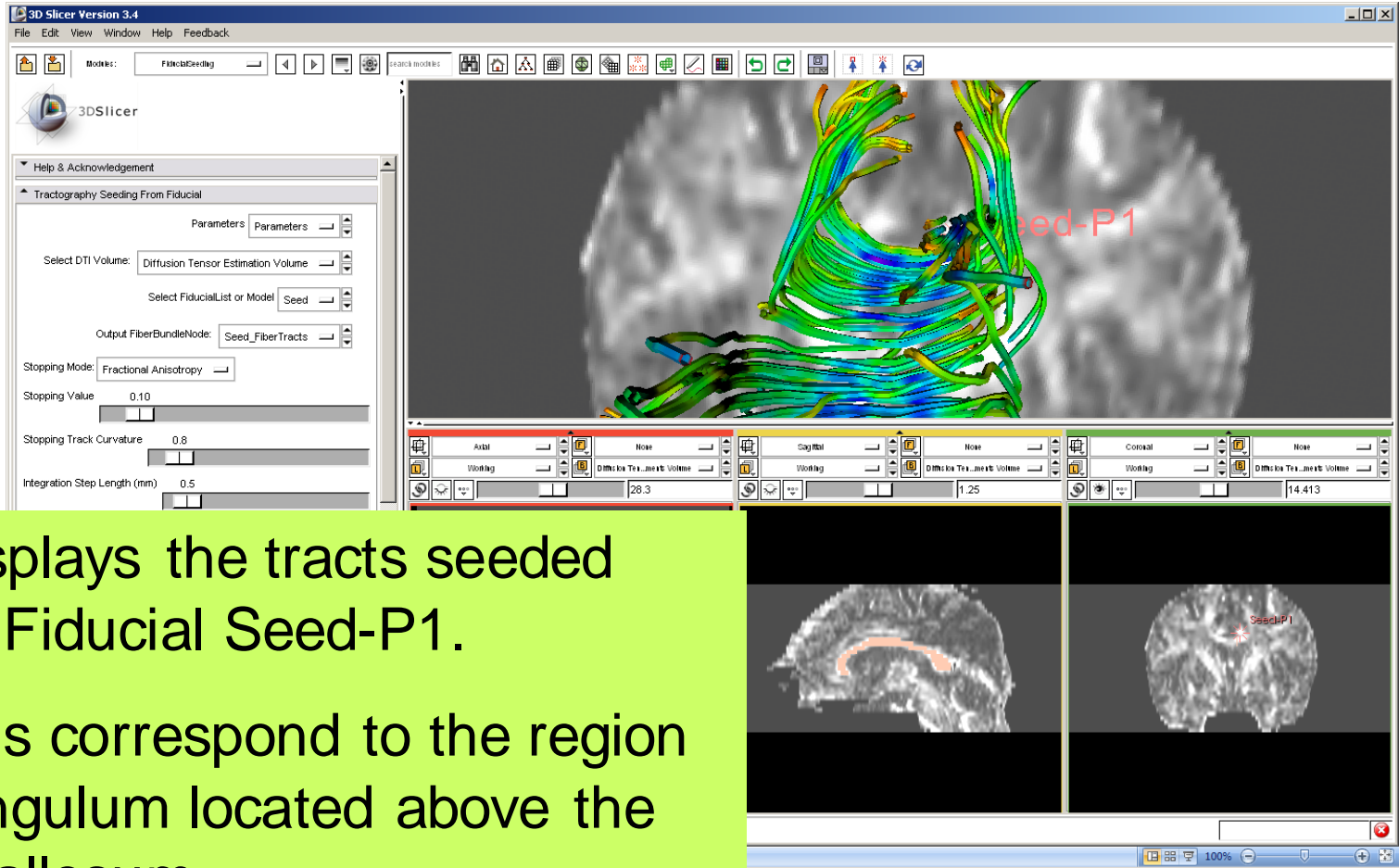
Stopping Track Curvature: 0.8

Step Length: 0.8 mm

Minimum Length: 10 mm

Fiducial Stepping Size: 1.5 mm

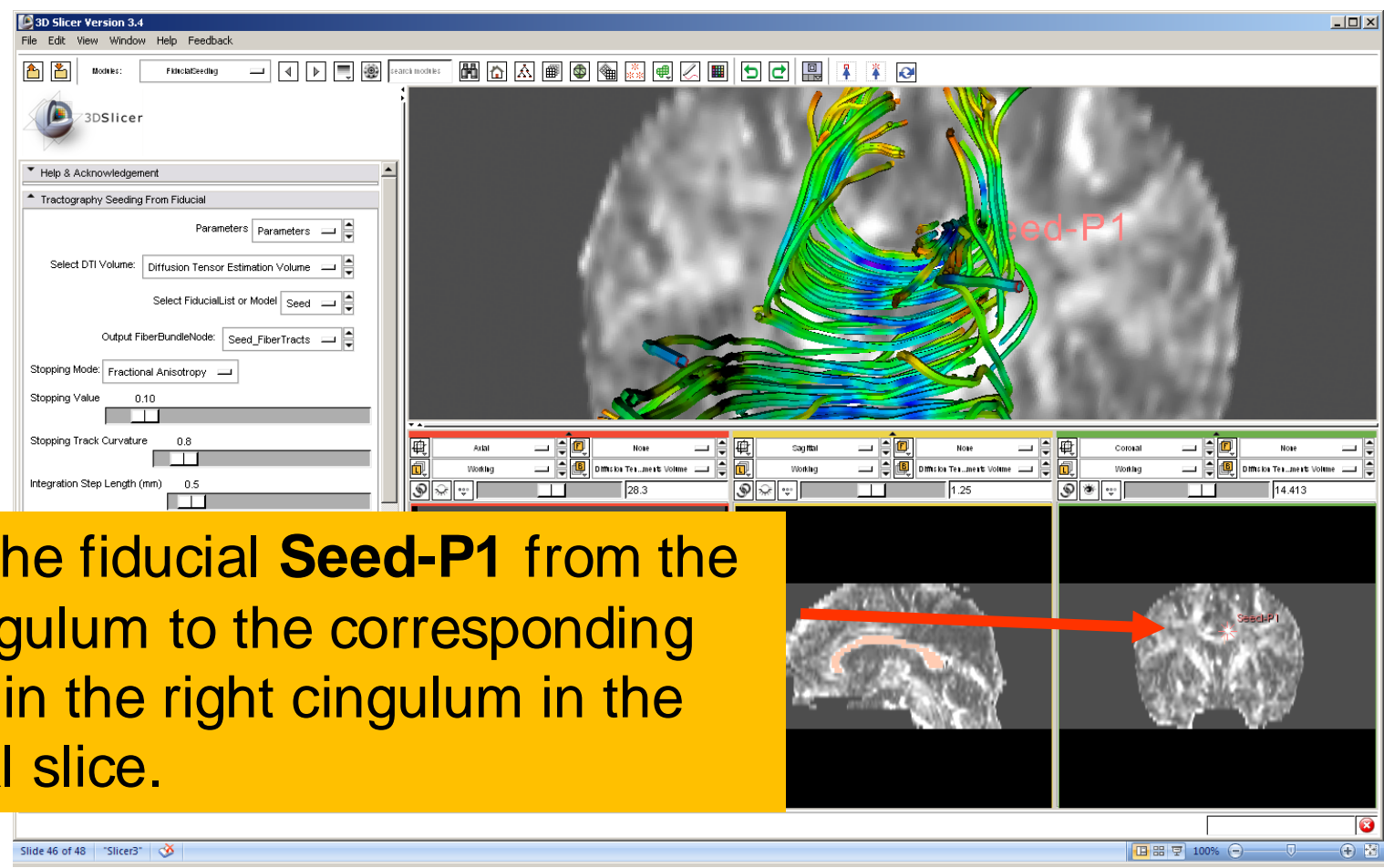
Fiducial Seeding



Slicer displays the tracts seeded from the Fiducial Seed-P1.

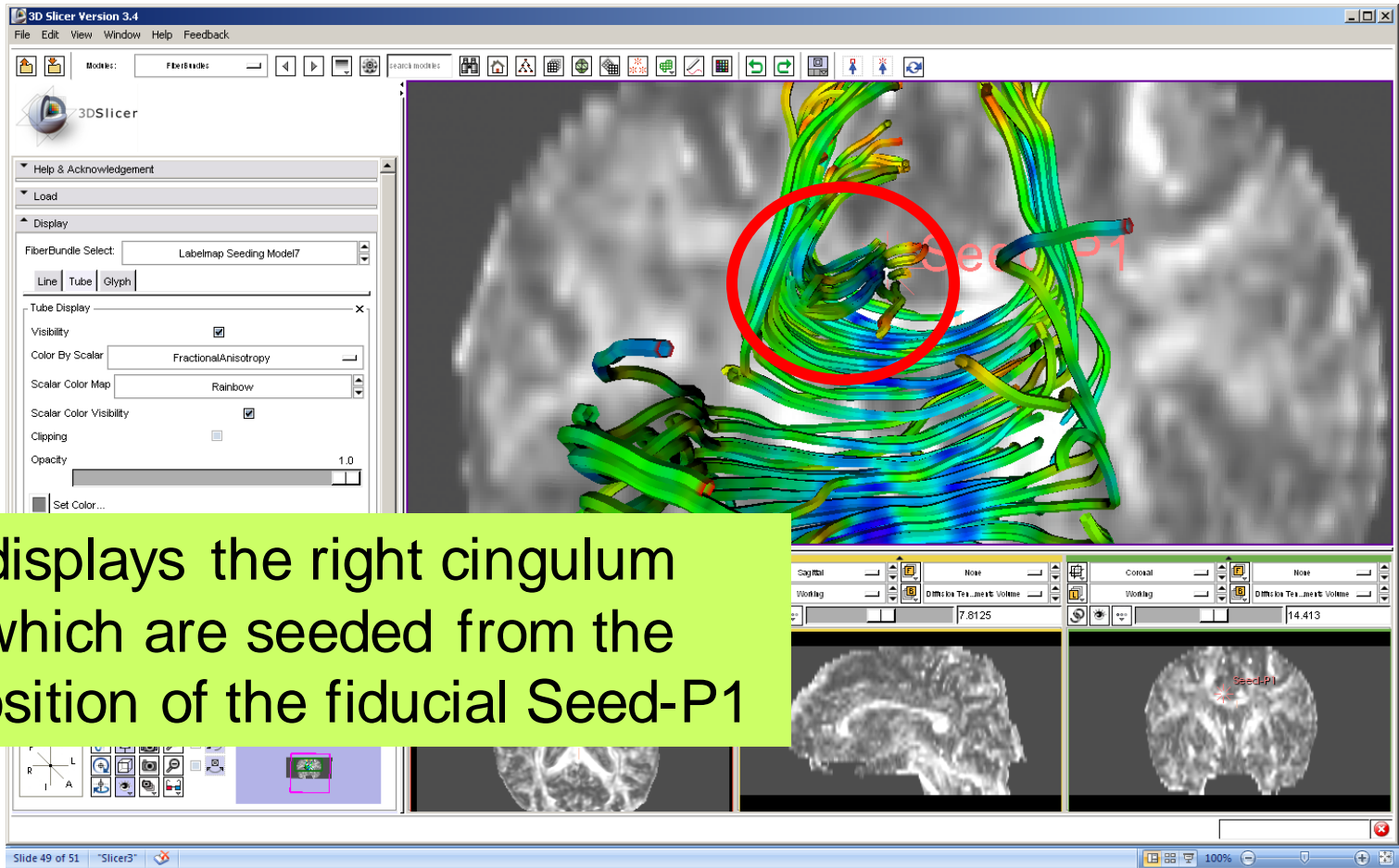
The tracts correspond to the region of the cingulum located above the corpus callosum.

Fiducial Seeding



Move the fiducial **Seed-P1** from the left cingulum to the corresponding region in the right cingulum in the coronal slice.

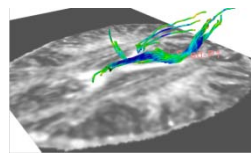
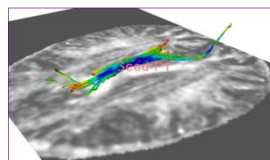
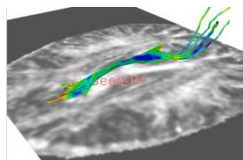
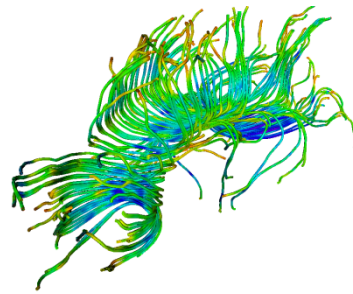
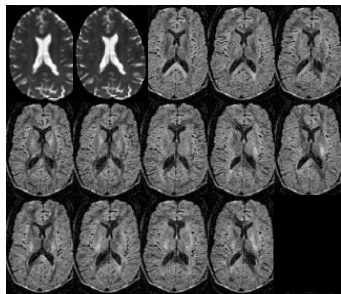
Fiducial Seeding

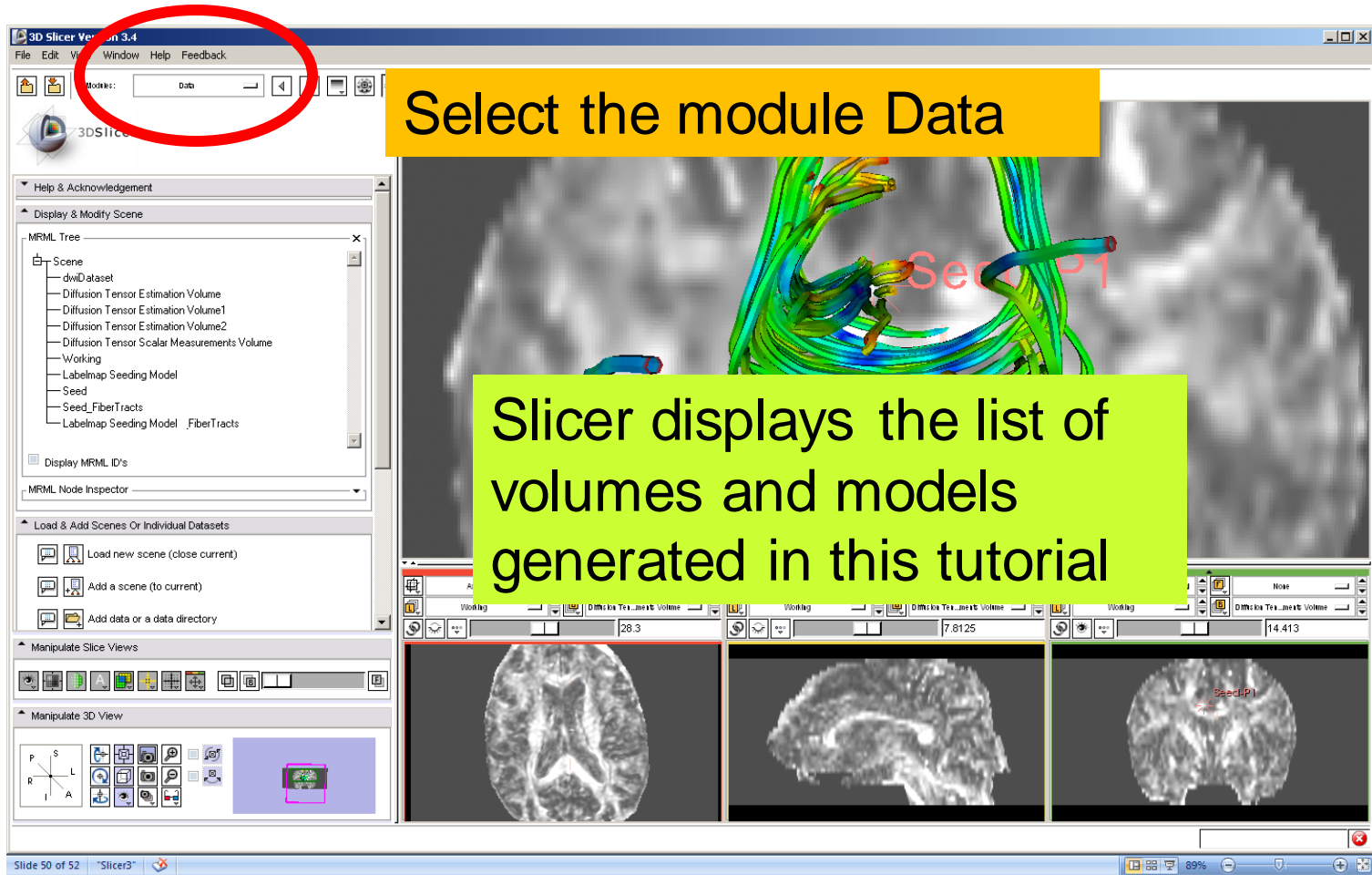


Slicer displays the right cingulum tracts which are seeded from the new position of the fiducial Seed-P1

Part 5:

Saving a DTI Scene



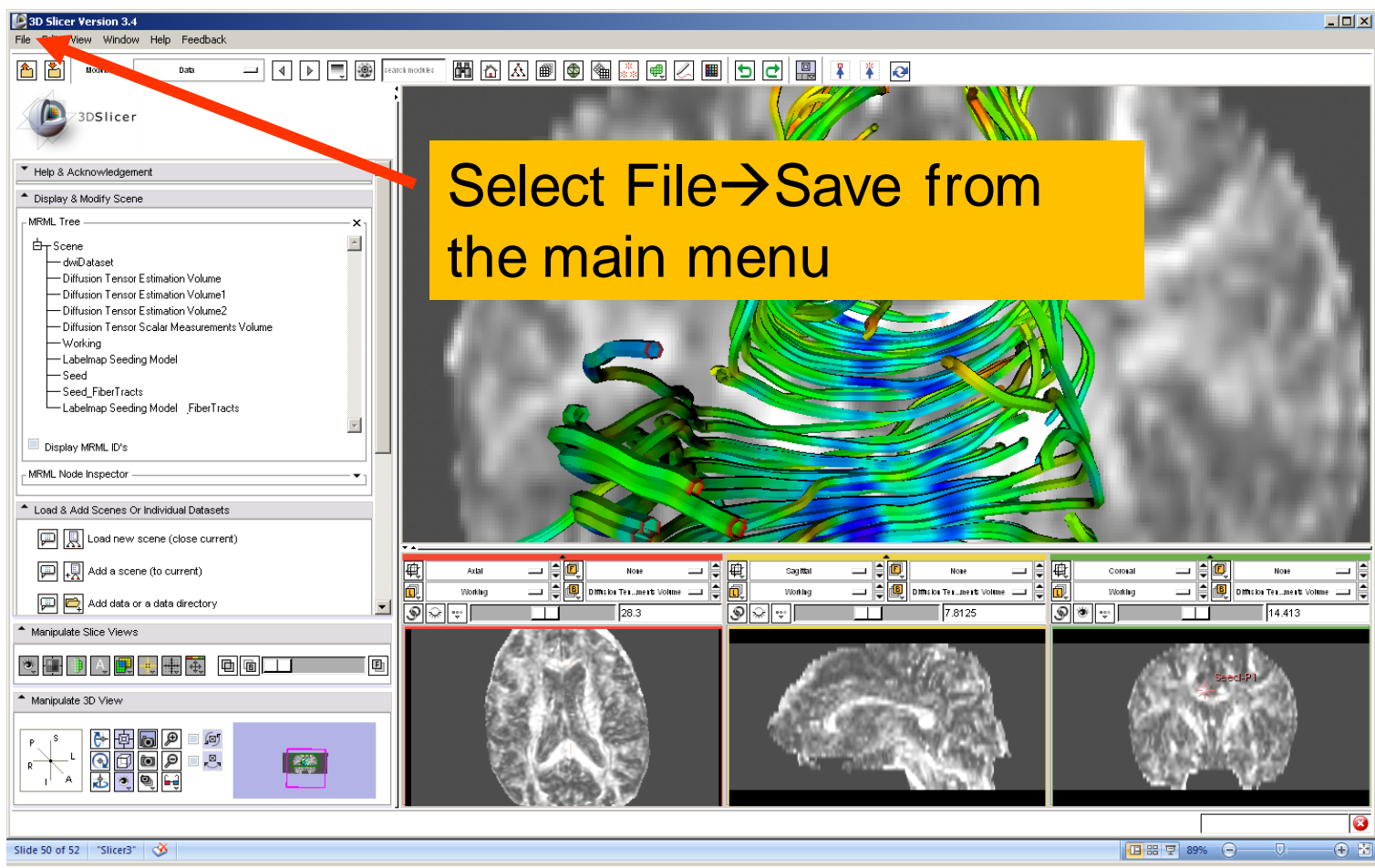


Select the module Data

Slicer displays the list of volumes and models generated in this tutorial

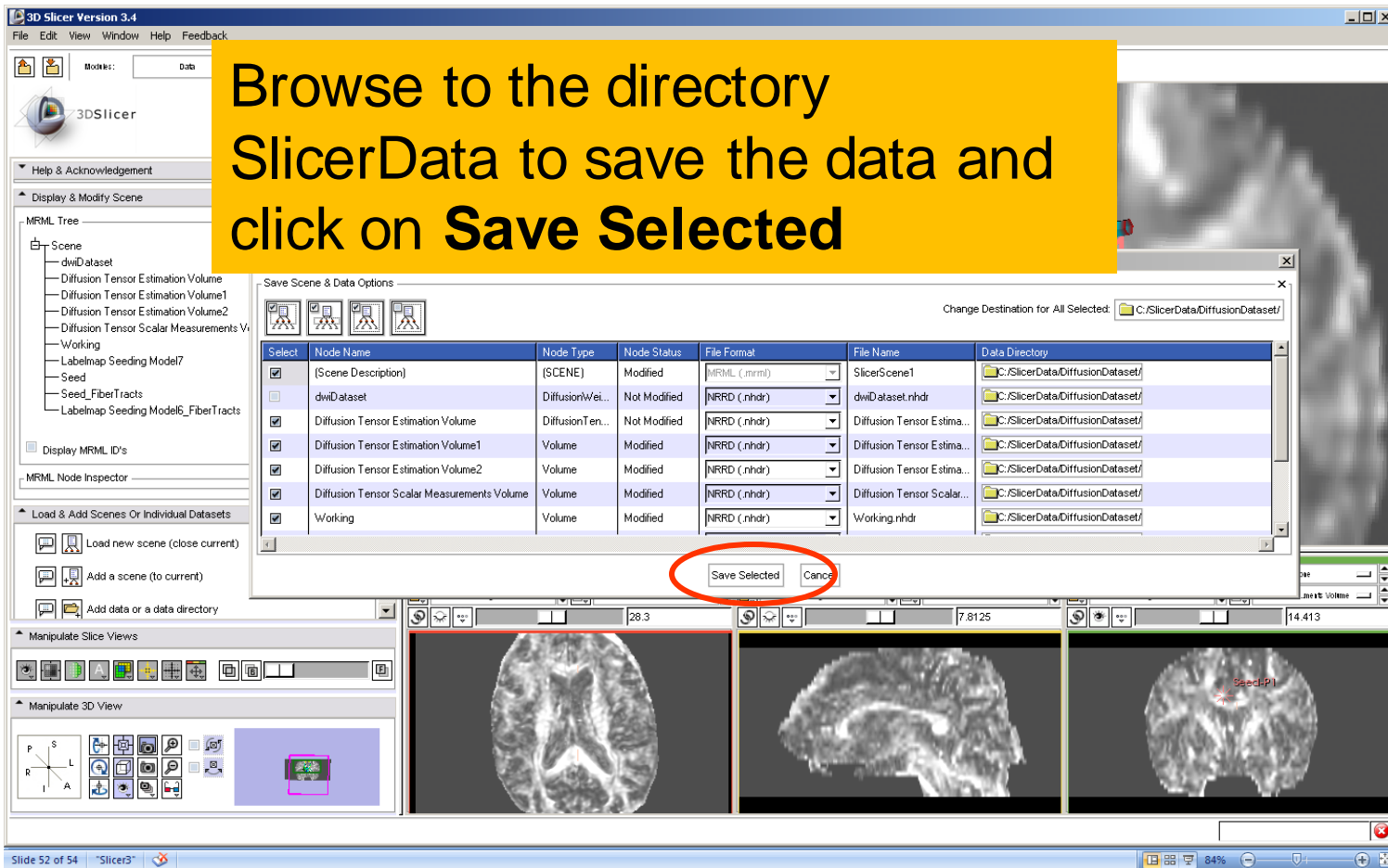
The screenshot shows the 3D Slicer 3.4 interface. The 'Data' module is highlighted with a red circle in the top toolbar. The MRML Tree on the left lists various volumes and models, including 'Diffusion Tensor Estimation Volume' and 'Seed_FiberTracts'. The main 3D view displays a brain slice with colorful fiber tracts and a red 'Seed: P1' label. The bottom panel shows three orthogonal slice views (axial, sagittal, and coronal) of the brain data.

Saving a DTI Scene



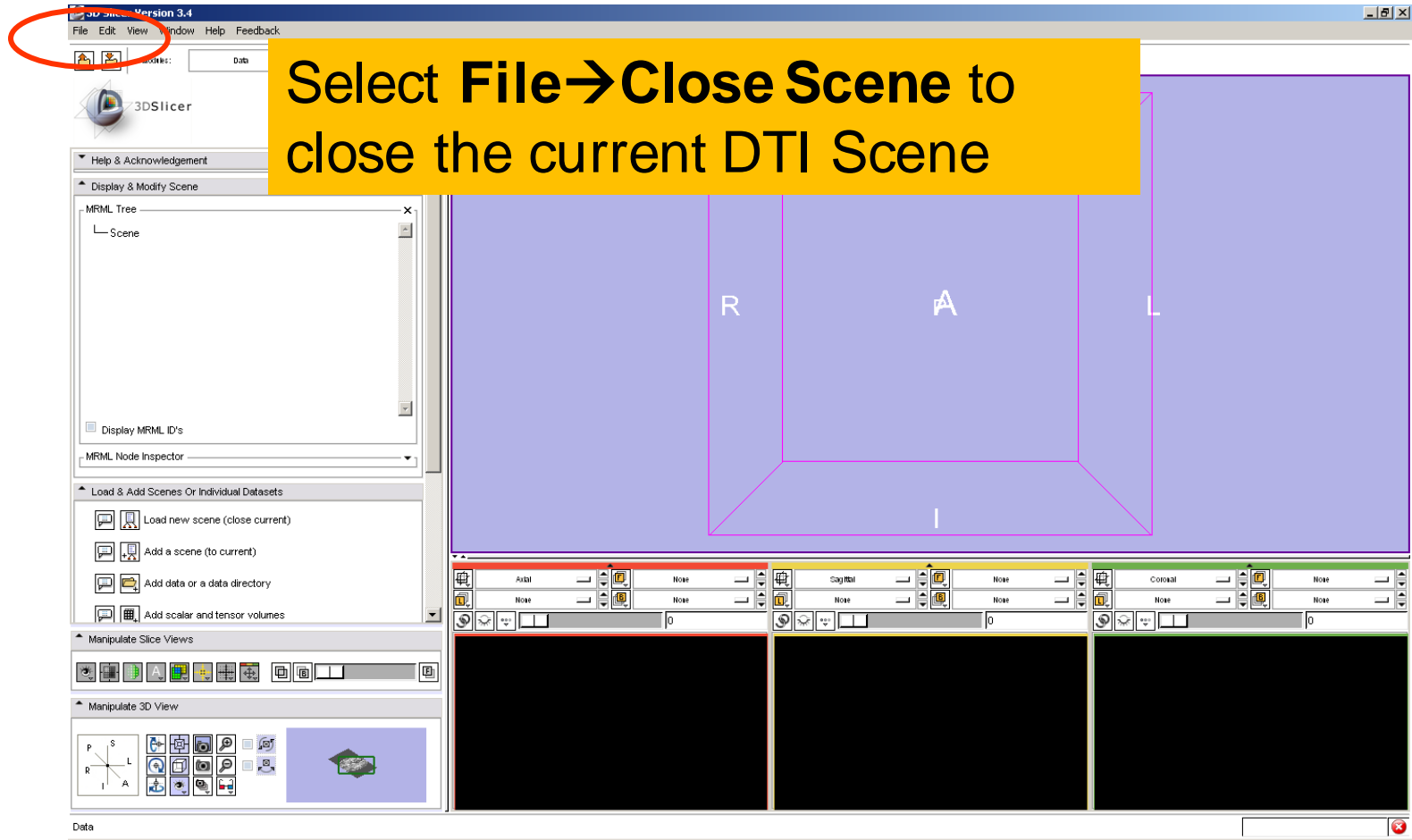
Saving a DTI Scene

Browse to the directory SlicerData to save the data and click on **Save Selected**

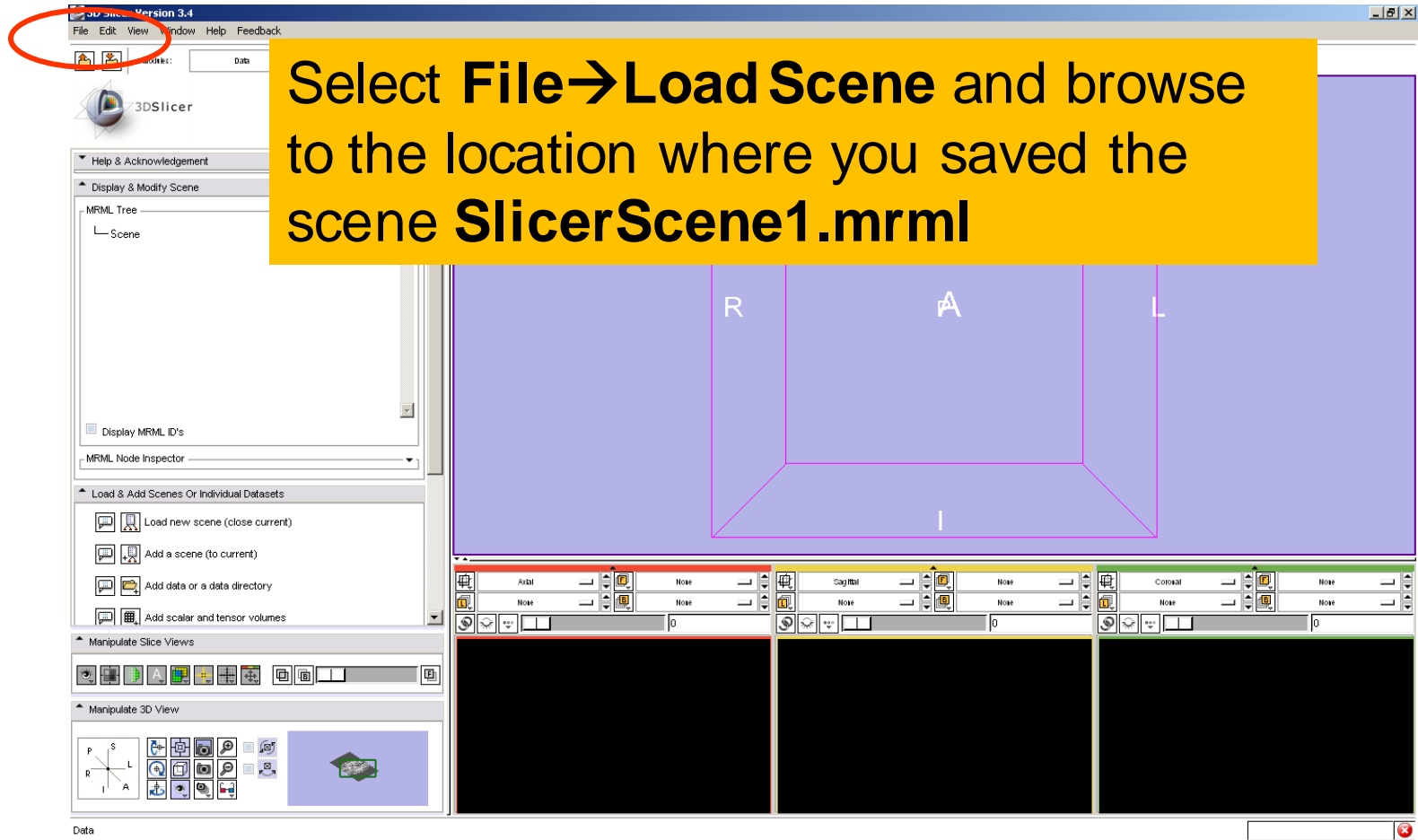


Select	Node Name	Node Type	Node Status	File Format	File Name	Data Directory
<input checked="" type="checkbox"/>	(Scene Description)	(SCENE)	Modified	MRML (.mrm)	SlicerScene1	C:/SlicerData/DiffusionDataset/
<input type="checkbox"/>	dwiDataset	DiffusionWei...	Not Modified	NRRD (.nhdr)	dwiDataset.nhdr	C:/SlicerData/DiffusionDataset/
<input checked="" type="checkbox"/>	Diffusion Tensor Estimation Volume	DiffusionTen...	Not Modified	NRRD (.nhdr)	Diffusion Tensor Estima...	C:/SlicerData/DiffusionDataset/
<input checked="" type="checkbox"/>	Diffusion Tensor Estimation Volume1	Volume	Modified	NRRD (.nhdr)	Diffusion Tensor Estima...	C:/SlicerData/DiffusionDataset/
<input checked="" type="checkbox"/>	Diffusion Tensor Estimation Volume2	Volume	Modified	NRRD (.nhdr)	Diffusion Tensor Estima...	C:/SlicerData/DiffusionDataset/
<input checked="" type="checkbox"/>	Diffusion Tensor Scalar Measurements Volume	Volume	Modified	NRRD (.nhdr)	Diffusion Tensor Scalar...	C:/SlicerData/DiffusionDataset/
<input checked="" type="checkbox"/>	Working	Volume	Modified	NRRD (.nhdr)	Working.nhdr	C:/SlicerData/DiffusionDataset/

Saving a DTI Scene

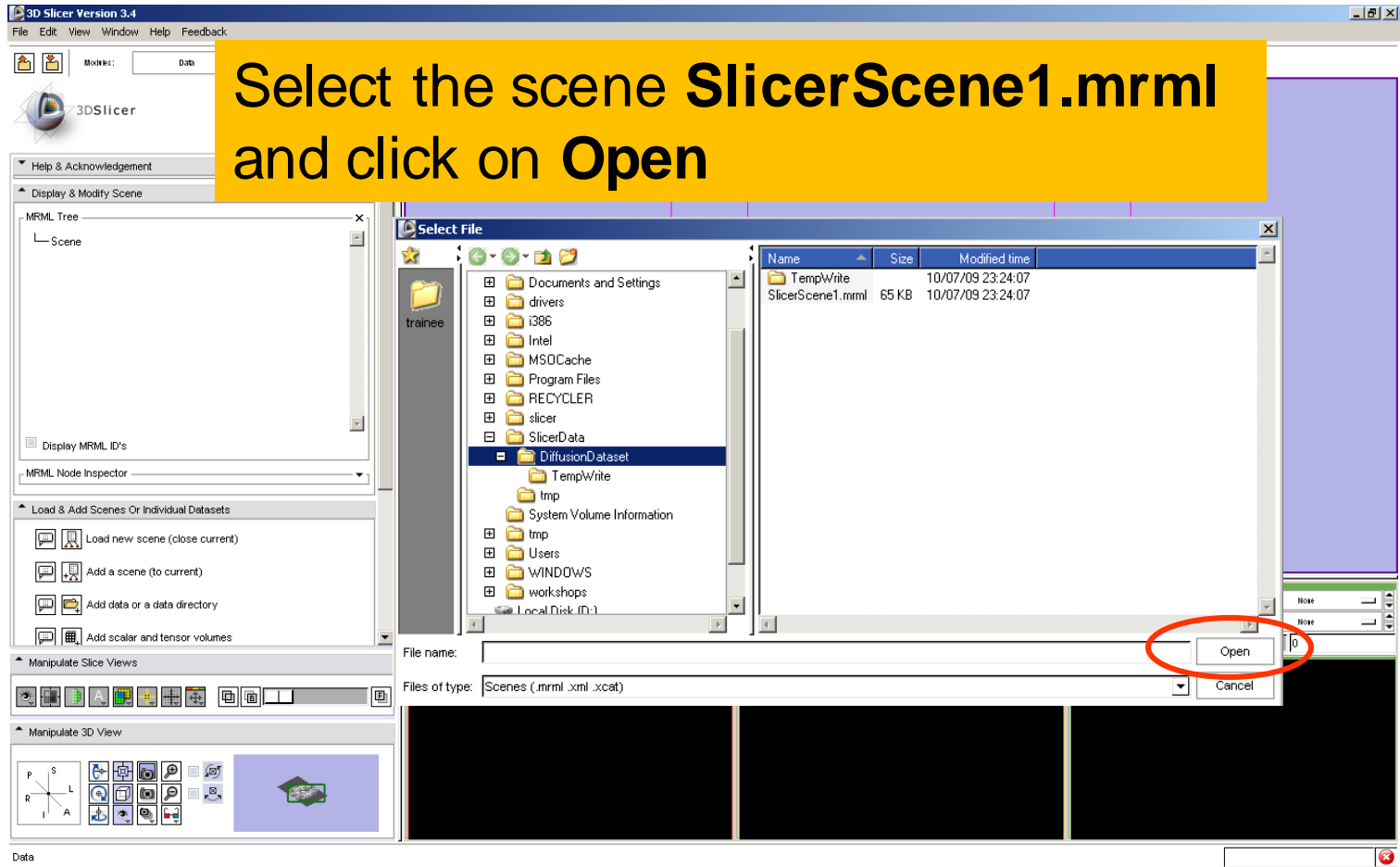


Loading a DTI Scene



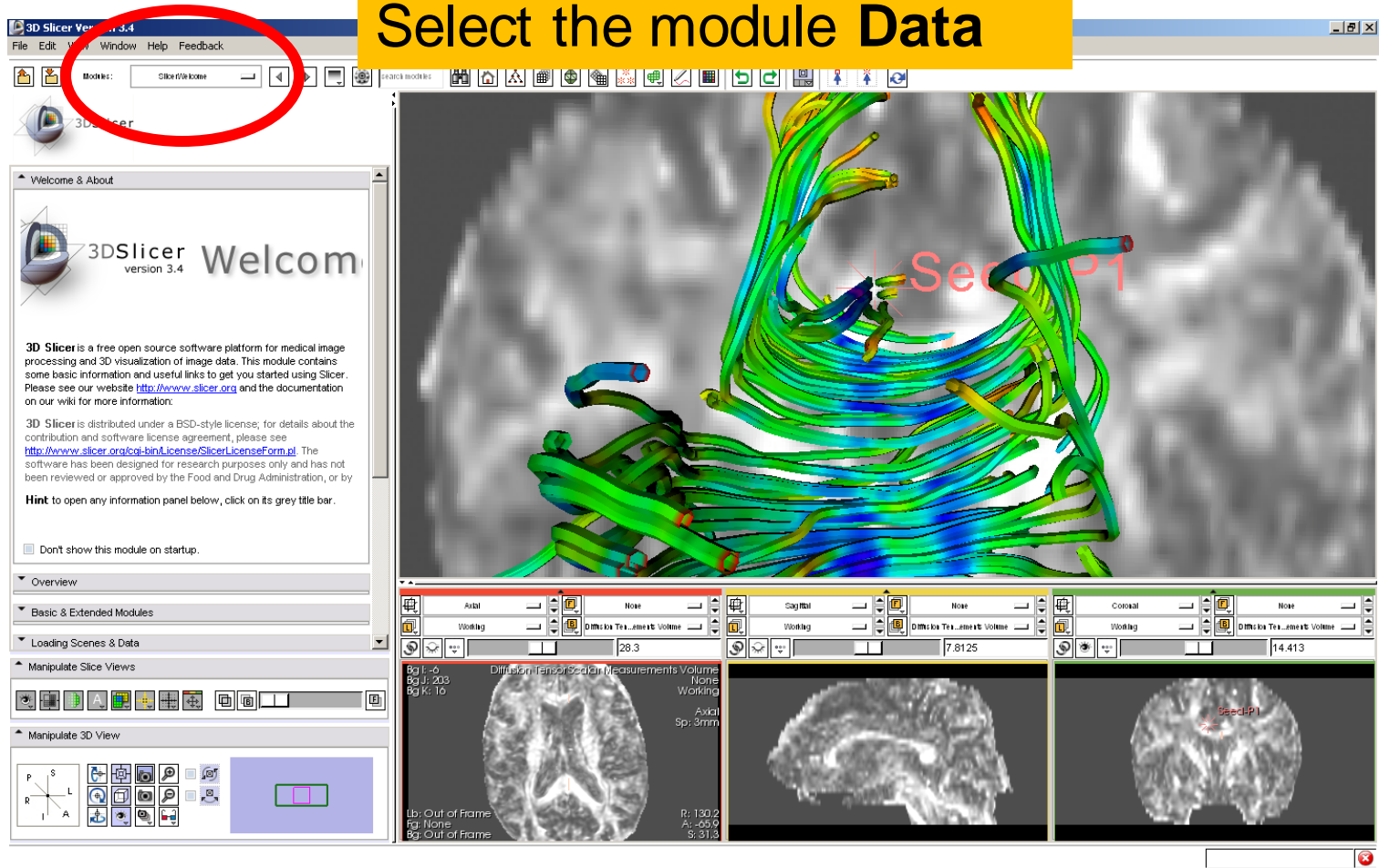
The screenshot shows the 3DSlicer Version 3.4 interface. A red circle highlights the 'File' menu in the top-left corner. A yellow callout box with black text is overlaid on the interface, containing the instruction: 'Select **File** → **Load Scene** and browse to the location where you saved the scene **SlicerScene1.mrml**'. The interface includes a menu bar (File, Edit, View, Window, Help, Feedback), a toolbar, a sidebar with panels like 'Help & Acknowledgement', 'Display & Modify Scene', 'Load & Add Scenes Or Individual Datasets', 'Manipulate Slice Views', and 'Manipulate 3D View', and a main 3D view area with 'R', 'A', 'L', and 'I' orientation markers. Below the 3D view are three slice view panels (Axial, Sagittal, Coronal) and a 'Data' panel at the bottom.

Loading a DTI Scene

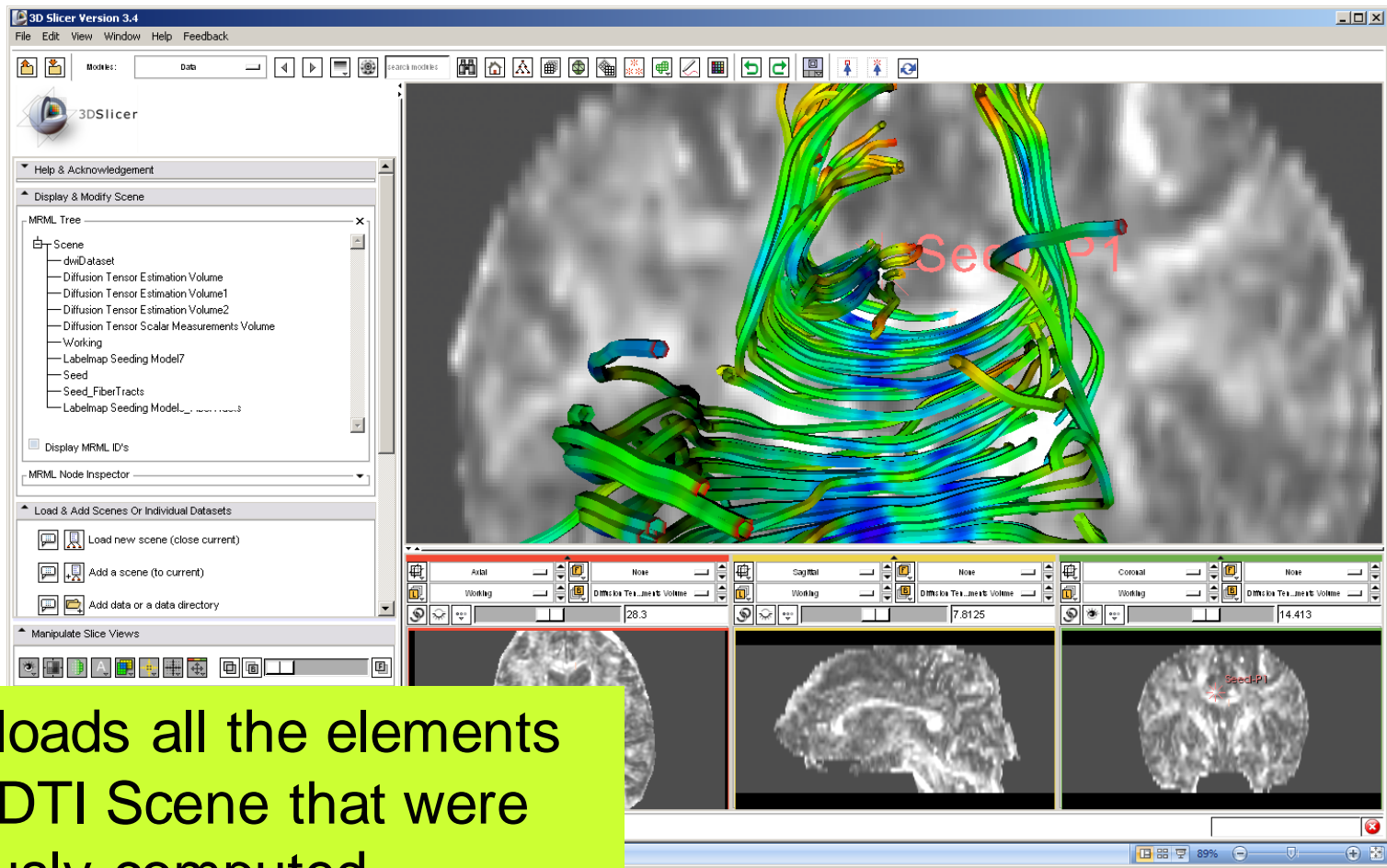


Loading a DTI Scene

Select the module **Data**

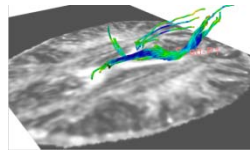
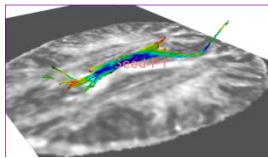
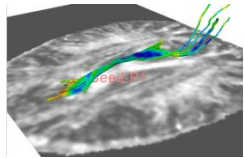
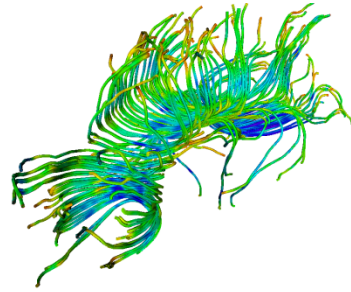
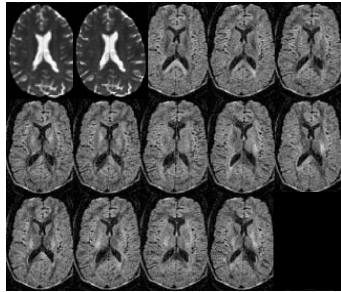


Loading a DTI Scene



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 more tutorials and teaching events, please visit

spujol@bwh.harvard.edu

www.slicer.org

www.na-mic.org/Wiki/index.php/Events



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