



NA-MIC

National Alliance for Medical Image Computing

<http://na-mic.org>

Diffusion Tensor Imaging tutorial

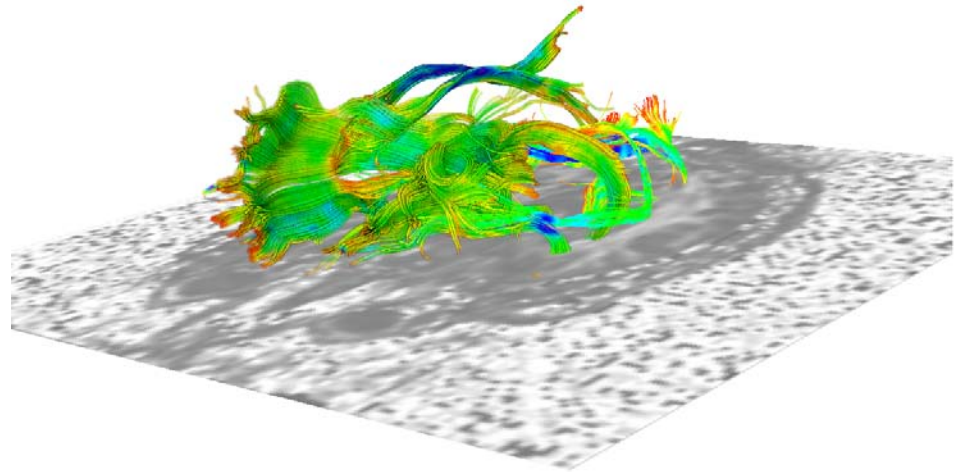


Sonia Pujol, PhD
Surgical Planning Laboratory
Harvard University



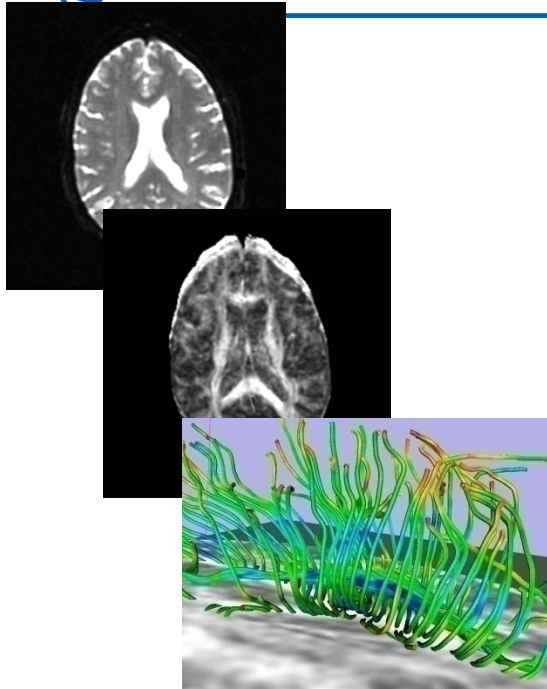
DTI tutorial

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





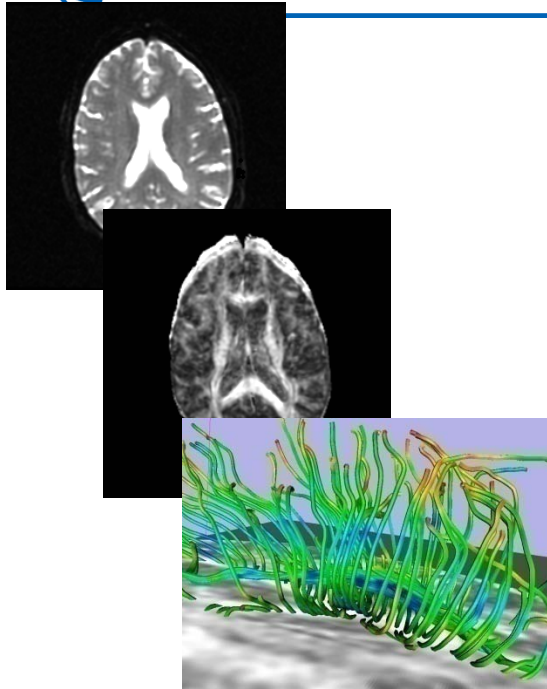
Outline



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



Outline



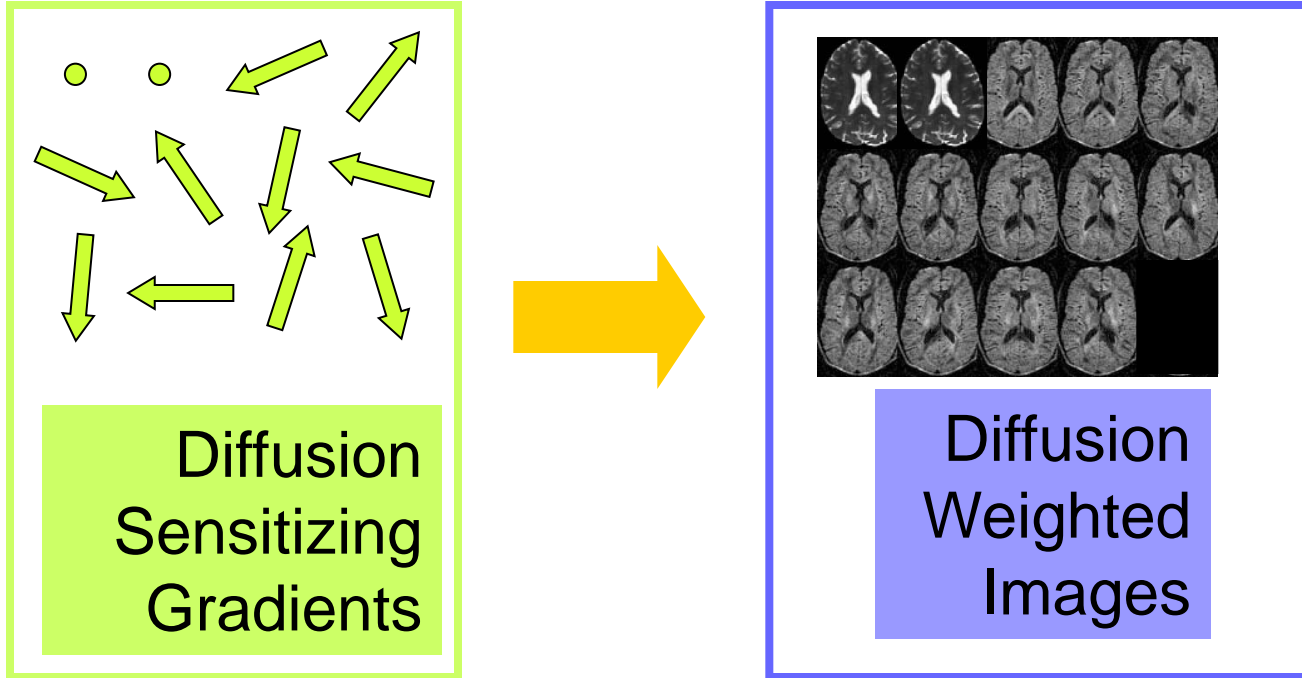
The processing pipeline uses **9 image analysis modules** of Slicer3.4

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



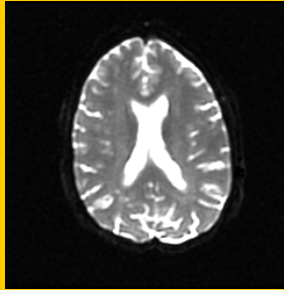
Tutorial Dataset

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

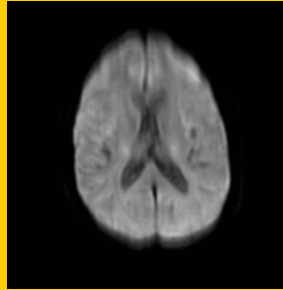




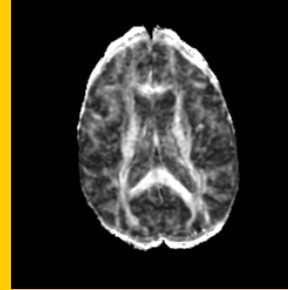
DTI Processing Pipeline



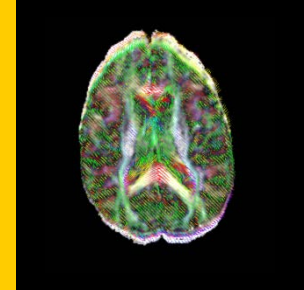
DWI
Acquisition



Tensor
Calculation



Scalar
Maps



3D
Visualization



Start Slicer3

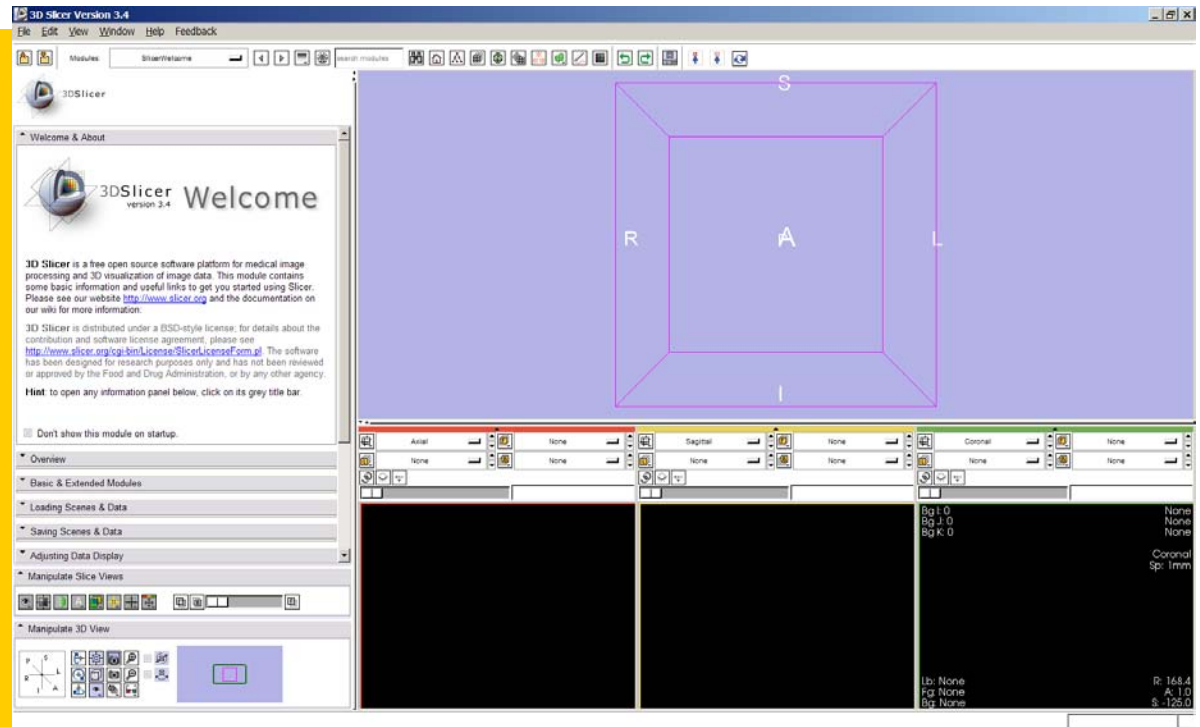
Linux/Mac users
Launch the Slicer3
executable located in
the Slicer3.4 directory

Windows users

Select

Start → All Programs

→ Slicer3 3.4 2009-05-21 → Slicer3

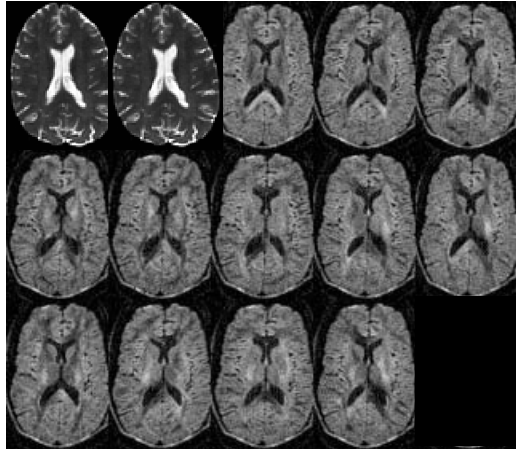




Slicer Welcome

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

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



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

Part 1:

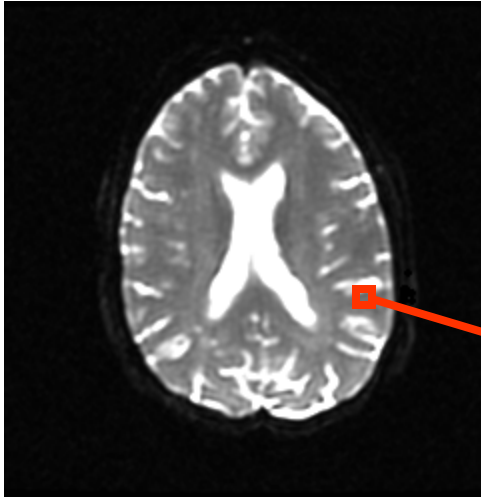
Diffusion data loading and tensor estimation



Diffusion Tensor

Stejskal-Tanner

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



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



Loading the DWI volume

3D Slicer Version 3.4

File Edit View Window Help Feedback

Modules: SlicerWelcome

3DSlicer

Welcome & About

3DSlicer version 3.4 Welcome

3D Slicer is a free open source software platform for medical image processing and 3D visualization of image data. This module contains some basic information and useful links to get you started using Slicer. Please see our website <http://www.slicer.org> and the documentation on our wiki for more information.

3D Slicer is distributed under a BSD-style license; for details about the contribution and software license agreement, please see http://www.slicer.org/cgi-bin/license/Slicer_licenseForm.pl. The software has been designed for research purposes only and has not been reviewed or approved by the Food and Drug Administration, or by any other agency.

Hint: to open any information panel below, click on its grey title bar.

Don't show this module on startup.

Overview

Basic & Extended Modules

Loading Scenes & Data

Saving Scenes & Data

Adjusting Data Display

Manipulate Slice Views

Manipulate 3D View

Axial None None None

Sagittal None None None

Coronal None None None

Bg I: 0 None
Bg J: 0 None
Bg K: 0 None

Coronal Sp: 1mm

R: 168.4
A: 1.0
Fg: None
Bg: None
S: -125.0



Loading the DWI volume

The screenshot shows the 3D Slicer interface with the 'Add Volume' dialog box open. The file list shows 'dwiDataset.nhdr' selected. The 'Volume Options' section is visible, and the 'Apply' button is circled in red. A red arrow points to the 'Volume Options' section.

Name	Size	0
dwiDataset.nhdr	2 KB	0
dwiDataset.raw.gz	31,903 KB	0

Description	Value
-------------	-------

Path: C:\SlicerData\DiffusionDataset\dwiDataset.nhdr

Volume Options: Centered Ignore File Orientation Label Map Single File Name: dwiDataset

Recent Volumes: -

Apply Cancel

Bg I: 0 None
Bg J: 0 None
Bg K: 0 None
Coronal Sp: 1mm

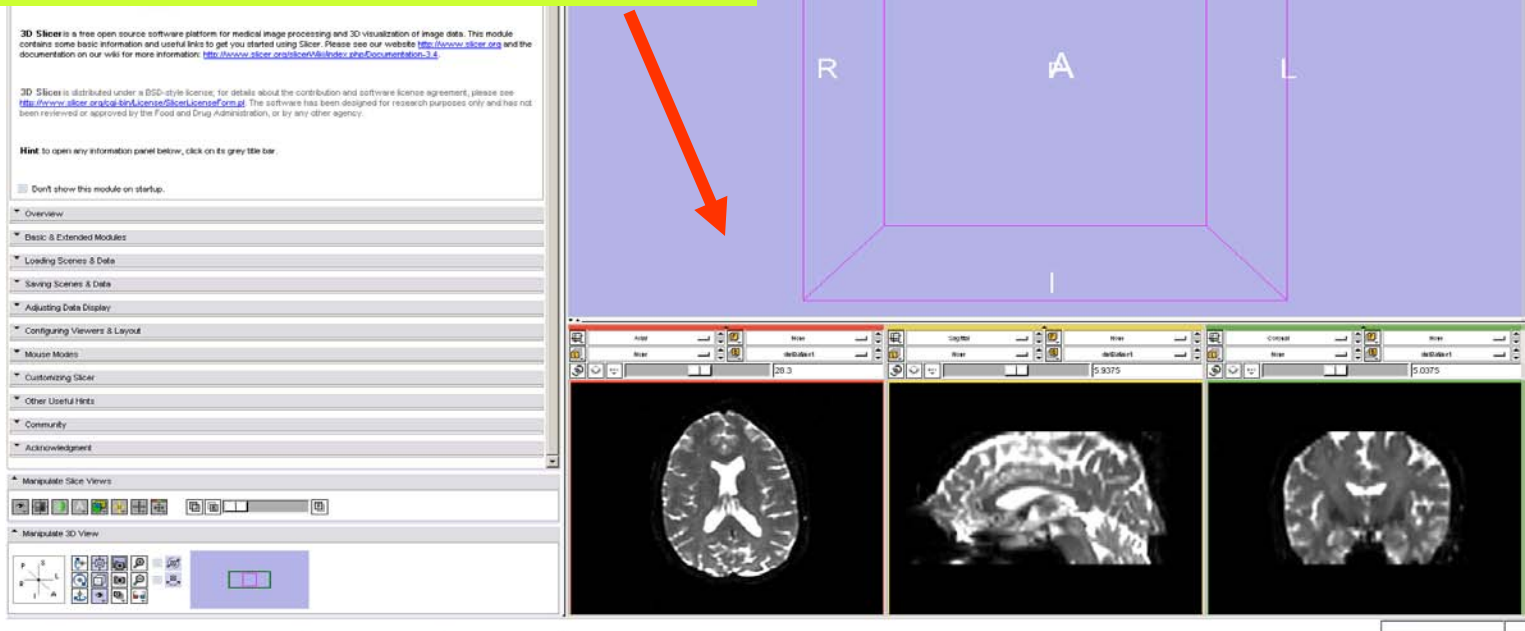
Browse to the location of the Diffusion tutorial dataset directory and select the file **dwiDataset.nhdr**

Click on **Apply** to load the volume



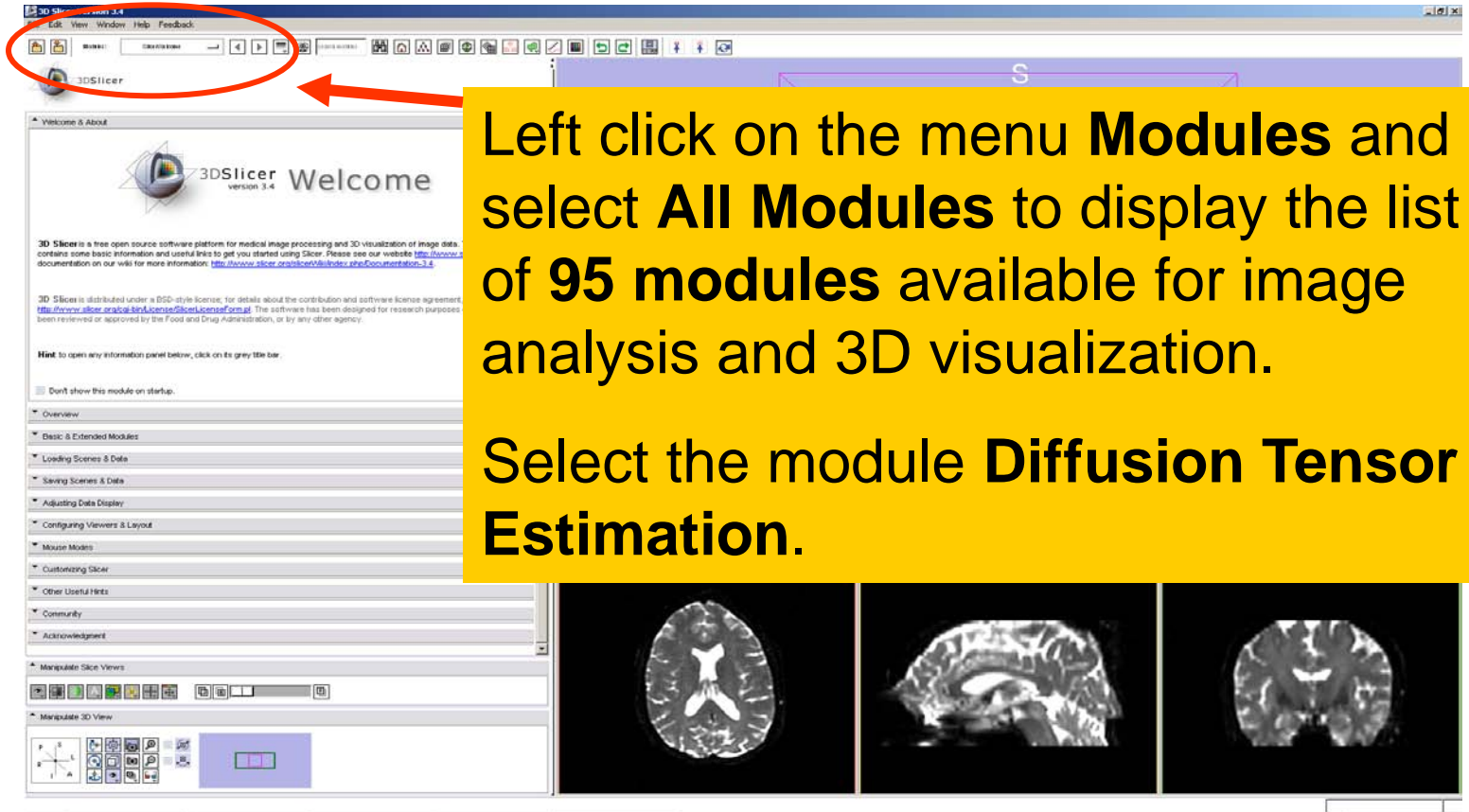
Loading the DWI volume

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





Tensor Estimation



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**.



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 Algorithm **LS** (Least Squares), and click on **Apply** to estimate the tensors.



Tensor Estimation

Left click on **Diffusion Tensor Volume 1** to display the list of volumes that have been computed by Slicer

The screenshot shows the 3D Slicer interface with the Diffusion Tensor Estimation panel on the left. The main window displays a brain slice with a purple bounding box. The volume list at the bottom shows several volumes, with 'Diffusion Tensor Volume 1' highlighted. The bottom panel shows three views of the brain slice: a top-down view, a side view, and a front view.

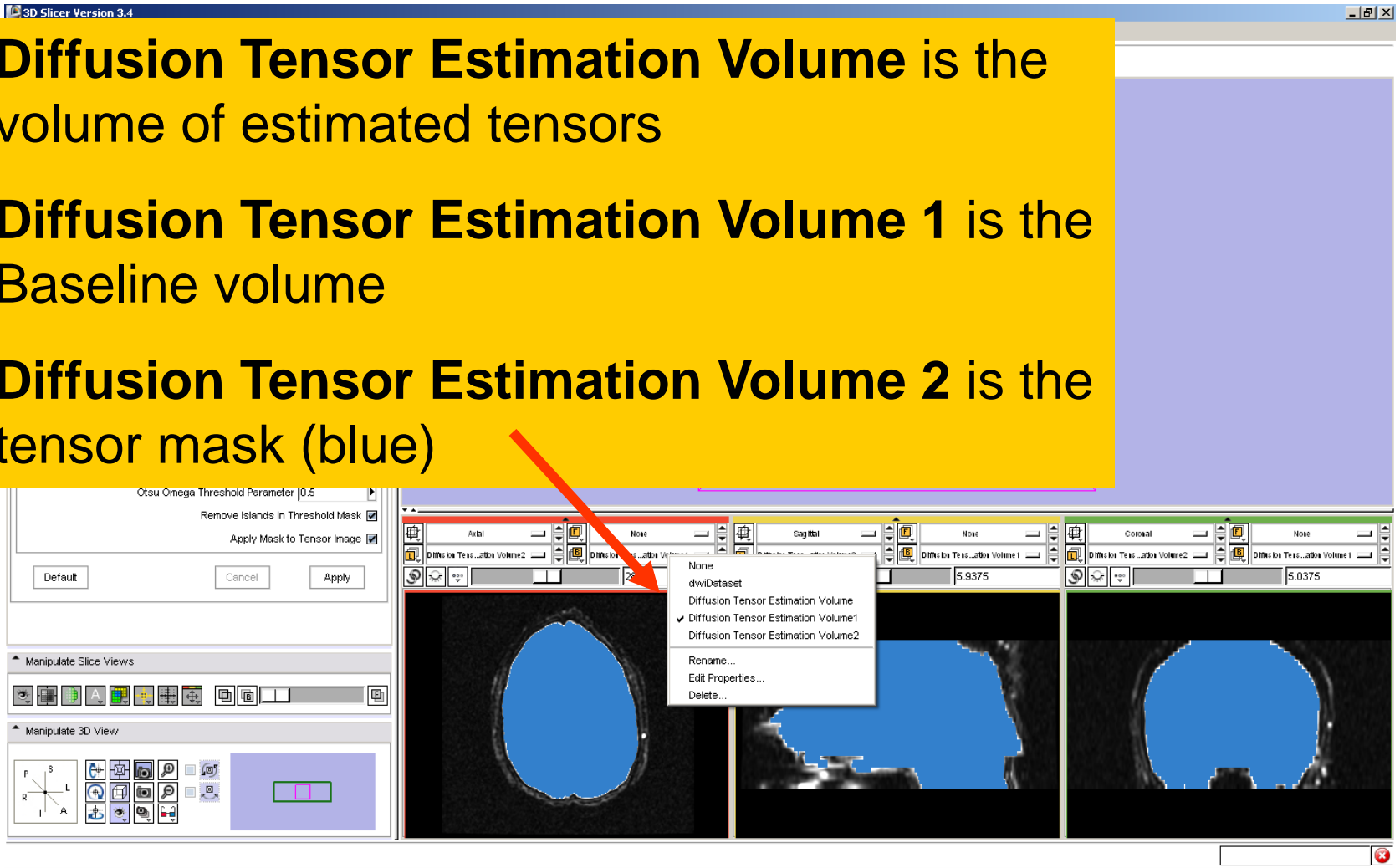


Tensor Estimation

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)



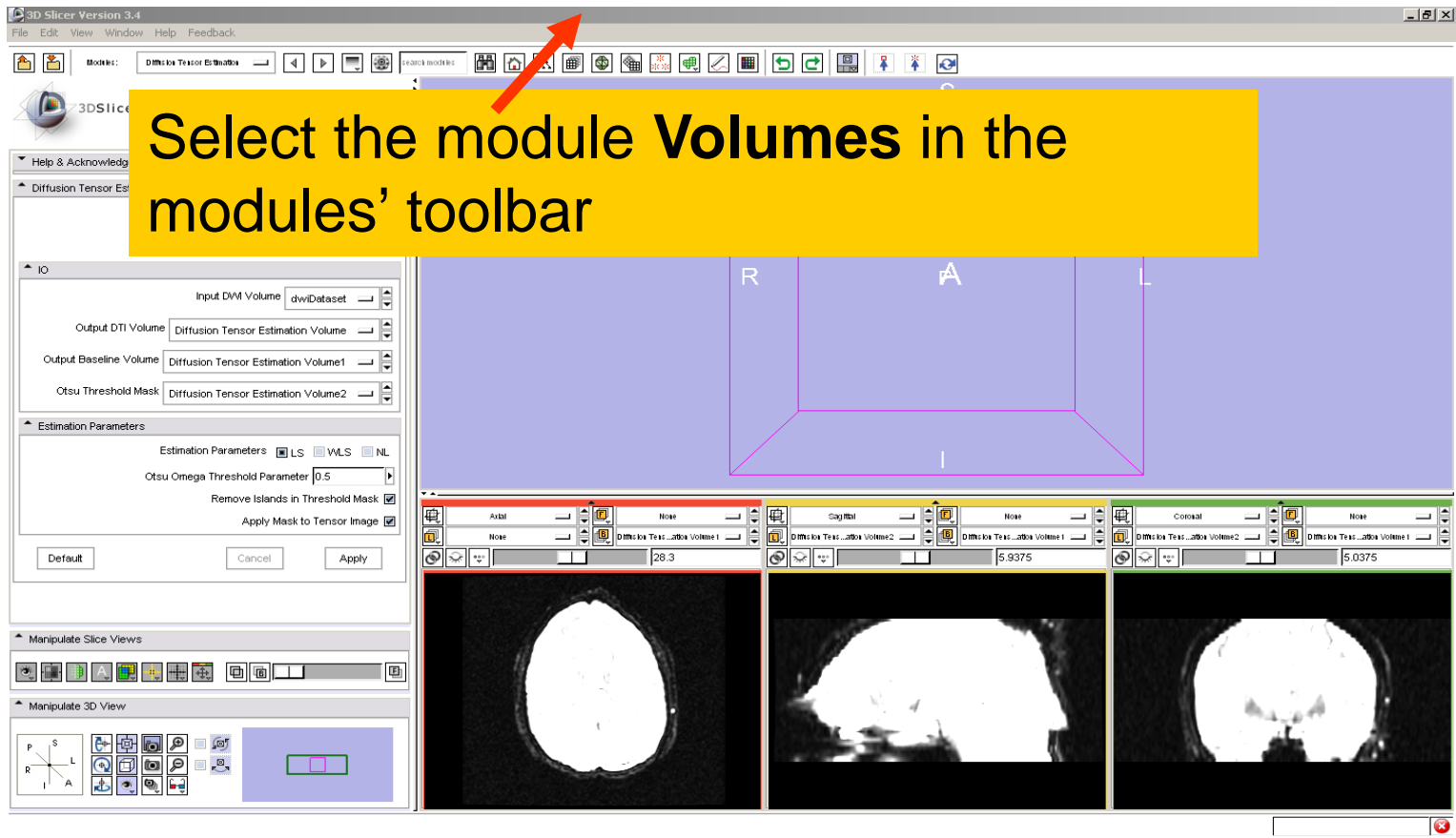


Tensor Estimation

Click on the link icon, left click on **Diffusion Tensor Volume 2** and select **None**



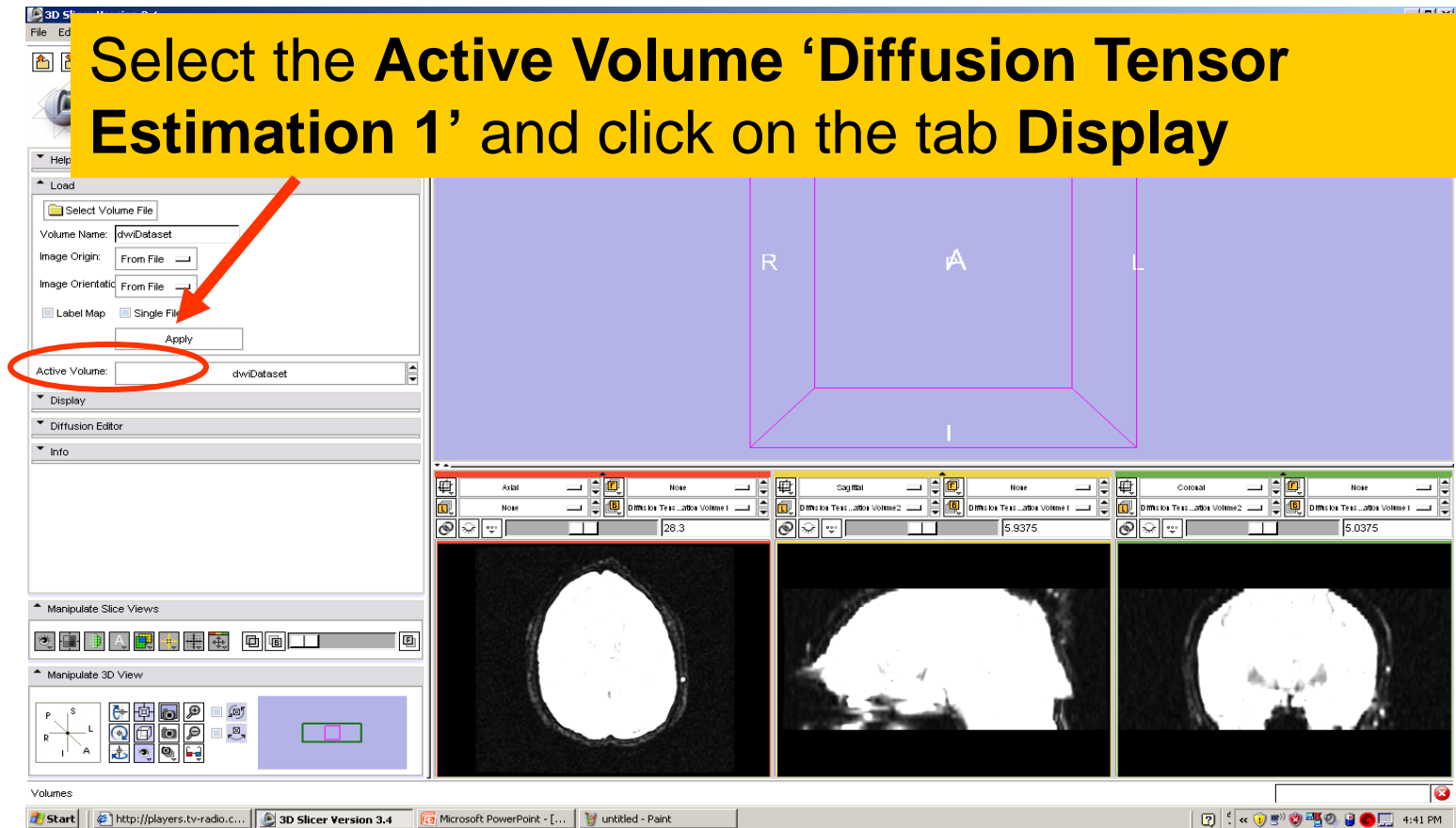
Tensor Estimation





Tensor Estimation

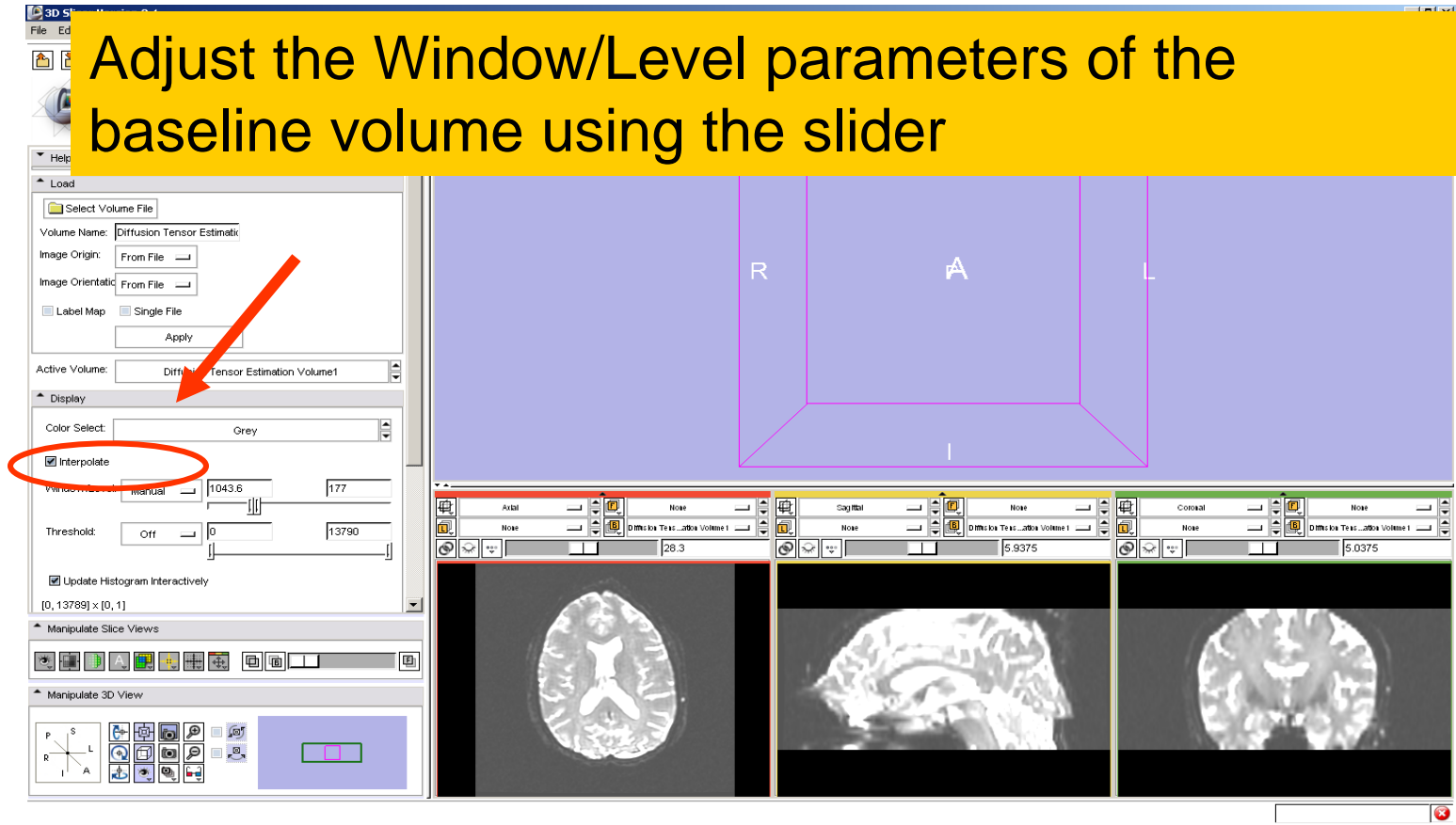
Select the Active Volume 'Diffusion Tensor Estimation 1' and click on the tab Display





Tensor Estimation

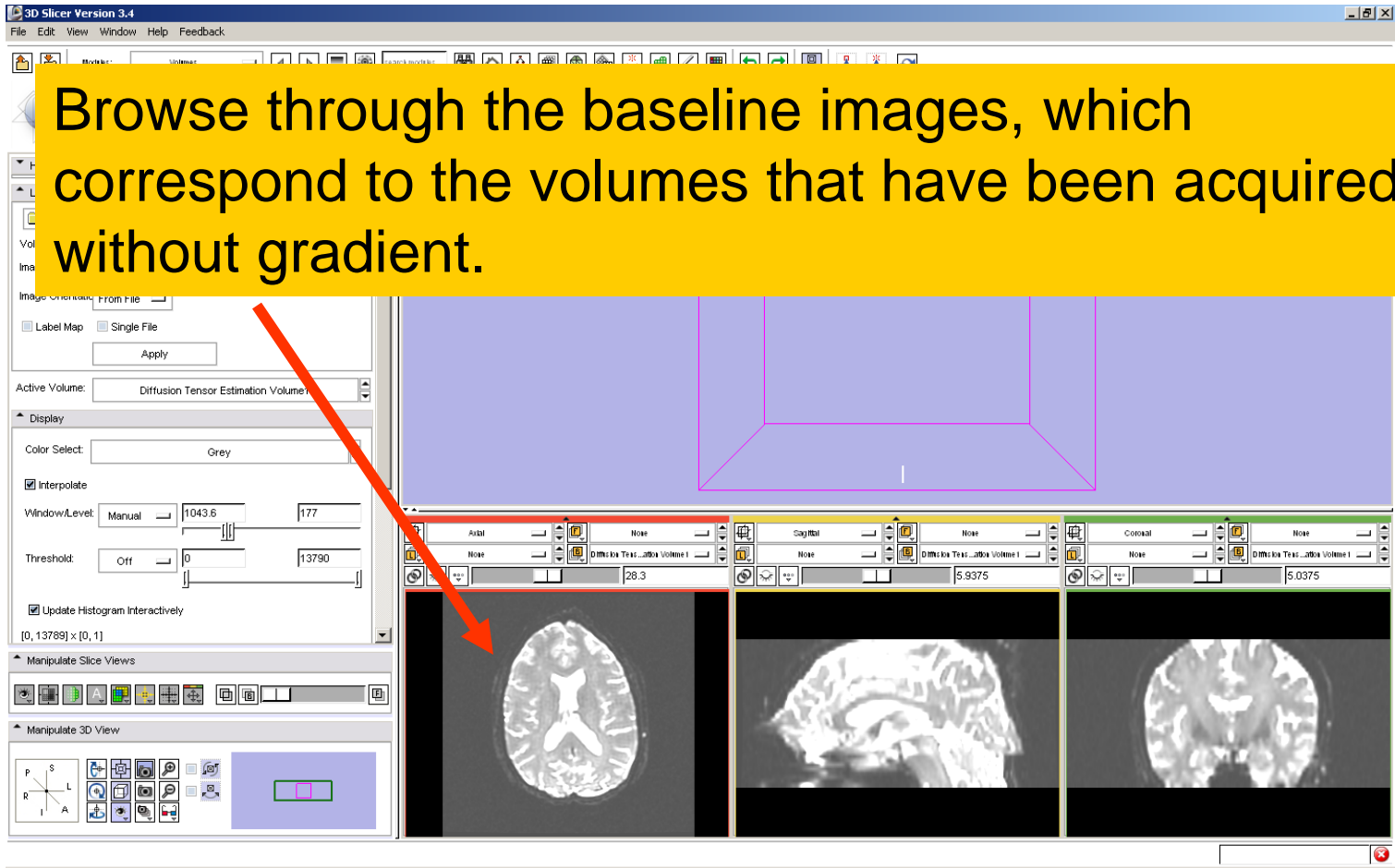
Adjust the Window/Level parameters of the baseline volume using the slider

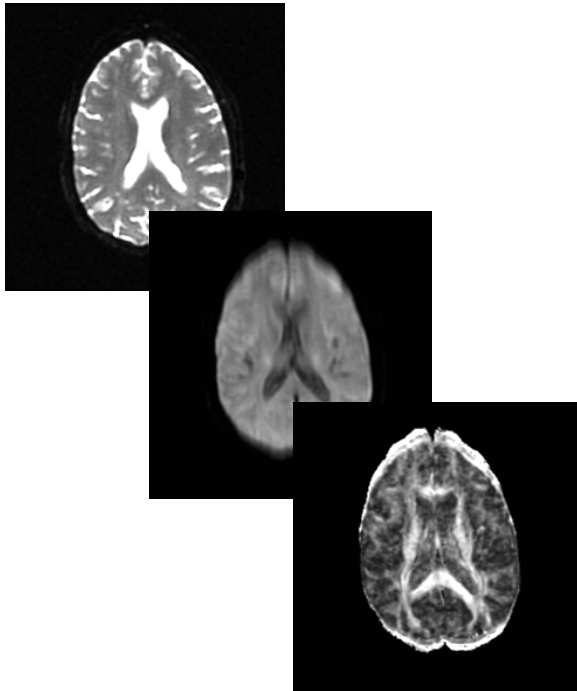




Tensor Estimation

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.

The screenshot shows the 3D Slicer 3.4 interface. The top menu bar has 'Diffusion' selected. The 'Diffusion Tensor Scalar Measurements' module is active, showing parameters for IO, Operation, and Manipulate Slice Views. The main 3D view shows a brain slice with axes R, A, L, and I. The bottom panel shows three orthogonal slices (Axial, Sagittal, Coronal) with numerical values: 37.3, 5.9375, and 5.0375 respectively.



Scalar Measurements

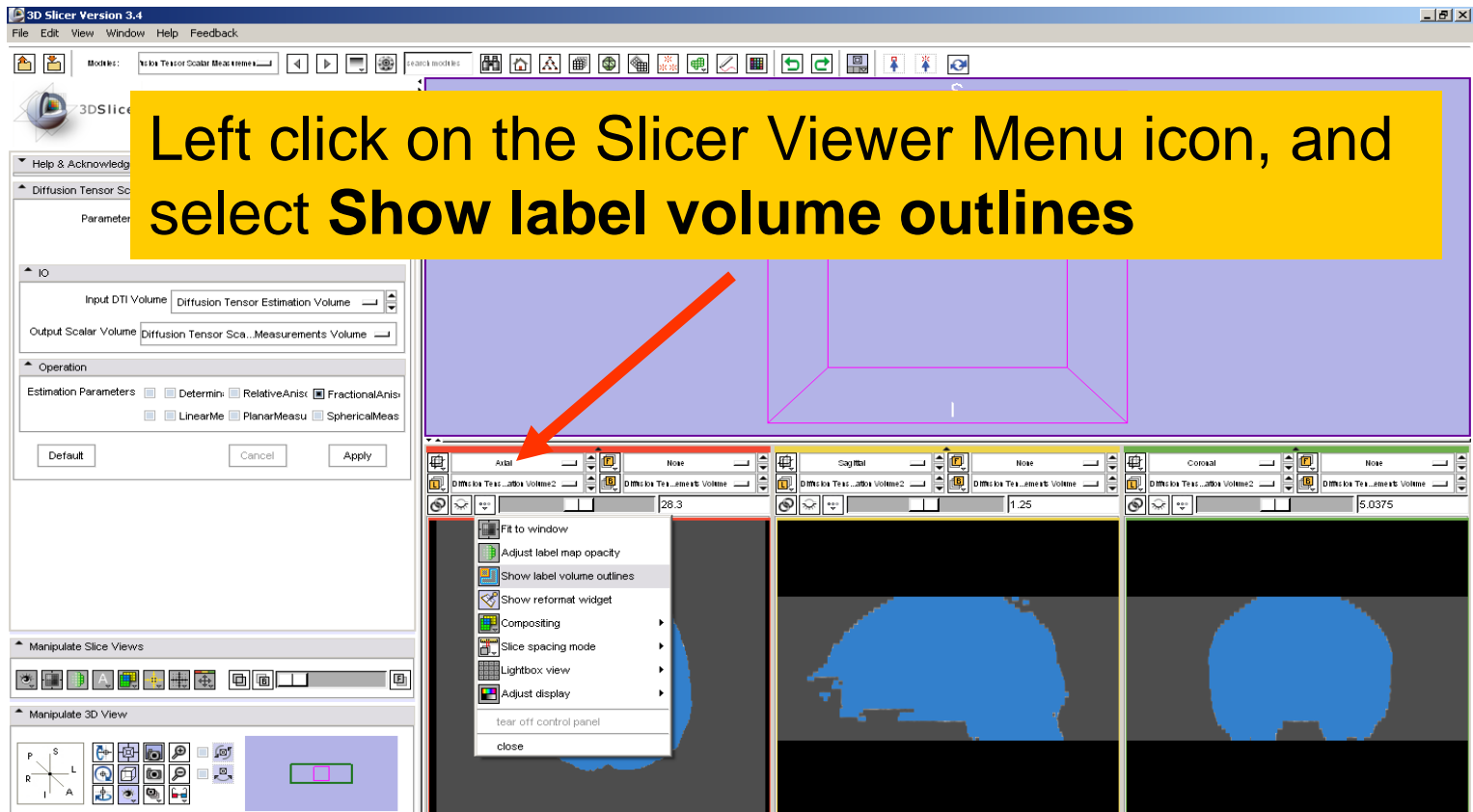
Select the Input DTI Volume **Diffusion Tensor Estimation Volume**

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

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

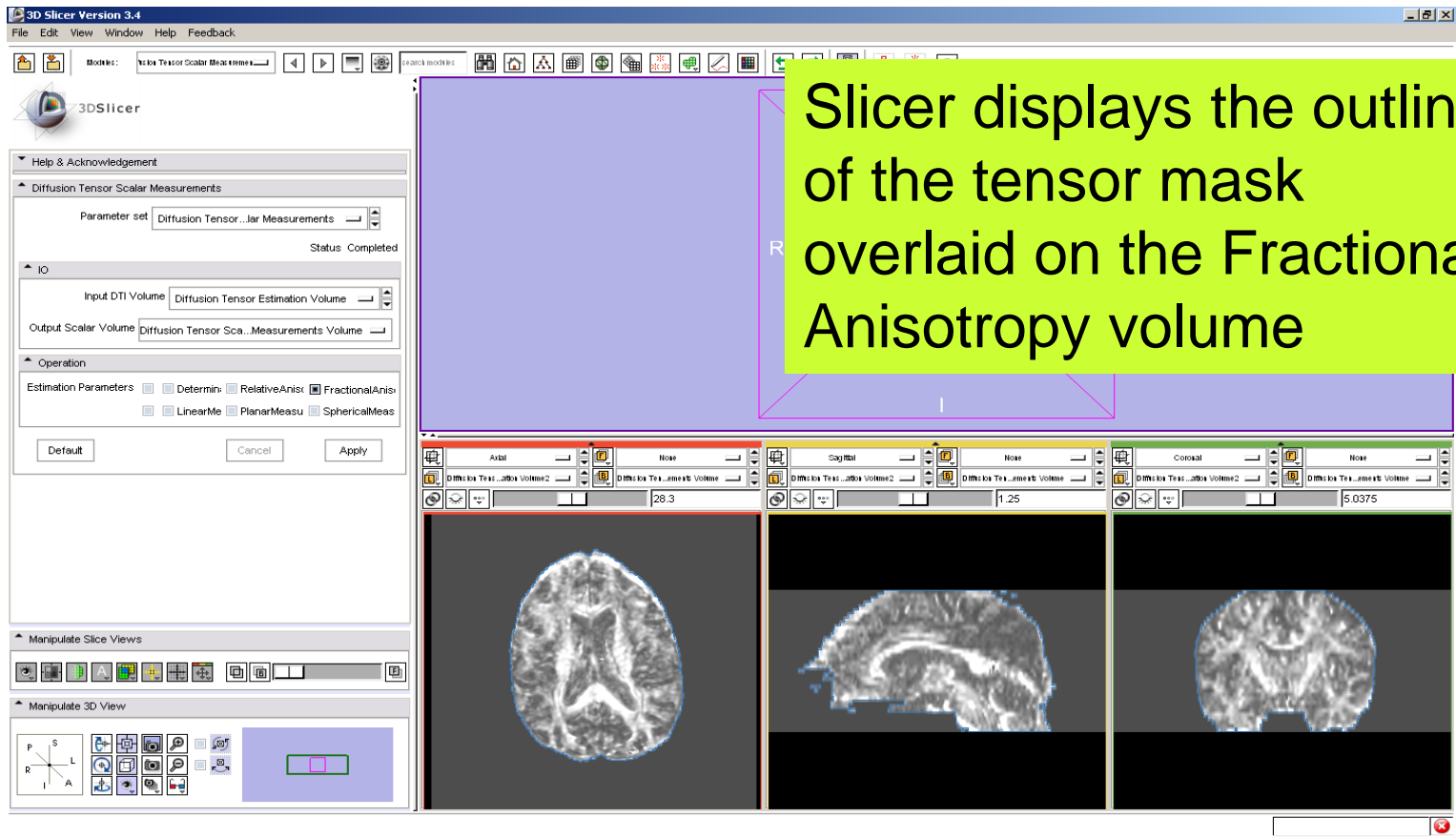


Fractional Anisotropy Volume



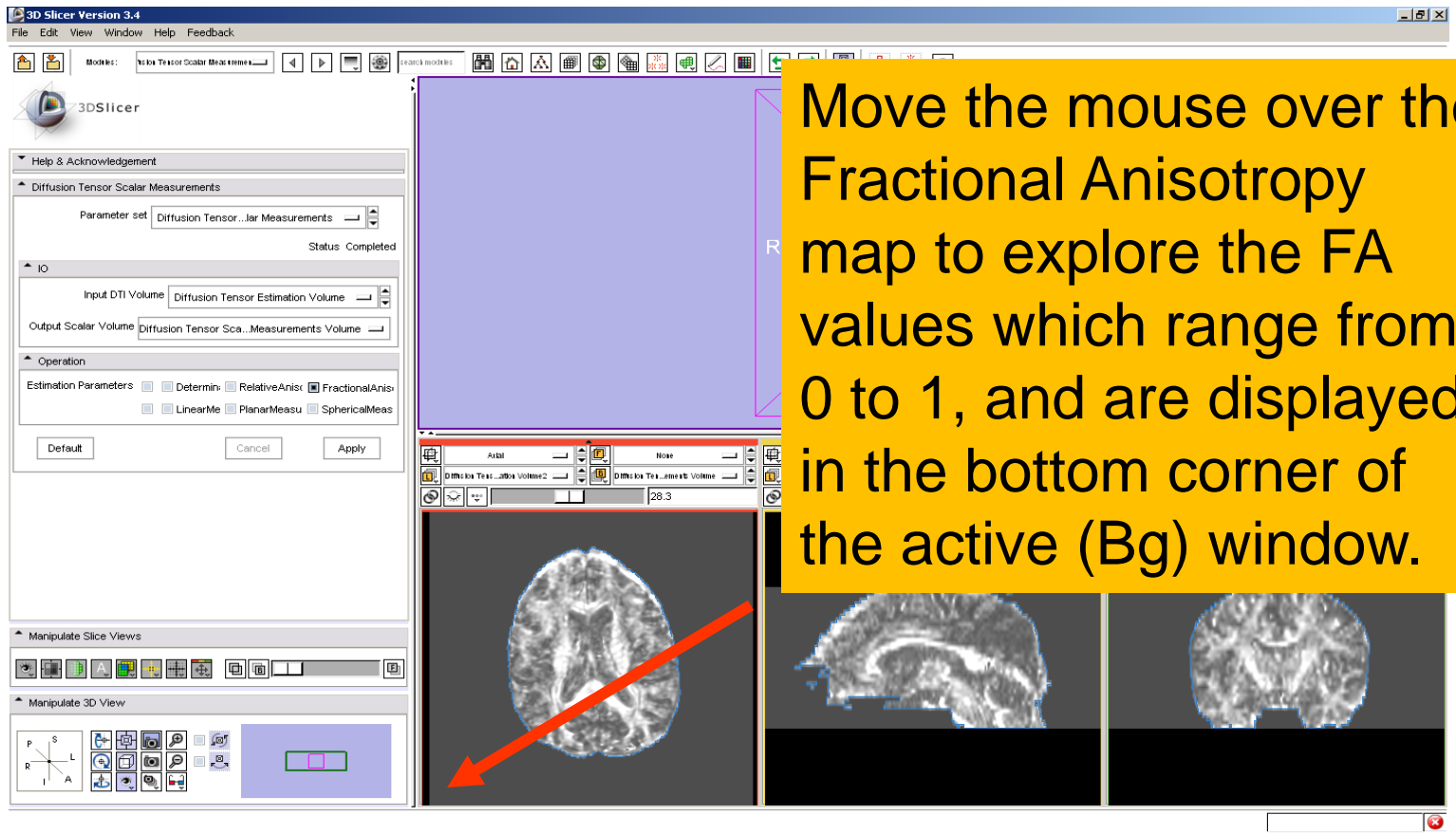


Fractional Anisotropy Volume





Fractional Anisotropy Volume





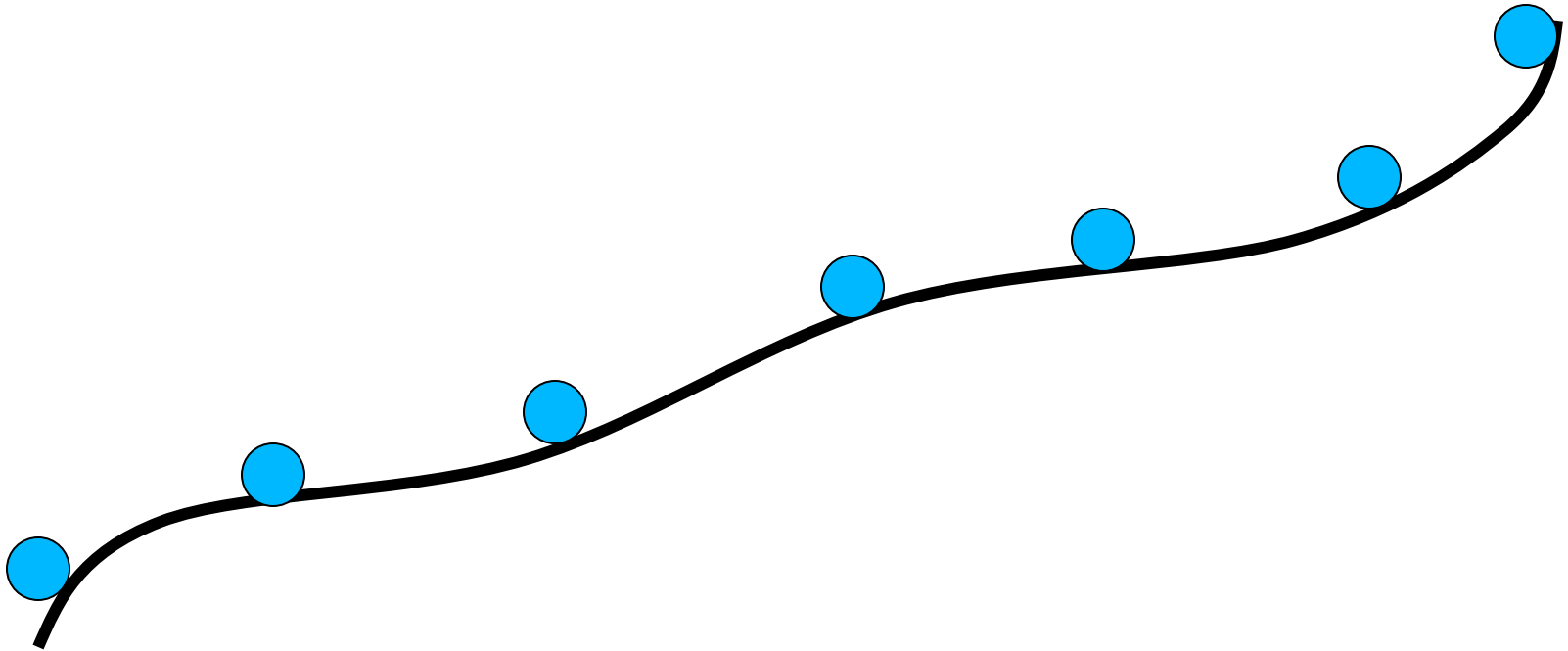
Part 3:

Region of Interest based Tractography





Tractography

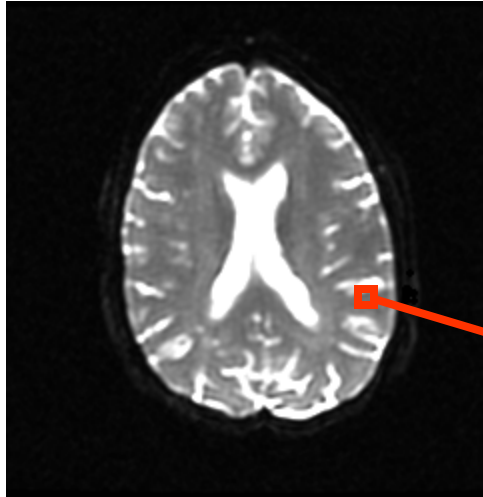




Diffusion Tensor

Stejskal-Tanner

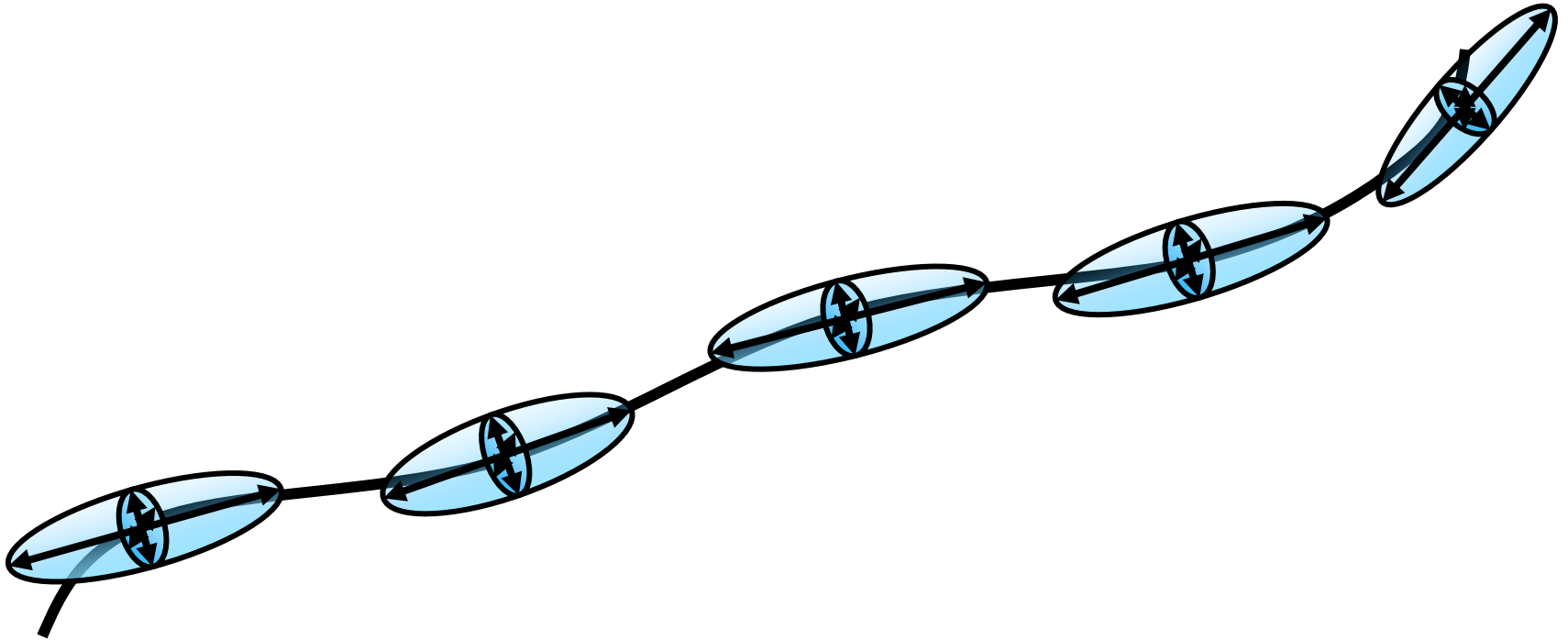
$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$



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



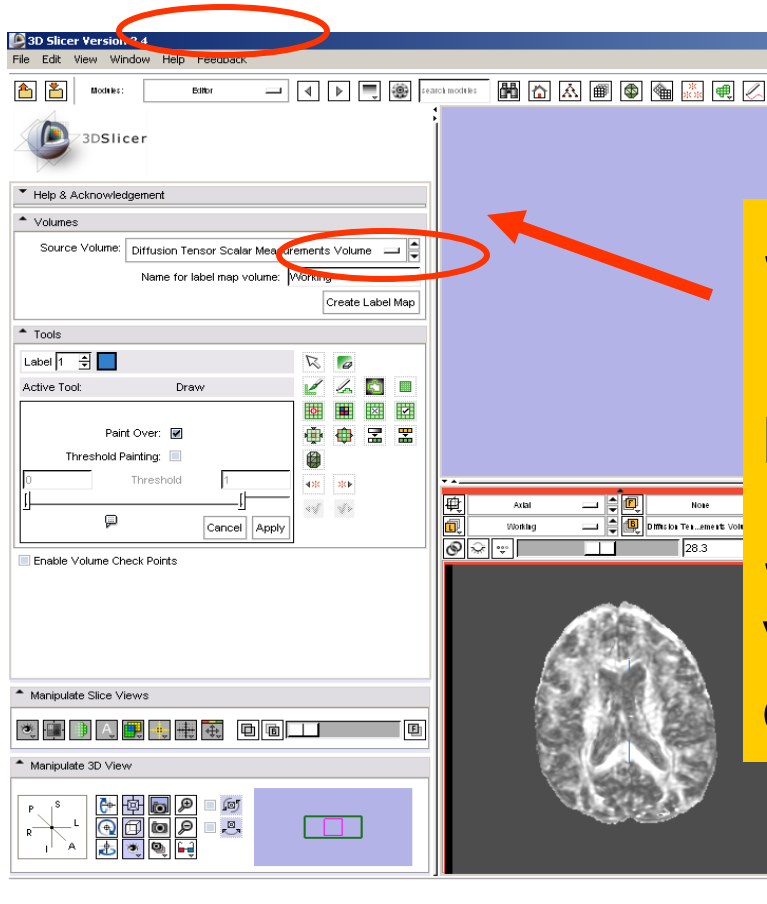
Tractography





LabelMap Generation

Select the module Editor in the modules' menu.

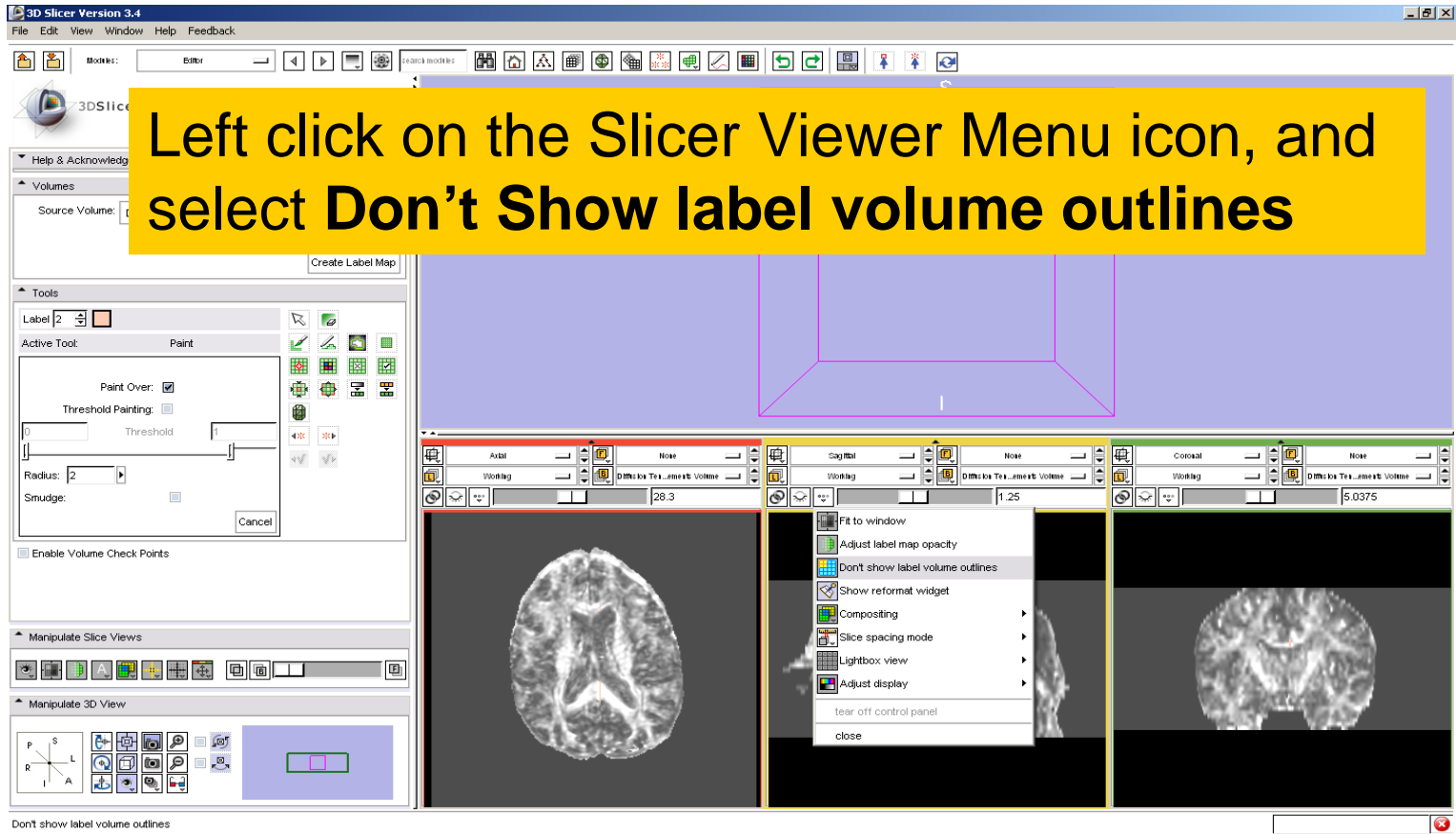


Select the Source Volume
**Diffusion Tensor Scalar
Measurements Volume**

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



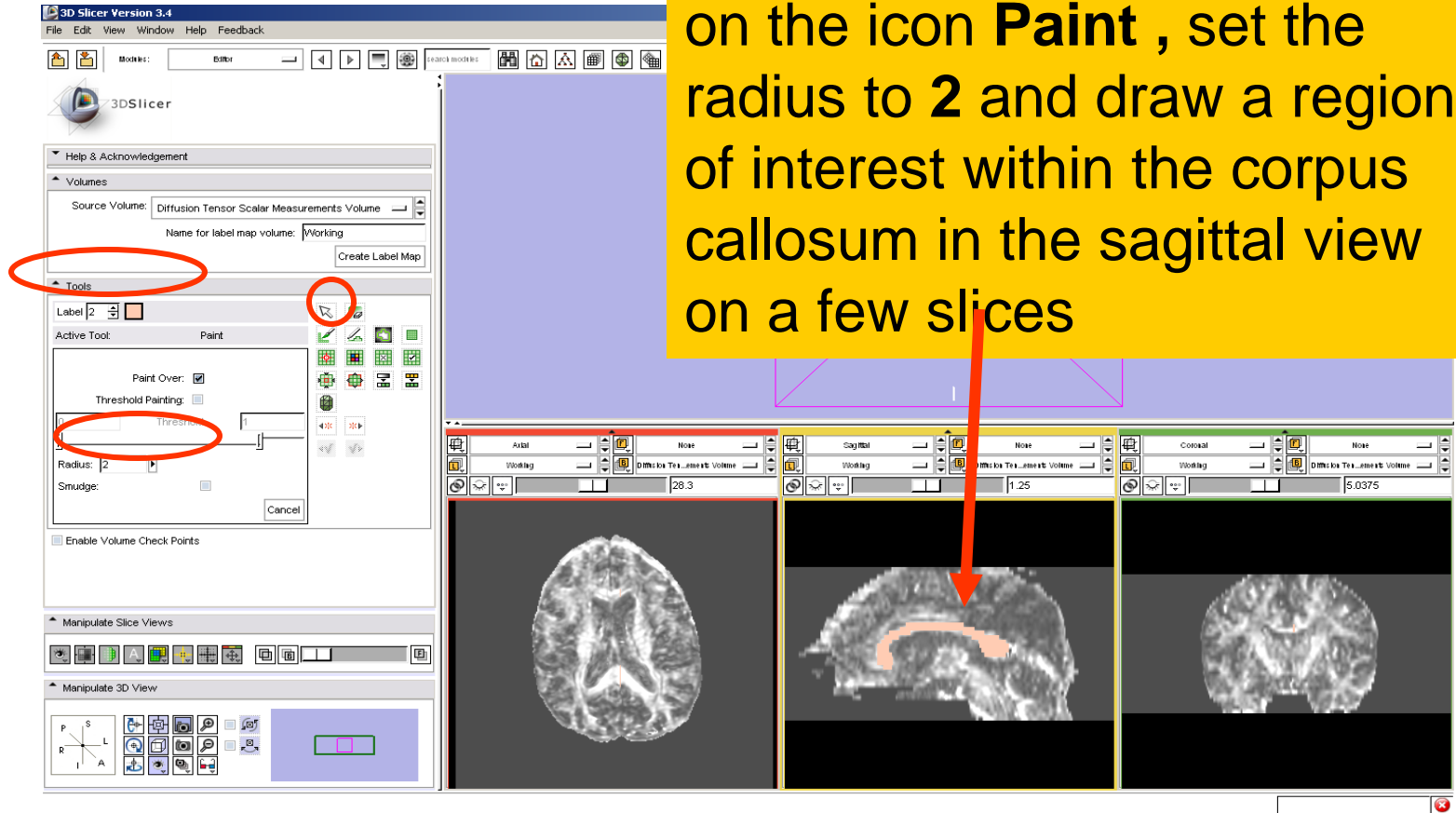
LabelMap Generation





LabelMap Generation

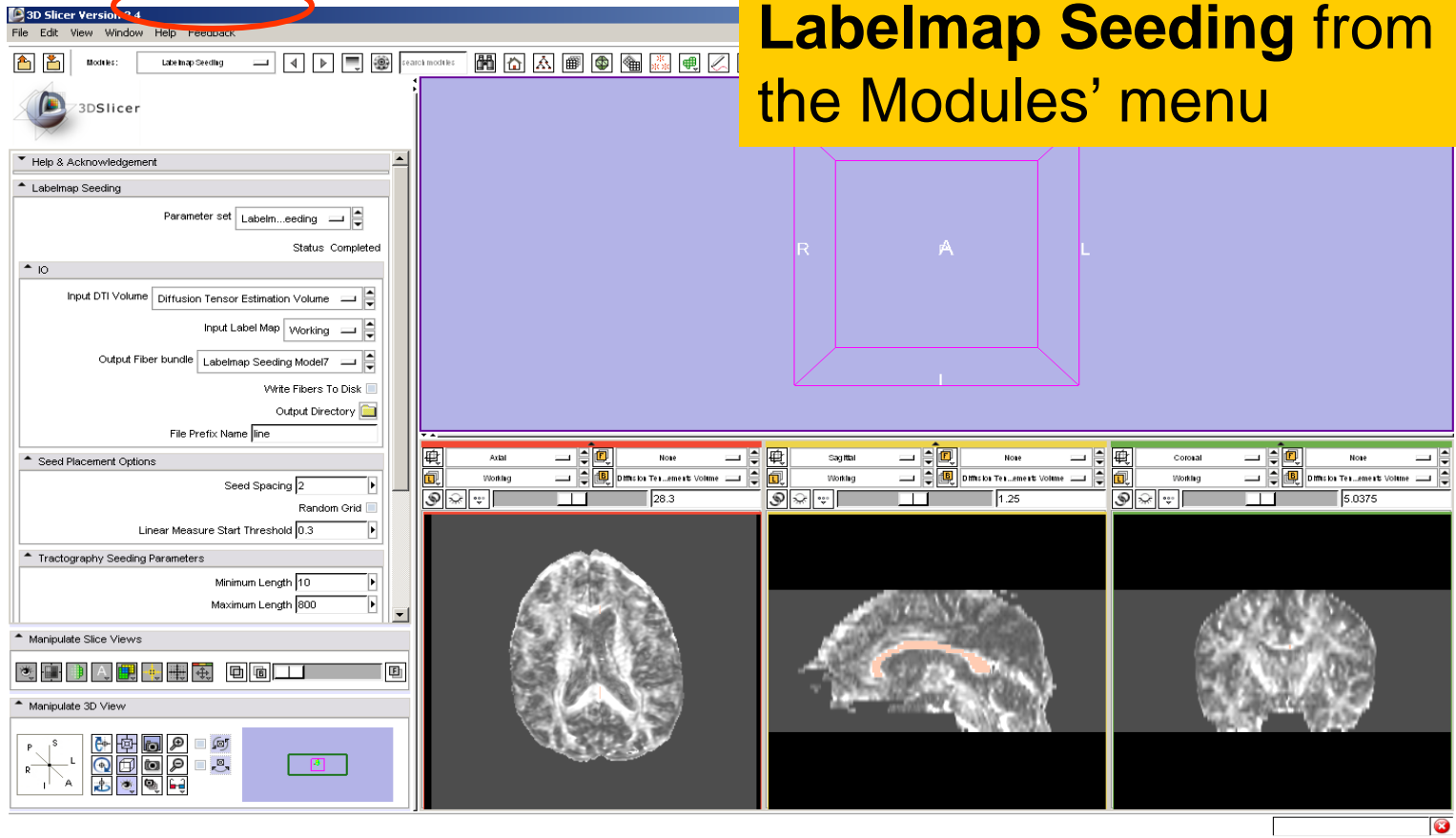
Select the label 2 (pink), click on the icon **Paint**, set the radius to **2** and draw a region of interest within the corpus callosum in the sagittal view on a few slices





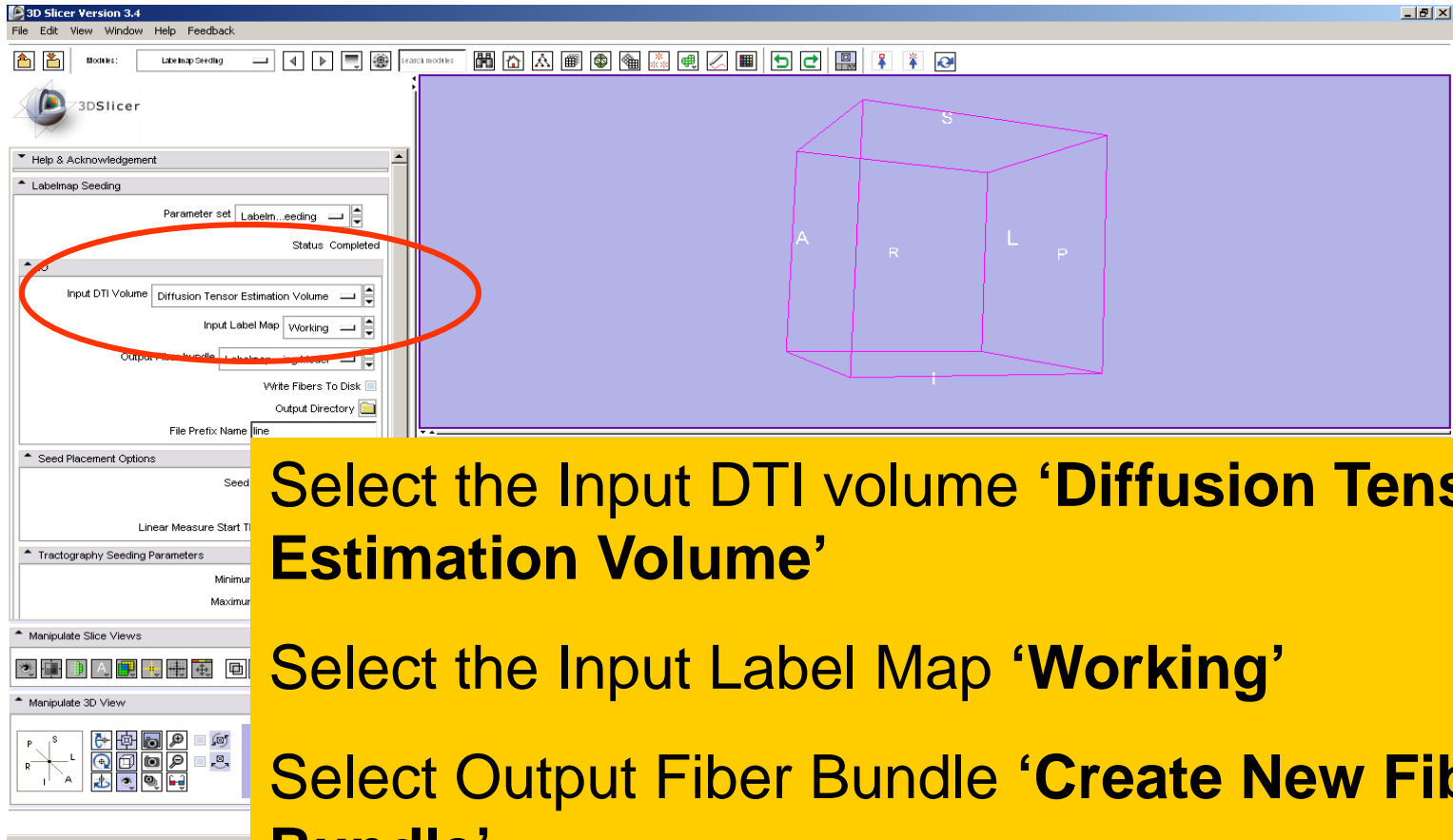
LabelMap Seeding

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

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.

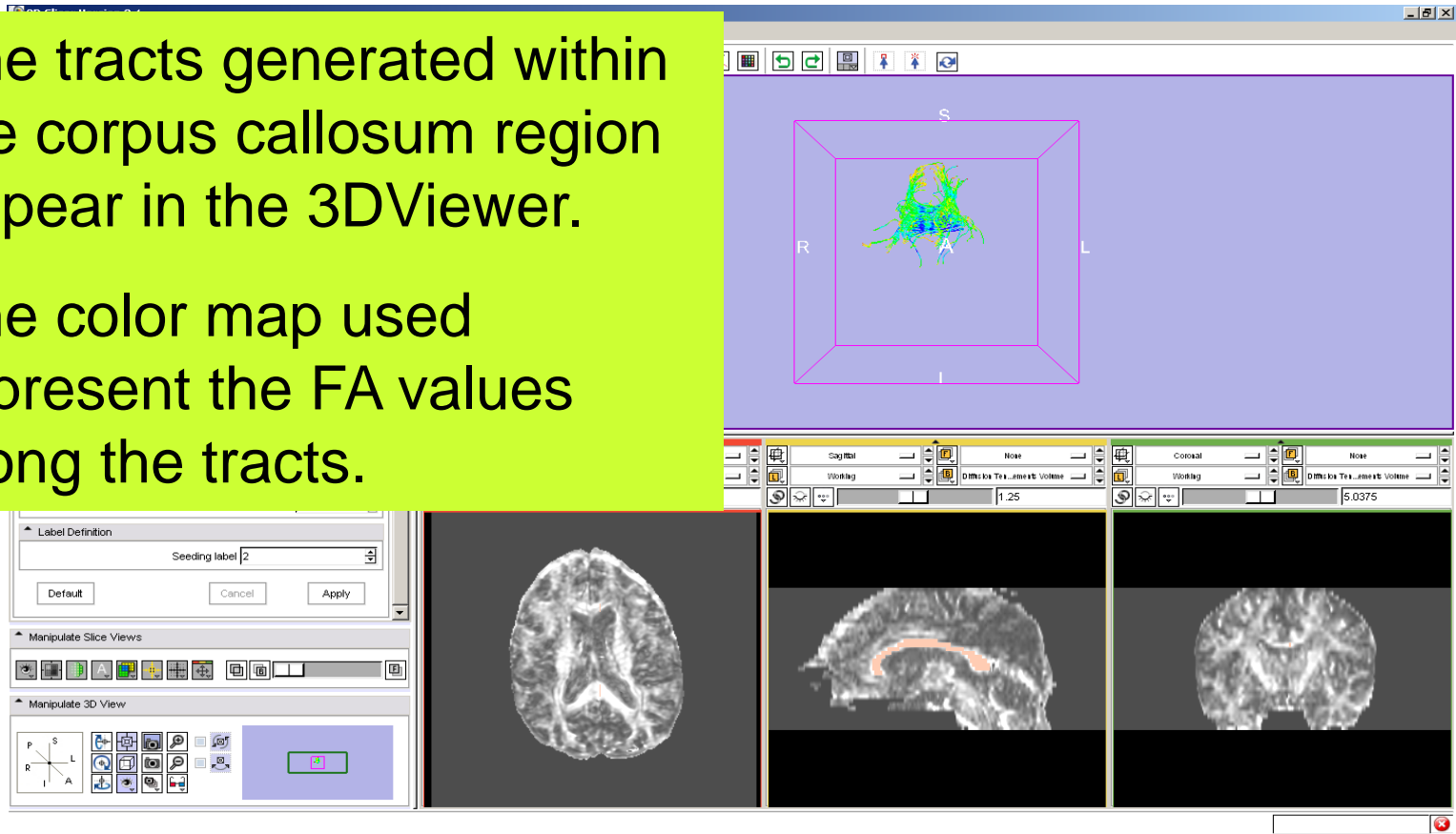
Set Seeding label to label 2, and click on **Apply**



LabelMap Seeding

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

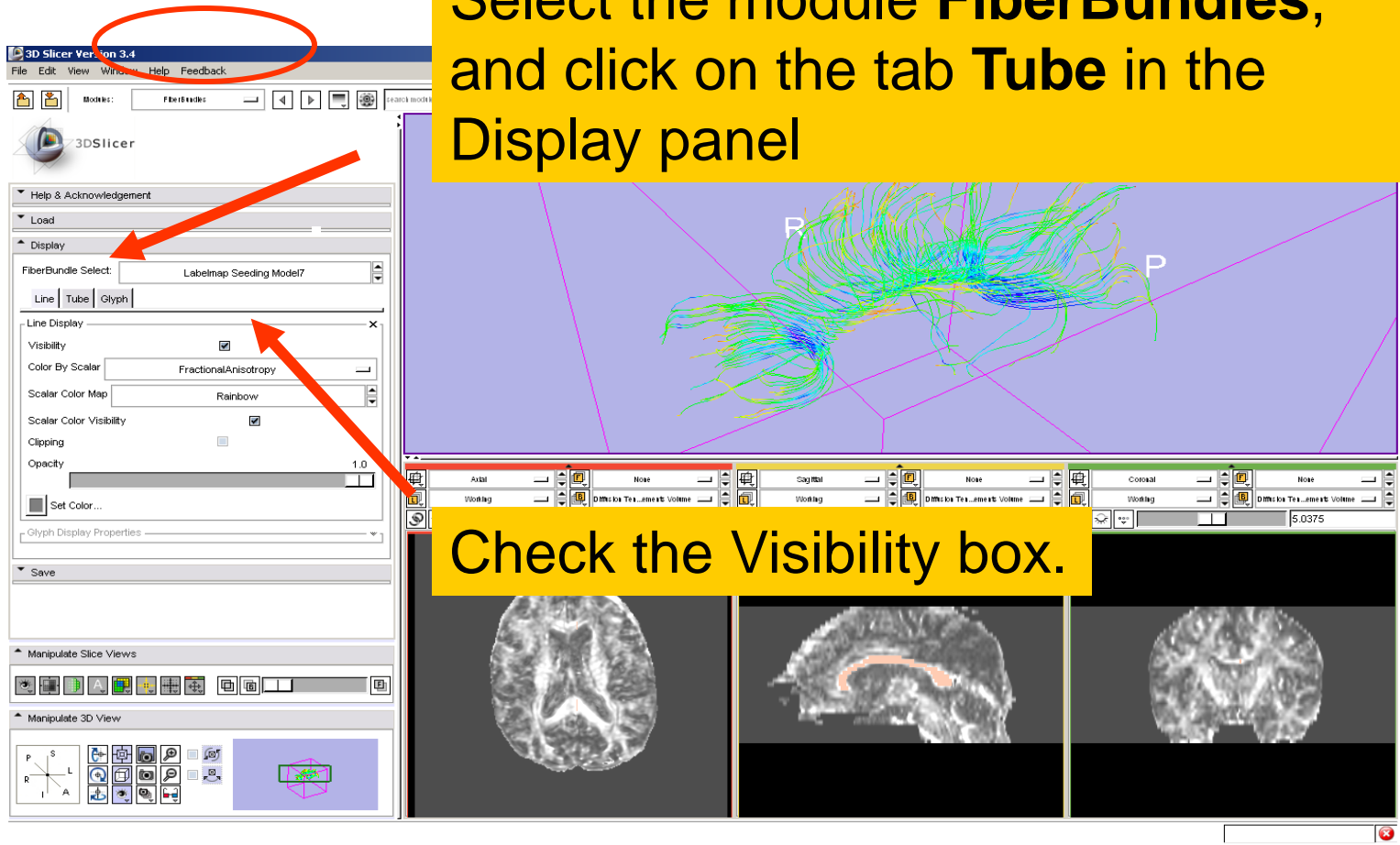
The color map used represent the FA values along the tracts.





LabelMap Seeding

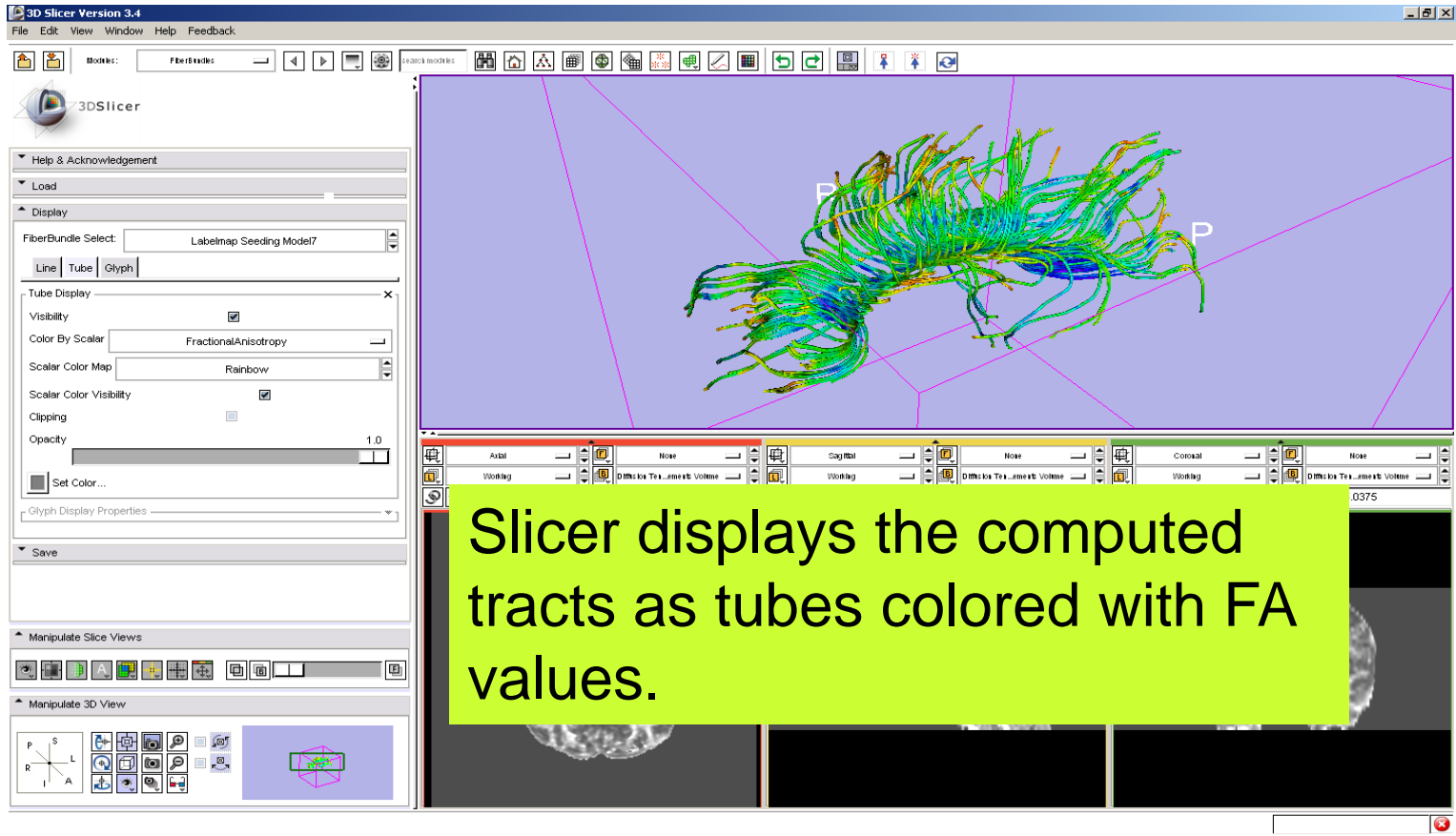
Select the module **FiberBundles**, and click on the tab **Tube** in the Display panel

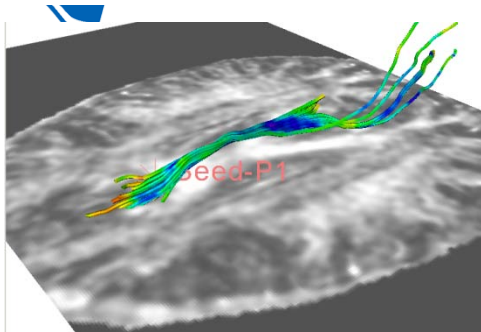


Check the Visibility box.



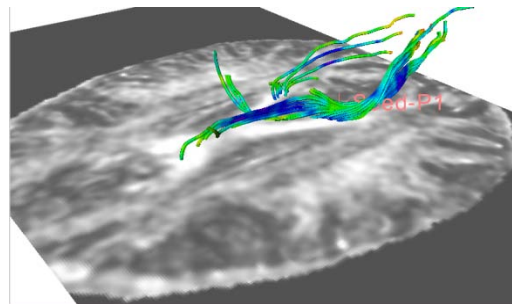
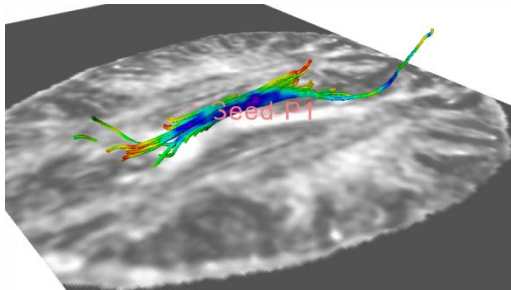
LabelMap Seeding





Part 4:

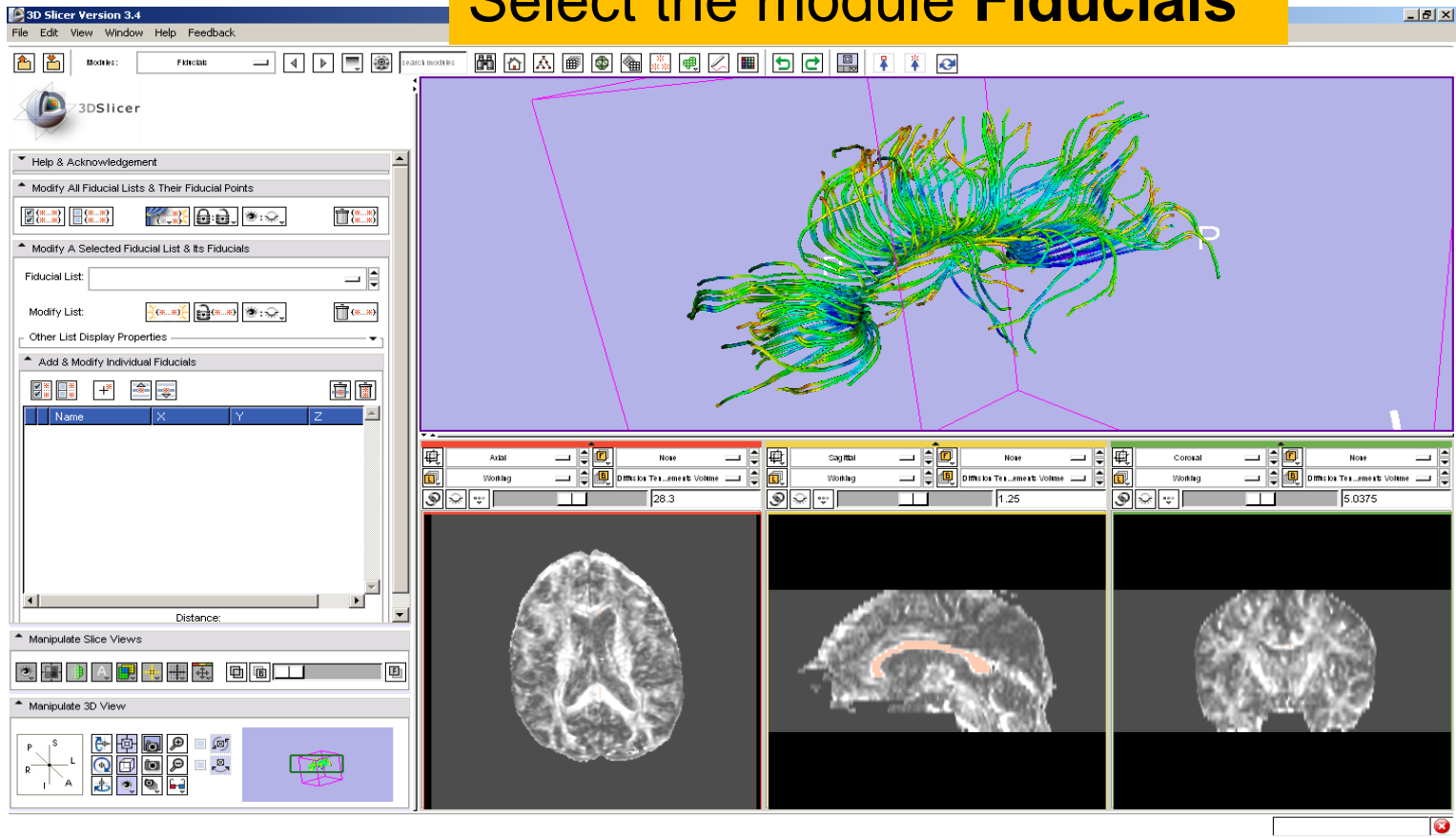
Tractography on-the-fly





Fiducial Seeding

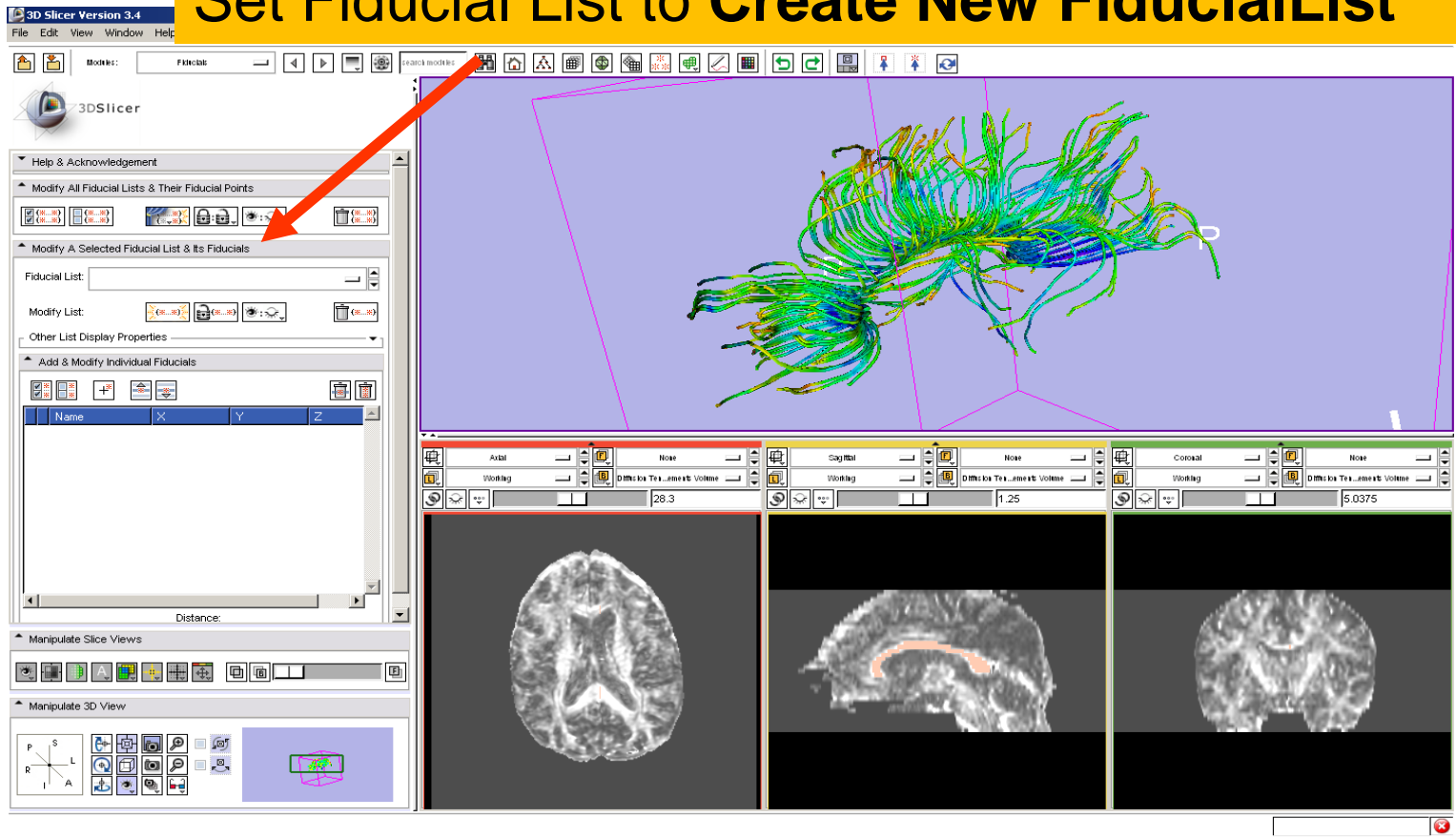
Select the module **Fiducials**





Fiducial Seeding

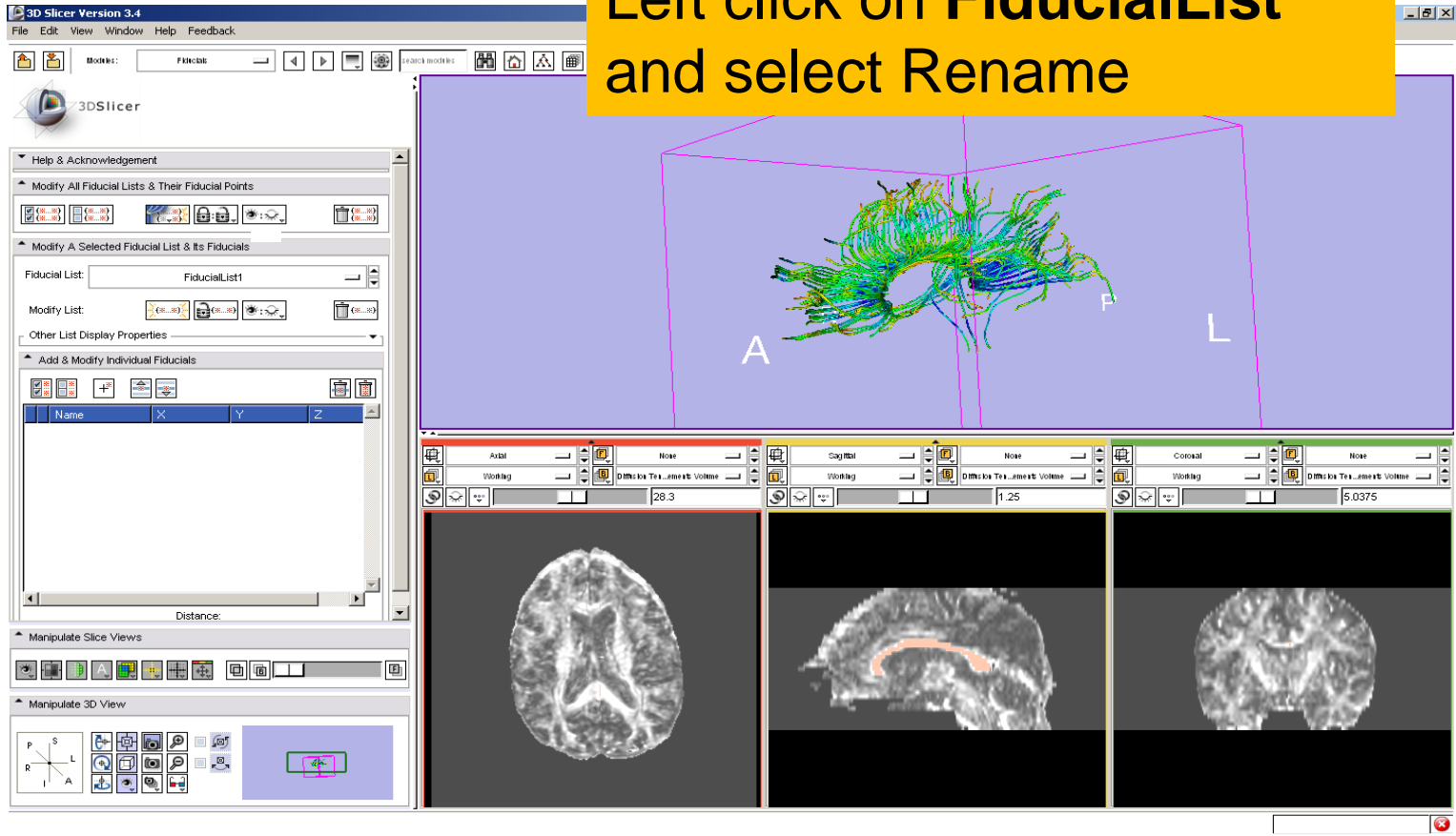
Set Fiducial List to Create New FiducialList





Fiducial Seeding

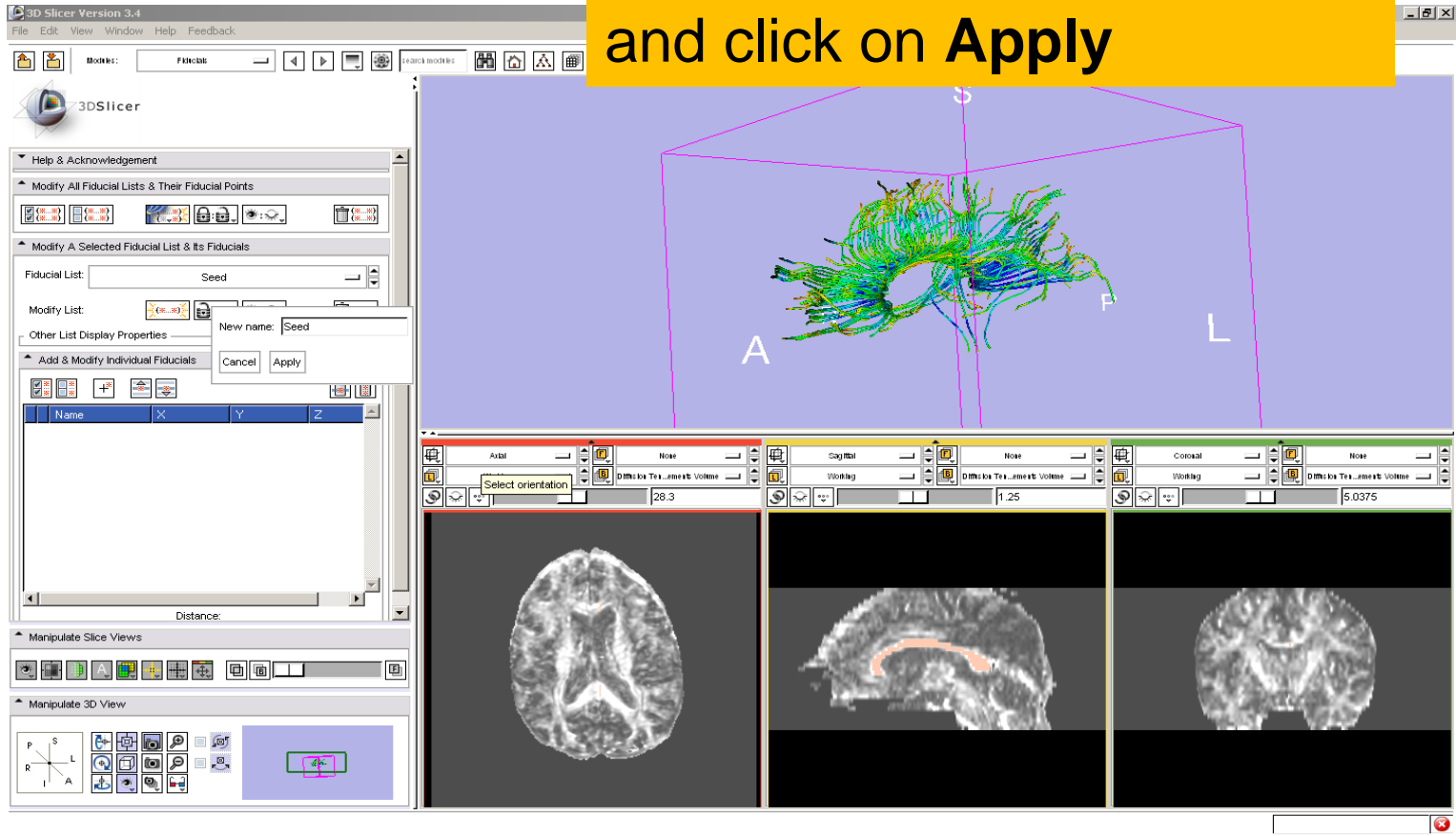
Left click on **FiducialList**
and select **Rename**





Fiducial Seeding

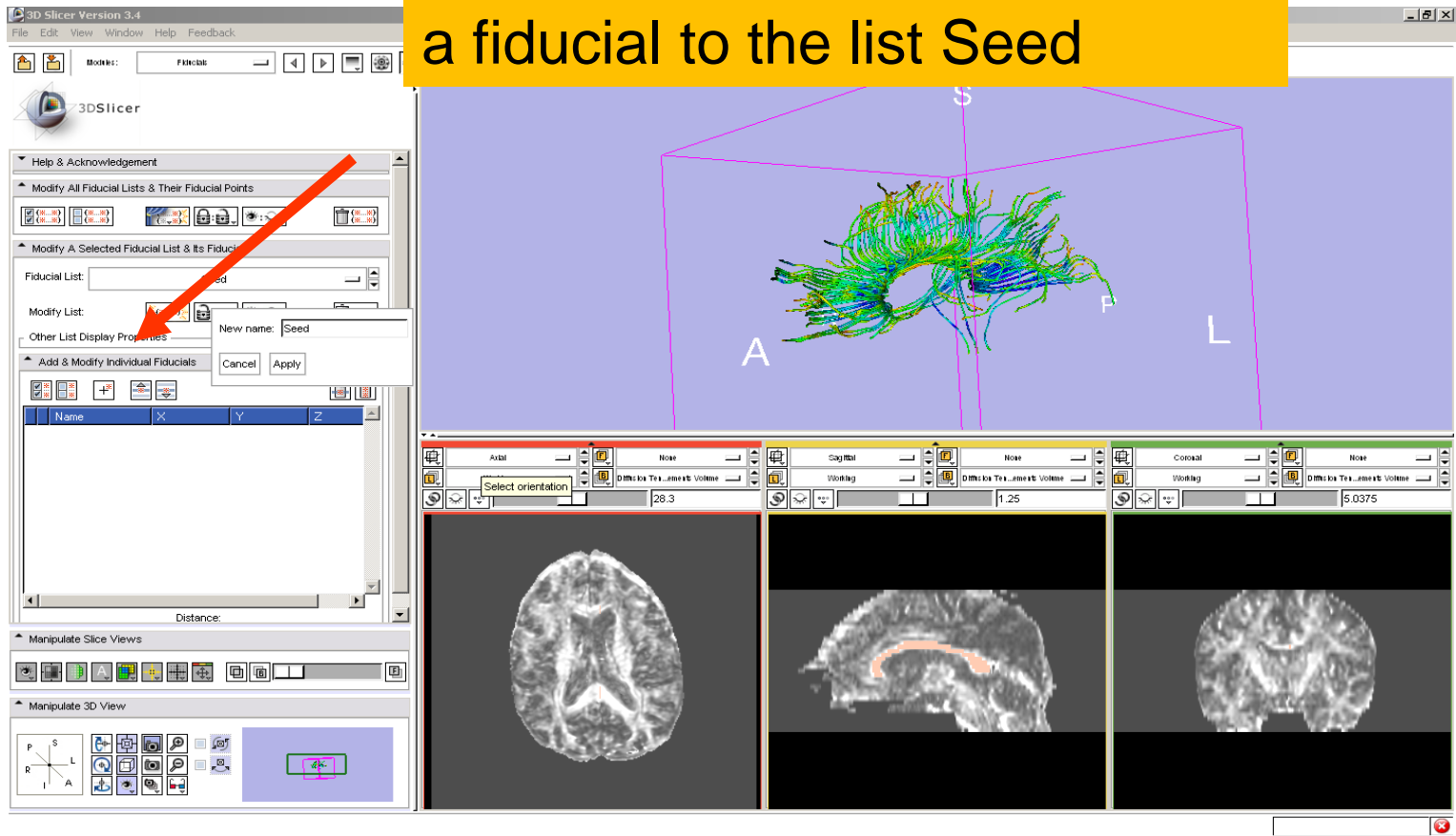
Enter the new name **Seed** and click on **Apply**





Fiducial Seeding

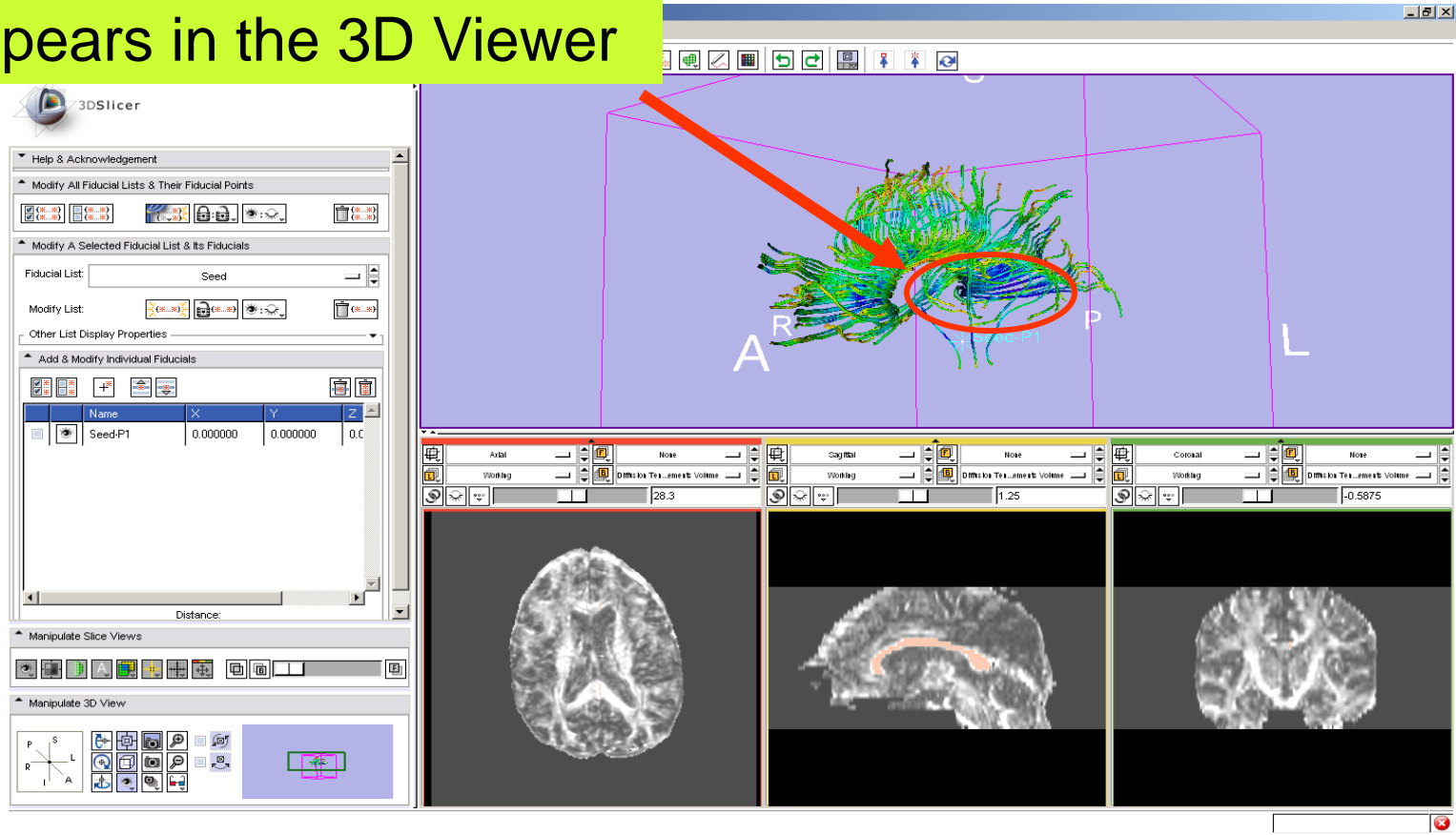
Click on the cross icon to add a fiducial to the list Seed





Fiducial Seeding

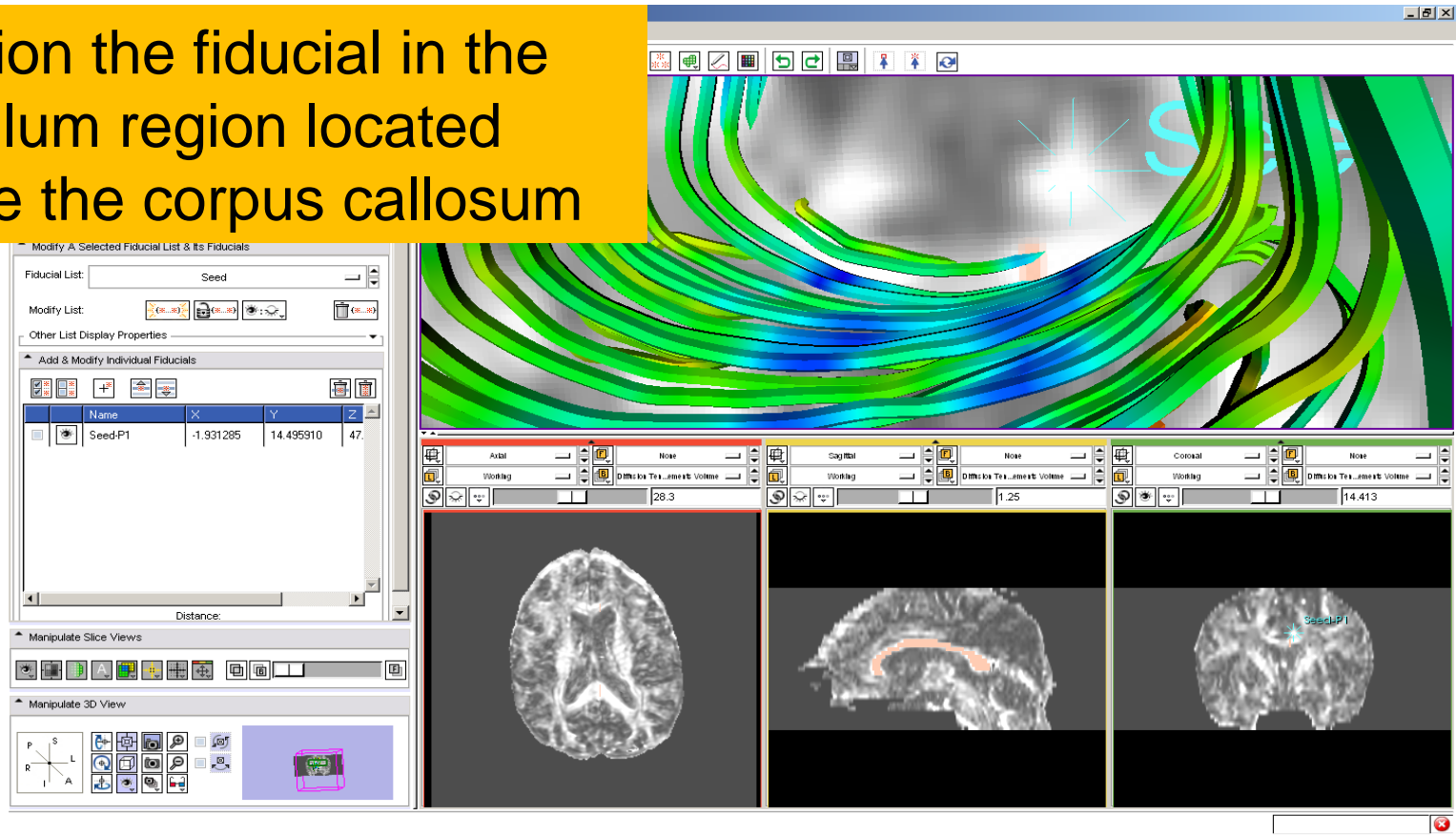
The fiducial **Seed-P1** appears in the 3D Viewer





Fiducial Seeding

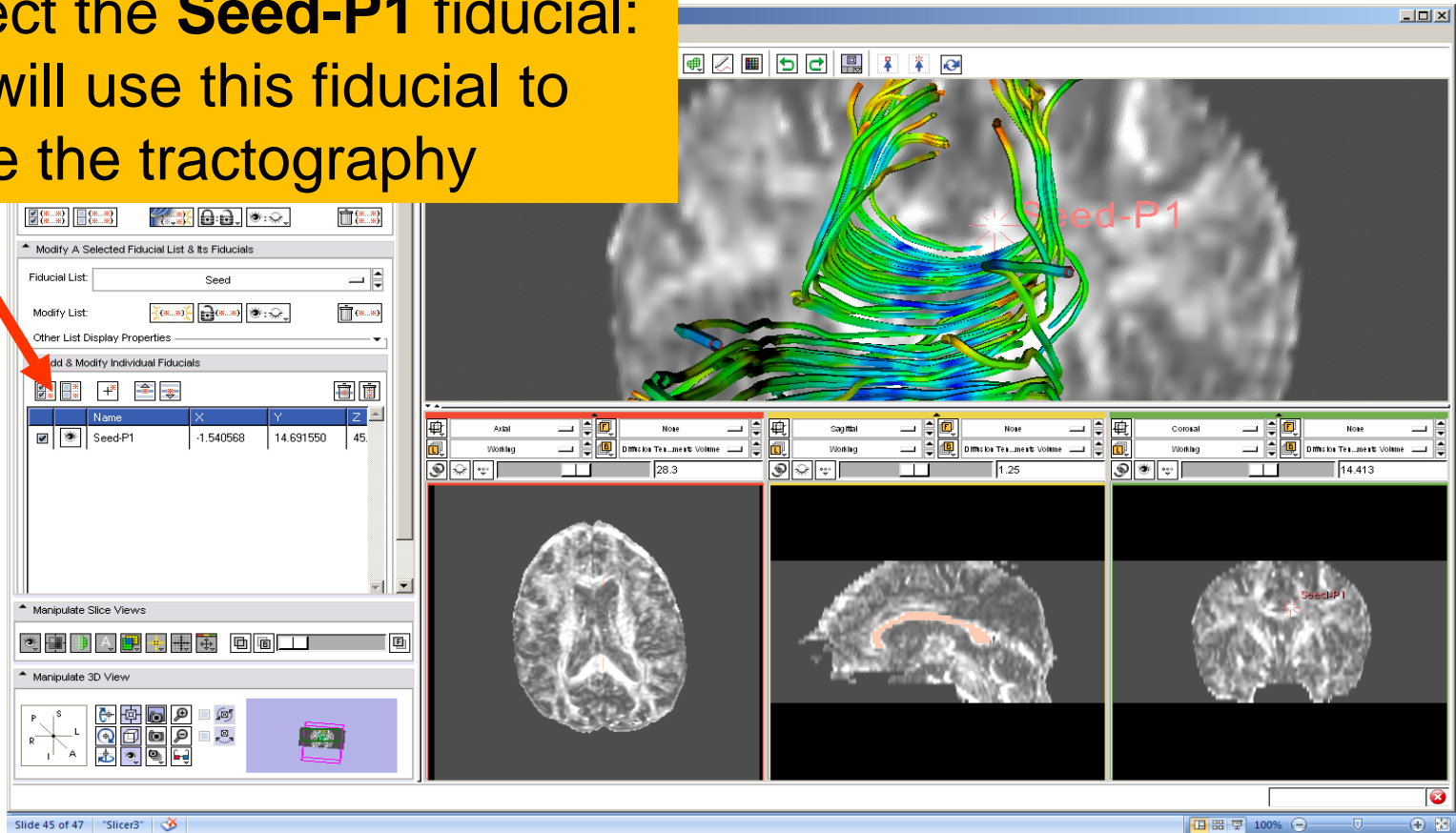
Position the fiducial in the cingulum region located above the corpus callosum





Fiducial Seeding

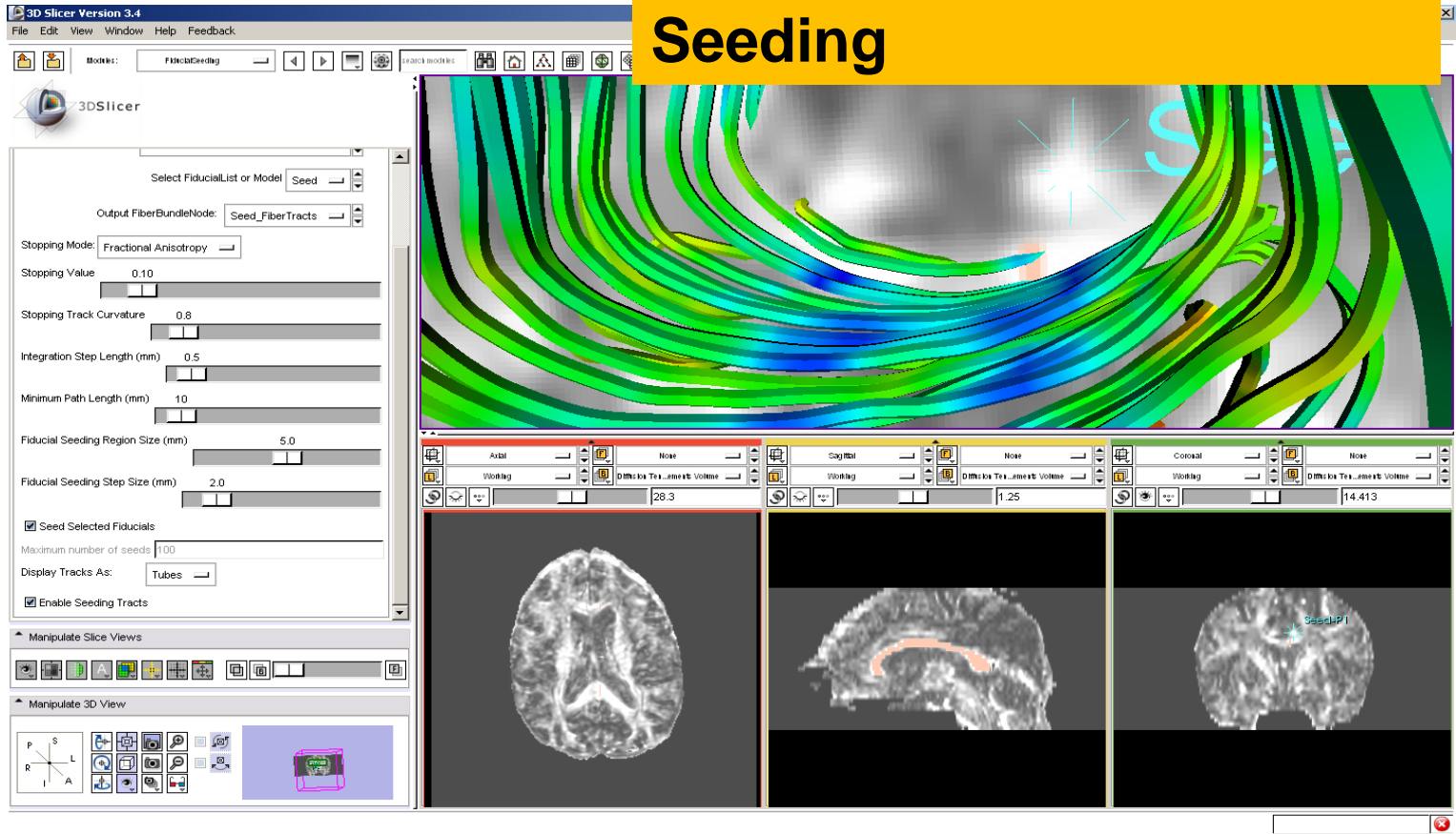
Select the **Seed-P1** fiducial:
we will use this fiducial to
drive the tractography





Fiducial Seeding

Select the module **Fiducial Seeding**



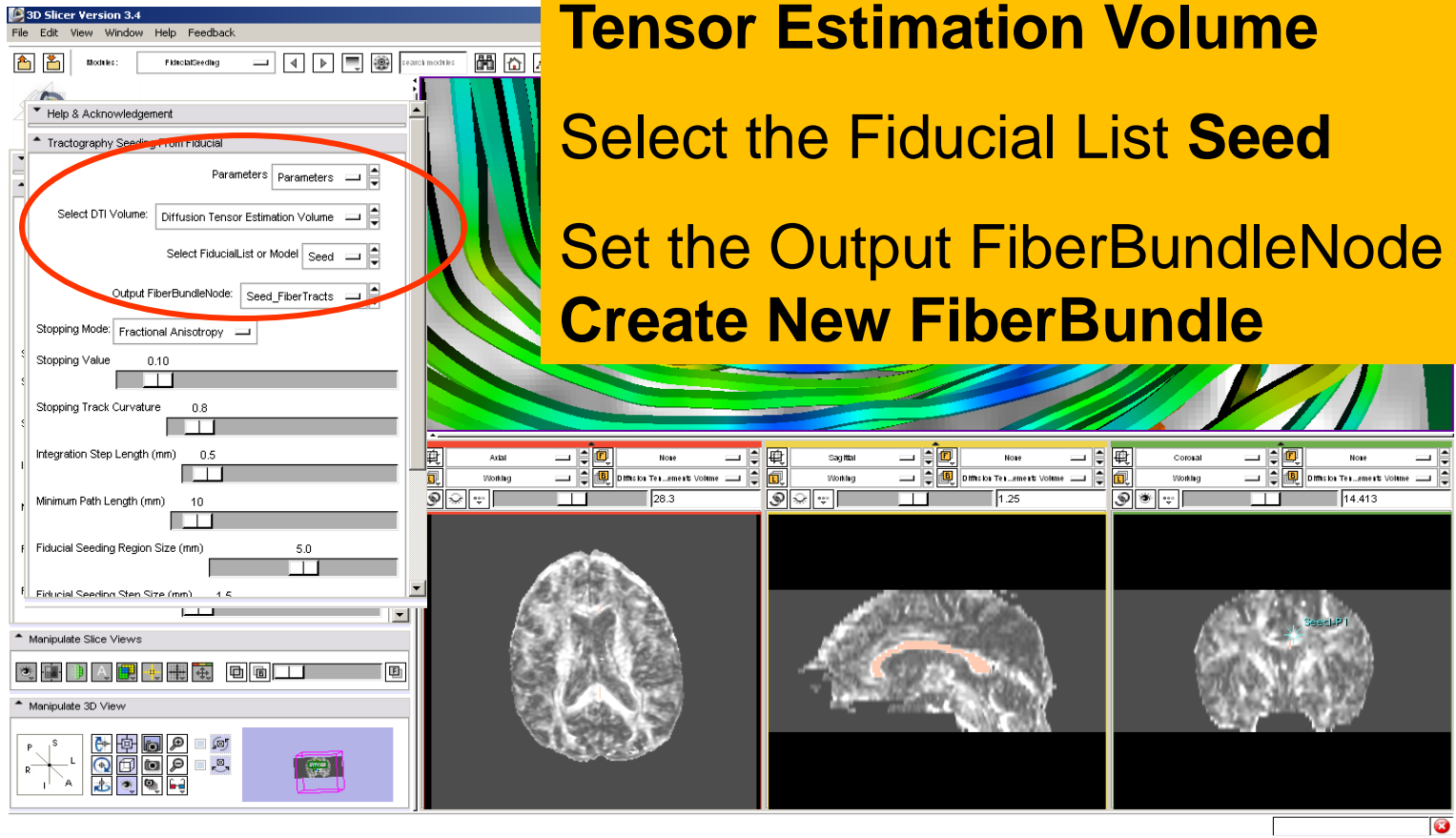


Fiducial Seeding

Set the DTI Volume to **Diffusion Tensor Estimation Volume**

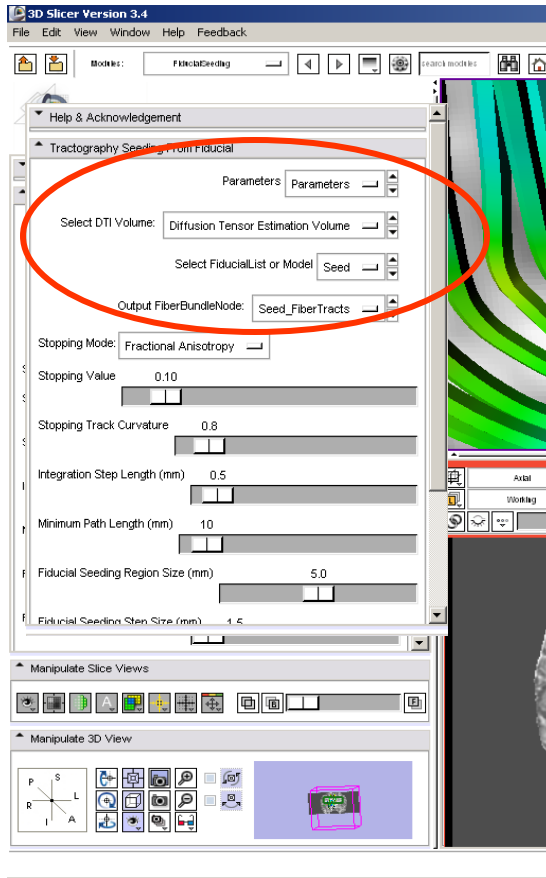
Select the Fiducial List **Seed**

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

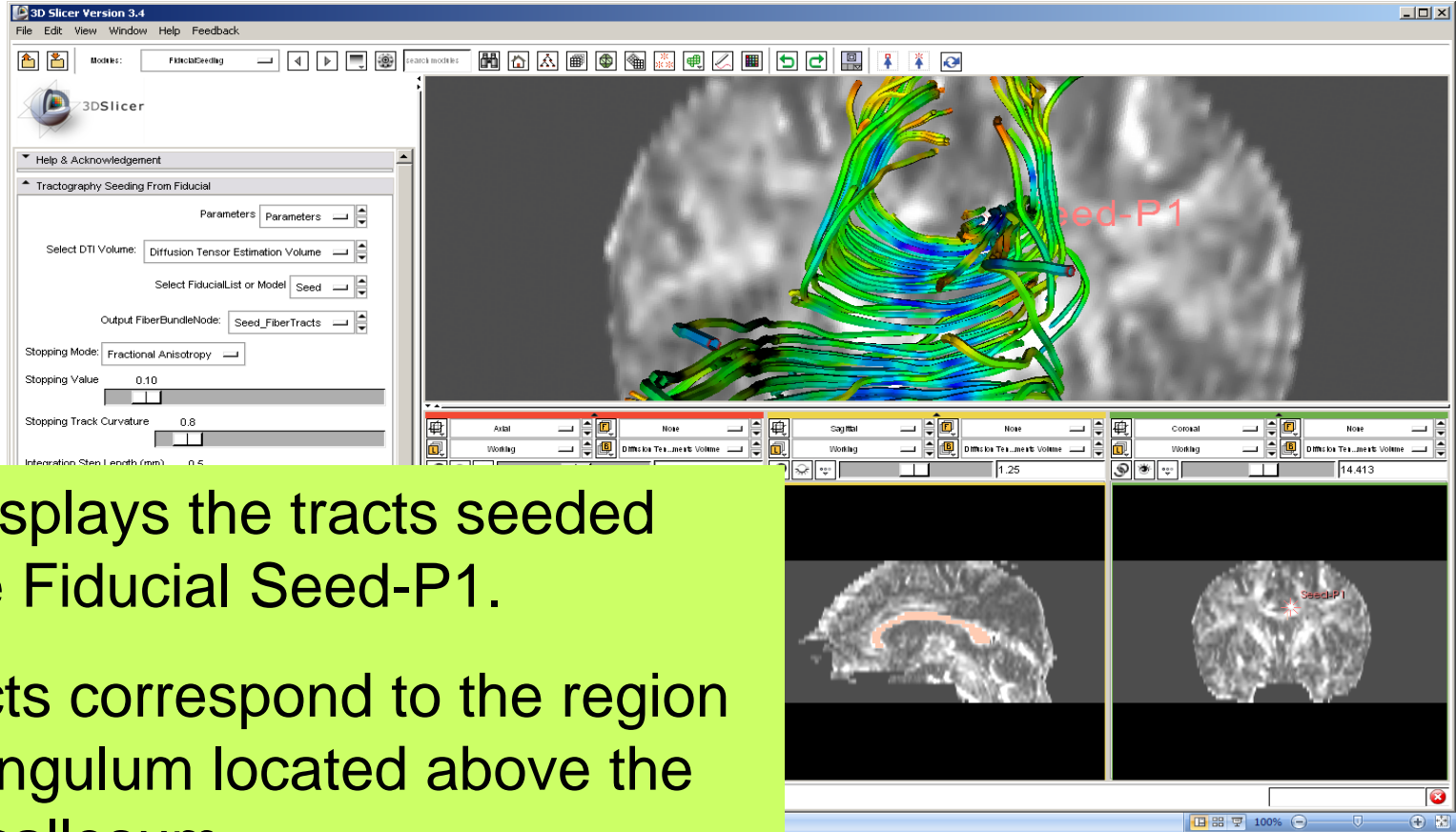
Step Length: 0.8 mm

Minimum Length: 10 mm

Fiducial Stepping Size: 1.5 mm



Fiducial Seeding

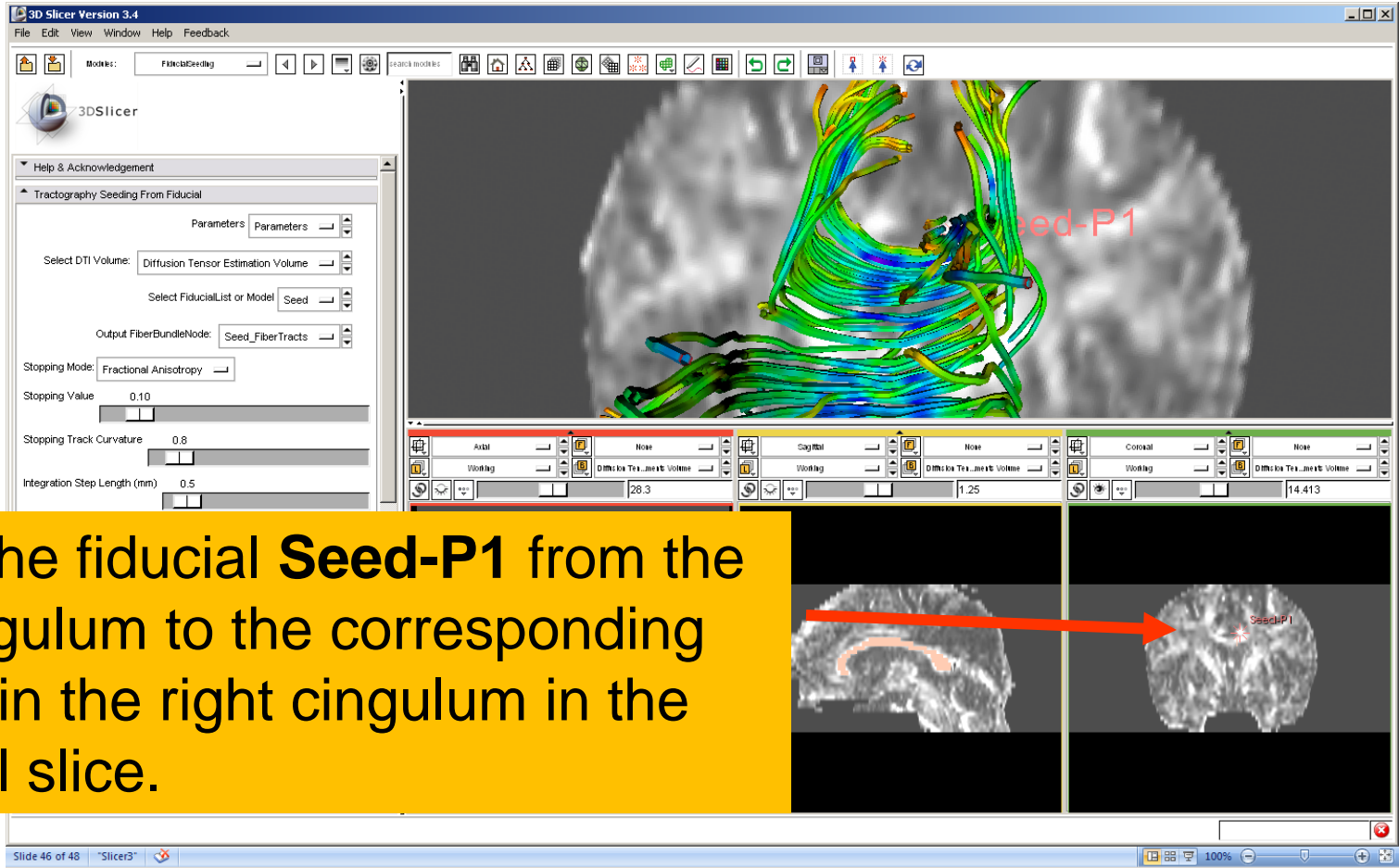


Slicer displays the tracts seeded from the Fiducial Seed-P1.

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

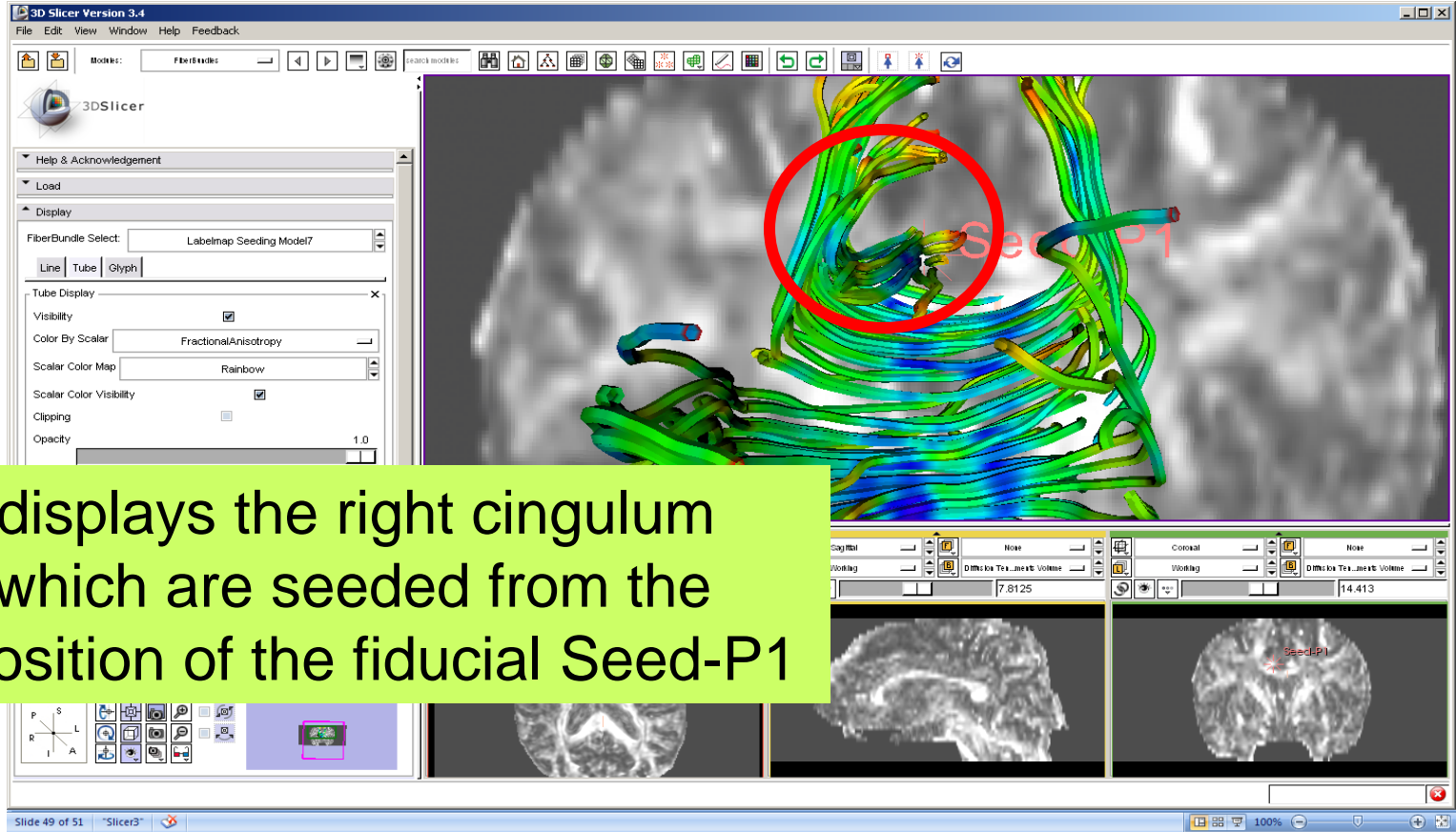


Fiducial Seeding





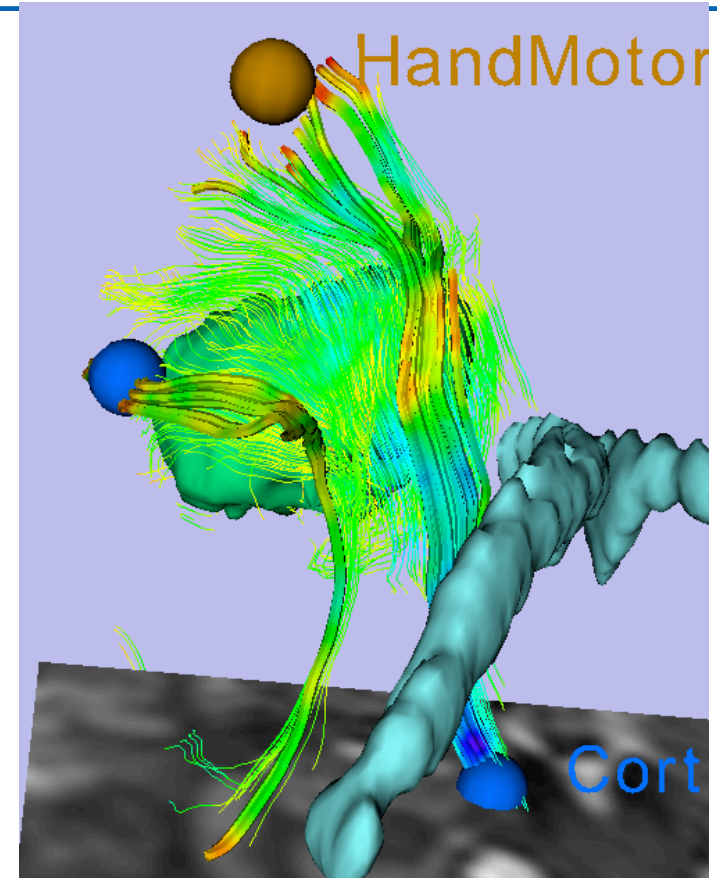
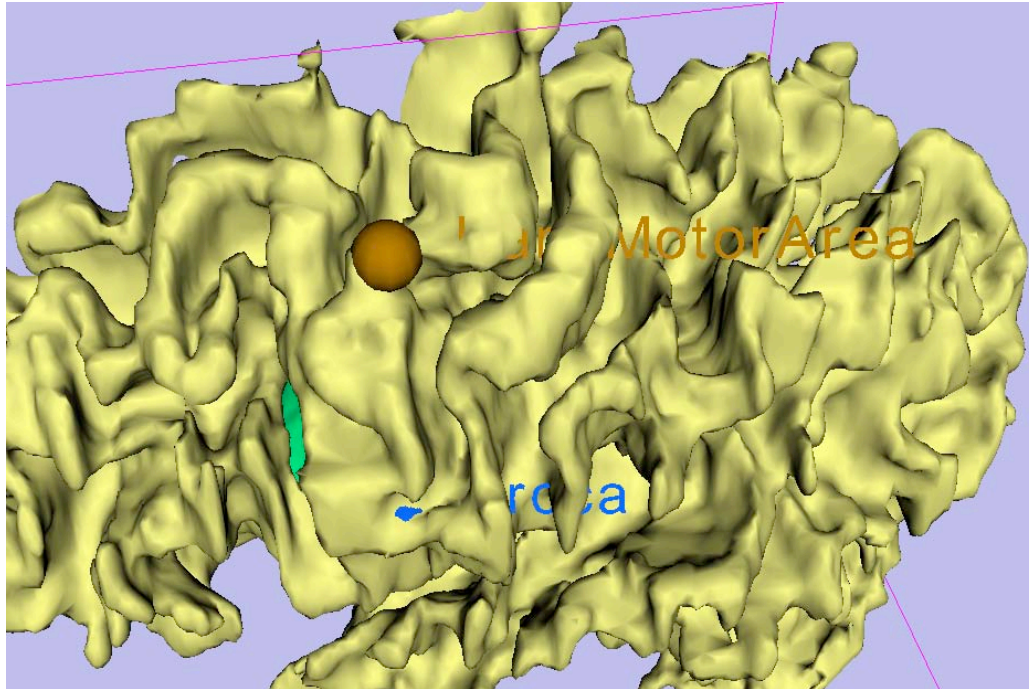
Fiducial Seeding



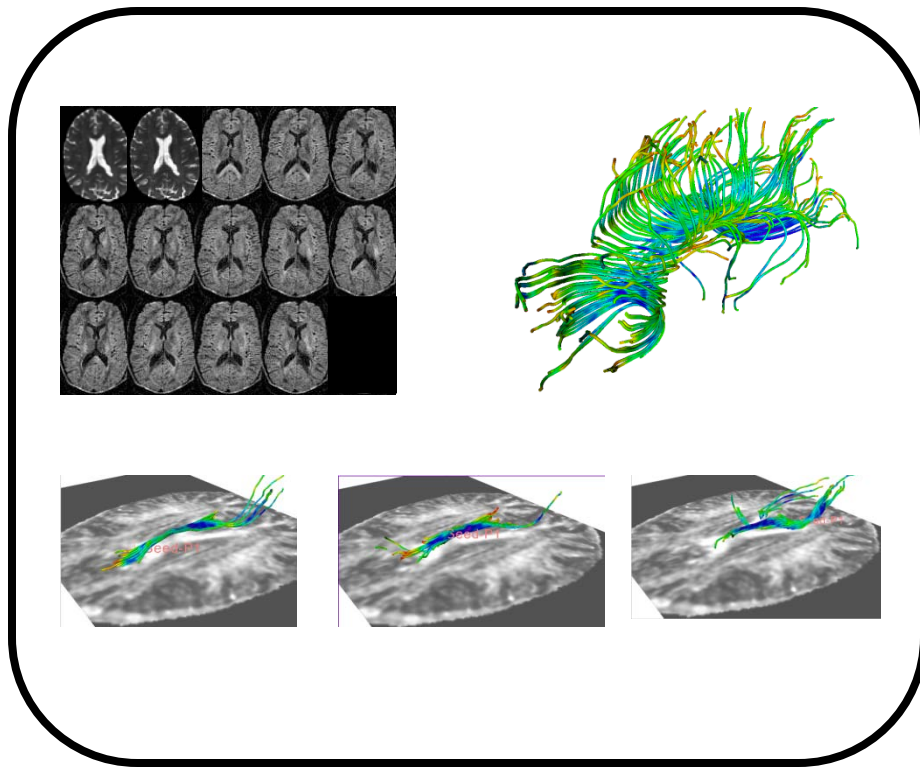
Slicer displays the right cingulum tracts which are seeded from the new position of the fiducial Seed-P1



Neurosurgical Application



Courtesy of Alexandra Golby, MD, Peter Black, MD and Ron Kikinis, MD
Brigham and Women's Hospital, Boston, MA



Part 5:

Saving a DTI Scene



DTI Scene

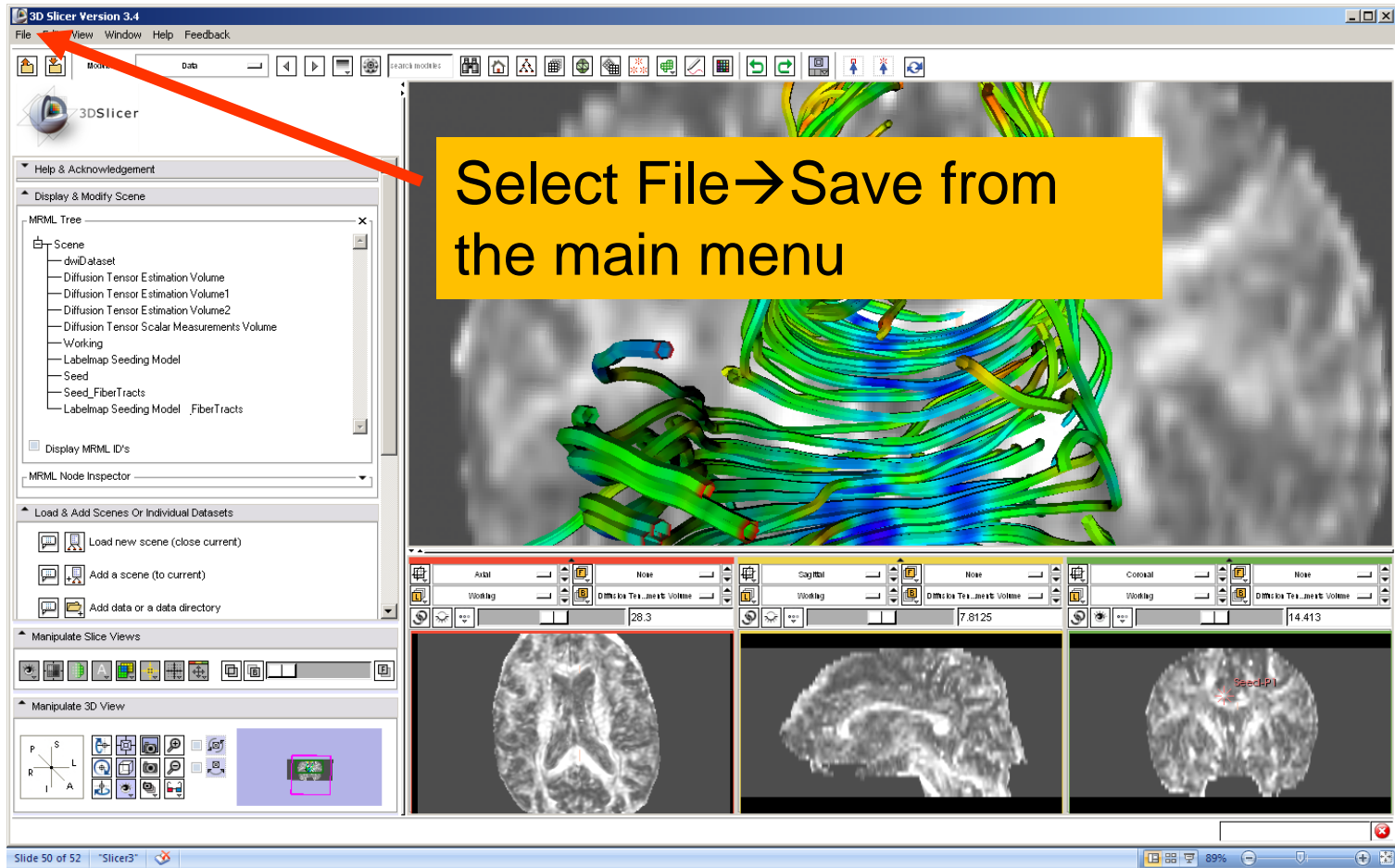
The screenshot shows the 3D Slicer Version 3.4 interface. A red circle highlights the 'Data' module in the top toolbar. A yellow text box with the text 'Select the module Data' is overlaid on the top right. A green text box with the text 'Slicer displays the list of volumes and models generated in this tutorial' is overlaid on the center. The MRML Tree on the left lists various volumes and models. The main 3D view shows a brain with fiber tracts and a red 'Seed: P1' label. The bottom panel shows three slice views: axial, sagittal, and coronal.

Select the module Data

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



Saving a DTI Scene





Saving a DTI Scene

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

The screenshot shows the 3D Slicer 3.4 interface with the 'Save Scene and Unsaved Data' dialog box open. The dialog box has a 'Save Scene & Data Options' section with a table of nodes to be saved. The 'Save Selected' button is circled in red.

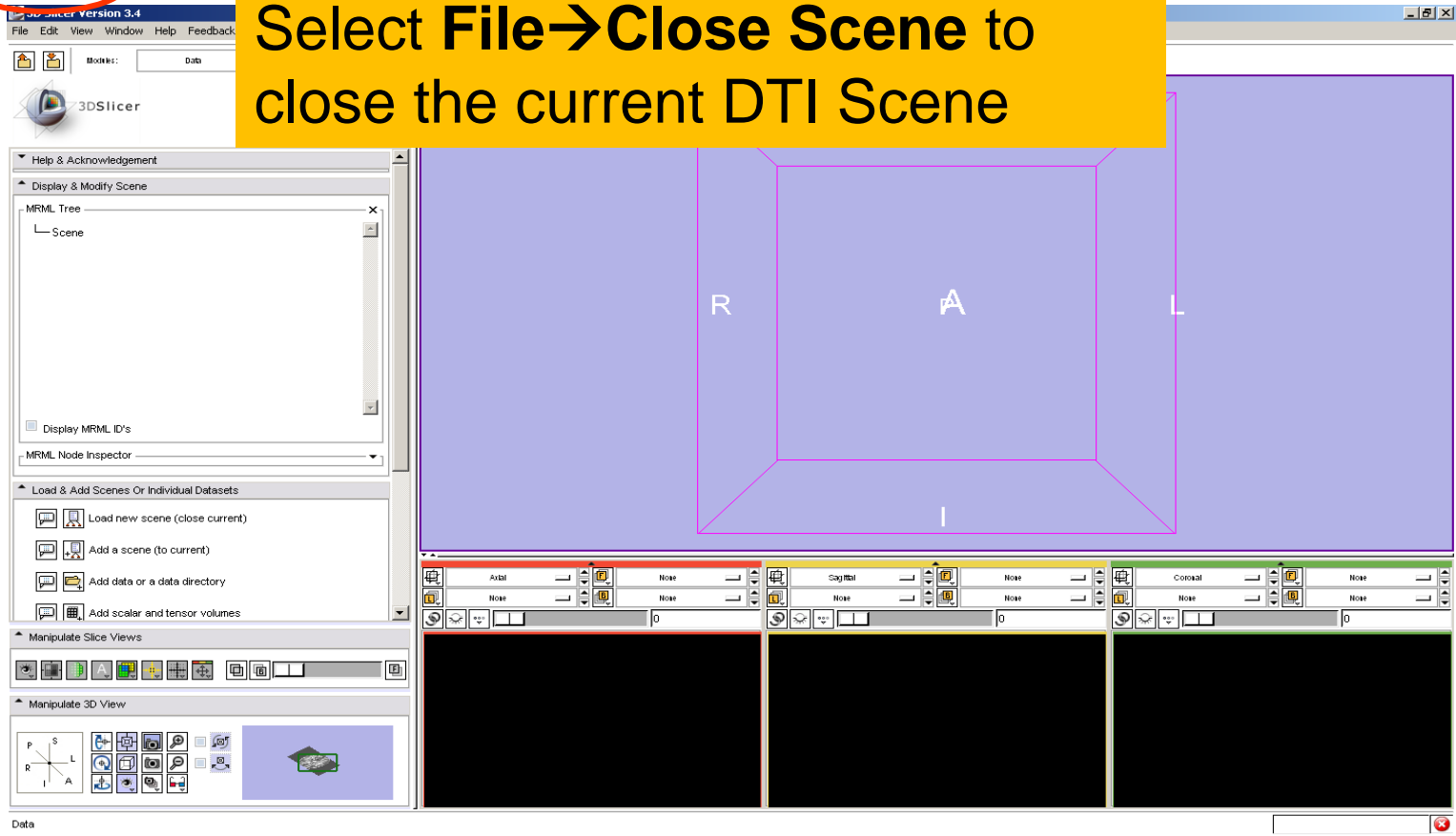
Select	Node Name	Node Type	Node Status	File Format	File Name	Data Directory
<input checked="" type="checkbox"/>	[Scene Description]	(SCENE)	Modified	MRRM (.mrm)	SlicerScene1	C:/SlicerData/DiffusionDataset/
<input type="checkbox"/>	dwiDataset	DiffusionWei...	Not Modified	NRRD (.nhdr)	dwiDataset.nhdr	C:/SlicerData/DiffusionDataset/
<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



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

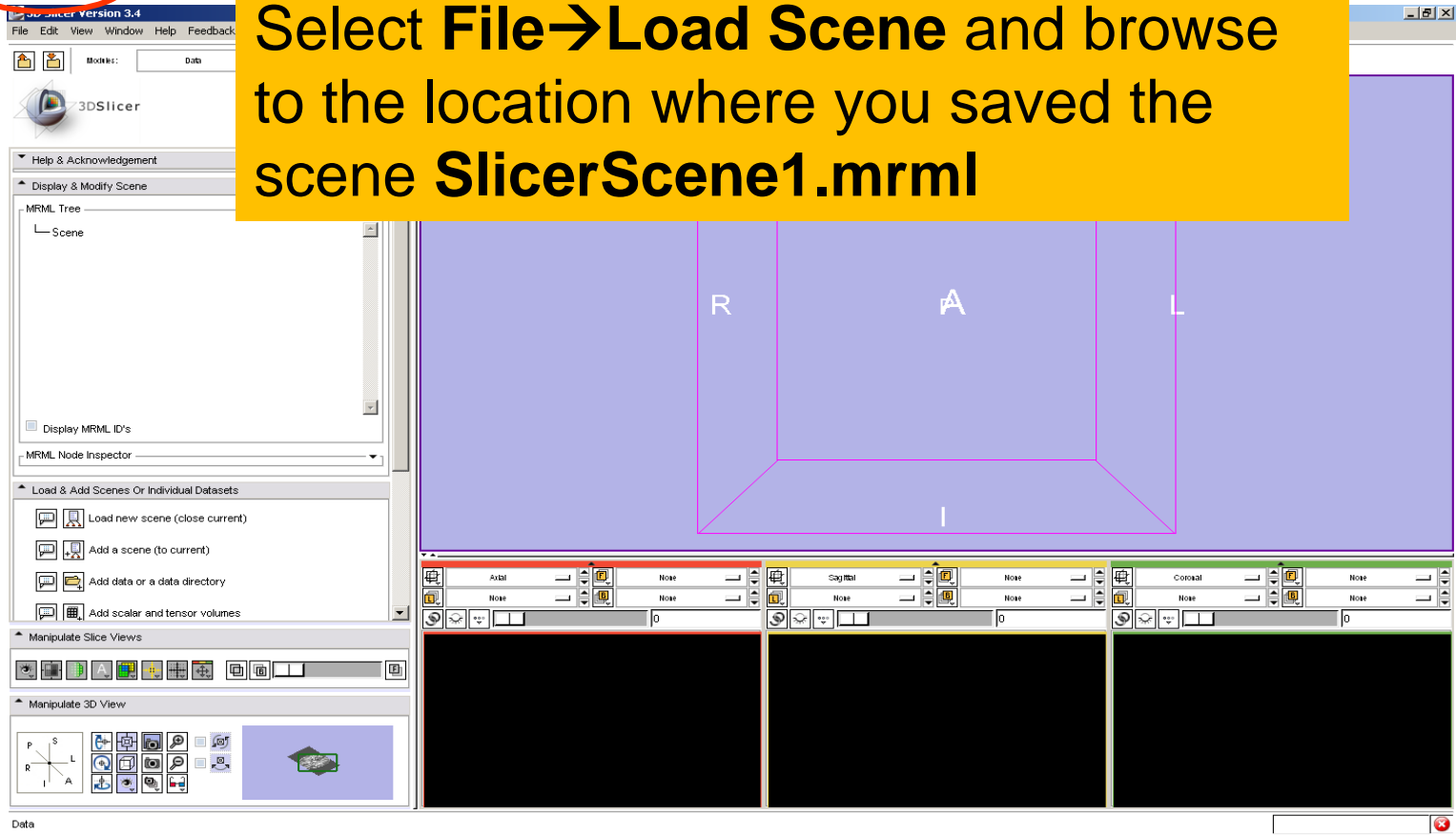




Loading a DTI Scene



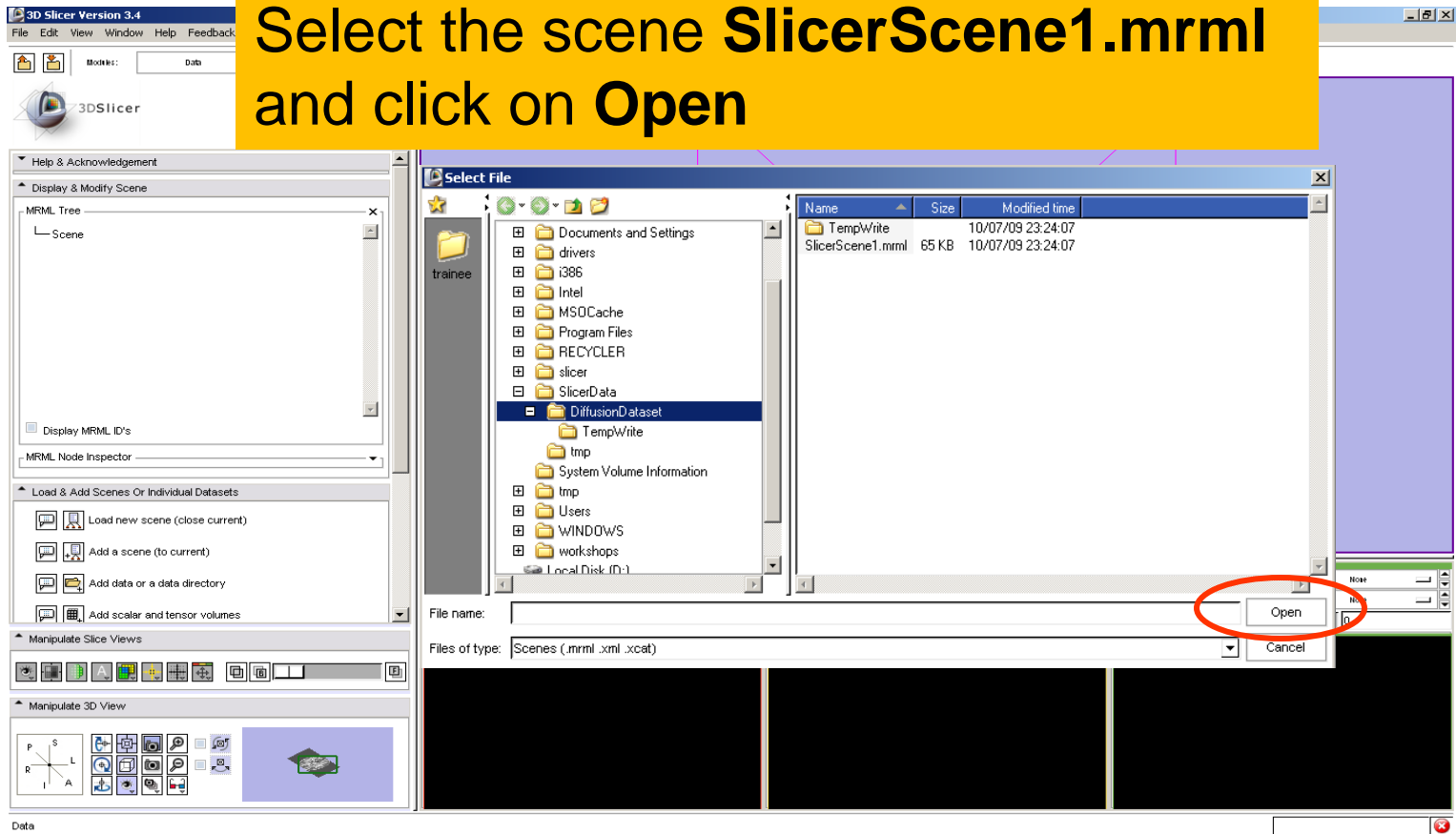
Select **File** → **Load Scene** and browse to the location where you saved the scene **SlicerScene1.mrml**





Loading a DTI Scene

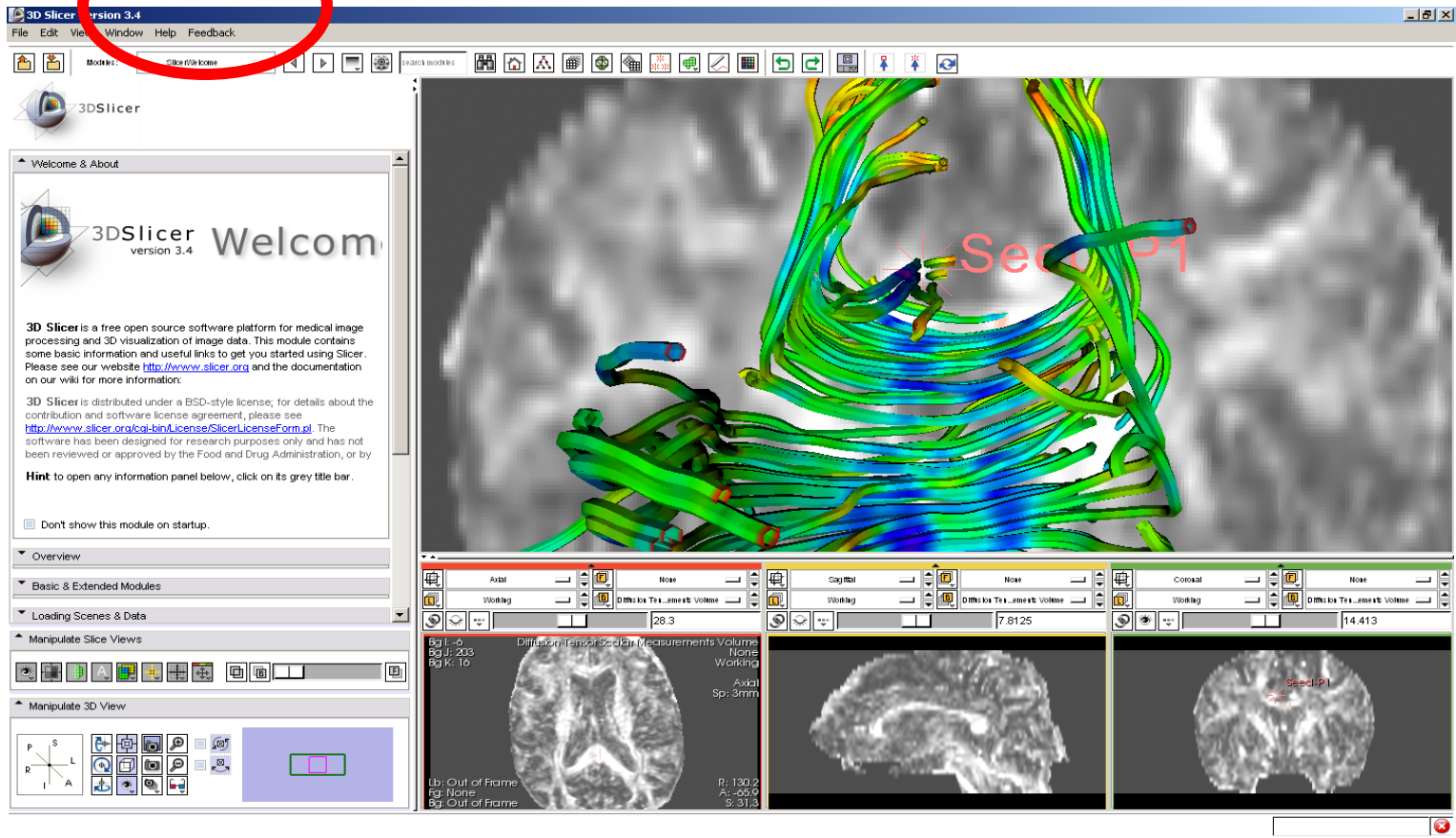
Select the scene **SlicerScene1.mrml** and click on **Open**





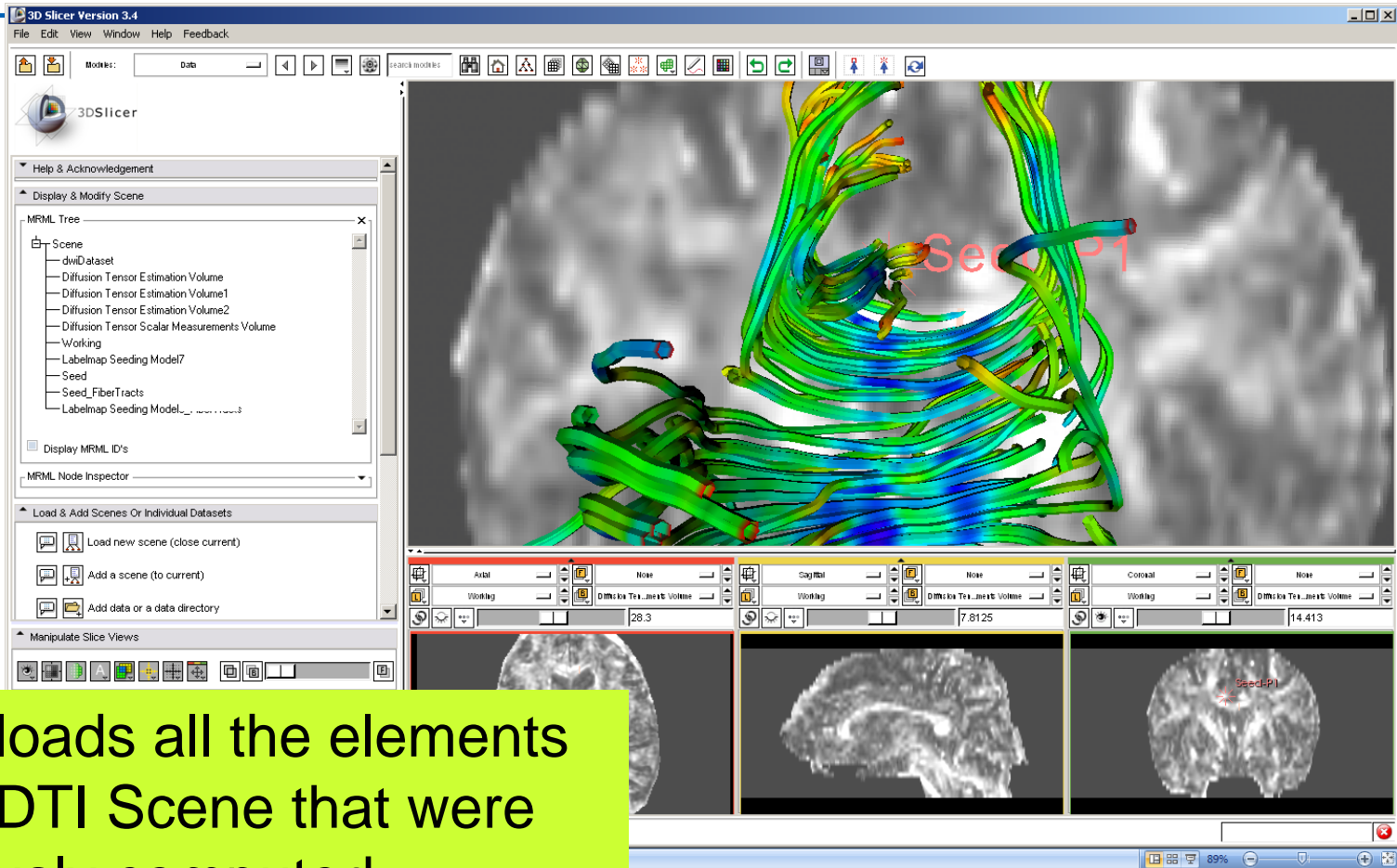
Loading a DTI Scene

Select the module **Data**





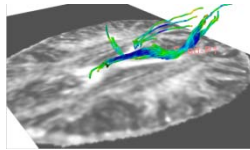
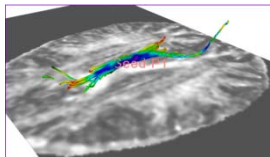
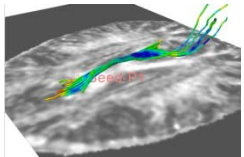
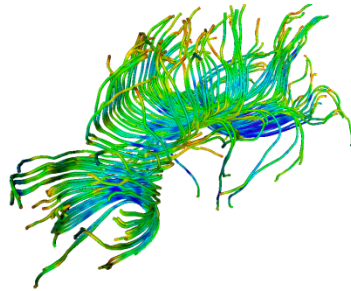
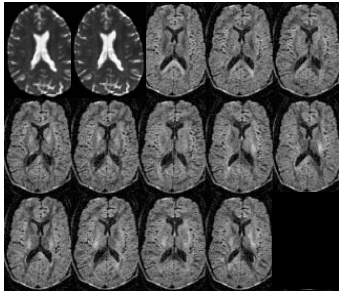
Loading a DTI Scene



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.

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