# Diffusion MRI Analysis

Sonia Pujol, Ph.D.

Surgical Planning Laboratory
Harvard University

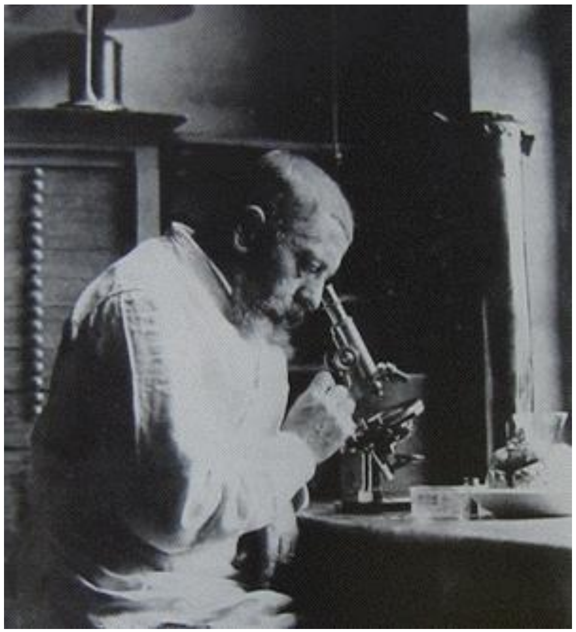
# Brain Anatomy

•White matter ~45% of the brain

•Myelinated nerve fibers

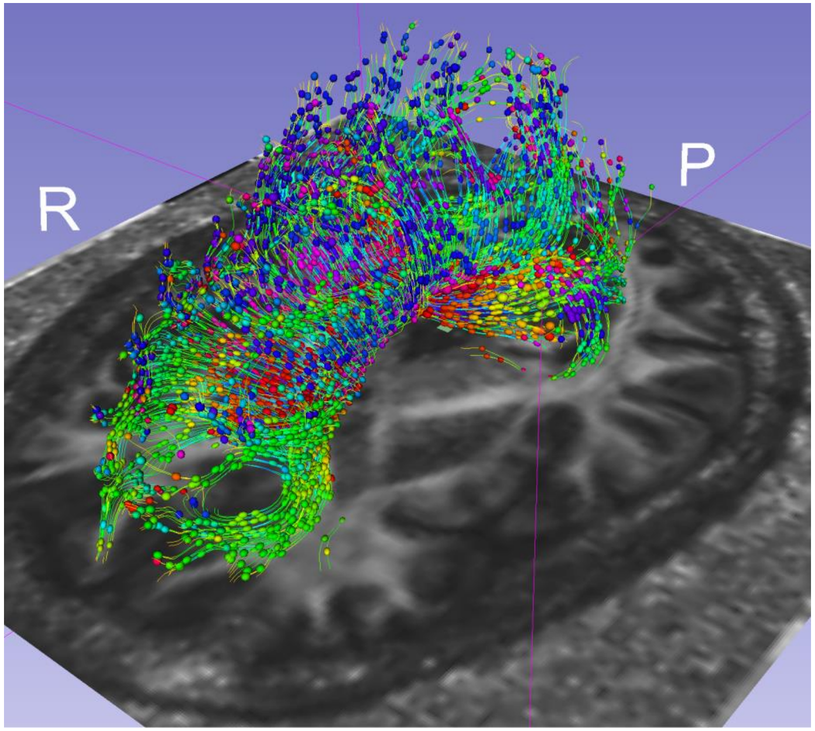
(~ 10 μm axon diameter)

# White Matter Exploration



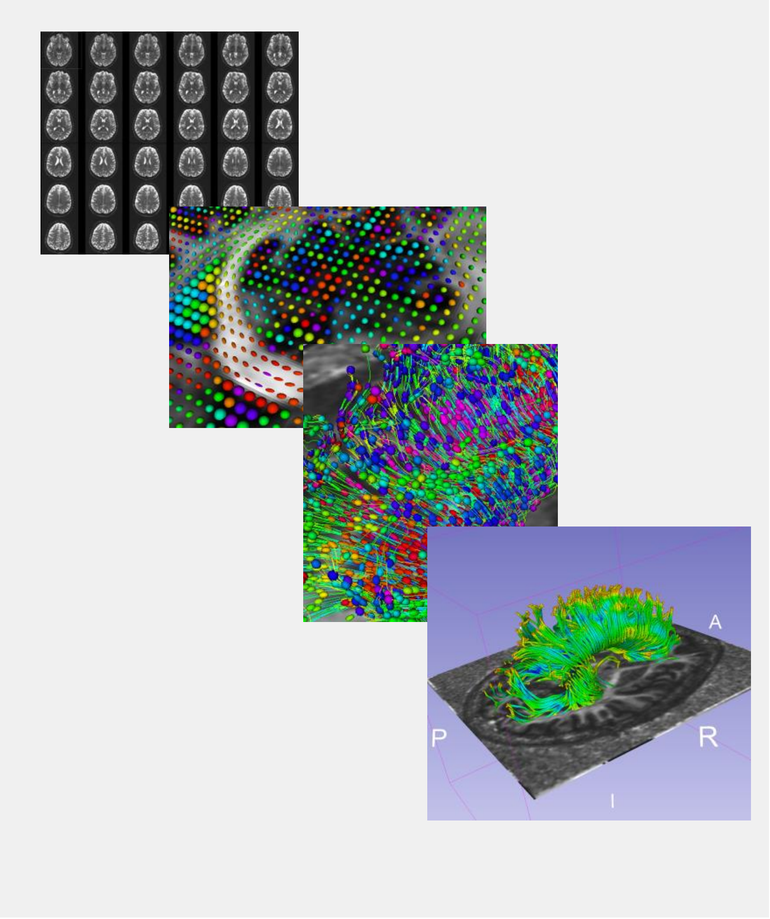
Jules Joseph Dejerine (*Anatomie des centres nerveux* (Paris, 1890-1901): Atlas of Neuroanatomy based on myelin stained preparation

# White Matter Exploration




First non-invasive window on the organization of brain white matter pathways *in-vivo*

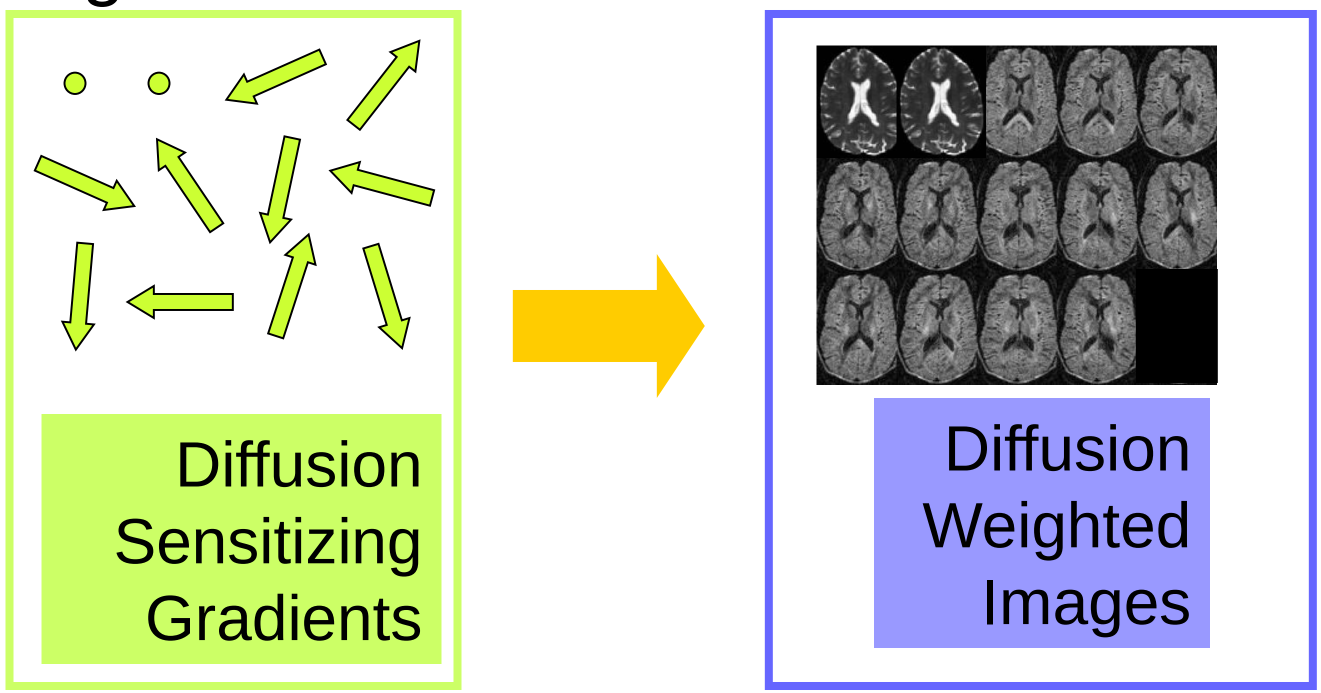
# Tutorial Outline




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.



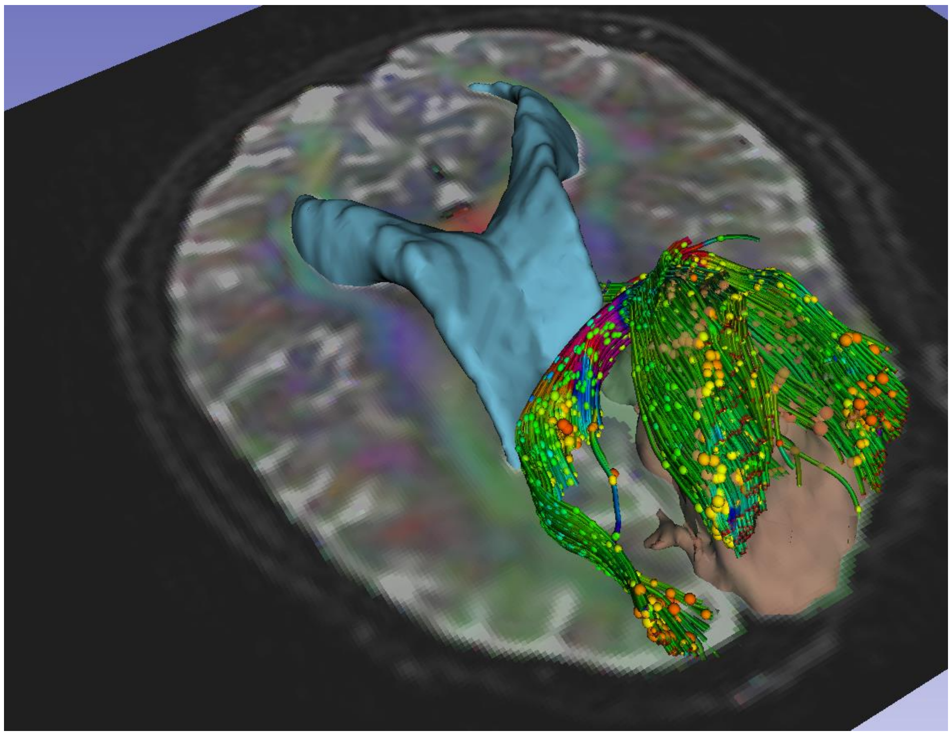
# Tutorial Software


The tutorial uses the 3DSlicer version 4.1 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

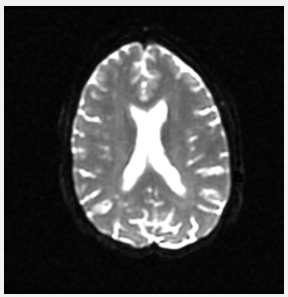
1) Estimate a tensor volume from a set of Diffusion Weighted Images

2) Understand the shape and size of the diffusion ellipsoid

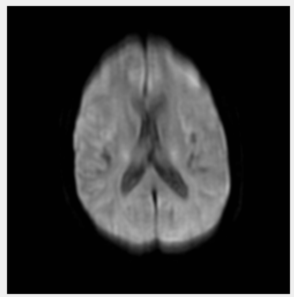
3) Reconstruct DTI tracts from a pre-defined region of interest

4) Interactively visualize DTI tracts seeded from a fiducial

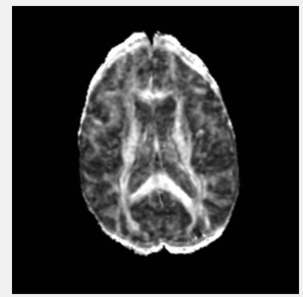
# MR Diffusion Analysis Pipeline



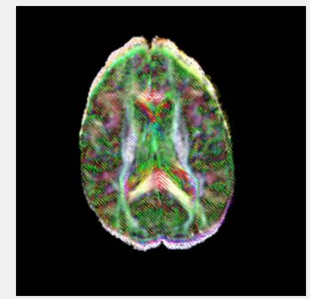
DWI
Acquisition



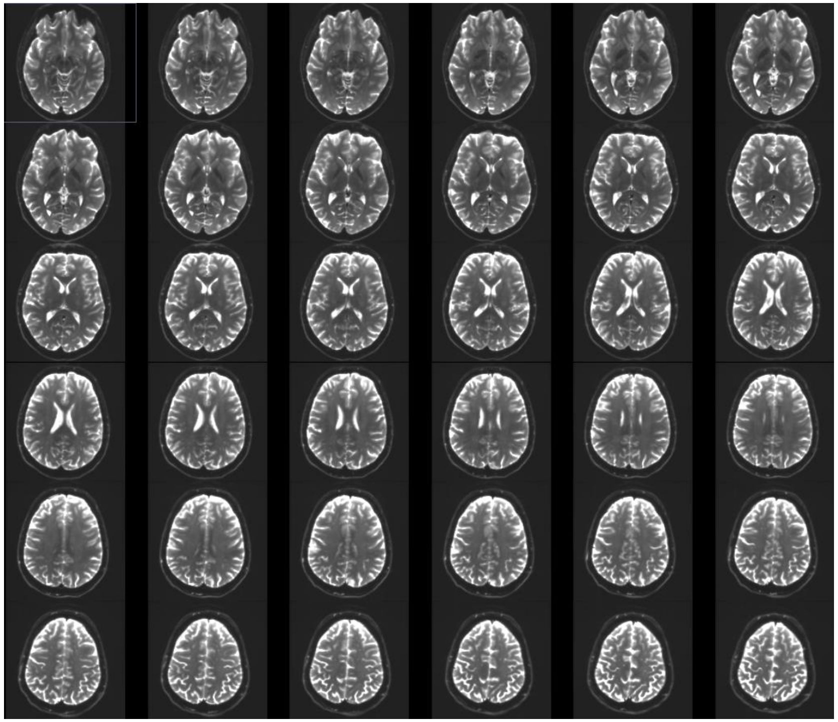
Tensor
Calculation



Scalar
Maps

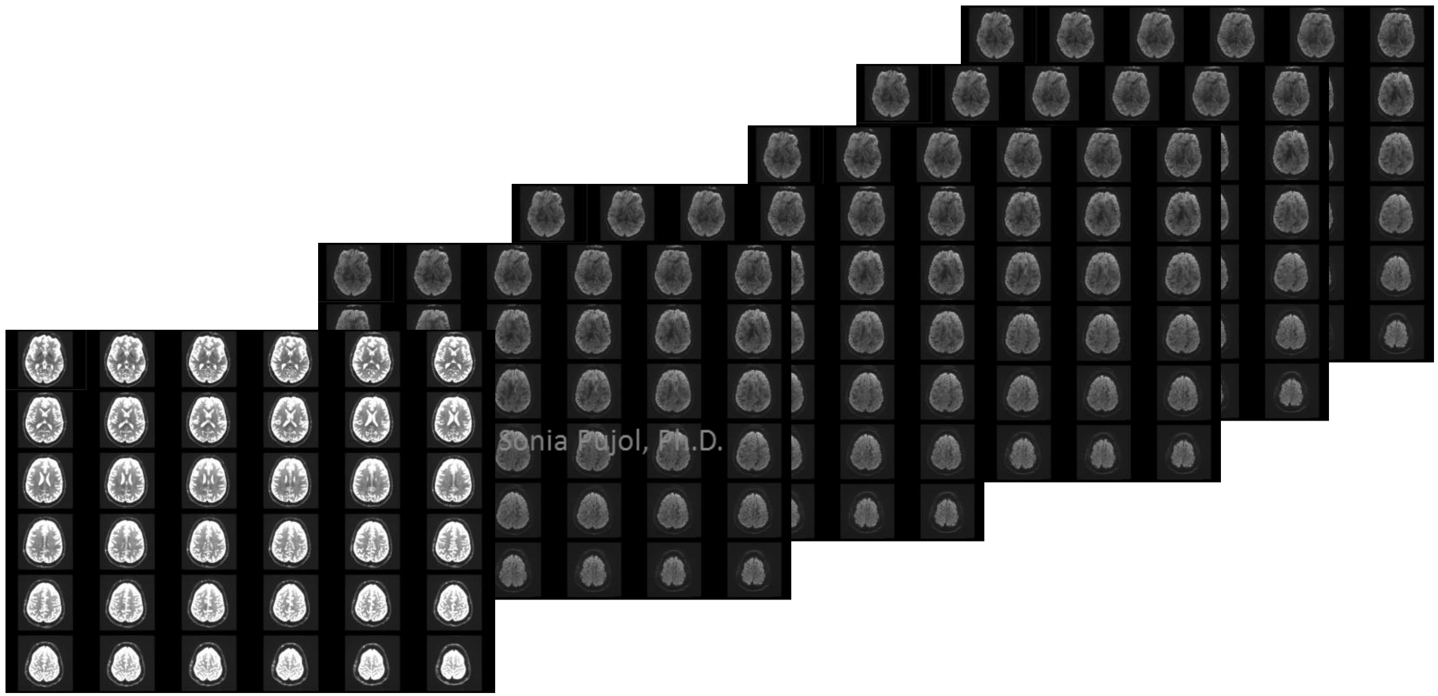


3D
Visualization



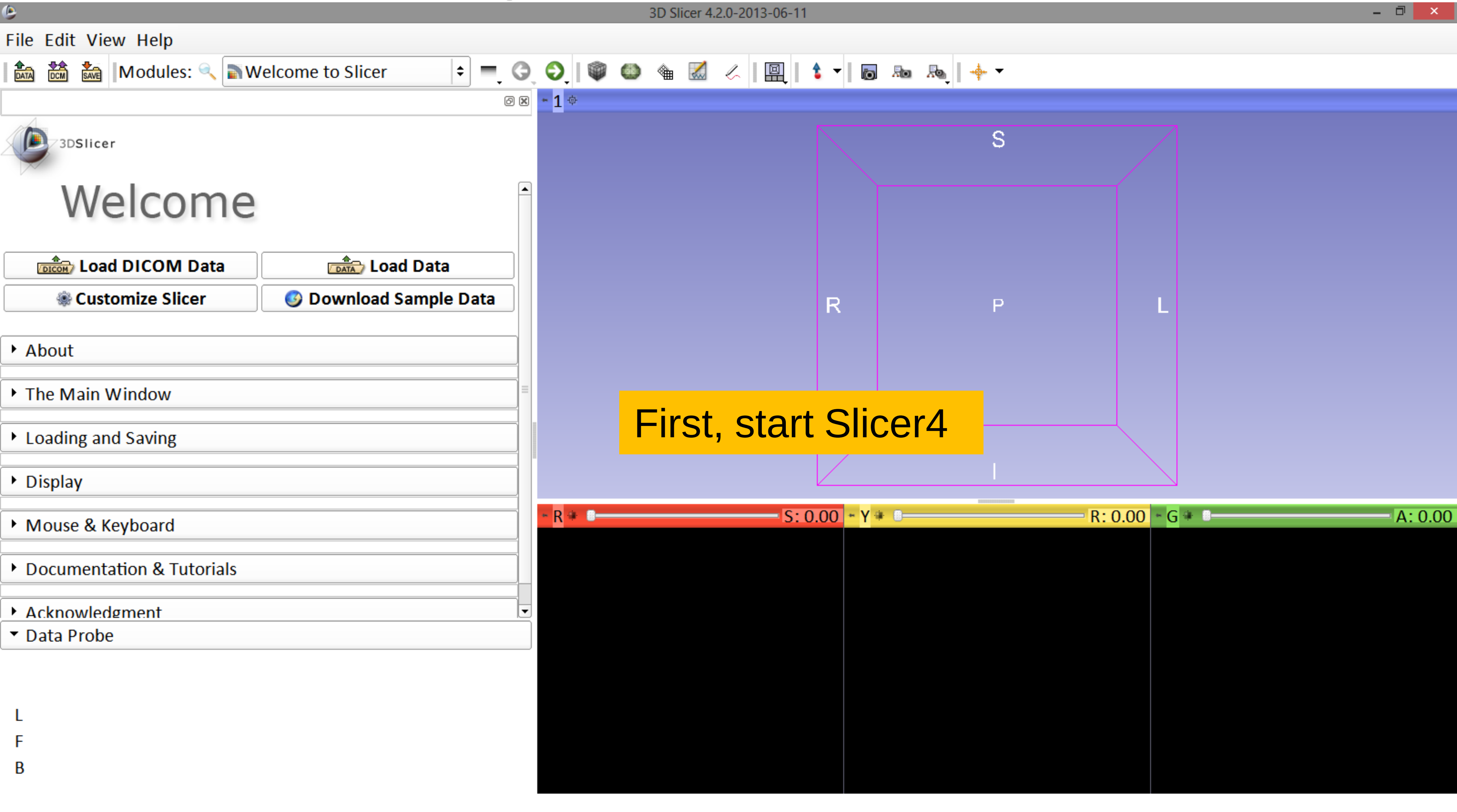
# Part 1: From DWI images to Tensors

# Understanding the DWI Dataset

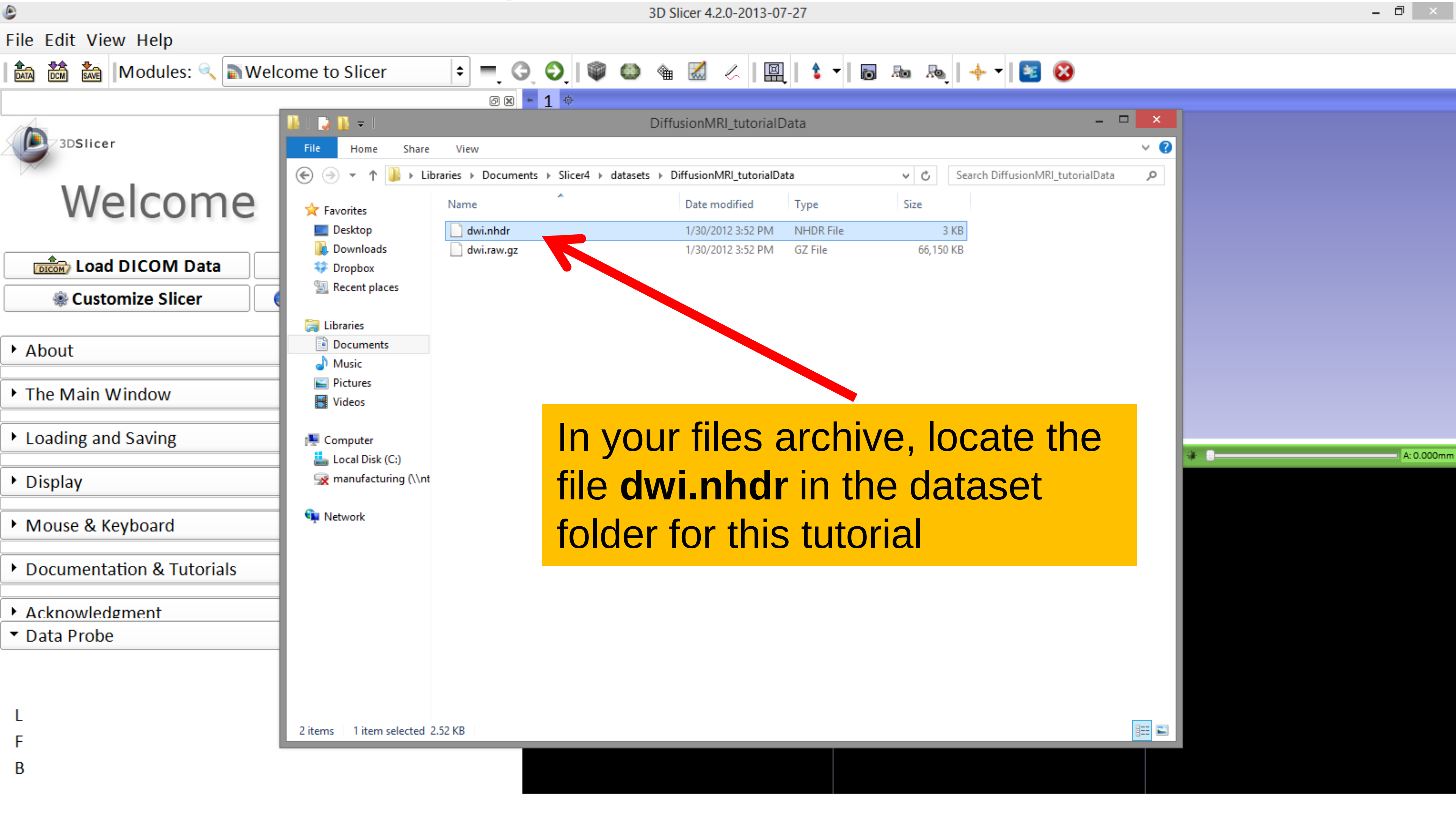



The Diffusion Weighted Imaging (DWI) dataset is composed of 1 volume acquired without diffusion-sensitizing gradient, and 41 volumes acquired with 41 different diffusion-sensitizing gradient directions.

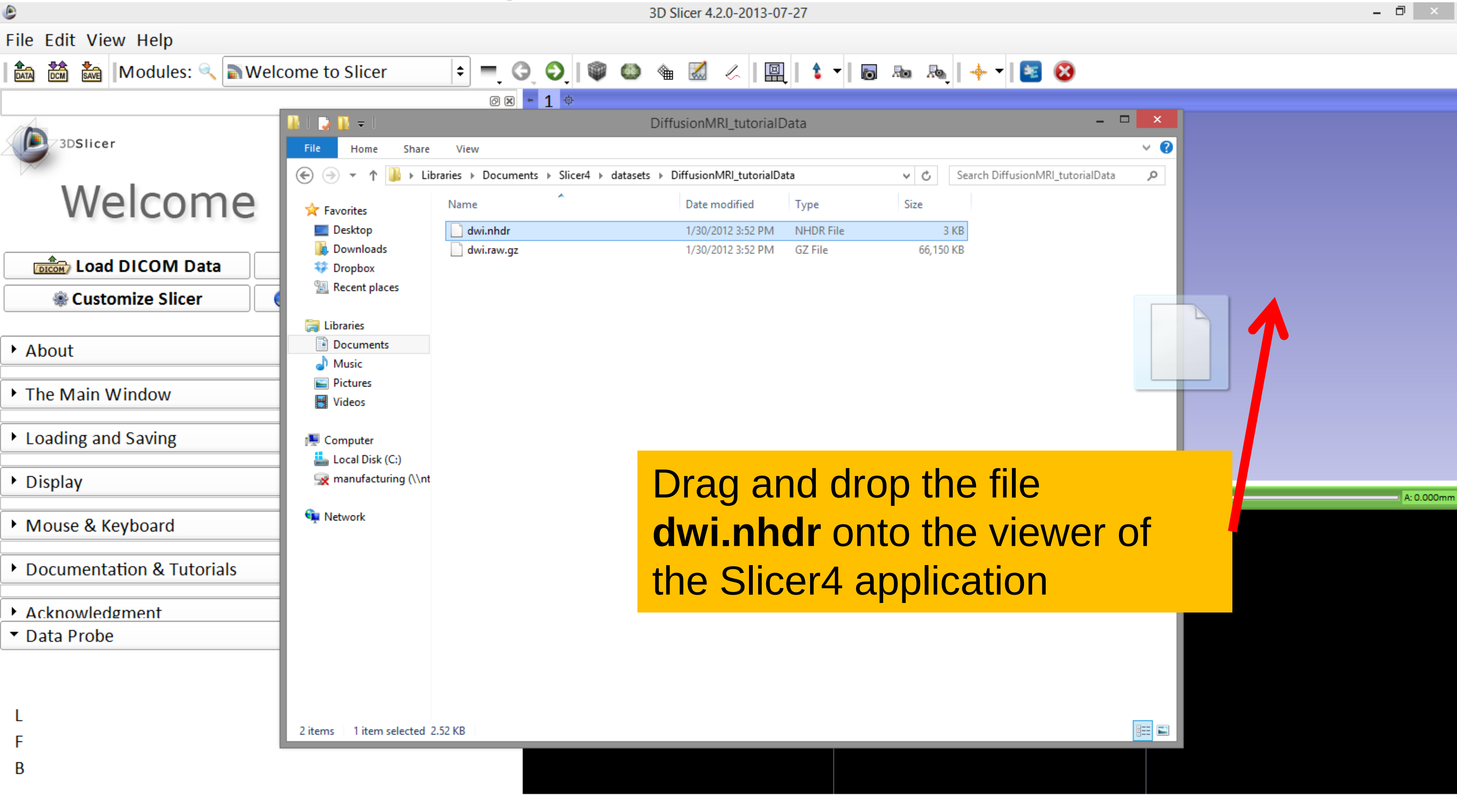
# Loading the DWI Dataset



# Loading the DWI Dataset

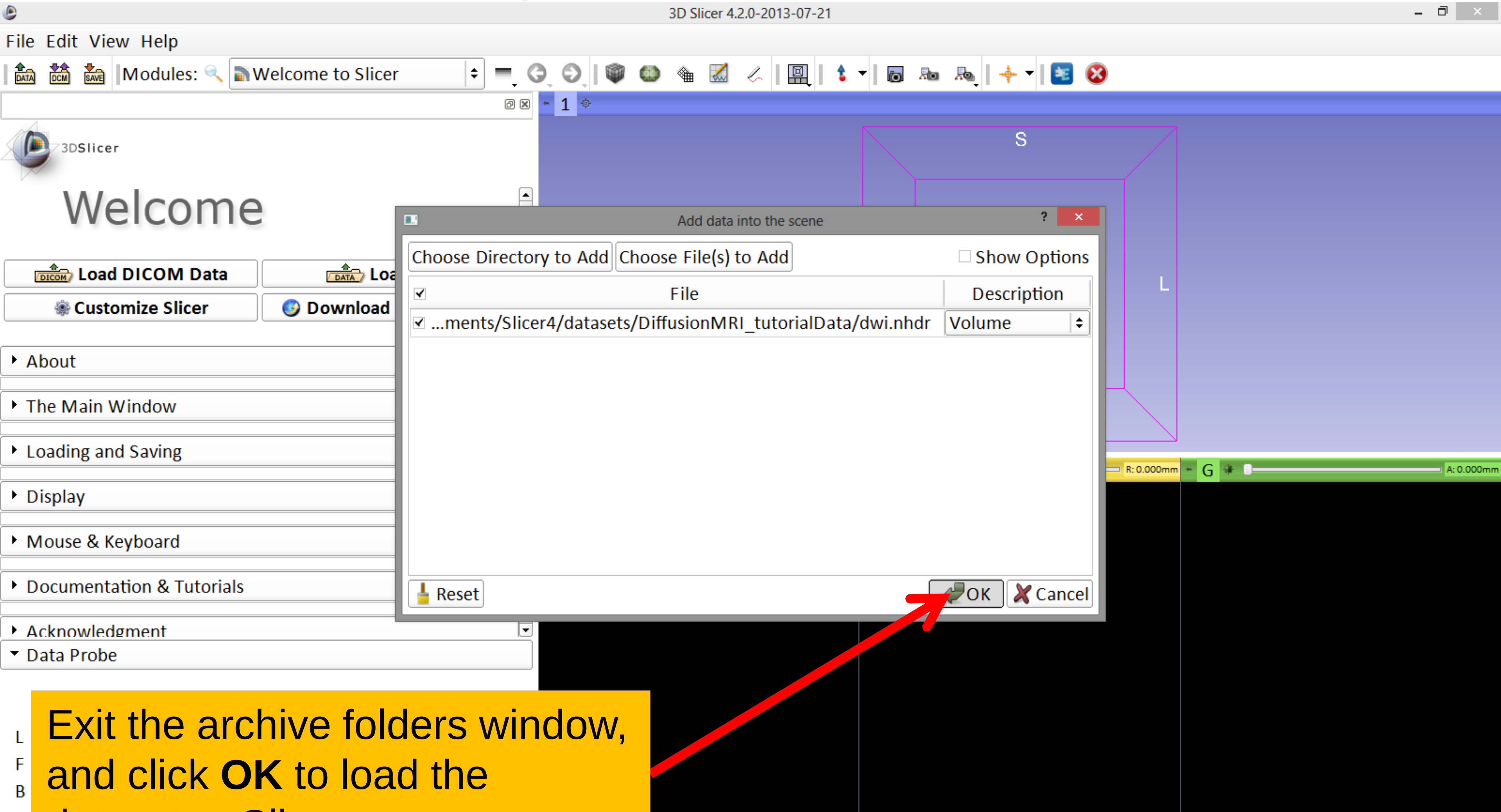


# Loading the DWI Dataset



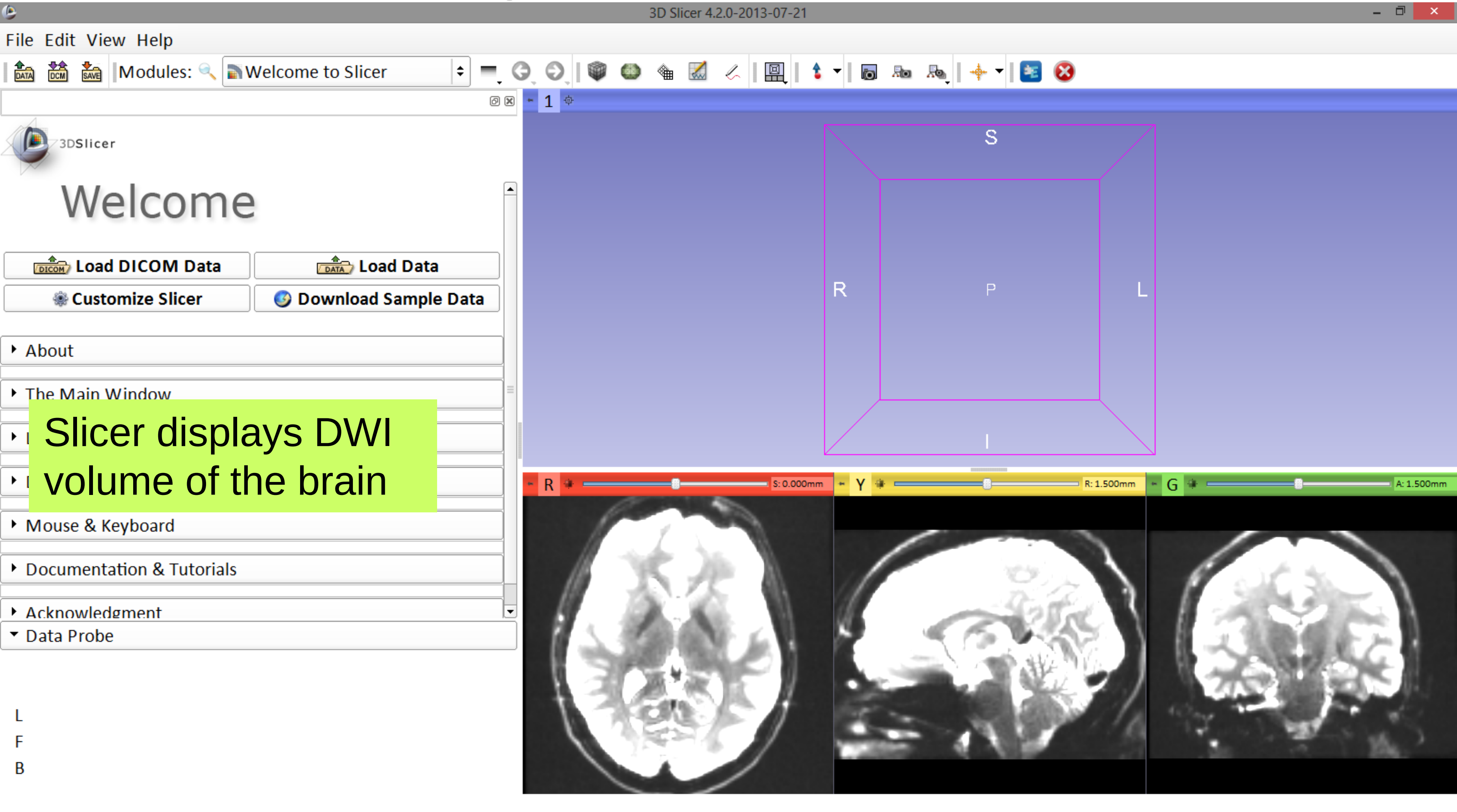

Drag and drop the file **dwi.nhdr** onto the viewer of the Slicer4 application

# Loading the DWI Dataset

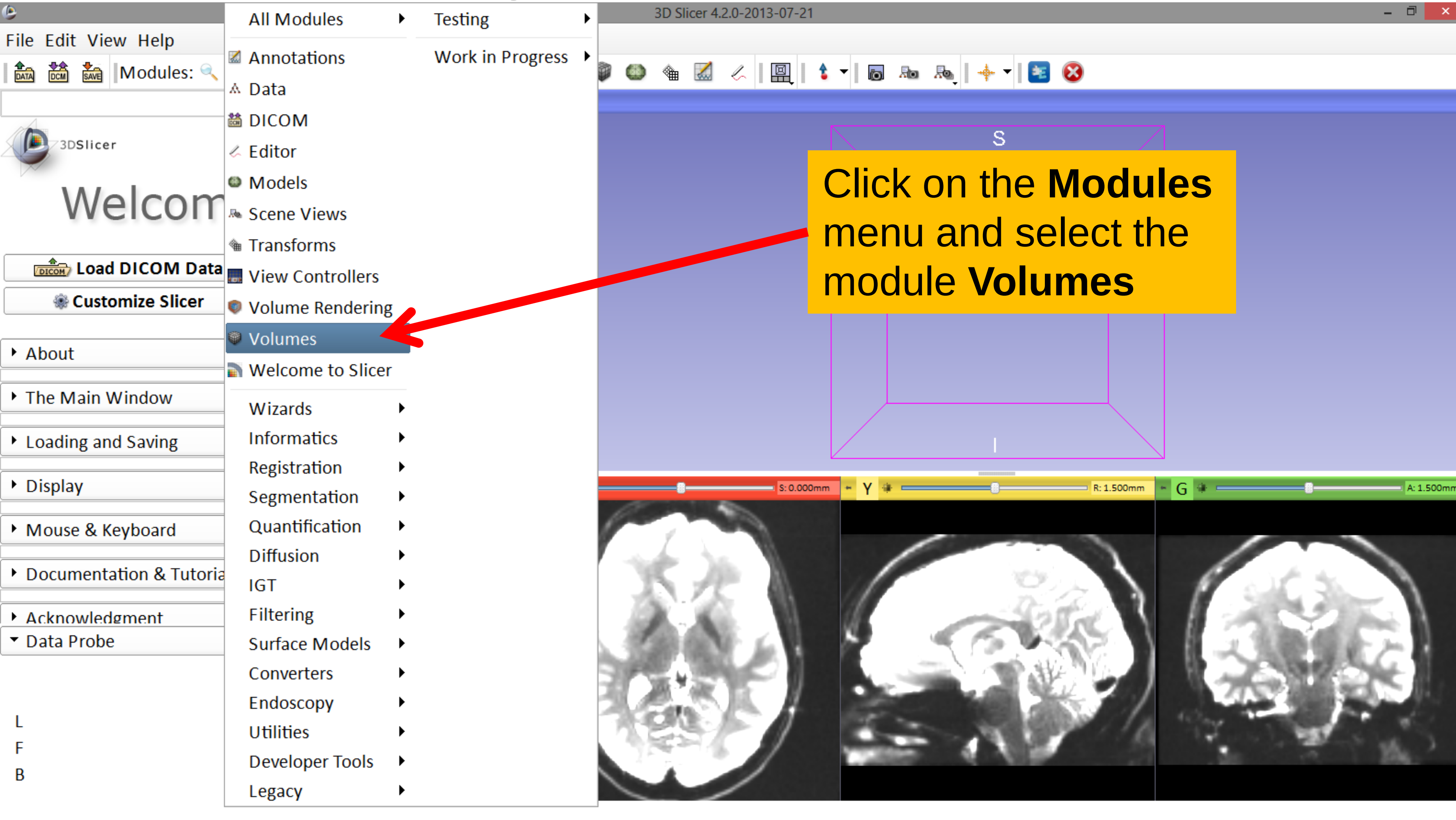



Exit the archive folders window, and click **OK** to load the dataset to Slicer

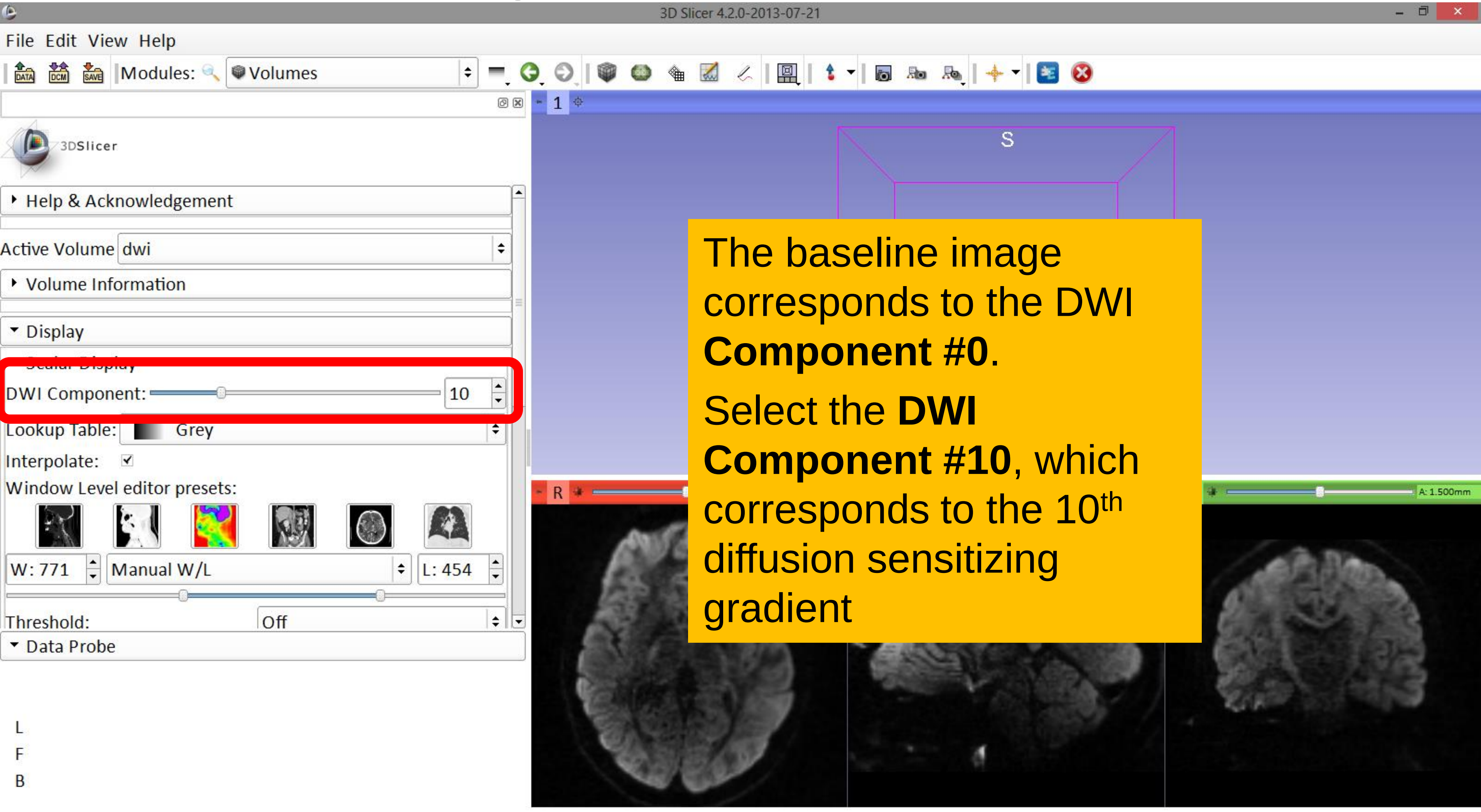
# Loading the DWI Dataset



# Loading the DWI Dataset



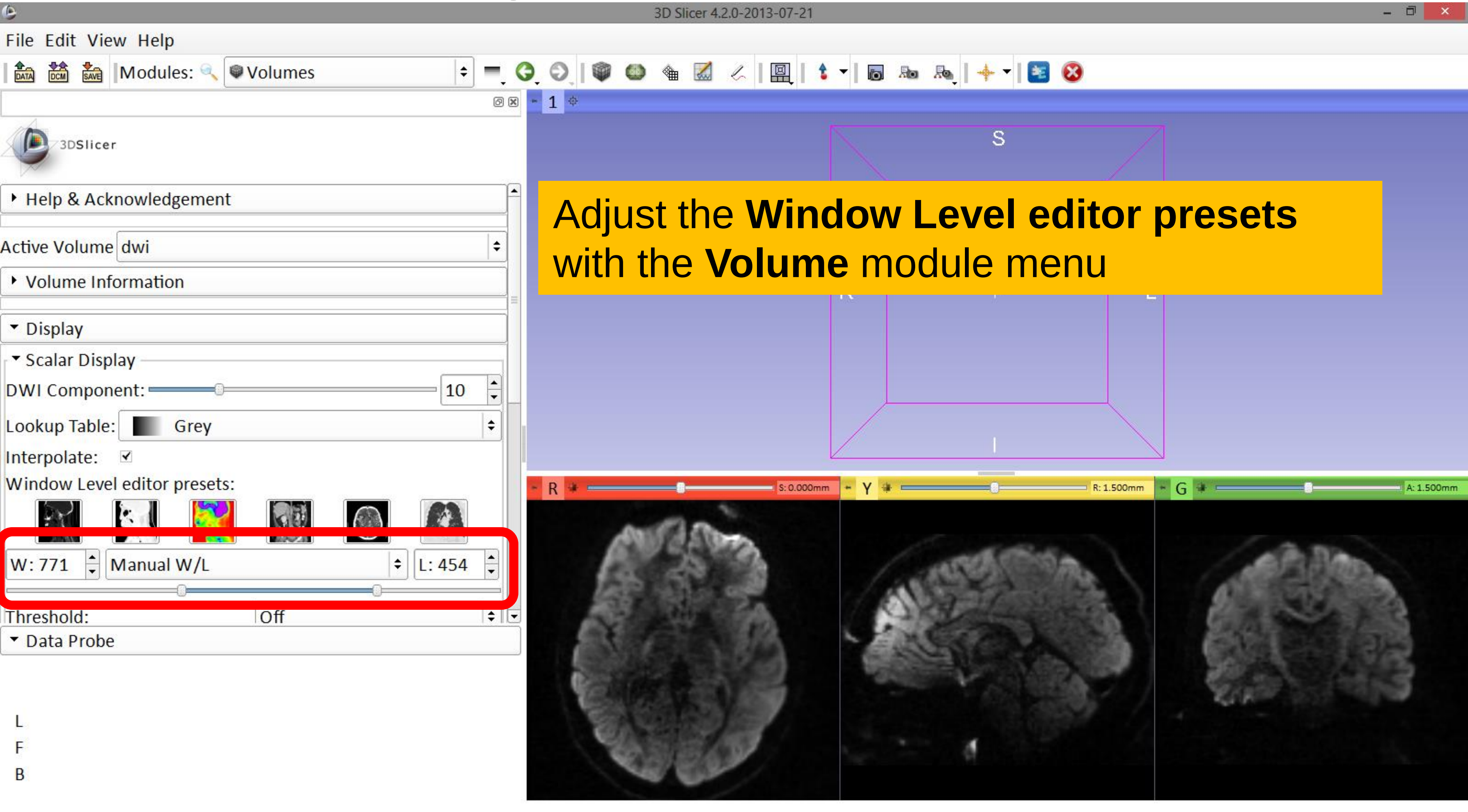
# Loading the DWI Dataset




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

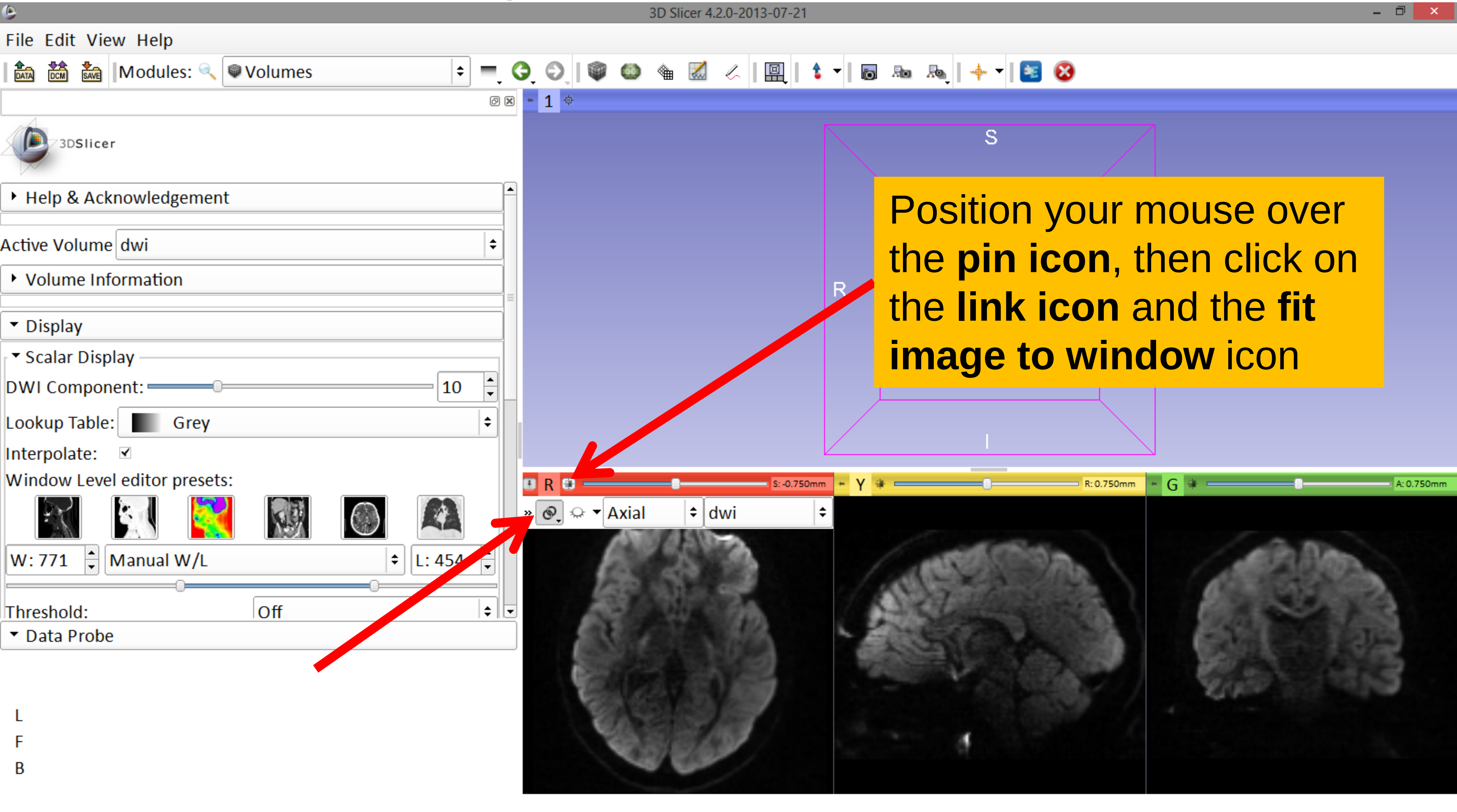
Select the **DWI Component #10**, which corresponds to the 10$^{th}$ diffusion sensitizing gradient

# Loading the DWI Dataset

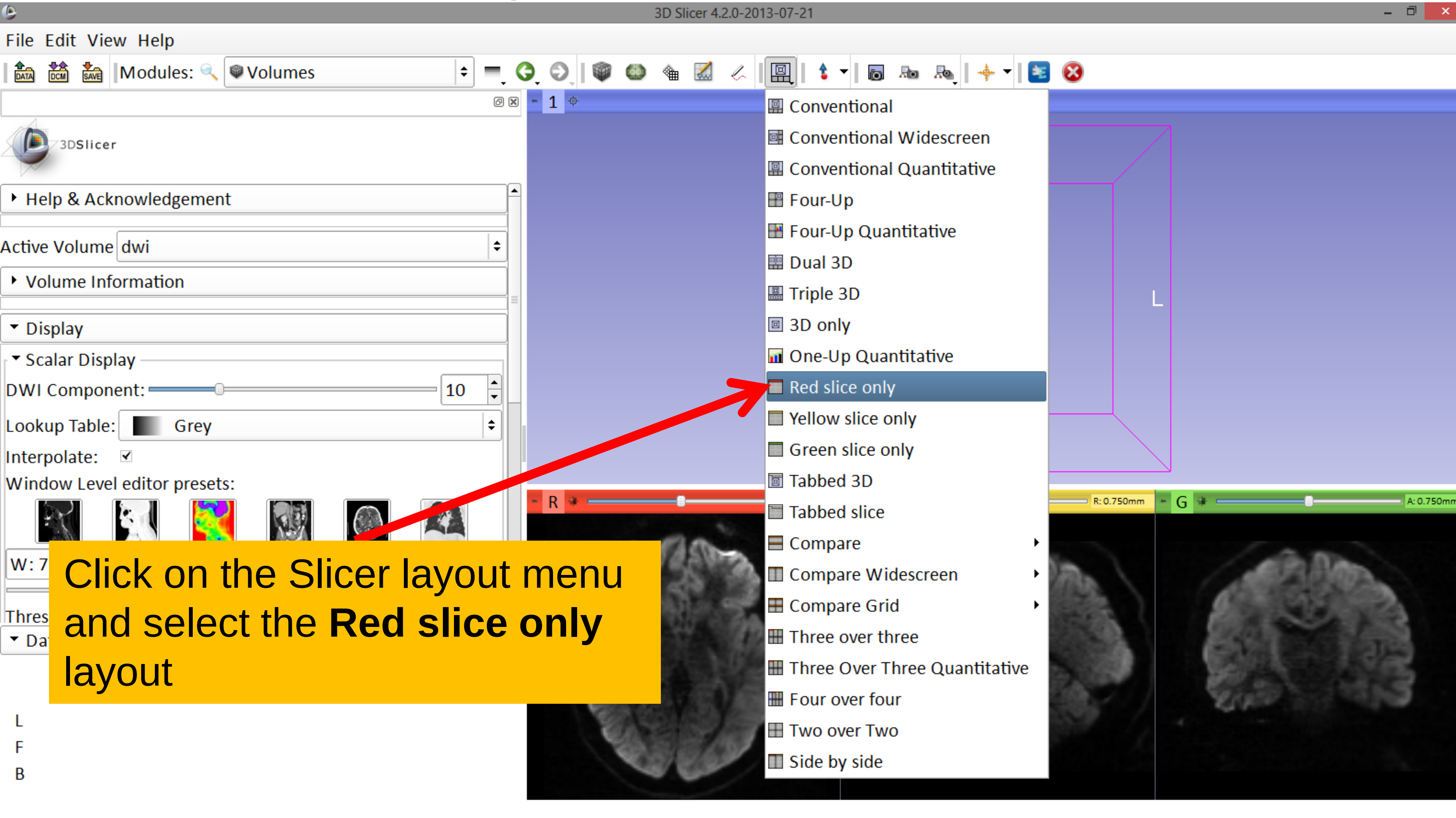



Adjust the **Window Level editor presets** with the **Volume** module menu

# Loading the DWI Dataset

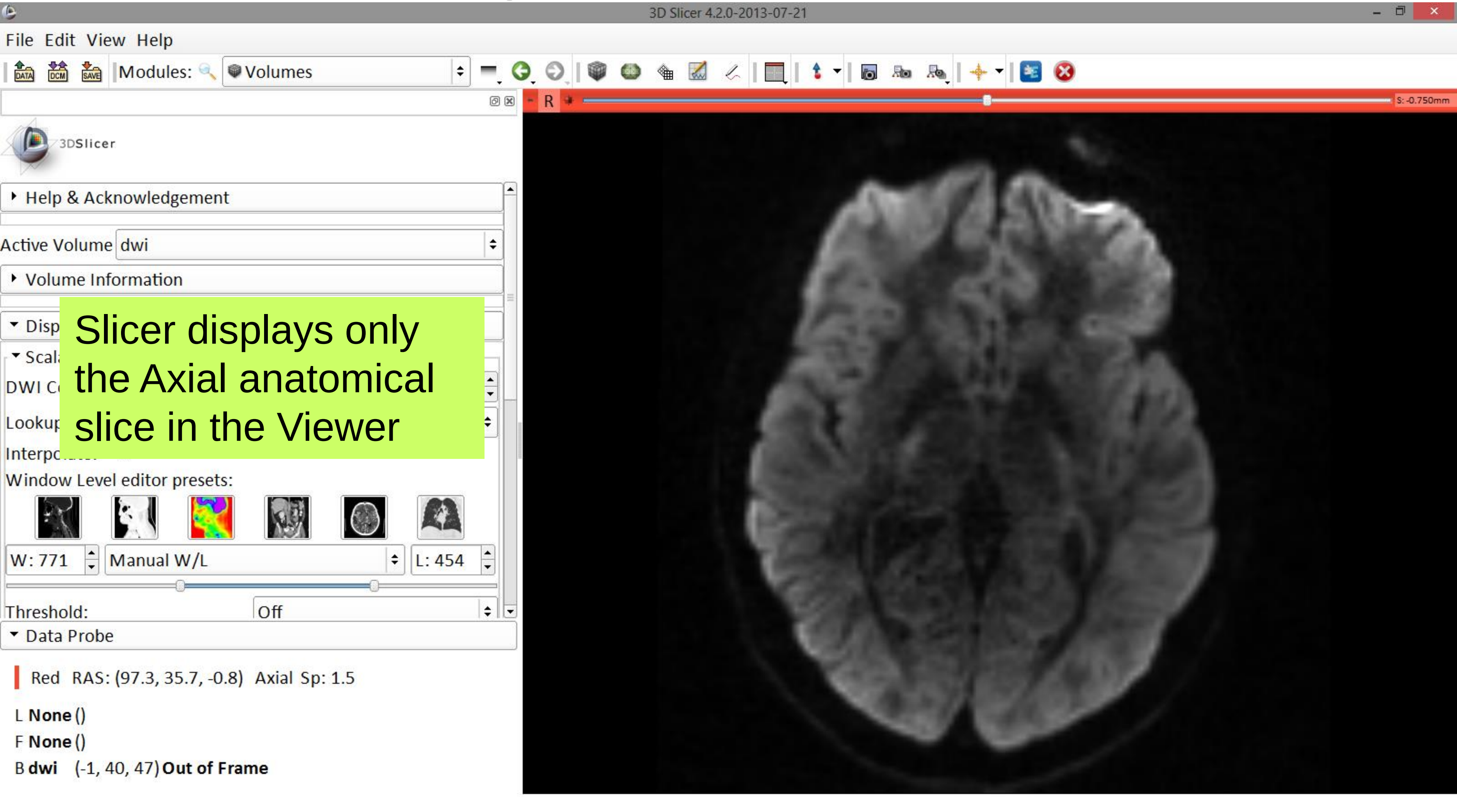


# Loading the DWI Dataset



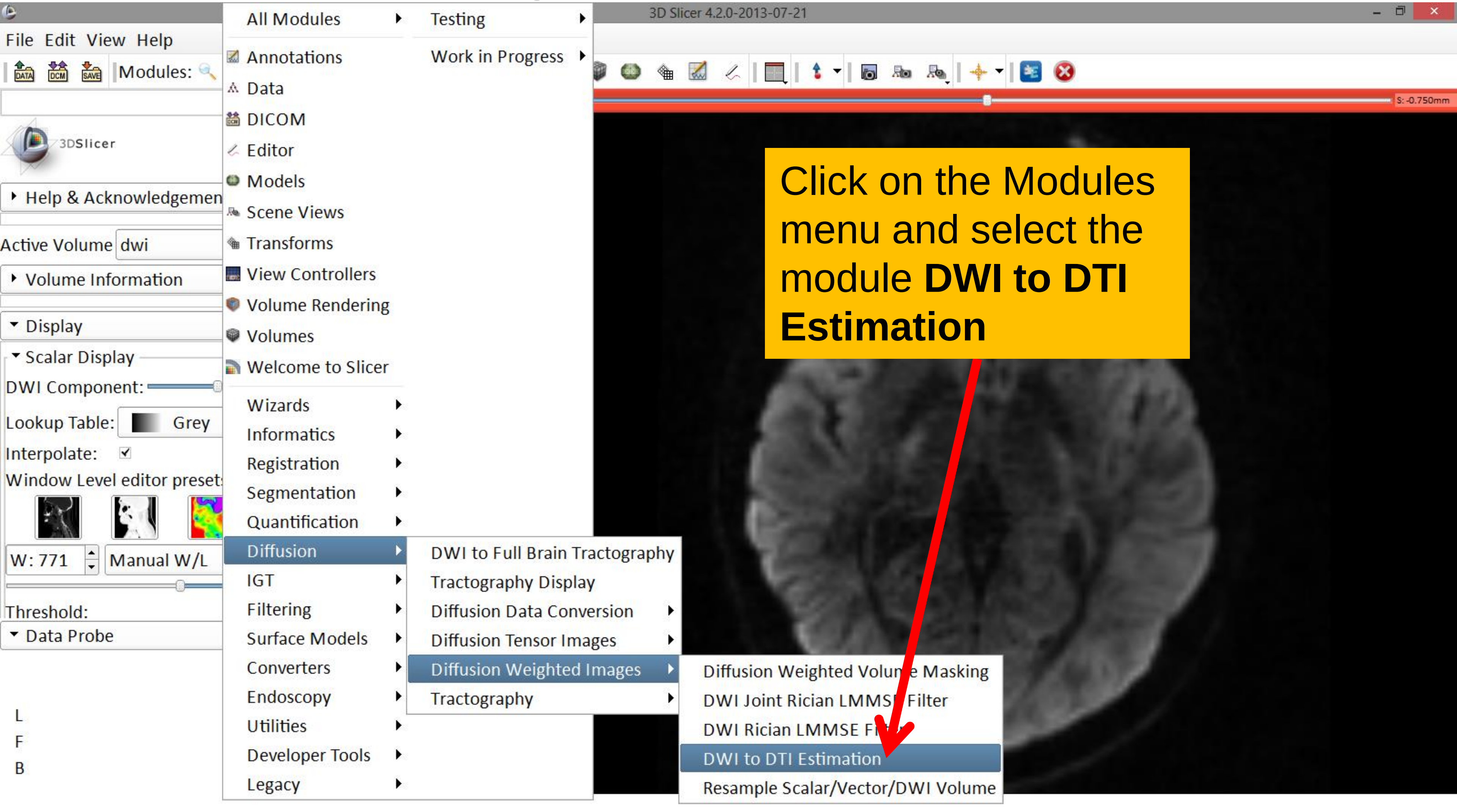

Click on the Slicer layout menu and select the **Red slice only** layout

# Loading the DWI Dataset

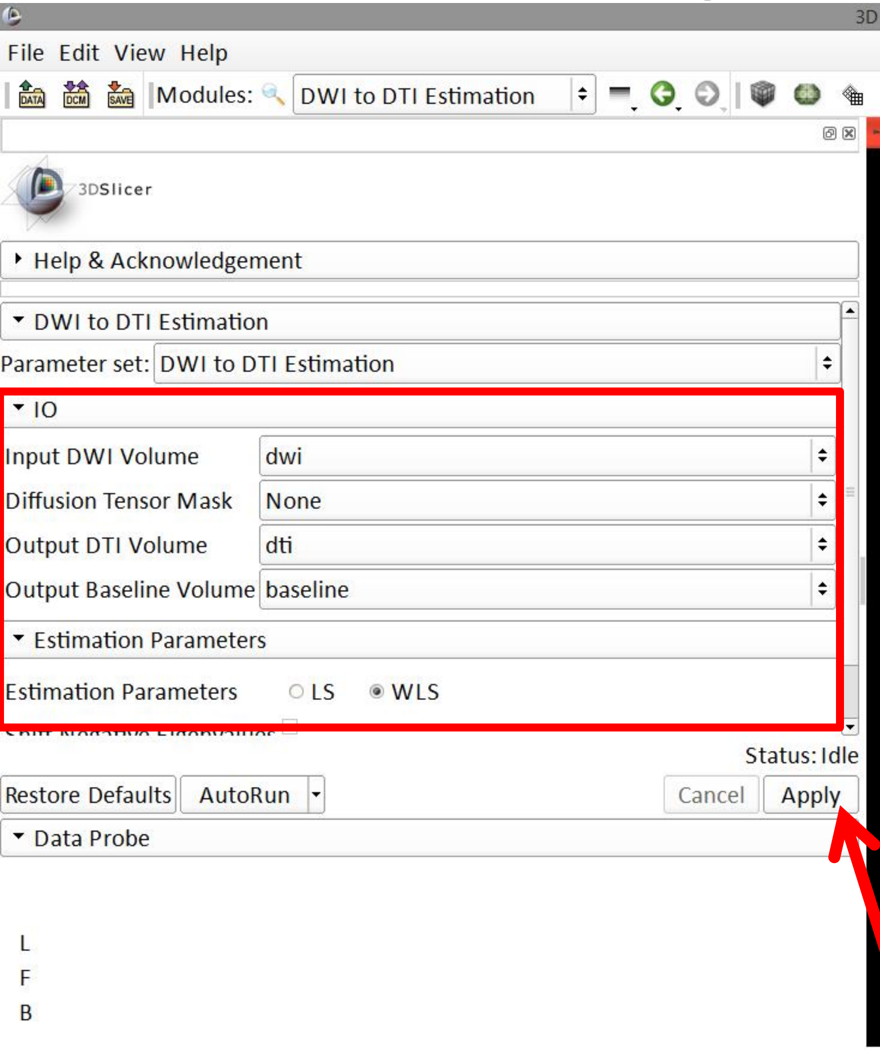



Slicer displays only the Axial anatomical slice in the Viewer

# Exploring the DWI Dataset



# Exploring the DWI Dataset




Select the module **DWI to DTI Estimation** in the modules menu:

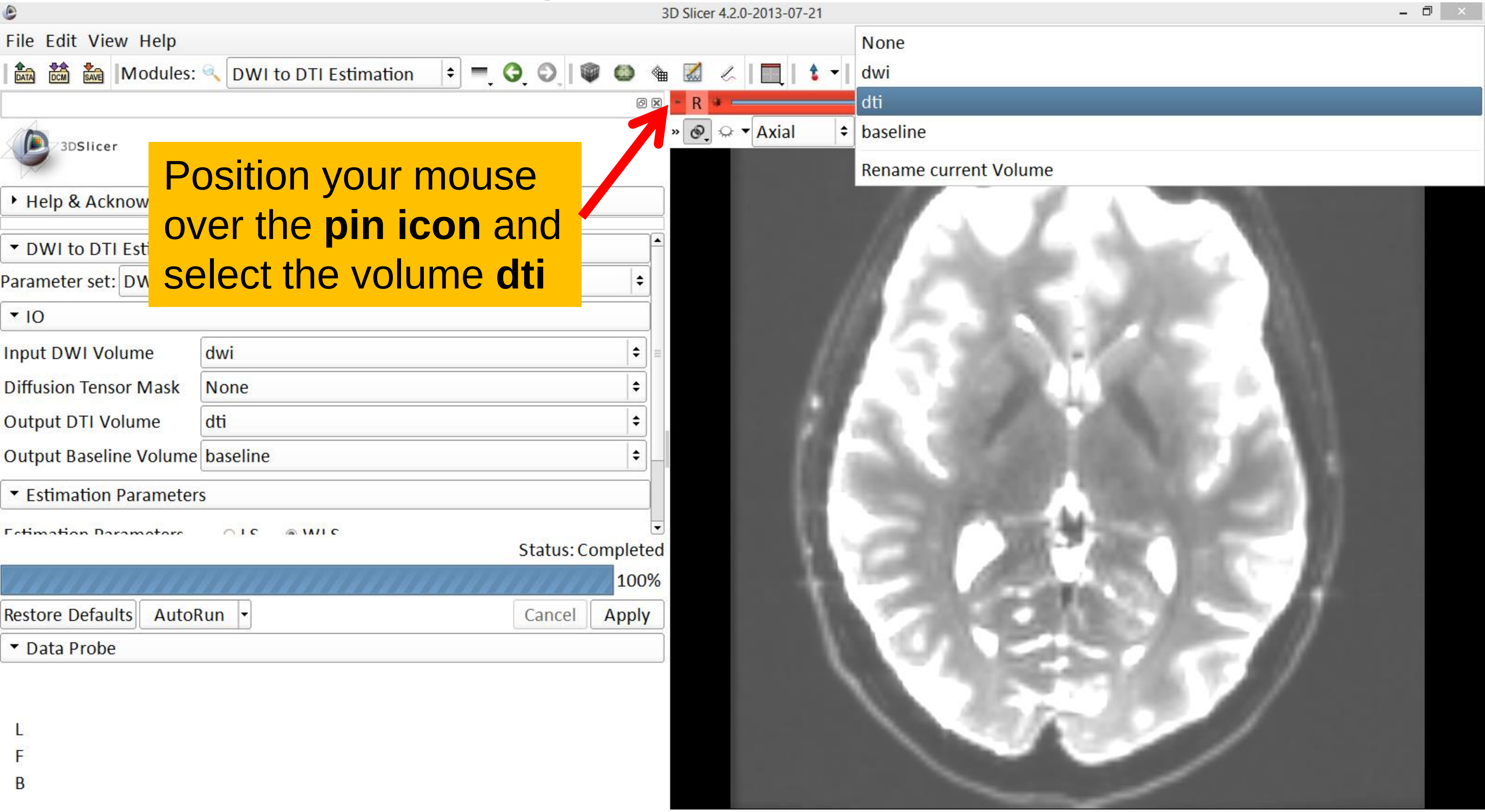
-select the **Input DWI volume 'dwi'**

-select **Output DTI Volume 'Create and Rename New Volume'**, and rename it '**dti**'

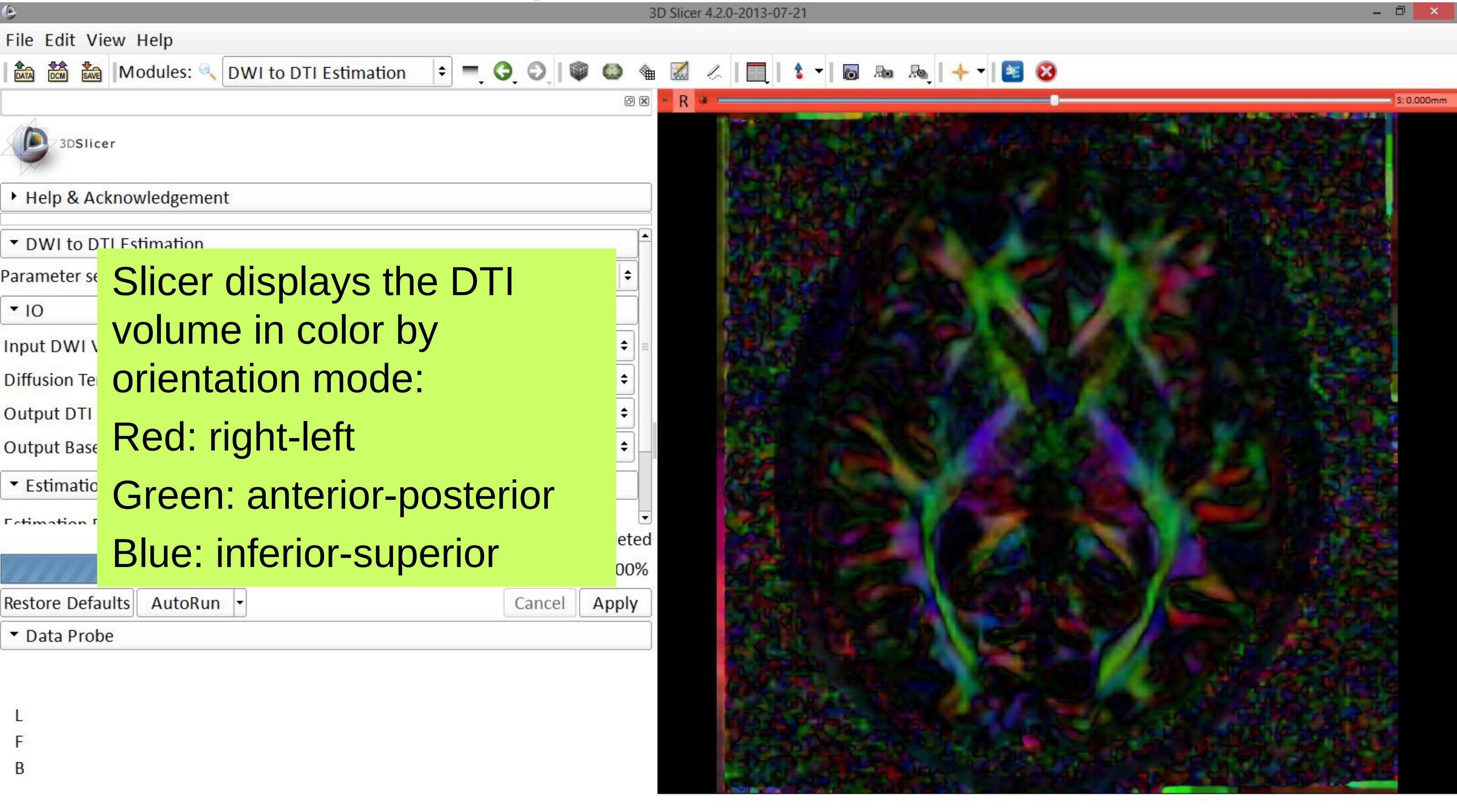
-select **Output Baseline Volume 'Create and Rename new Volume'**, and rename it '**baseline**'

-select the **Estimation Parameter 'WLS'** (Weighted Least Squares) and click on **Apply**.

# Exploring the DWI Dataset



# Exploring the DWI Dataset



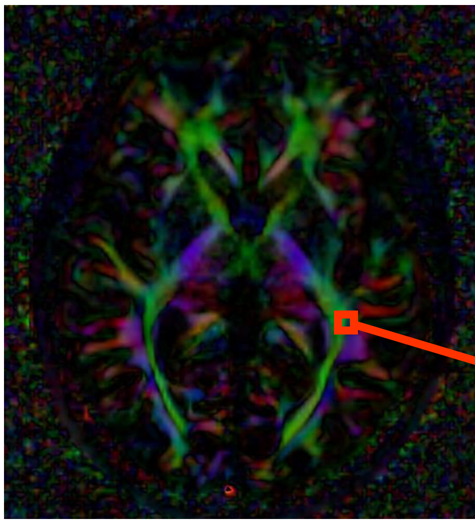

Slicer displays the DTI volume in color by orientation mode:

Red: right-left

Green: anterior-posterior

Blue: inferior-superior

# Diffusion Tensor Data



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

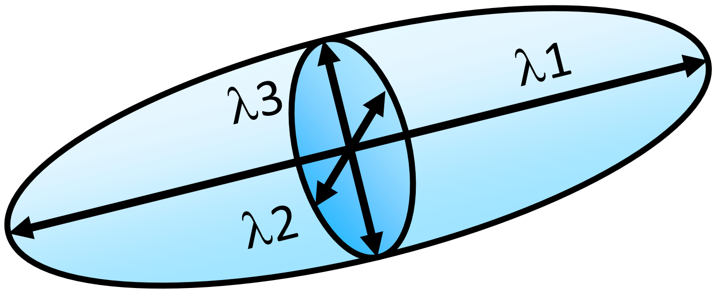
Stejskal-Tanner equation (1965)

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

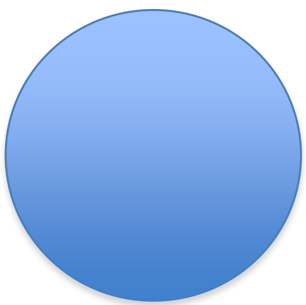
The diffusion tensor D in the voxel (I,J,K) is a 3x3 symmetric matrix.

# Diffusion Tensor

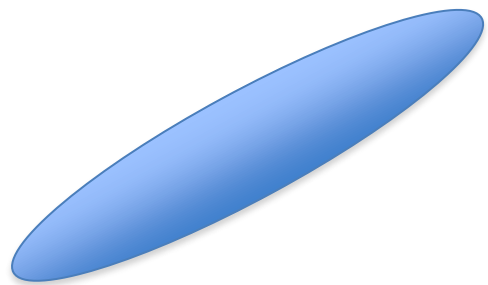
- The diffusion tensor D in the voxel (I,J,K) can be visualized as an ellipsoid, with the eigenvectors indicating the directions of the principal axes, and the square root of the eigenvalues defining the ellipsoidal radii.
- Scalar maps can be derived from the rotationally invariant eigenvalues λ1, λ2,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



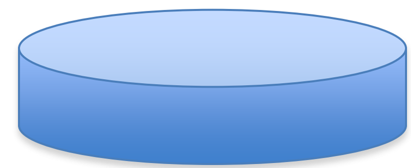
# Diffusion Tensor Shape



$\lambda1 = \lambda2 = \lambda3$



$\lambda1 >> \lambda2, \lambda3$

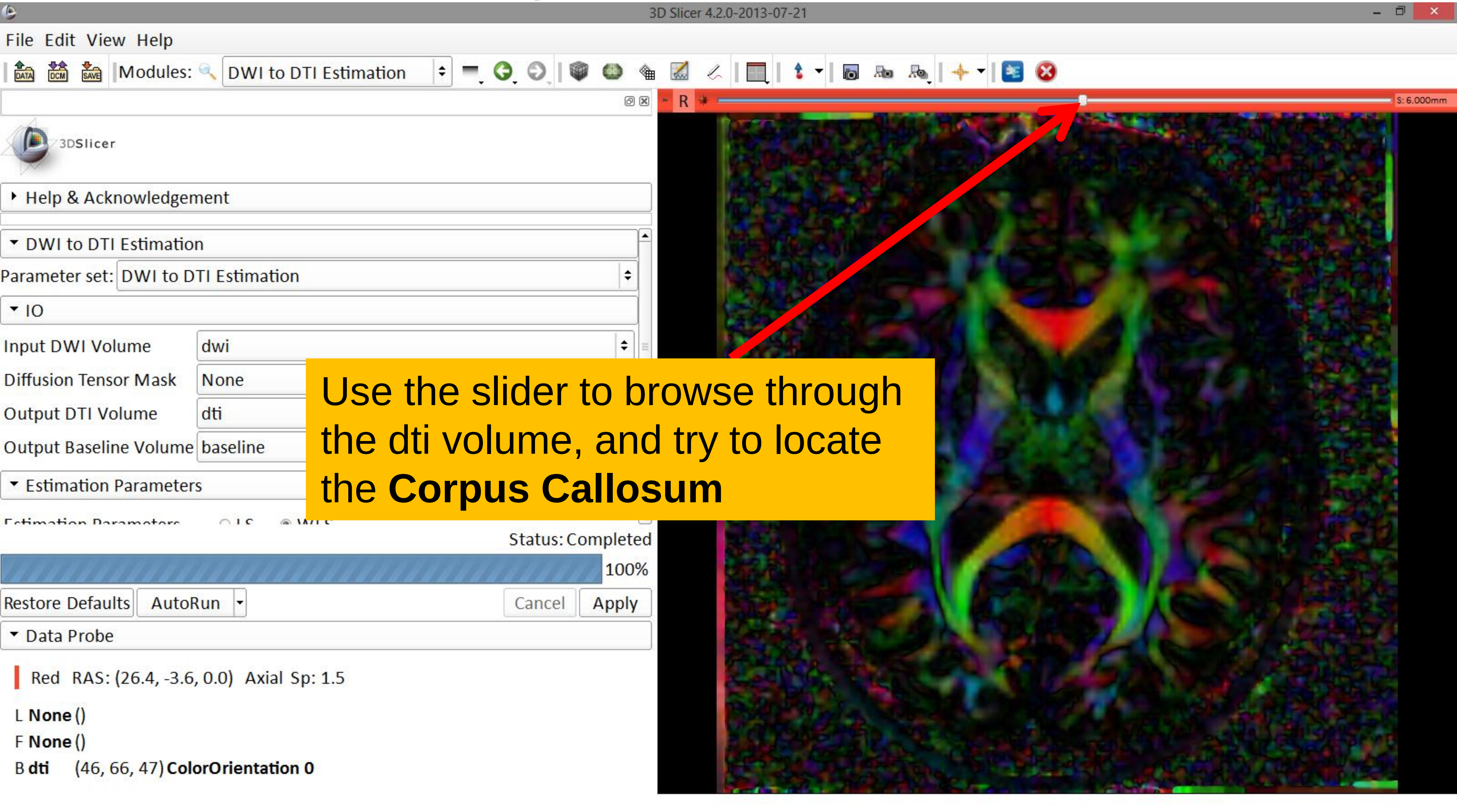


$\lambda1 \sim \lambda2 >> \lambda3$

Isotropic media
(CSF, gray matter)

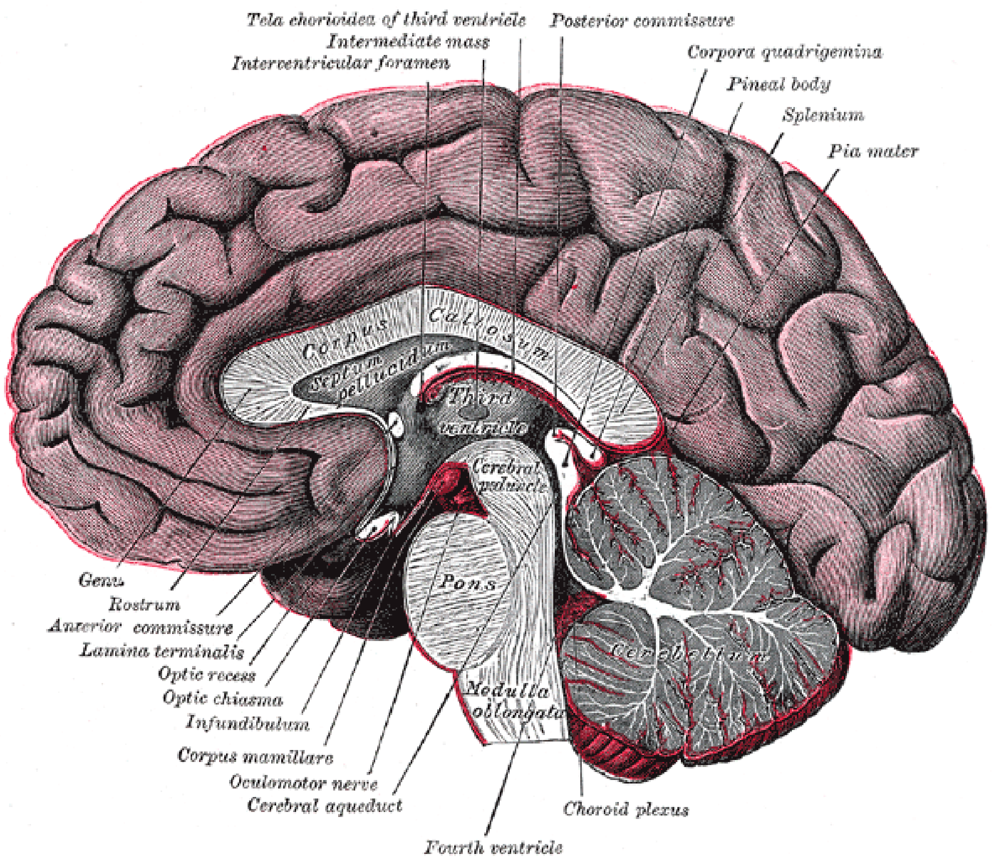
Anisotropic media
(white matter)

# Exploring the DWI Dataset




Use the slider to browse through the dti volume, and try to locate the **Corpus Callosum**

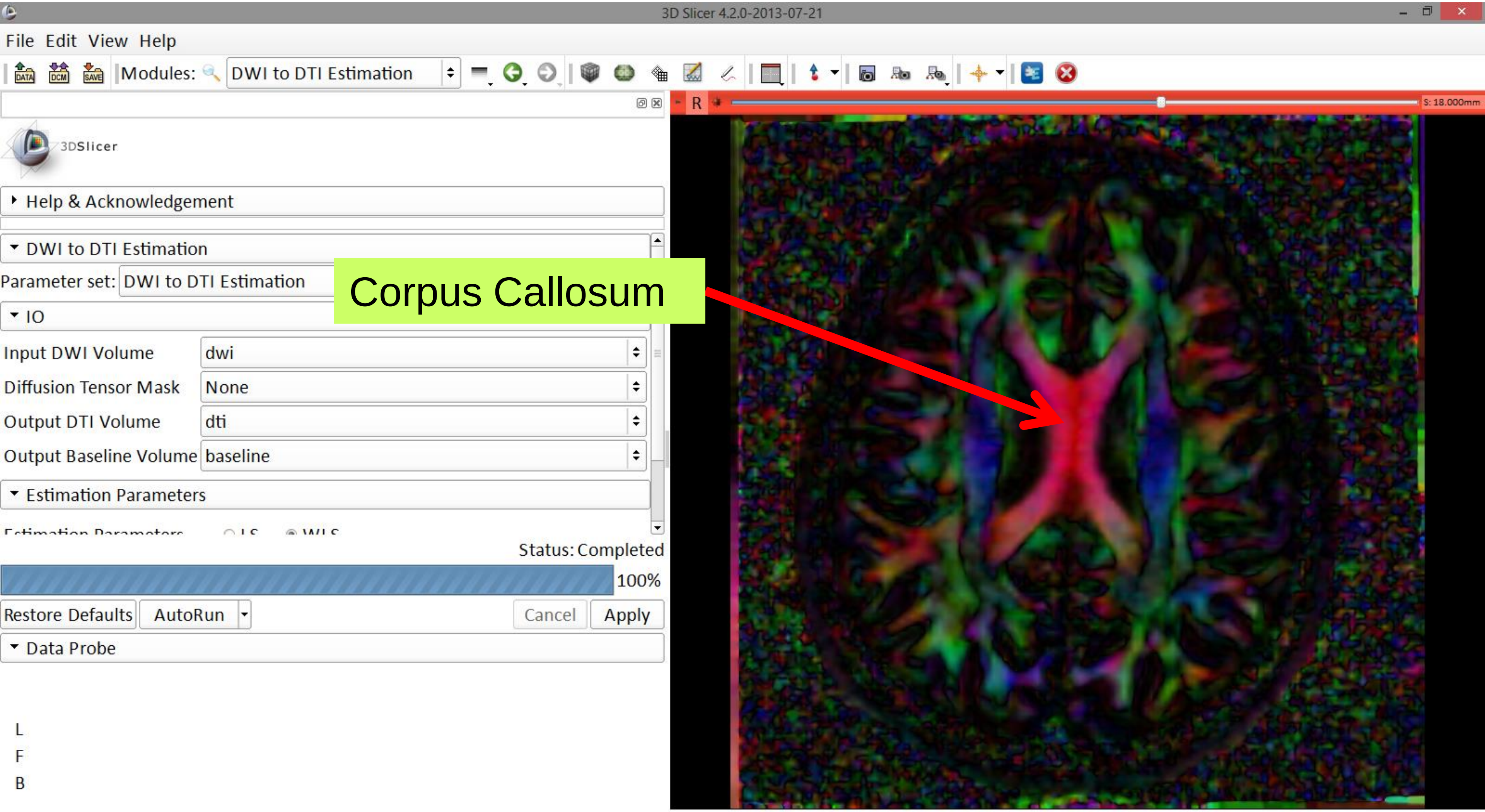
# Corpus Callosum




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



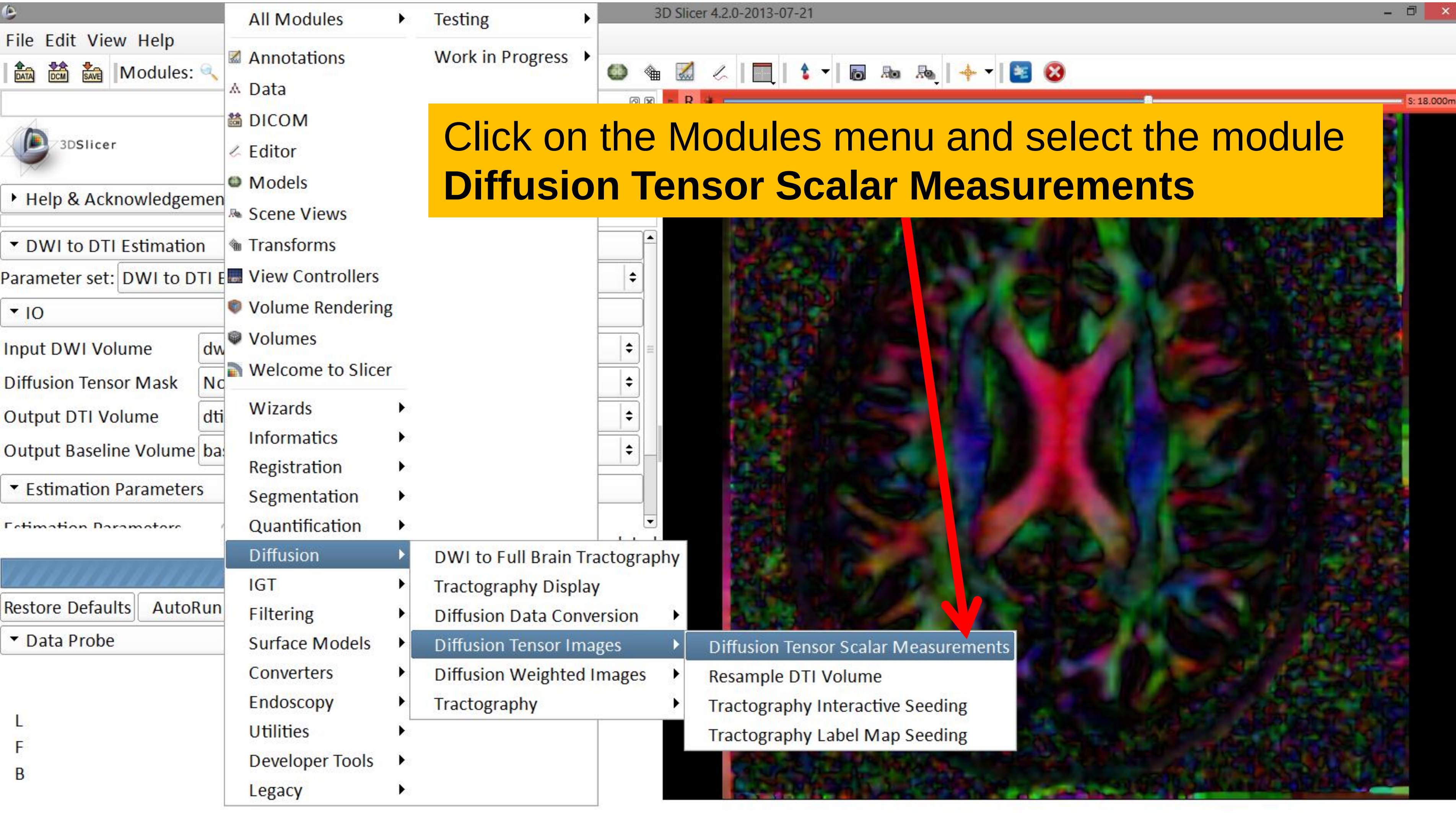
# Characterizing the Size of the tensor: Trace

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

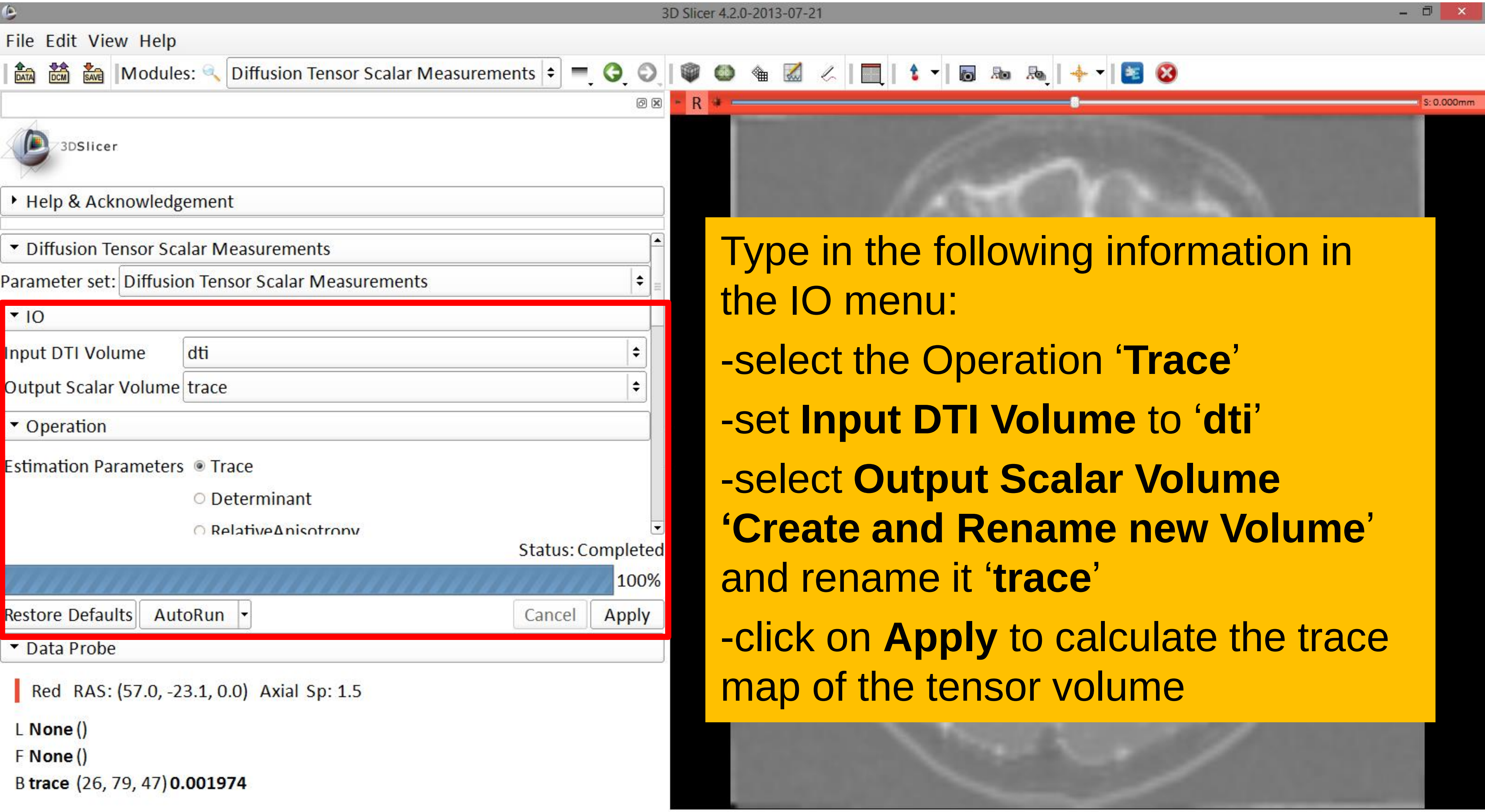
- Trace(D) is intrinsic to the tissue and is independent of fiber orientation, and diffusion sensitizing gradient directions
- Trace(D) is a clinically relevant parameter for monitoring stroke and neurological condition ( degree of structural coherence in tissue)
- Trace(D) is useful to characterize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

# Trace

Click on the Modules menu and select the module **Diffusion Tensor Scalar Measurements**



# Trace




Type in the following information in the IO menu:

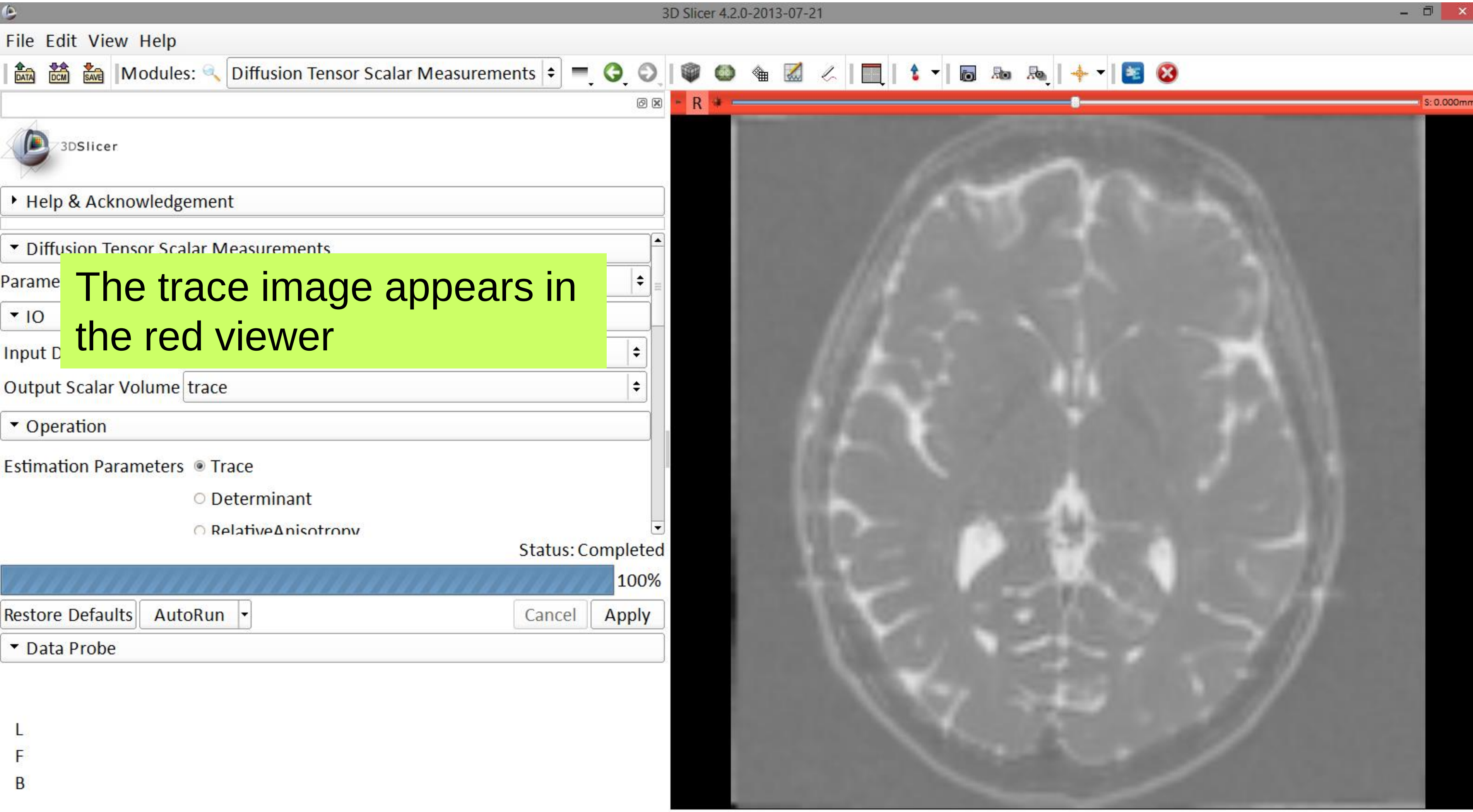
-select the Operation ‘**Trace**’

-set **Input DTI Volume** to ‘**dti**’

-select **Output Scalar Volume** ‘**Create and Rename new Volume**’ and rename it ‘**trace**’

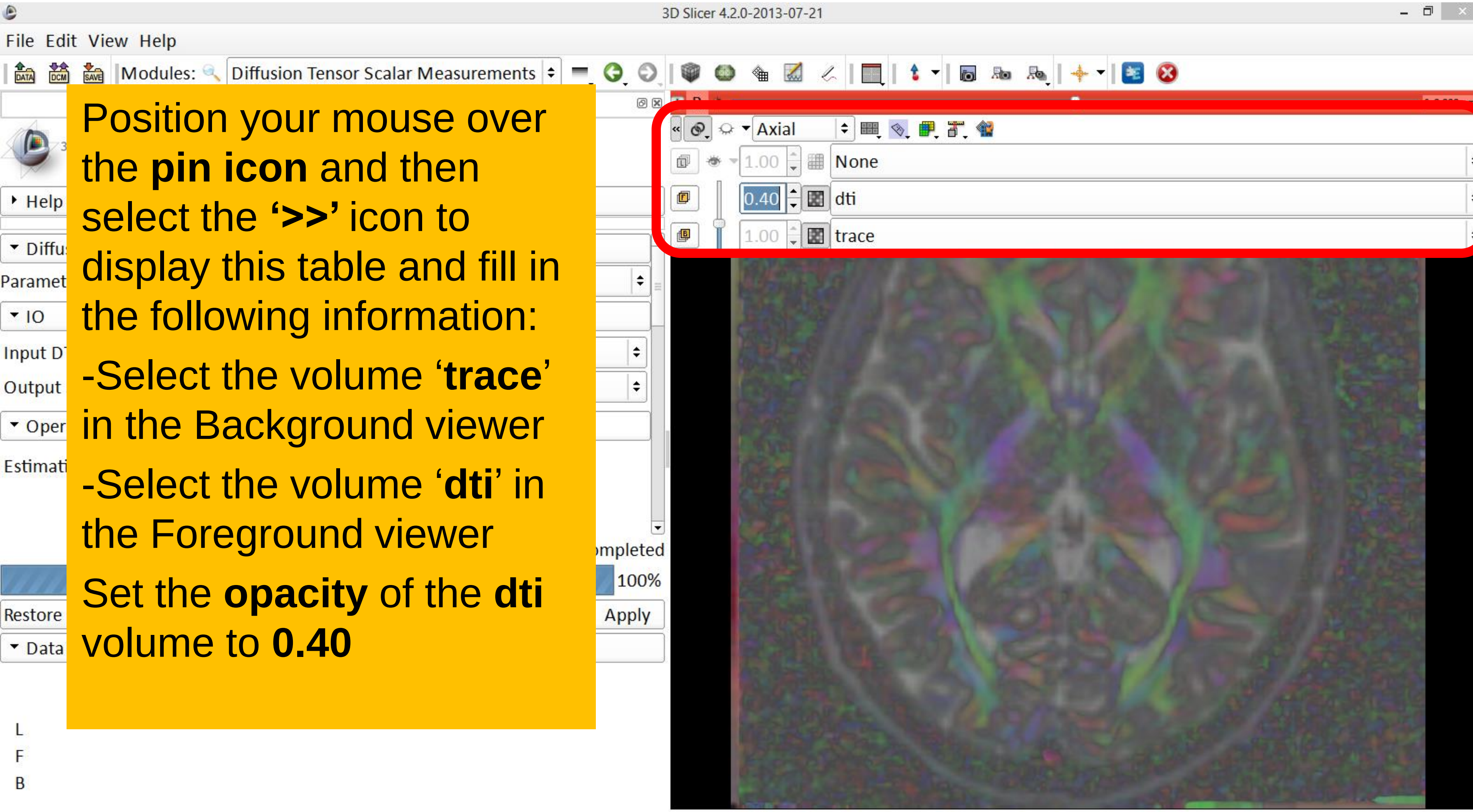
-click on **Apply** to calculate the trace map of the tensor volume

# 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:

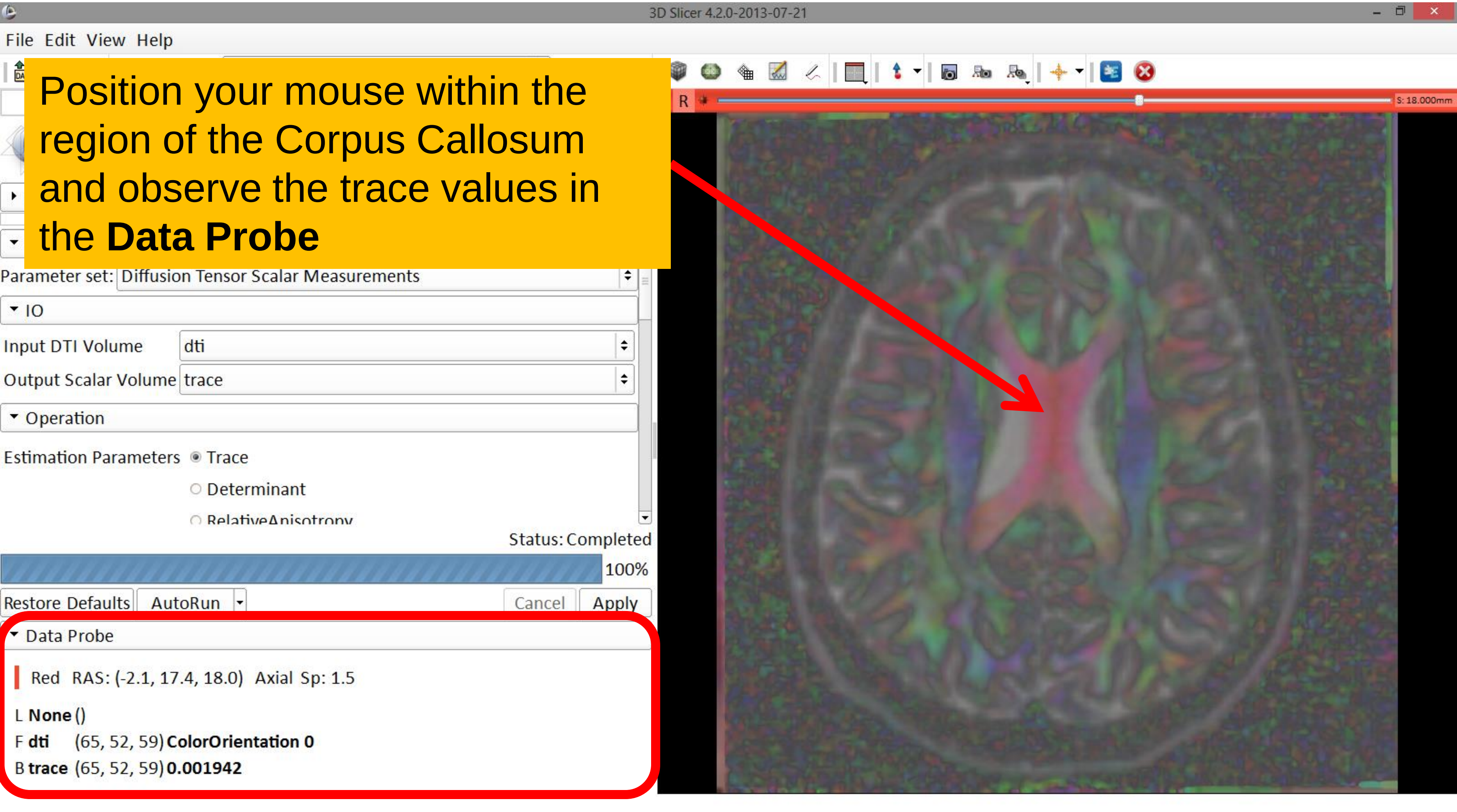
-Select the volume '**trace**' in the Background viewer

-Select the volume '**dti**' in the Foreground viewer

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

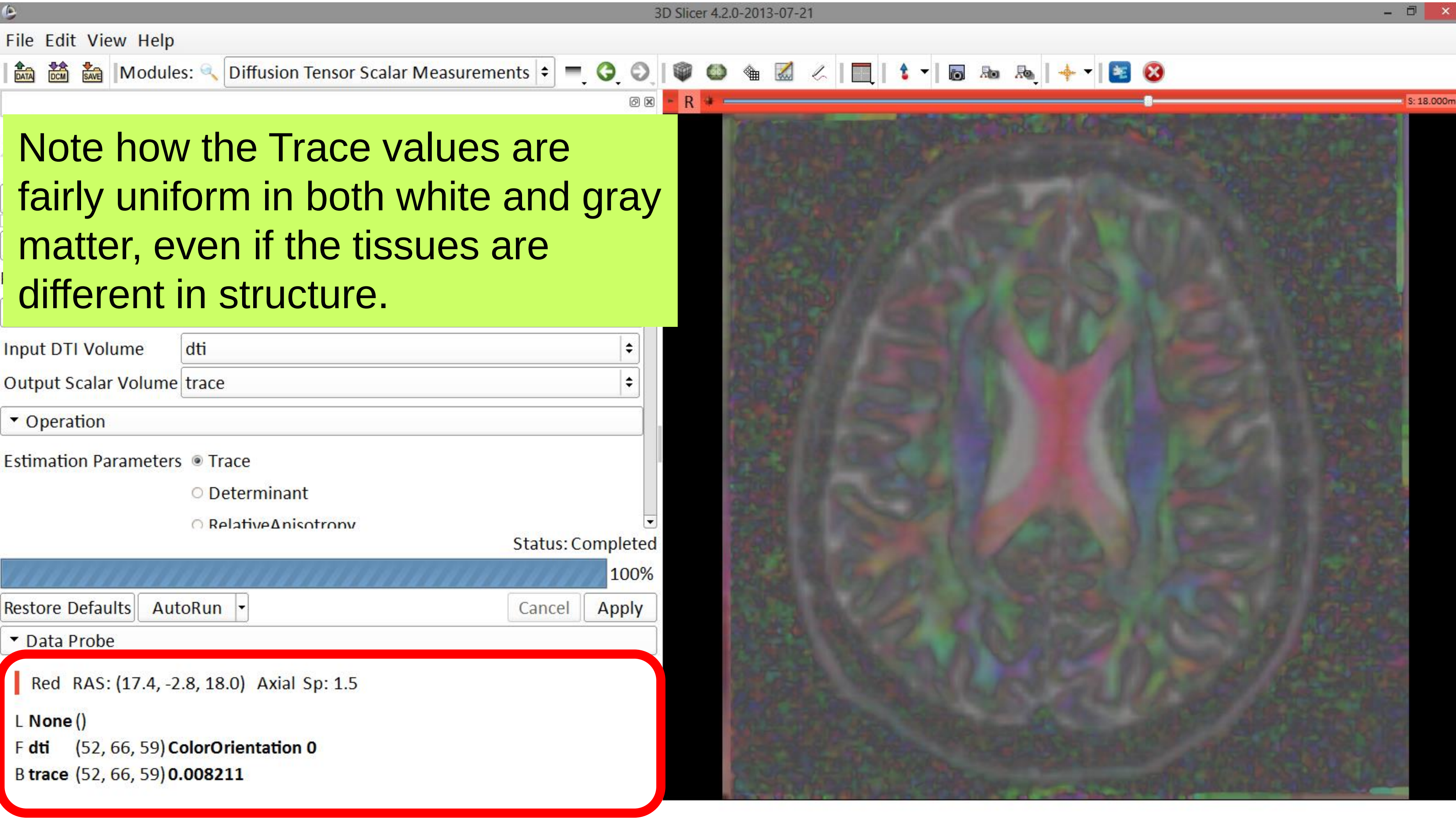
# Trace

Position your mouse within the region of the Corpus Callosum and observe the trace values in the **Data Probe**



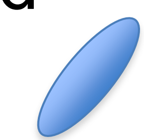
# Trace

Note how the Trace values are fairly uniform in both white and gray matter, even if the tissues are different in structure.

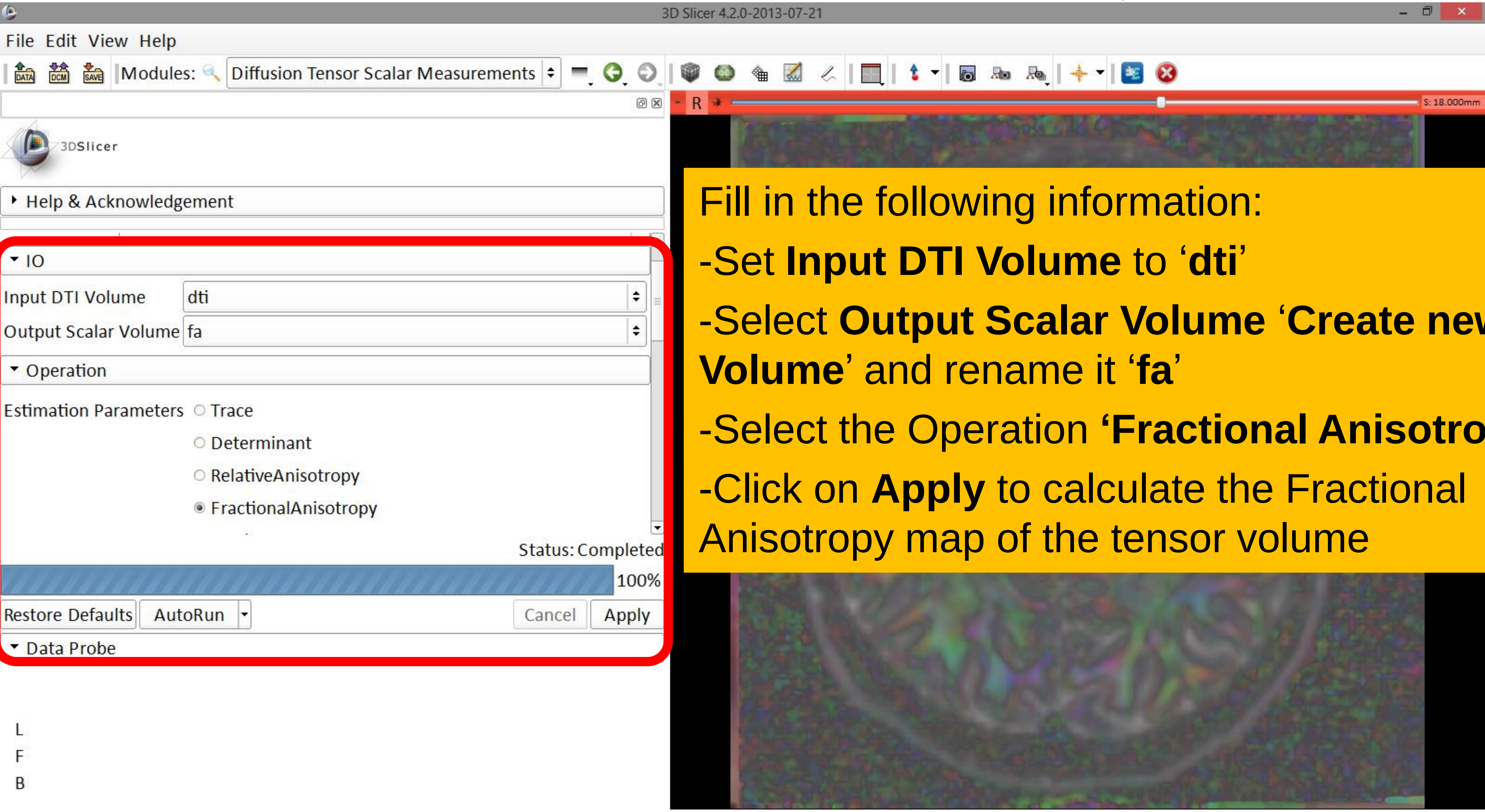


# Scalar Maps: Fractional Anisotropy

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

- 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:

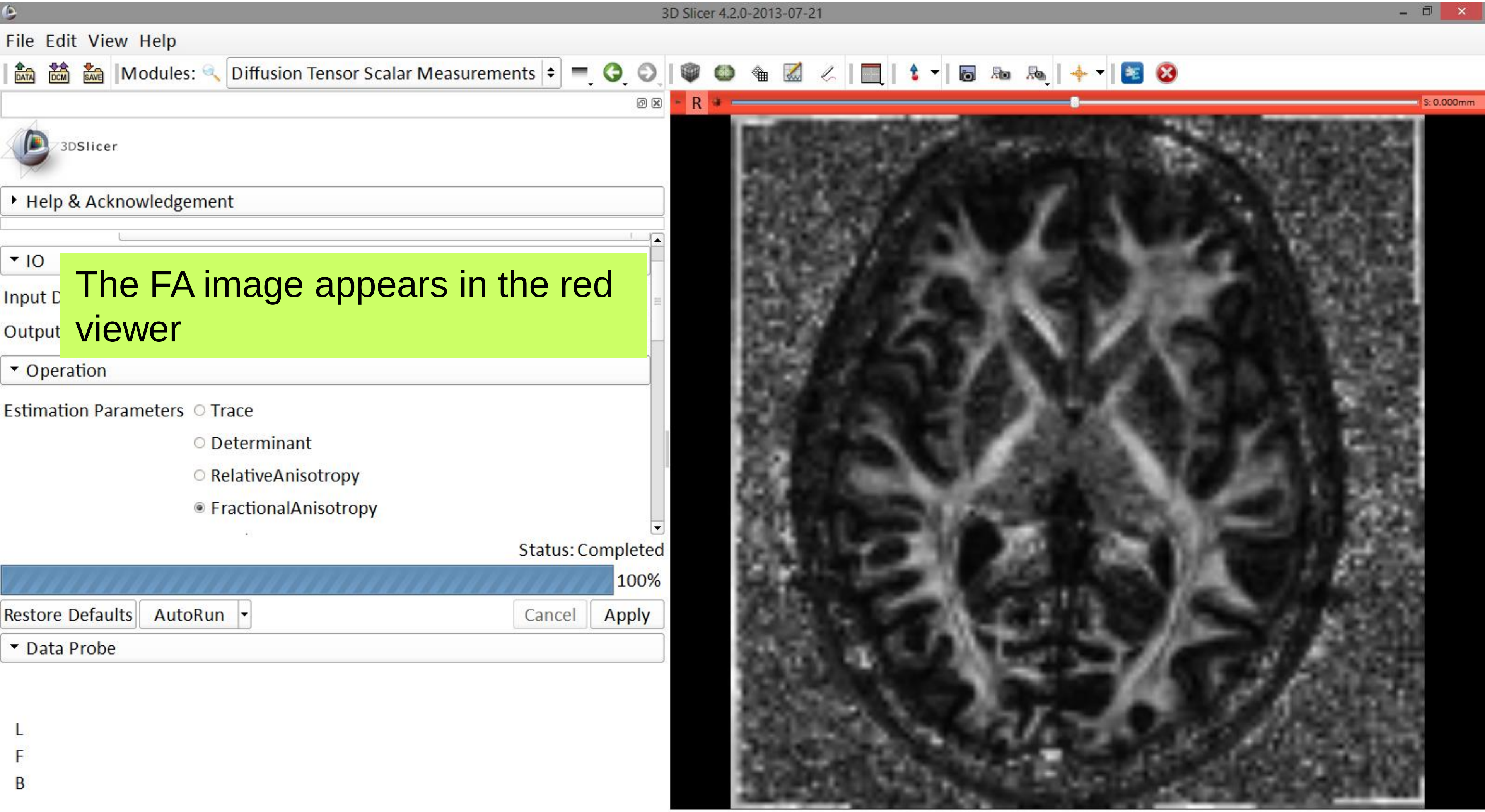
-Set **Input DTI Volume** to '**dti**'

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

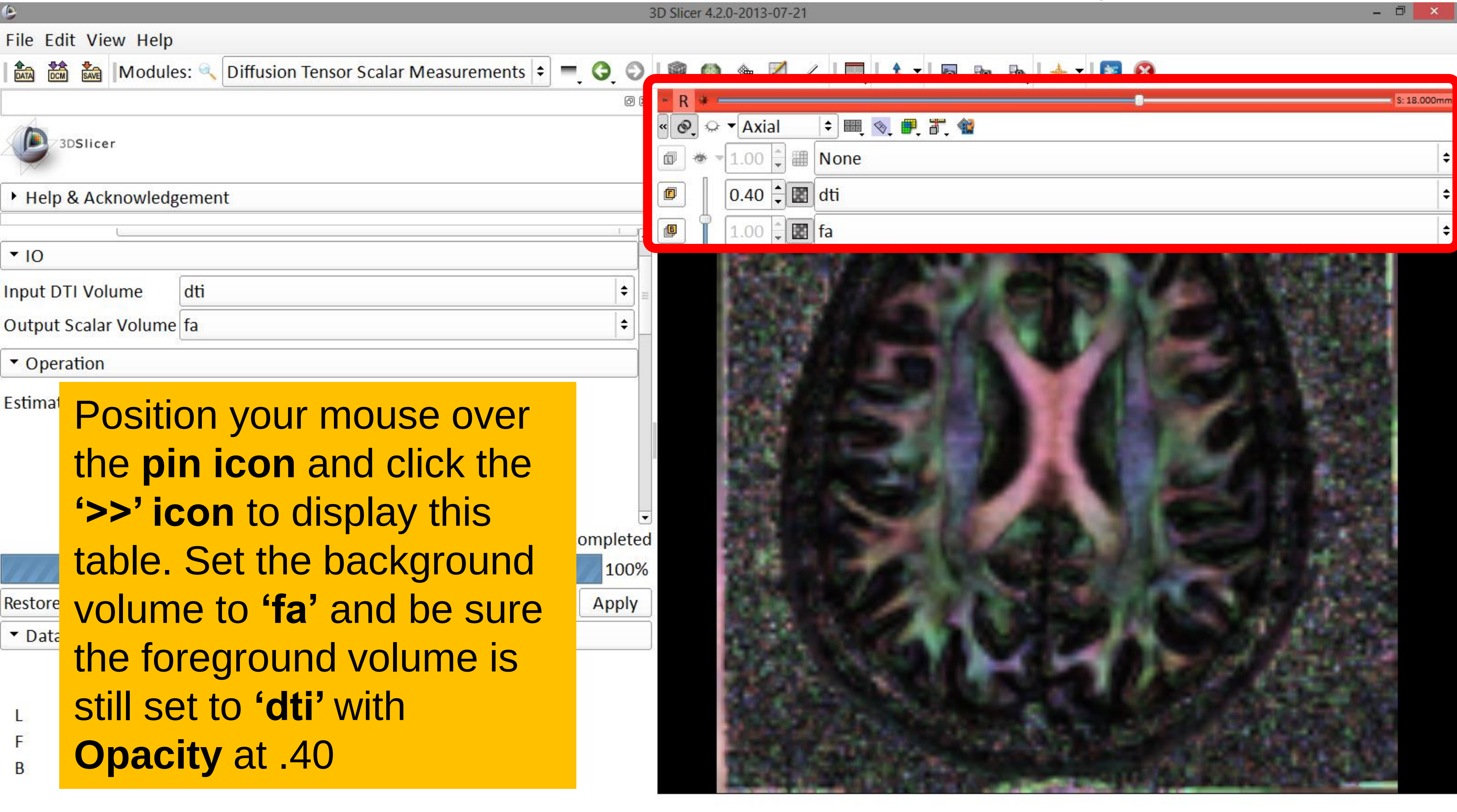
-Select the Operation **'Fractional Anisotro**

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

# Fractional Anisotropy



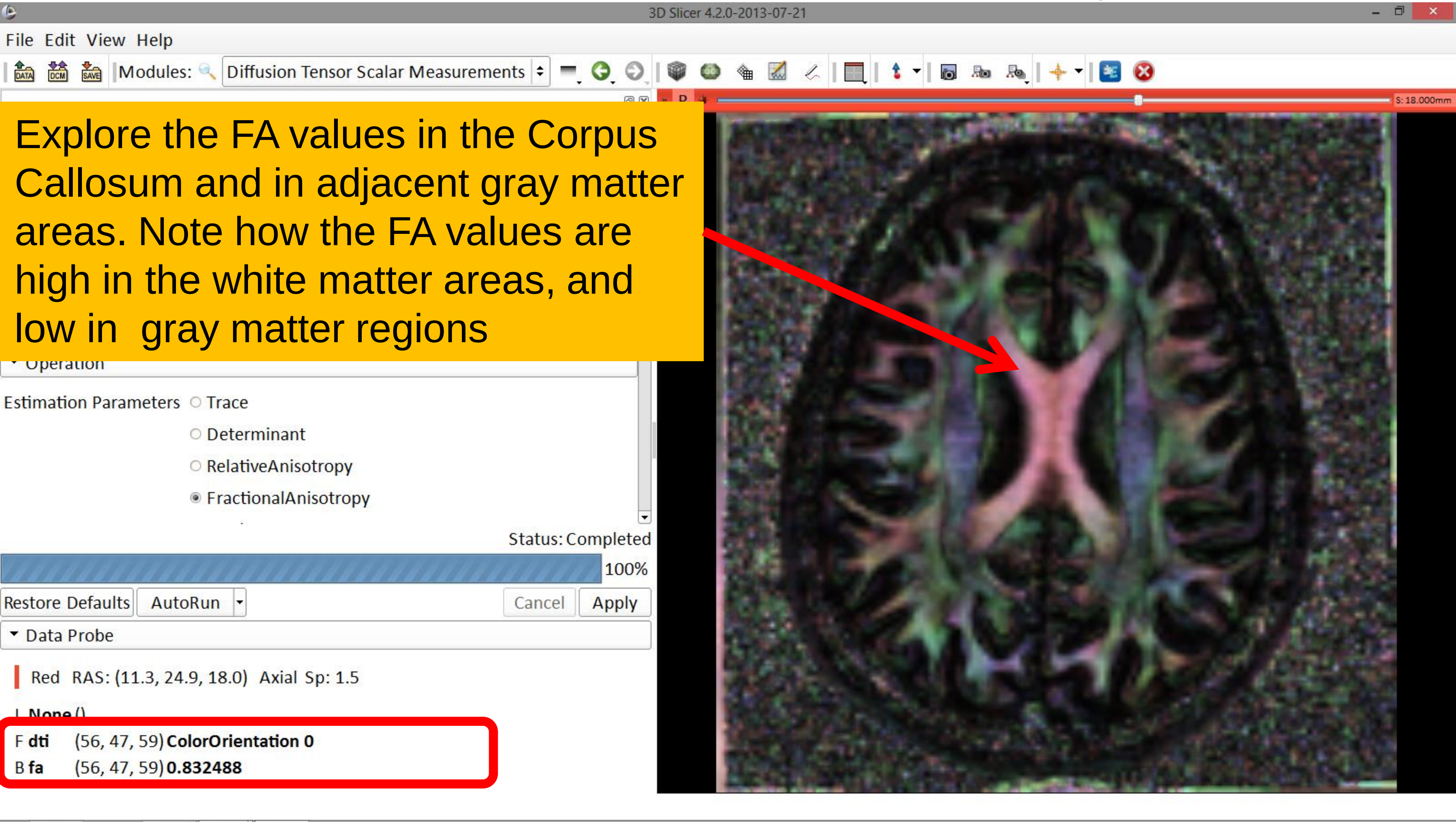
# Fractional Anisotropy



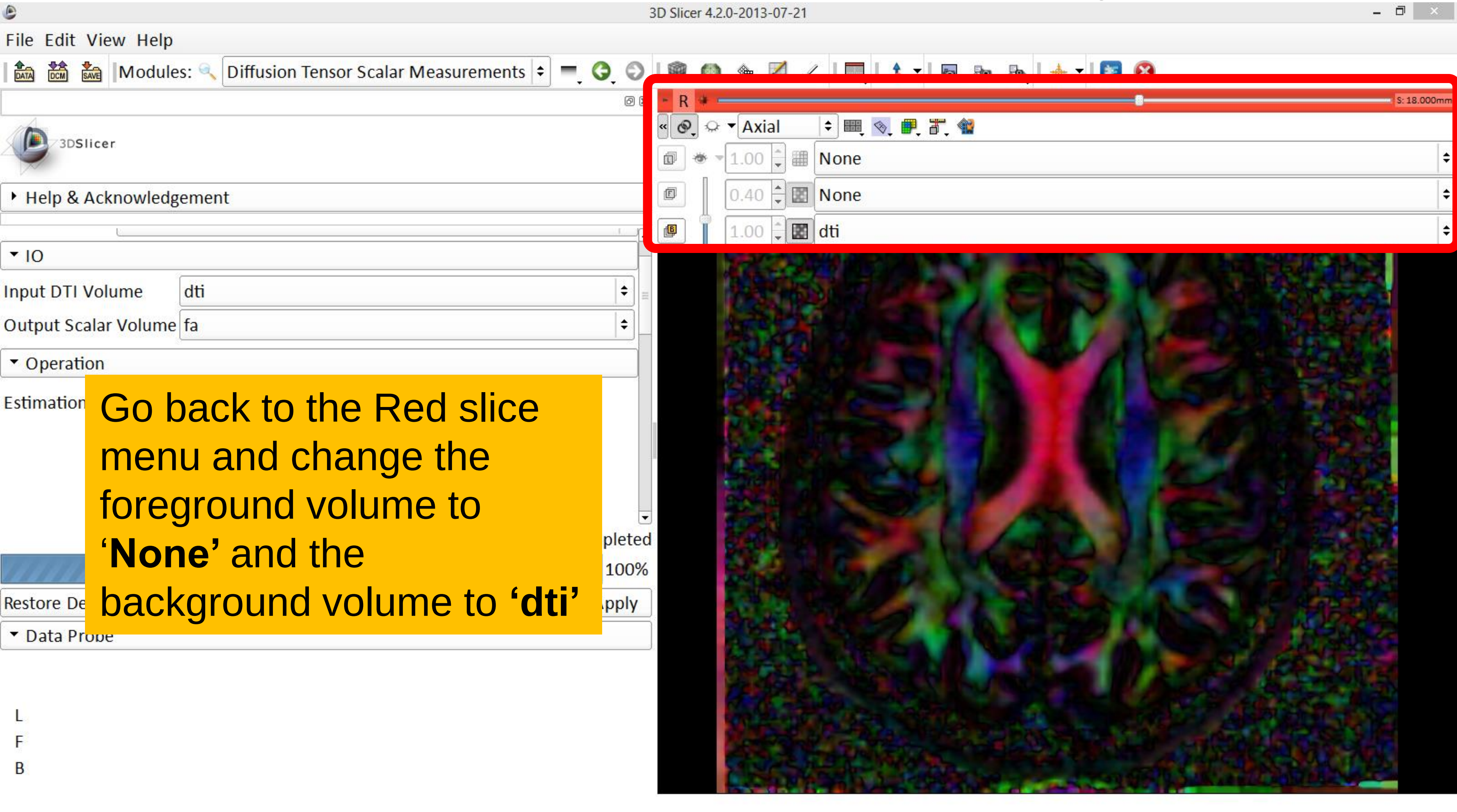

Position your mouse over the **pin icon** and click the **'>>' icon** to display this table. Set the background volume to **'fa'** and be sure the foreground volume is still set to **'dti'** with **Opacity** at .40

# Fractional Anisotropy

Explore the FA values in the Corpus Callosum and in adjacent gray matter areas. Note how the FA values are high in the white matter areas, and low in gray matter regions

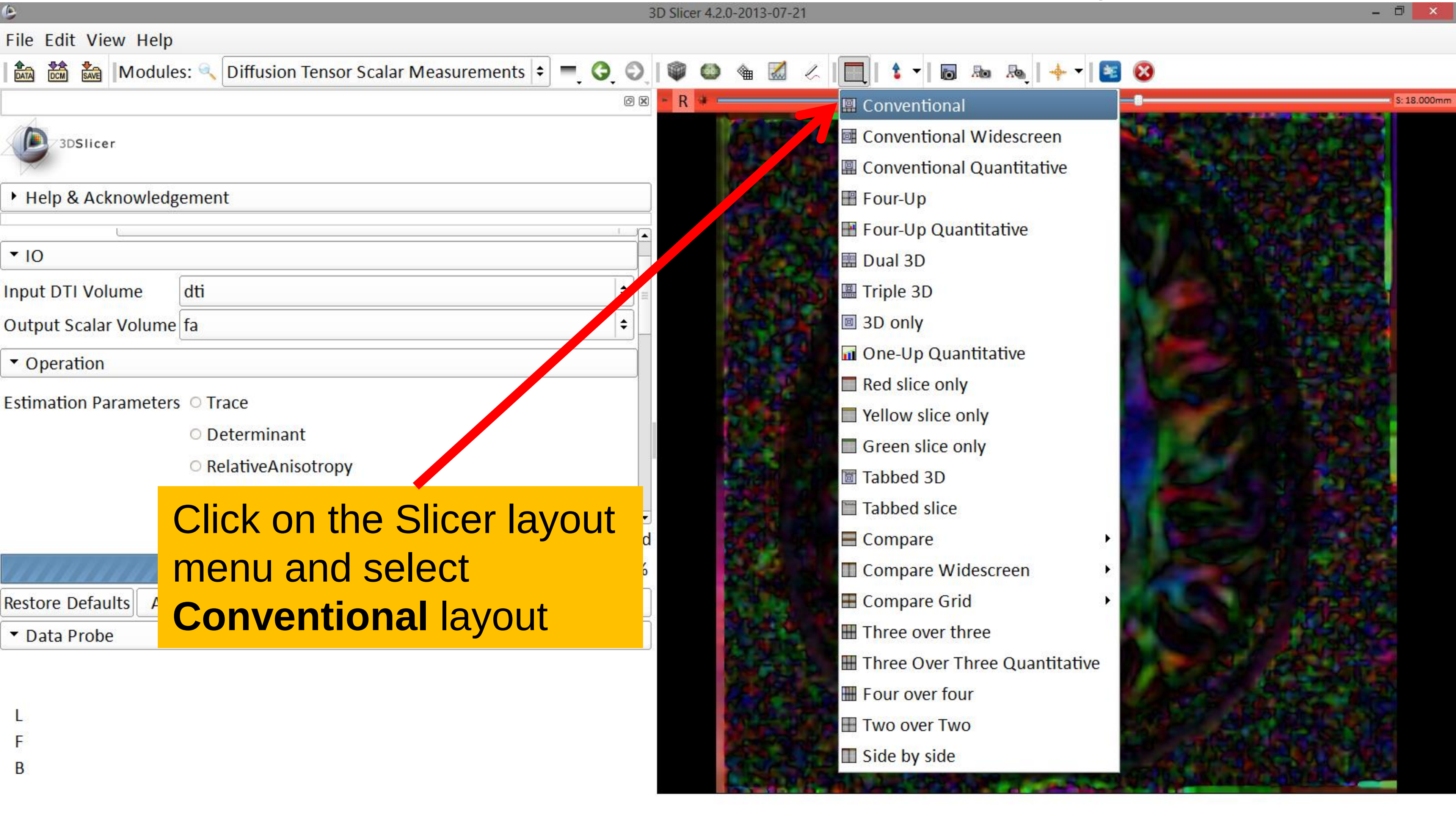


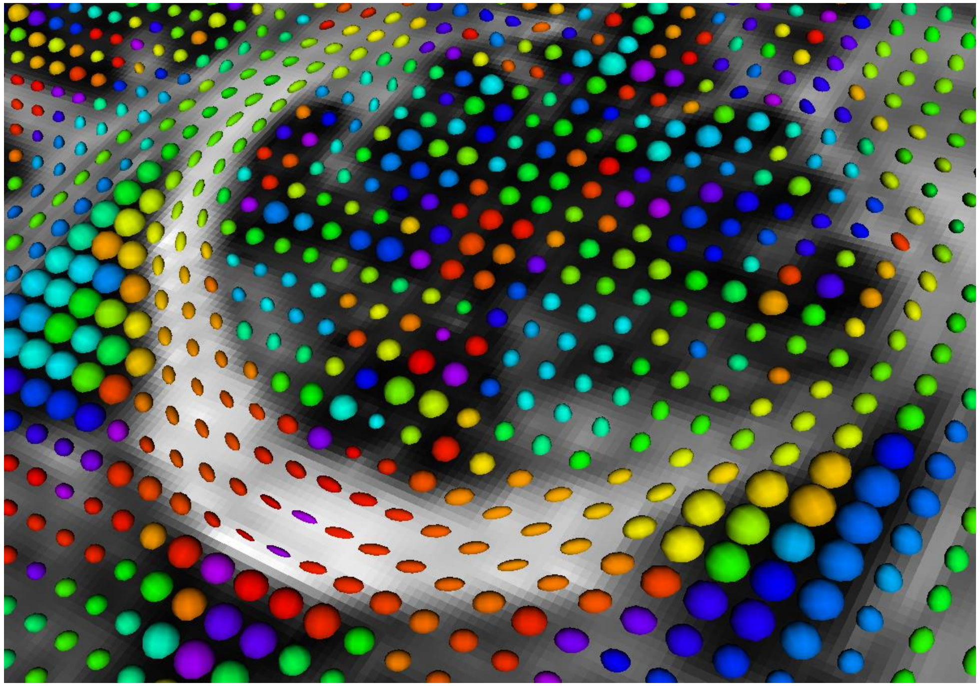
# Fractional Anisotropy




Go back to the Red slice menu and change the foreground volume to ‘**None**’ and the background volume to **‘dti’**

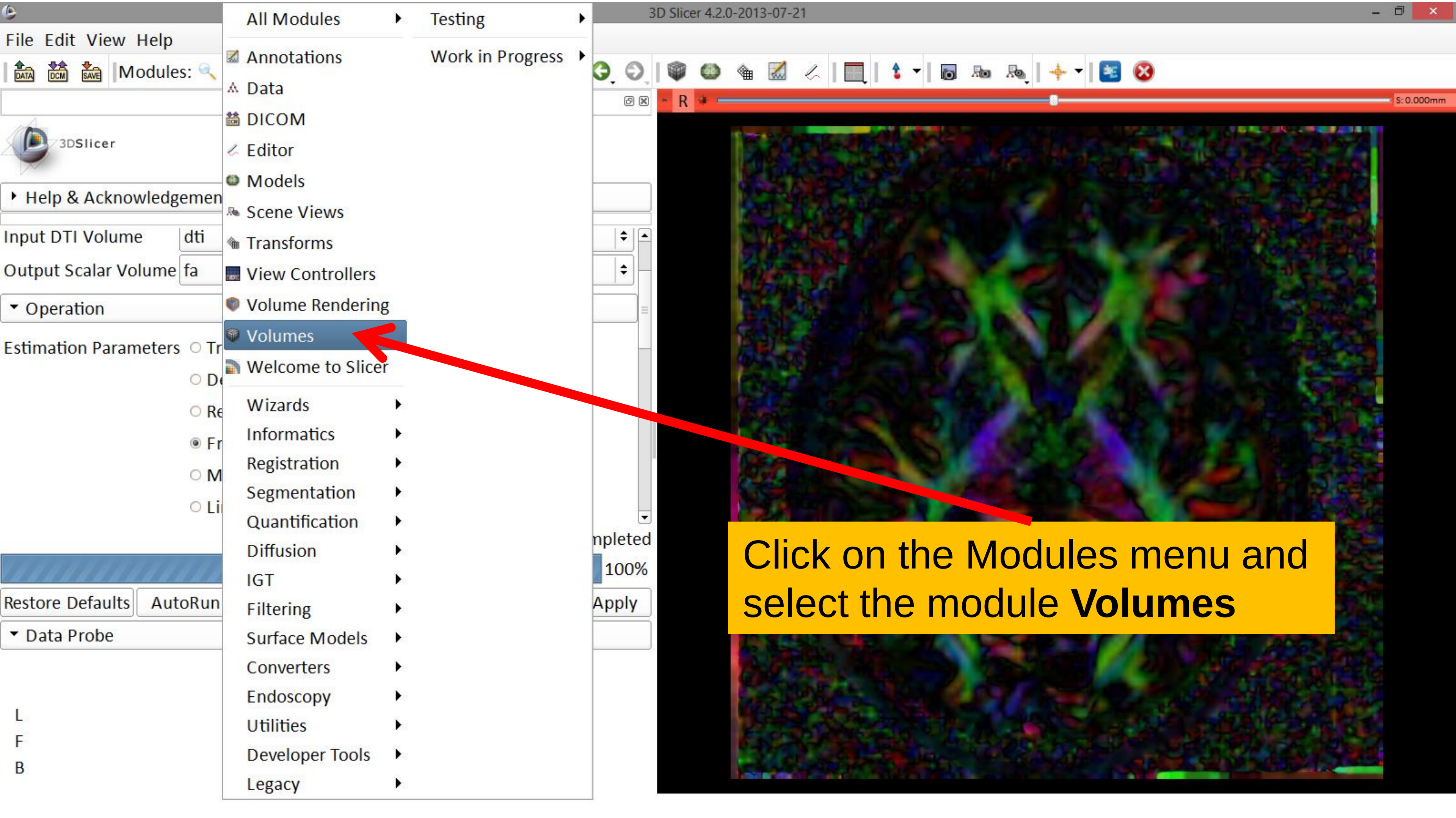
# Fractional Anisotropy



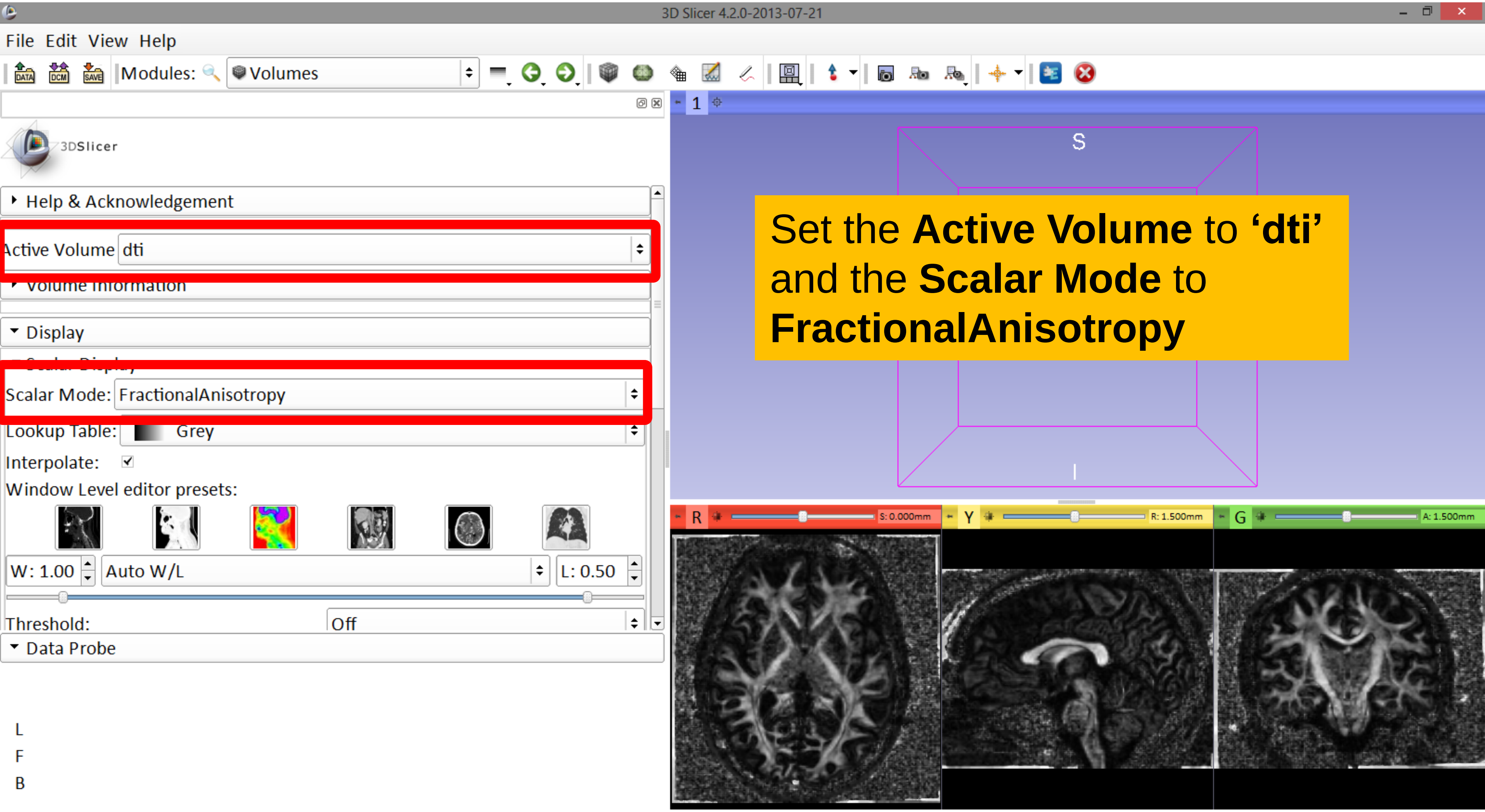


# Part 2: Visualizing the tensor data

# 3D Visualization: Glyphs

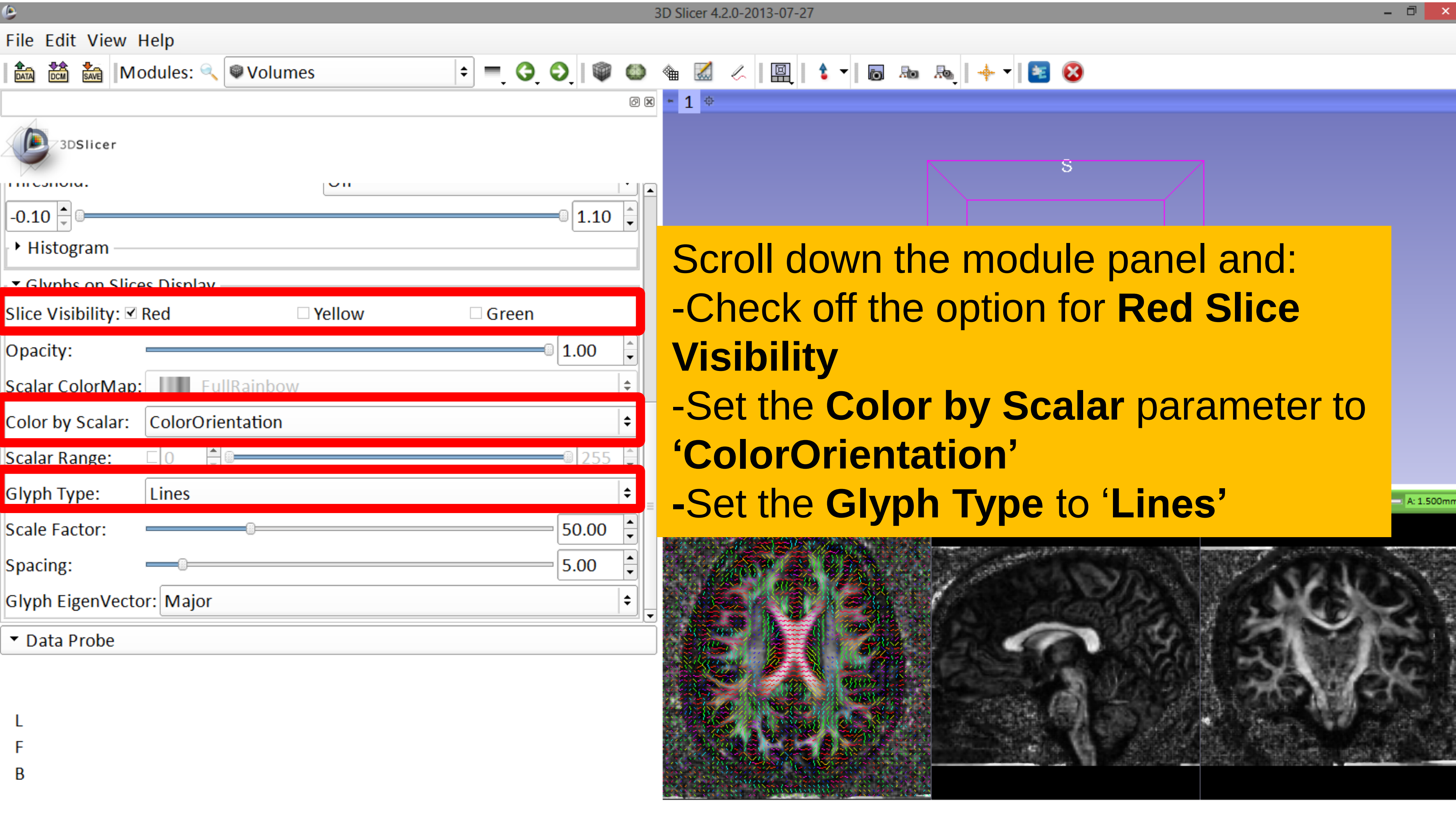


# 3D Visualization: Glyphs




Set the **Active Volume** to **'dti'** and the **Scalar Mode** to **FractionalAnisotropy**

# 3D Visualization: Glyphs



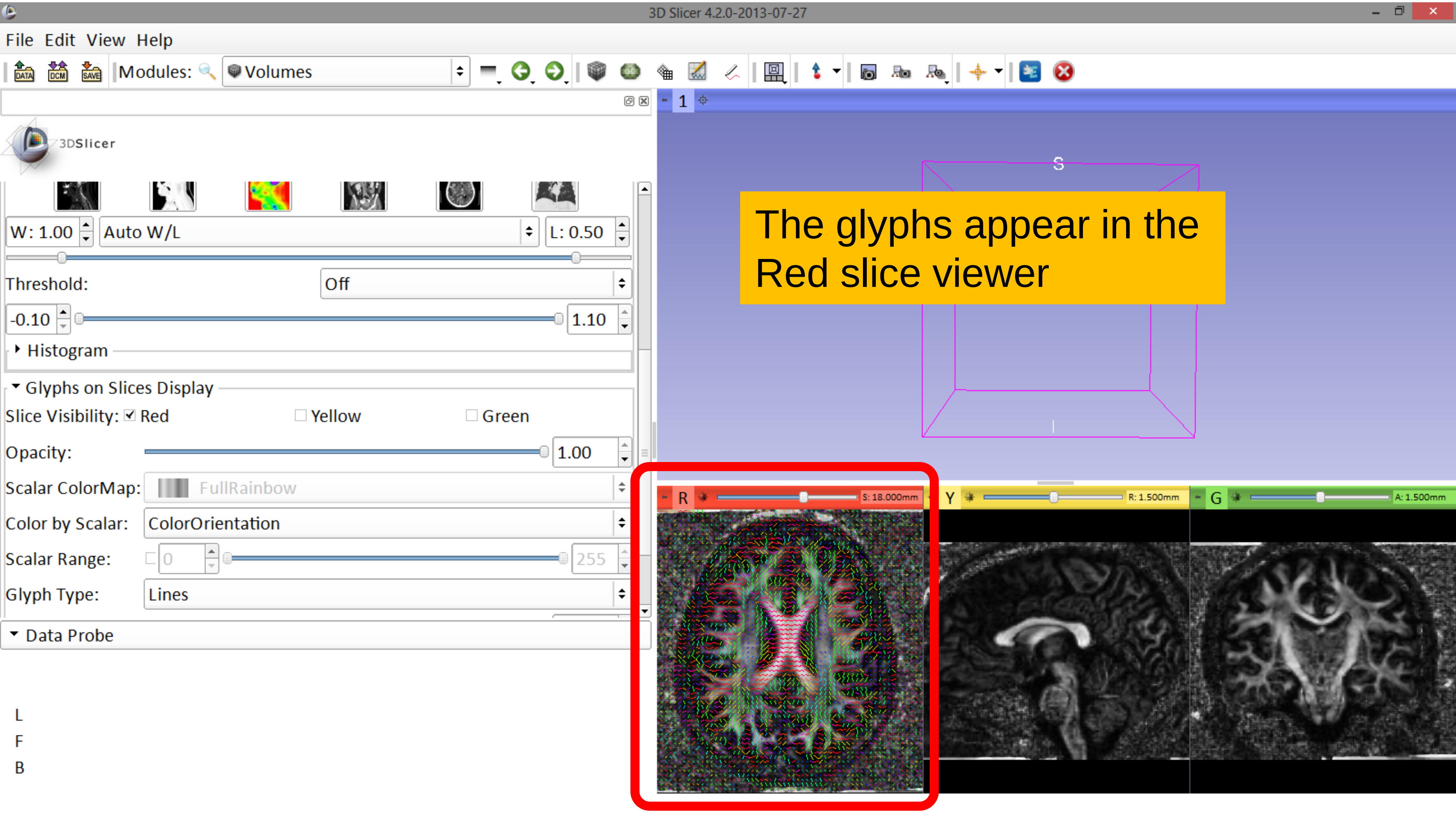

Scroll down the module panel and:

-Check off the option for **Red Slice Visibility**

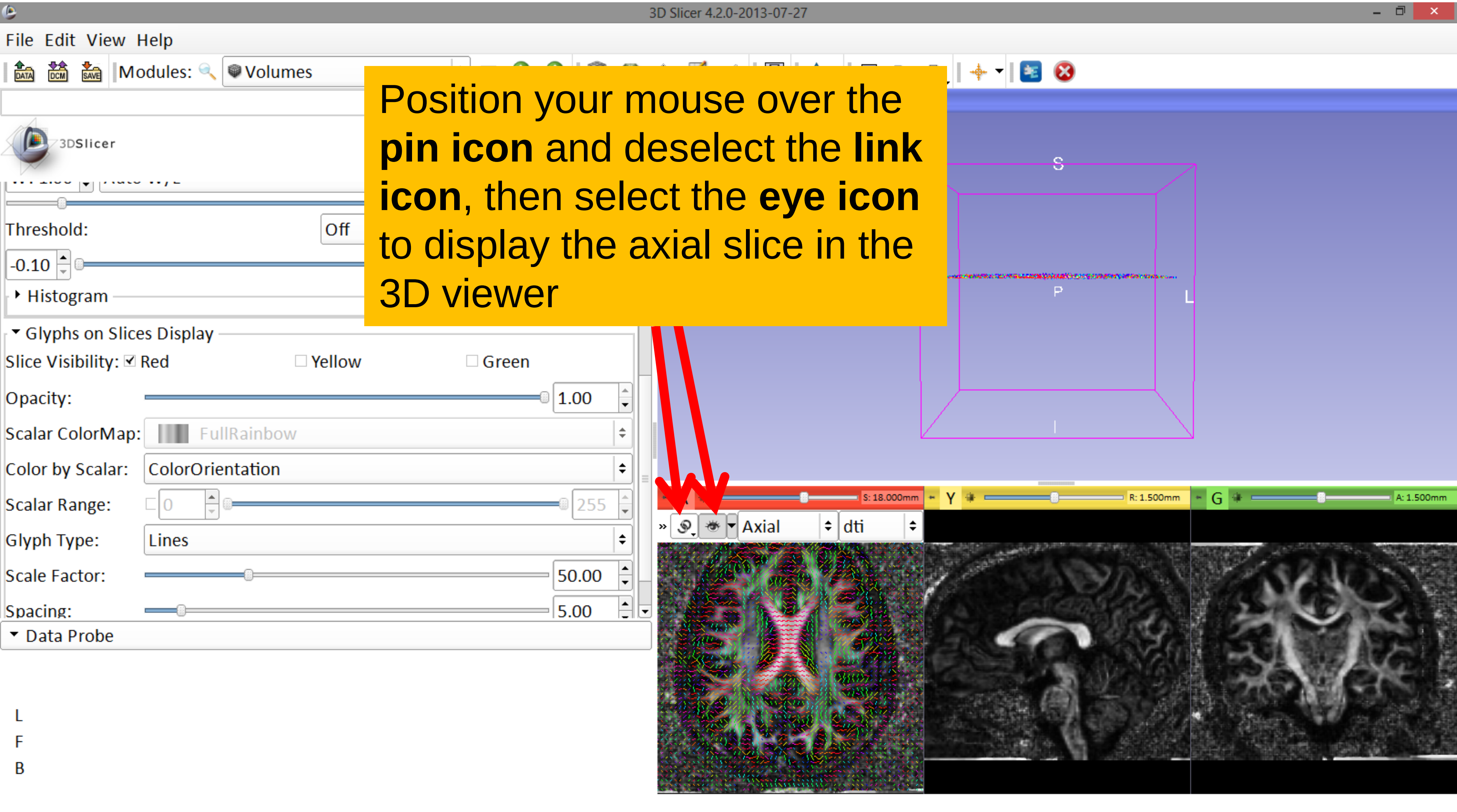
-Set the **Color by Scalar** parameter to **'ColorOrientation'**

-Set the **Glyph Type** to '**Lines'**

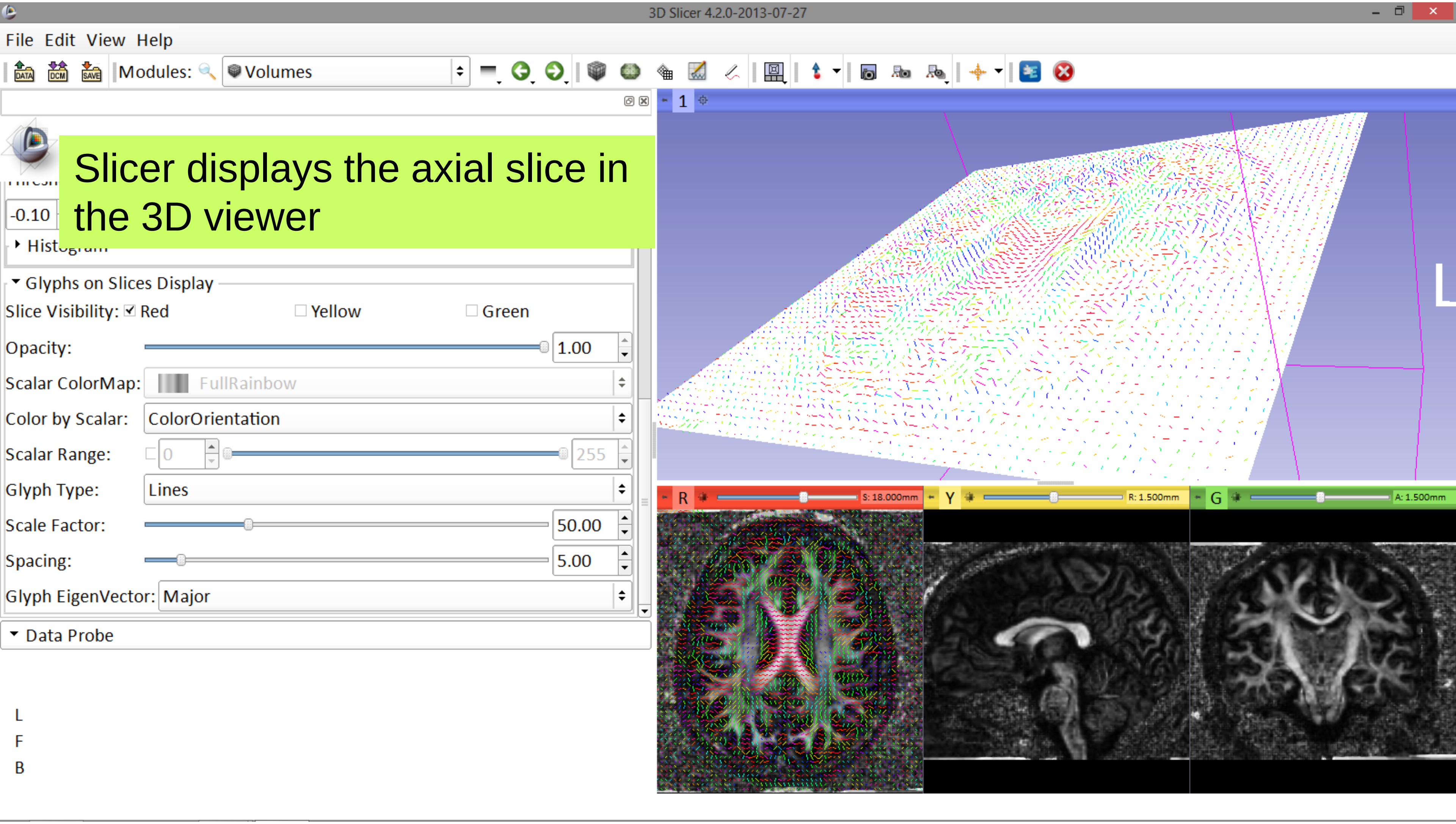
# 3D Visualization: Glyphs



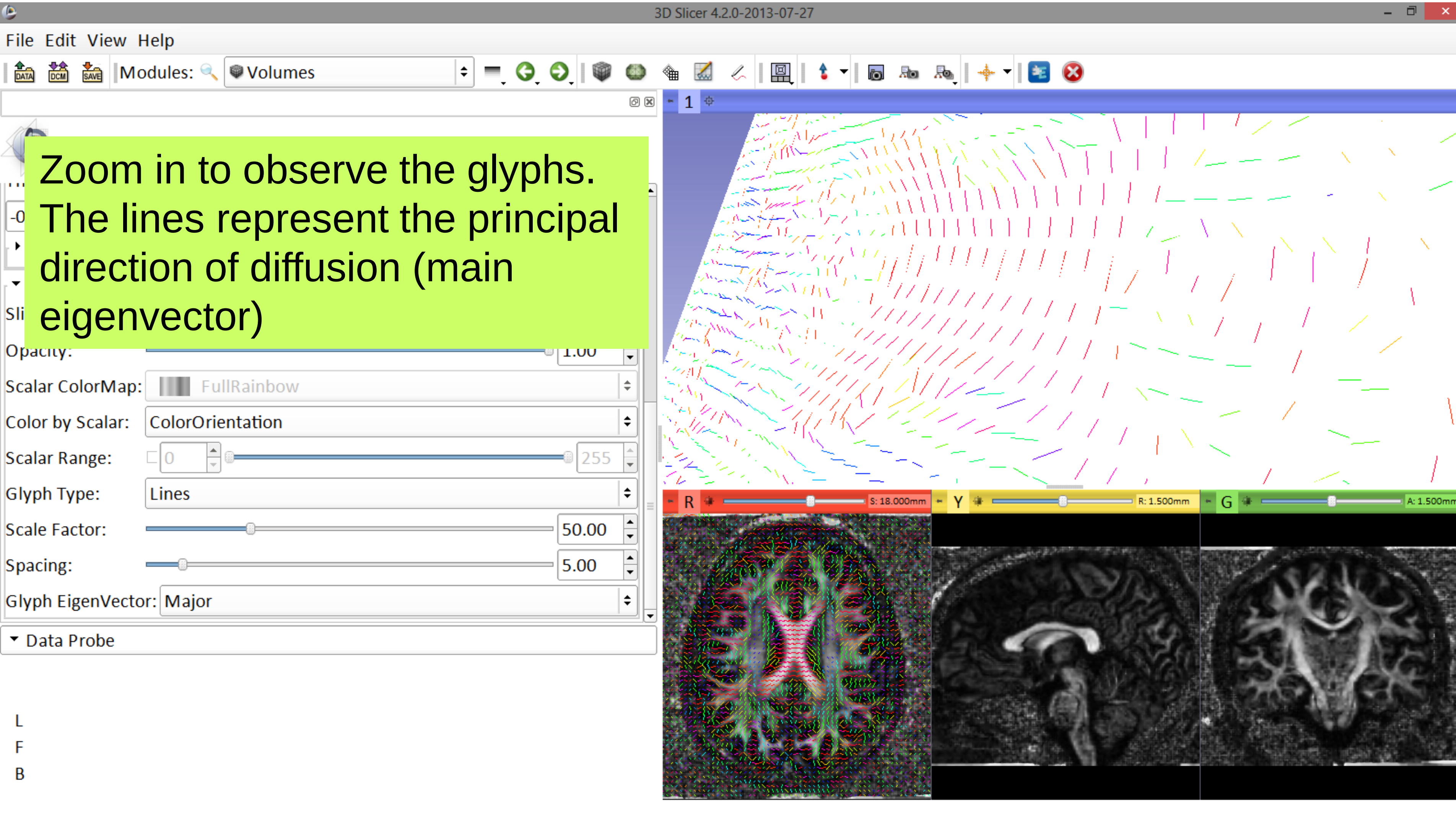
# 3D Visualization: Glyphs



# 3D Visualization: Glyphs

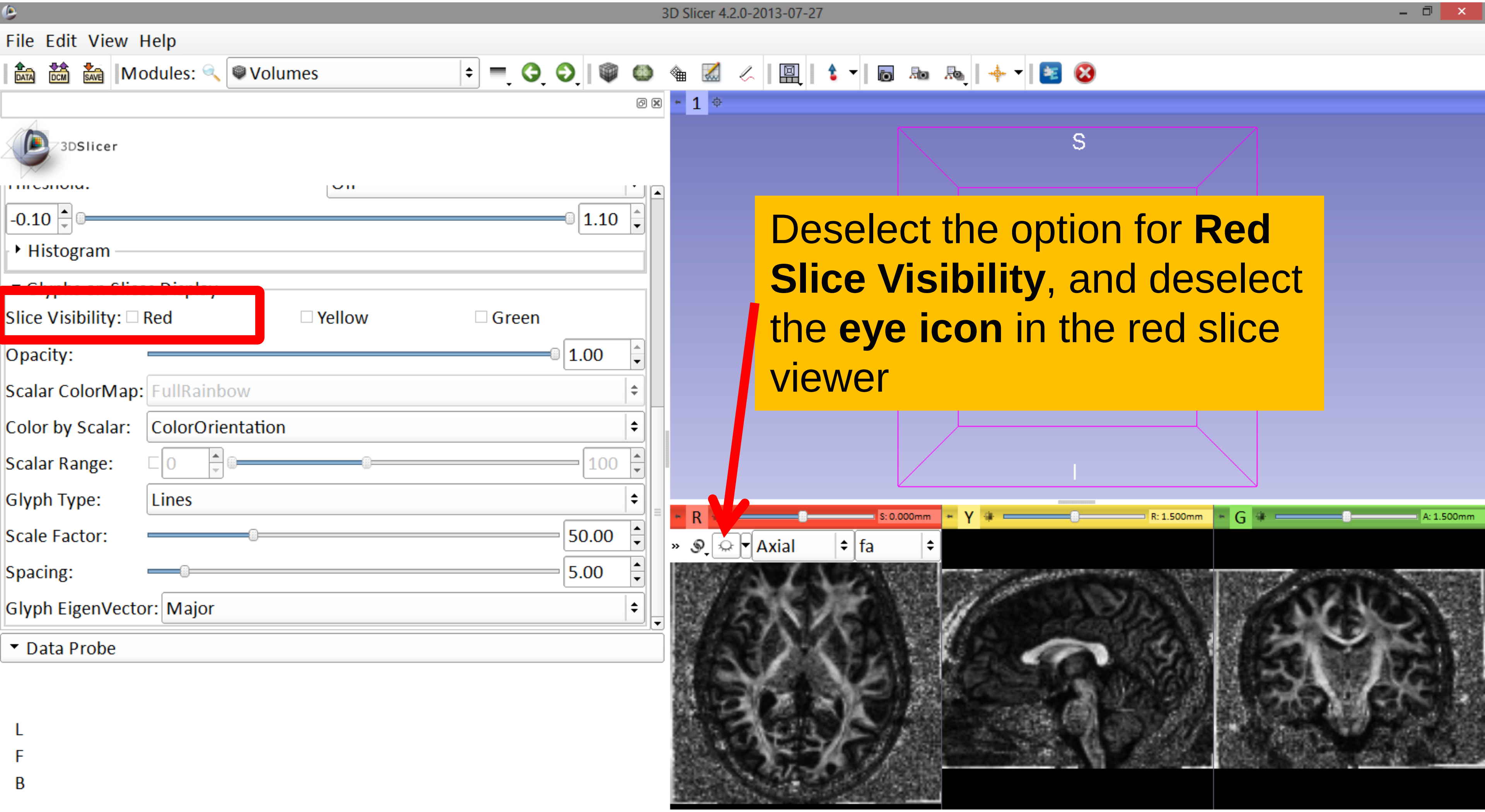


# 3D Visualization: Glyphs

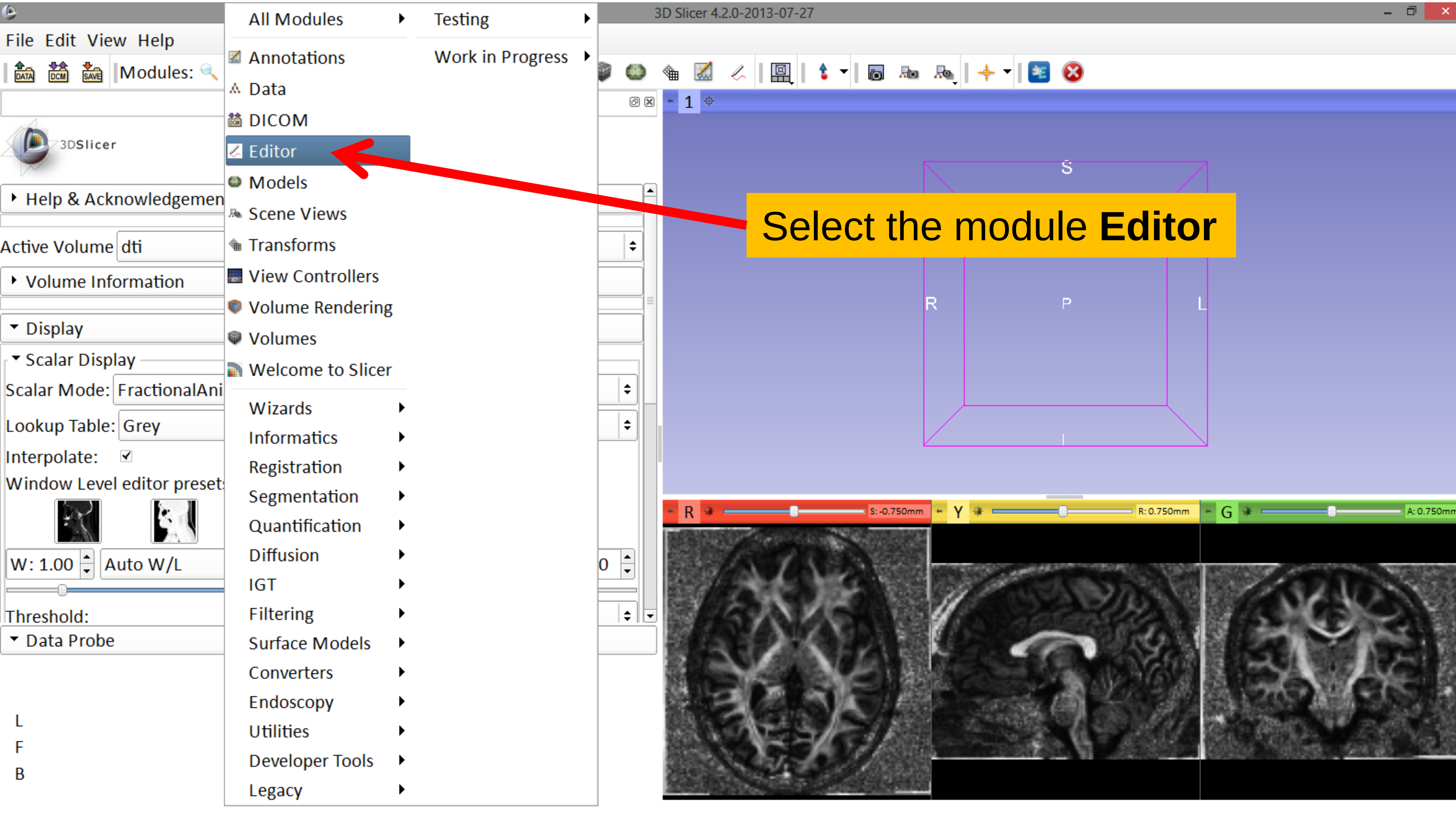



Zoom in to observe the glyphs. The lines represent the principal direction of diffusion (main eigenvector)

# Diffusion MRI tractography

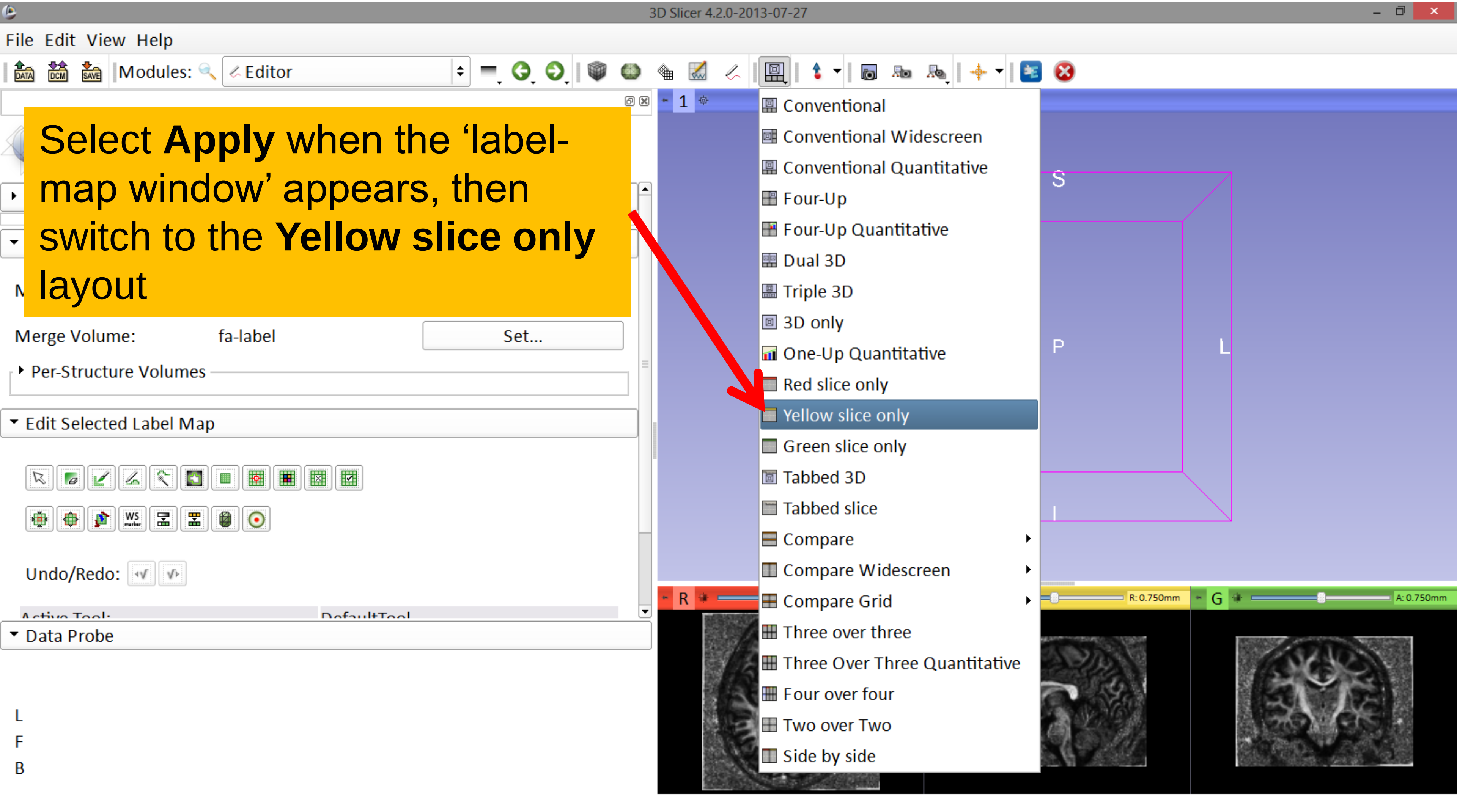


# Diffusion MRI tractography

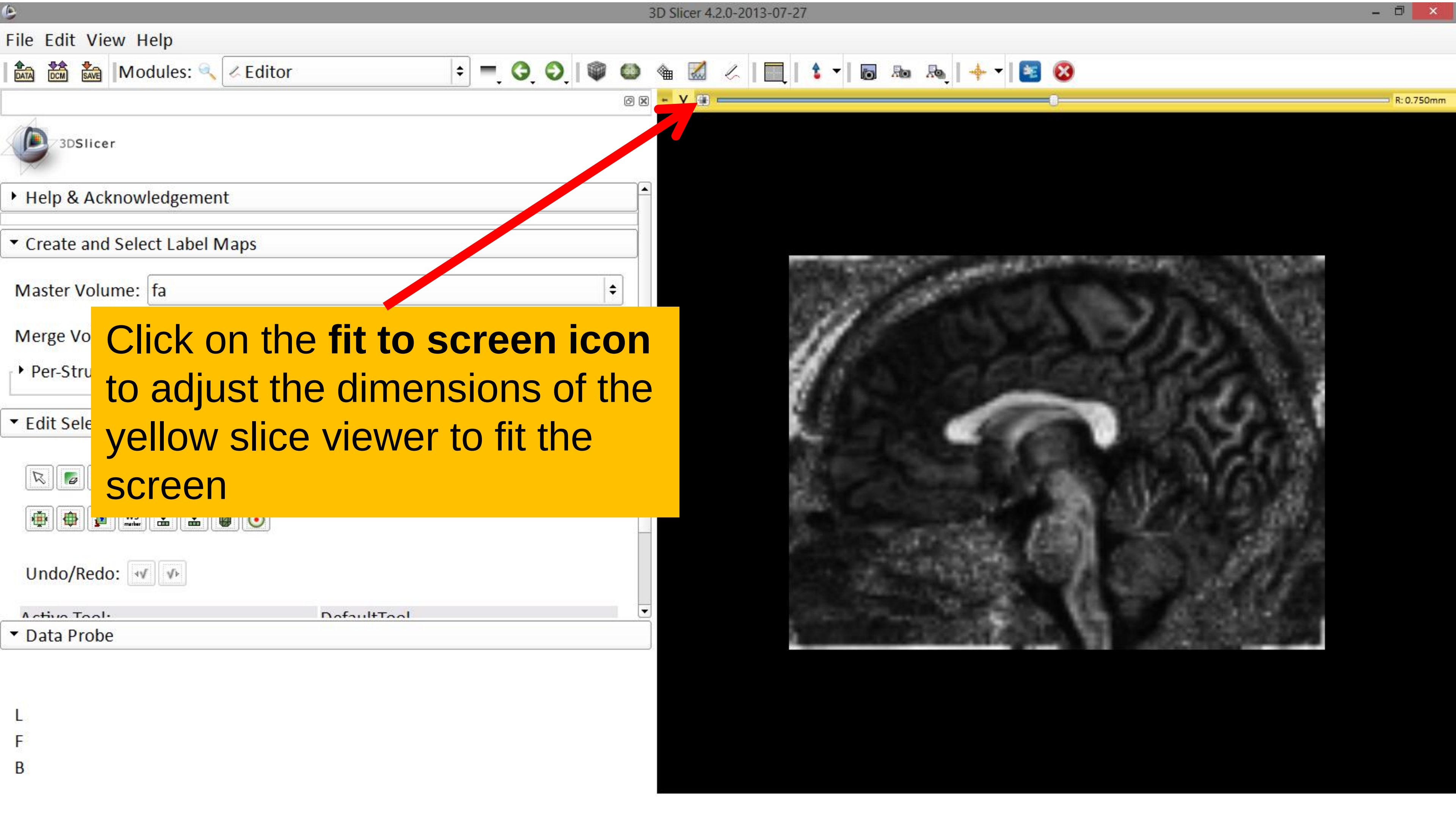


# Diffusion MRI tractography

Select **Apply** when the 'label-map window' appears, then switch to the **Yellow slice only** layout

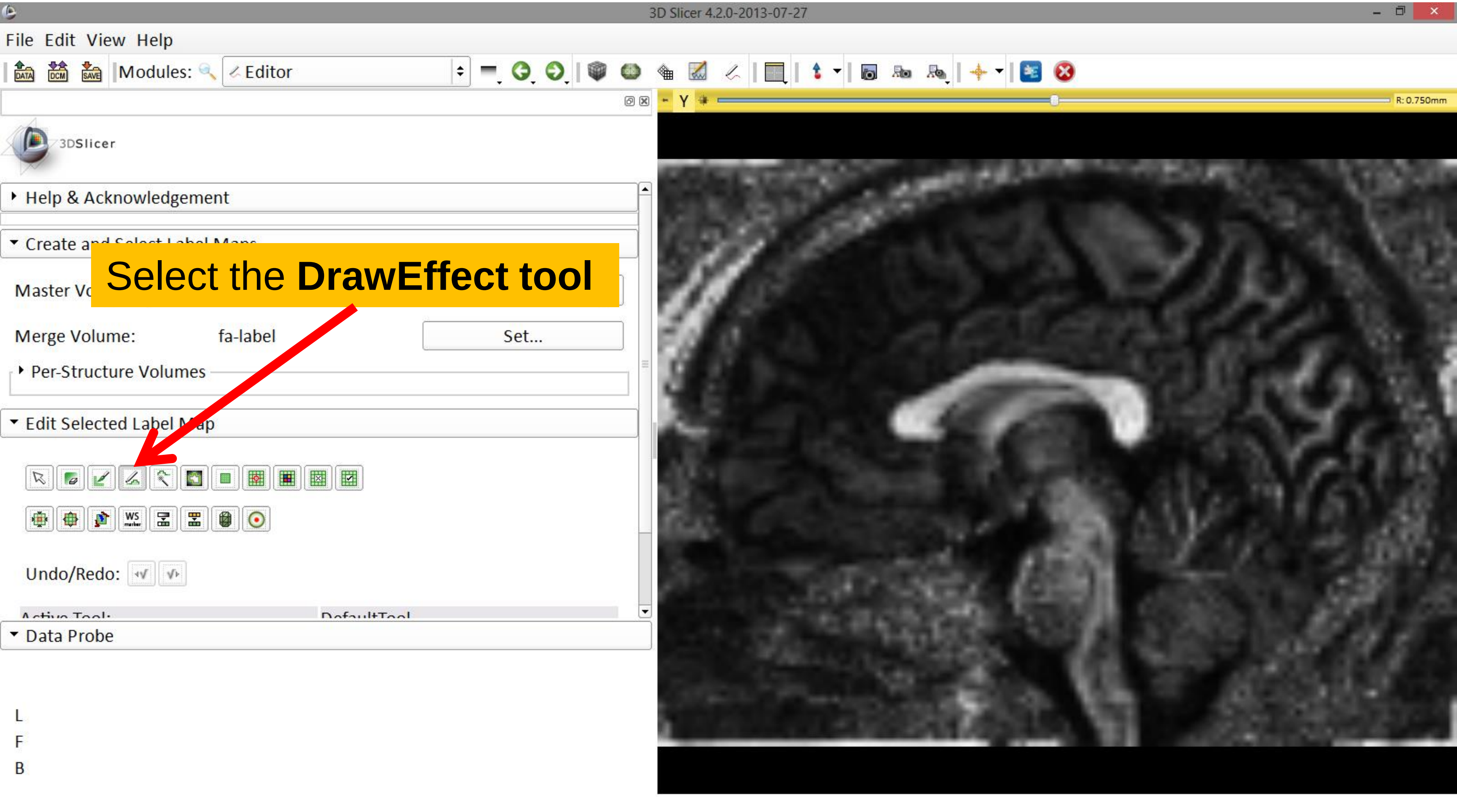


# Diffusion MRI tractography

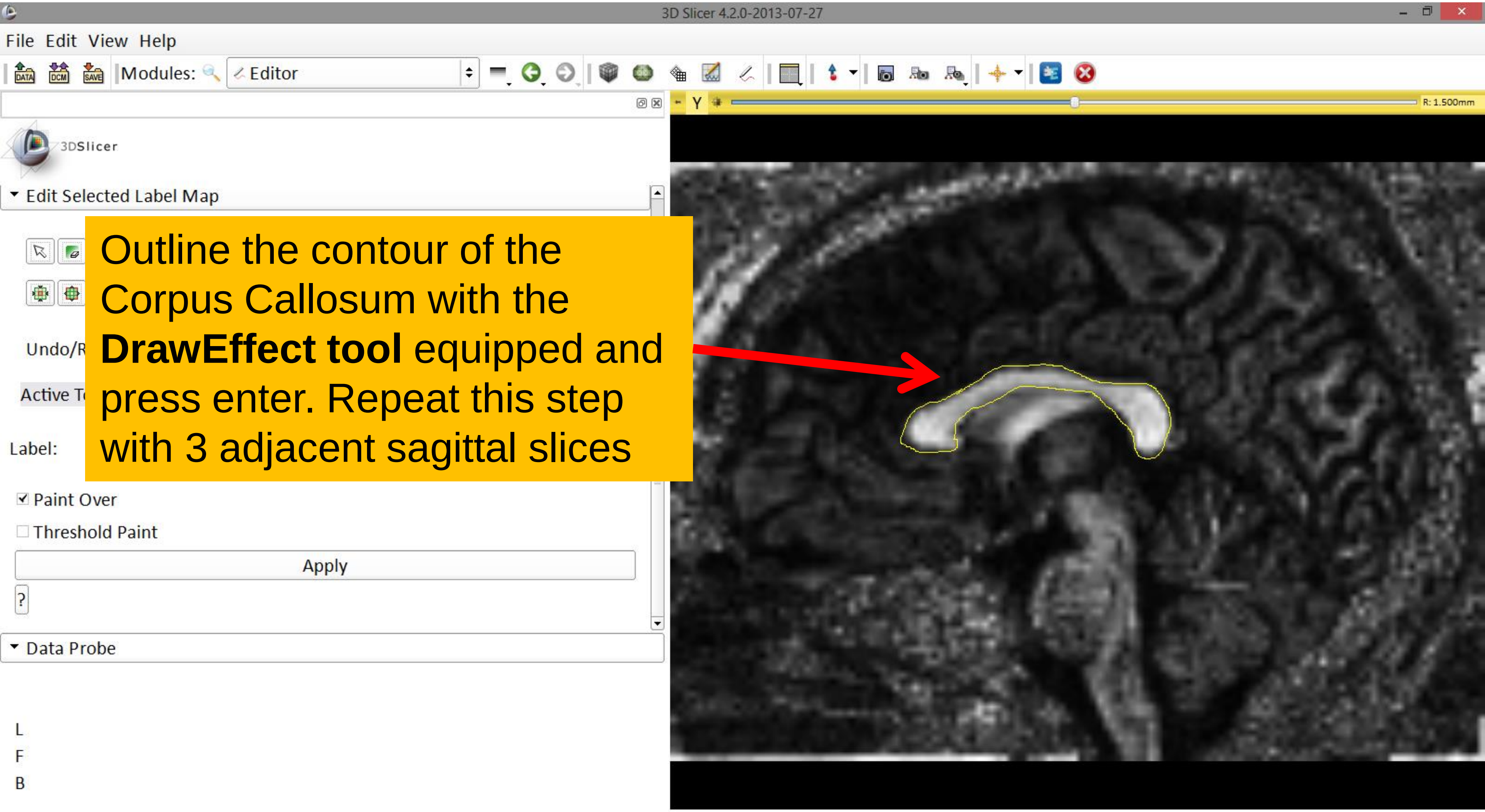



Click on the **fit to screen icon** to adjust the dimensions of the yellow slice viewer to fit the screen

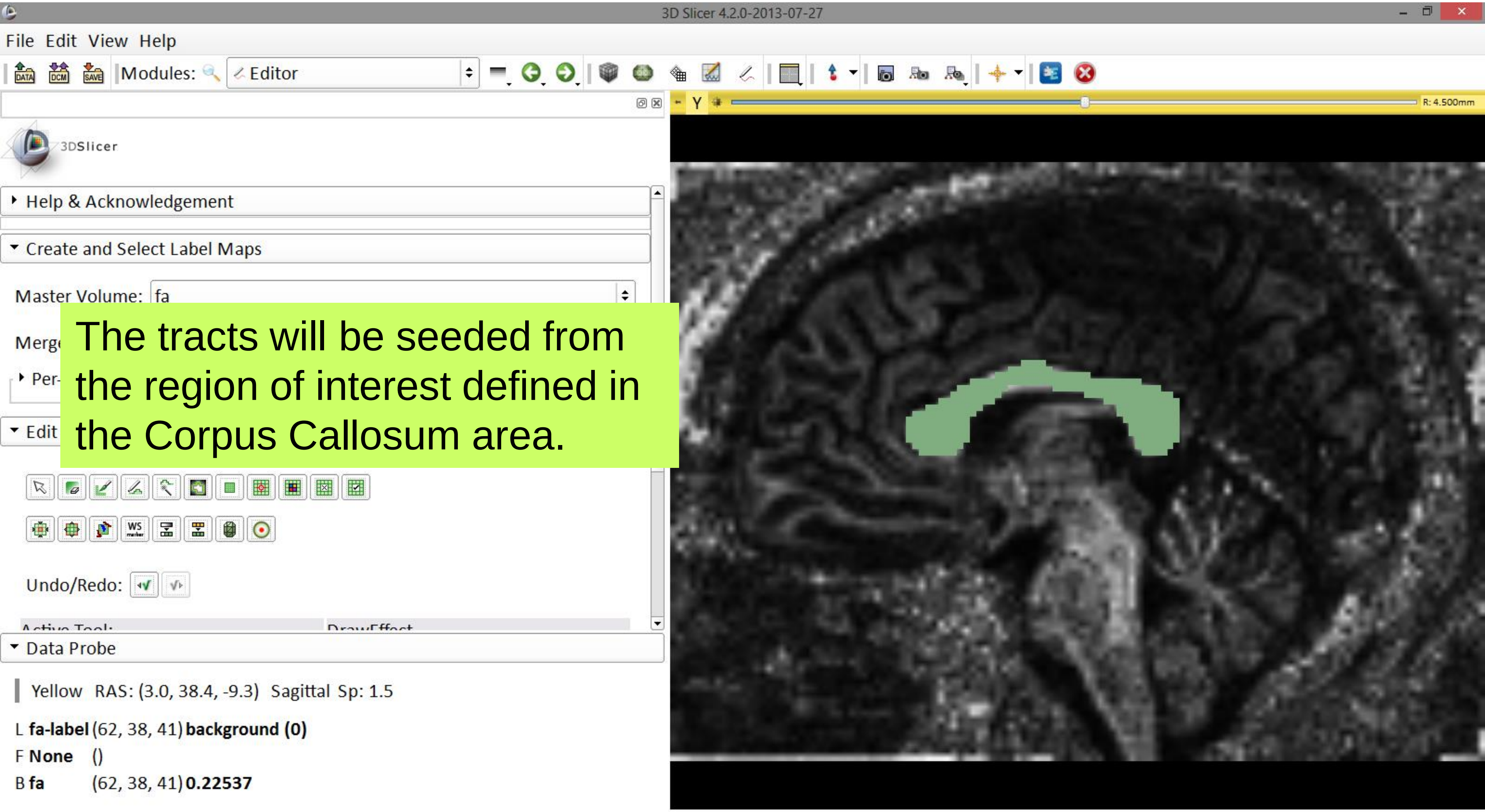
# Diffusion MRI tractography



# Diffusion MRI tractography

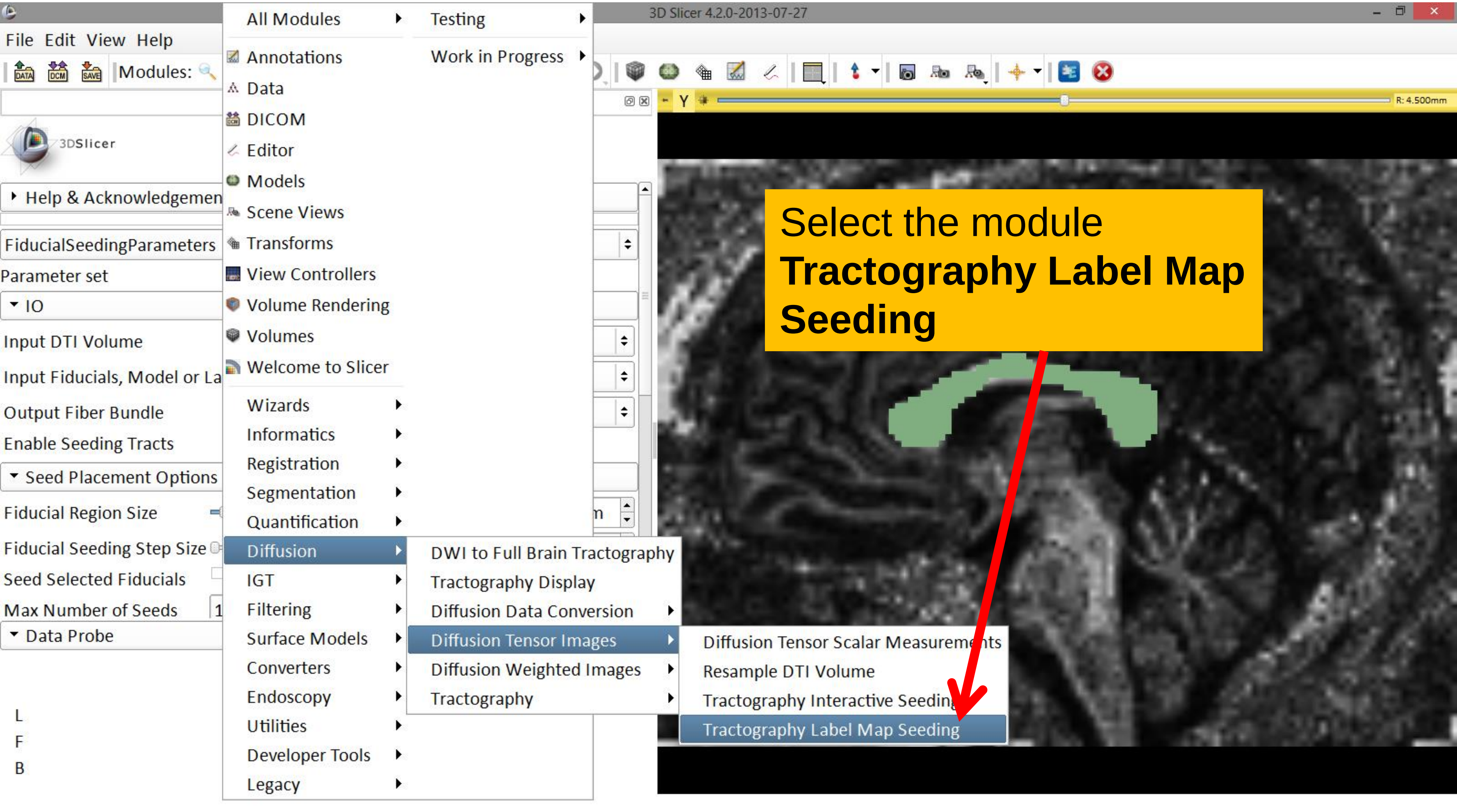


# Diffusion MRI tractography

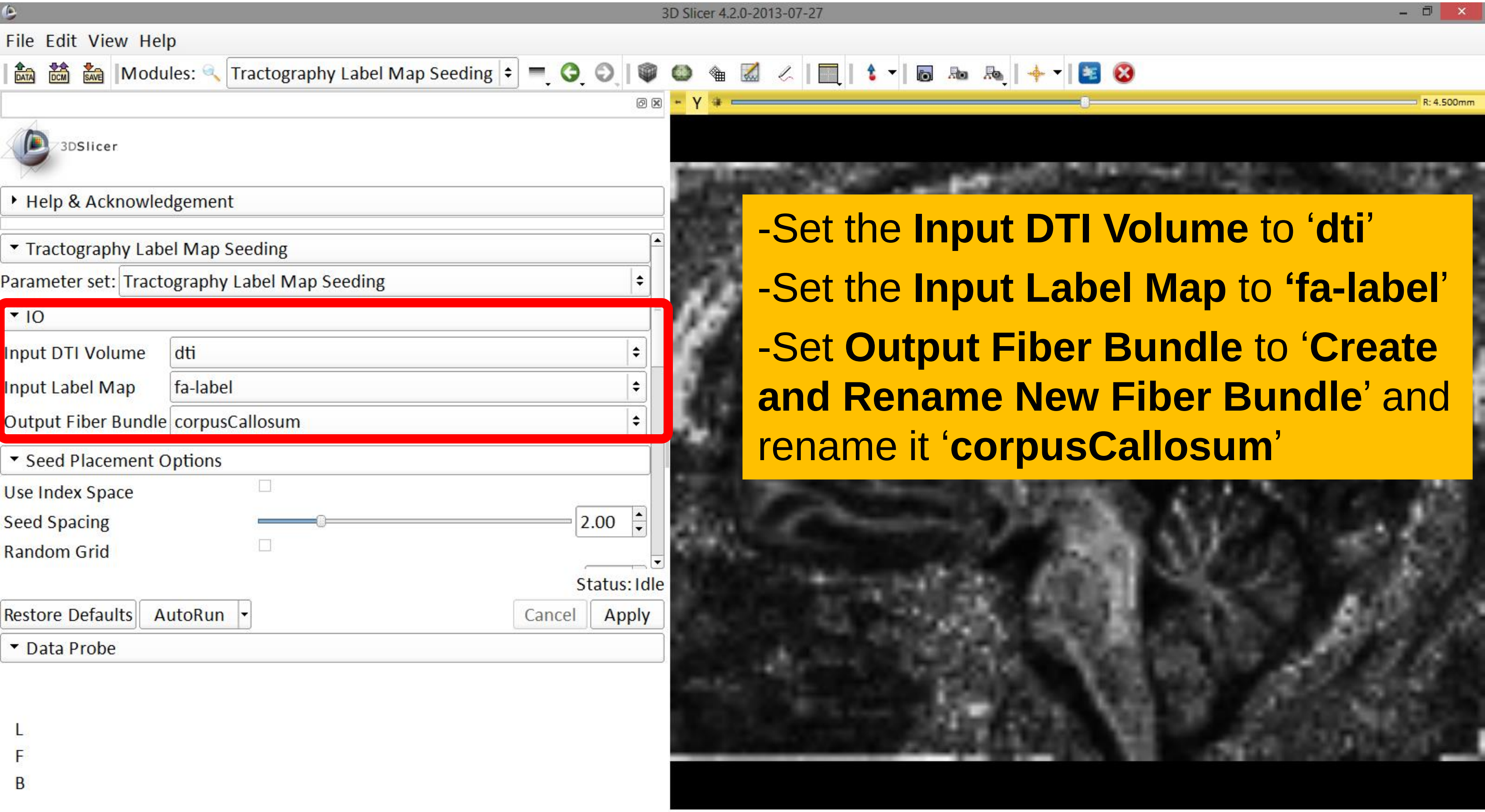



The tracts will be seeded from the region of interest defined in the Corpus Callosum area.

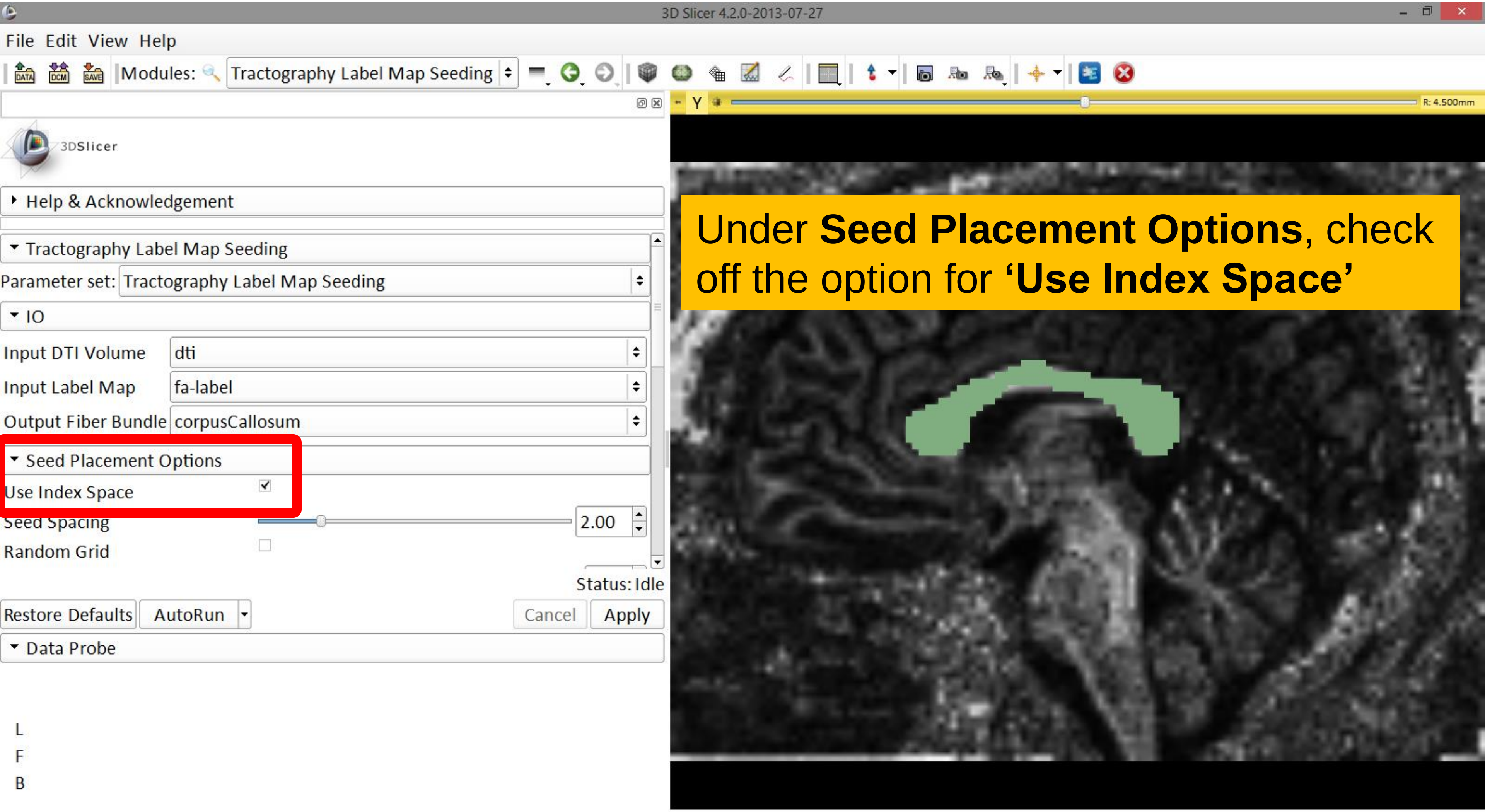
# Diffusion MRI tractography



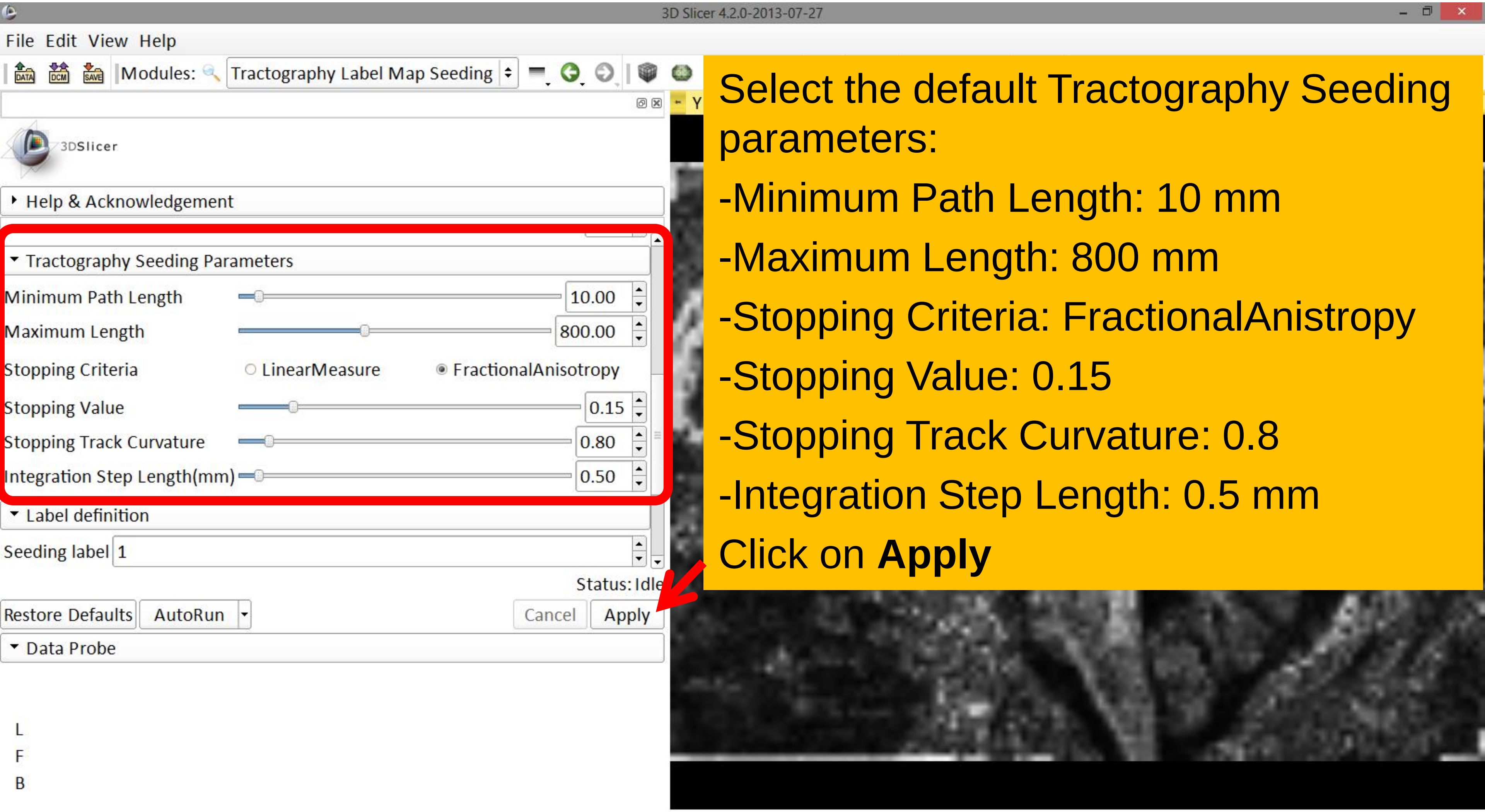
# Diffusion MRI tractography



# 3D Visualization: Glyphs



# 3D Visualization: Glyphs




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**

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  NIH P41RR013218

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