Diffusion MRI Analysis

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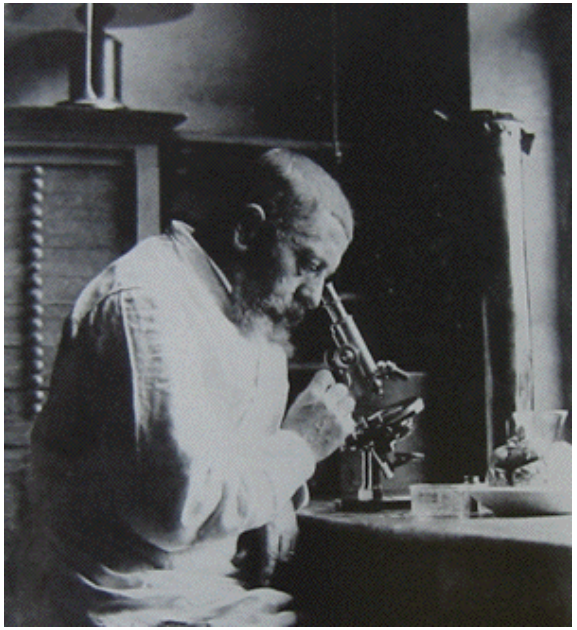
Brain Anatomy

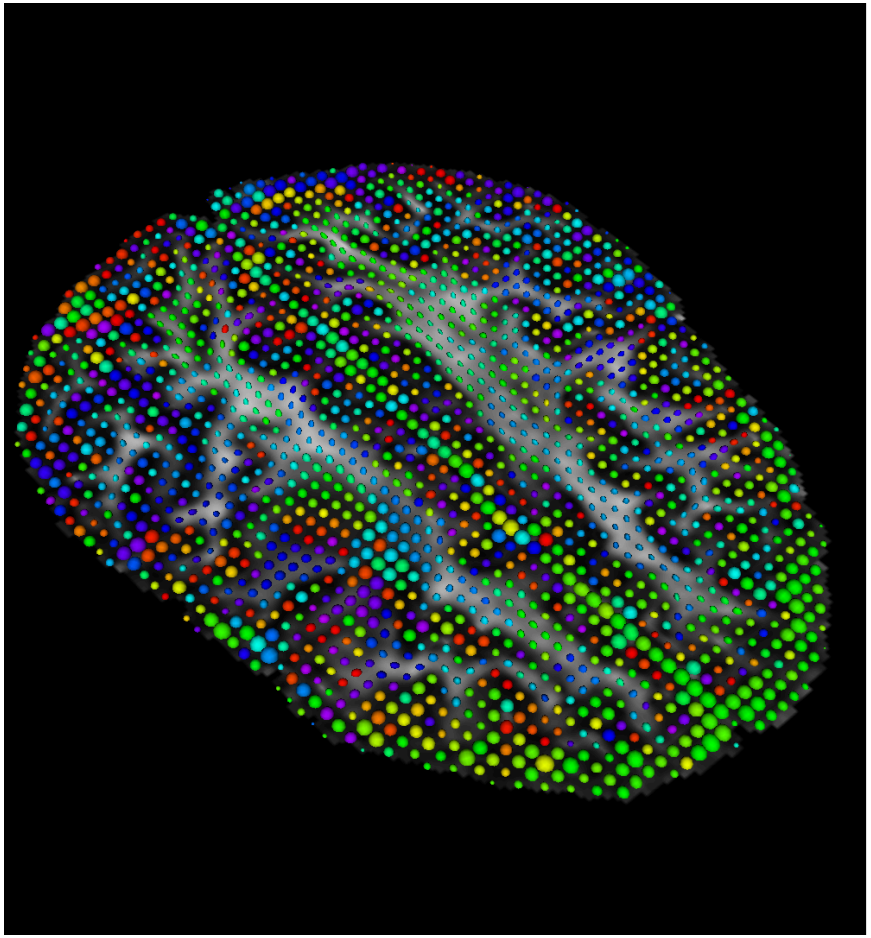
- White matter ~45% of the brain
- Myelinated nerve fibers (~ 10 μm axon diameter)

White Matter Exploration



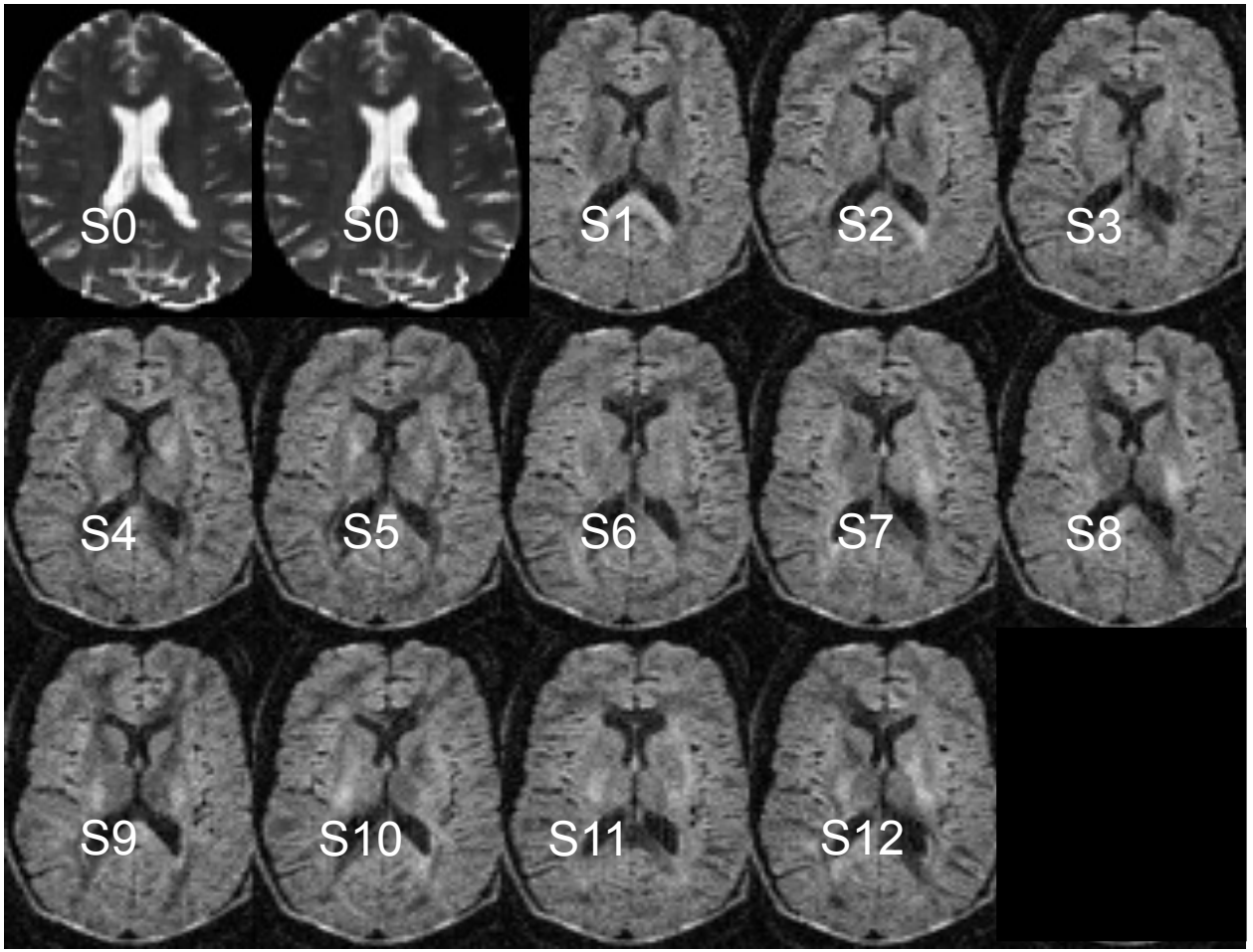
Jules Joseph Dejerine (*Anatomie des centres nerveux* (Paris, 1890-1901): Atlas of Neuroanatomy based on myelin stained preparation

Diffusion Tensor Imaging (DTI)



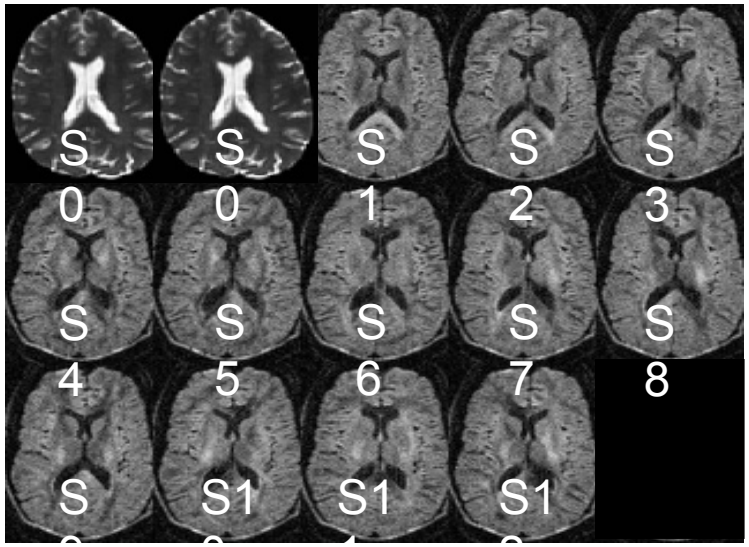
- First non-invasive window on white matter anatomy
- Measurement of the motion of water molecules using MRI techniques.
- Three-dimensional reconstruction of the trajectory of white matter bundles

Diffusion Weighted Imaging (DWI)



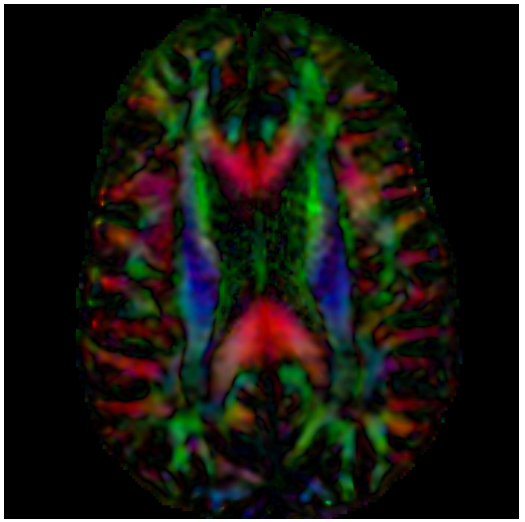
From DWI to DTI

DWI



DWI dataset acquired with
12 gradient and 2 baseline

DTI



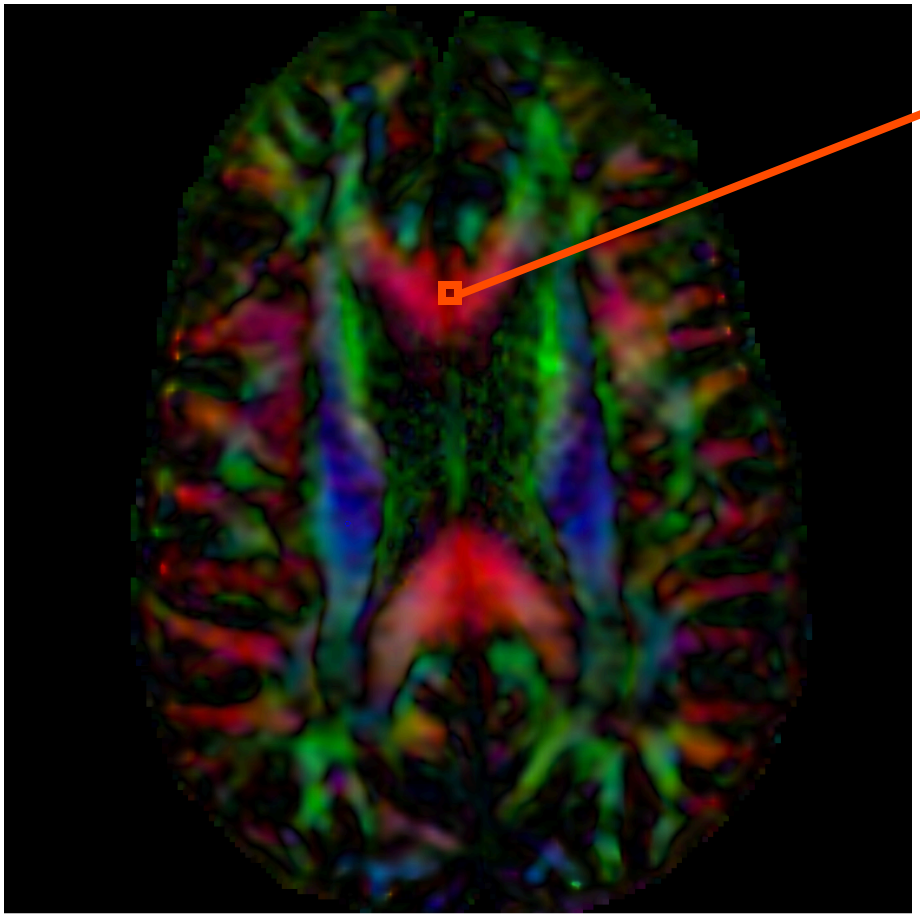
DTI dataset

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

Stejskal-Tanner (1965)

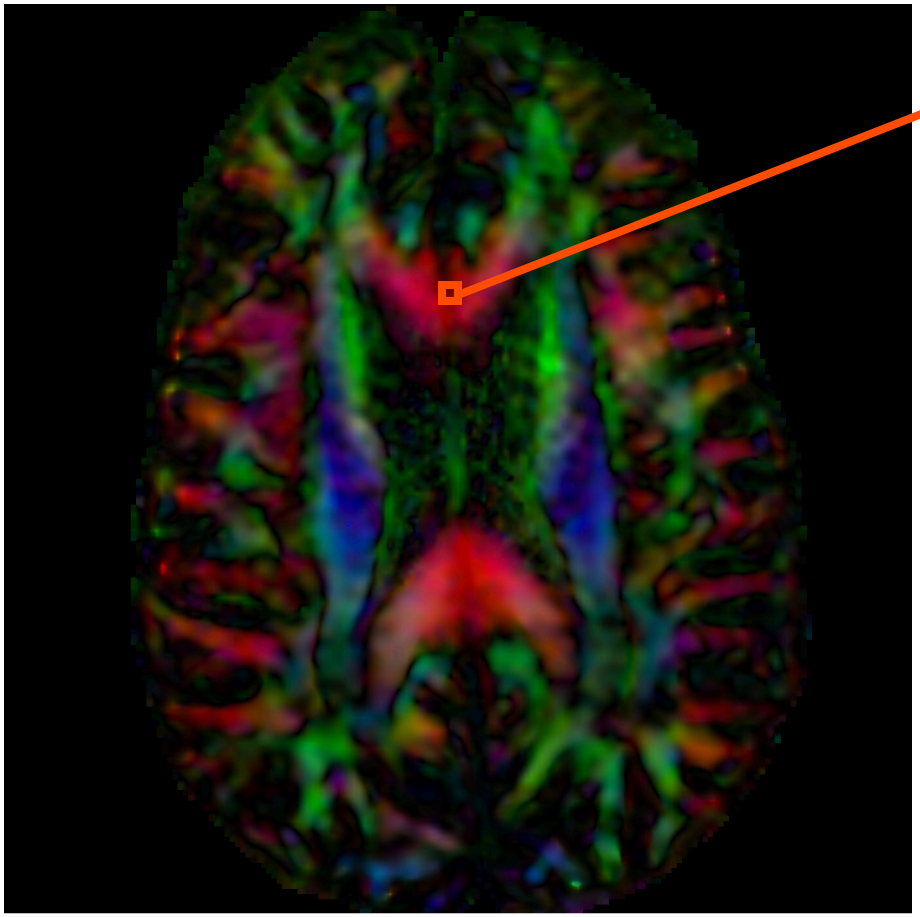
Si: DWI volume acquired with ith gradient
So: Baseline volume

Diffusion Tensor Imaging



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

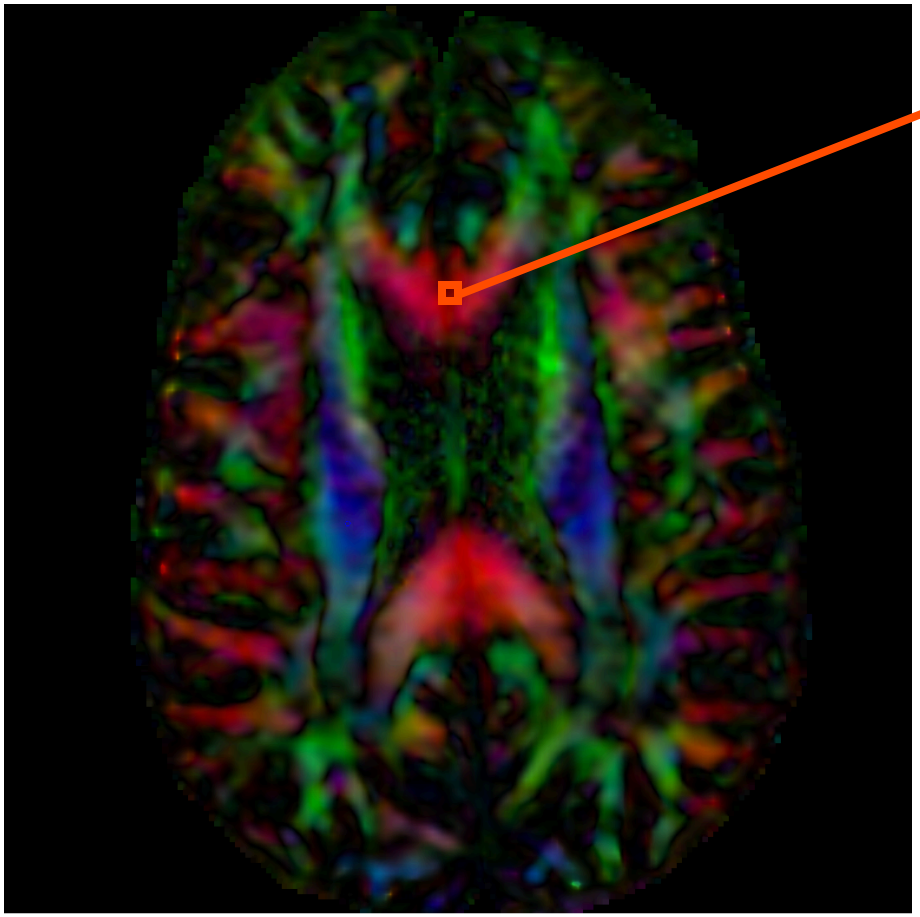
Diffusion Tensor Imaging



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

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

Diffusion Tensor Imaging



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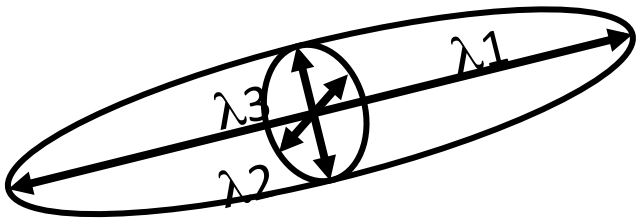
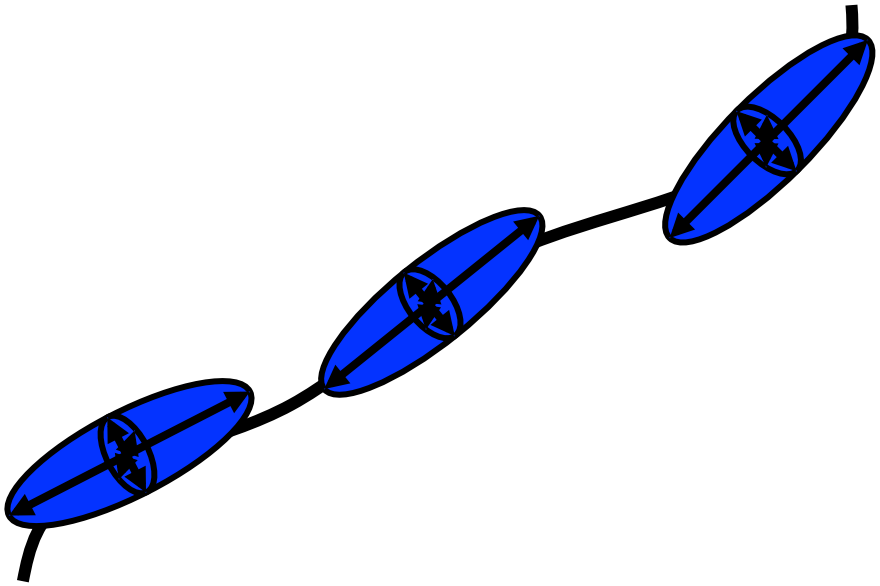
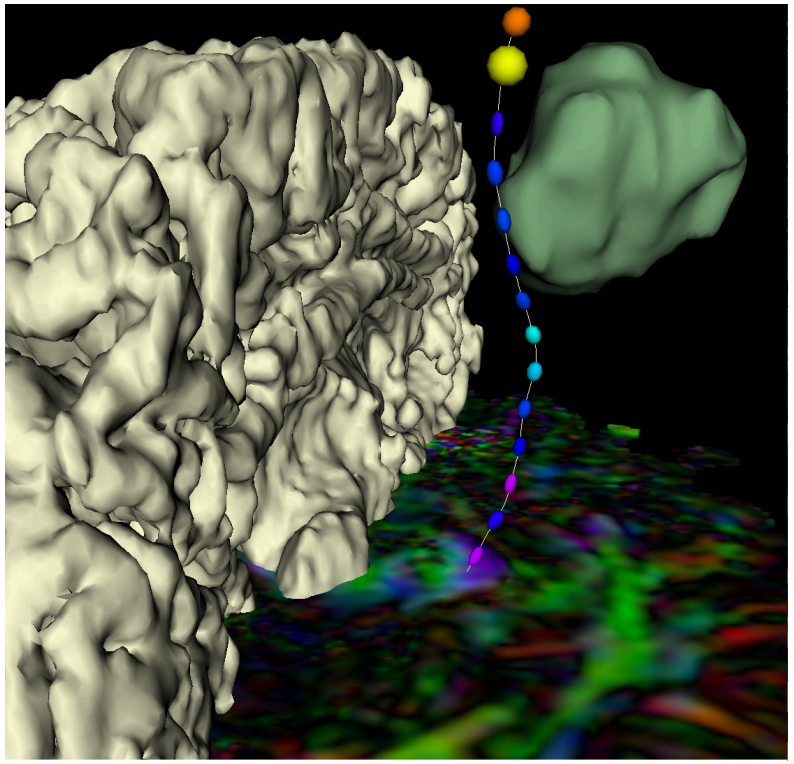


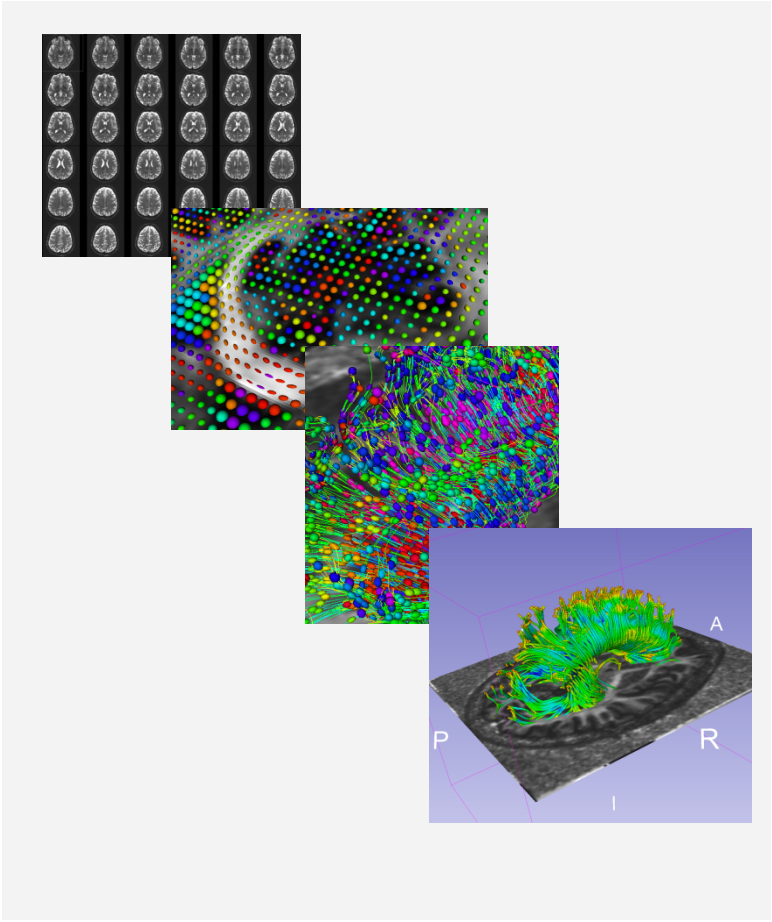
Tractography





DTI tractography provides 3D reconstruction of the trajectory of white matter pathways

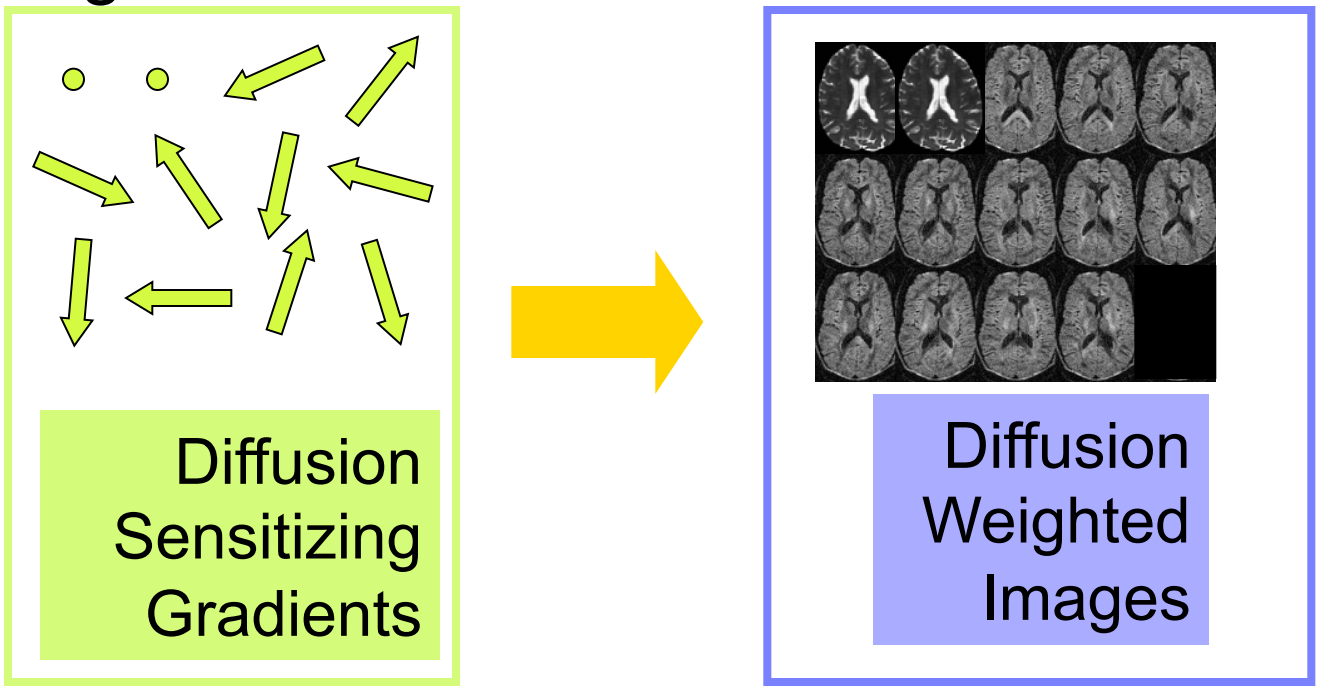
Tutorial Outline



This tutorial is an introduction to the fundamentals of Diffusion MRI analysis, from the estimation of diffusion tensors to the interactive 3D visualization of fiber tracts.

Tutorial Dataset

The tutorial dataset DiffusionMRI_tutorialData is a Diffusion Weighted MR scan of the brain acquired with 41 gradient directions and one baseline.



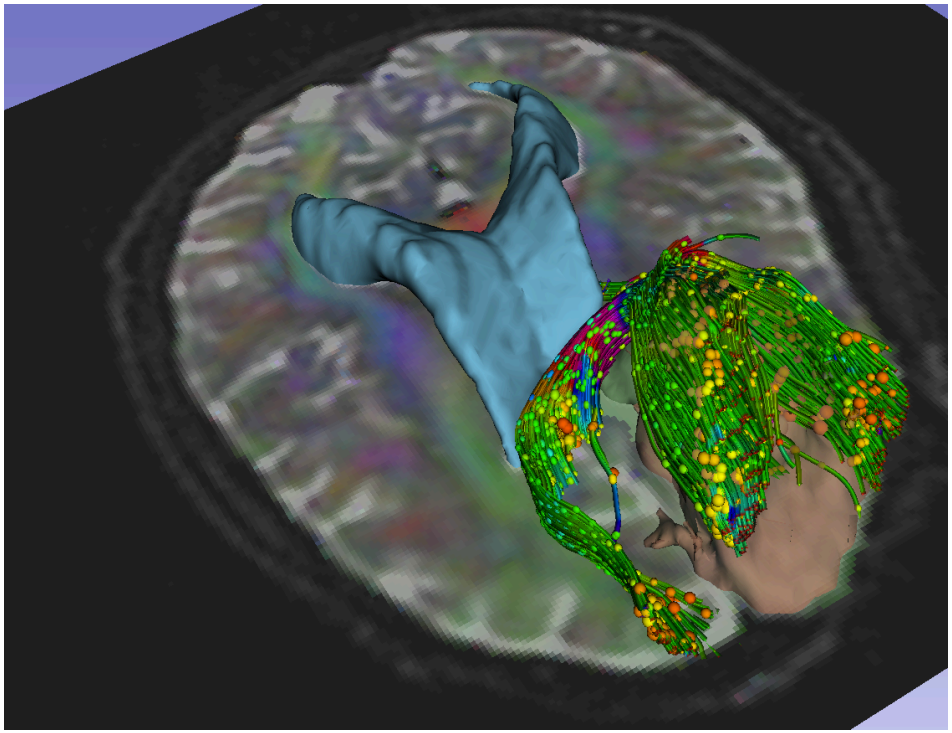
Tutorial Software

The tutorial uses the 3DSlicer version 4.3 software available at www.slicer.org

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. Slicer is a tool for research, and is not FDA approved.

3DSlicer



3D Slicer is a multi-institution effort supported by the National Institutes of Health.

- An end-user application for image analysis
- An open-source environment for software development
- A software platform that is both easy to use for clinical researchers and easy to extend for programmers

Learning Objectives

Following this tutorial, you'll be able to

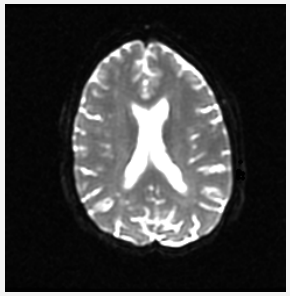
1) Estimate a tensor volume from a set of Diffusion Weighted Images

2) Understand the shape and size of the diffusion ellipsoid

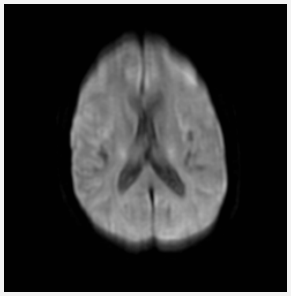
3) Reconstruct DTI tracts from a pre-defined region of interest

4) Interactively visualize DTI tracts seeded from a fiducial

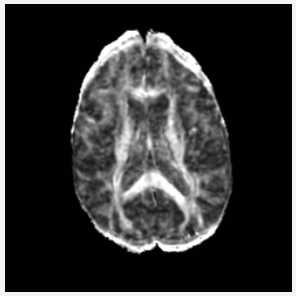
MR Diffusion Analysis Pipeline



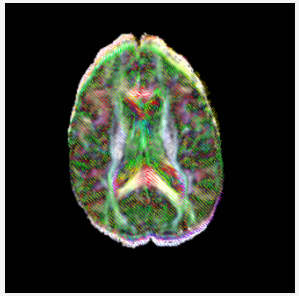
DWI
Acquisition



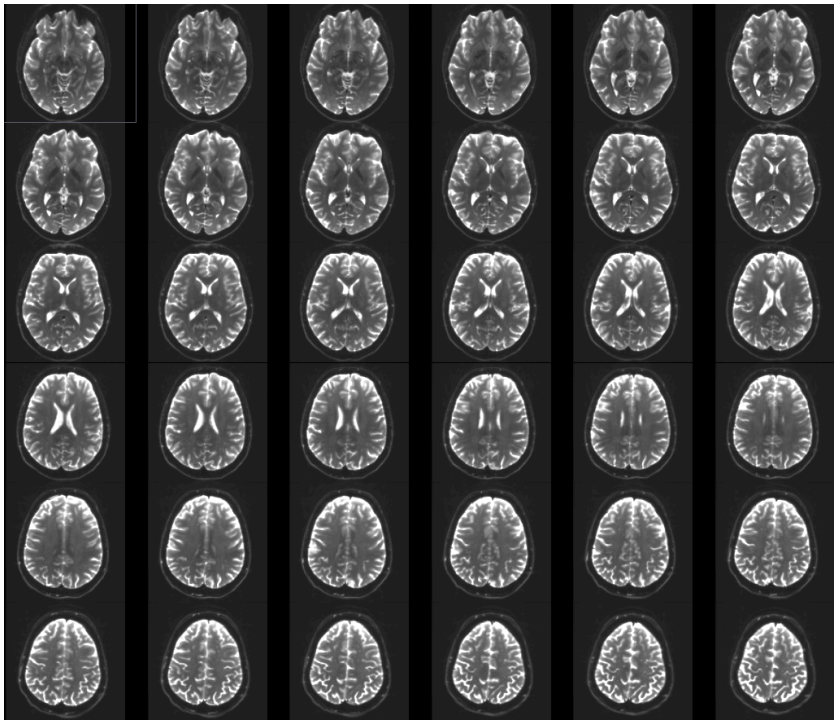
Tensor
Calculation



Scalar
Maps

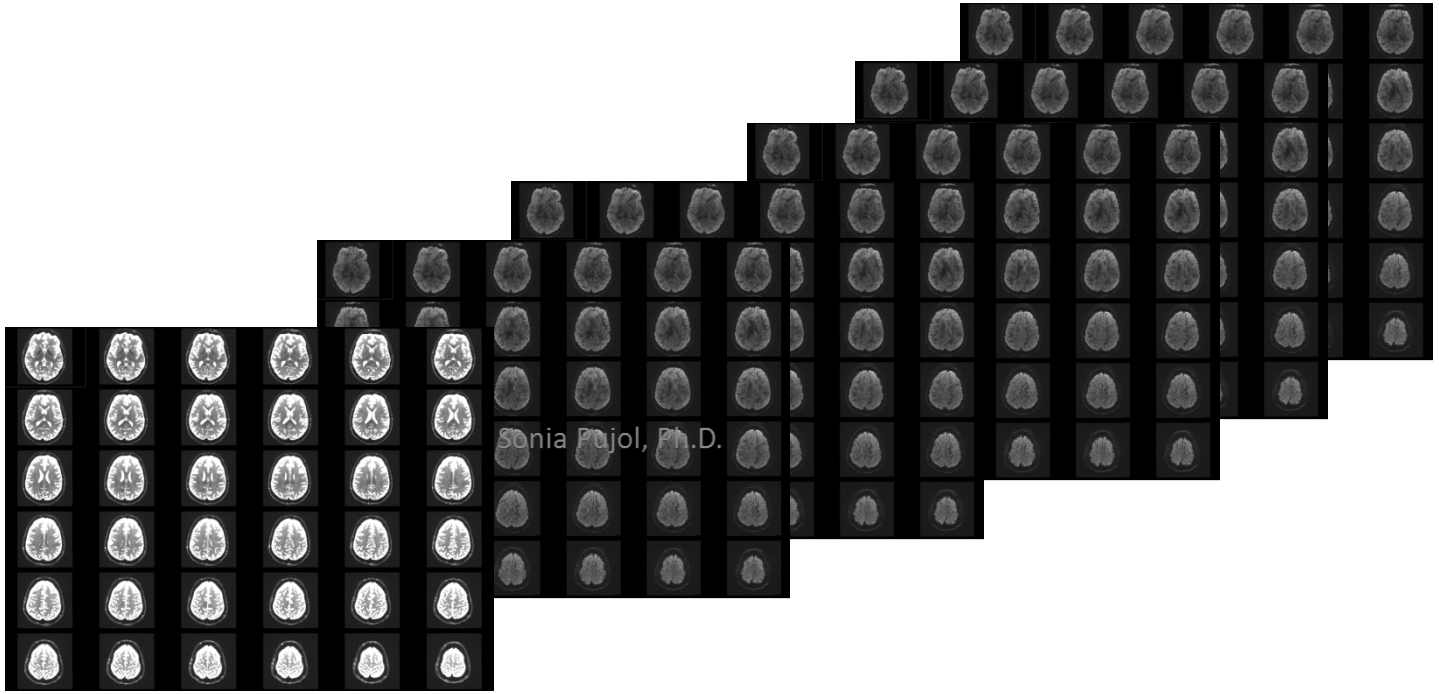


3D
Visualization



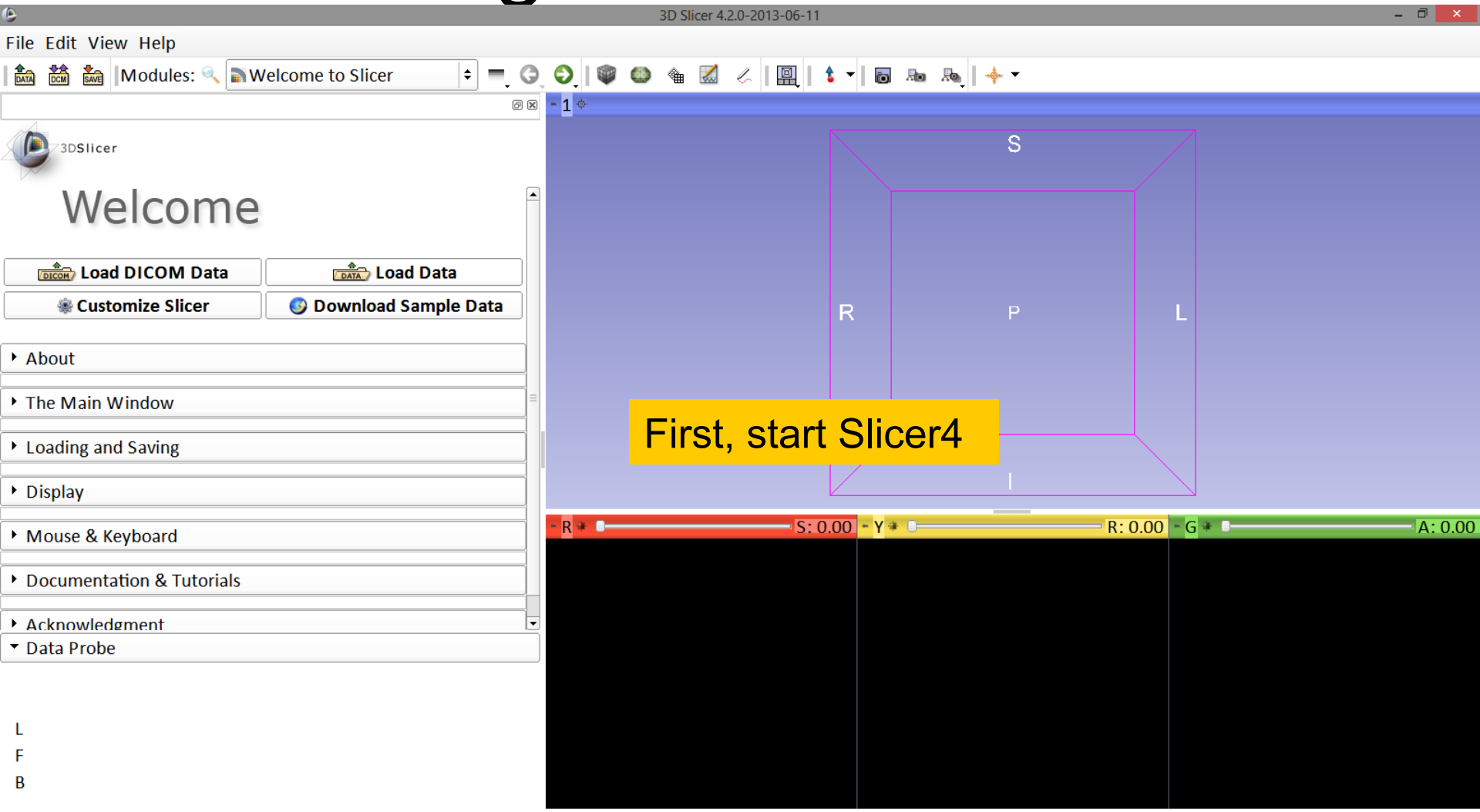
Part 1: From DWI images to Tensors

Understanding the DWI Dataset

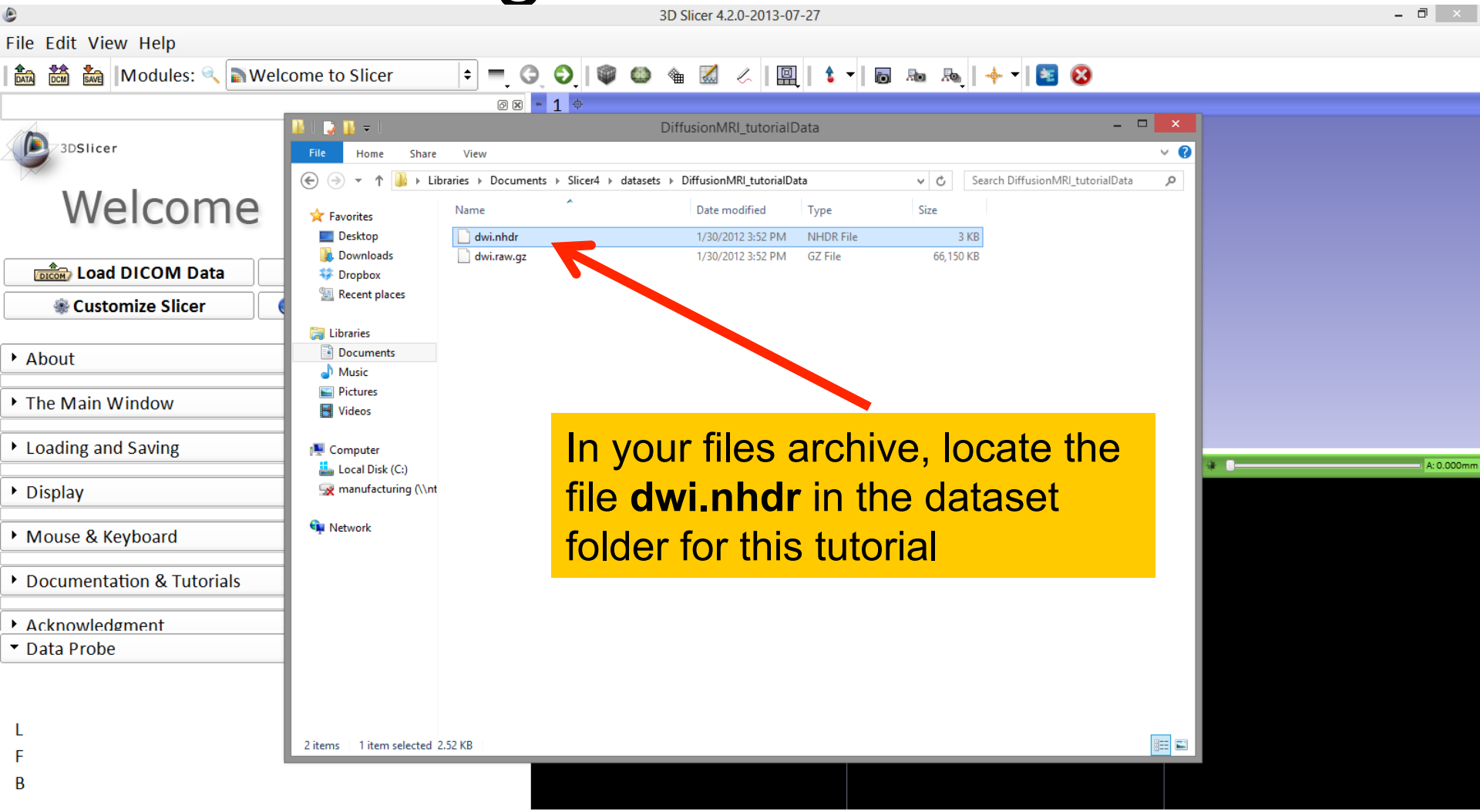


The Diffusion Weighted Imaging (DWI) dataset is composed of 1 volume acquired without diffusion-sensitizing gradient, and 41 volumes acquired with 41 different diffusion-sensitizing gradient directions.

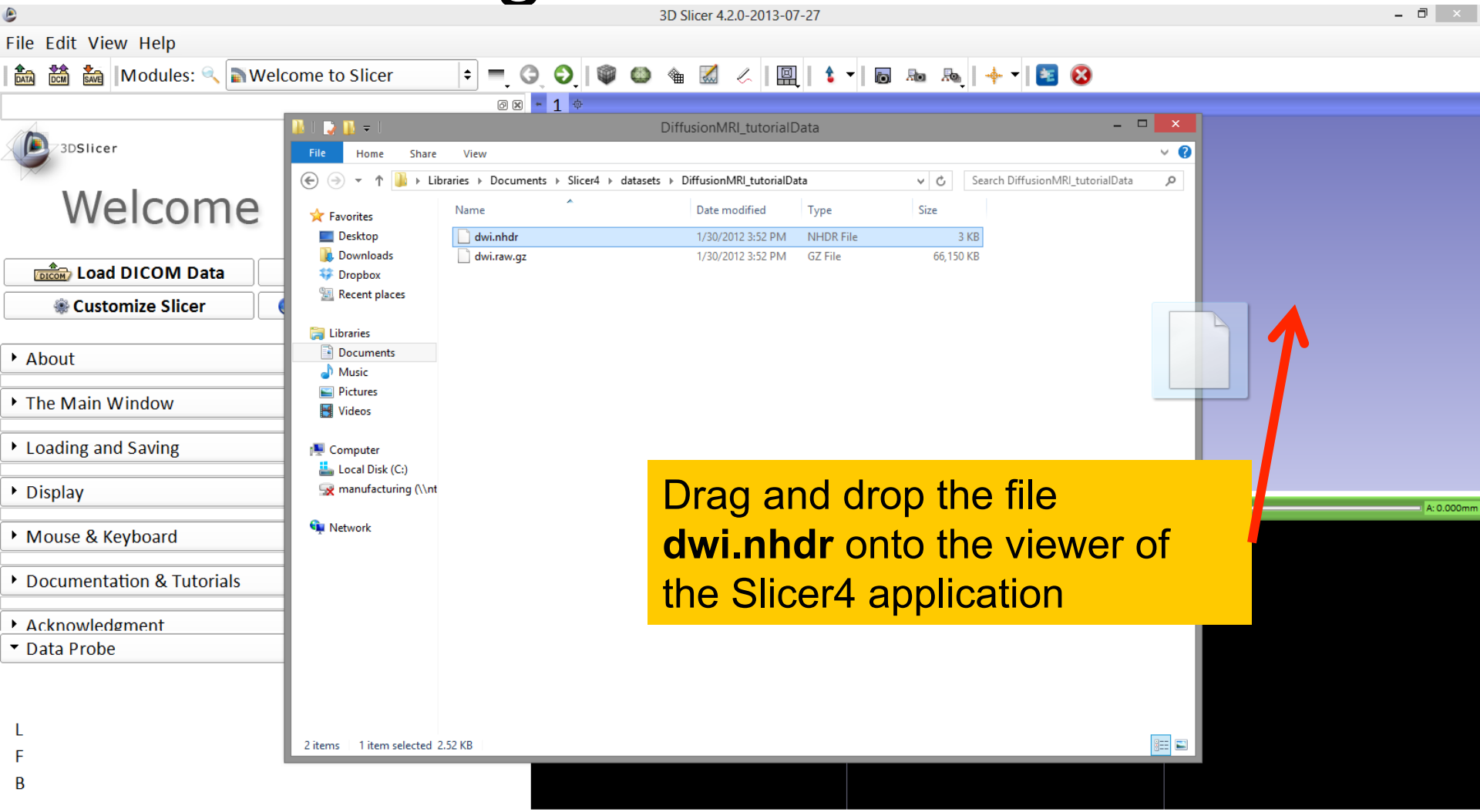
Loading the DWI Dataset



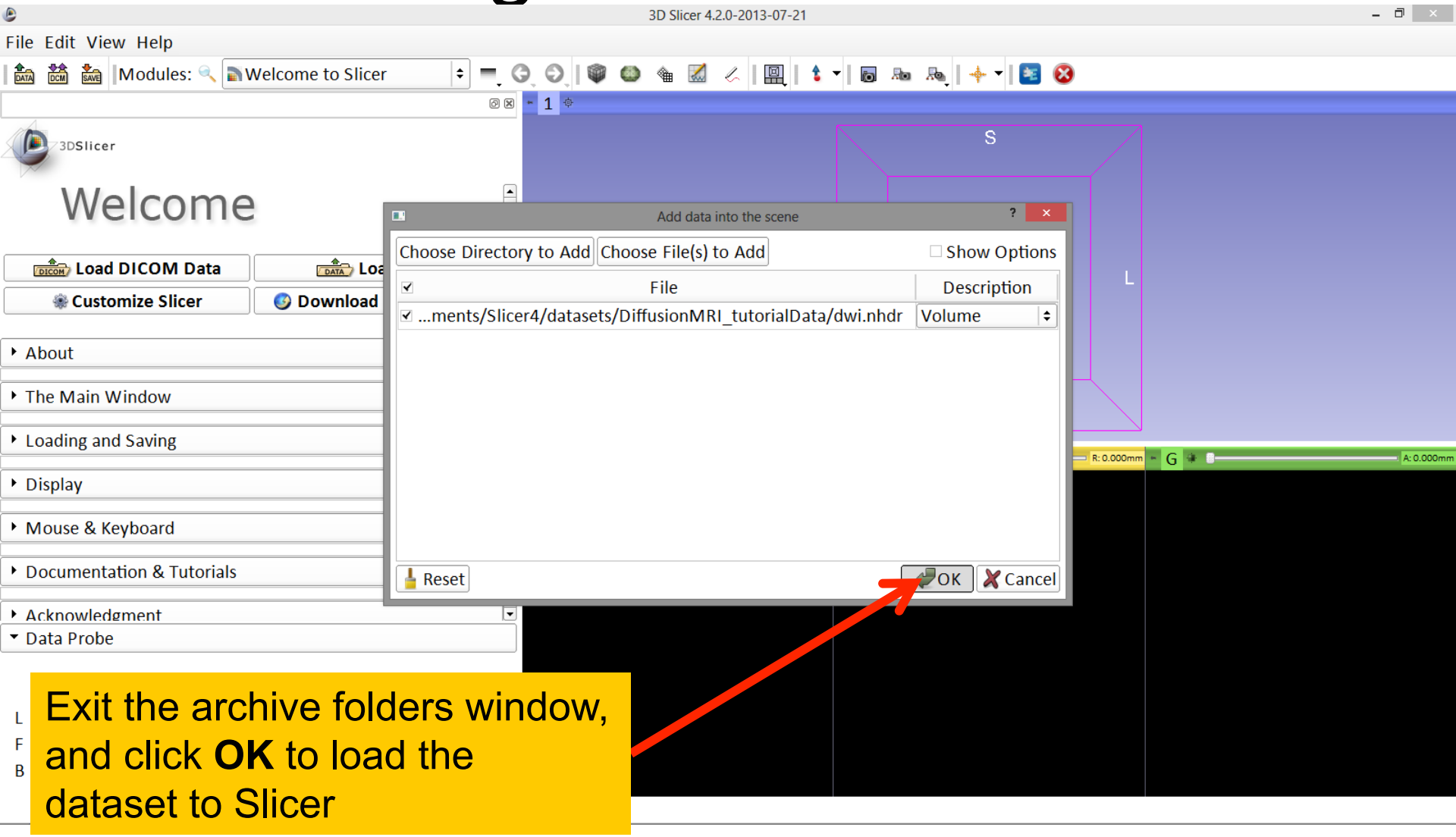
Loading the DWI Dataset



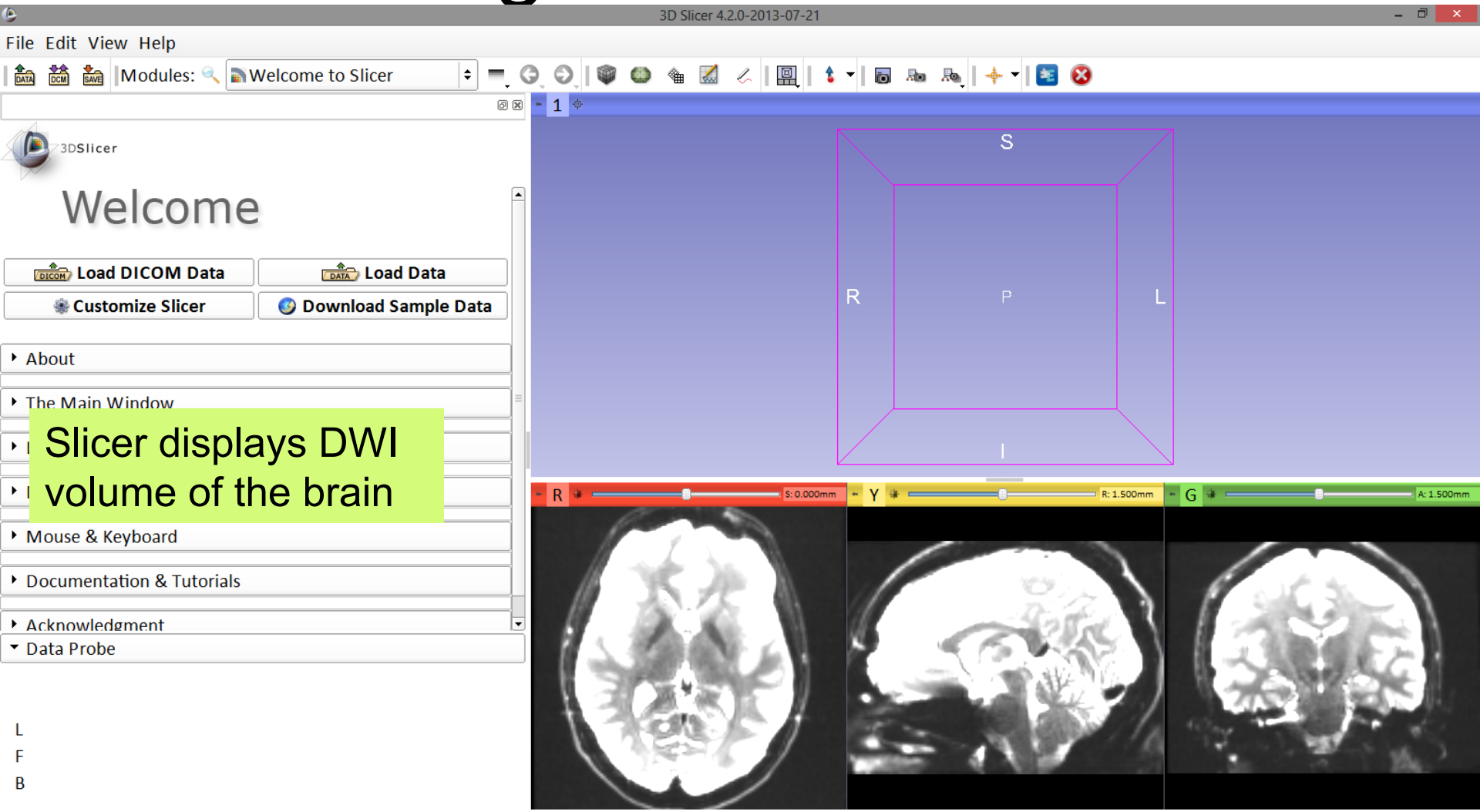
Loading the DWI Dataset



Loading the DWI Dataset

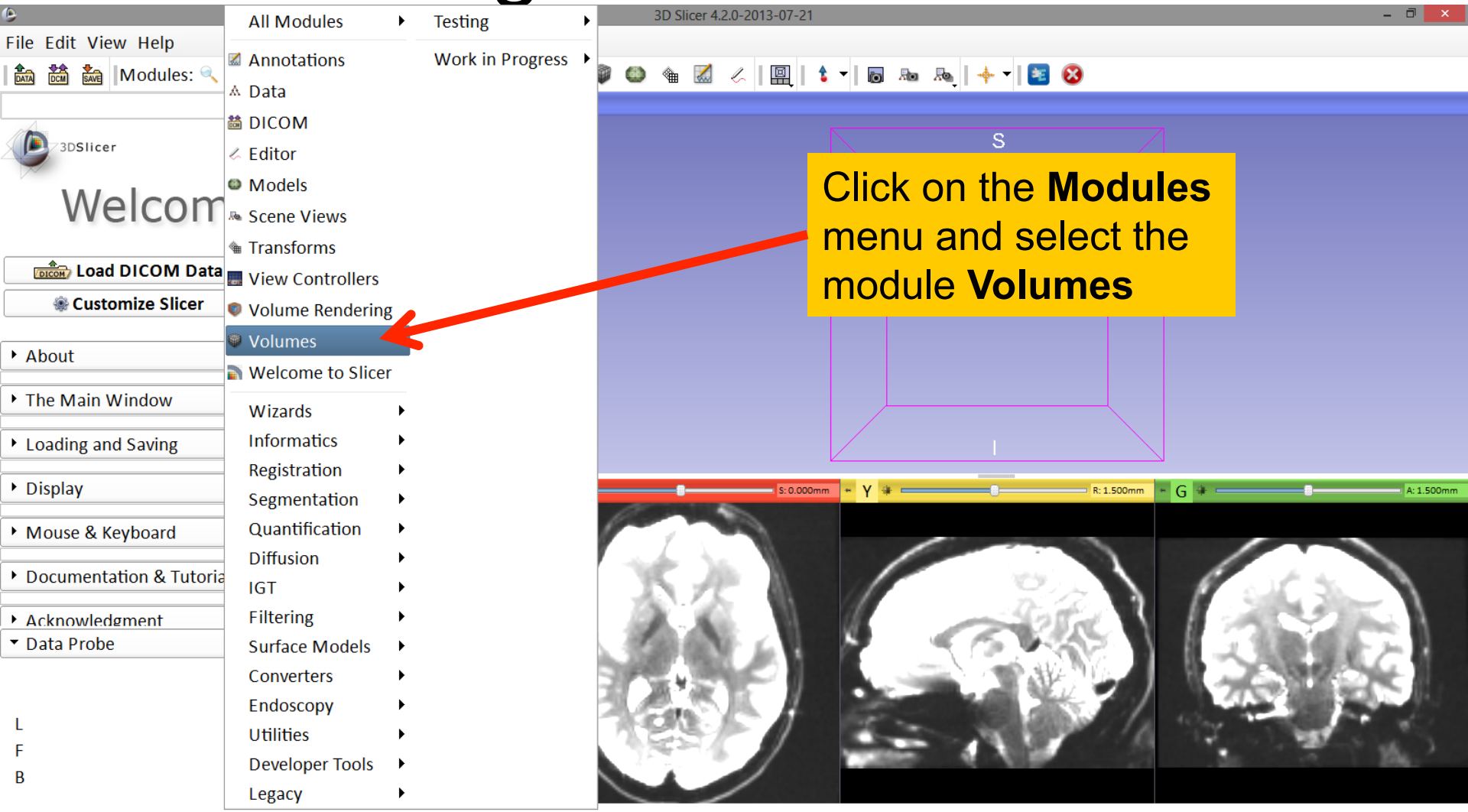


Loading the DWI Dataset

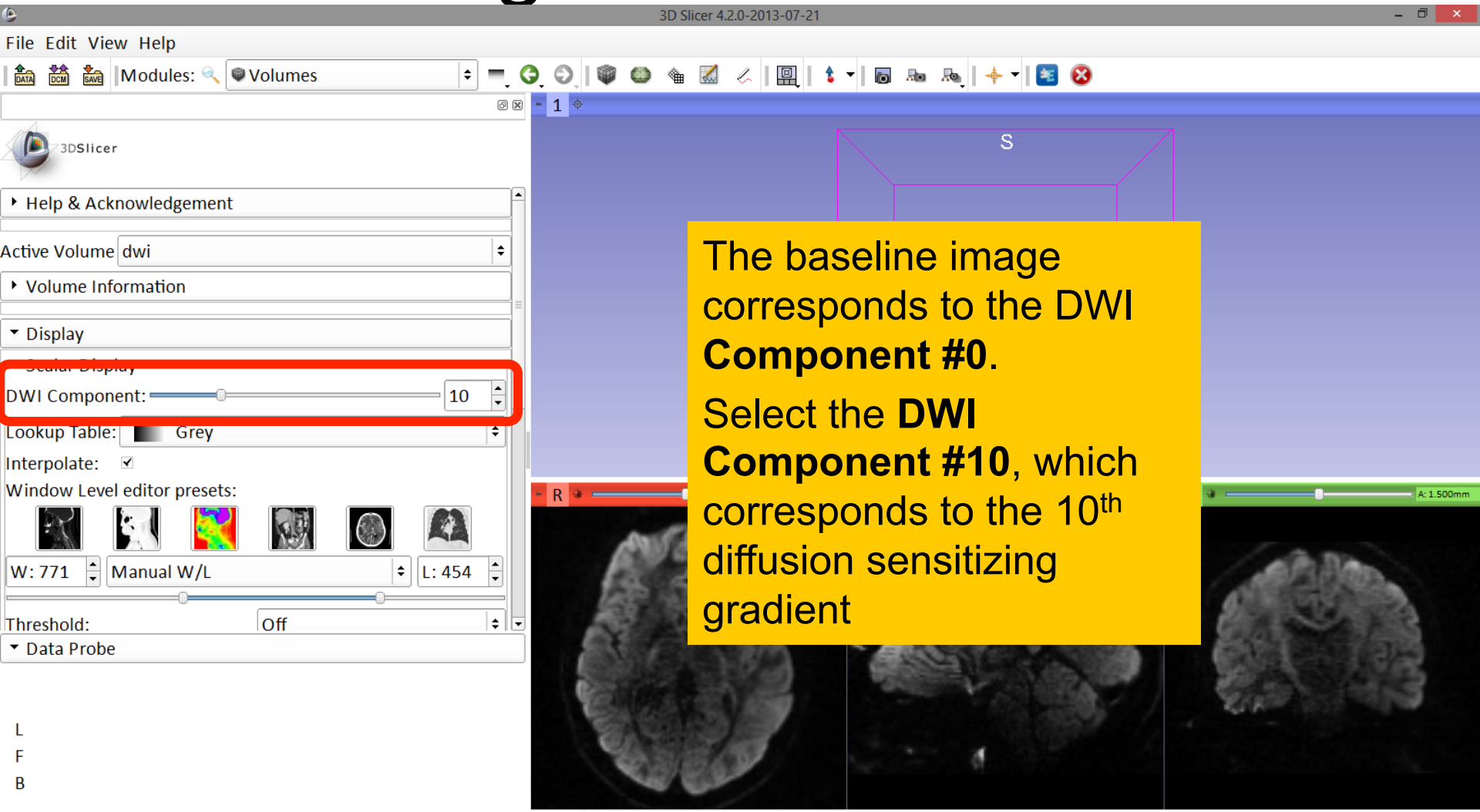


Slicer displays DWI volume of the brain

Loading the DWI Dataset



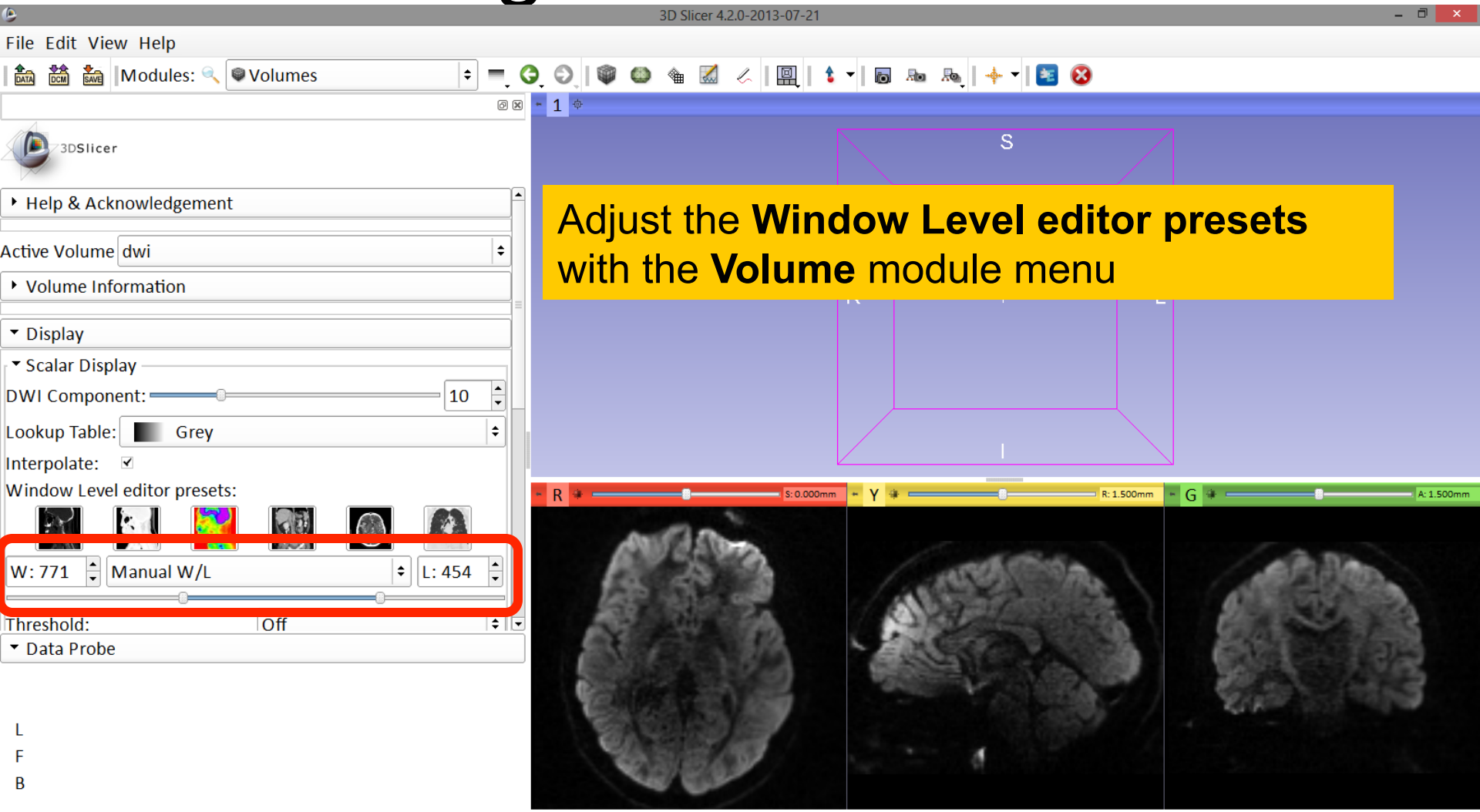
Loading the DWI Dataset



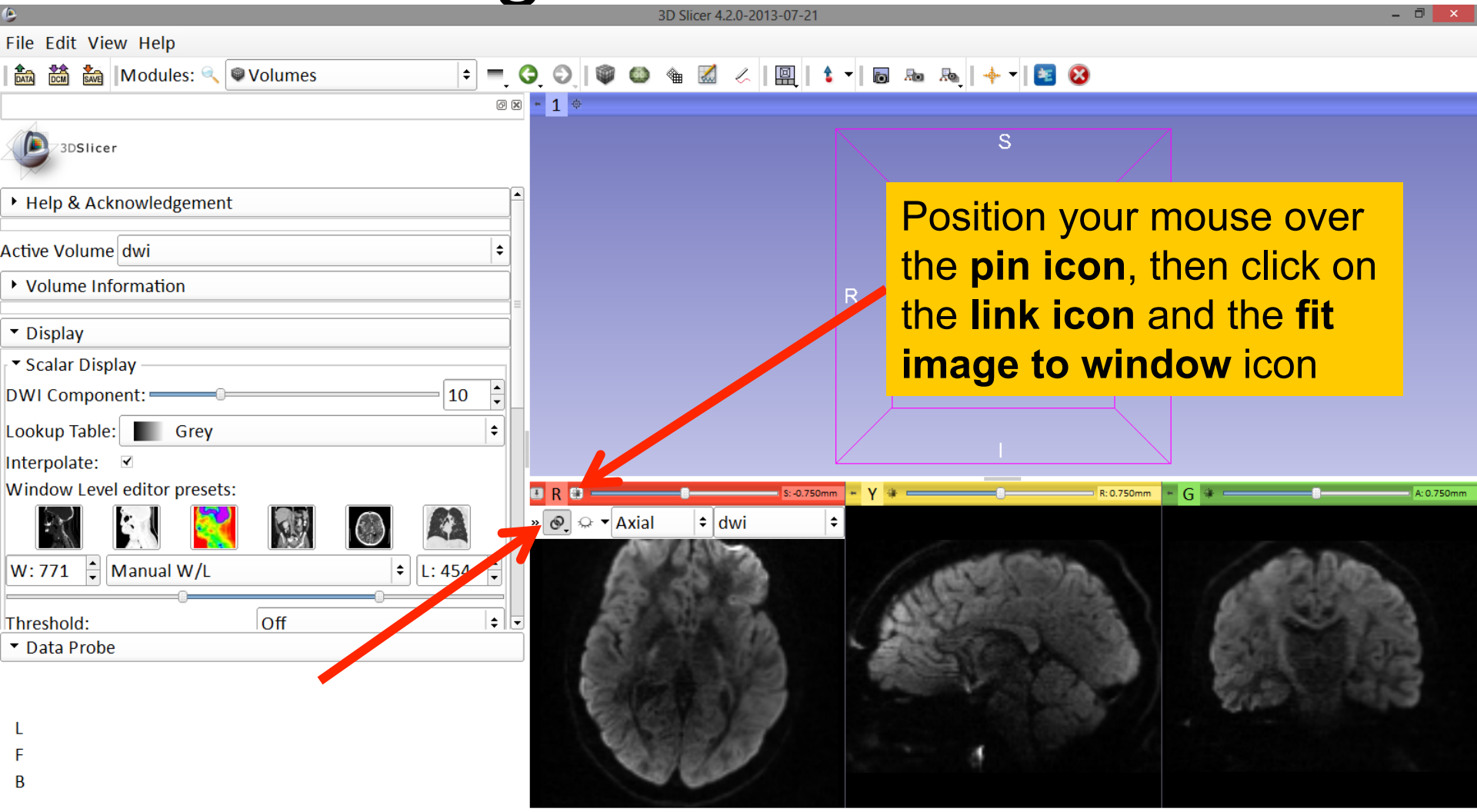
The baseline image corresponds to the DWI **Component #0**.

Select the **DWI Component #10**, which corresponds to the 10th diffusion sensitizing gradient

Loading the DWI Dataset



Loading the DWI Dataset



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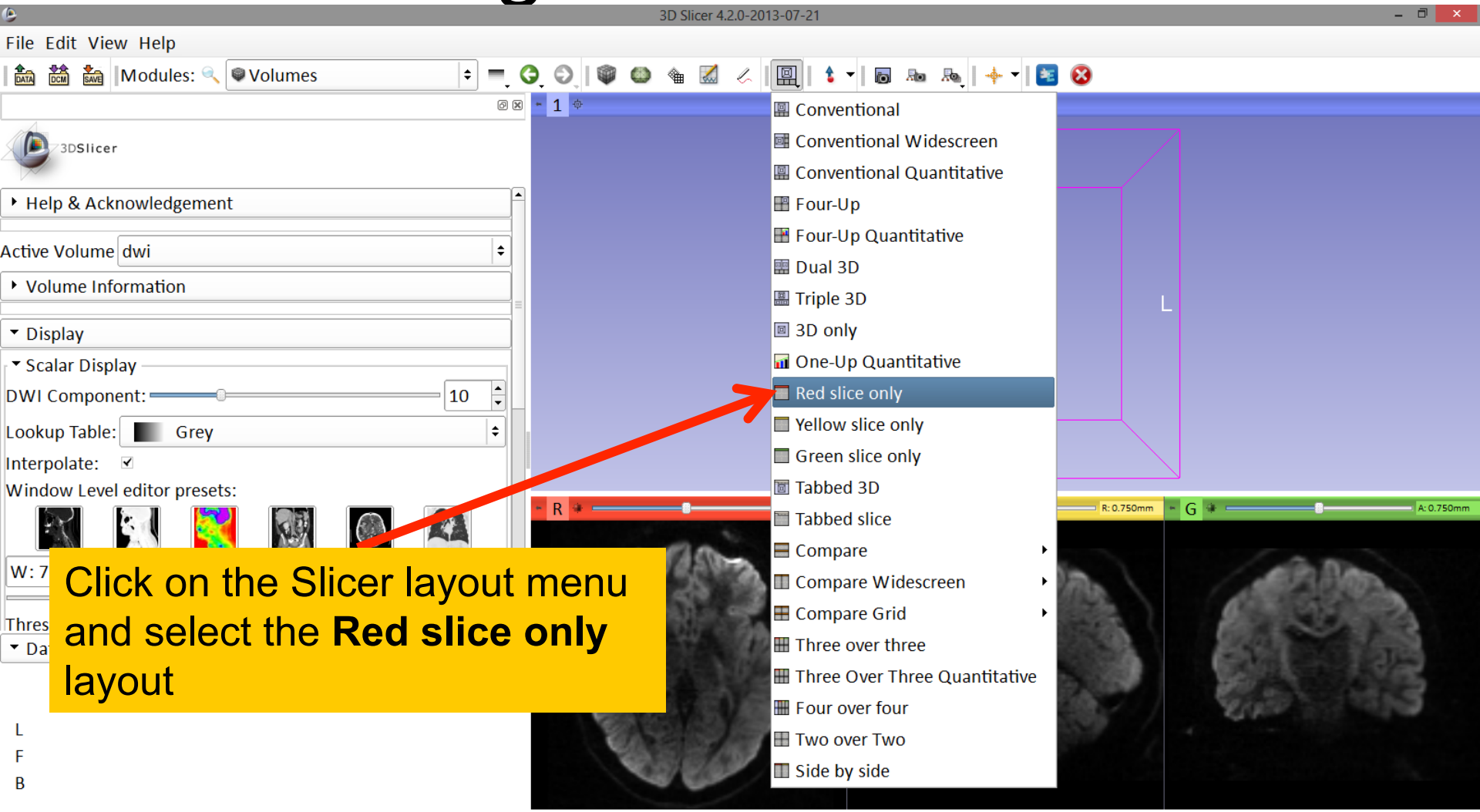
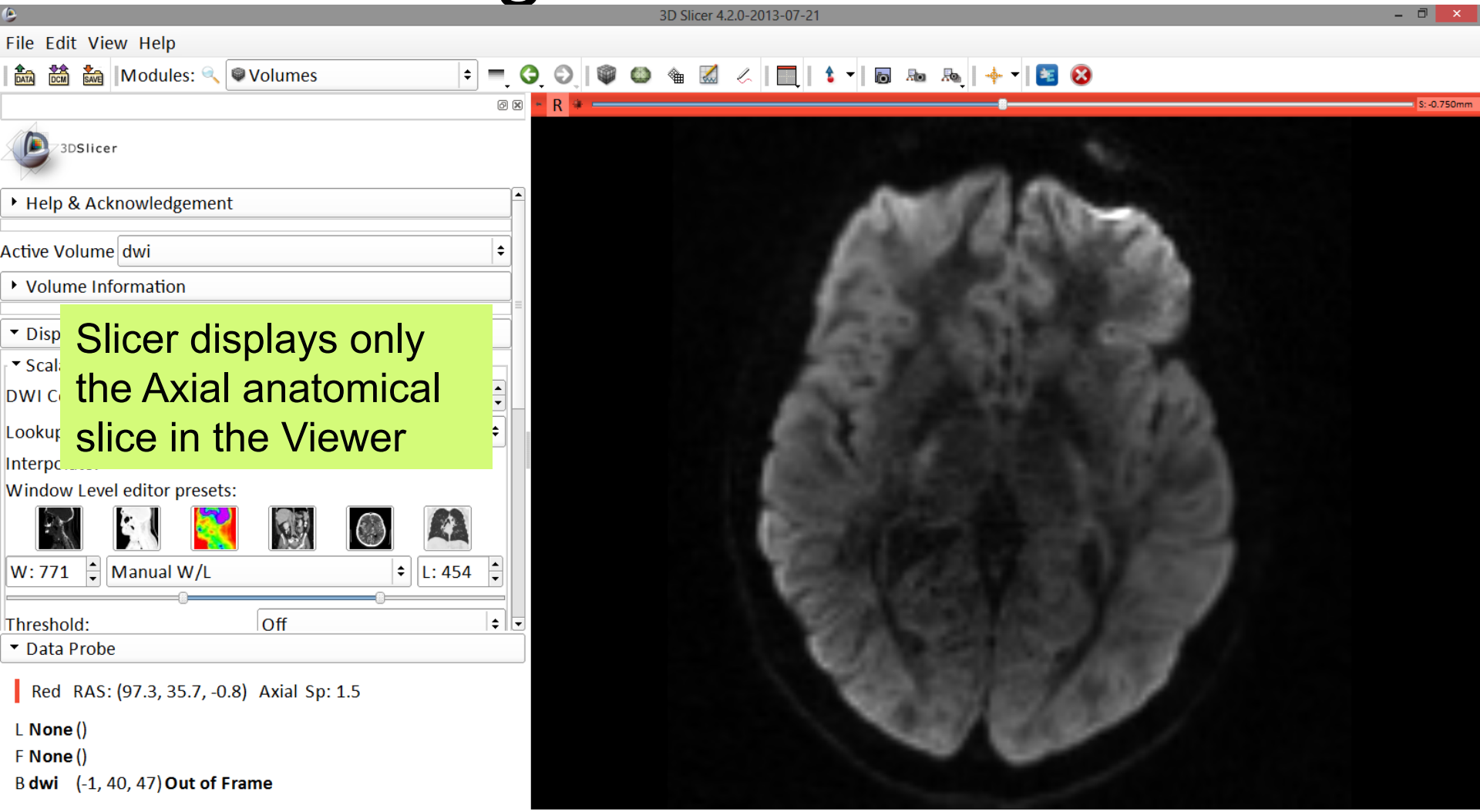
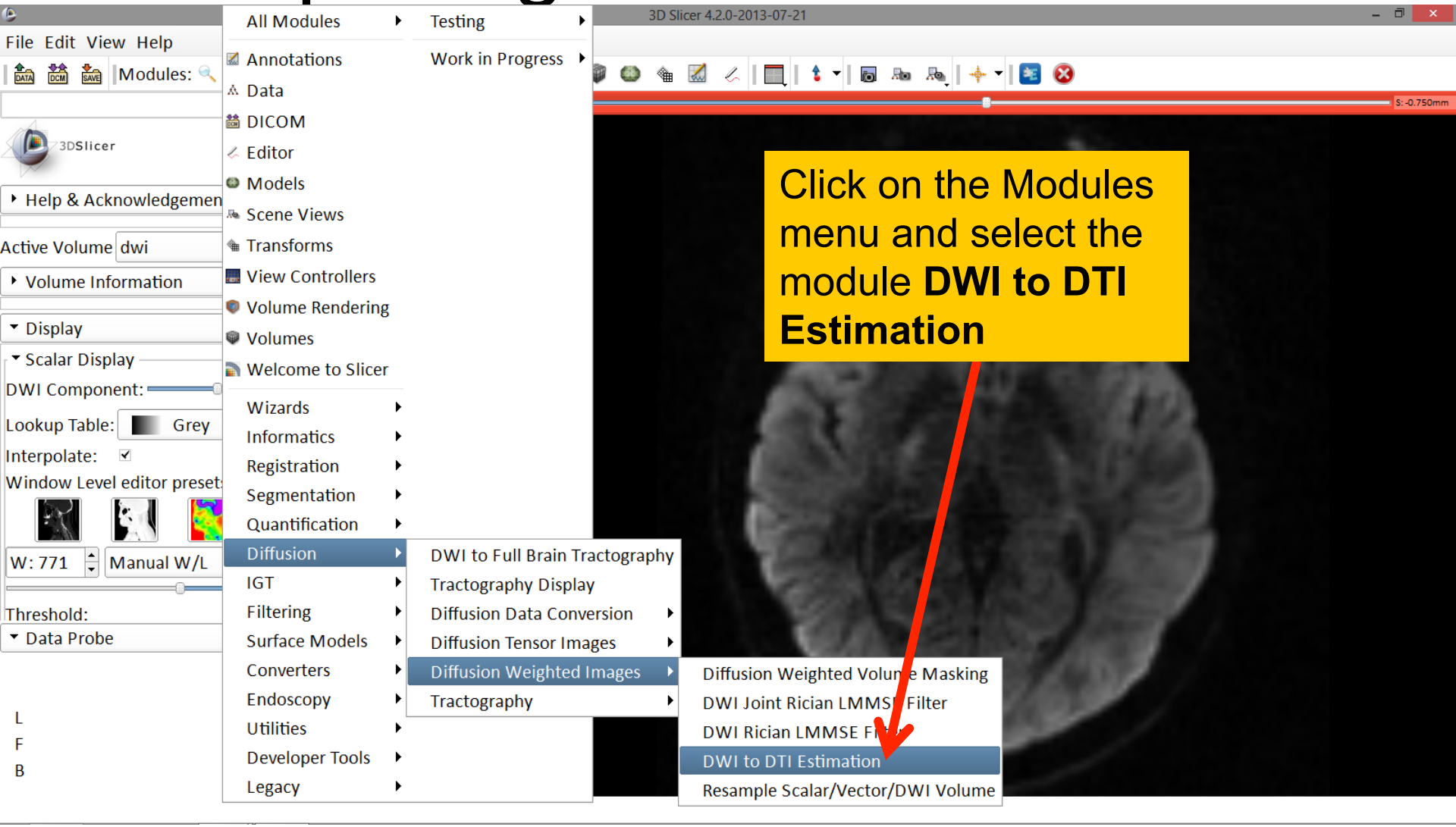


Loading the DWI Dataset



Exploring the DWI Dataset



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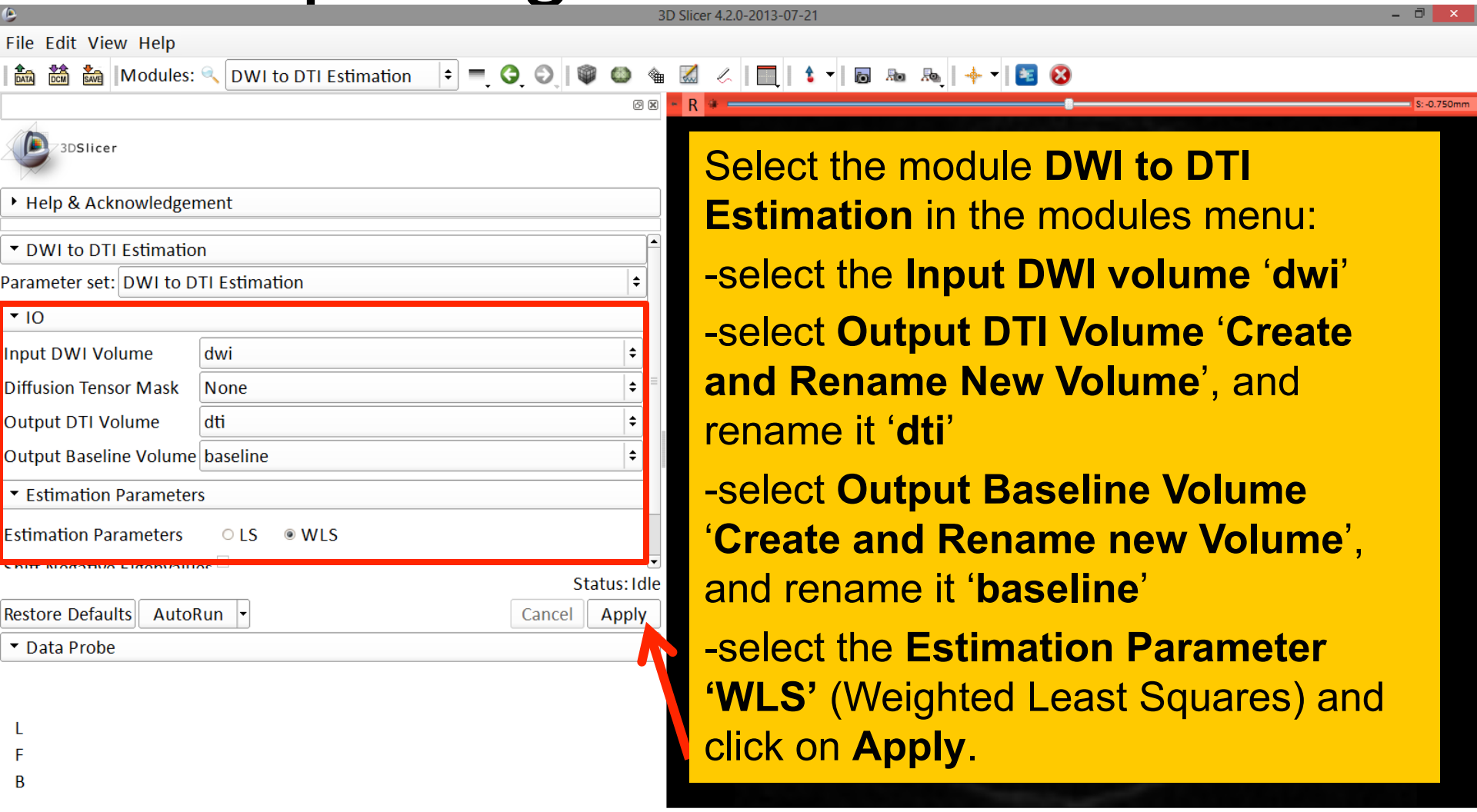
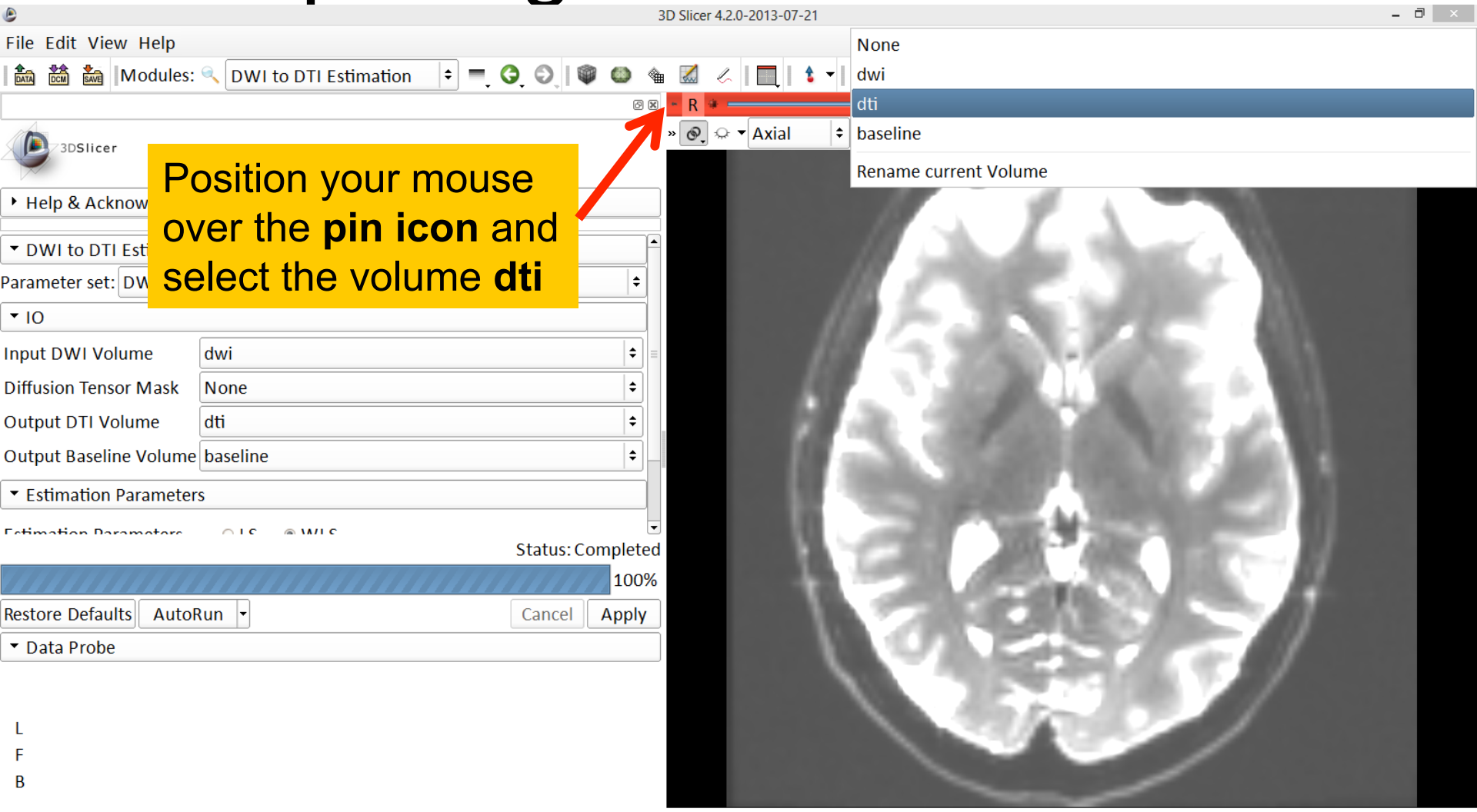
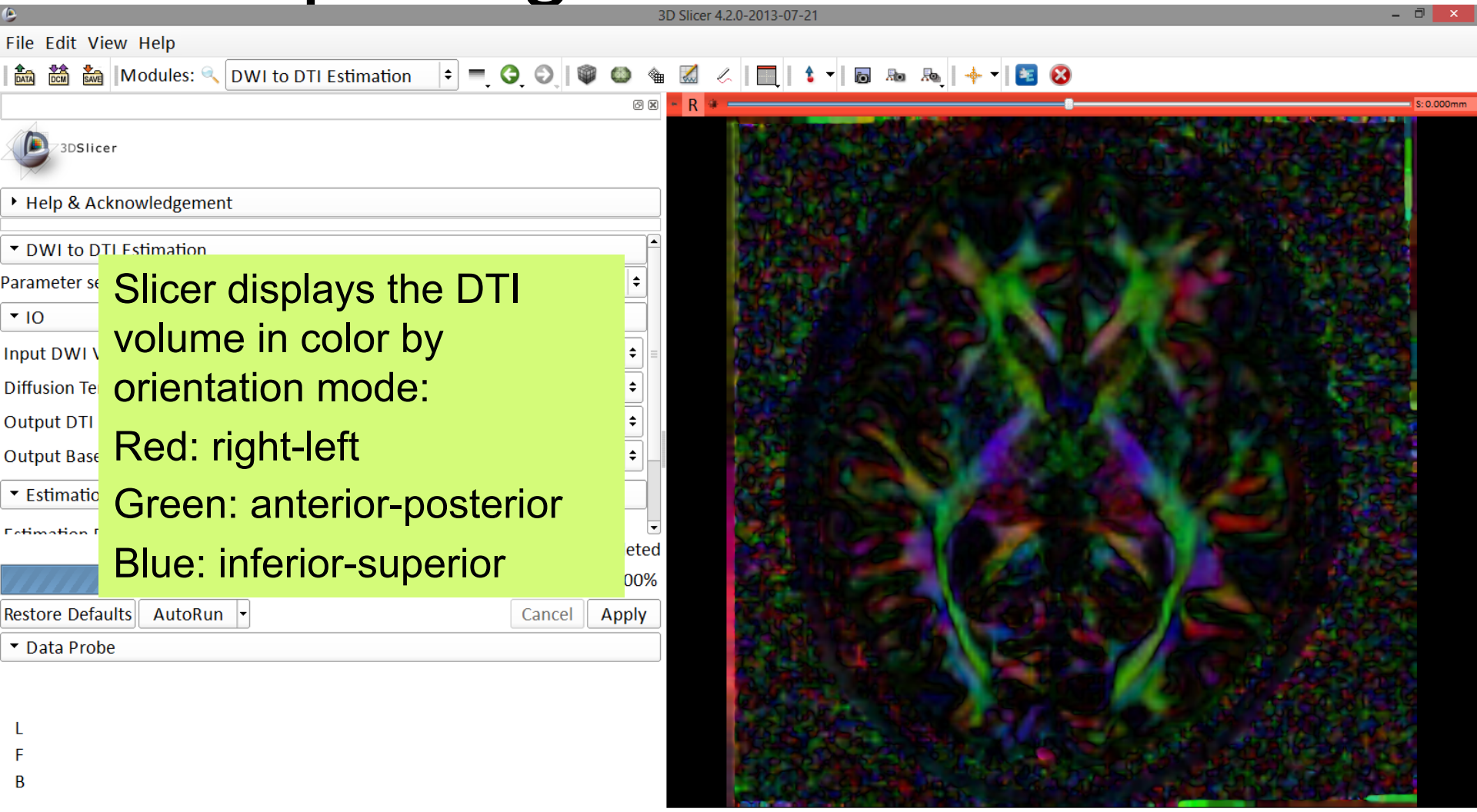


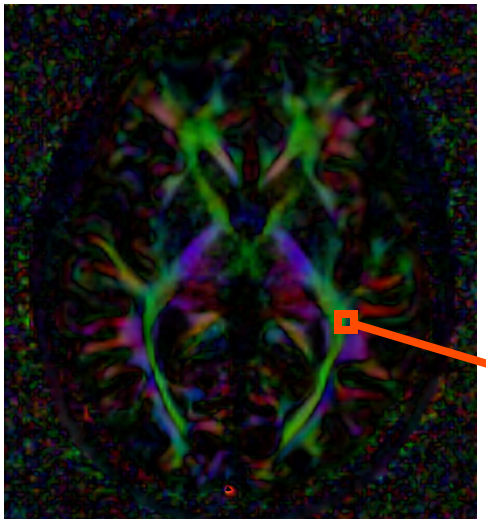
Exploring the DWI Dataset



Exploring the DWI Dataset



Diffusion Tensor Data



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

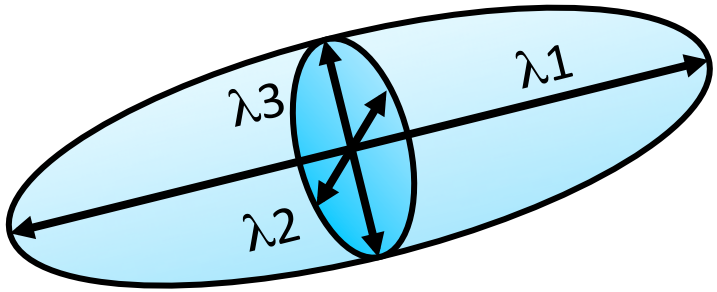
Stejskal-Tanner equation (1965)

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

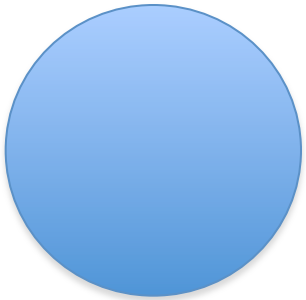
The diffusion tensor D in the voxel (I,J,K) is a 3x3 symmetric matrix.

Diffusion Tensor

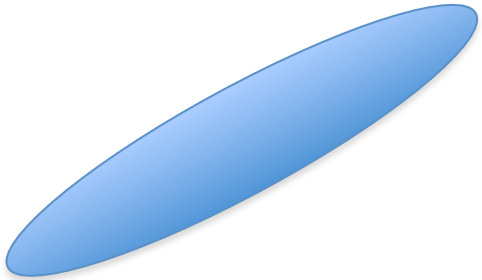
- The diffusion tensor $\underline{D}$ in the voxel (I,J,K) can be visualized as an ellipsoid, with the eigenvectors indicating the directions of the principal axes, and the square root of the eigenvalues defining the ellipsoidal radii.
- Scalar maps can be derived from the rotationally invariant eigenvalues λ1, λ2, λ3 to characterize the size and shape of the diffusion tensor.



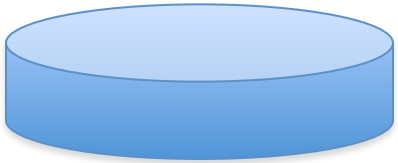
Diffusion Tensor Shape



$\lambda 1 = \lambda 2 = \lambda 3$



$\lambda 1 >> \lambda 2, \lambda 3$

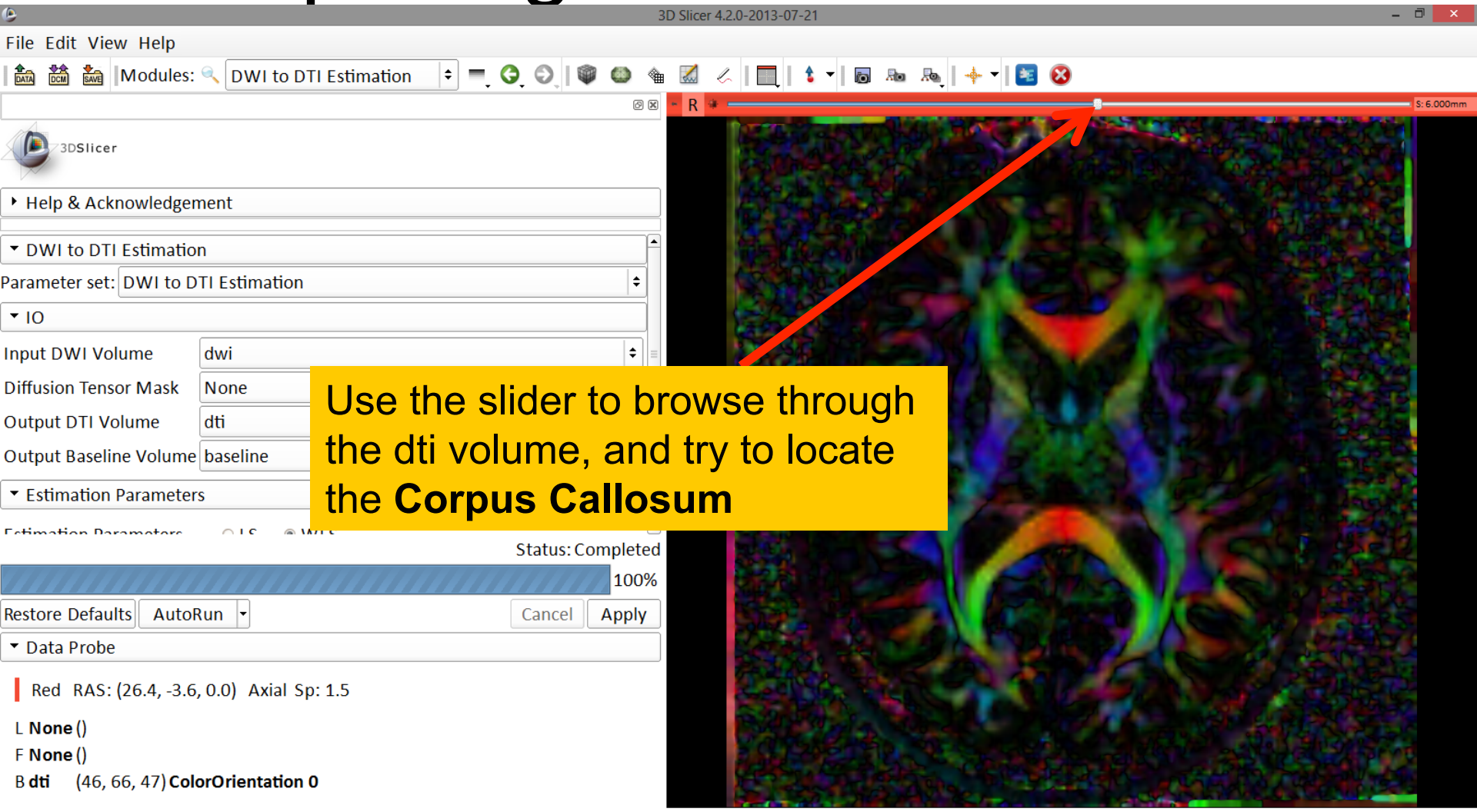


$\lambda 1 \sim \lambda 2 >> \lambda 3$

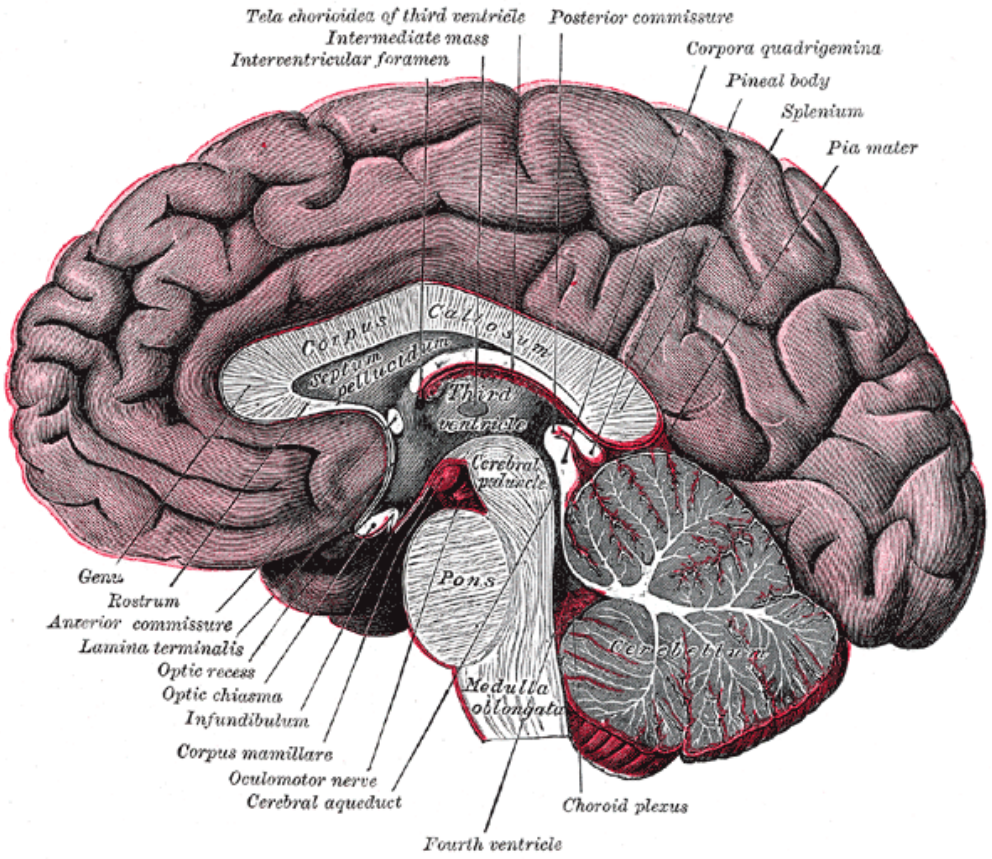
Isotropic media
(CSF, gray matter)

Anisotropic media
(white matter)

Exploring the DWI Dataset



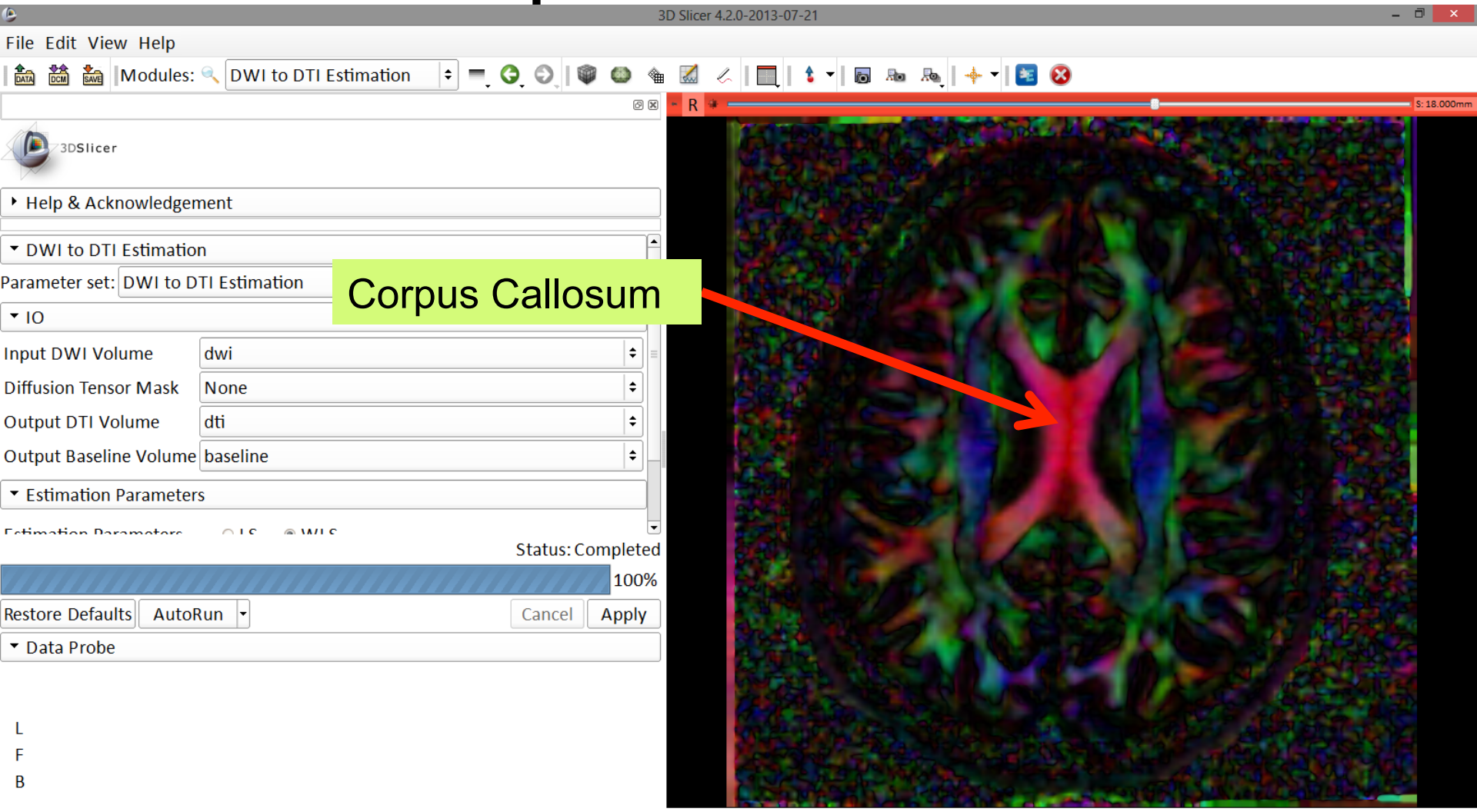
Corpus Callosum



The corpus callosum is a broad thick bundle of dense myelinated fibers that connect the left and right hemisphere. It is the largest white matter structure in the brain

Image from Gray's Anatomy

Corpus Callosum

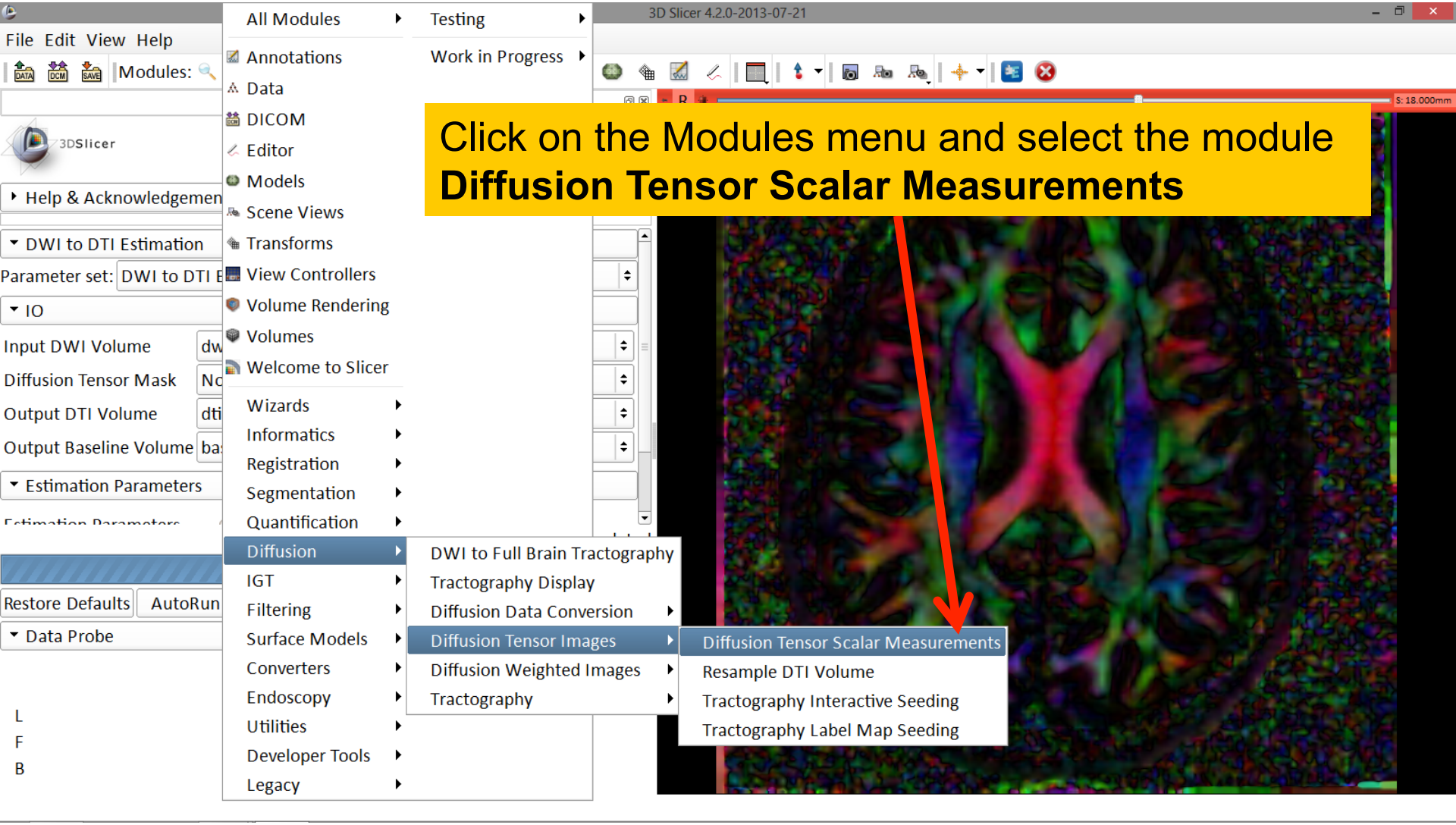


Characterizing the Size of the tensor: Trace

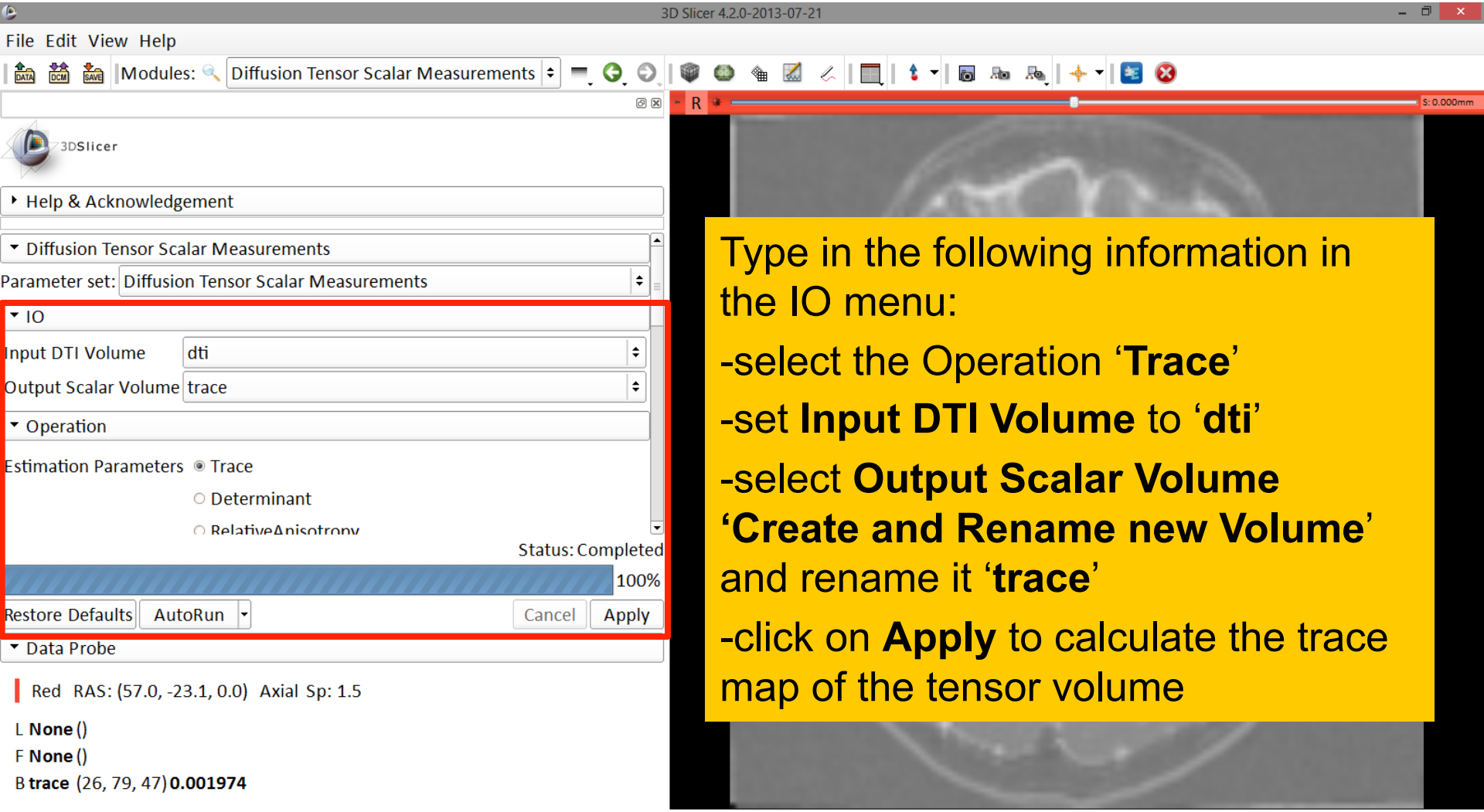
$$Trace(D) = \lambda 1 + \lambda 2 + \lambda 3$$

- Trace(D) is intrinsic to the tissue and is independent of fiber orientation, and diffusion sensitizing gradient directions
- Trace(D) is a clinically relevant parameter for monitoring stroke and neurological condition (degree of structural coherence in tissue)
- Trace(D) is useful to characterize the size of the diffusion ellipsoid

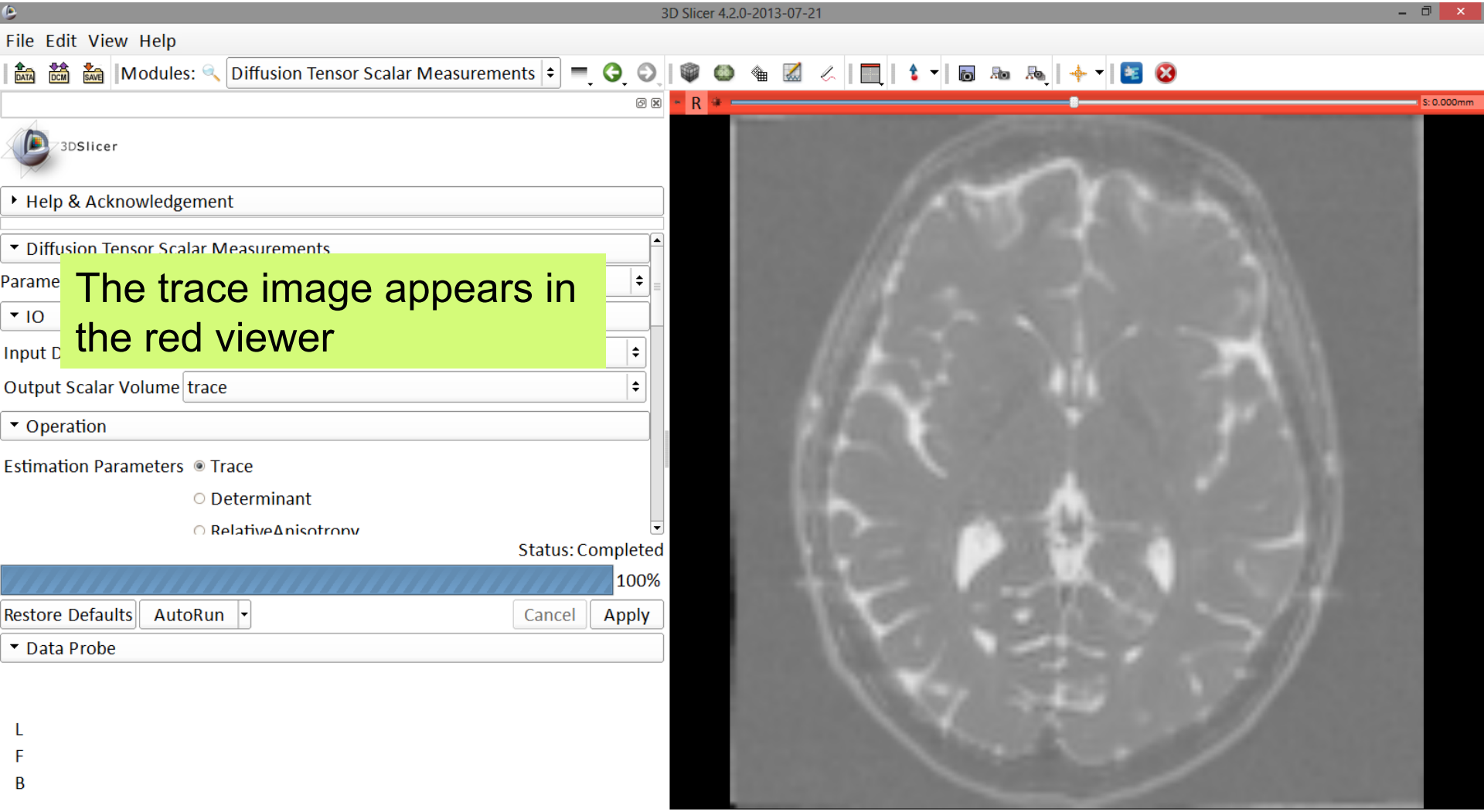
Trace


Click on the Modules menu and select the module
Diffusion Tensor Scalar Measurements
File Edit View Help
Modules:
3DSlicer
Help & Acknowledgemen
DWI to DTI Estimation
Parameter set: DWI to DTI E
IO
Input DWI Volume
Diffusion Tensor Mask
Output DTI Volume
Output Baseline Volume
Estimation Parameters
Restore Defaults
AutoRun
Data Probe
All Modules
Annotations
Data
DICOM
Editor
Models
Scene Views
Transforms
View Controllers
Volume Rendering
Volumes
Welcome to Slicer
Wizards
Informatics
Registration
Segmentation
Quantification
Diffusion
IGT
Filtering
Surface Models
Converters
Endoscopy
Utilities
Developer Tools
Legacy
Testing
Work in Progress
DWI to Full Brain Tractography
Tractography Display
Diffusion Data Conversion
Diffusion Tensor Images
Diffusion Weighted Images
Tractography
Diffusion Tensor Scalar Measurements
Resample DTI Volume
Tractography Interactive Seeding
Tractography Label Map Seeding
3D Slicer 4.2.0-2013-07-21

Trace

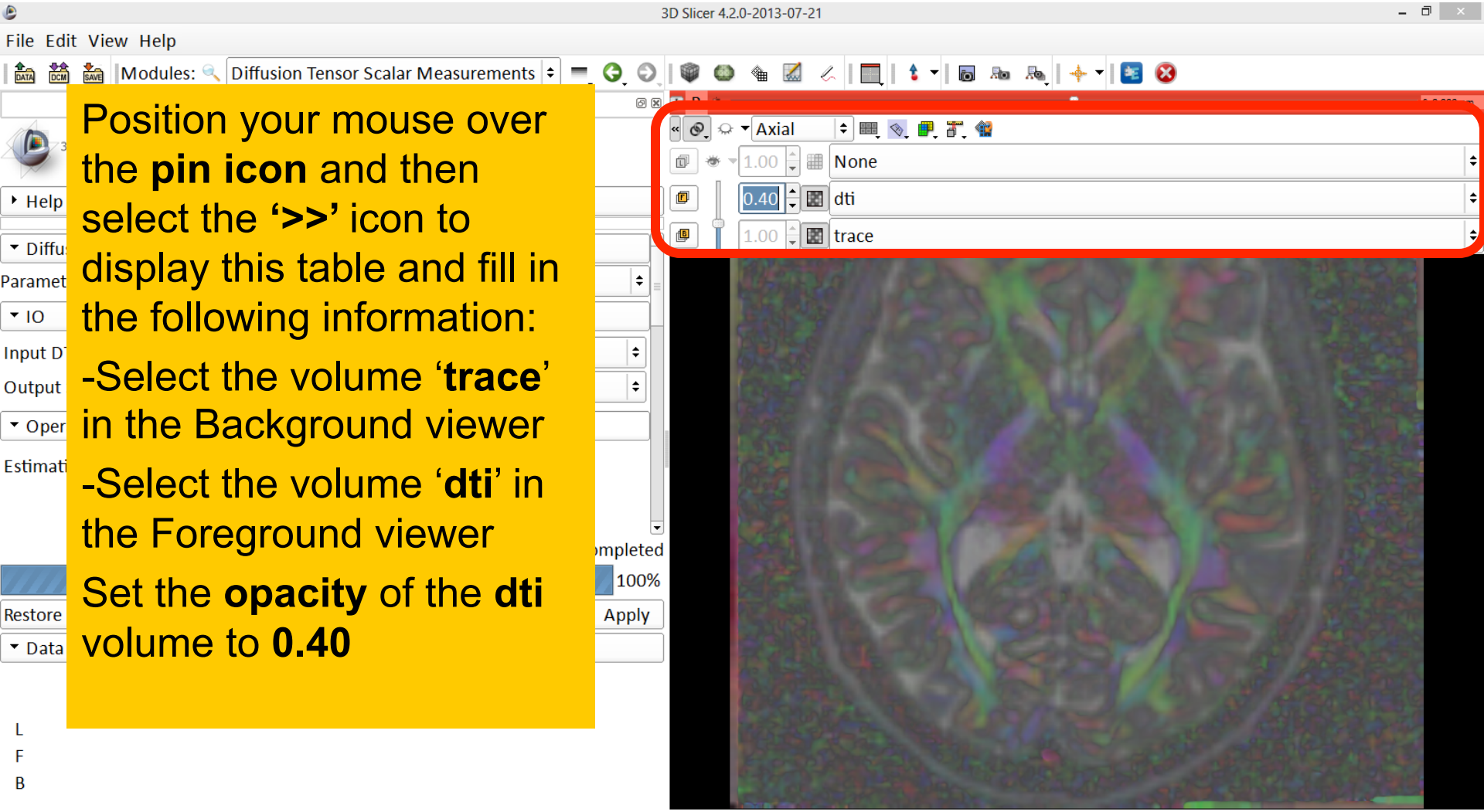

3D Slicer 4.2.0-2013-07-21
File Edit View Help
Modules: Diffusion Tensor Scalar Measurements
3DSlicer
Help & Acknowledgement
Diffusion Tensor Scalar Measurements
Parameter set: Diffusion Tensor Scalar Measurements
IO
Input DTI Volume dti
Output Scalar Volume trace
Operation
Estimation Parameters Trace
Determinant
RelativeAnisotropy
Status: Completed
100%
Restore Defaults AutoRun Cancel Apply
Data Probe
Red RAS: (57.0, -23.1, 0.0) Axial Sp: 1.5
L None ()
F None ()
B trace (26, 79, 47) 0.001974
Type in the following information in the IO menu:
-select the Operation 'Trace'
-set Input DTI Volume to 'dti'
-select Output Scalar Volume 'Create and Rename new Volume' and rename it 'trace'
-click on Apply to calculate the trace map of the tensor volume

Trace



The trace image appears in the red viewer

Trace



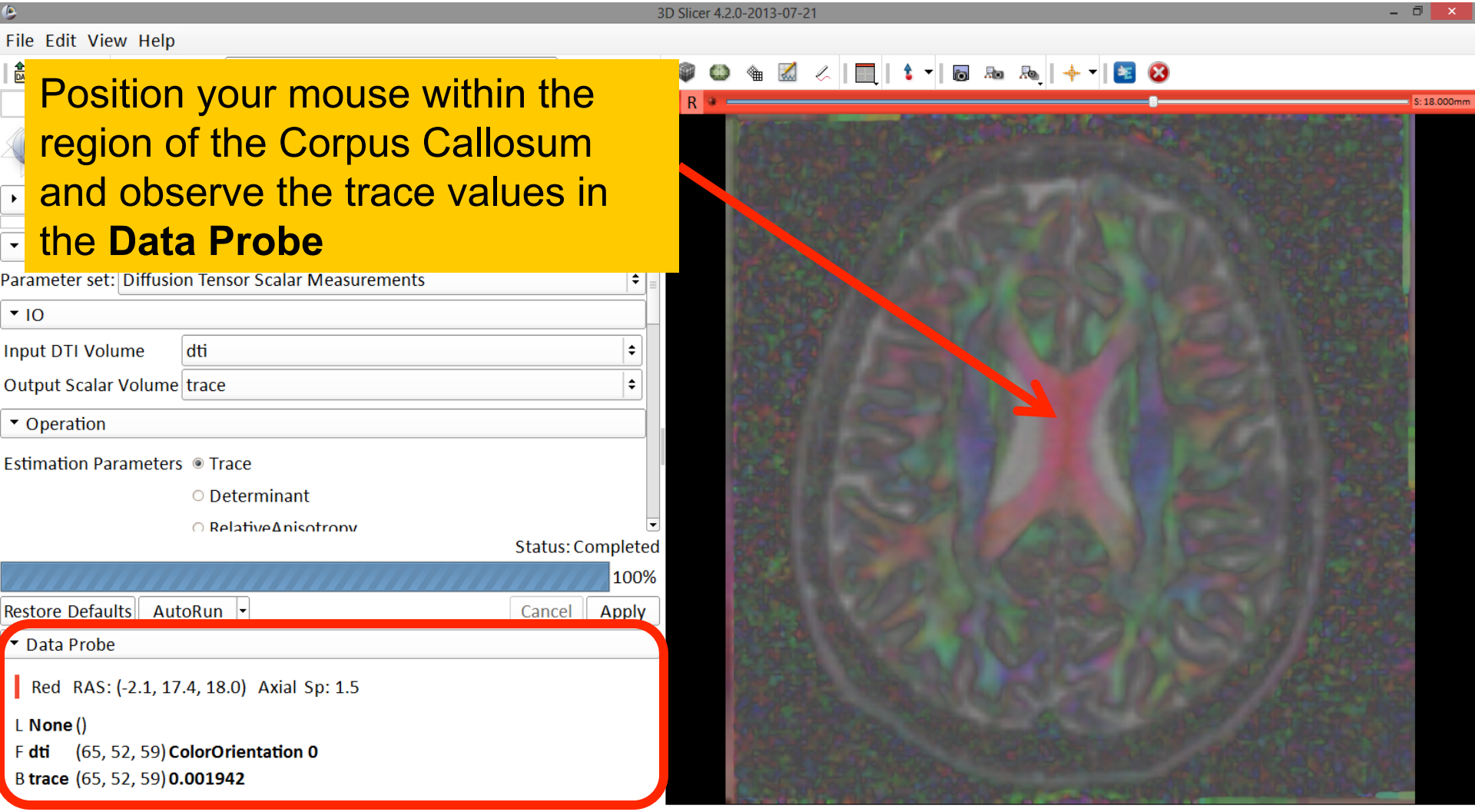
Position your mouse over the **pin icon** and then select the **‘>>’** icon to display this table and fill in the following information:

-Select the volume ‘**trace**’ in the Background viewer

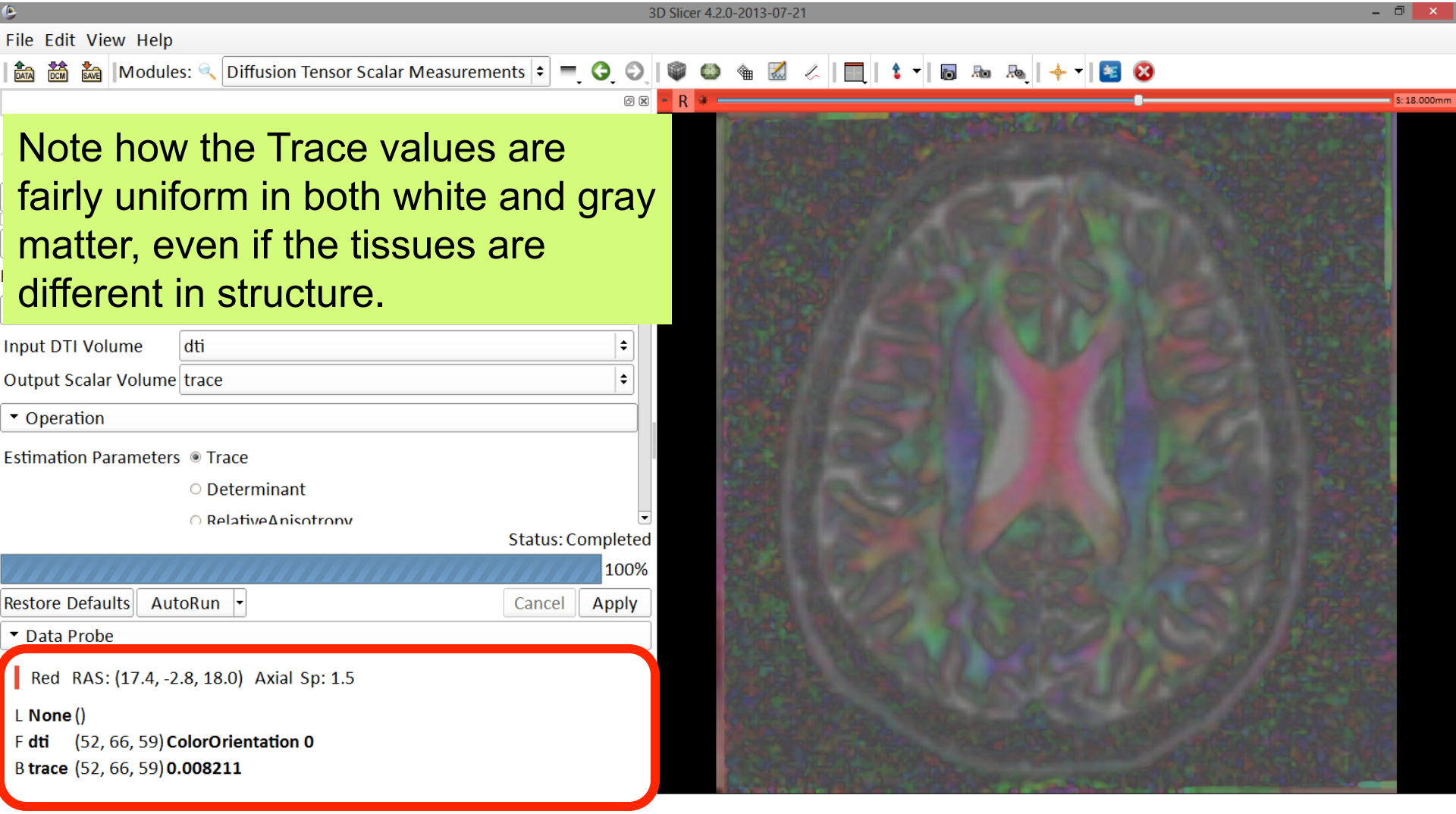
-Select the volume ‘**dti**’ in the Foreground viewer

Set the **opacity** of the **dti** volume to **0.40**

Trace


3D Slicer 4.2.0-2013-07-21
File Edit View Help
Position your mouse within the region of the Corpus Callosum and observe the trace values in the **Data Probe**
Parameter set: Diffusion Tensor Scalar Measurements
IO
Input DTI Volume dti
Output Scalar Volume trace
Operation
Estimation Parameters Trace
Determinant
RelativeAnisotropy
Status: Completed
100%
Restore Defaults AutoRun Cancel Apply
Data Probe
Red RAS: (-2.1, 17.4, 18.0) Axial Sp: 1.5
L None ()
F dti (65, 52, 59) ColorOrientation 0
B trace (65, 52, 59) 0.001942
R
S: 18.000mm

Trace

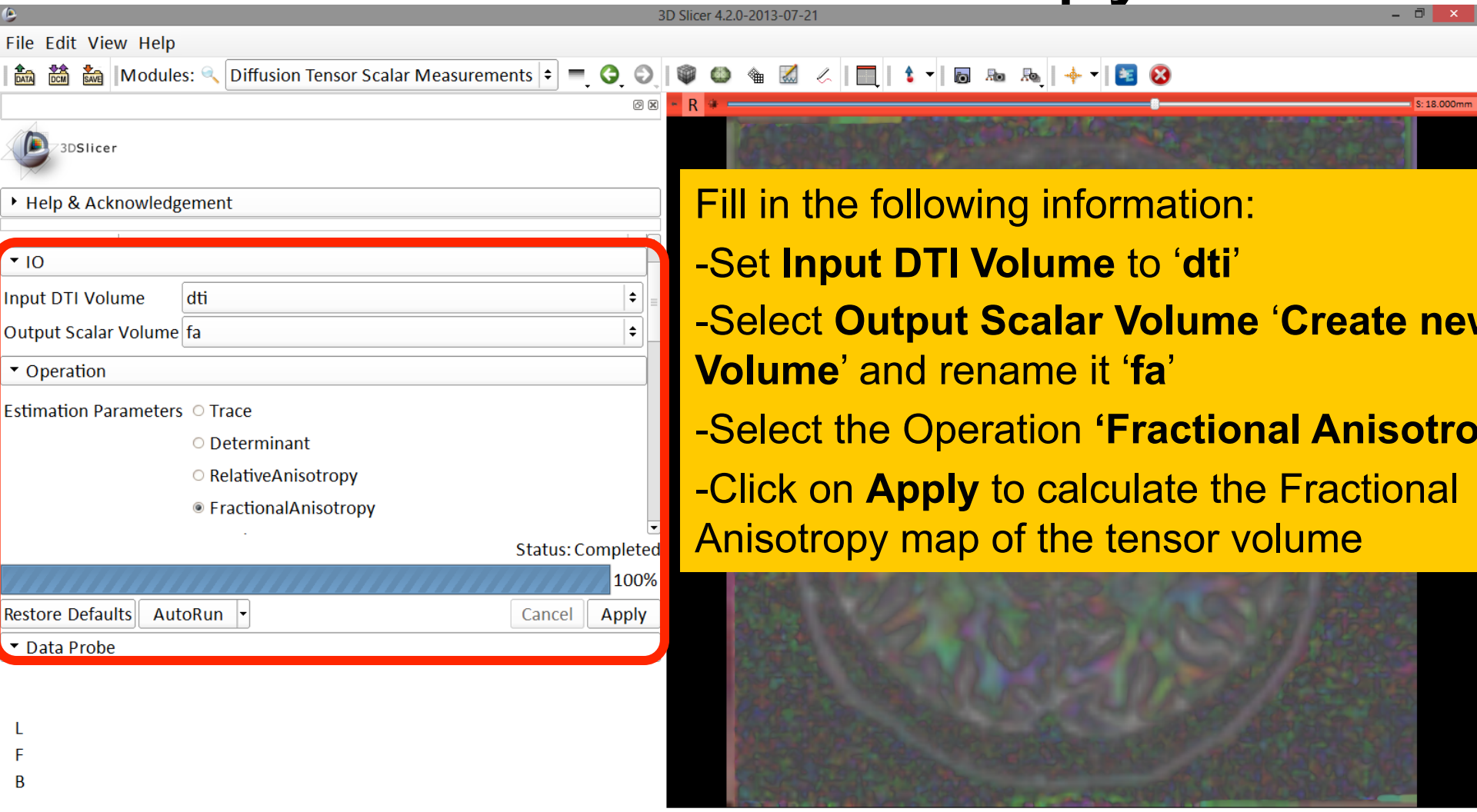

3D Slicer 4.2.0-2013-07-21
File Edit View Help
Modules: Diffusion Tensor Scalar Measurements
Note how the Trace values are fairly uniform in both white and gray matter, even if the tissues are different in structure.
Input DTI Volume dti
Output Scalar Volume trace
Operation
Estimation Parameters Trace
Determinant
RelativeAnisotropy
Status: Completed
100%
Restore Defaults AutoRun Cancel Apply
Data Probe
Red RAS: (17.4, -2.8, 18.0) Axial Sp: 1.5
L None ()
F dti (52, 66, 59) ColorOrientation 0
B trace (52, 66, 59) 0.008211
R
S: 18.000mm

Scalar Maps: Fractional Anisotropy

$$FA(D) = \frac{\sqrt{(\lambda_1 - \lambda_2)^2 + (\lambda_1 - \lambda_3)^2 + (\lambda_2 - \lambda_3)^2}}{\sqrt{2}\sqrt{\lambda_1^2 + \lambda_2^2 + \lambda_3^2}}$$

- FA(D) is intrinsic to the tissue and is independent of fiber orientation, and diffusion sensitizing gradient directions
- FA(D) is useful to characterize the shape (degree of 'out-of-roundness') of the diffusion ellipsoid'
- Low FA:  → High FA: 

Fractional Anisotropy



Fill in the following information:

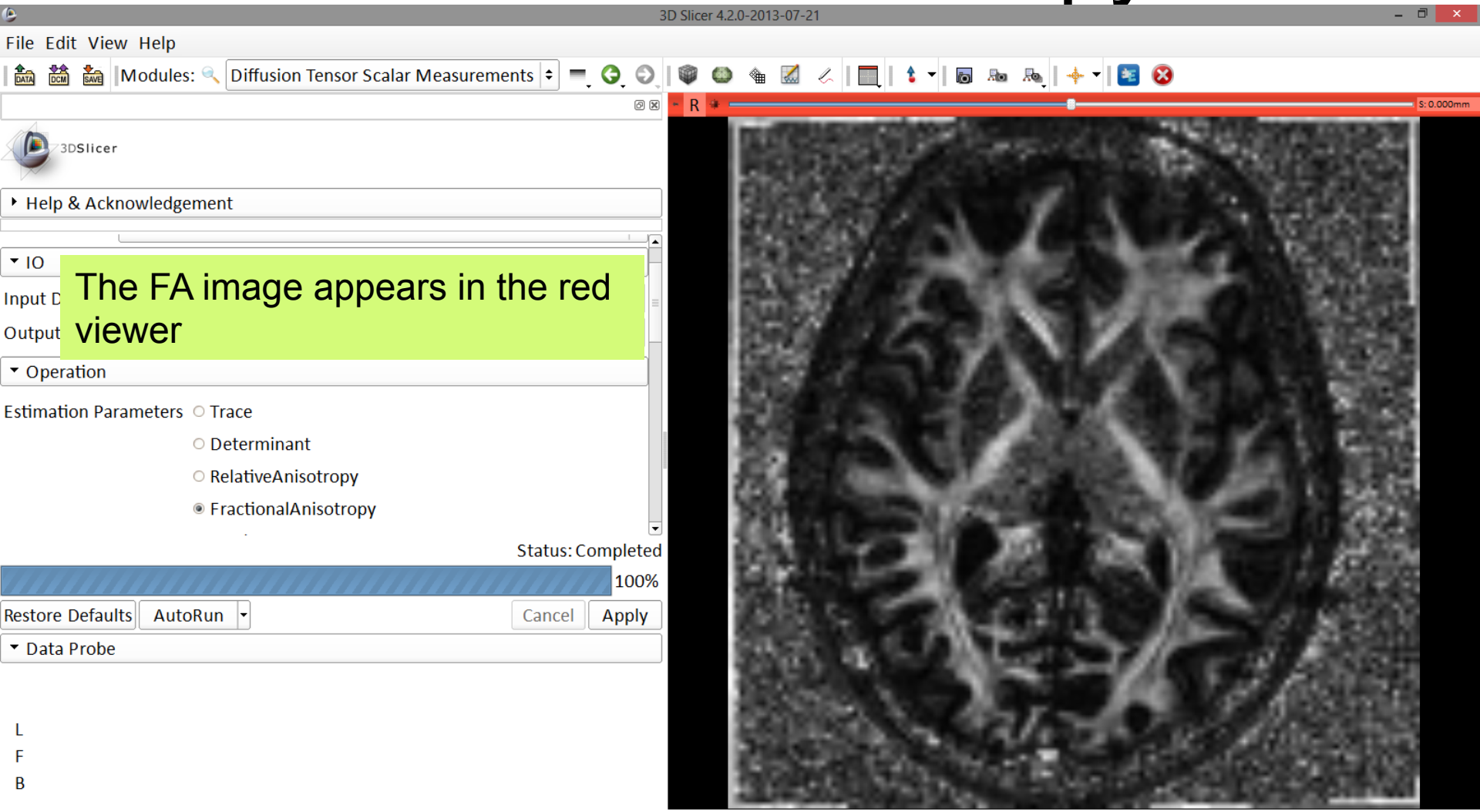
-Set **Input DTI Volume** to '**dti**'

-Select **Output Scalar Volume** '**Create new Volume**' and rename it '**fa**'

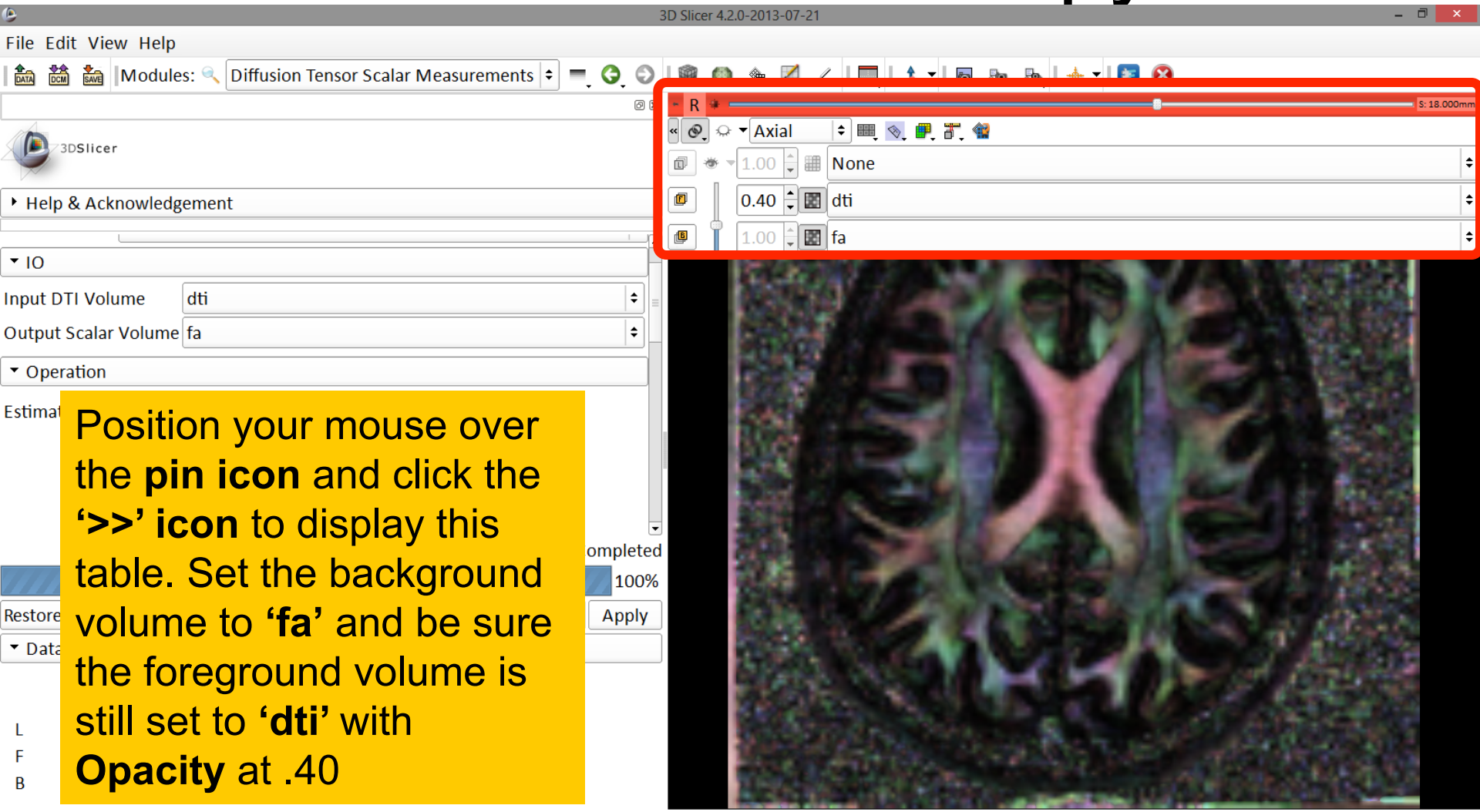
-Select the Operation '**Fractional Anisotropy**'

-Click on **Apply** to calculate the Fractional Anisotropy map of the tensor volume

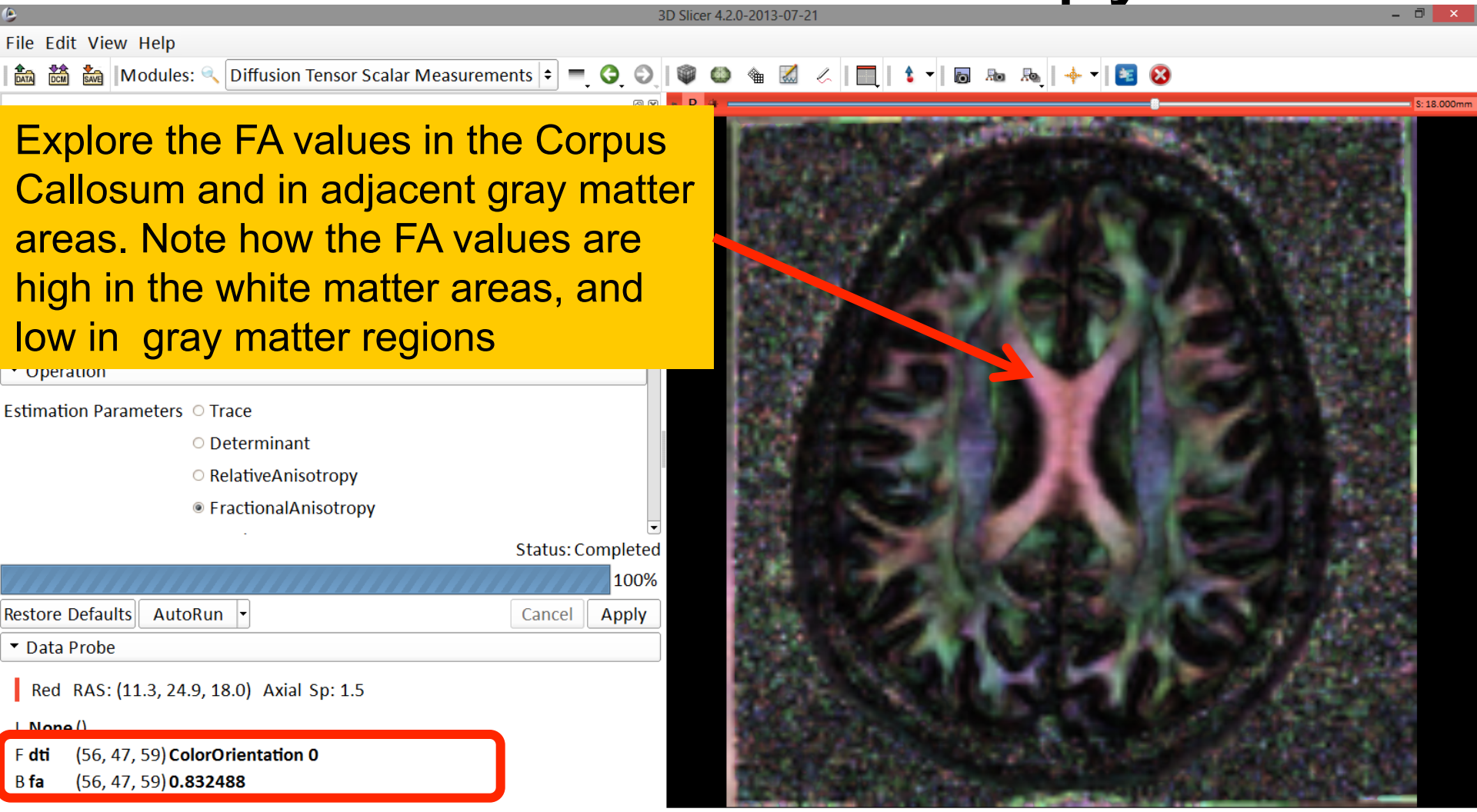
Fractional Anisotropy



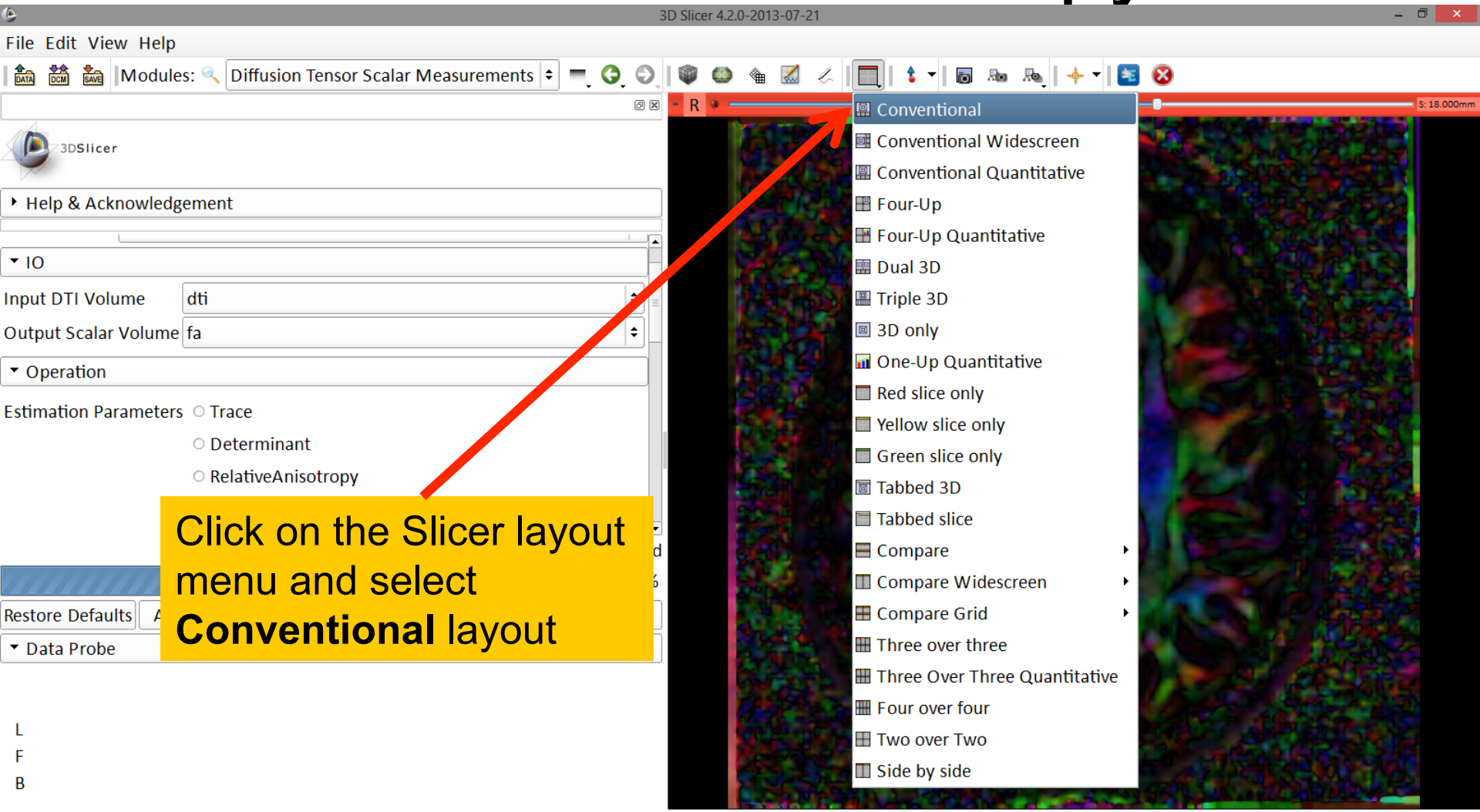
Fractional Anisotropy

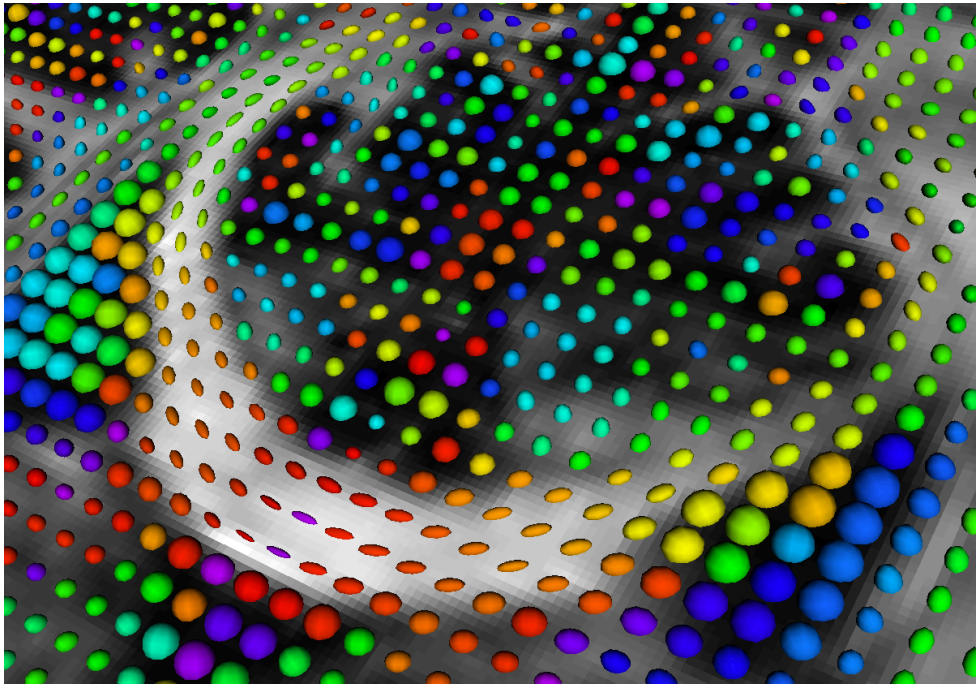


Fractional Anisotropy



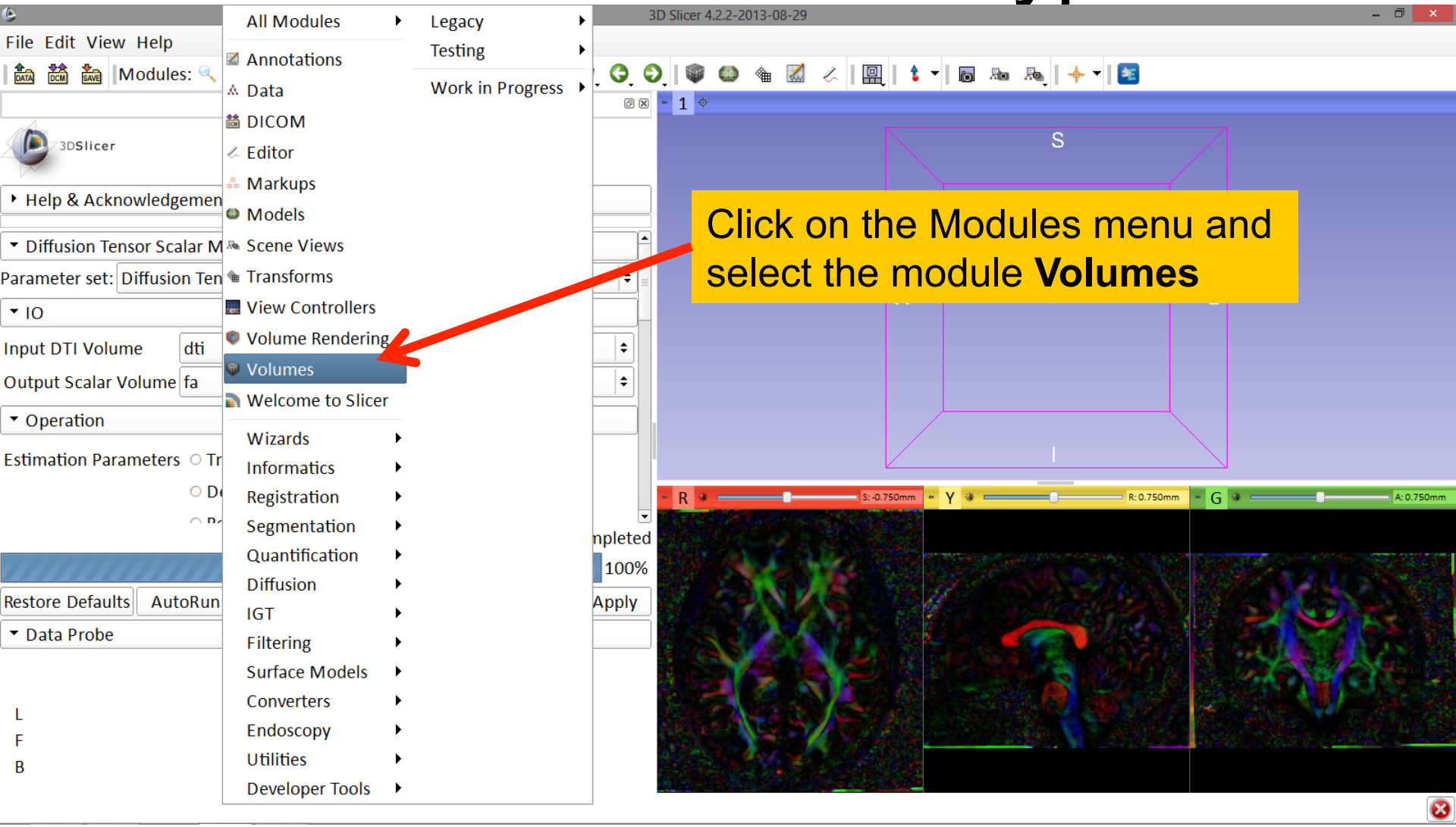
Fractional Anisotropy



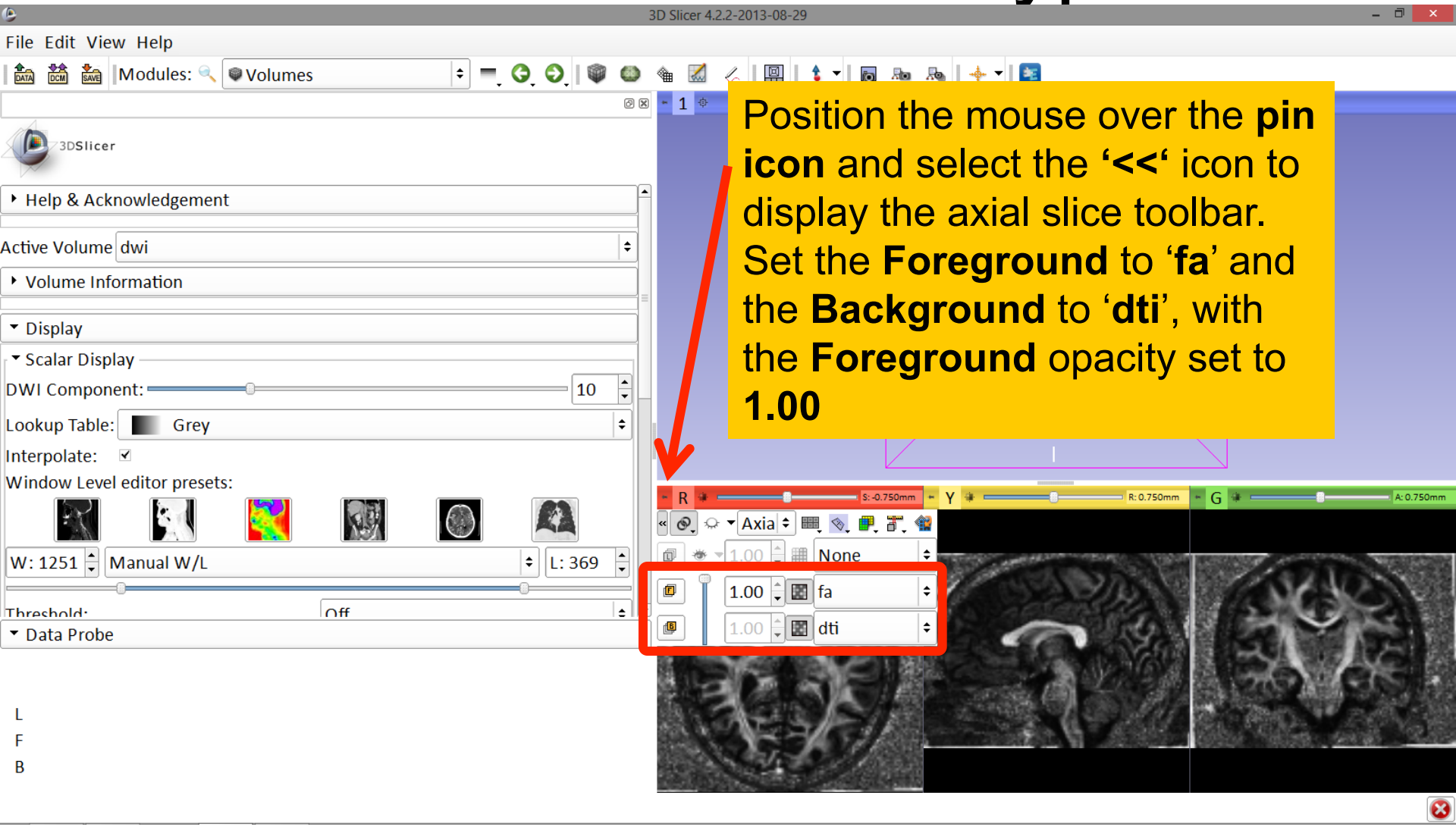


Part 2: Visualizing the tensor data

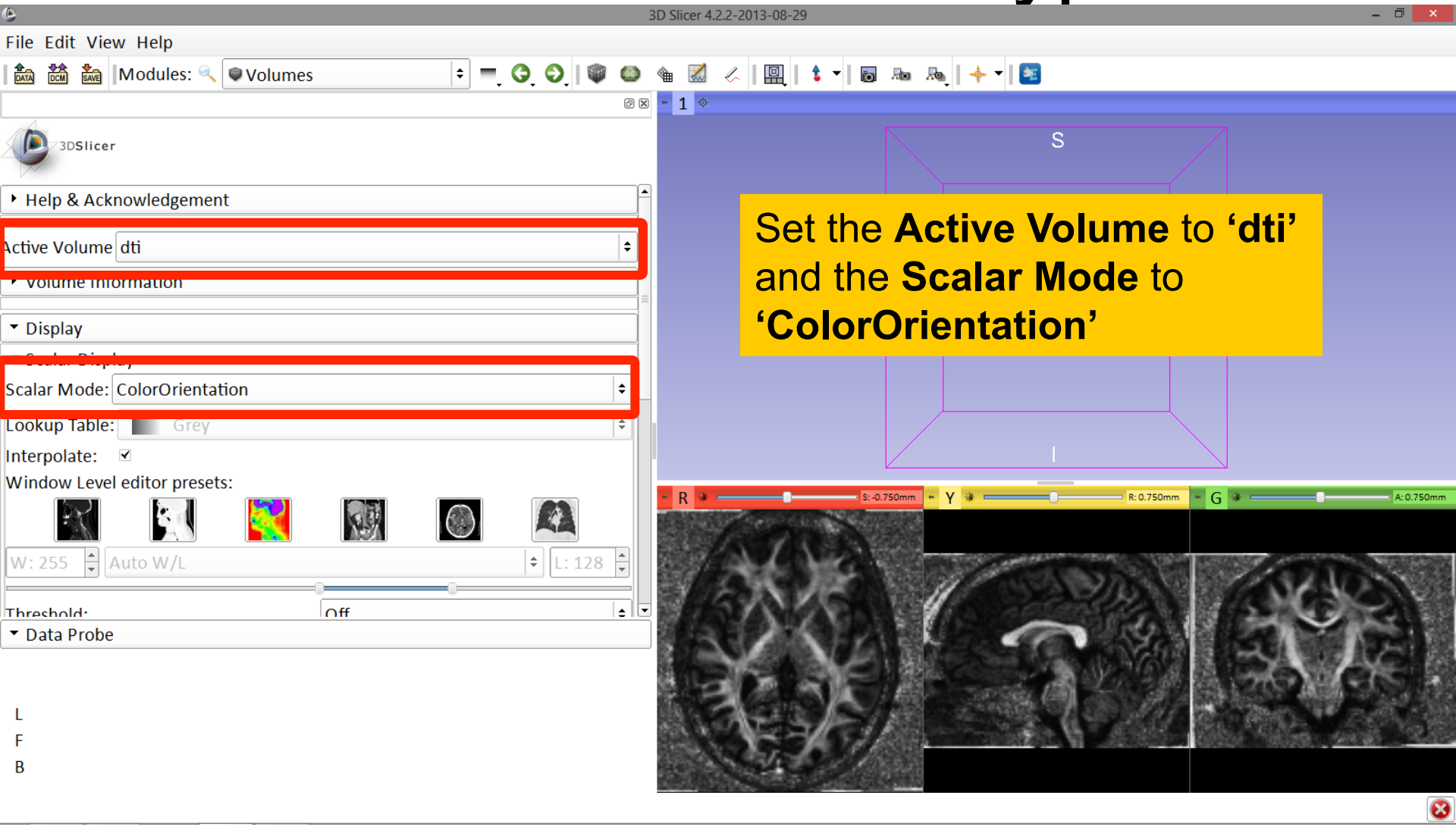
3D Visualization: Glyphs



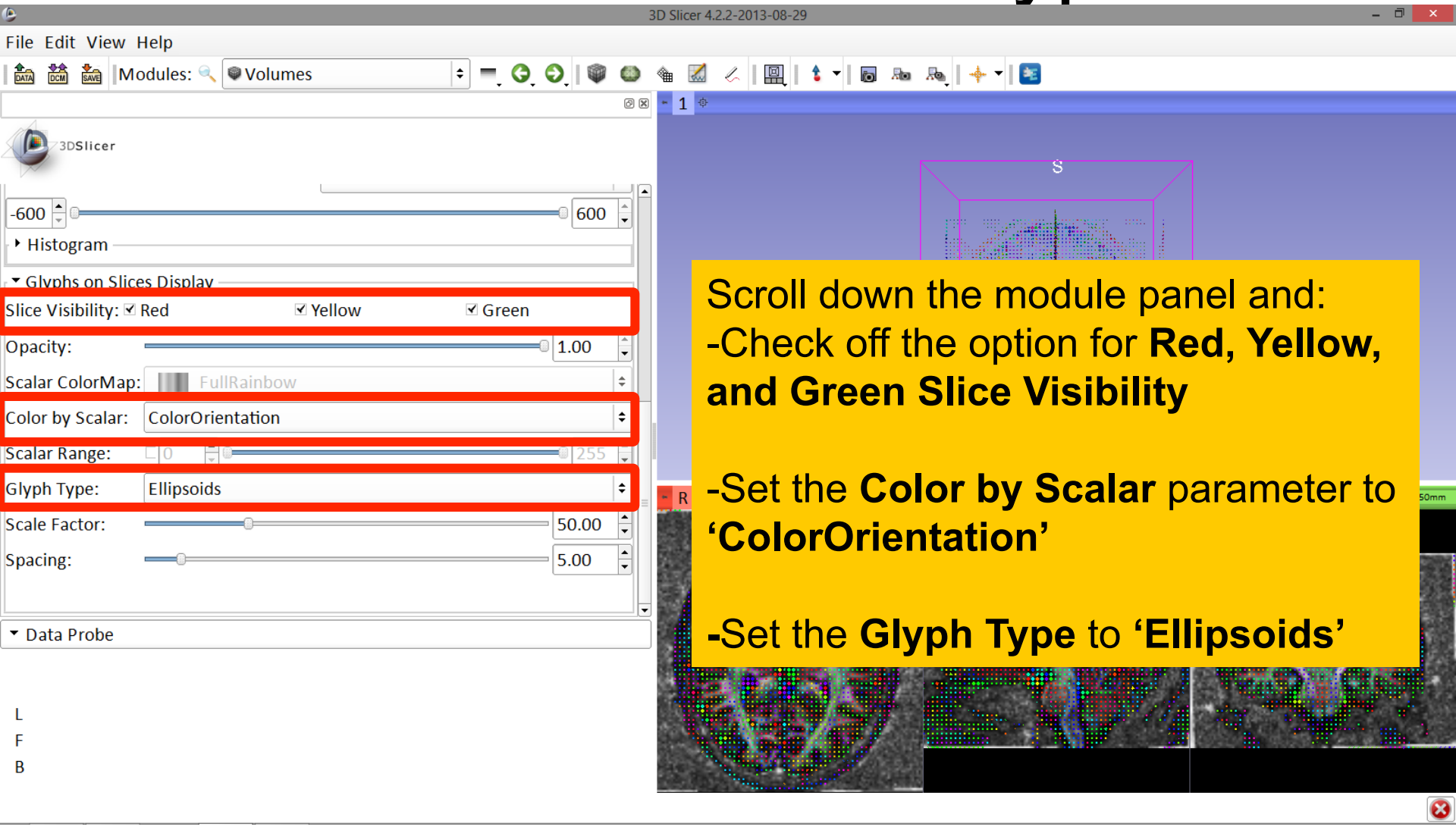
3D Visualization: Glyphs



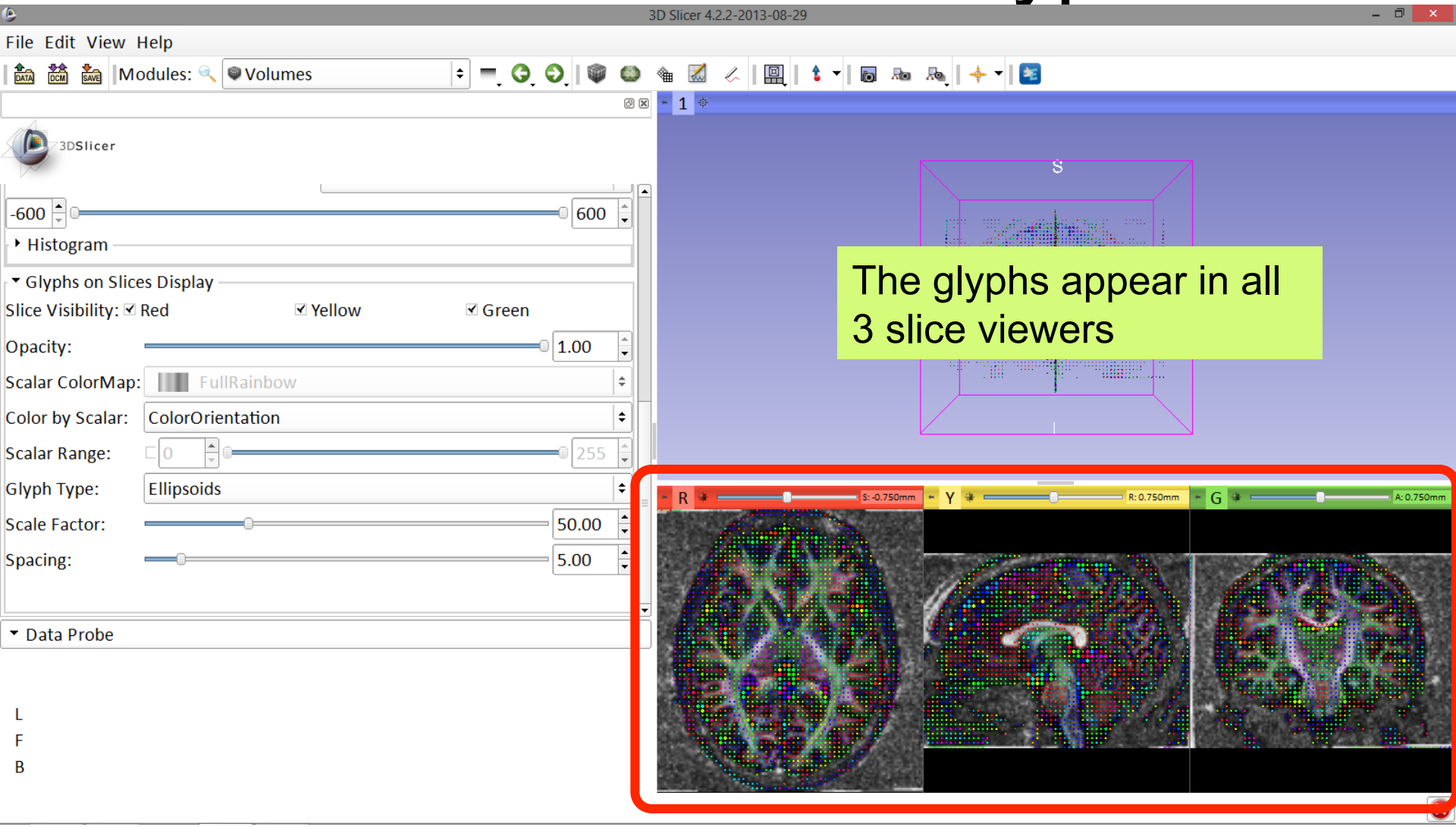
3D Visualization: Glyphs



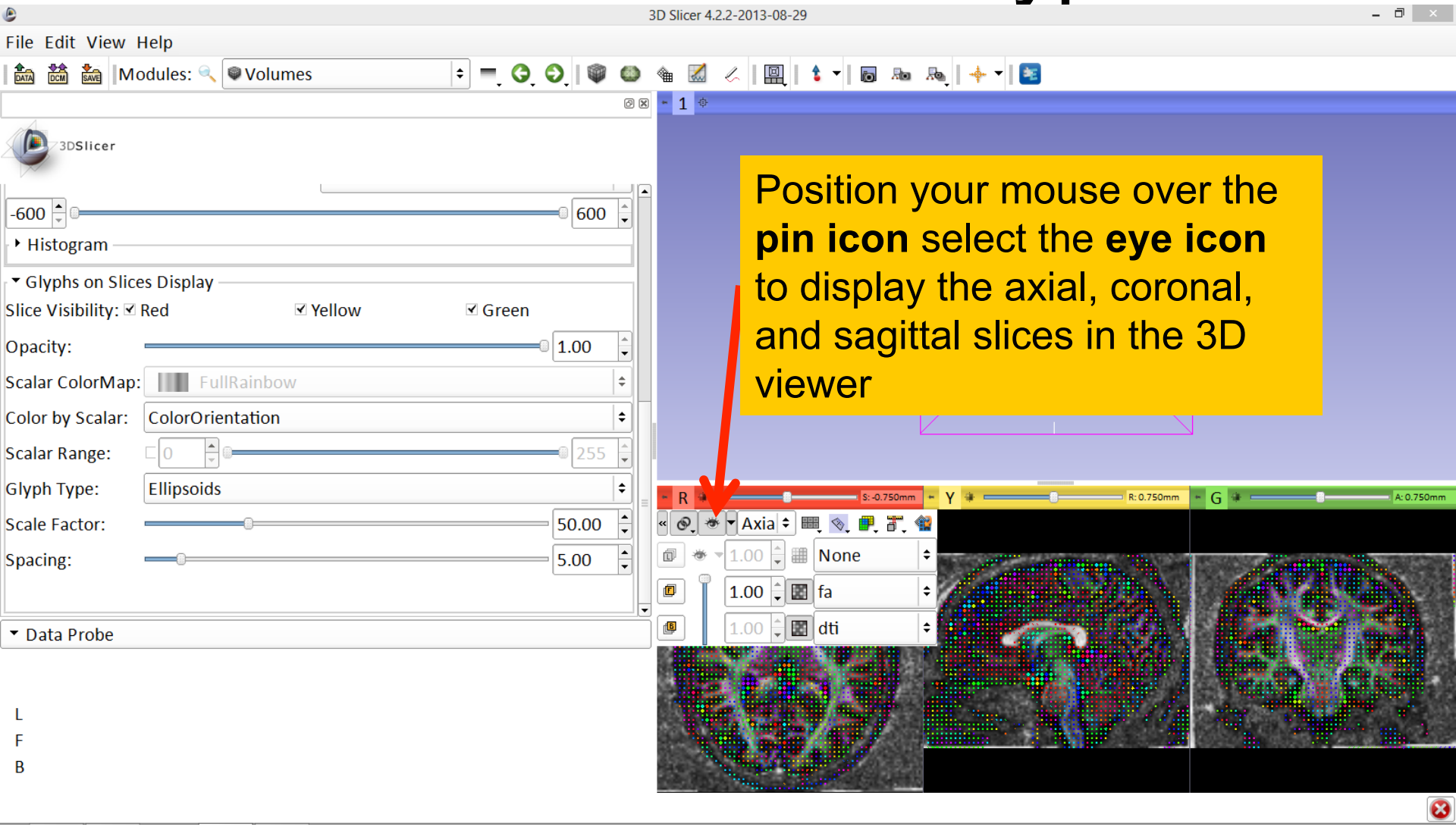
3D Visualization: Glyphs



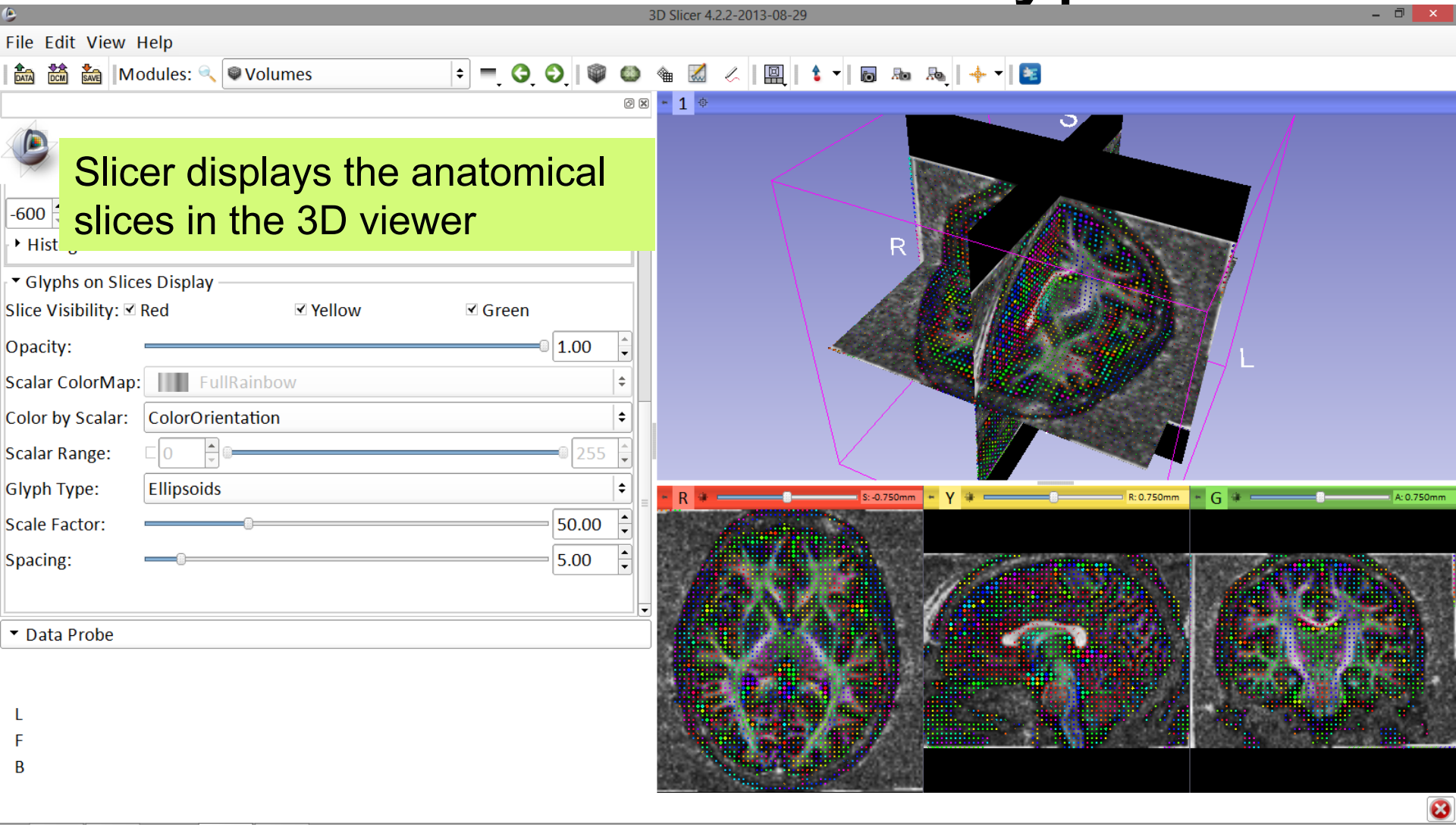
3D Visualization: Glyphs



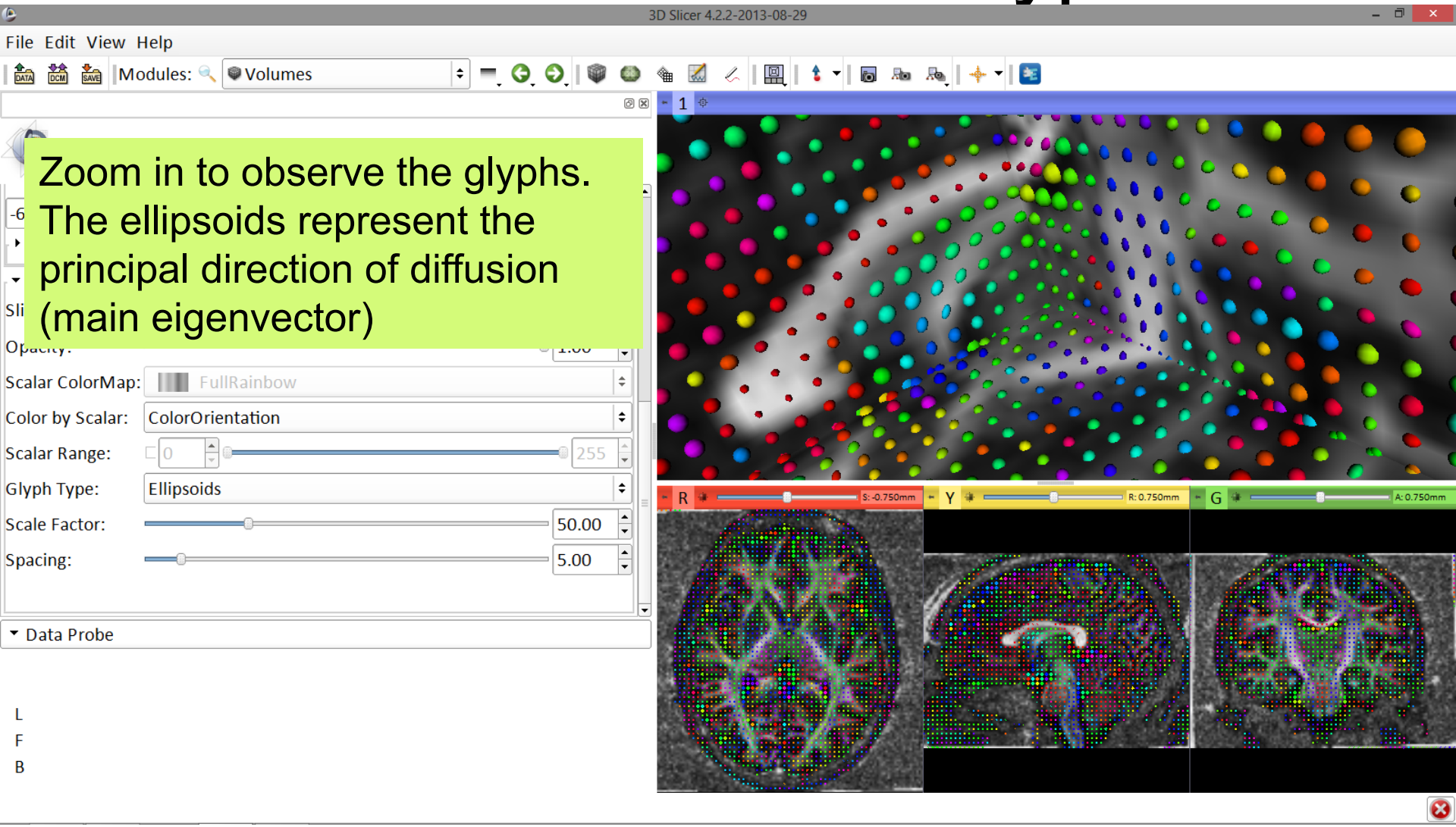
3D Visualization: Glyphs



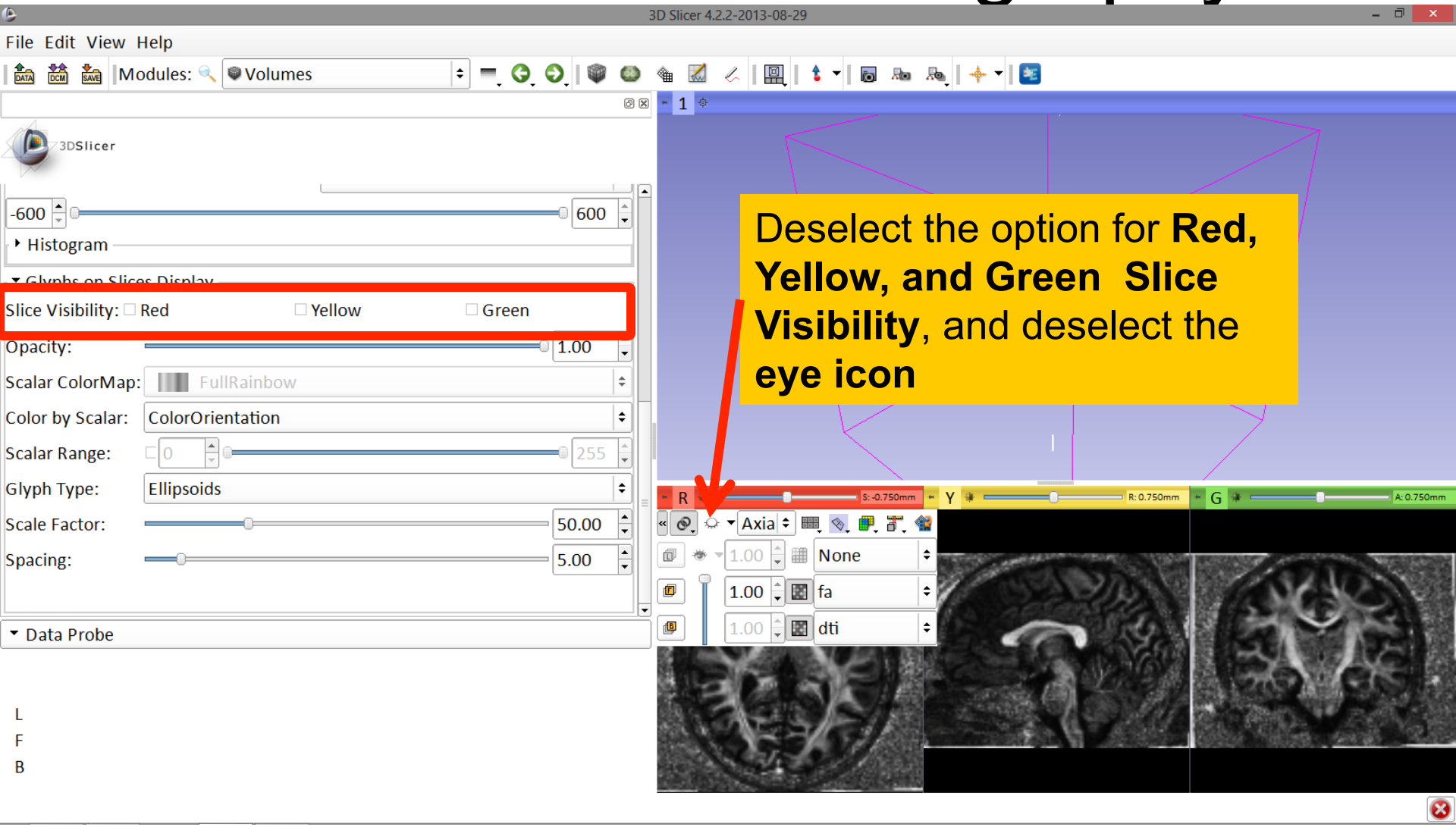
3D Visualization: Glyphs



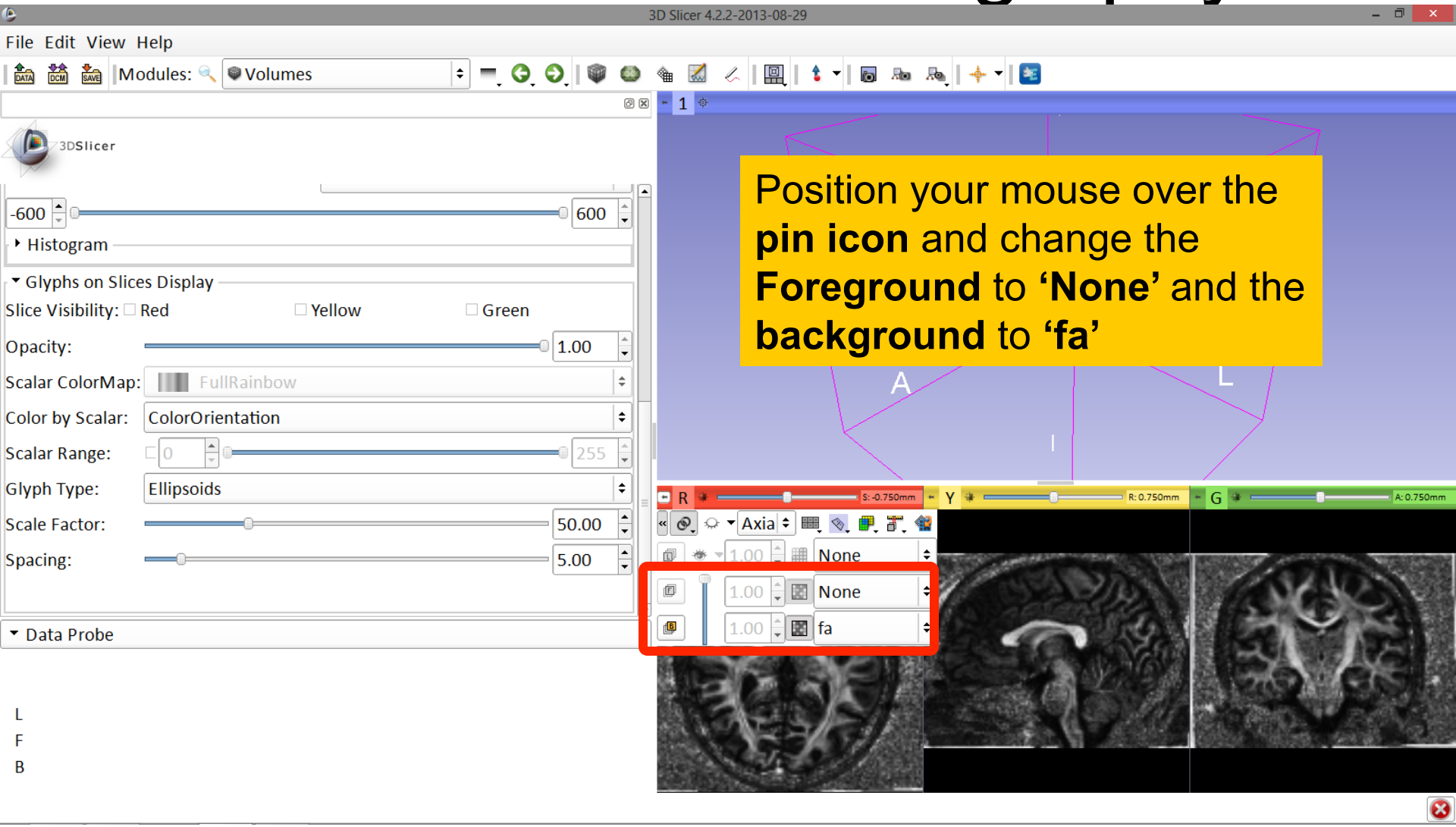
3D Visualization: Glyphs



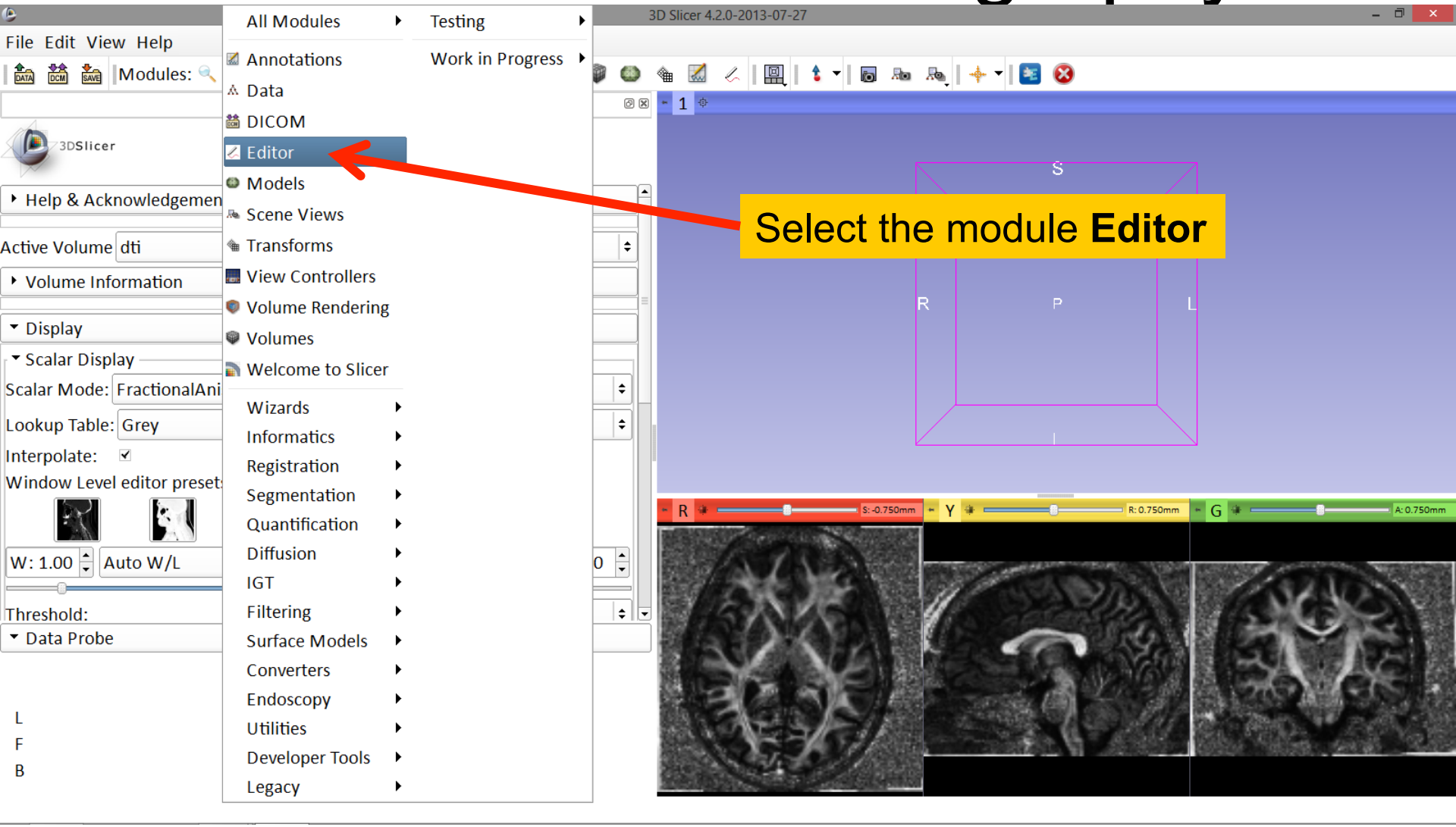
Diffusion MRI tractography



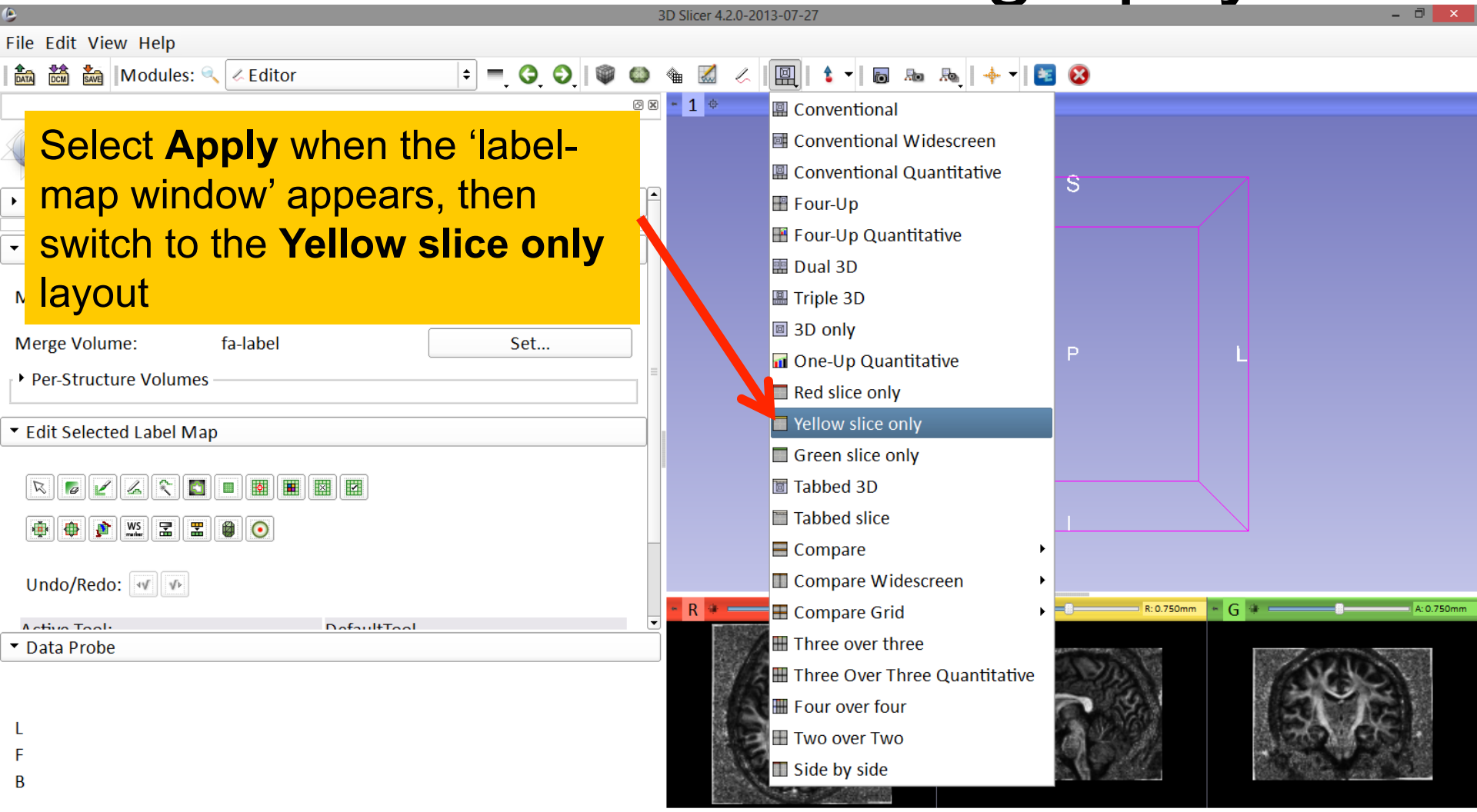
Diffusion MRI tractography



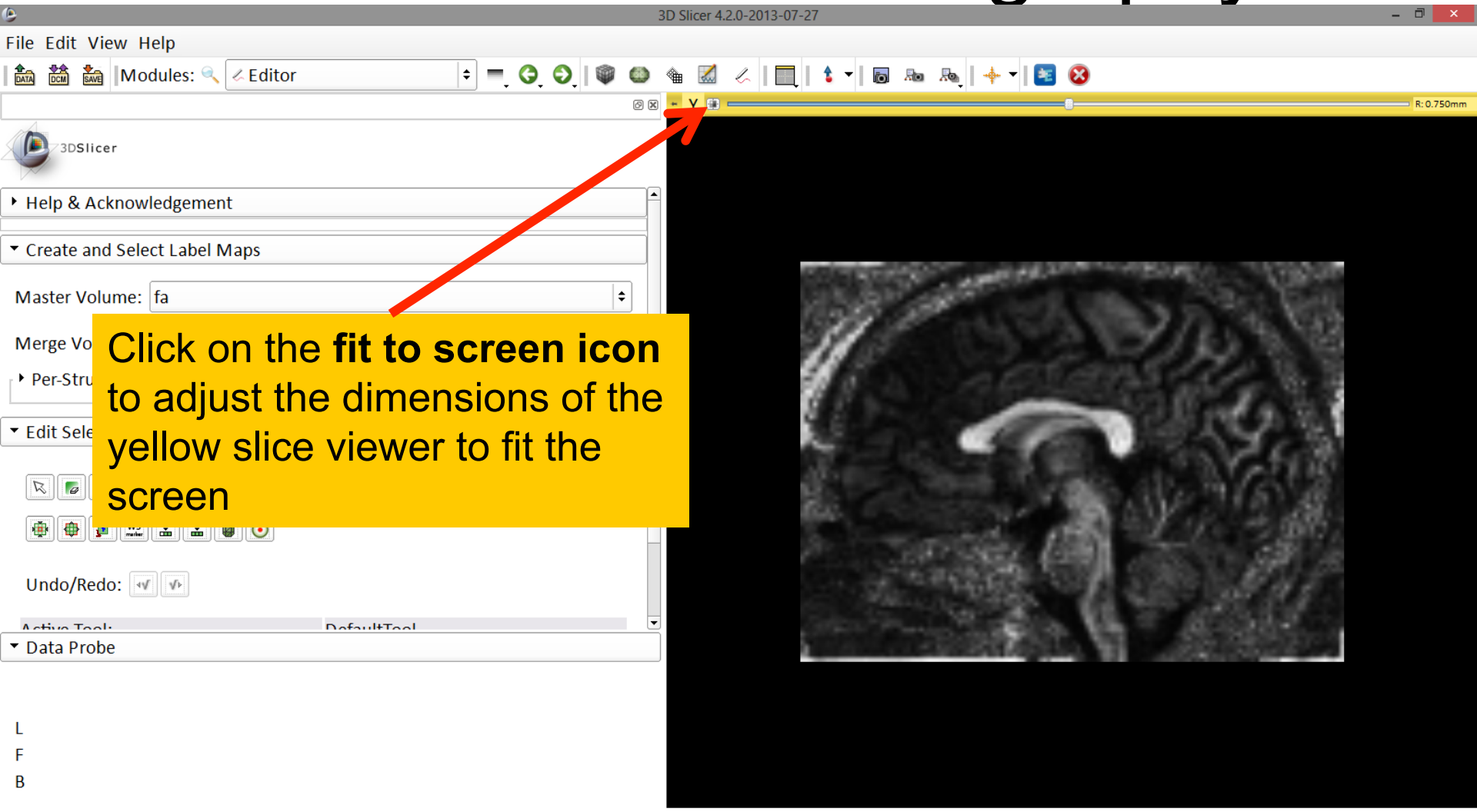
Diffusion MRI tractography



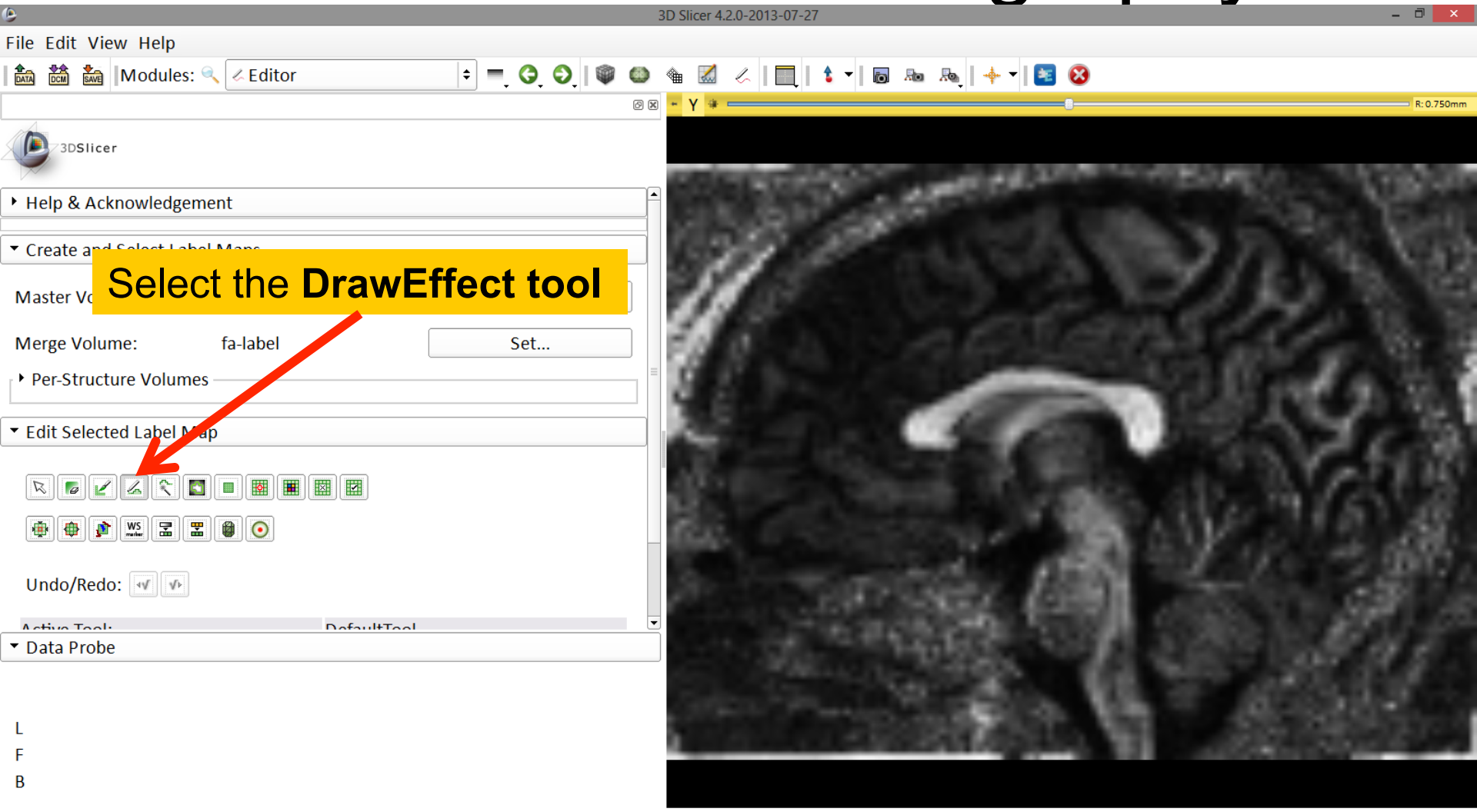
Diffusion MRI tractography



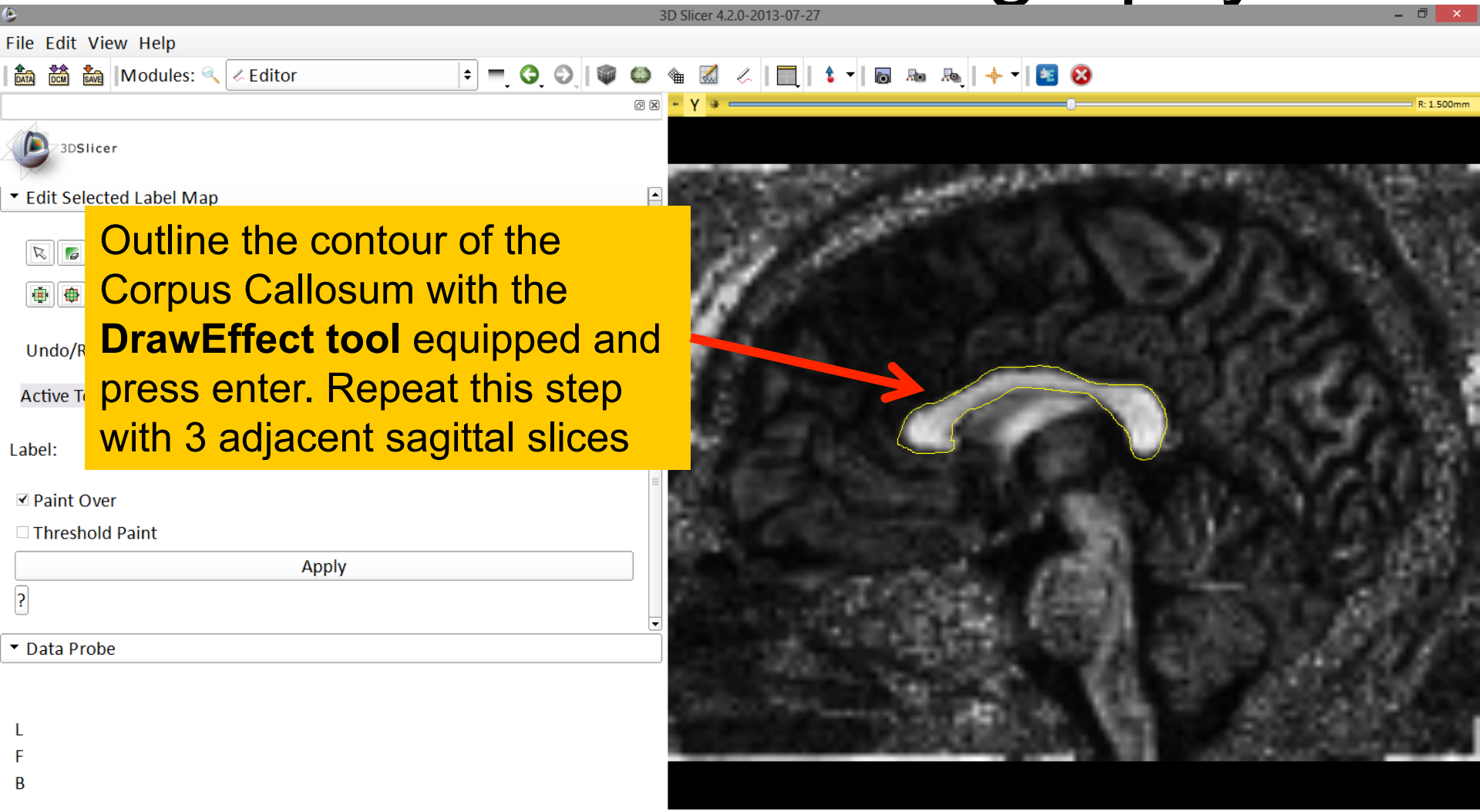
Diffusion MRI tractography



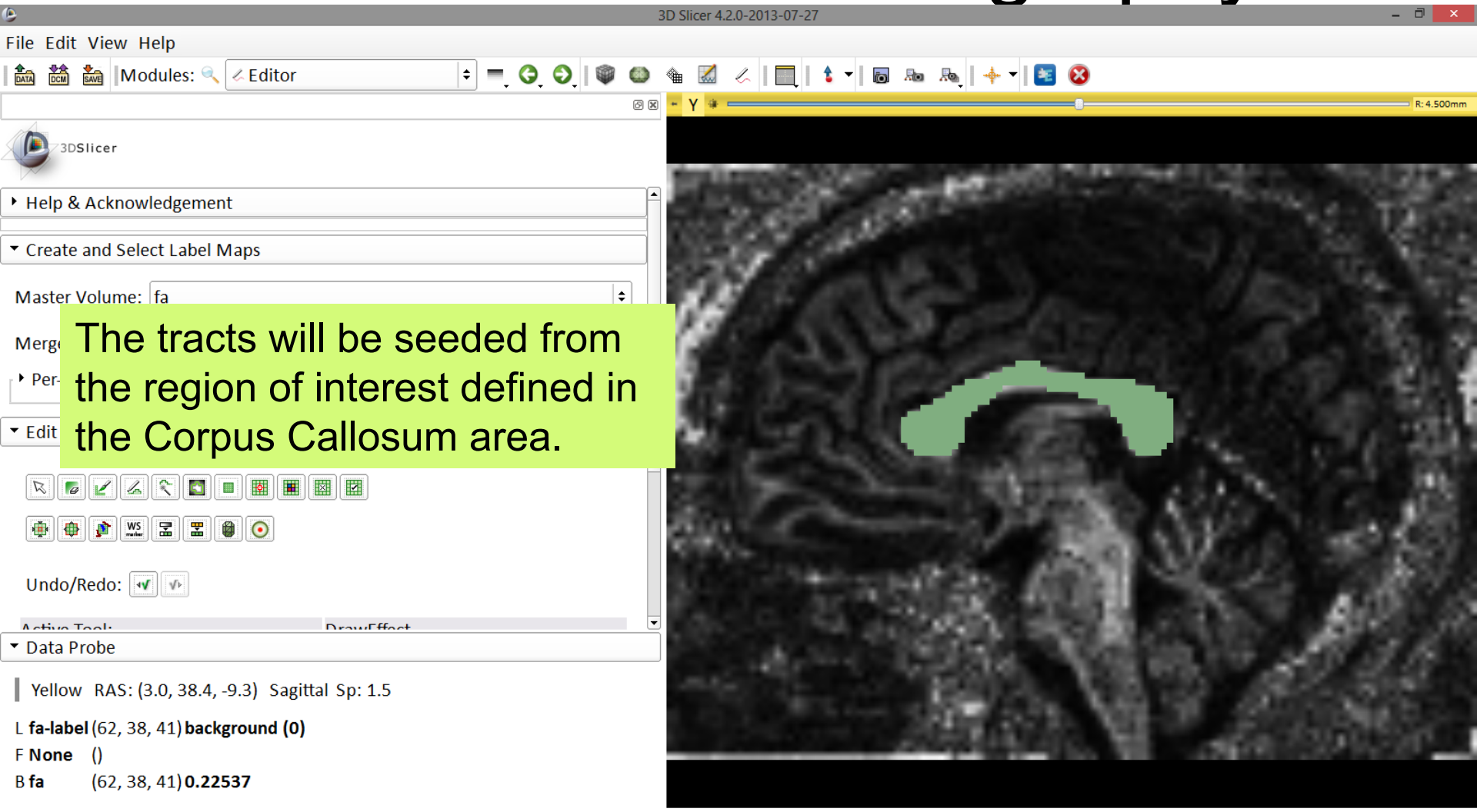
Diffusion MRI tractography



Diffusion MRI tractography

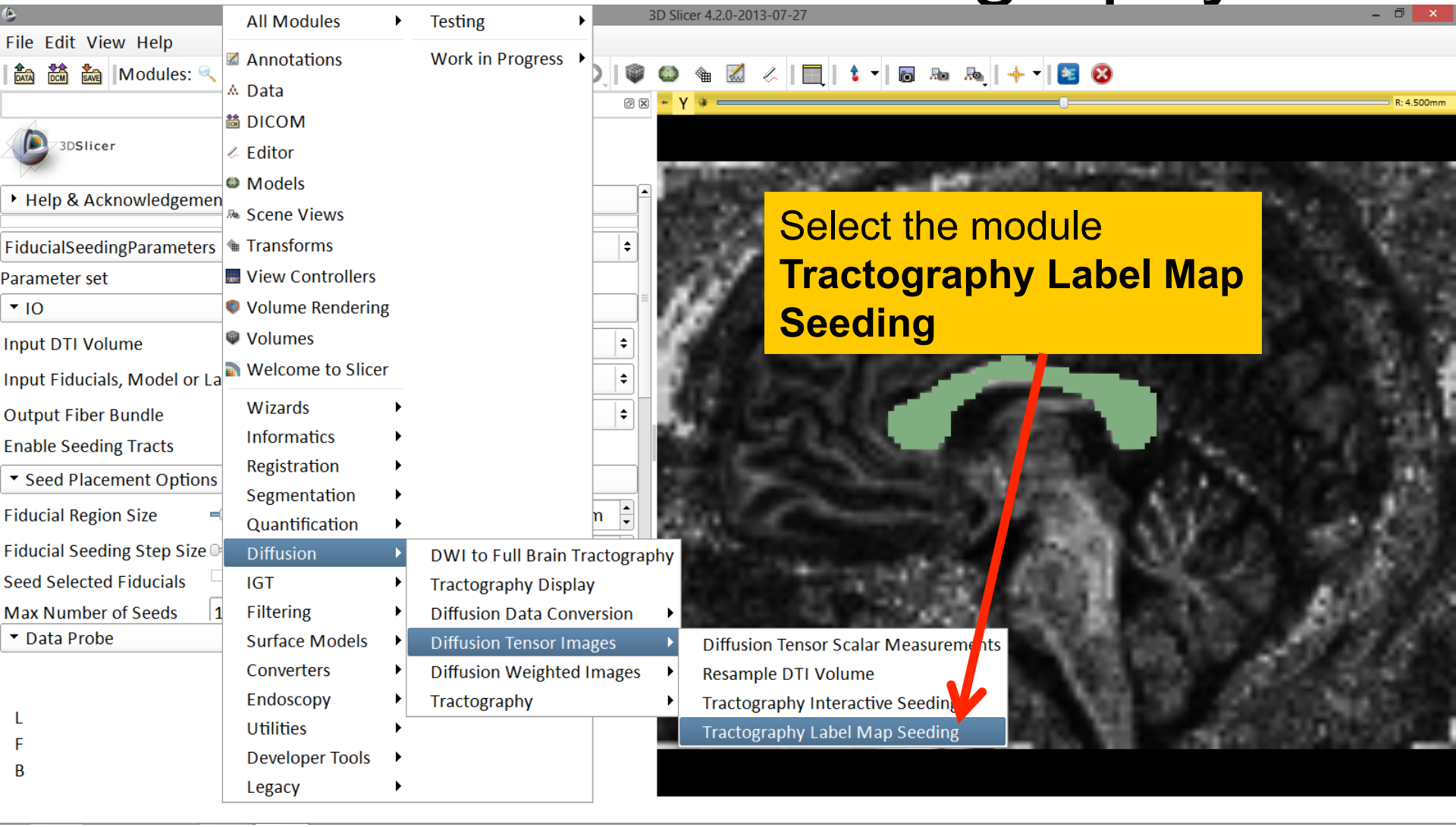


Diffusion MRI tractography

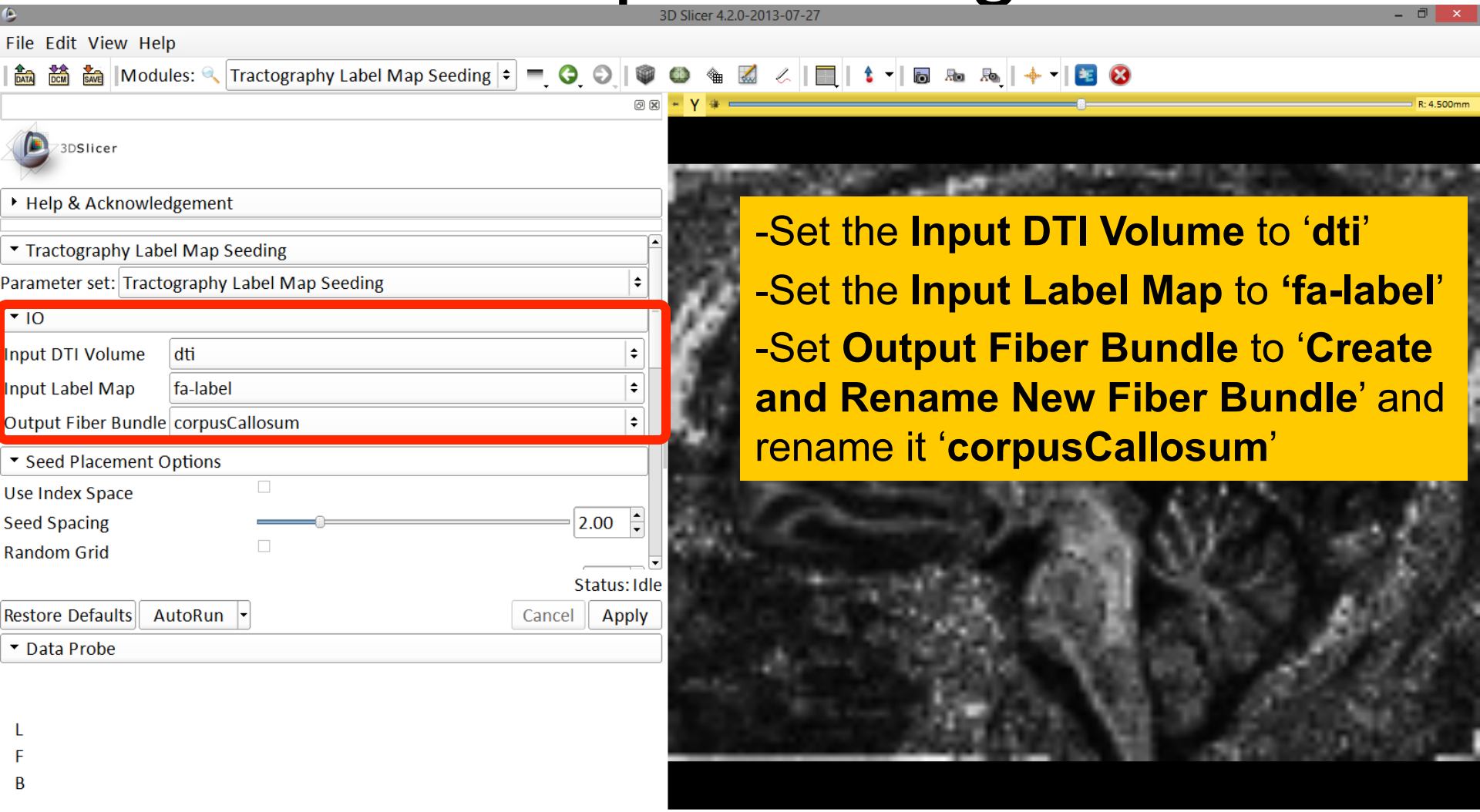


The tracts will be seeded from the region of interest defined in the Corpus Callosum area.

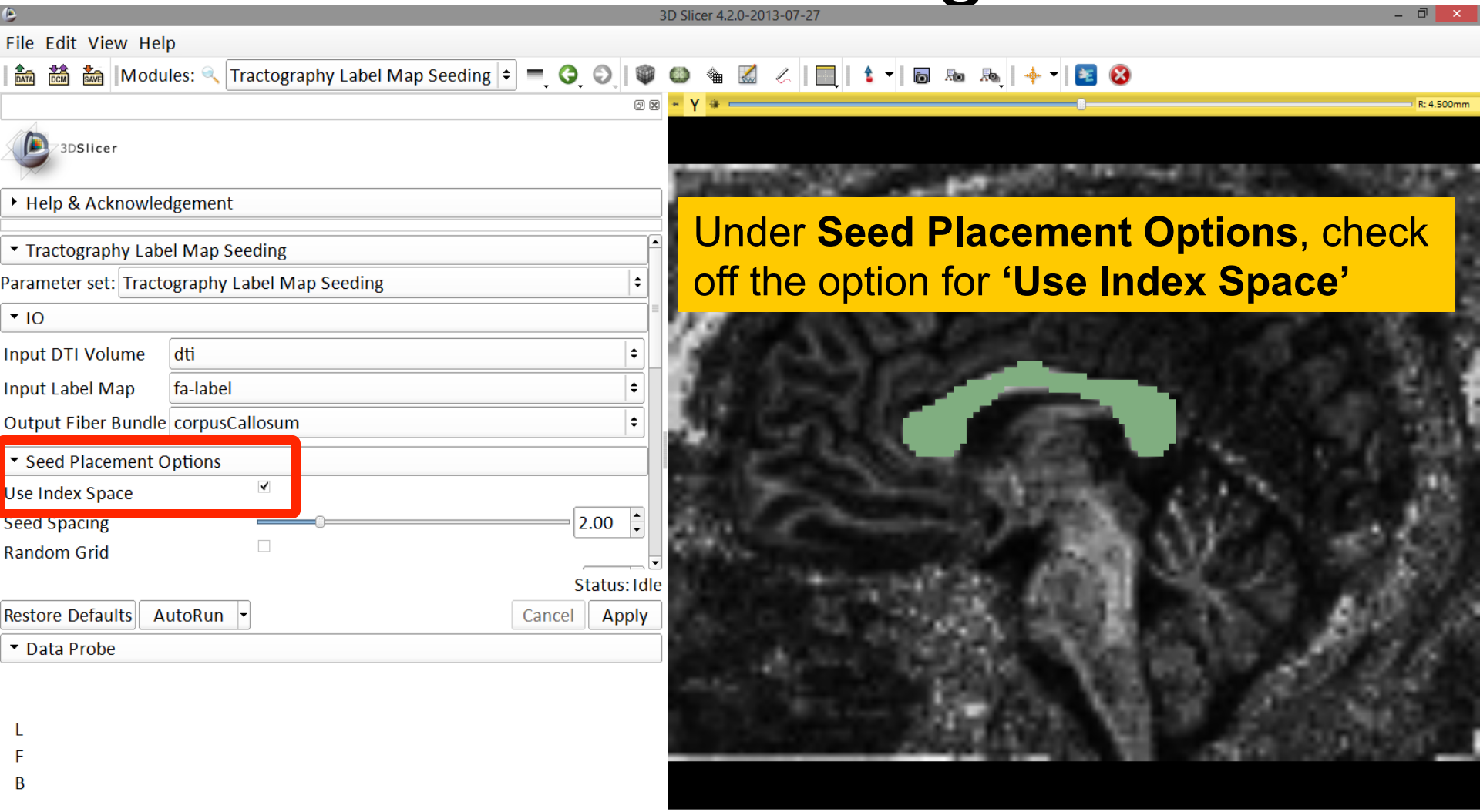
Diffusion MRI tractography



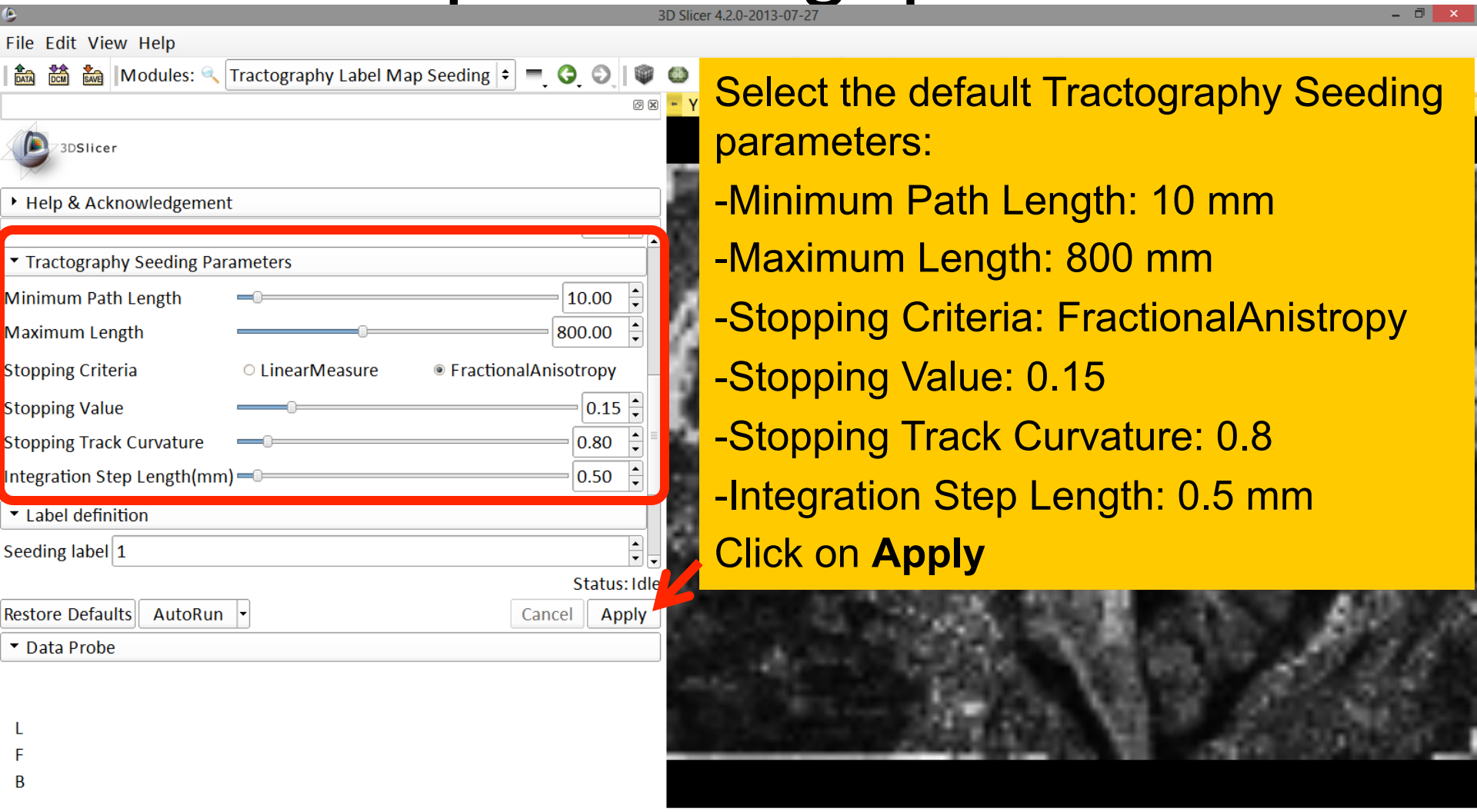
LabelMap Seeding: I/O



ROI Drawing


3D Slicer 4.2.0-2013-07-27
File Edit View Help
Modules: Tractography Label Map Seeding
3DSlicer
Help & Acknowledgement
Tractography Label Map Seeding
Parameter set: Tractography Label Map Seeding
IO
Input DTI Volume dti
Input Label Map fa-label
Output Fiber Bundle corpusCallosum
Seed Placement Options
Use Index Space
Seed Spacing 2.00
Random Grid
Status: Idle
Restore Defaults AutoRun Cancel Apply
Data Probe
L
F
B
Under **Seed Placement Options**, check off the option for **'Use Index Space'**

LabelMap Seeding: parameters



Select the default Tractography Seeding parameters:

-Minimum Path Length: 10 mm

-Maximum Length: 800 mm

-Stopping Criteria: FractionalAnistropy

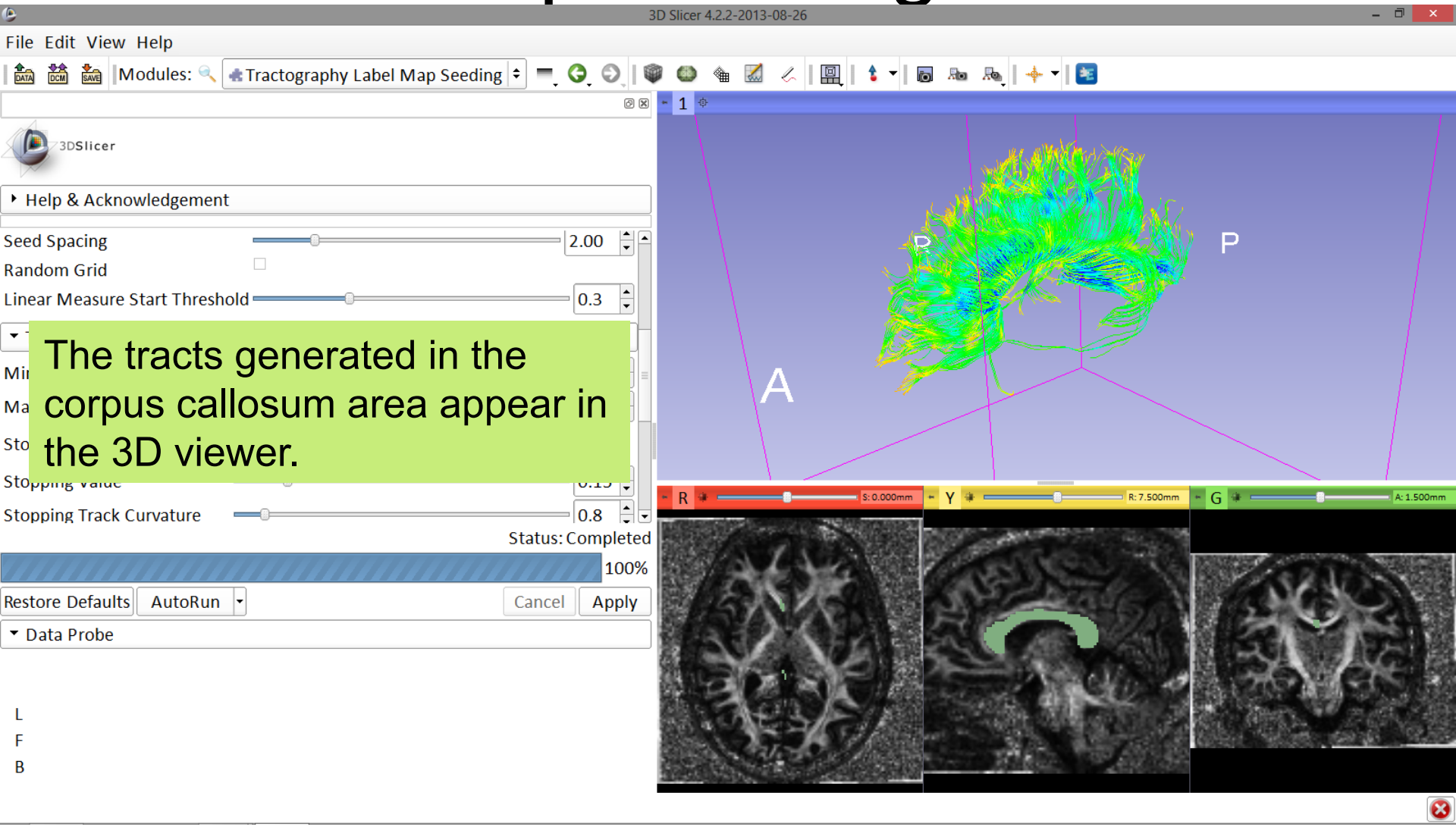
-Stopping Value: 0.15

-Stopping Track Curvature: 0.8

-Integration Step Length: 0.5 mm

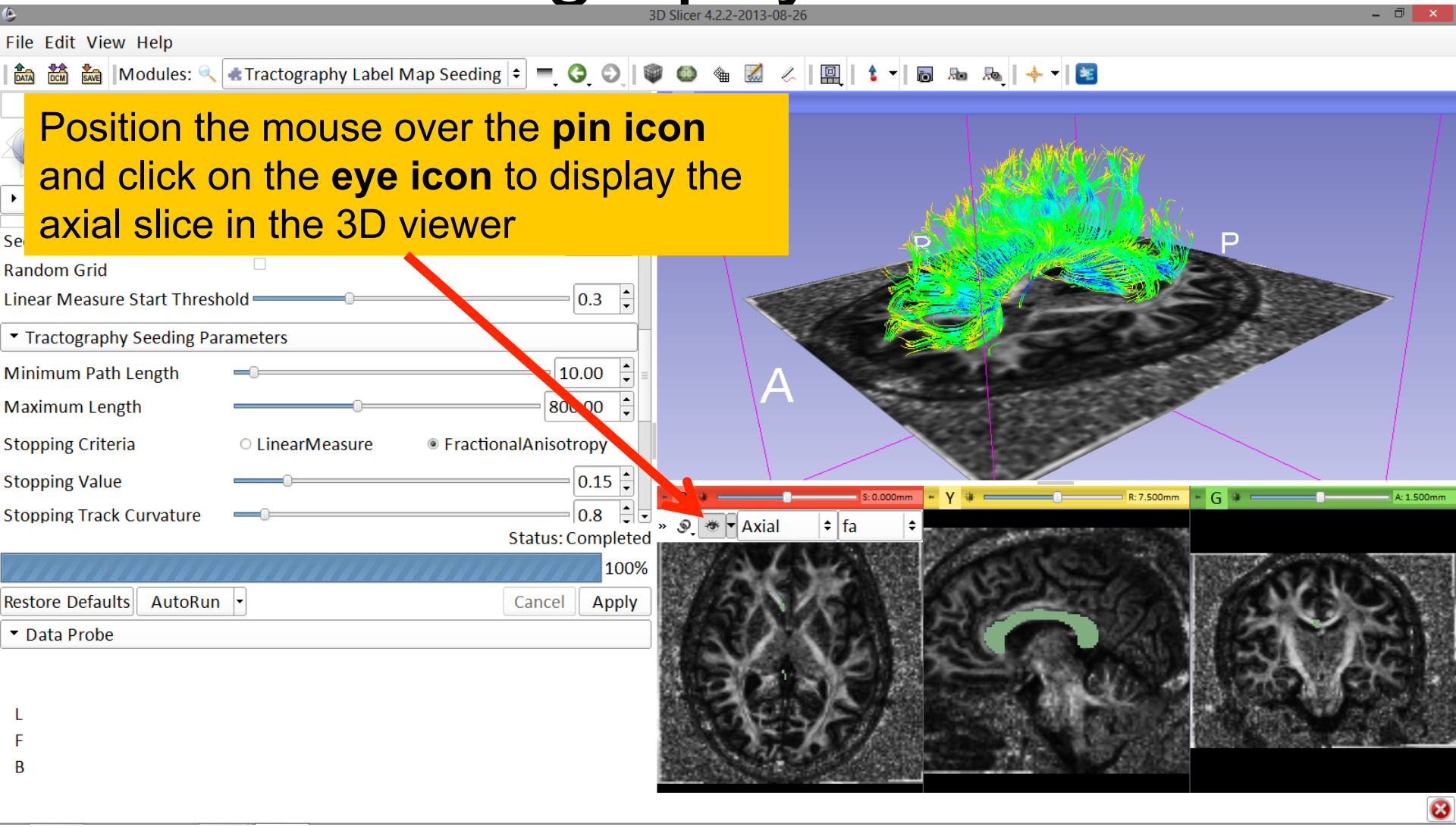
Click on **Apply**

LabelMap Seeding: Tracts

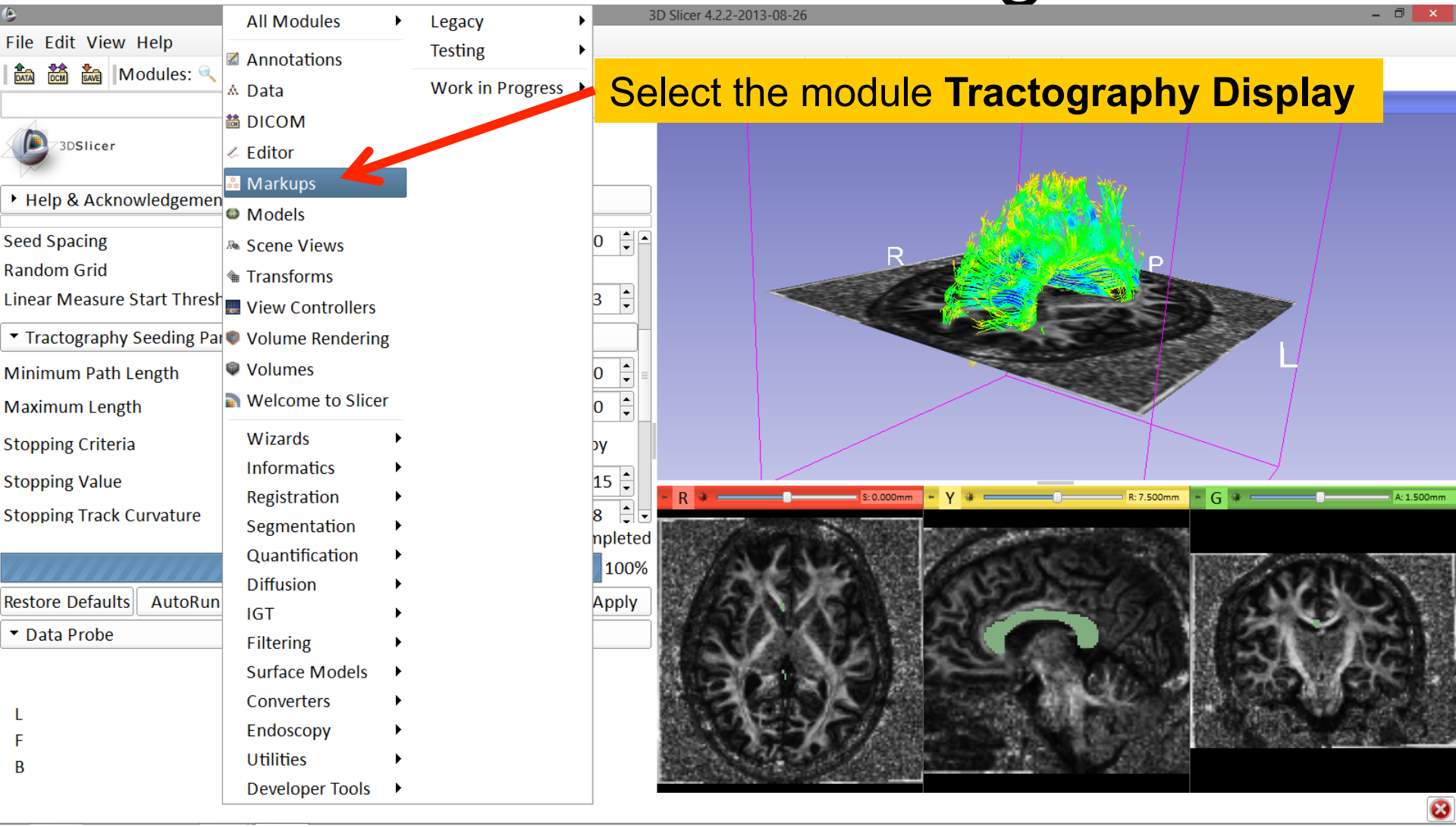


The tracts generated in the corpus callosum area appear in the 3D viewer.

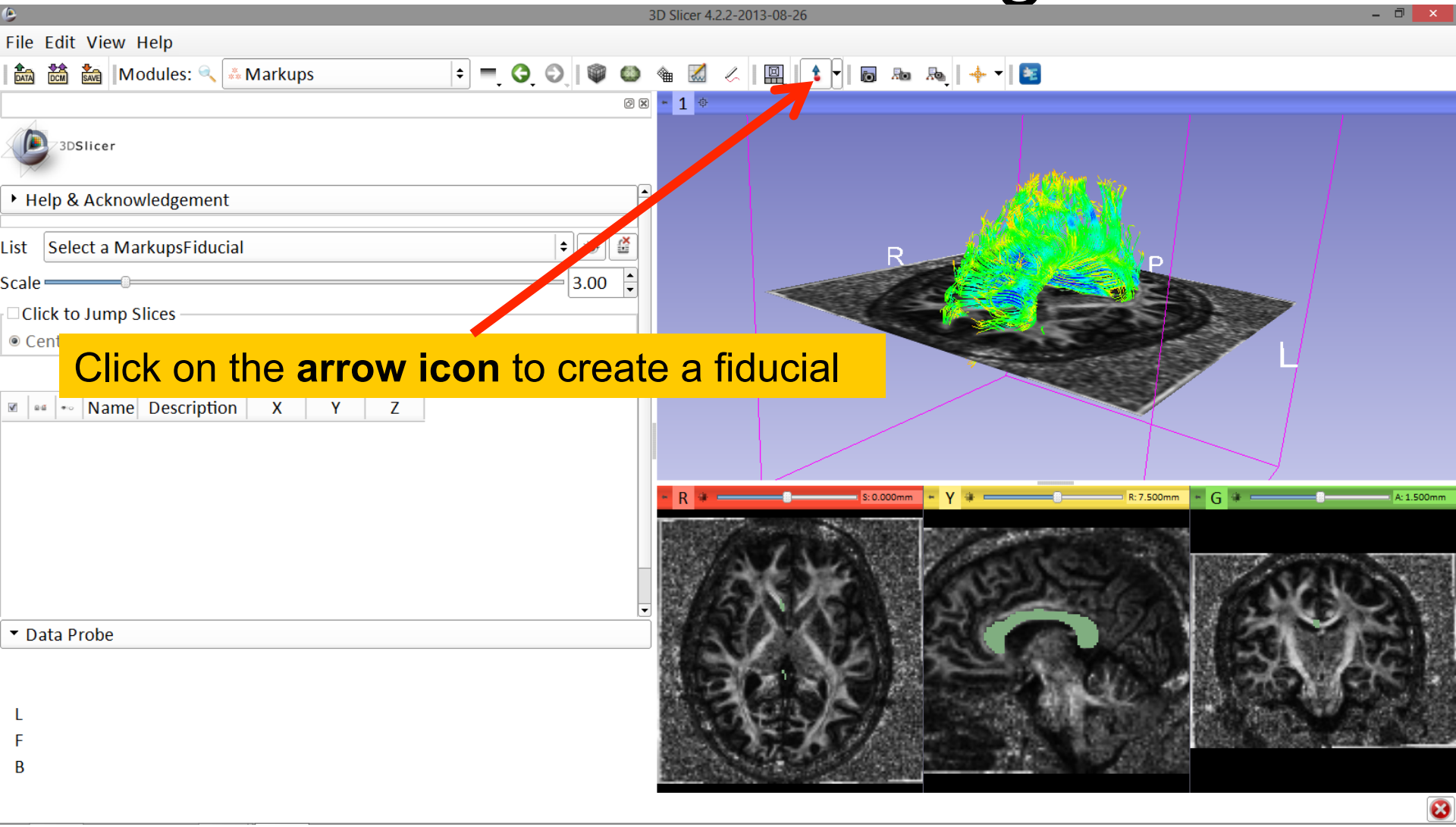
Tractography Results



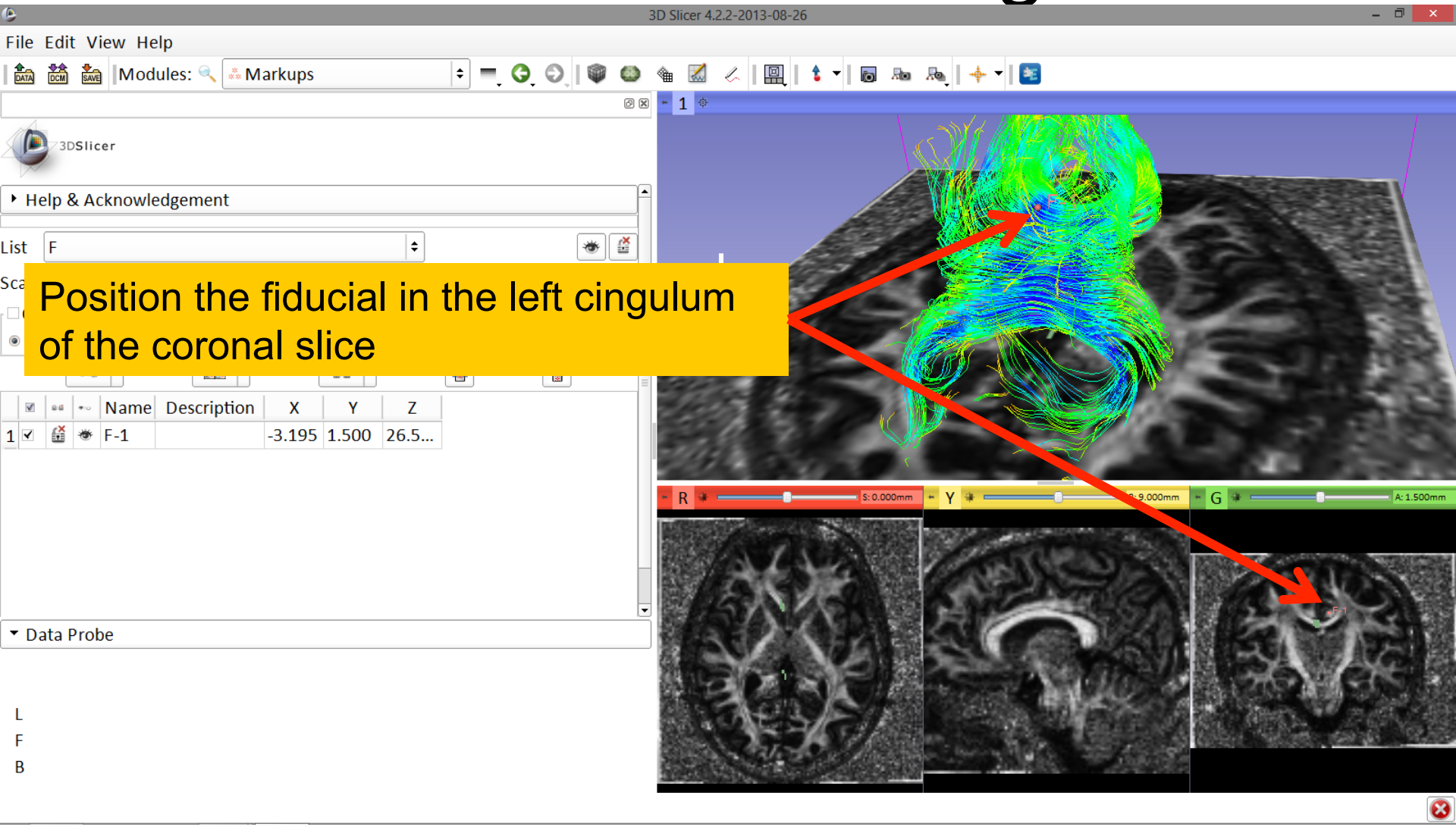
Fiducial Seeding



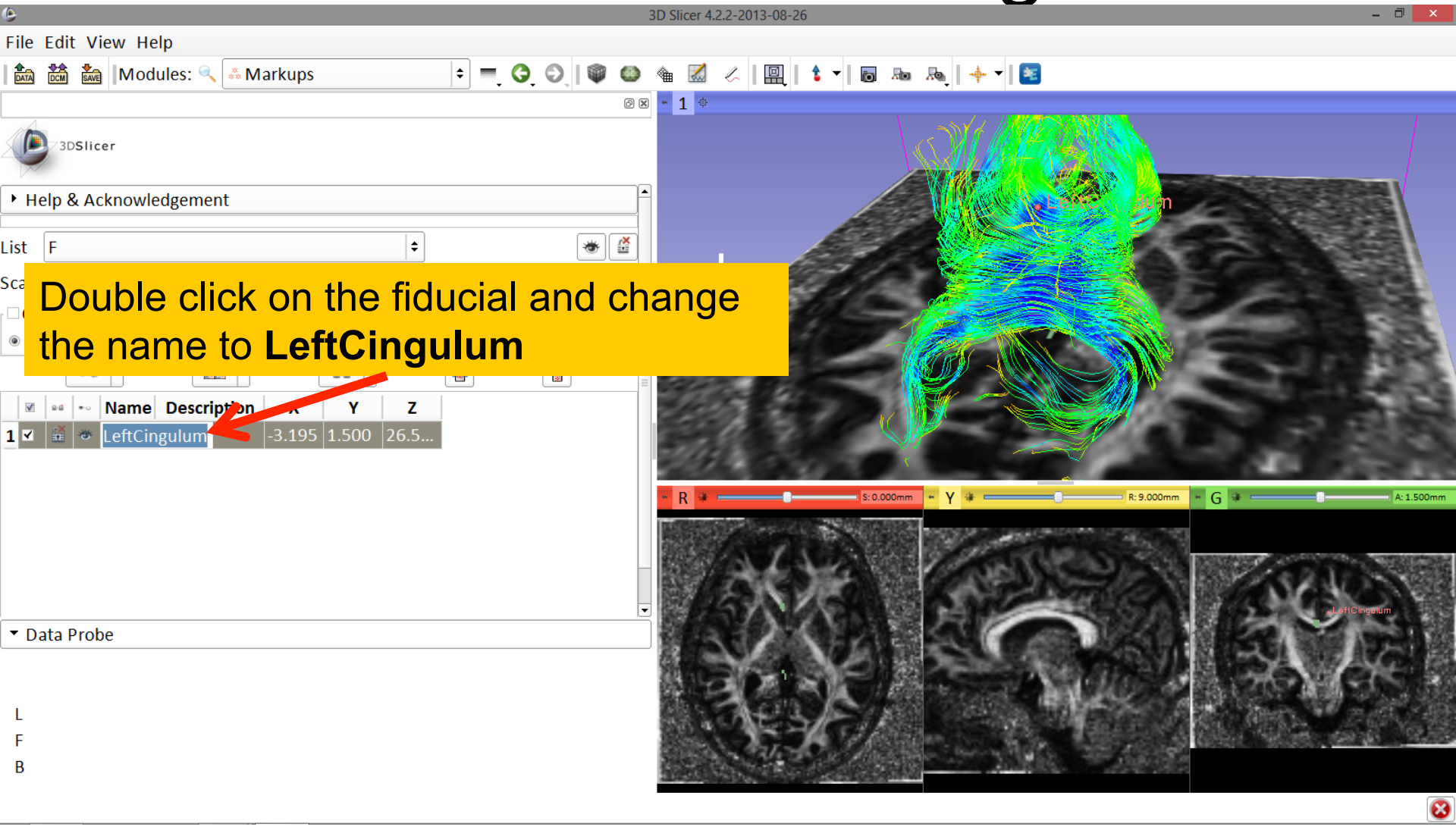
Fiducial Seeding



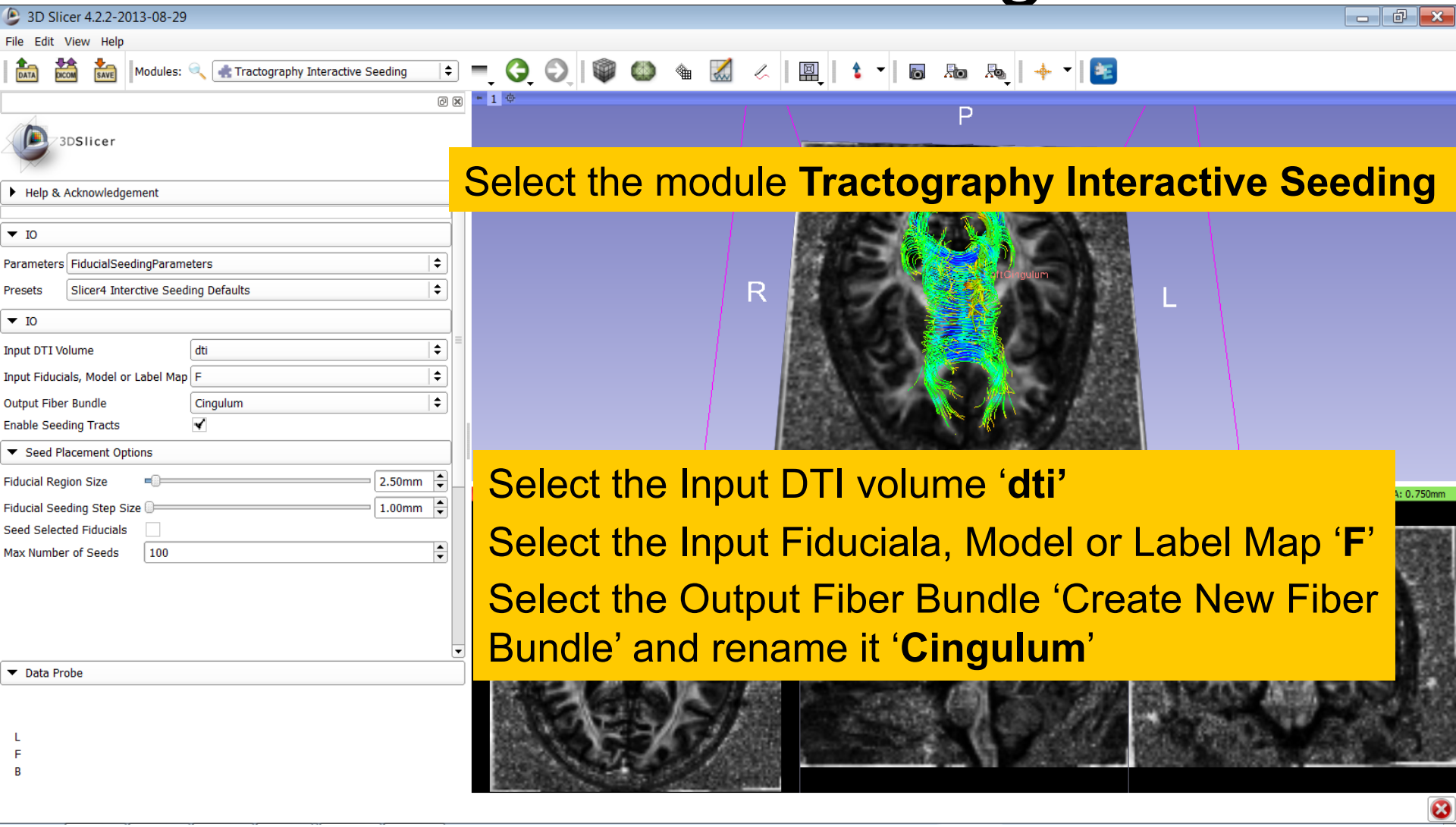
Fiducial Seeding



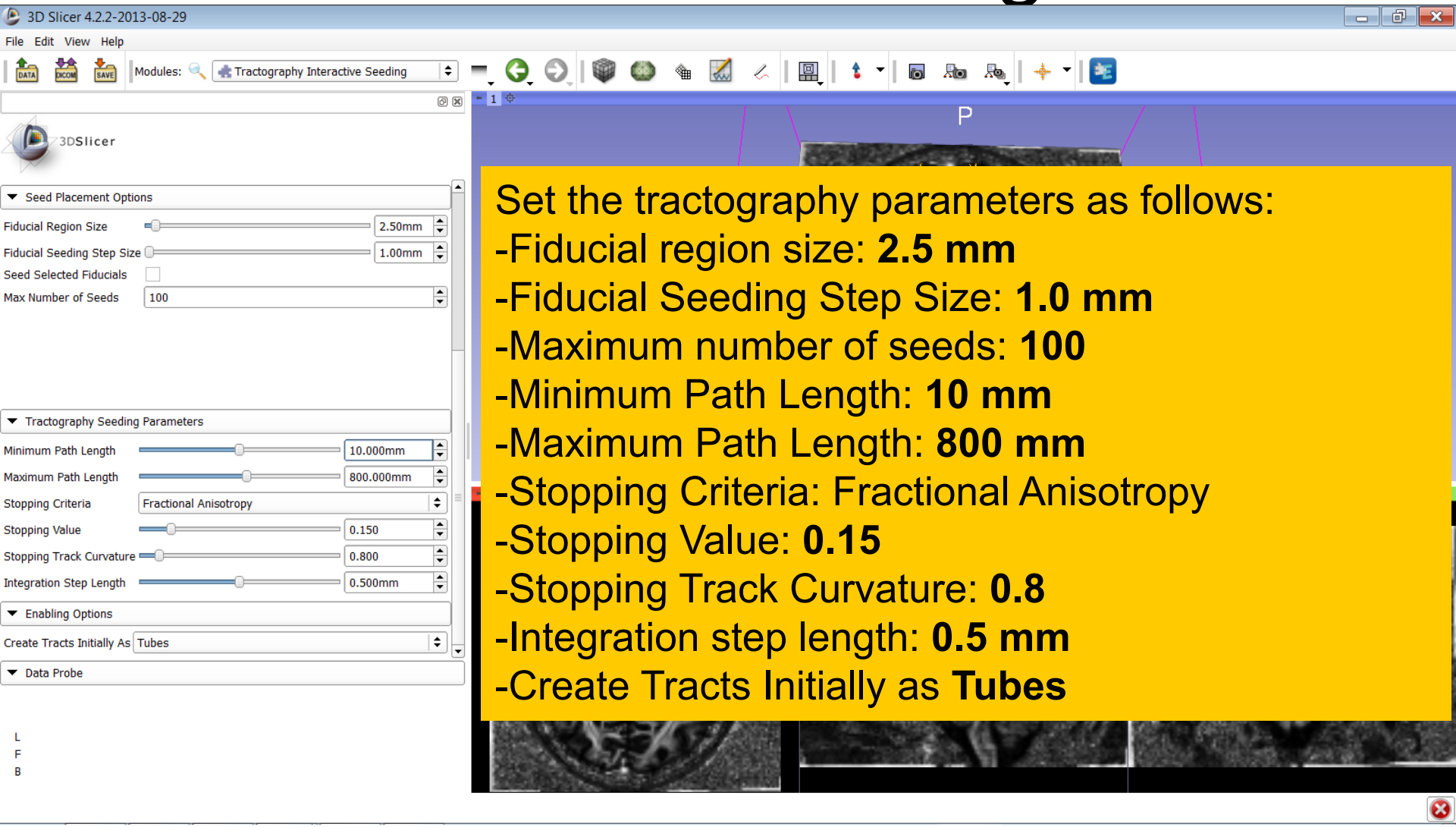
Fiducial Seeding



Fiducial Seeding



Fiducial Seeding



Set the tractography parameters as follows:

-Fiducial region size: **2.5 mm**

-Fiducial Seeding Step Size: **1.0 mm**

-Maximum number of seeds: **100**

-Minimum Path Length: **10 mm**

-Maximum Path Length: **800 mm**

-Stopping Criteria: Fractional Anisotropy

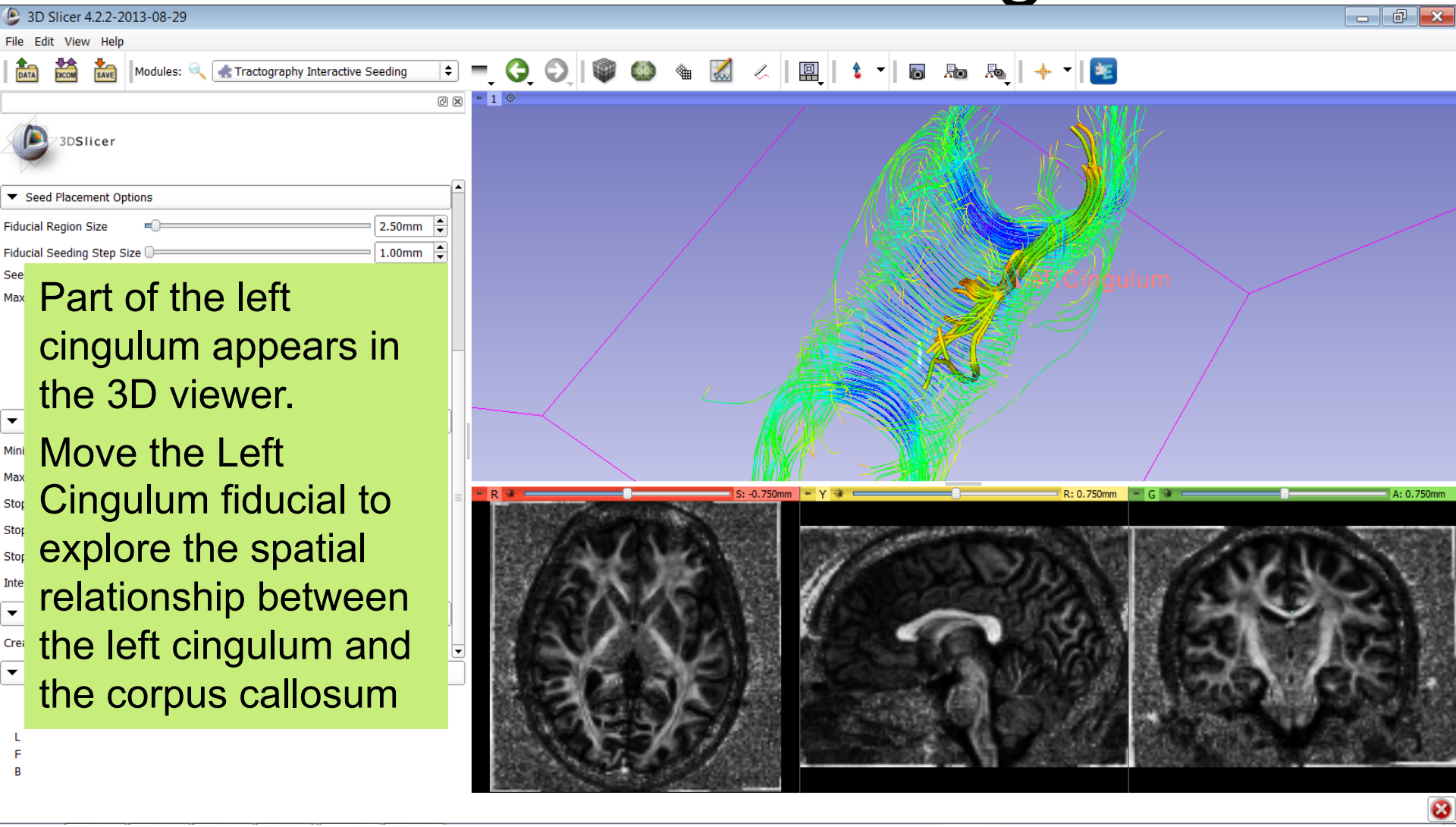
-Stopping Value: **0.15**

-Stopping Track Curvature: **0.8**

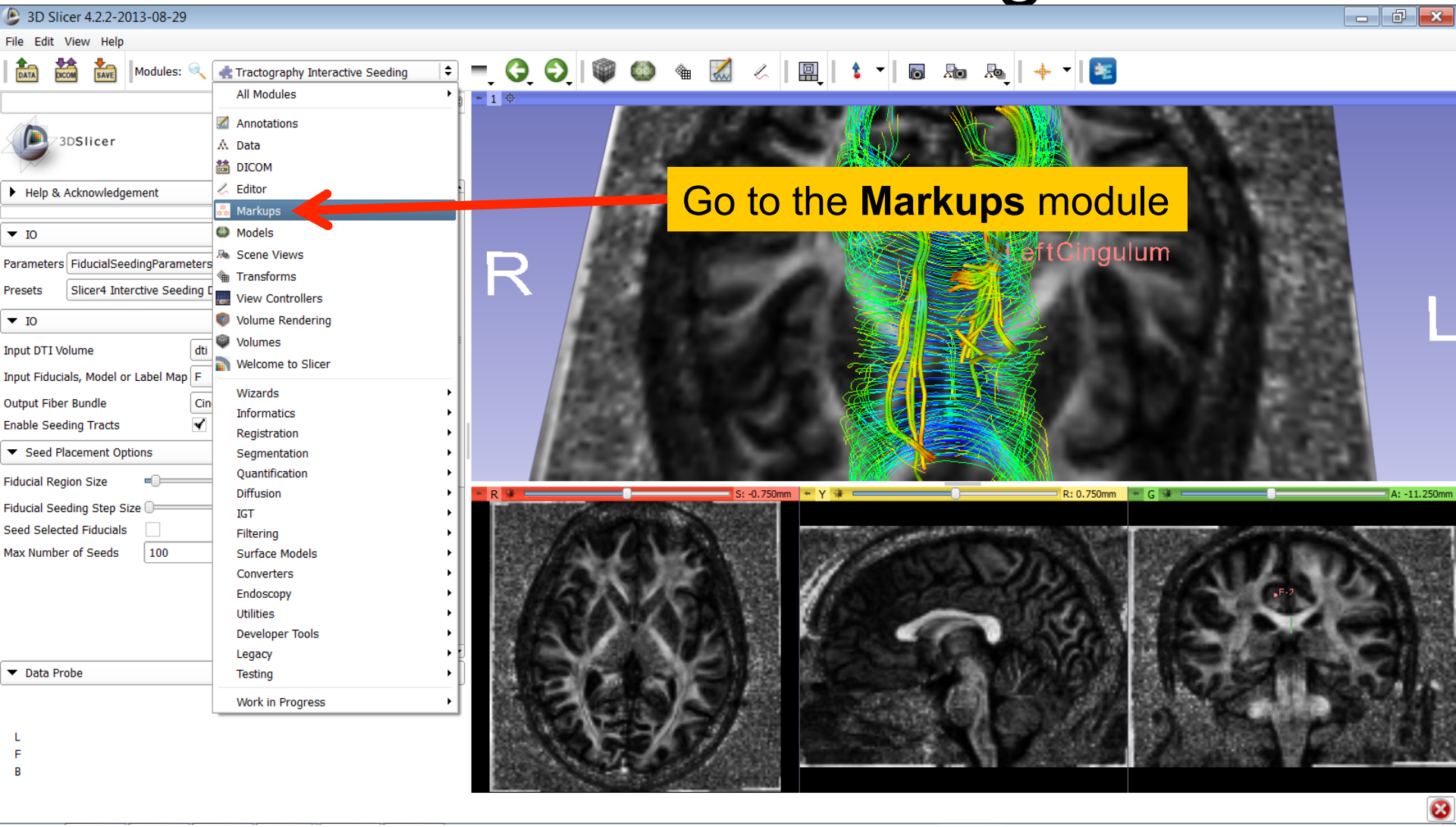
-Integration step length: **0.5 mm**

-Create Tracts Initially as **Tubes**

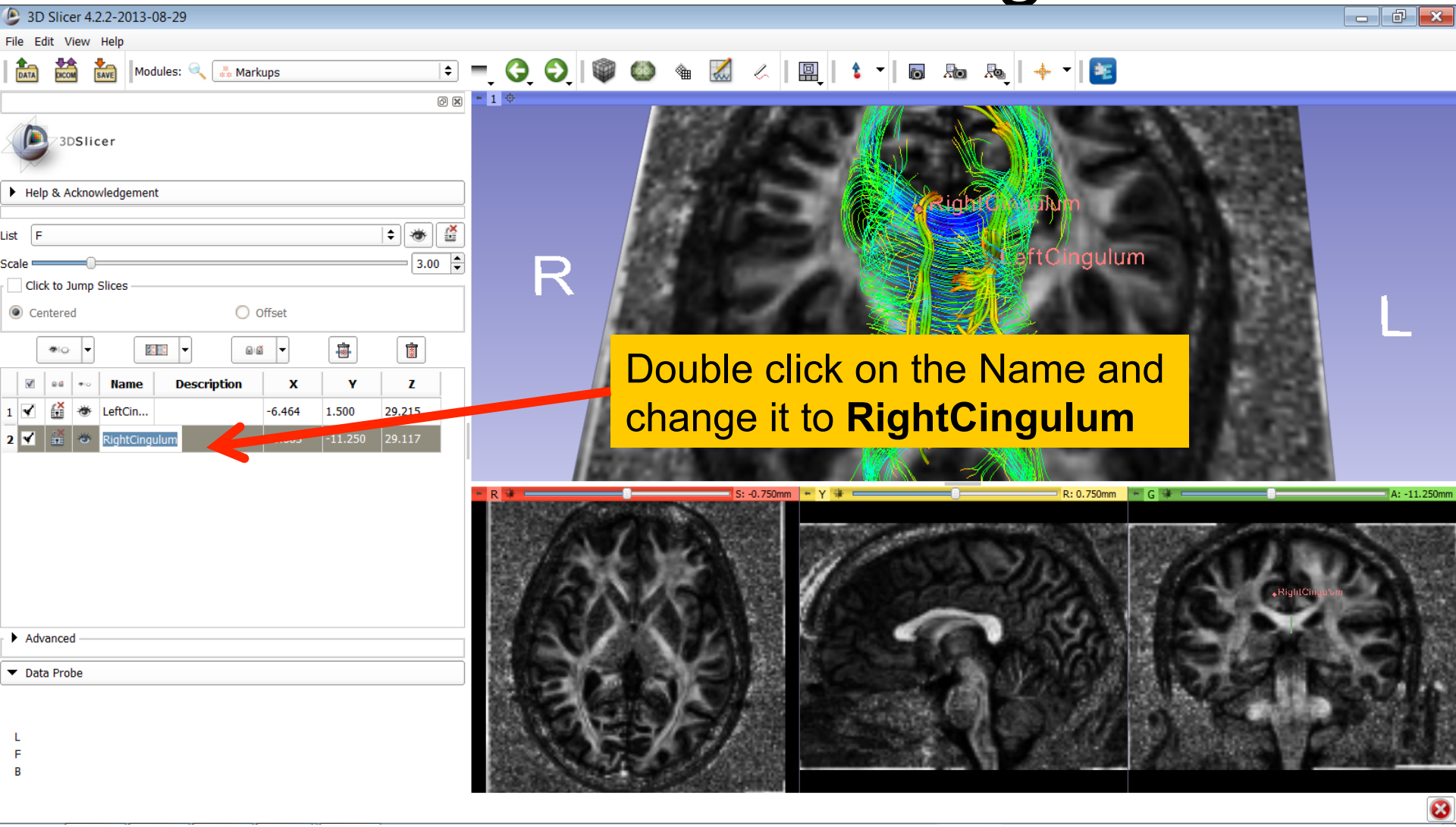
Fiducial Seeding



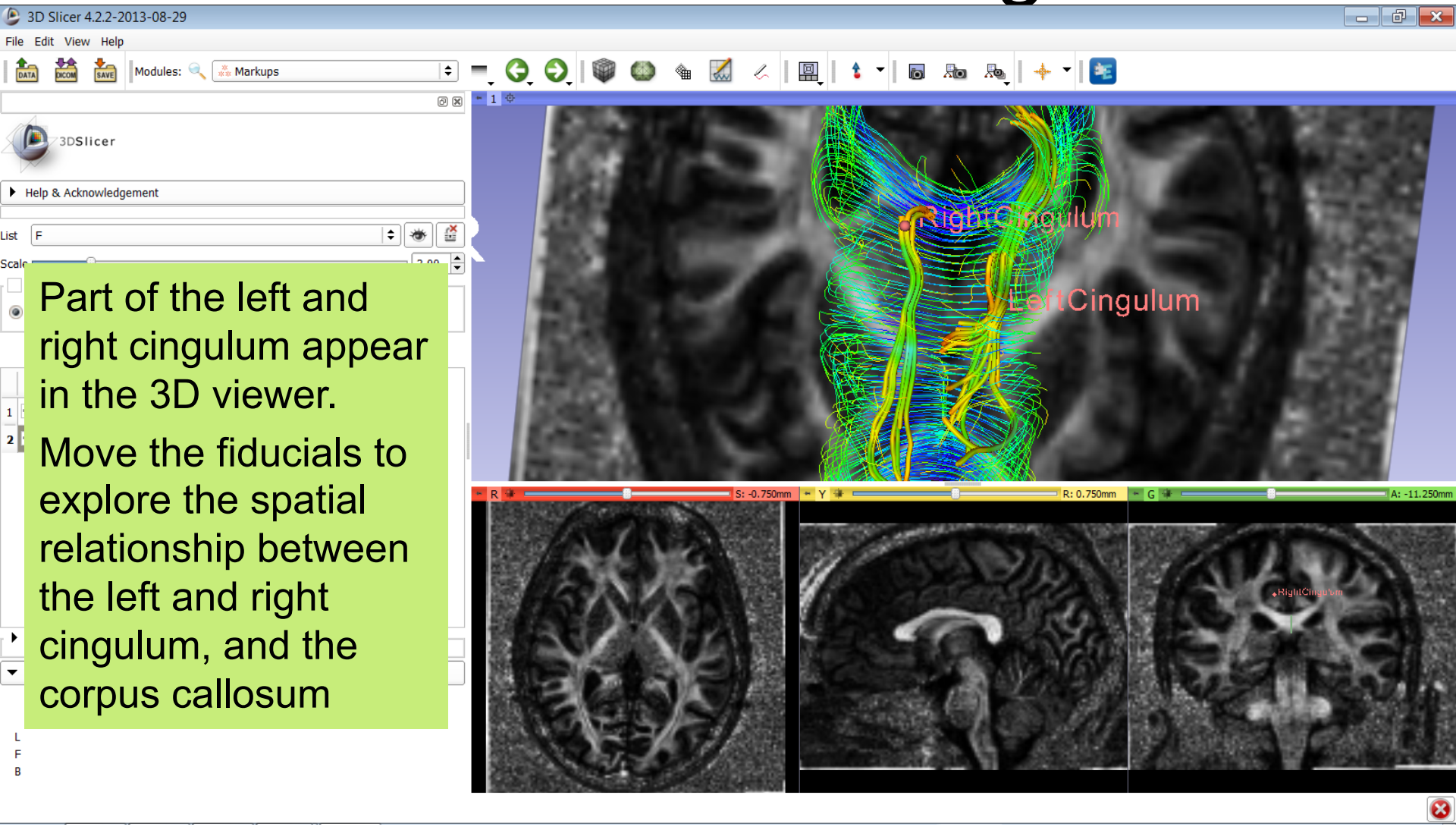
Fiducial Seeding



Fiducial Seeding



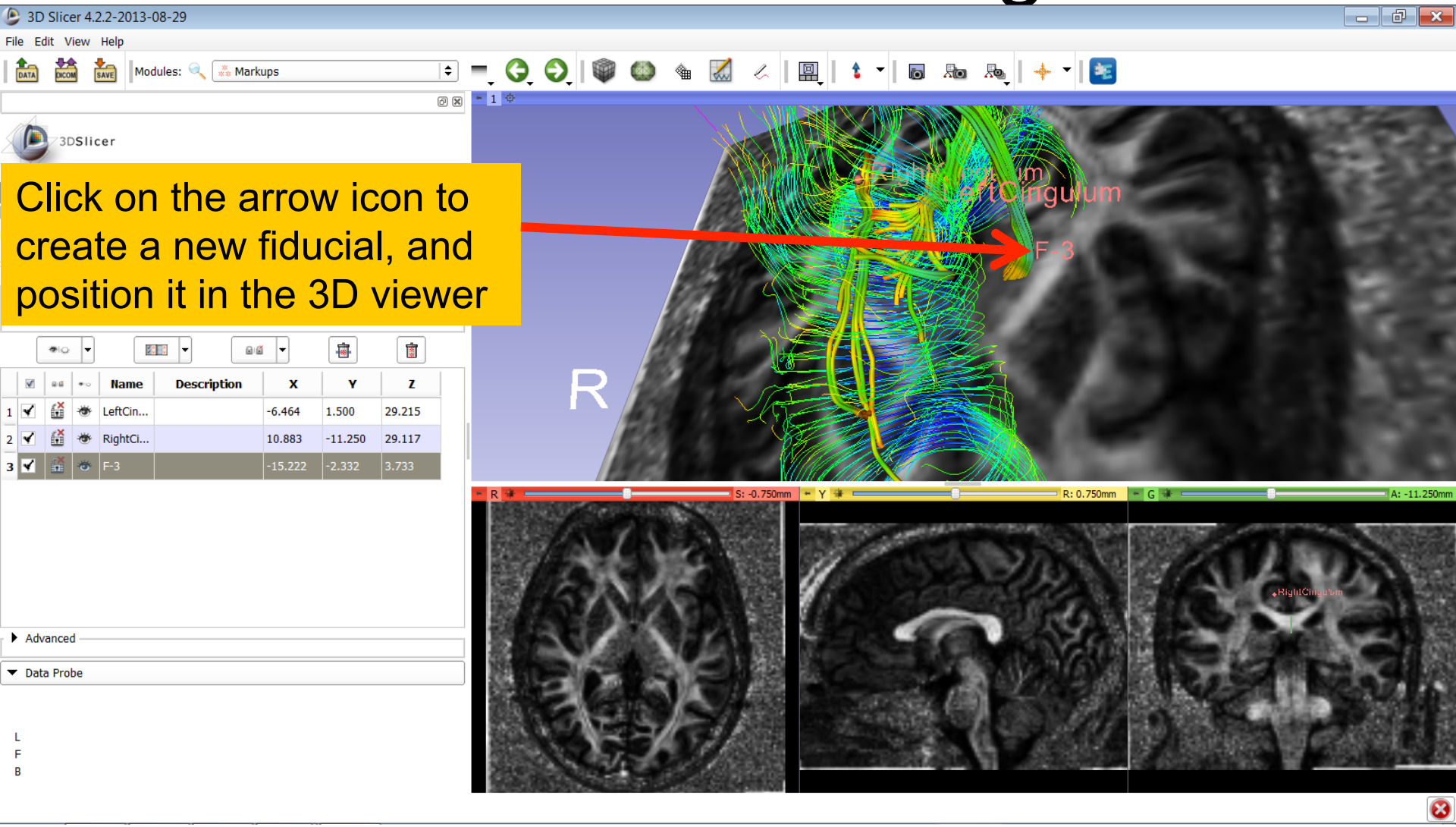
Fiducial Seeding



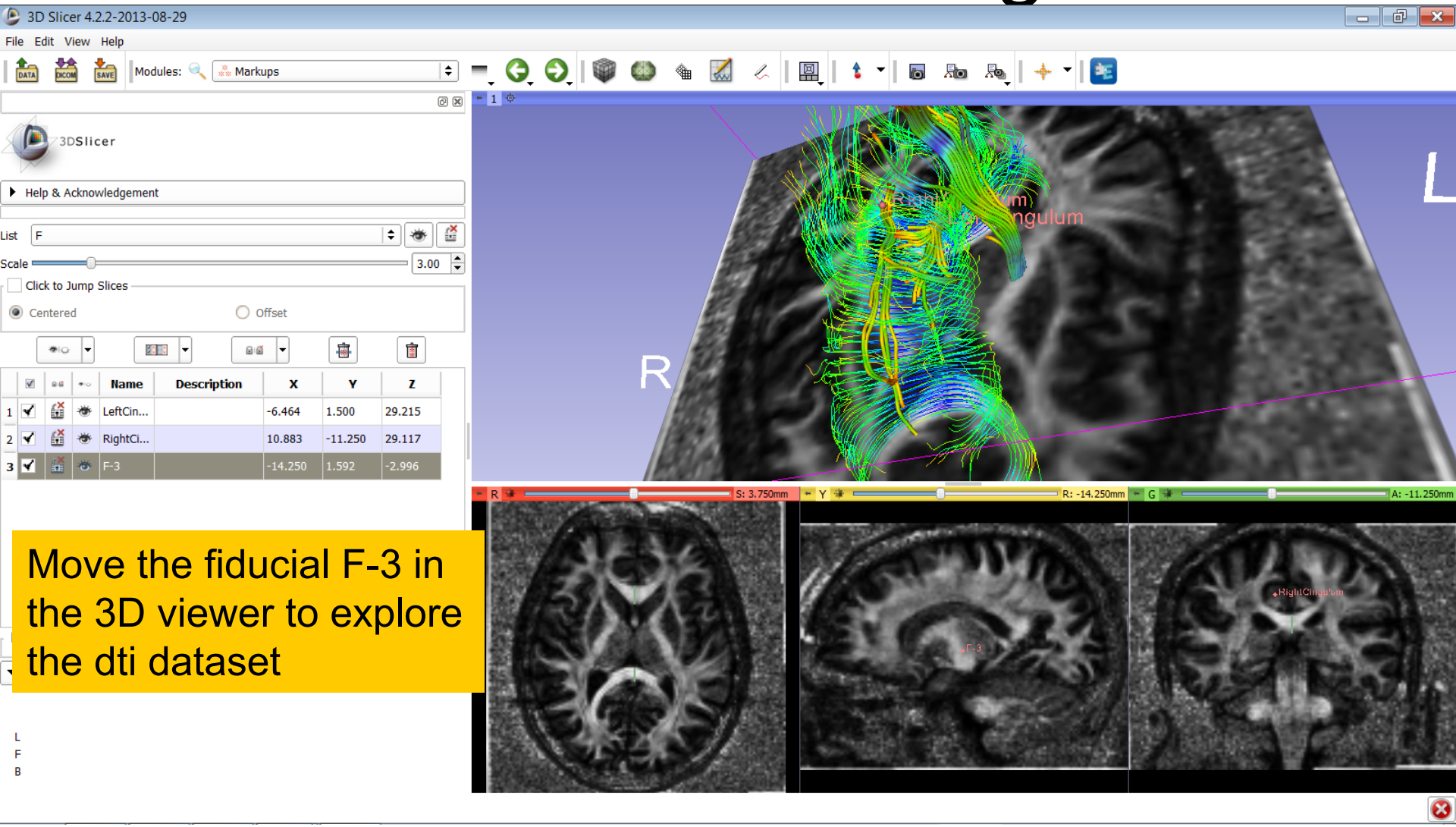
Part of the left and right cingulum appear in the 3D viewer.

Move the fiducials to explore the spatial relationship between the left and right cingulum, and the corpus callosum

Fiducial Seeding

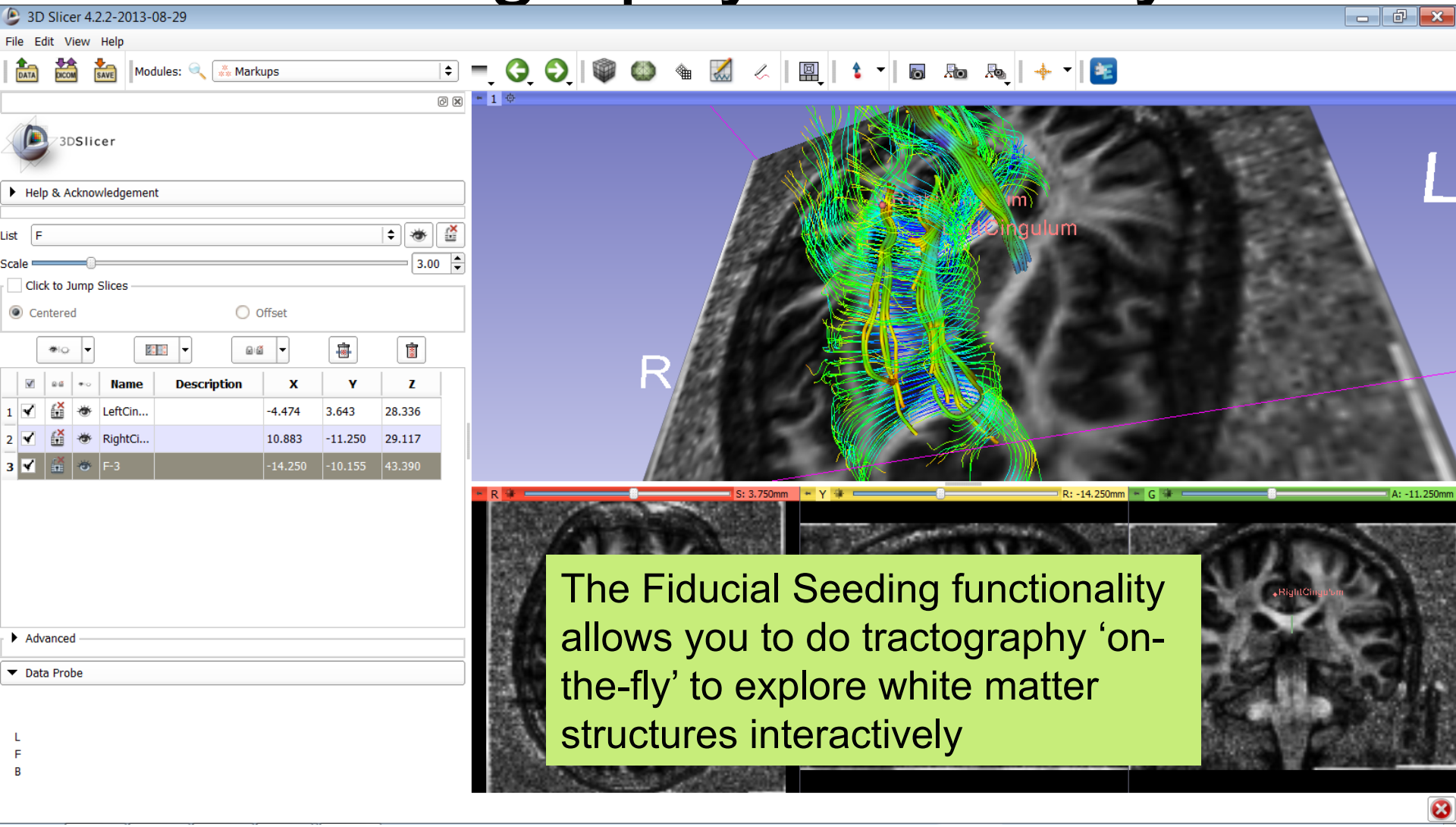


Fiducial Seeding

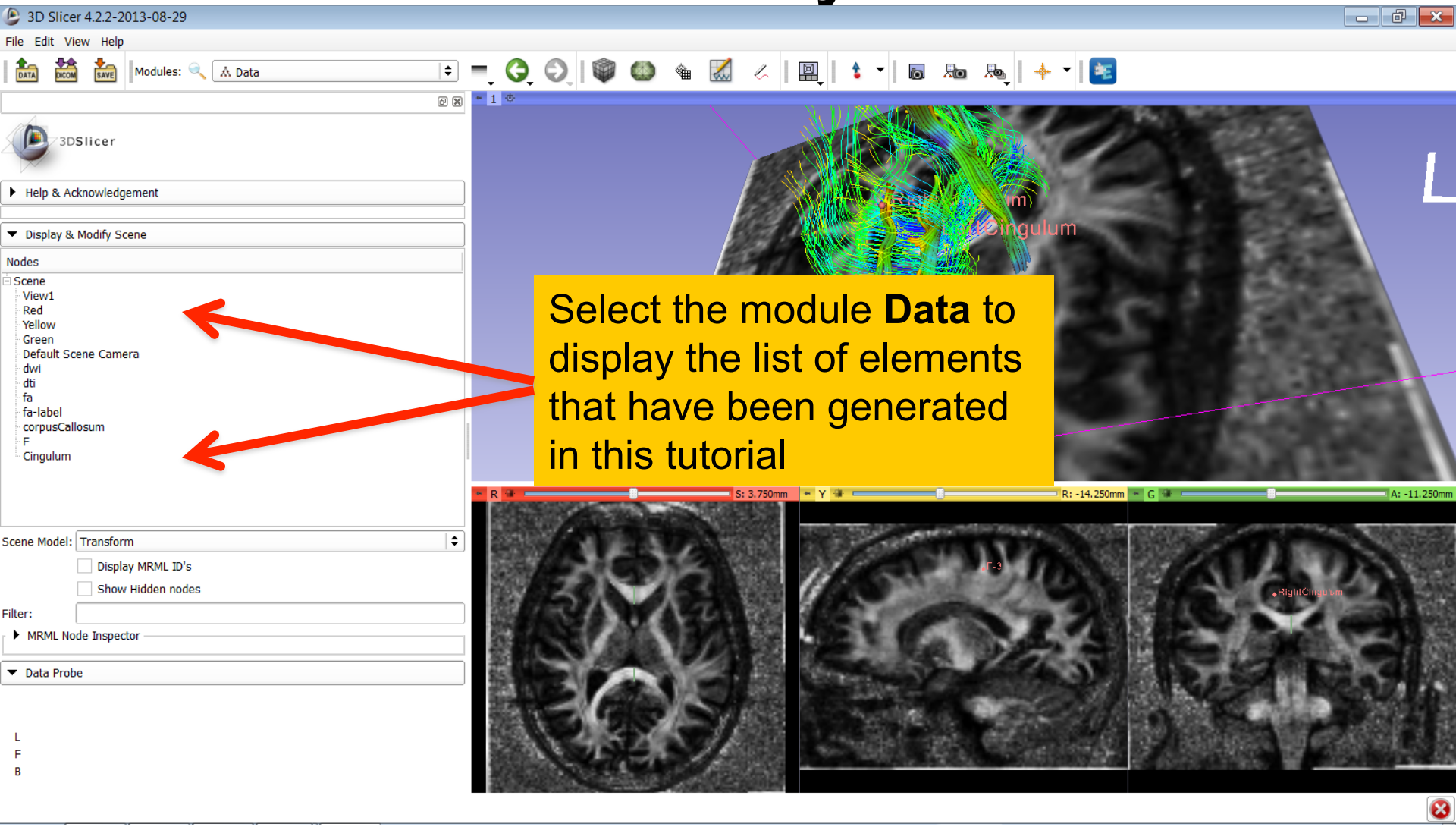


Move the fiducial F-3 in the 3D viewer to explore the dti dataset

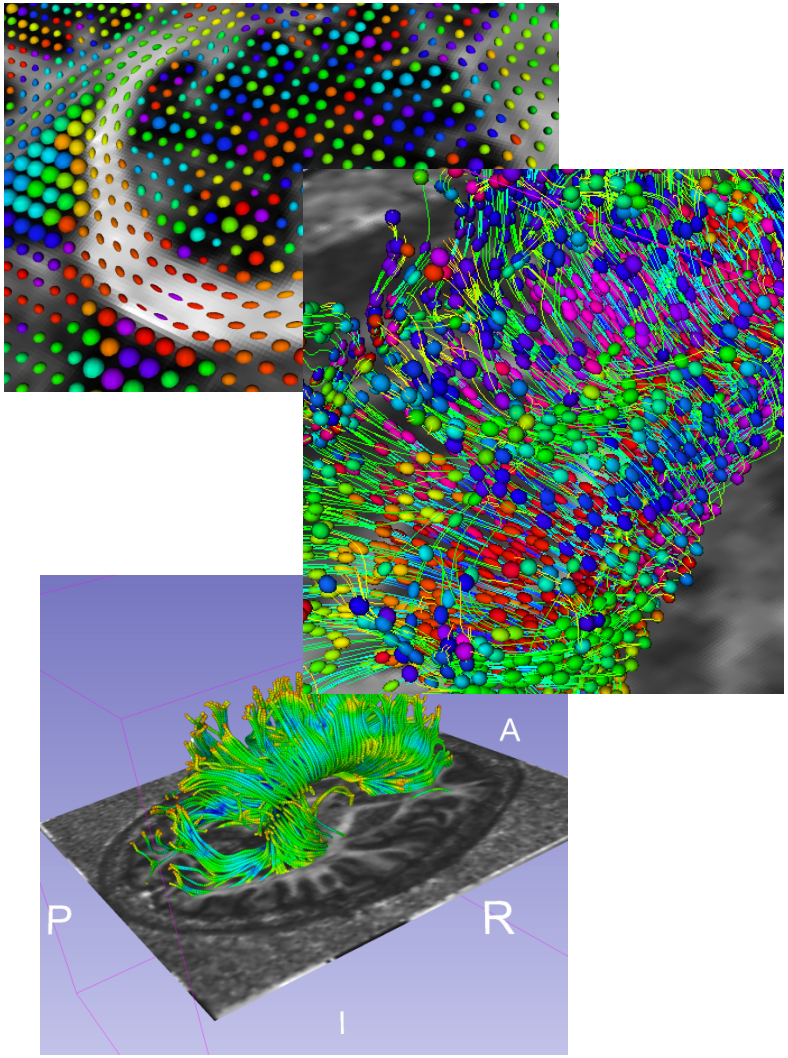
Tractography ‘on-the-fly’



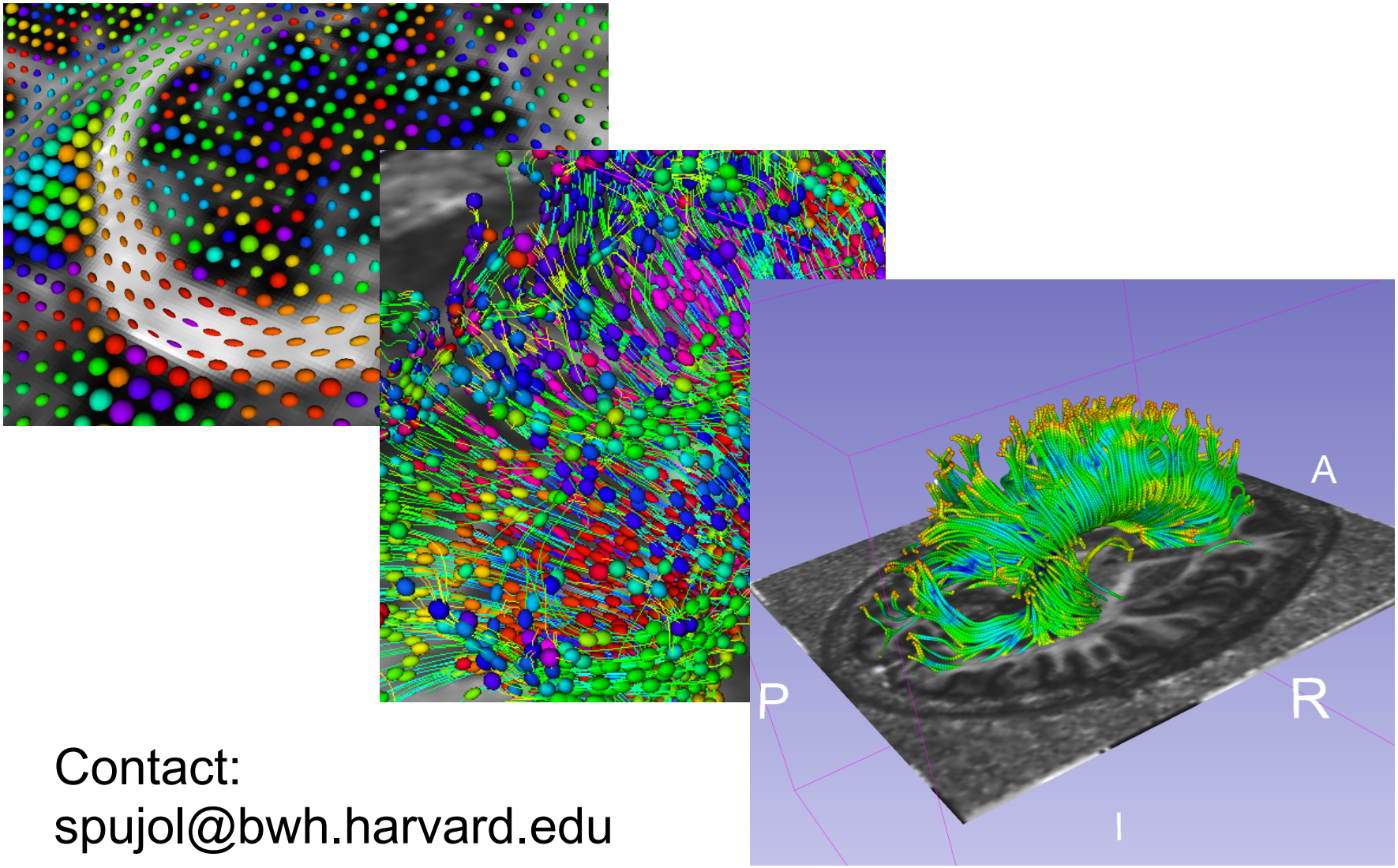
DTI Analysis



Conclusion



This tutorial guided you through the different steps of a Diffusion MR Analysis pipeline, from tensor estimation to 3D tracts visualization, for exploring and studying the brain white matter pathways.



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  NIH P41RR013218

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- Matthew Flynn, WIT ‘16