Diffusion MRI Analysis

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Brain Anatomy

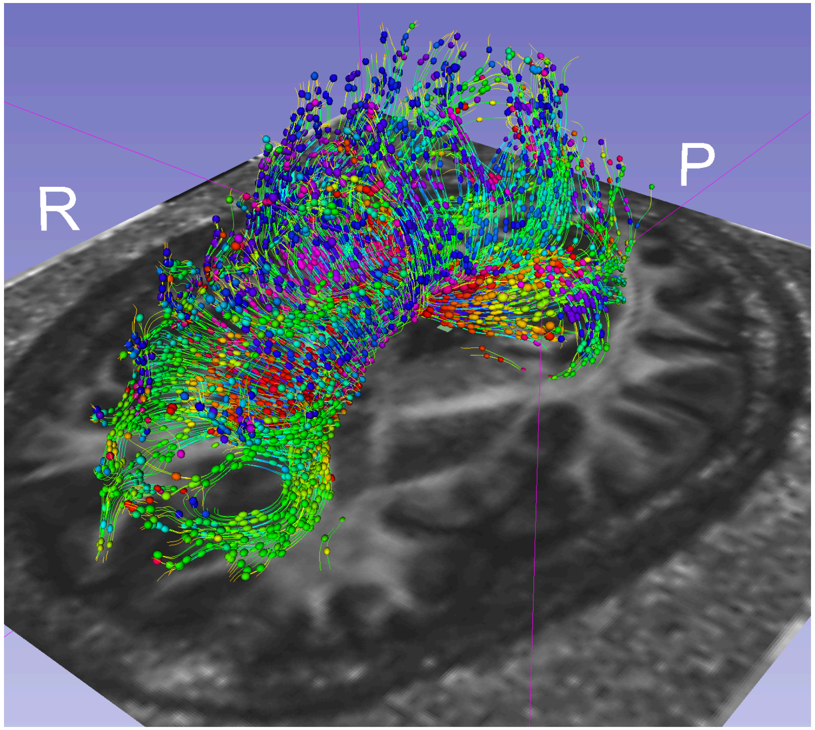
- White matter ~45% of the brain
- Myelinated nerve fibers

(~ 10 µm axon diameter)

White Matter Exploration

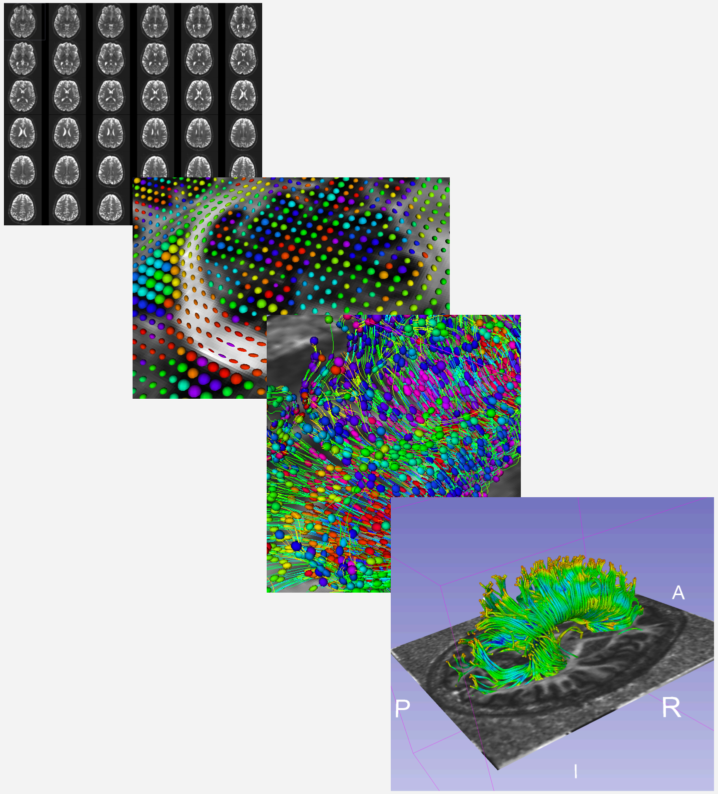
Jules Joseph Dejerine (*Anatomie des centres nerveux* (Paris, 1890-1901): Atlas of Neuroanatomy based on myelin stained preparation

White Matter Exploration



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

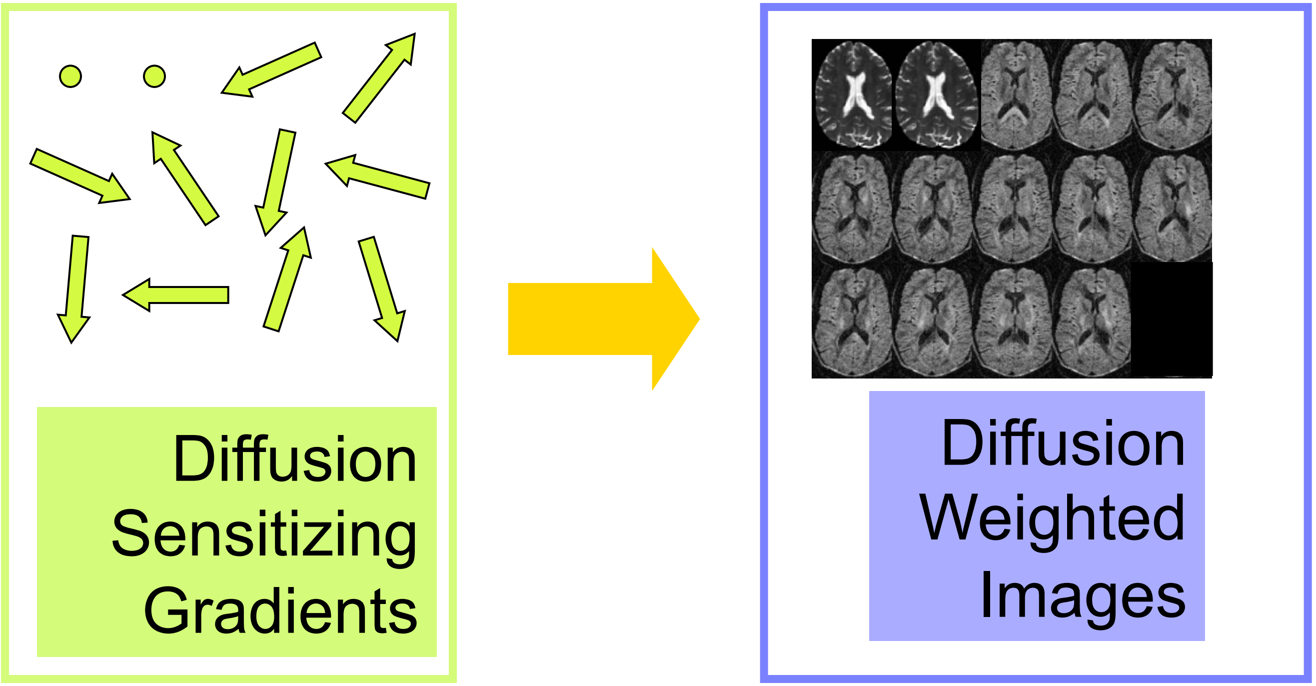
Tutorial Outline



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.



Diffusion Sensitizing Gradients

Diffusion Weighted Images

The dataset is available on the Slicer Training Compendium (www.slicer.org)

Tutorial software

A multi-platform, free and open source software package for visualization and medical image computing

The community of Slicer developers is proud to announce the release of Slicer 4.0. Find out more...

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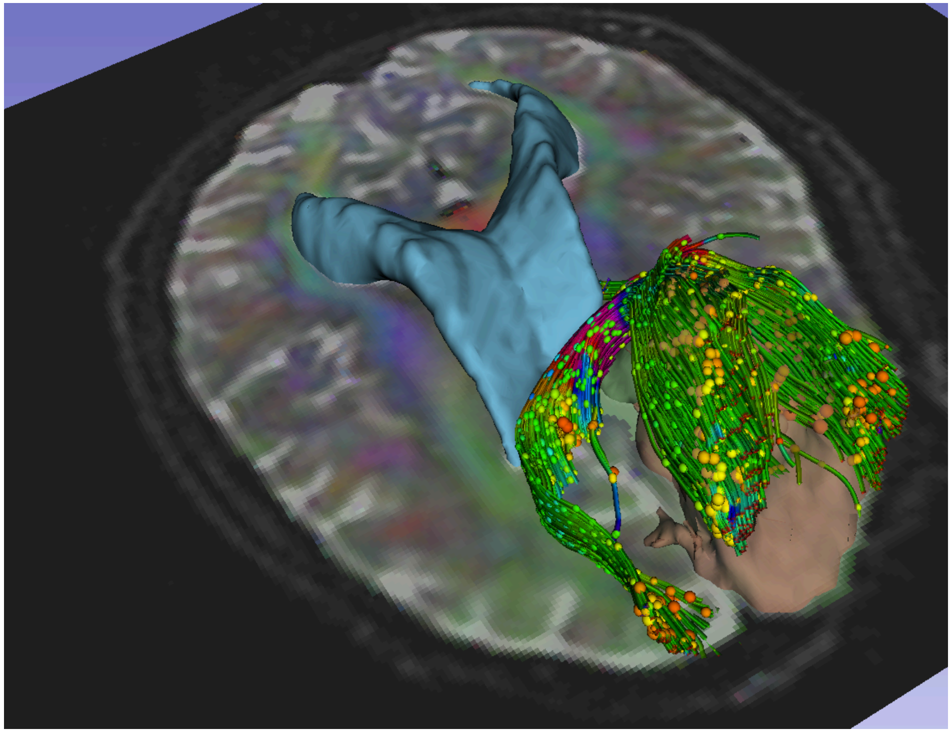
Contact webmaster@bwh.harvard.edu for questions about the use of this site's content.
See here for more information about the web infrastructure.

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

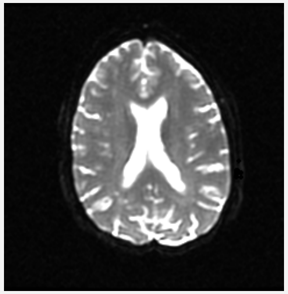
1) Estimate a tensor volume from a set of Diffusion Weighted Images

2) Understand the shape and size of the diffusion ellipsoid

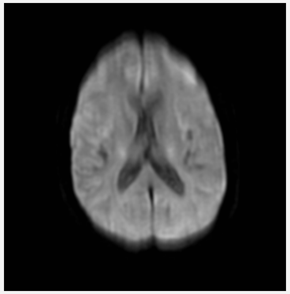
3) Reconstruct DTI tracts from a pre-defined region of interest

4) Interactively visualize DTI tracts seeded from a fiducial

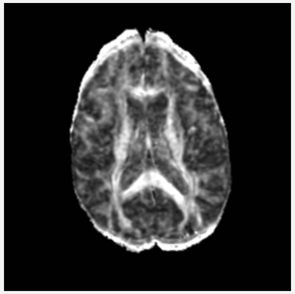
MR Diffusion Analysis Pipeline



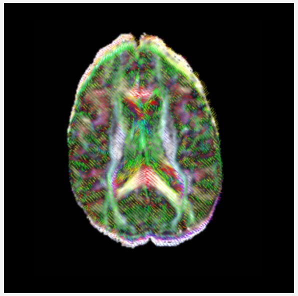
DWI
Acquisition



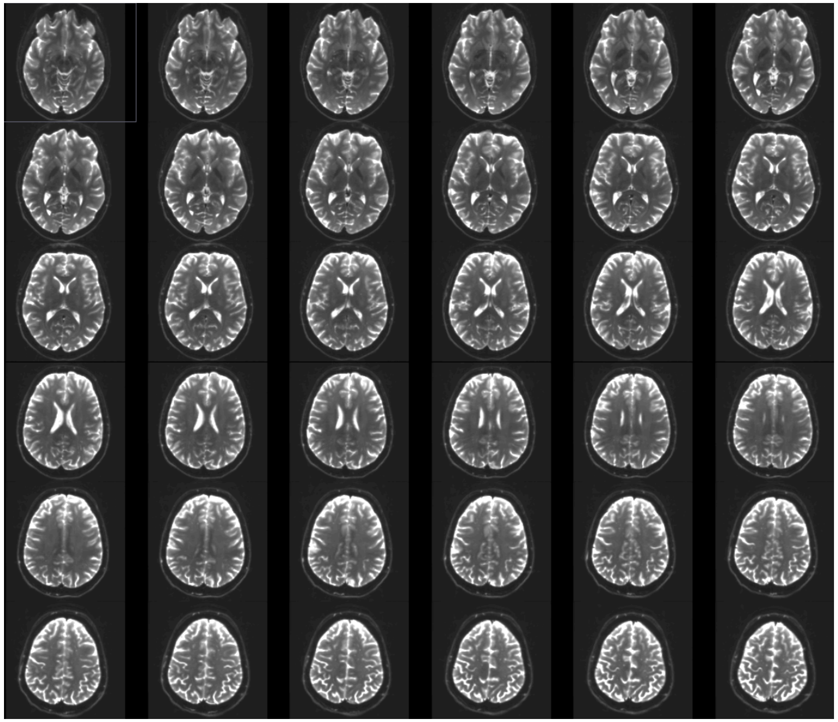
Tensor
Calculation



Scalar
Maps

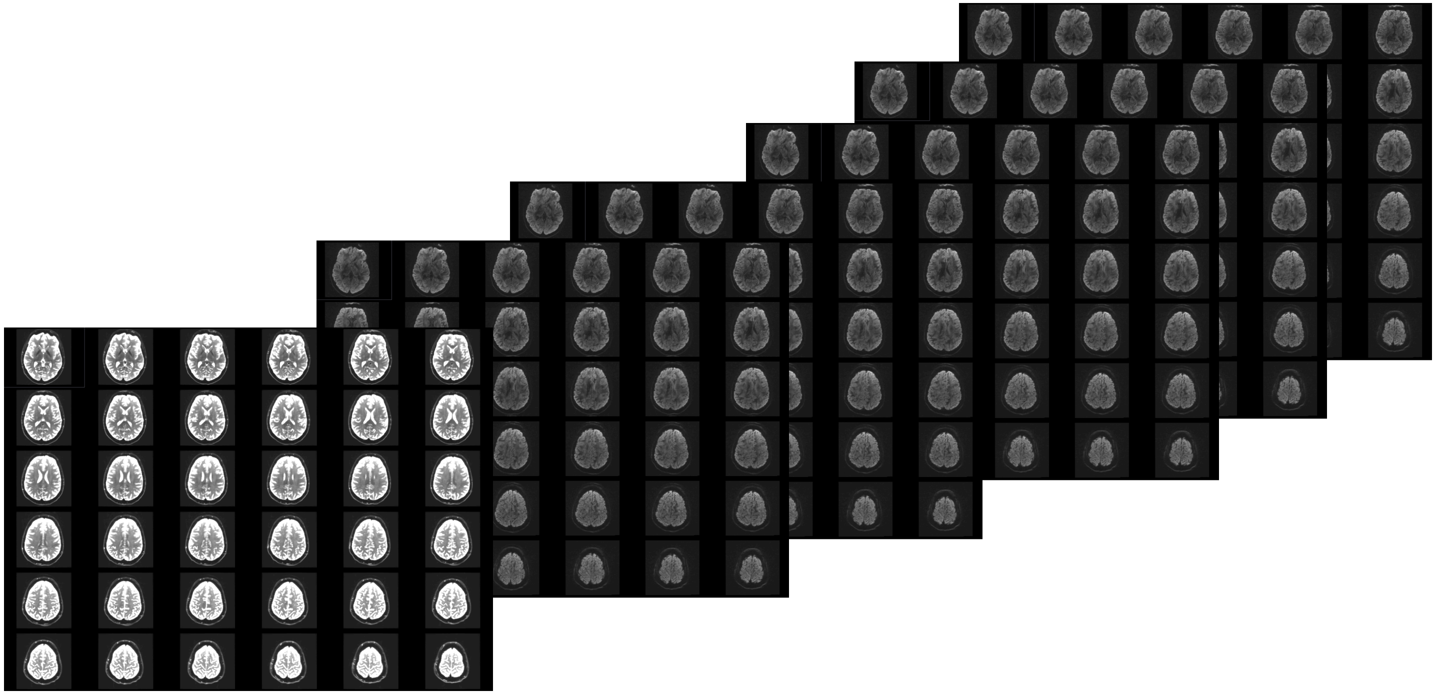


3D
Visualization



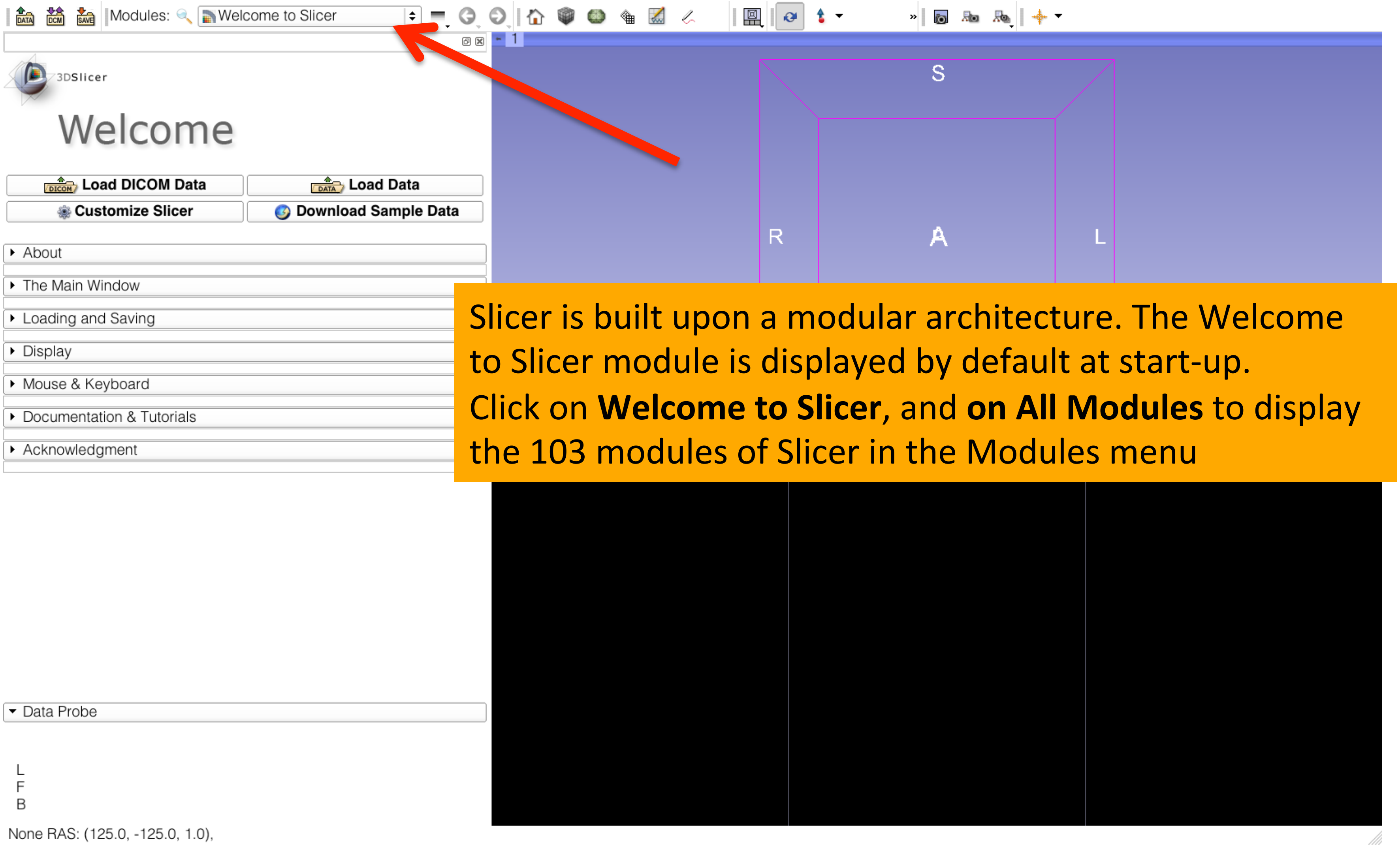
Part 1:
From DWI images to Tensors

Understanding the DWI dataset



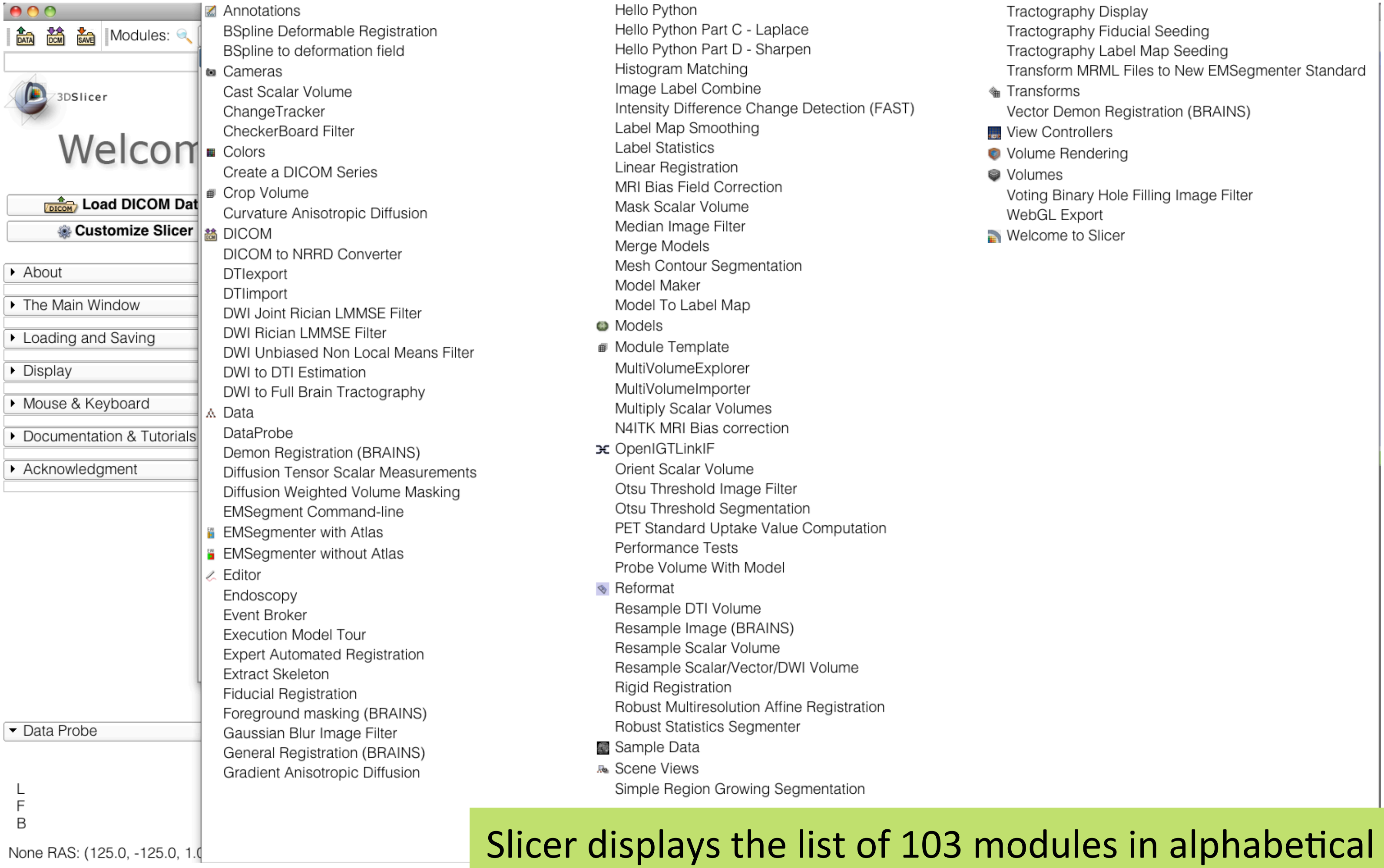
The Diffusion Weighted Imaging (DWI) dataset is composed of 1 volume acquired without diffusion-sensitizing gradient, and 41 volumes acquired with 41 different diffusion-sensitizing gradient directions.

Start the Slicer Software



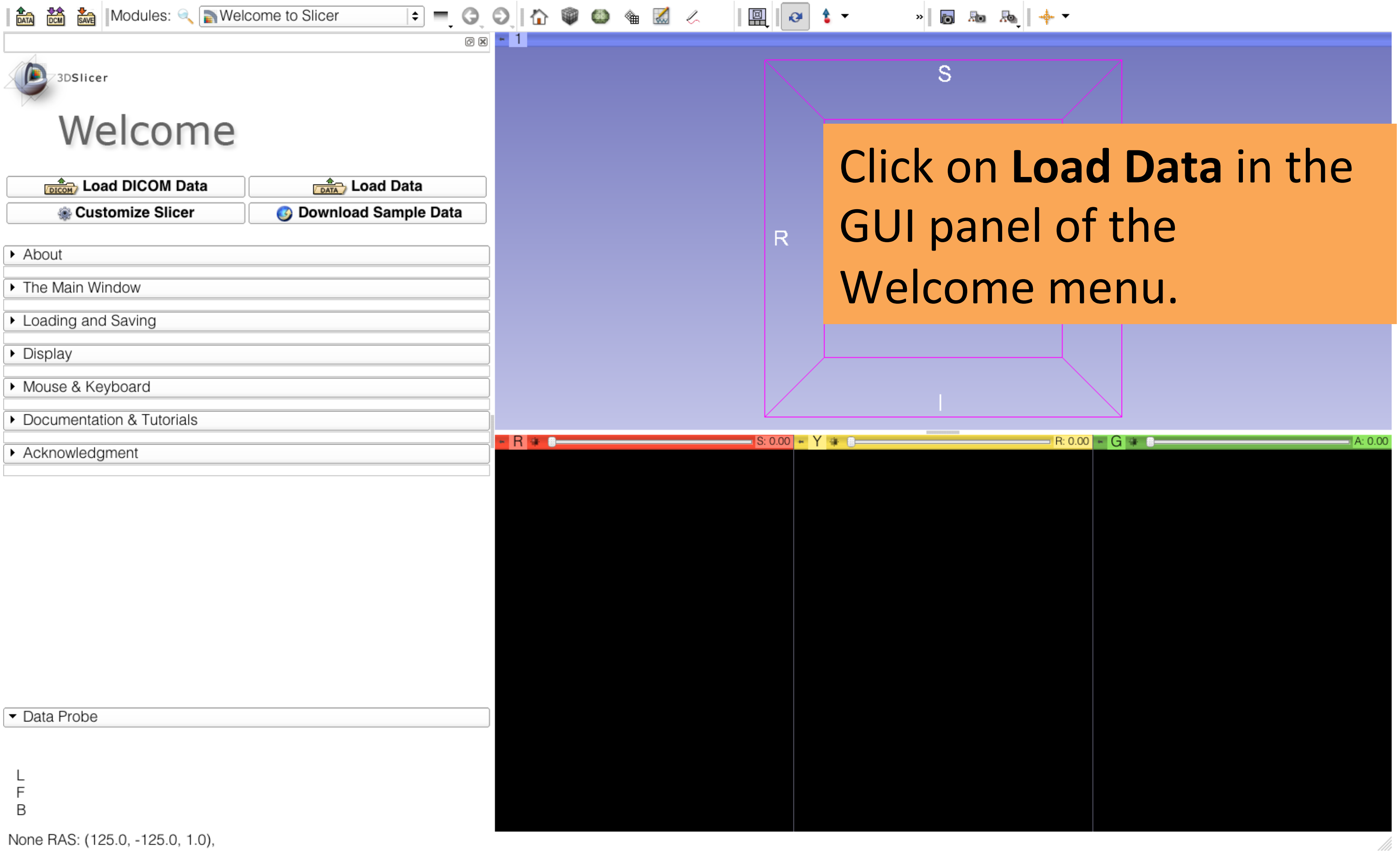
Slicer is built upon a modular architecture. The Welcome to Slicer module is displayed by default at start-up.
Click on **Welcome to Slicer**, and **on All Modules** to display the 103 modules of Slicer in the Modules menu

Start the Slicer software



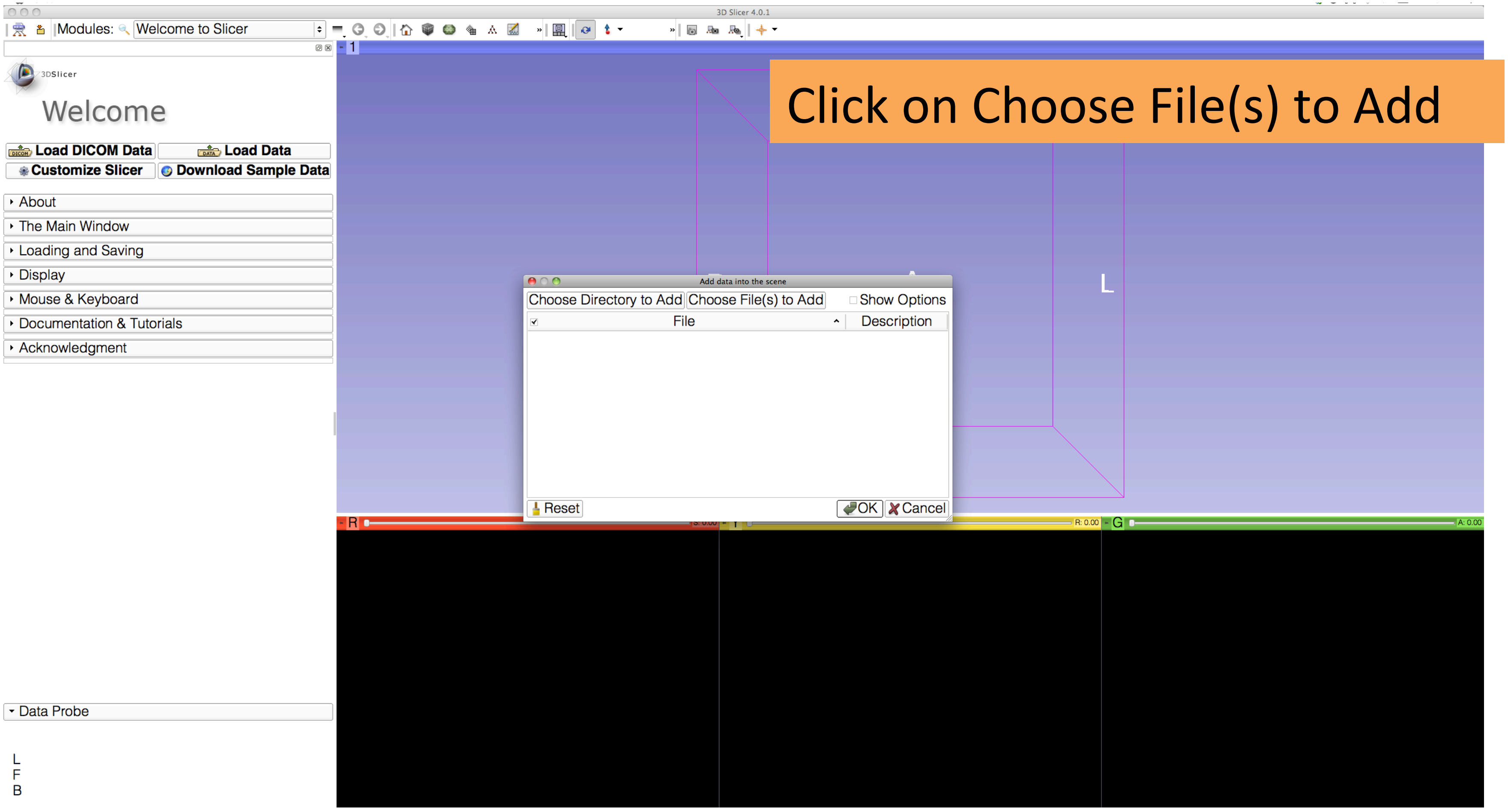
Slicer displays the list of 103 modules in alphabetical order.

Loading the DWI dataset



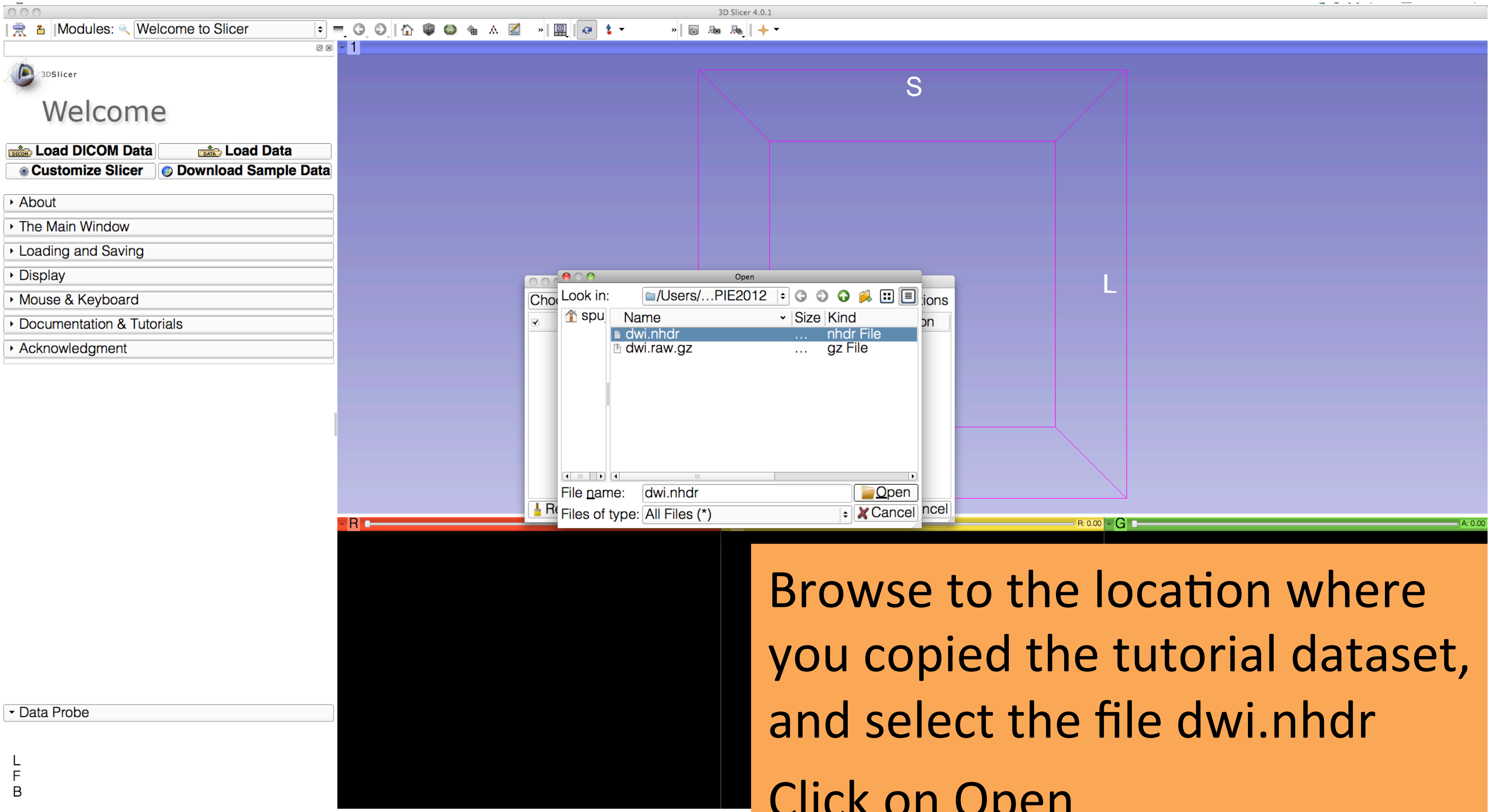
Click on **Load Data** in the GUI panel of the Welcome menu.

Loading the DWI dataset



Click on Choose File(s) to Add

Loading the DWI dataset



Look in: /Users/…PIE2012

Name	Size	Kind
dwi.nhdr	…	nhdr File
dwi.raw.gz	…	gz File

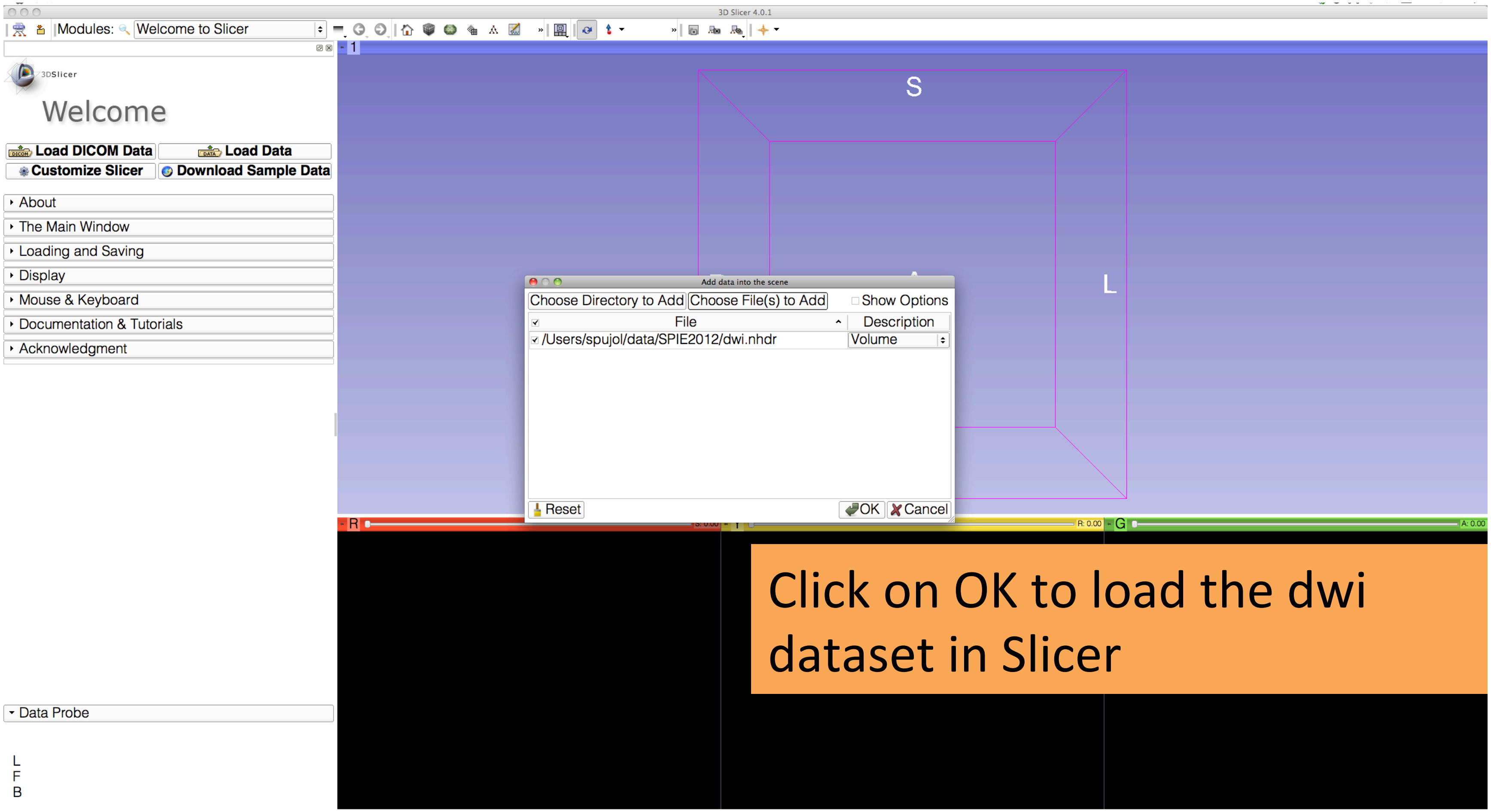
File name: dwi.nhdr

Files of type: All Files (*)

Browse to the location where you copied the tutorial dataset, and select the file dwi.nhdr

Click on Open

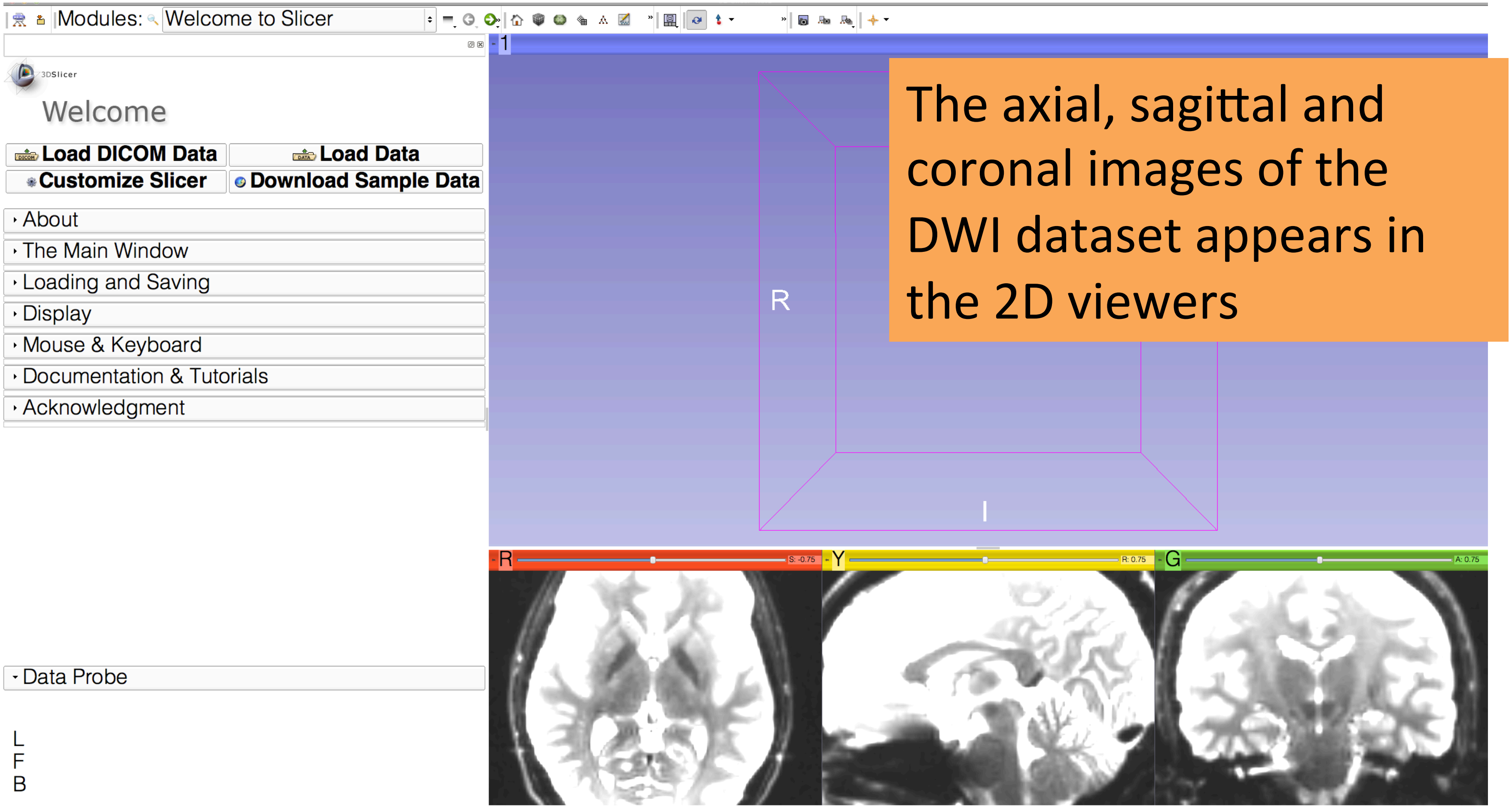
Loading the DWI dataset



☑	File	Description
☑	/Users/spujol/data/SPIE2012/dwi.nhdr	Volume

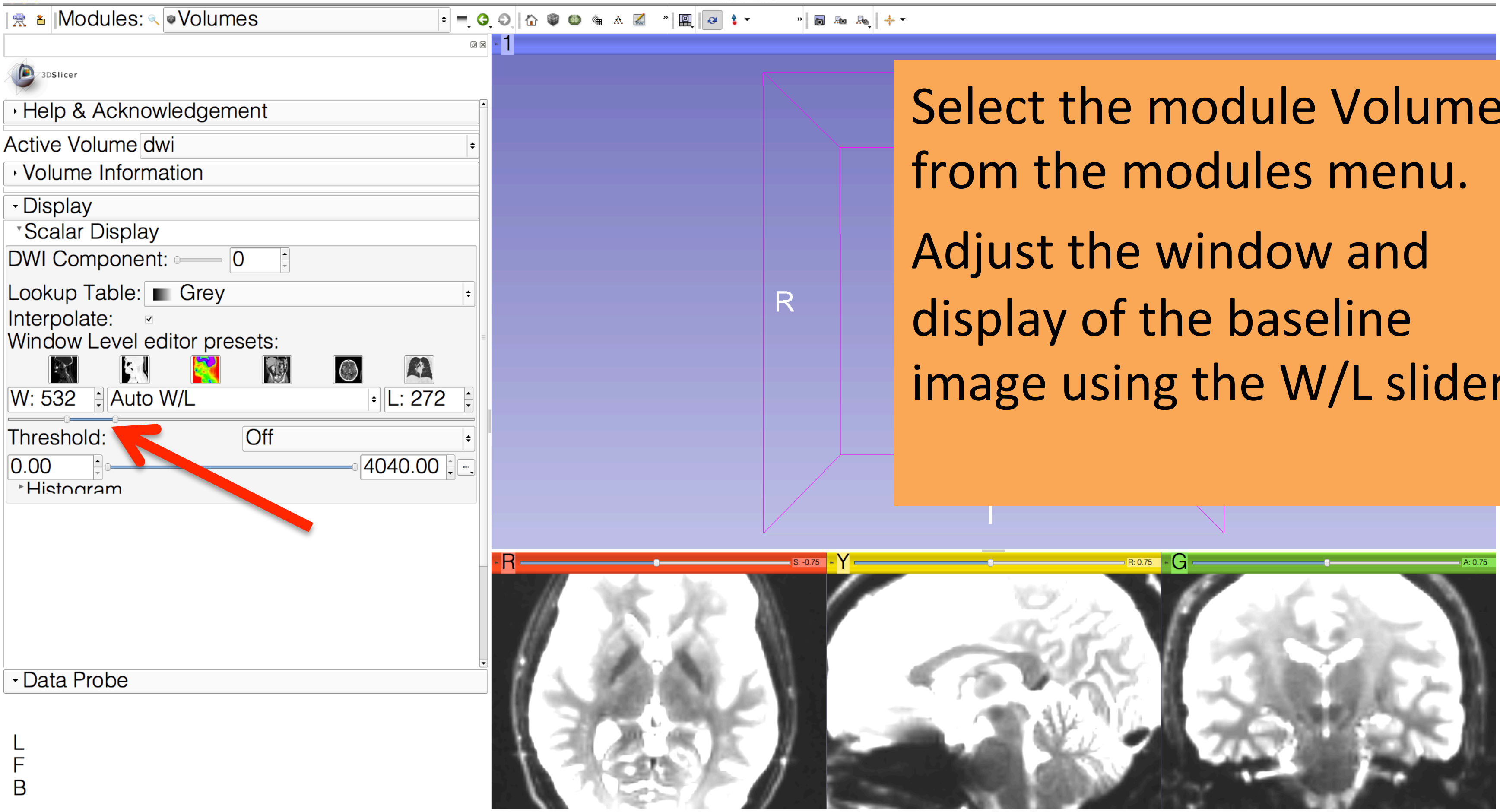
Click on OK to load the dwi dataset in Slicer

Loading the DWI dataset



The axial, sagittal and coronal images of the DWI dataset appears in the 2D viewers

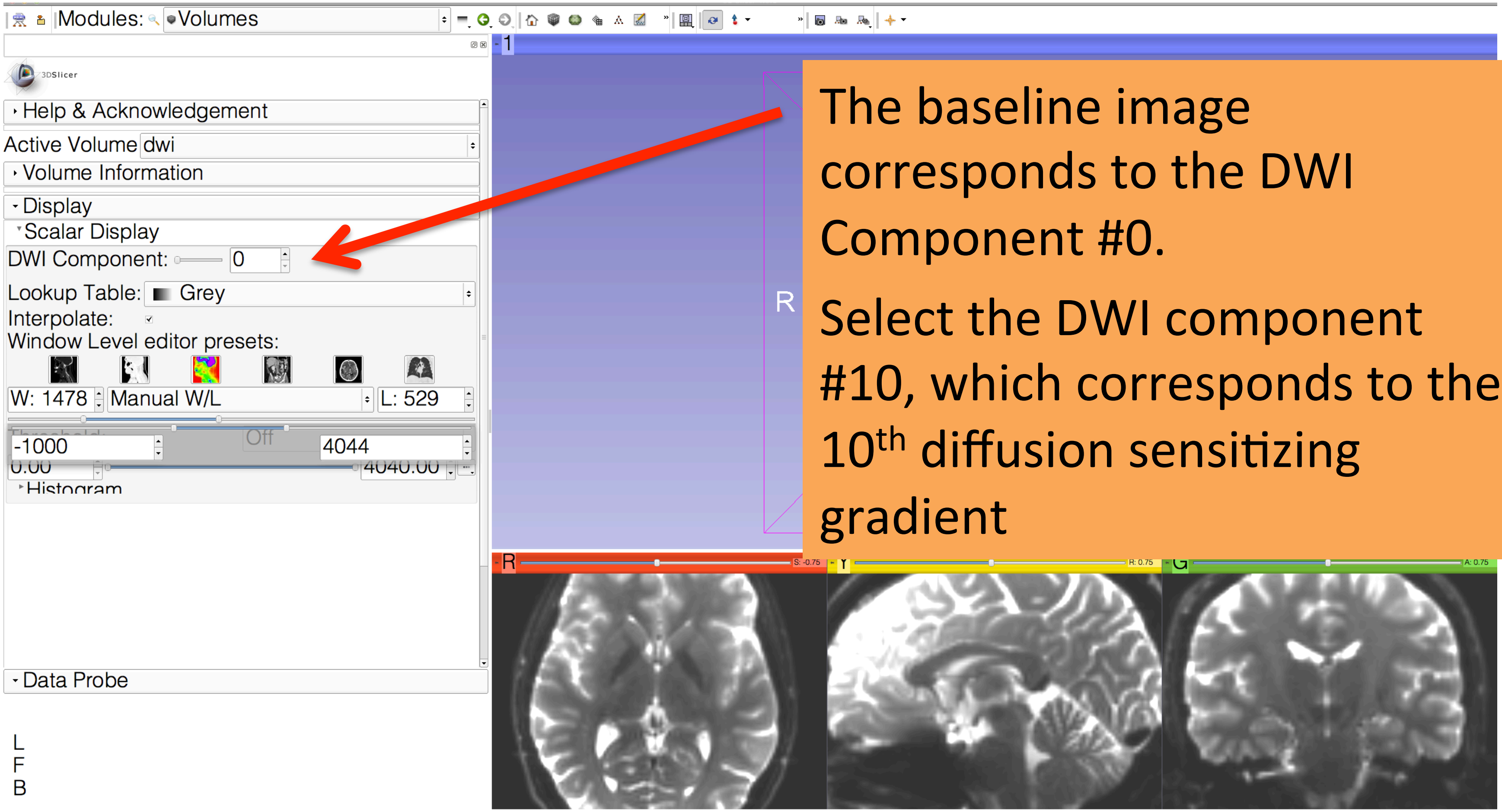
Adjusting Window and Level



Select the module Volumes from the modules menu.

Adjust the window and display of the baseline image using the W/L slider

Exploring the DWI dataset



Modules: Volumes

Active Volume dwi

DWI Component: 0

Lookup Table: Grey

Interpolate: ☑

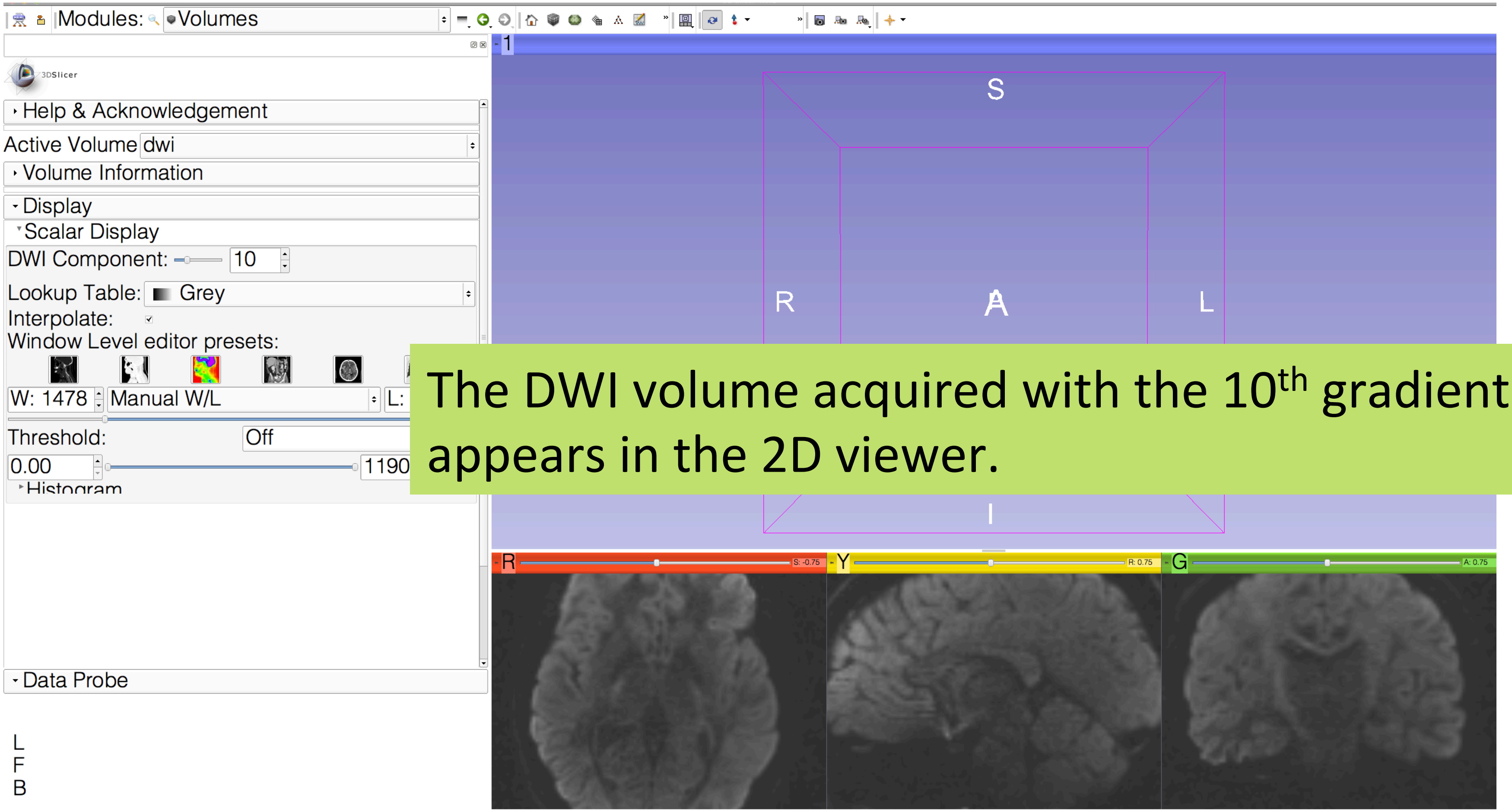
W: 1478 Manual W/L L: 529

-1000 Off 4044

The baseline image corresponds to the DWI Component #0.

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

Exploring the DWI dataset



Modules: Volumes

Active Volume: dwi

DWI Component: 10

Lookup Table: Grey

Interpolate: ☑

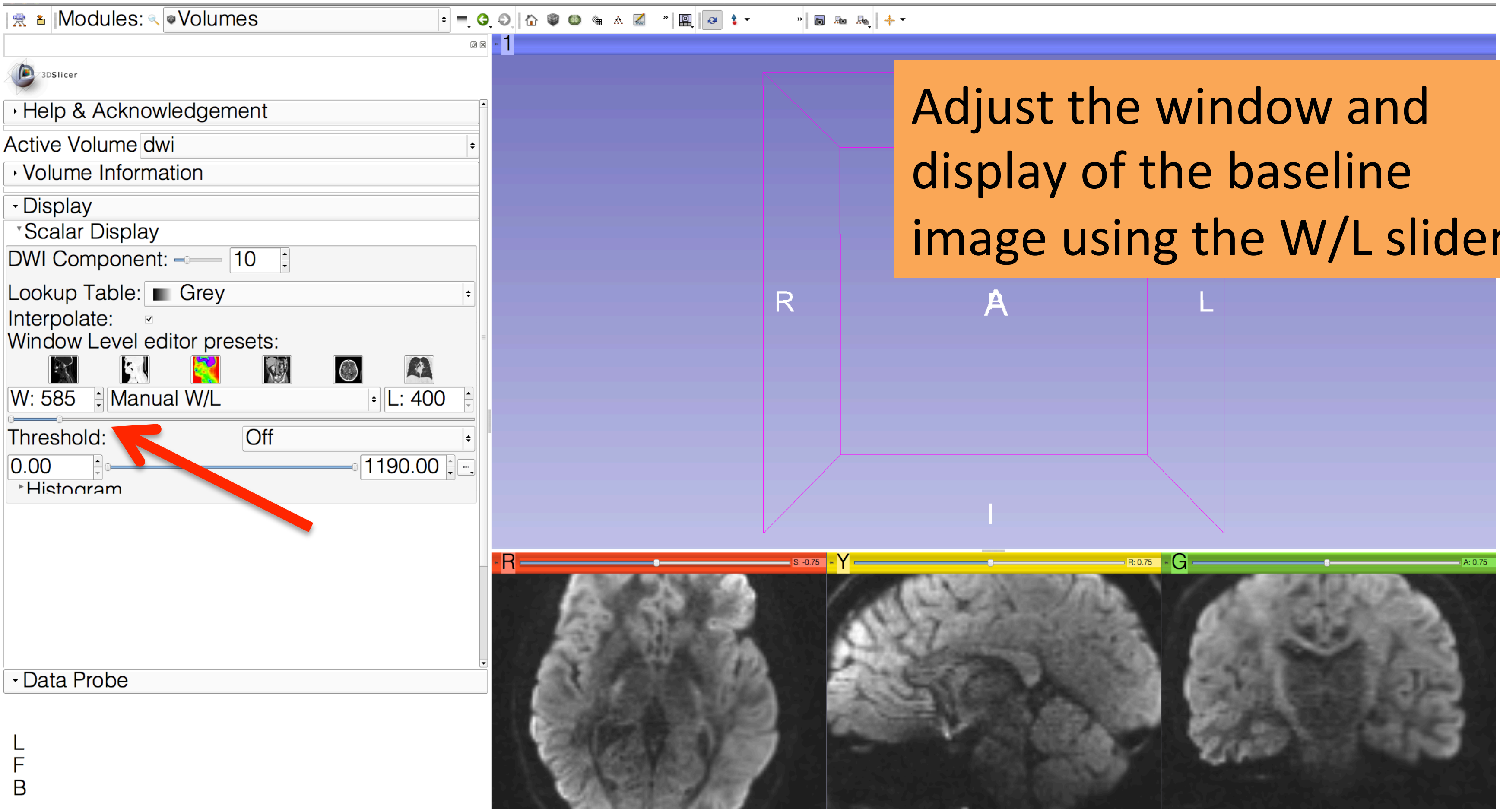
W: 1478 Manual W/L L:

Threshold: Off

0.00 1190

The DWI volume acquired with the 10th gradient appears in the 2D viewer.

Exploring the DWI dataset



Modules: Volumes

Active Volume: dwi

DWI Component: 10

Lookup Table: Grey

Interpolate: ☑

W: 585

Manual W/L

L: 400

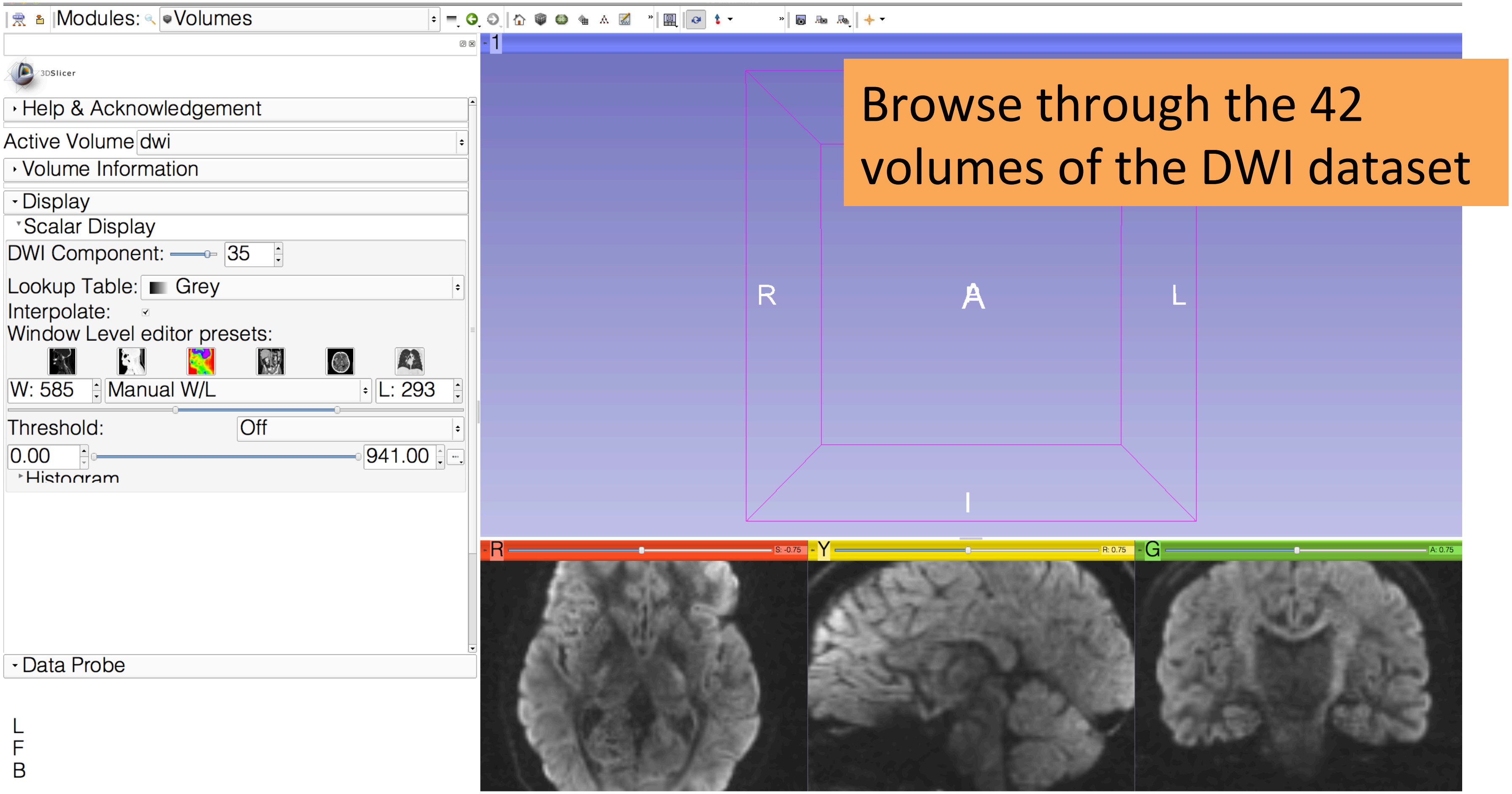
Threshold: Off

0.00

1190.00

Adjust the window and display of the baseline image using the W/L slider

Exploring the DWI dataset



Modules: Volumes

Active Volume dwi

DWI Component: 35

Lookup Table: Grey

Interpolate: ☑

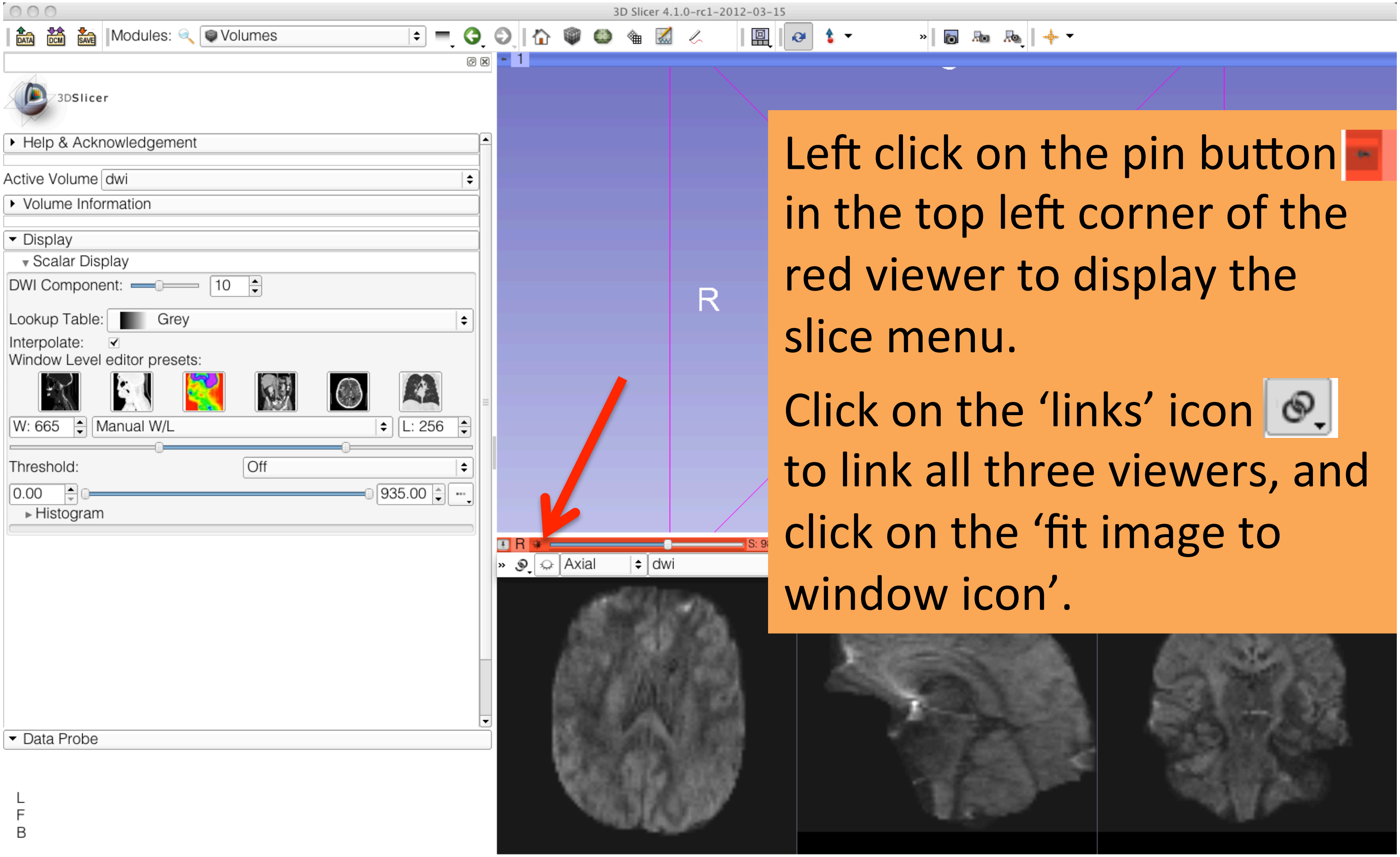
W: 585 Manual W/L L: 293

Threshold: Off

0.00 941.00

Browse through the 42 volumes of the DWI dataset

Exploring the DWI dataset



Active Volume: dwi

DWI Component: 10

Lookup Table: Grey

Interpolate: ☑

W: 665 Manual W/L L: 256

Threshold: Off

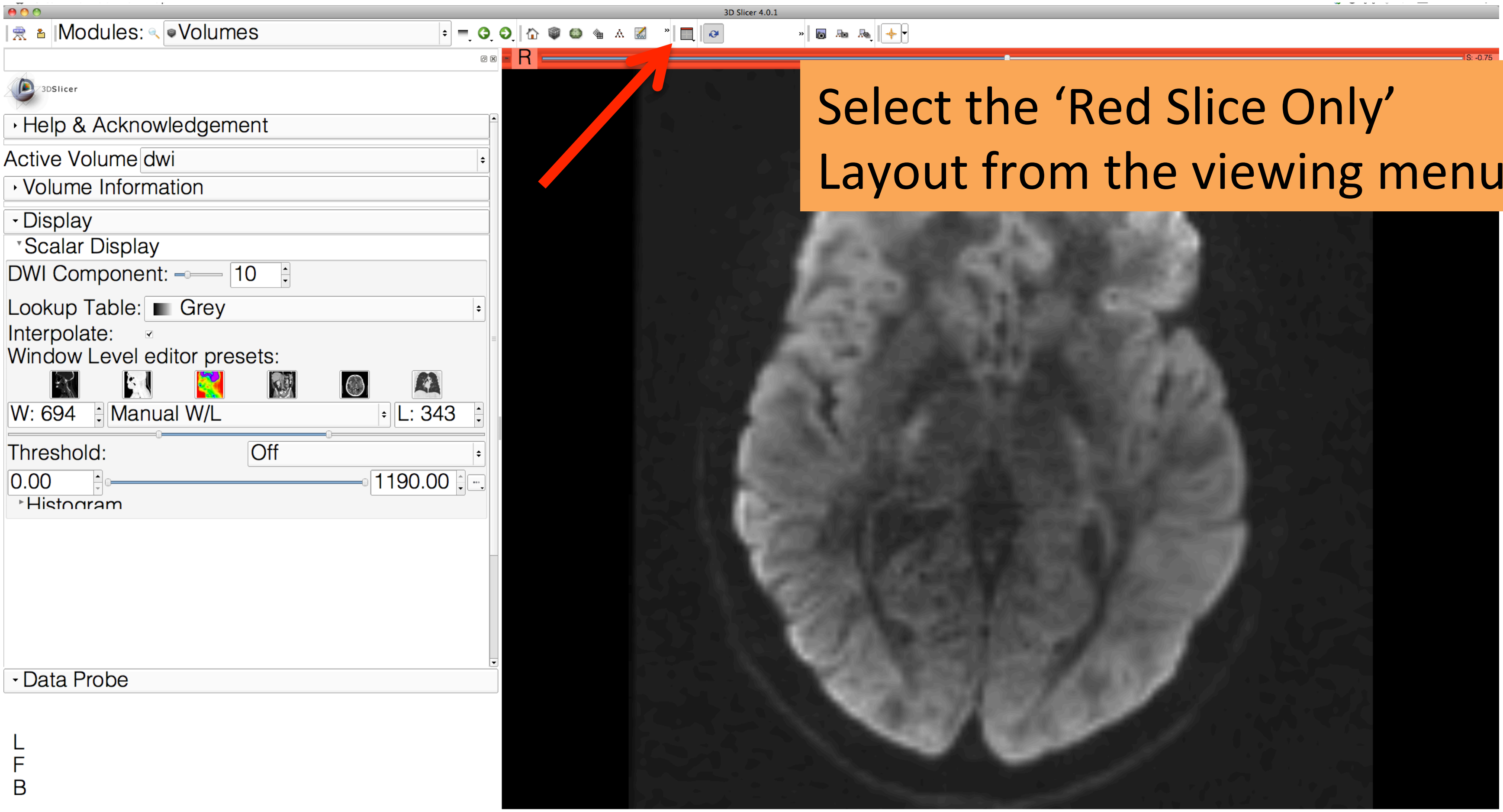
0.00 935.00

Axial dwi

Left click on the pin button in the top left corner of the red viewer to display the slice menu.

Click on the ‘links’ icon to link all three viewers, and click on the ‘fit image to window icon’.

Exploring the DWI dataset



Active Volume dwi

DWI Component: 10

Lookup Table: Grey

Interpolate: ☑

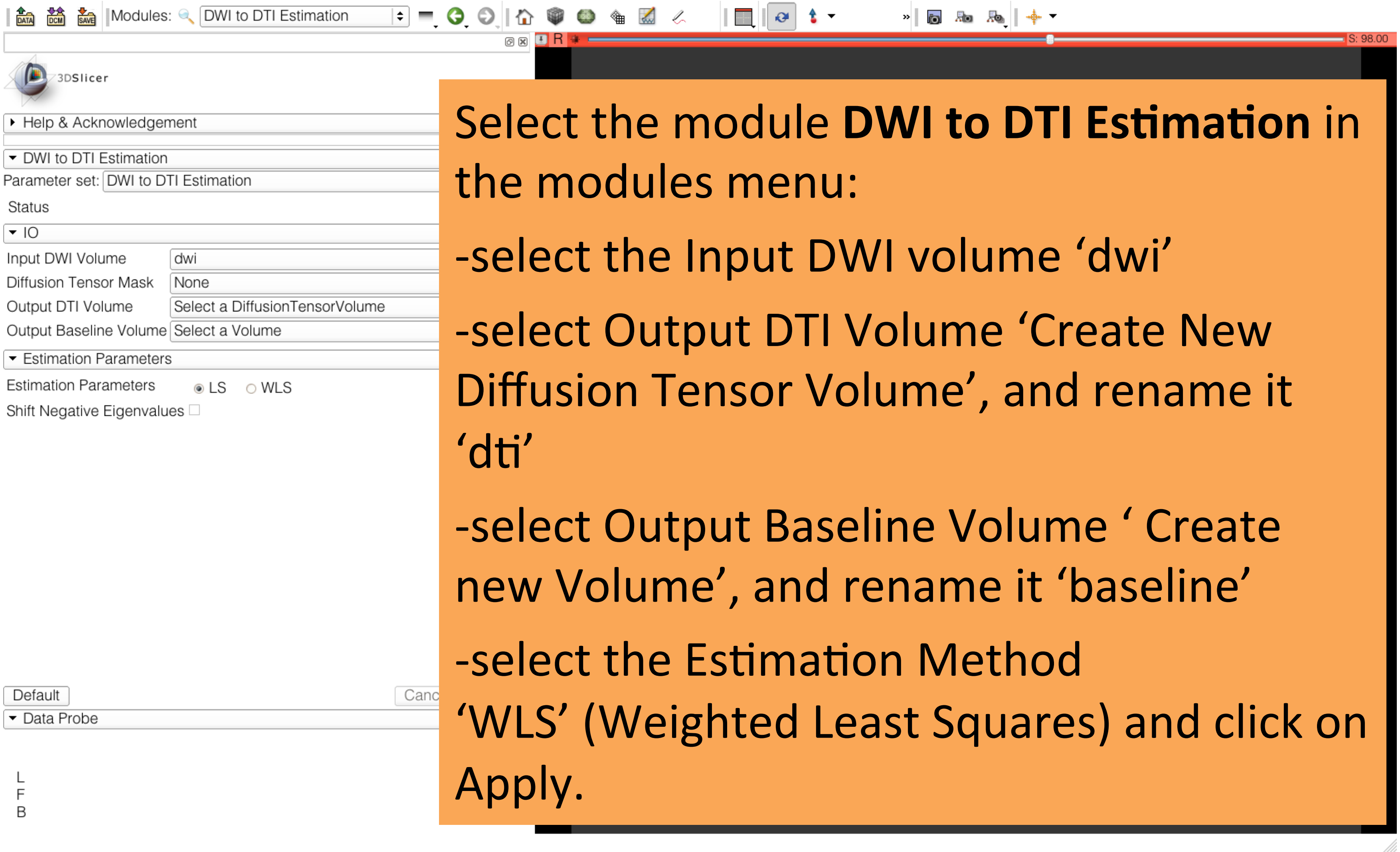
W: 694 Manual W/L L: 343

Threshold: Off

0.00 1190.00

Select the ‘Red Slice Only’ Layout from the viewing menu

Diffusion Tensor Estimation



Modules: DWI to DTI Estimation

Parameter set: DWI to DTI Estimation

Input DWI Volume: dwi

Diffusion Tensor Mask: None

Output DTI Volume: Select a DiffusionTensorVolume

Output Baseline Volume: Select a Volume

Estimation Parameters: ● LS ○ WLS

Shift Negative Eigenvalues ☐

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

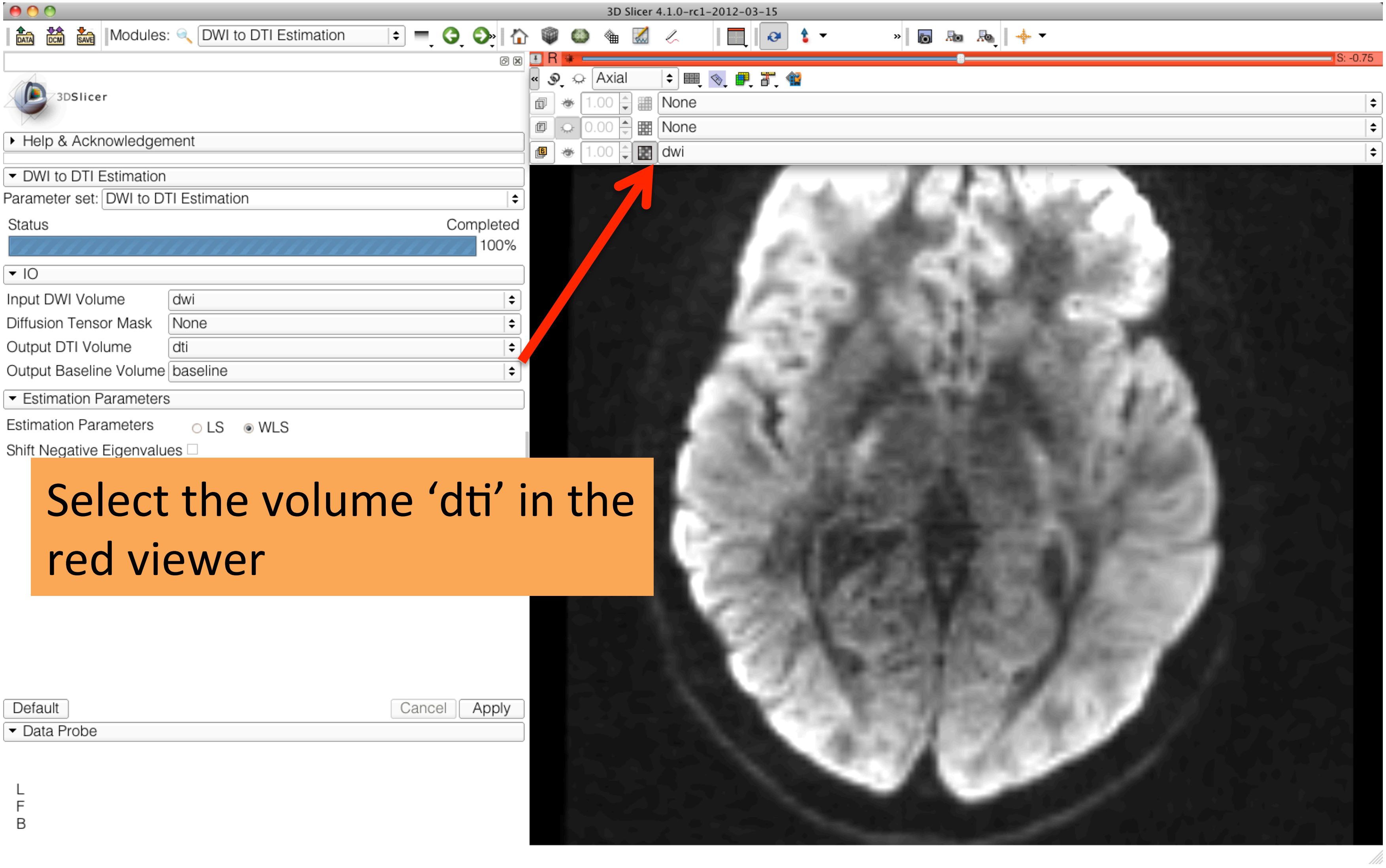
-select the Input DWI volume ‘dwi’

-select Output DTI Volume ‘Create New Diffusion Tensor Volume’, and rename it ‘dti’

-select Output Baseline Volume ‘ Create new Volume’, and rename it ‘baseline’

-select the Estimation Method ‘WLS’ (Weighted Least Squares) and click on Apply.

Diffusion Tensor Estimation



3D Slicer 4.1.0-rc1-2012-03-15

Modules: DWI to DTI Estimation

DWI to DTI Estimation

Parameter set: DWI to DTI Estimation

Status: Completed 100%

IO

Input DWI Volume: dwi

Diffusion Tensor Mask: None

Output DTI Volume: dti

Output Baseline Volume: baseline

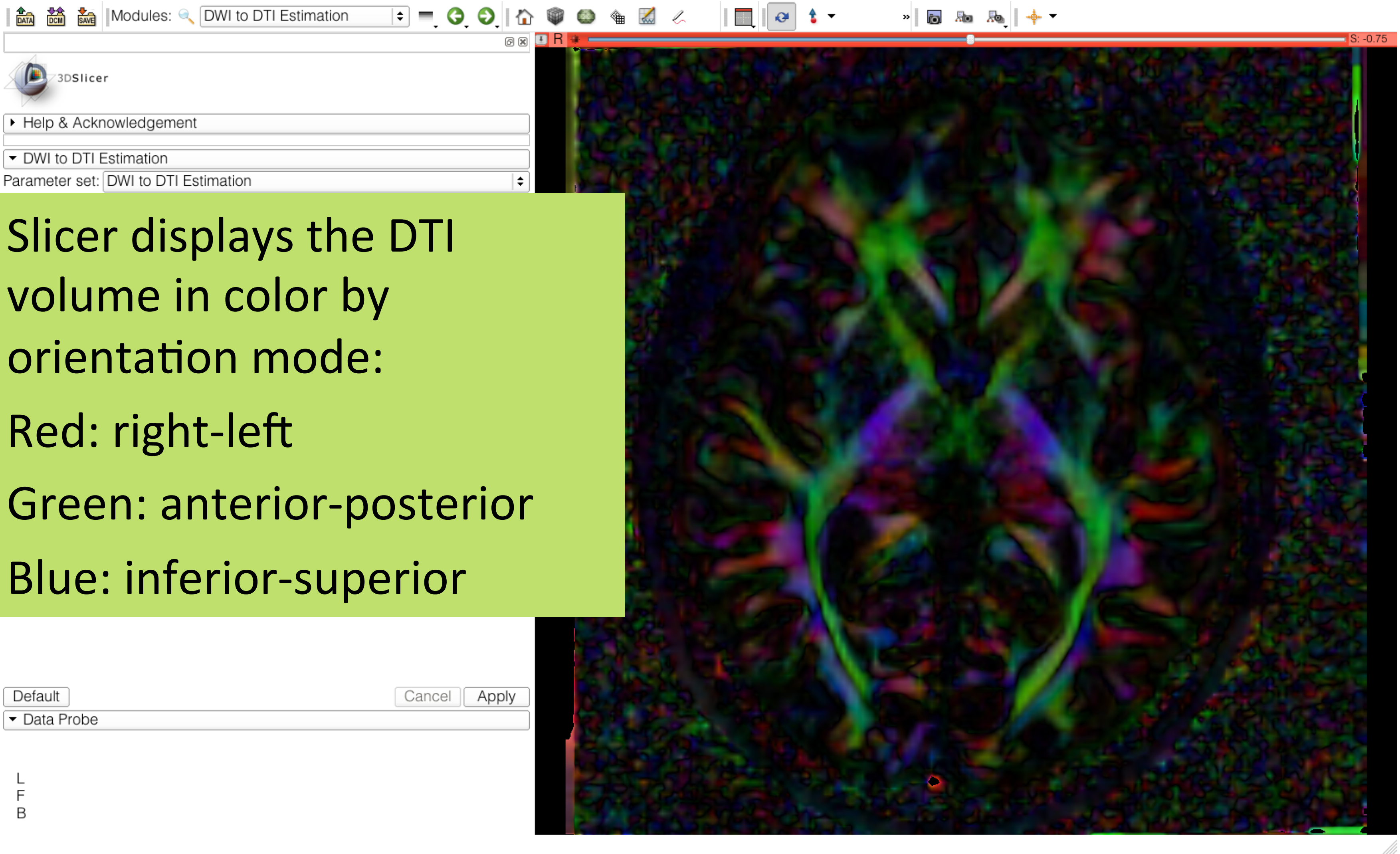
Estimation Parameters

Estimation Parameters: ○ LS ● WLS

Shift Negative Eigenvalues ☐

Select the volume ‘dti’ in the red viewer

Diffusion Tensor Estimation



Parameter set: DWI to DTI Estimation

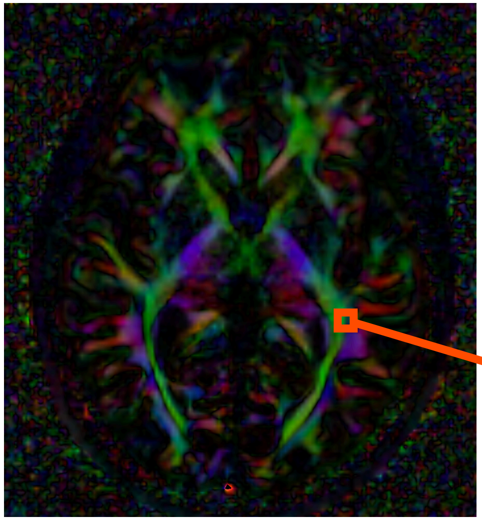
Slicer displays the DTI volume in color by orientation mode:

Red: right-left

Green: anterior-posterior

Blue: inferior-superior

Diffusion Tensor Data



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

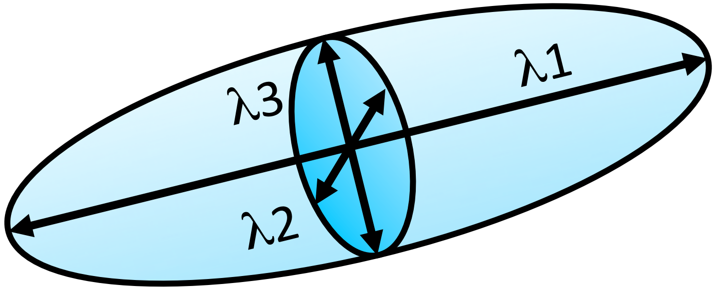
Stejskal-Tanner equation (1965)

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

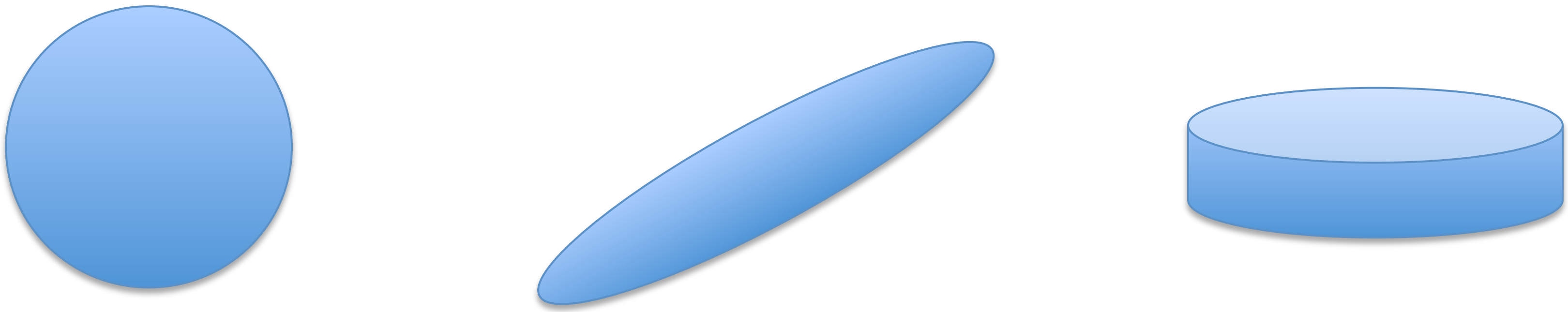
The diffusion tensor D in the voxel (I,J,K) is a 3x3 symmetric matrix.

Diffusion Tensor

- The diffusion tensor <u>D</u> 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



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

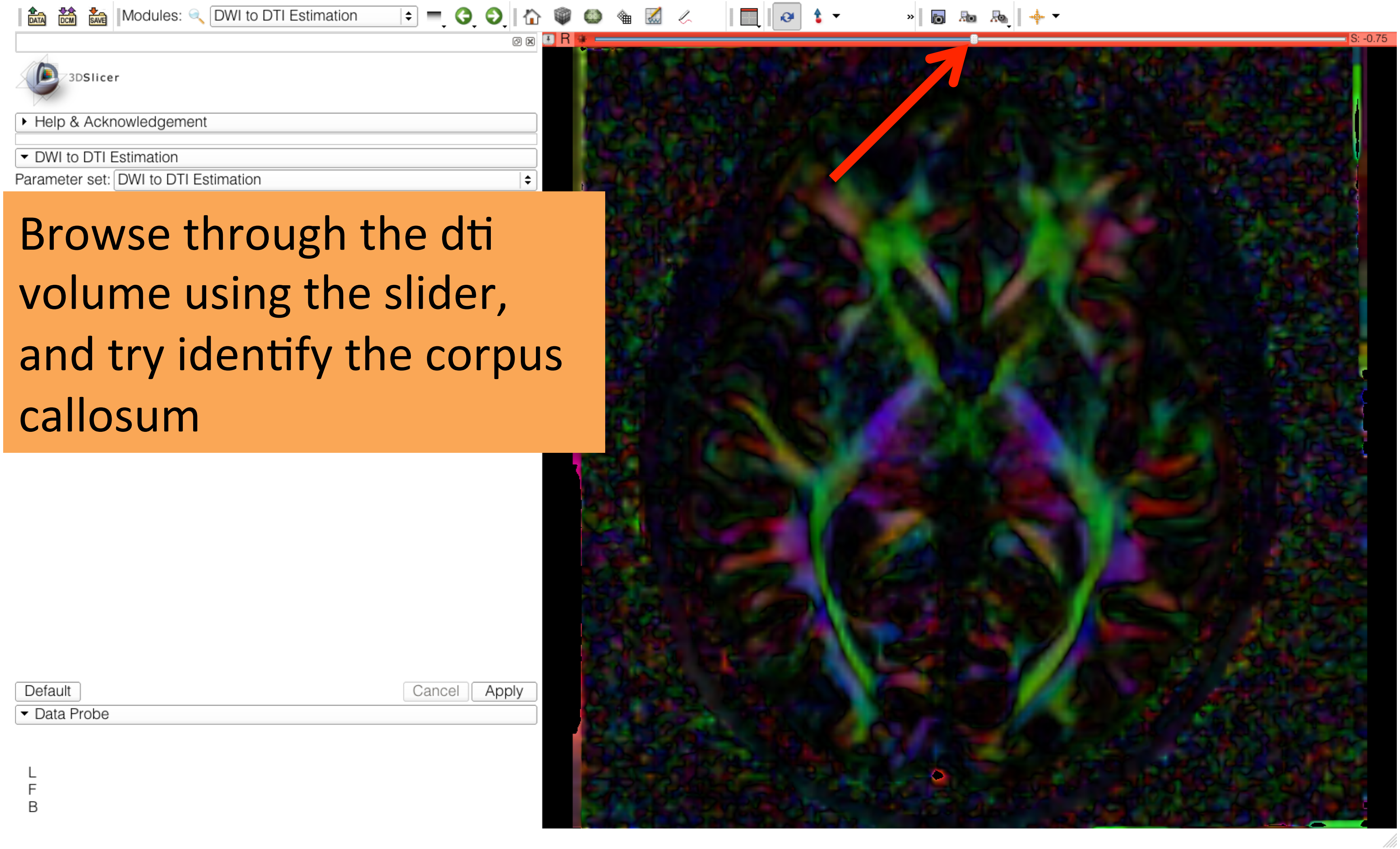
$\lambda 1 >> \lambda 2, \lambda 3$

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

Isotropic media
(CSF, gray matter)

Anisotropic media
(white matter)

Exploring the Diffusion Tensor Data

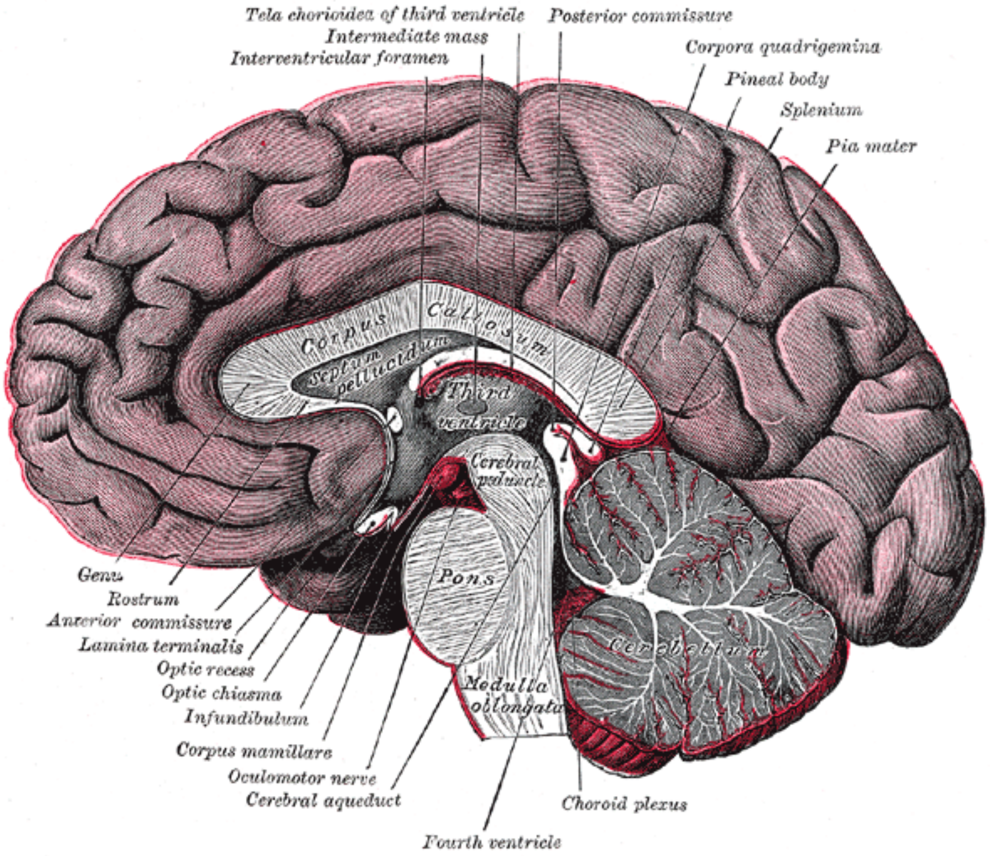


Modules: DWI to DTI Estimation

Parameter set: DWI to DTI Estimation

Browse through the dti volume using the slider, and try identify the corpus callosum

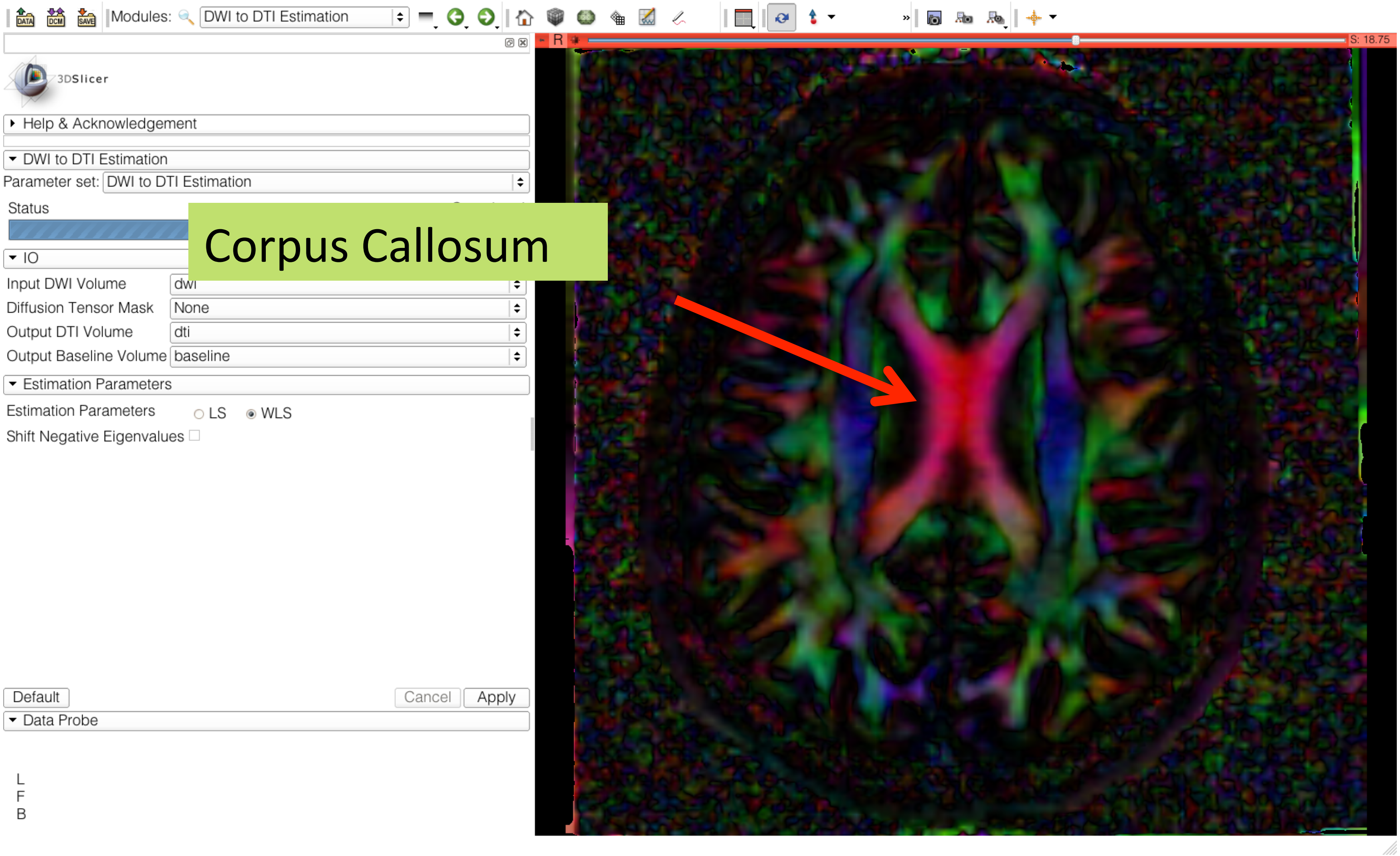
Corpus Callosum



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

Exploring the Diffusion Tensor Data



Corpus Callosum

Modules: DWI to DTI Estimation

DWI to DTI Estimation

Parameter set: DWI to DTI Estimation

Status

IO

Input DWI Volume: dwi

Diffusion Tensor Mask: None

Output DTI Volume: dti

Output Baseline Volume: baseline

Estimation Parameters

Estimation Parameters: ○ LS ● WLS

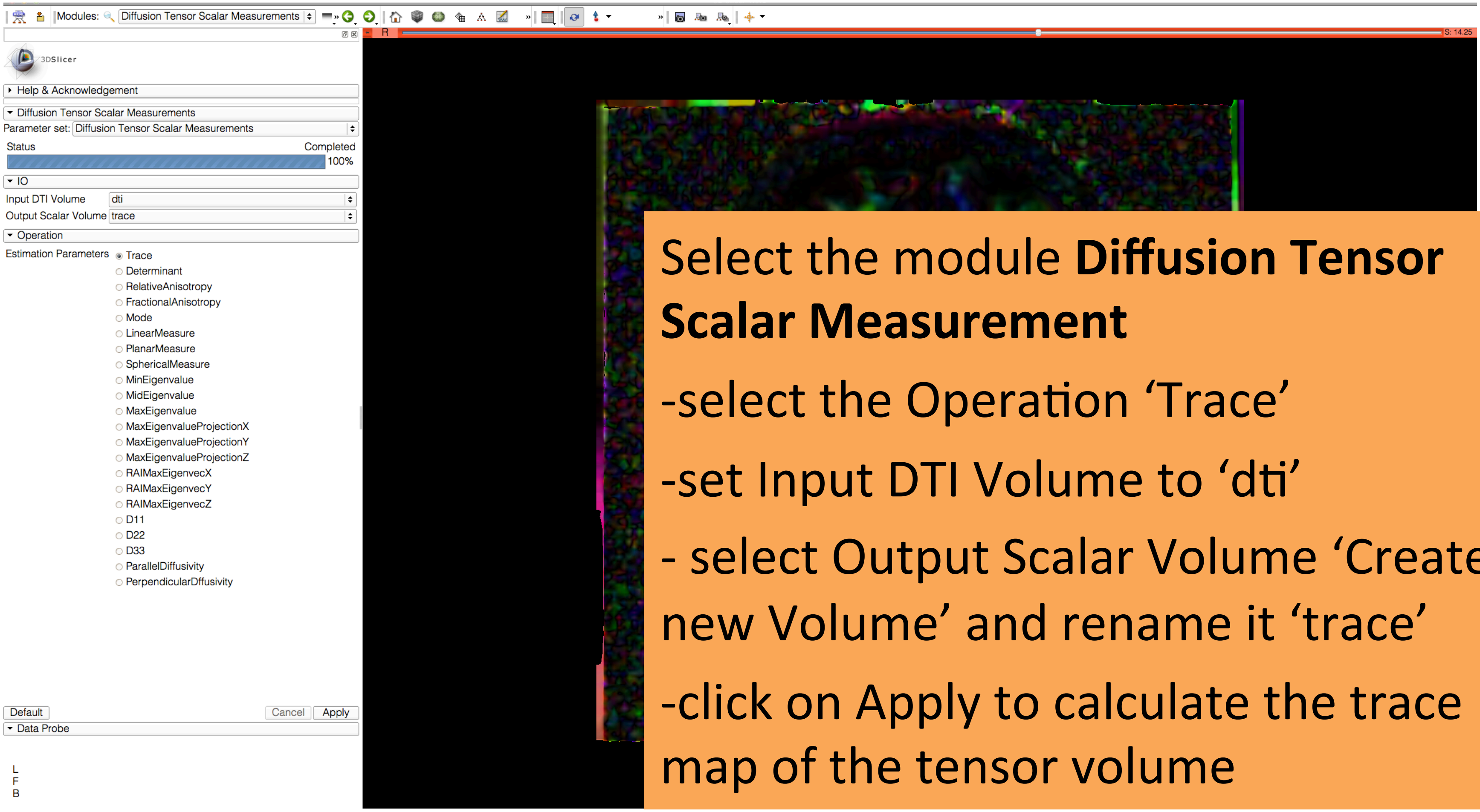
Shift Negative Eigenvalues ☐

Characterizing the Size of the tensor: Trace

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

- 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

Characterizing the Size of the tensor: Trace



Modules: Diffusion Tensor Scalar Measurements

Parameter set: Diffusion Tensor Scalar Measurements

Status: Completed 100%

Input DTI Volume: dti

Output Scalar Volume: trace

Estimation Parameters:
- ● Trace
- ○ Determinant
- ○ RelativeAnisotropy
- ○ FractionalAnisotropy
- ○ Mode
- ○ LinearMeasure
- ○ PlanarMeasure
- ○ SphericalMeasure
- ○ MinEigenvalue
- ○ MidEigenvalue
- ○ MaxEigenvalue
- ○ MaxEigenvalueProjectionX
- ○ MaxEigenvalueProjectionY
- ○ MaxEigenvalueProjectionZ
- ○ RAIMaxEigenvecX
- ○ RAIMaxEigenvecY
- ○ RAIMaxEigenvecZ
- ○ D11
- ○ D22
- ○ D33
- ○ ParallelDiffusivity
- ○ PerpendicularDffusivity

Select the module **Diffusion Tensor Scalar Measurement**

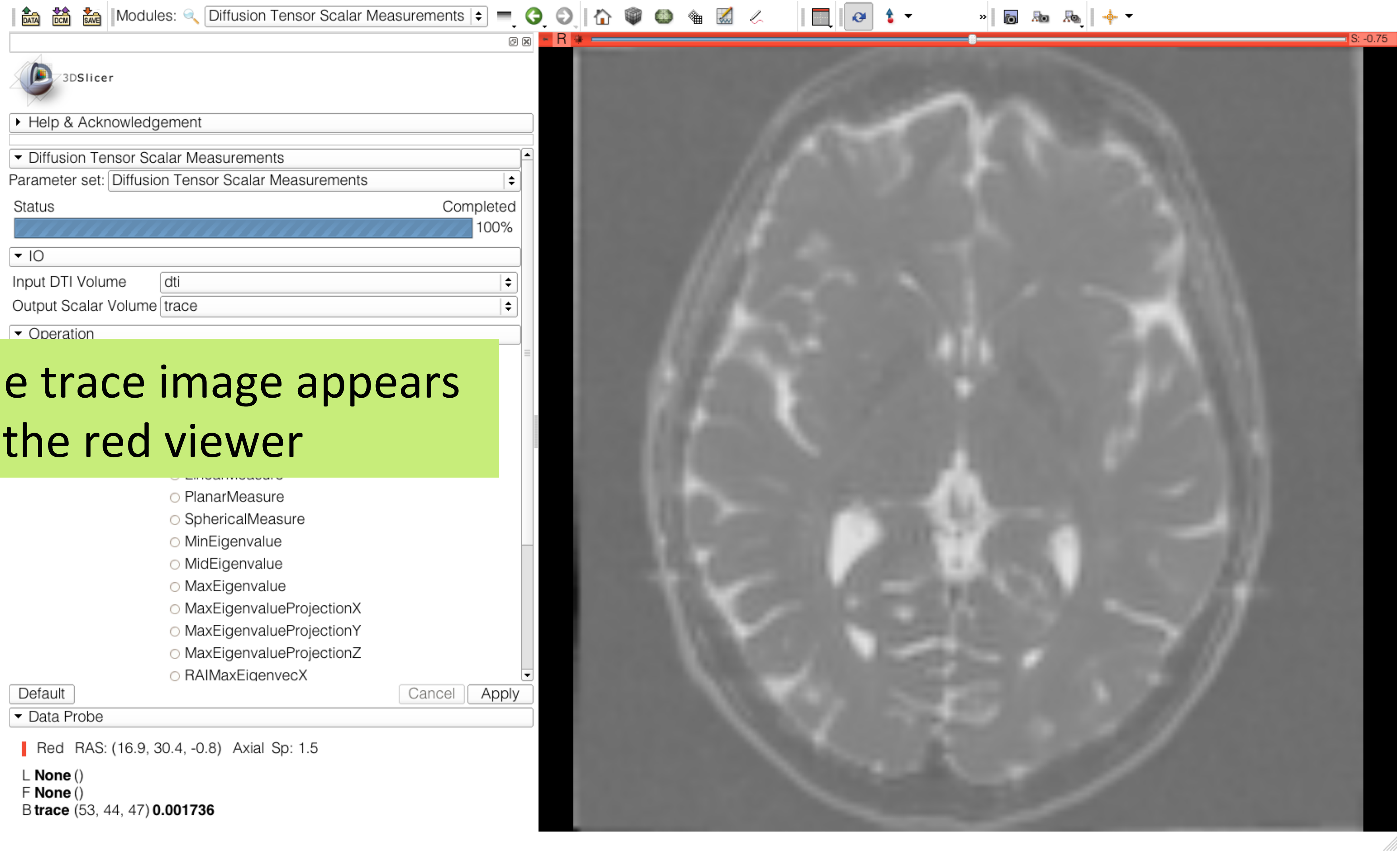
-select the Operation ‘Trace’

-set Input DTI Volume to ‘dti’

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

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

Trace


Modules: Diffusion Tensor Scalar Measurements

3DSlicer

Help & Acknowledgement

Diffusion Tensor Scalar Measurements

Parameter set: Diffusion Tensor Scalar Measurements

Status Completed

100%

IO

Input DTI Volume dti

Output Scalar Volume trace

Operation

○ PlanarMeasure
○ SphericalMeasure
○ MinEigenvalue
○ MidEigenvalue
○ MaxEigenvalue
○ MaxEigenvalueProjectionX
○ MaxEigenvalueProjectionY
○ MaxEigenvalueProjectionZ
○ RAIMaxEigenvecX

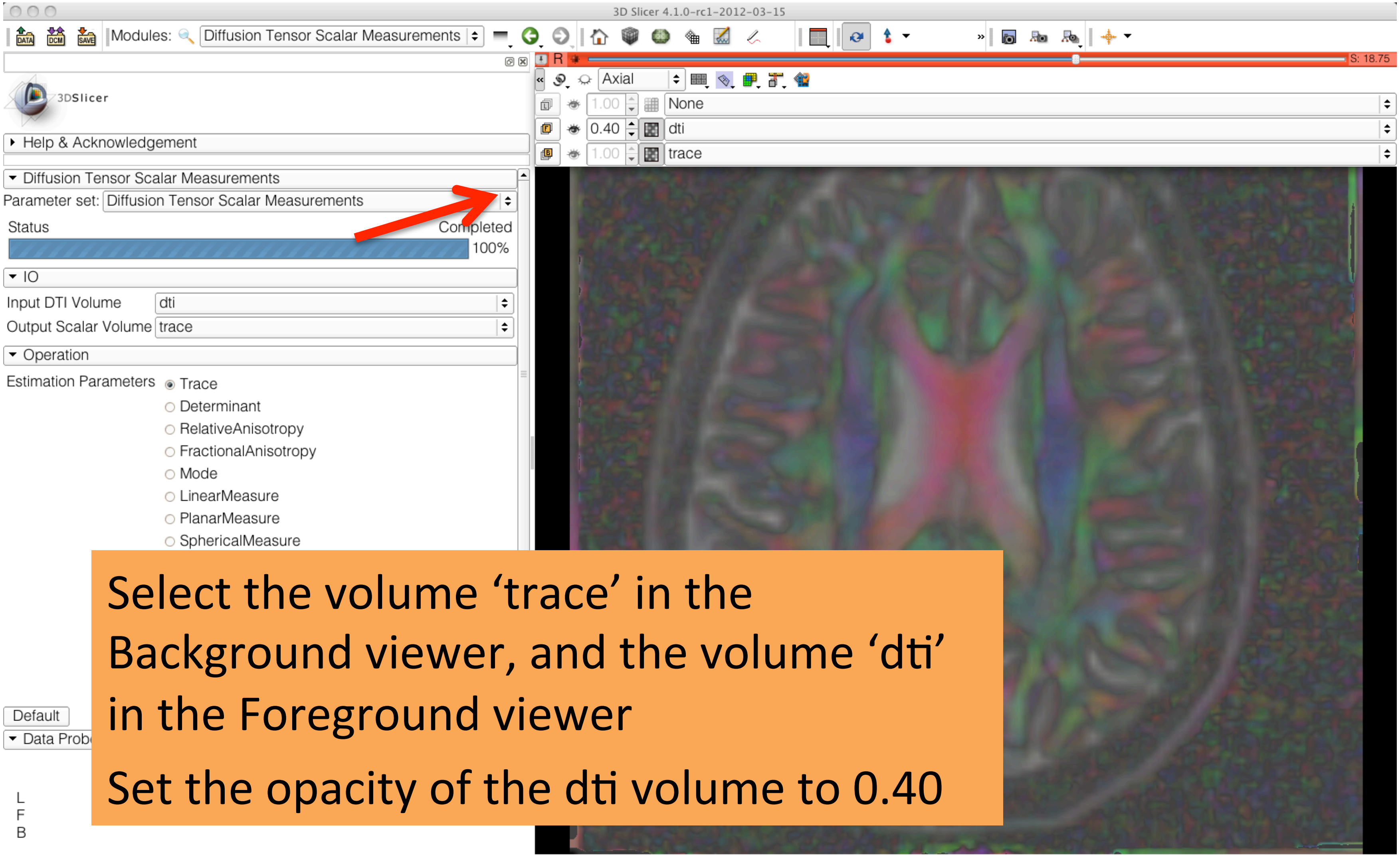
Data Probe

Red RAS: (16.9, 30.4, -0.8) Axial Sp: 1.5

L **None** ()
F **None** ()
B **trace** (53, 44, 47) **0.001736**

The trace image appears in the red viewer

Trace



3D Slicer 4.1.0-rc1-2012-03-15

Modules: Diffusion Tensor Scalar Measurements

Diffusion Tensor Scalar Measurements

Parameter set: Diffusion Tensor Scalar Measurements

Status Completed 100%

IO

Input DTI Volume: dti

Output Scalar Volume: trace

Operation

Estimation Parameters
- ● Trace
- ○ Determinant
- ○ RelativeAnisotropy
- ○ FractionalAnisotropy
- ○ Mode
- ○ LinearMeasure
- ○ PlanarMeasure
- ○ SphericalMeasure

Axial

1.00 None

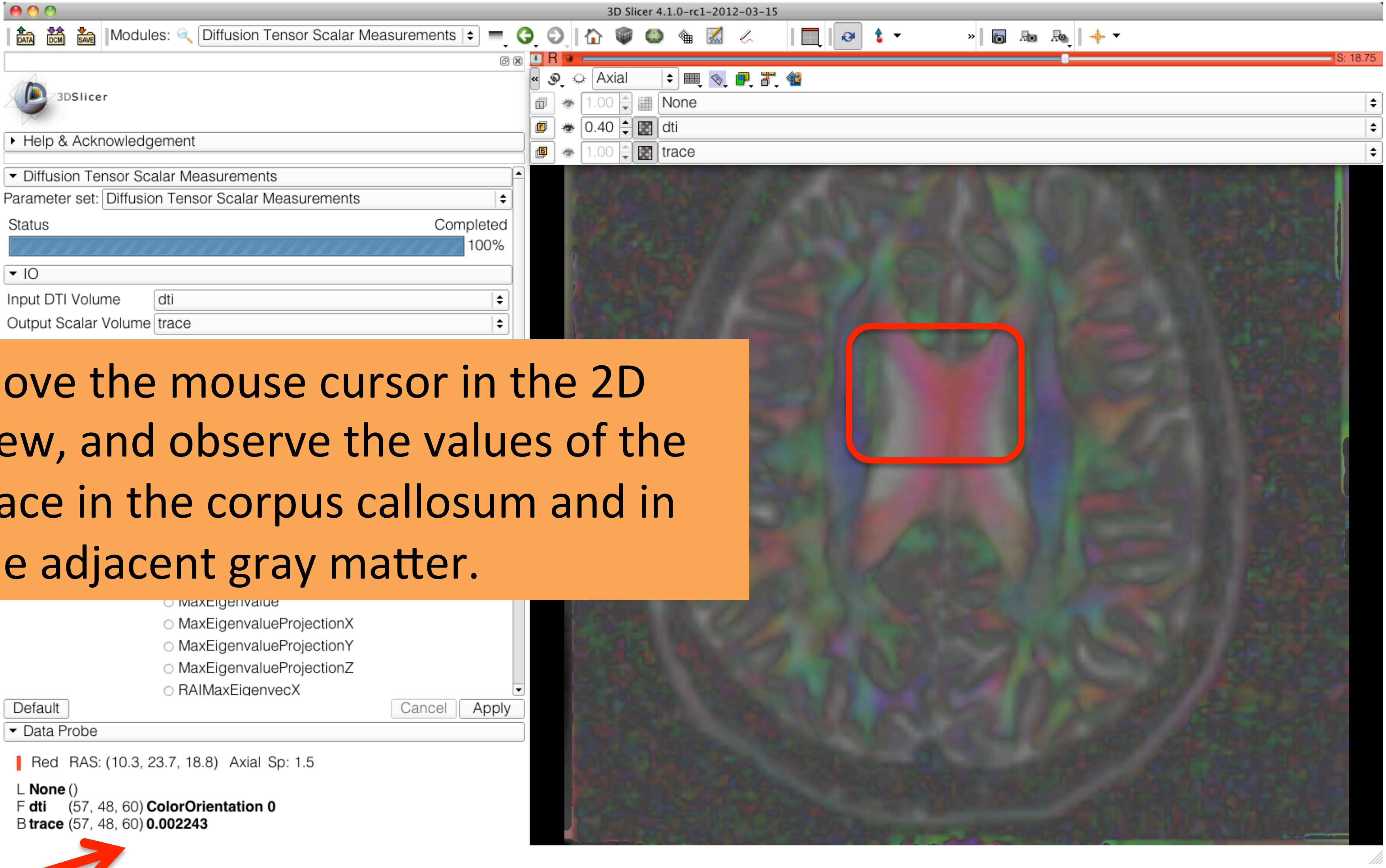
0.40 dti

1.00 trace

Select the volume ‘trace’ in the Background viewer, and the volume ‘dti’ in the Foreground viewer

Set the opacity of the dti volume to 0.40

Trace



Modules: Diffusion Tensor Scalar Measurements

Diffusion Tensor Scalar Measurements

Parameter set: Diffusion Tensor Scalar Measurements

Status Completed 100%

IO

Input DTI Volume dti

Output Scalar Volume trace

○ MaxEigenvalue
○ MaxEigenvalueProjectionX
○ MaxEigenvalueProjectionY
○ MaxEigenvalueProjectionZ
○ RAIMaxEigenvecX

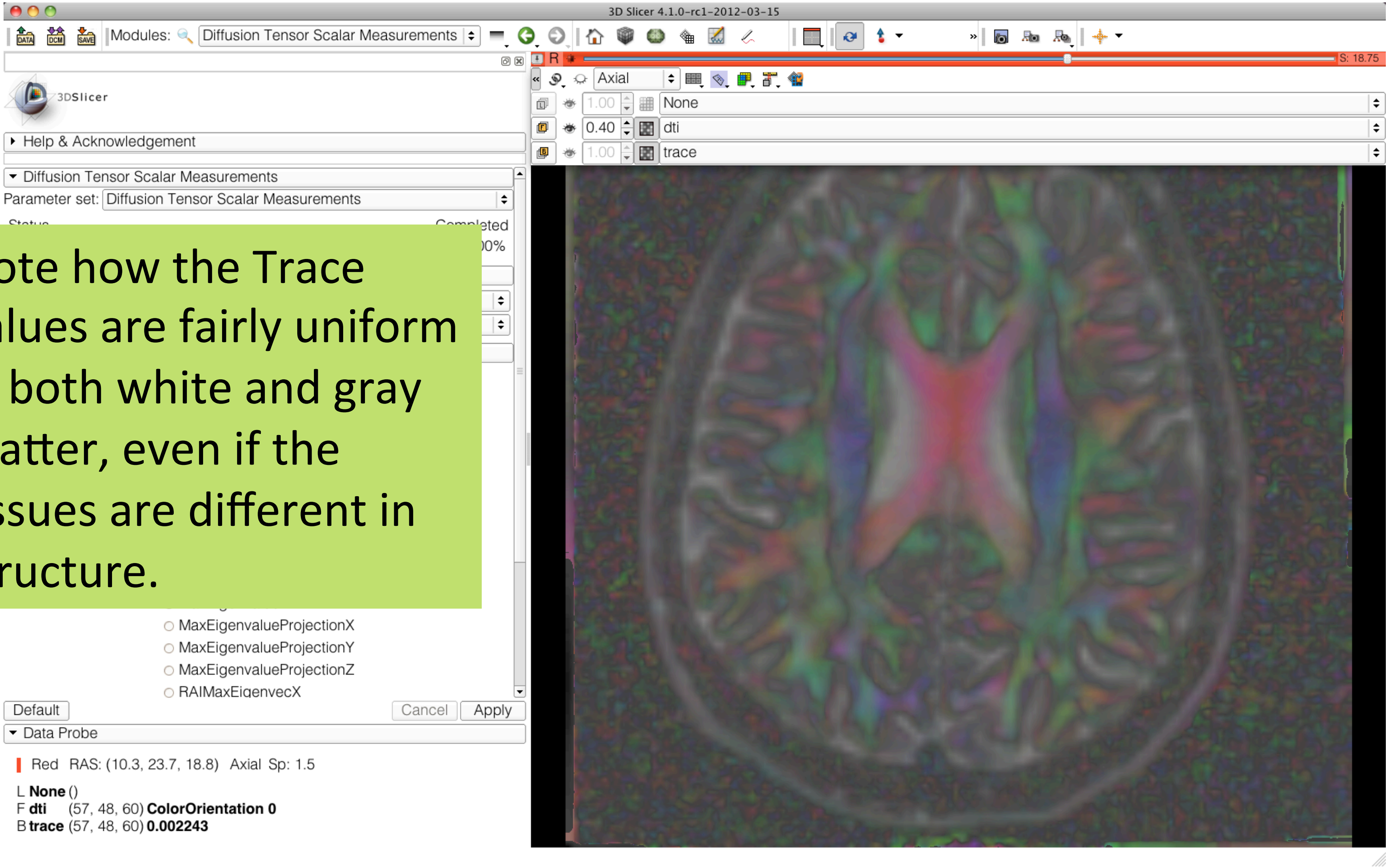
Data Probe

Red RAS: (10.3, 23.7, 18.8) Axial Sp: 1.5

L **None** ()
F **dti** (57, 48, 60) **ColorOrientation 0**
B **trace** (57, 48, 60) **0.002243**

Move the mouse cursor in the 2D view, and observe the values of the trace in the corpus callosum and in the adjacent gray matter.

Trace



Modules: Diffusion Tensor Scalar Measurements

Parameter set: Diffusion Tensor Scalar Measurements

Status Completed

S: 18.75

1.00 None

0.40 dti

1.00 trace

Red RAS: (10.3, 23.7, 18.8) Axial Sp: 1.5

L **None** ()

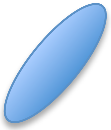
F **dti** (57, 48, 60) **ColorOrientation 0**

B **trace** (57, 48, 60) **0.002243**

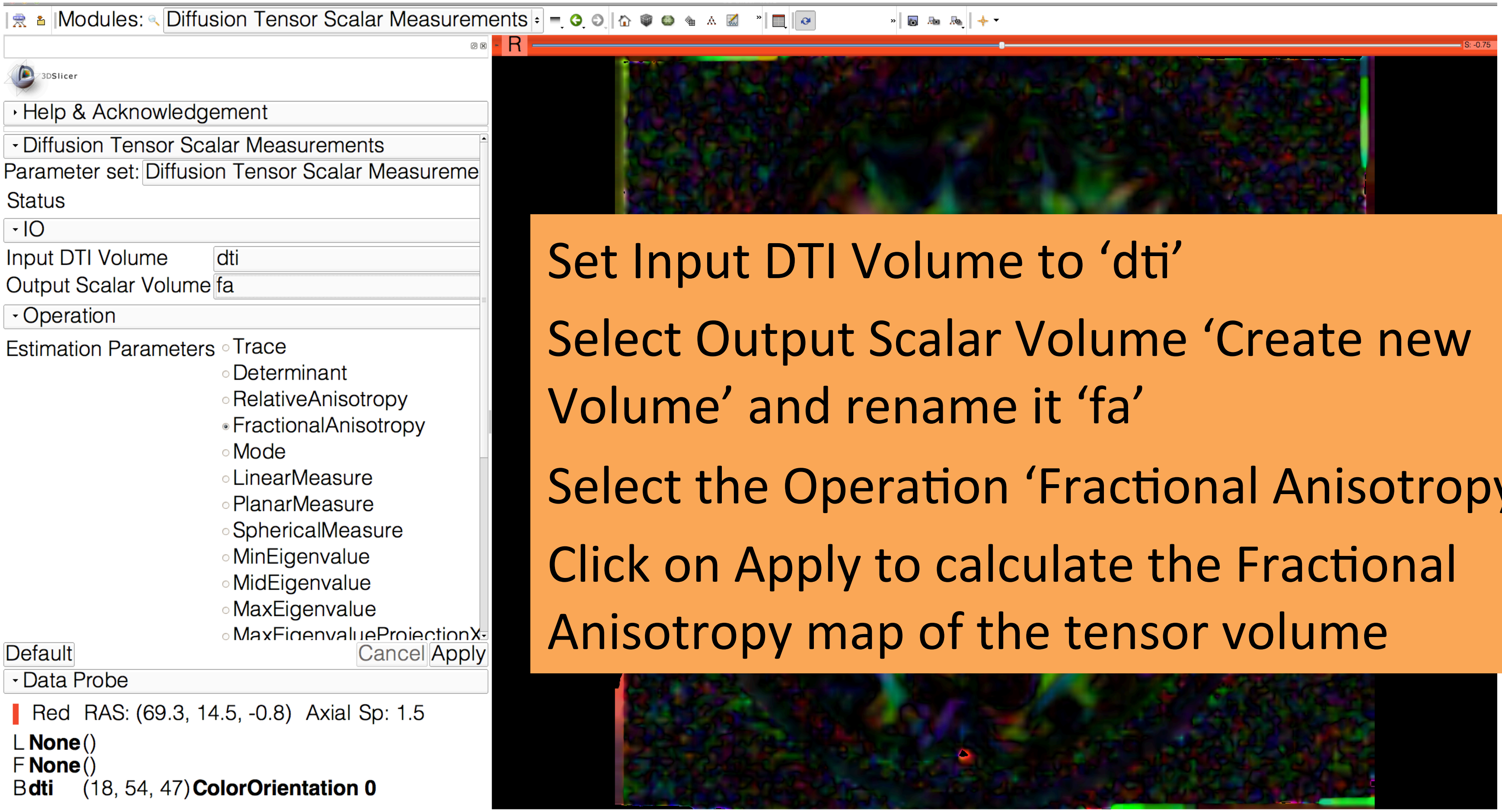
Note how the Trace values are fairly uniform in both white and gray matter, even if the tissues are different in structure.

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: 

Characterizing the Shape of the tensor: Fractional Anisotropy



Modules: Diffusion Tensor Scalar Measurements

Help & Acknowledgement

Diffusion Tensor Scalar Measurements

Parameter set: Diffusion Tensor Scalar Measureme

Status

IO

Input DTI Volume: dti

Output Scalar Volume: fa

Operation

Estimation Parameters
- ○ Trace
- ○ Determinant
- ○ RelativeAnisotropy
- ● FractionalAnisotropy
- ○ Mode
- ○ LinearMeasure
- ○ PlanarMeasure
- ○ SphericalMeasure
- ○ MinEigenvalue
- ○ MidEigenvalue
- ○ MaxEigenvalue
- ○ MaxEigenvalueProjectionX

Data Probe

Red RAS: (69.3, 14.5, -0.8) Axial Sp: 1.5

L **None** ()
F **None** ()
B **dti** (18, 54, 47) **ColorOrientation 0**

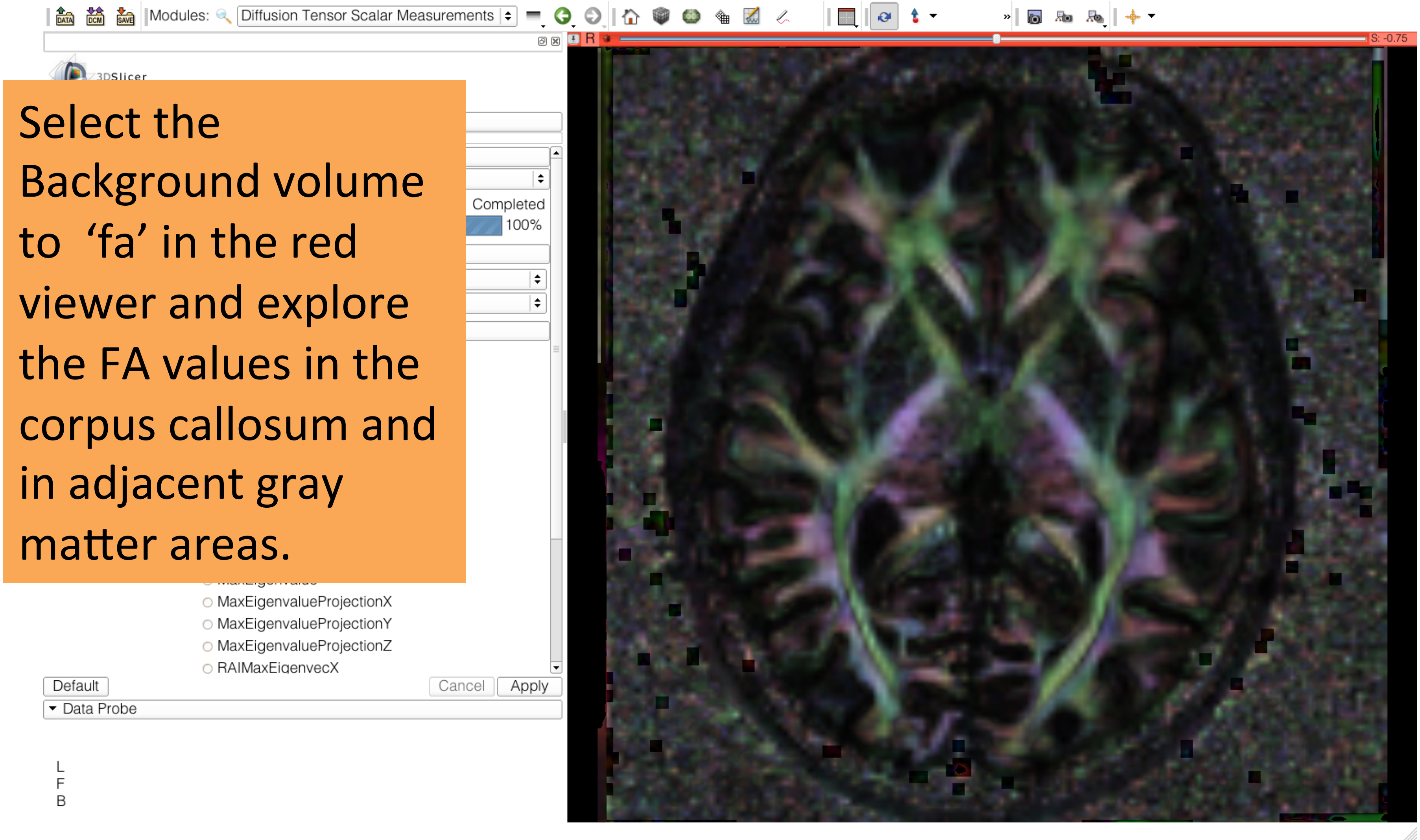
Set Input DTI Volume to ‘dti’

Select Output Scalar Volume ‘Create new Volume’ and rename it ‘fa’

Select the Operation ‘Fractional Anisotropy’

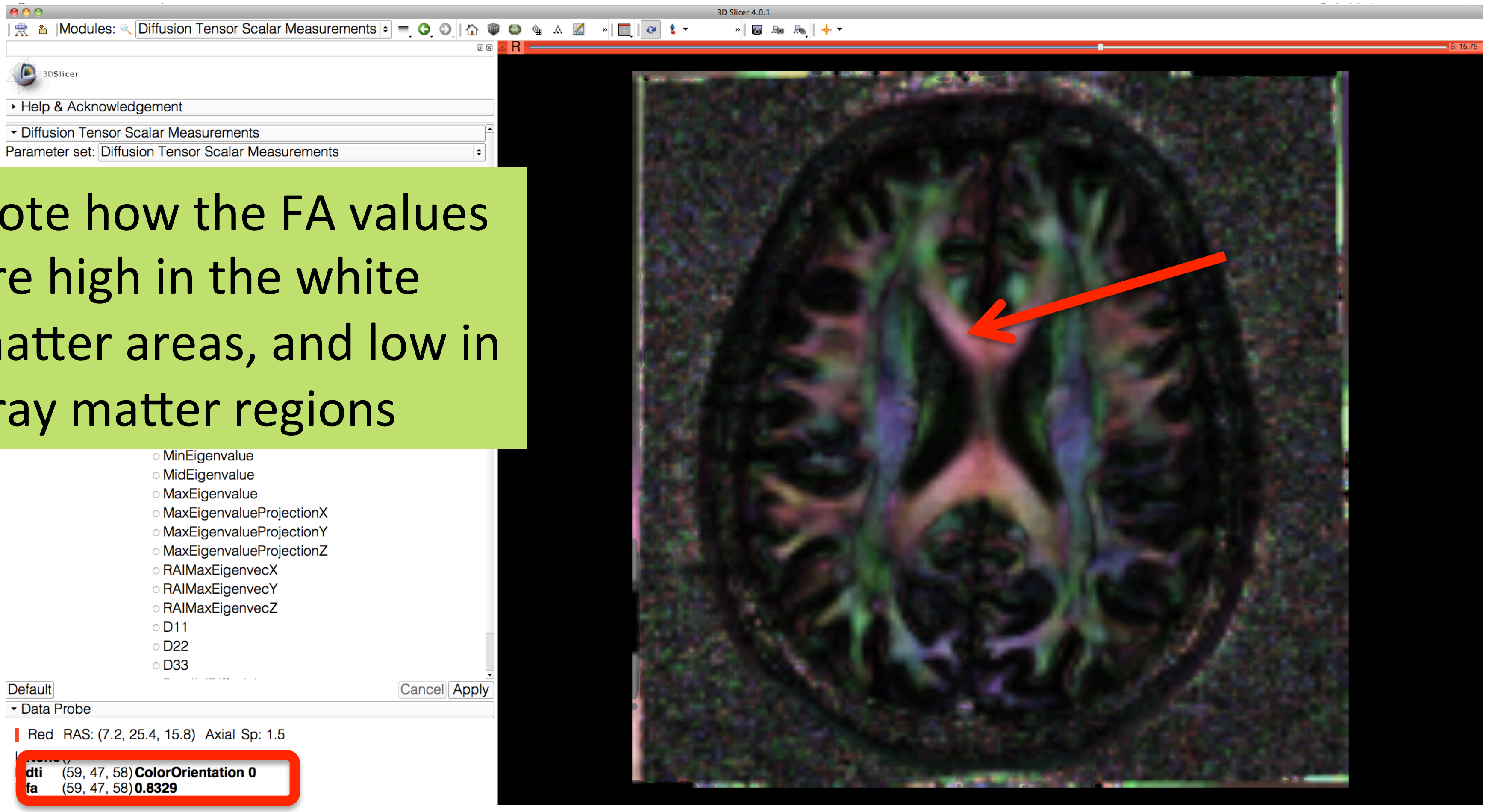
Click on Apply to calculate the Fractional Anisotropy map of the tensor volume

Fractional Anisotropy



Select the Background volume to ‘fa’ in the red viewer and explore the FA values in the corpus callosum and in adjacent gray matter areas.

Fractional Anisotropy



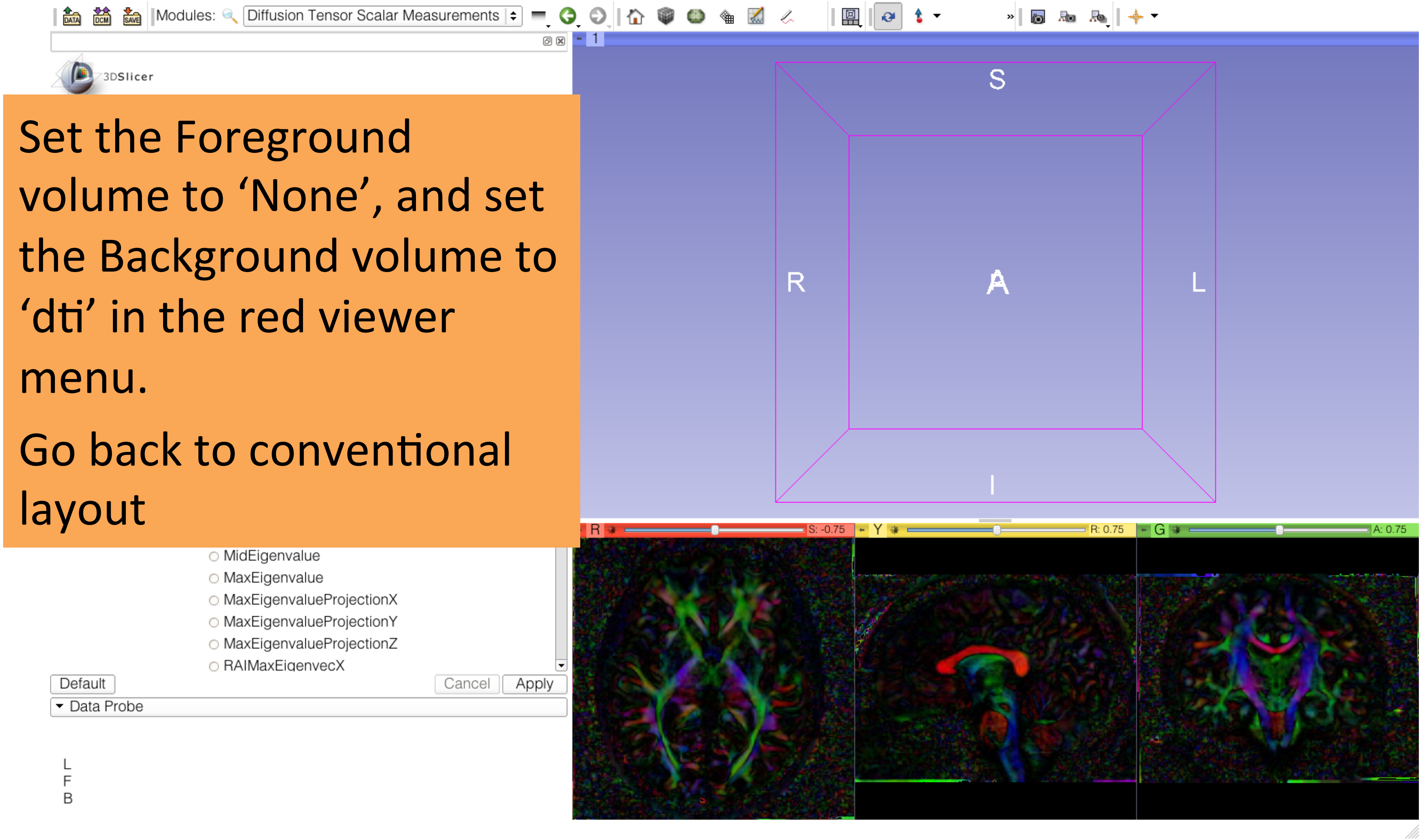
Parameter set: Diffusion Tensor Scalar Measurements

Red RAS: (7.2, 25.4, 15.8) Axial Sp: 1.5

dti (59, 47, 58) **ColorOrientation 0**
fa (59, 47, 58) **0.8329**

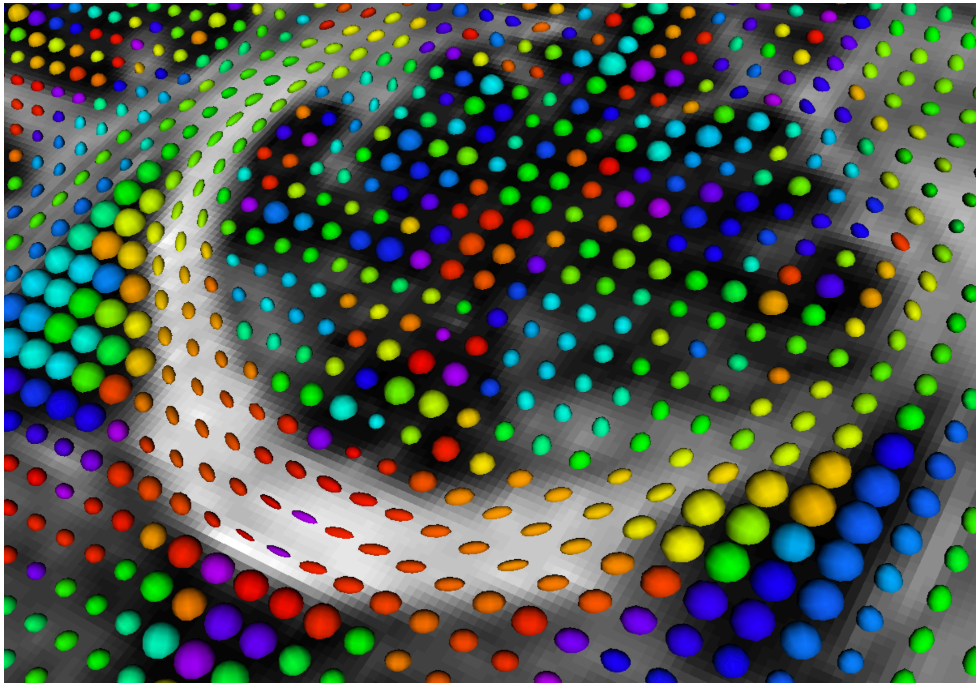
Note how the FA values are high in the white matter areas, and low in gray matter regions

Fractional Anisotropy



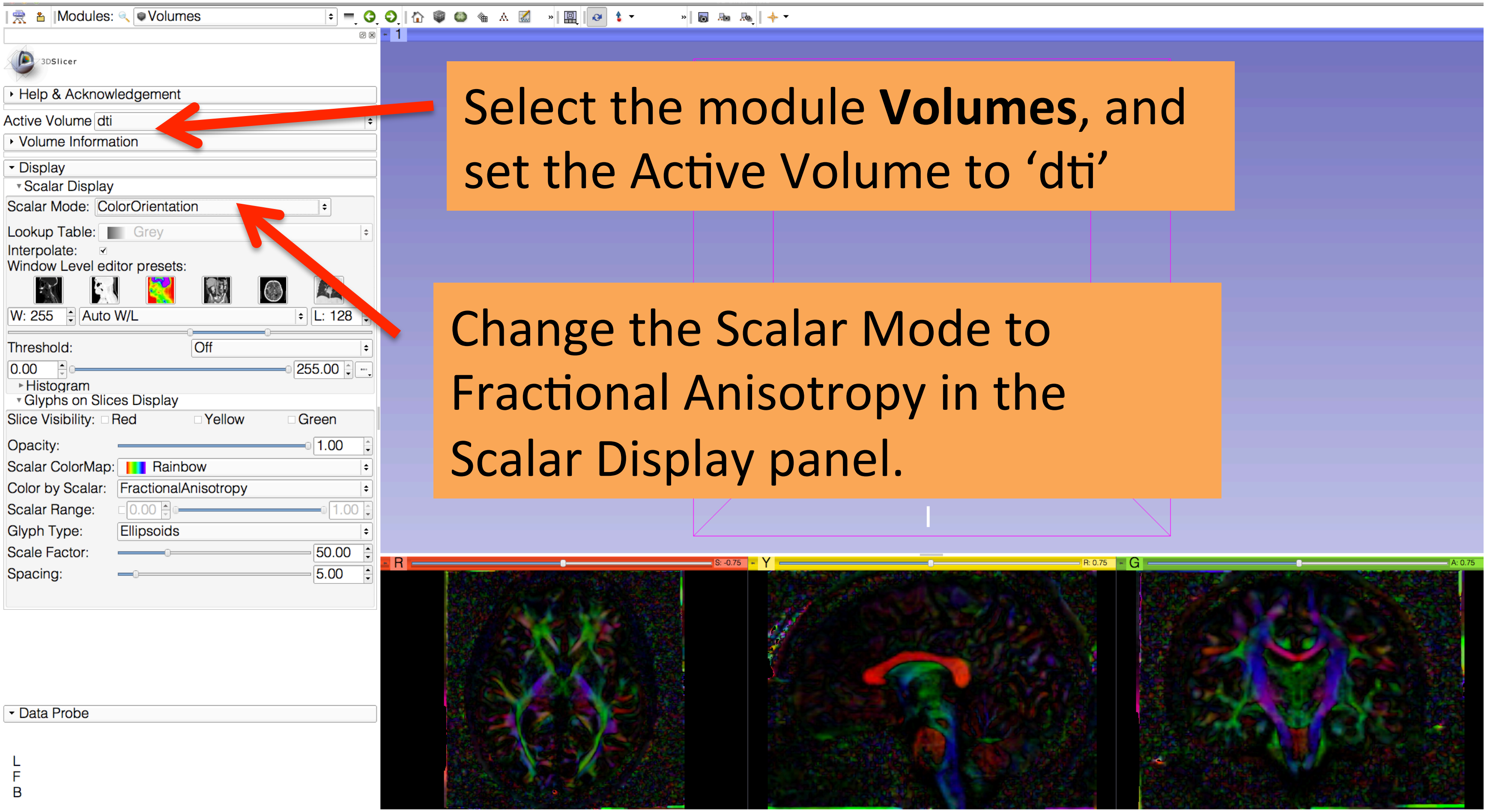
Set the Foreground volume to 'None', and set the Background volume to 'dti' in the red viewer menu.

Go back to conventional layout



Part 2: Visualizing the tensor data

3D Visualization: Glyphs



Select the module **Volumes**, and set the Active Volume to ‘dti’

Change the Scalar Mode to Fractional Anisotropy in the Scalar Display panel.

Modules: Volumes

Active Volume dti

Scalar Mode: ColorOrientation

Lookup Table: Grey

Interpolate: ☑

W: 255 Auto W/L L: 128

Threshold: Off

0.00 255.00

Slice Visibility: ☐ Red ☐ Yellow ☐ Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Color by Scalar: FractionalAnisotropy

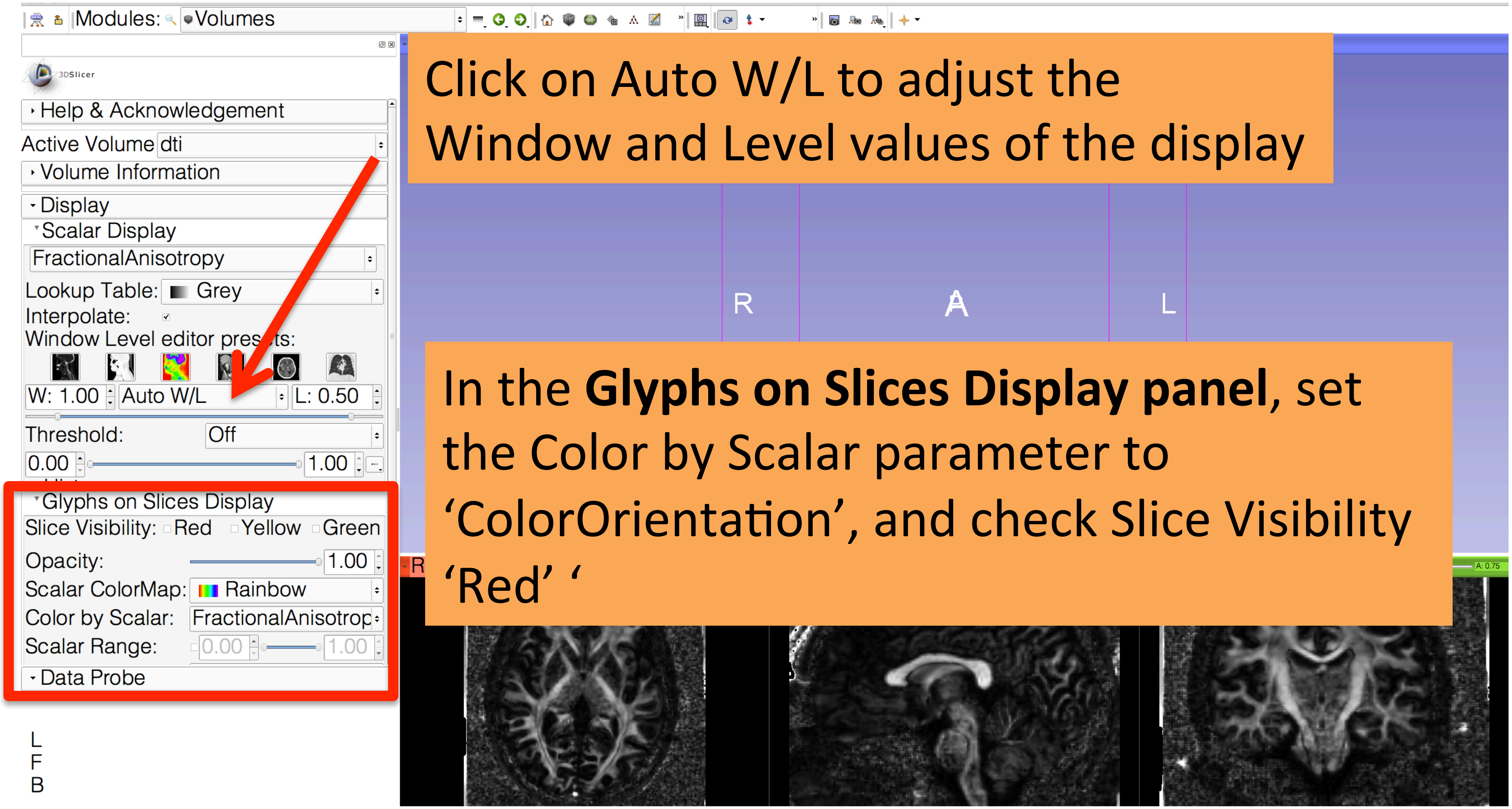
Scalar Range: 0.00 1.00

Glyph Type: Ellipsoids

Scale Factor: 50.00

Spacing: 5.00

3D Visualization: Glyphs



Modules: Volumes

Help & Acknowledgement

Active Volume: dti

Volume Information

Display

Scalar Display

FractionalAnisotropy

Lookup Table: Grey

Interpolate: ☑

Window Level editor presets:

W: 1.00 Auto W/L L: 0.50

Threshold: Off

0.00 1.00

Glyphs on Slices Display

Slice Visibility: ☐ Red ☐ Yellow ☐ Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Color by Scalar: FractionalAnisotrop

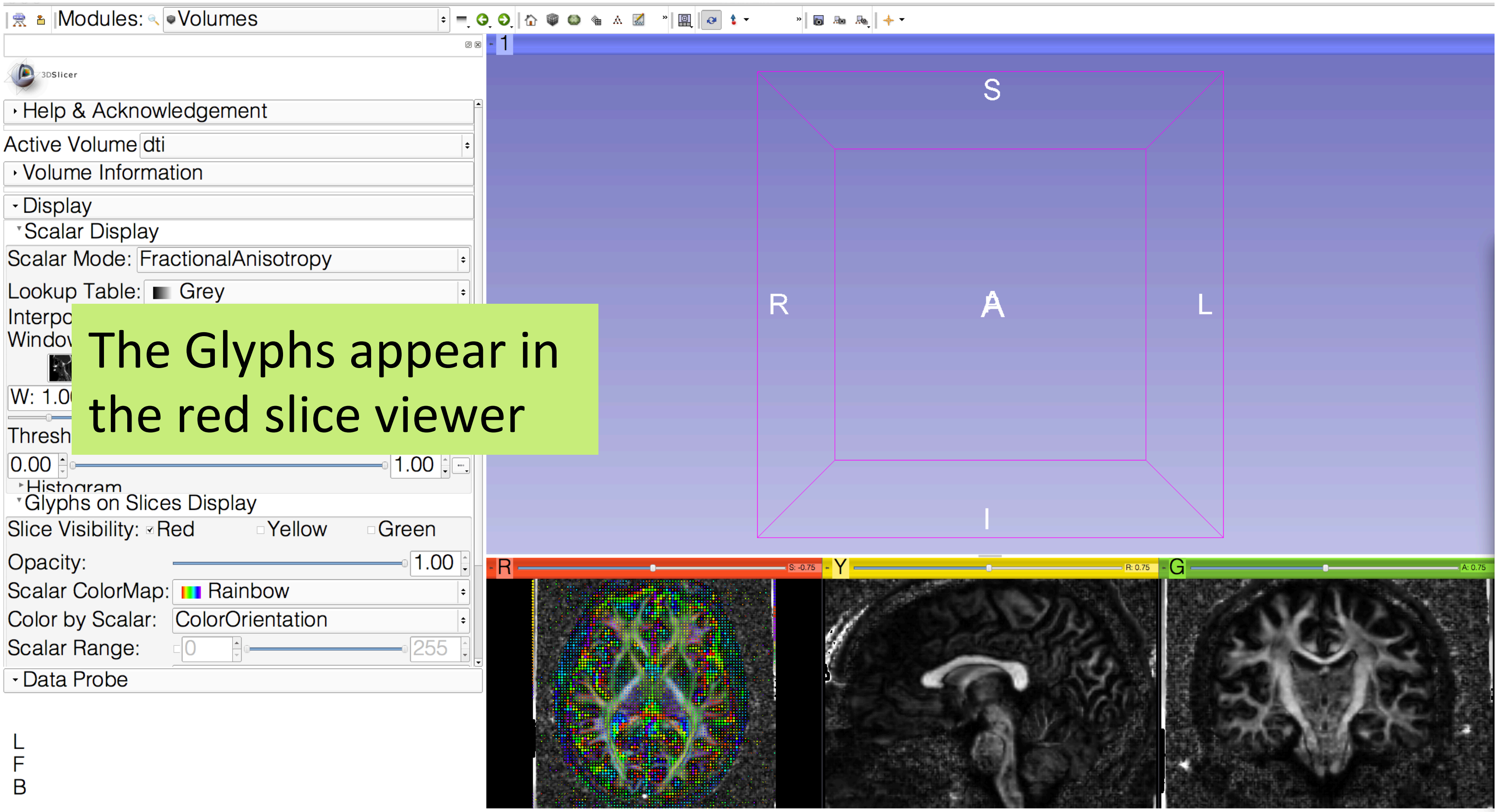
Scalar Range: 0.00 1.00

Data Probe

Click on Auto W/L to adjust the Window and Level values of the display

In the **Glyphs on Slices Display panel**, set the Color by Scalar parameter to ‘ColorOrientation’, and check Slice Visibility ‘Red’ ‘

3D Visualization: Glyphs



Modules: Volumes

Help & Acknowledgement

Active Volume dti

Volume Information

Display

Scalar Display

Scalar Mode: FractionalAnisotropy

Lookup Table: Grey

Threshold: 0.00 – 1.00

Histogram

Glyphs on Slices Display

Slice Visibility: ☑ Red ☐ Yellow ☐ Green

Opacity: 1.00

Scalar ColorMap: Rainbow

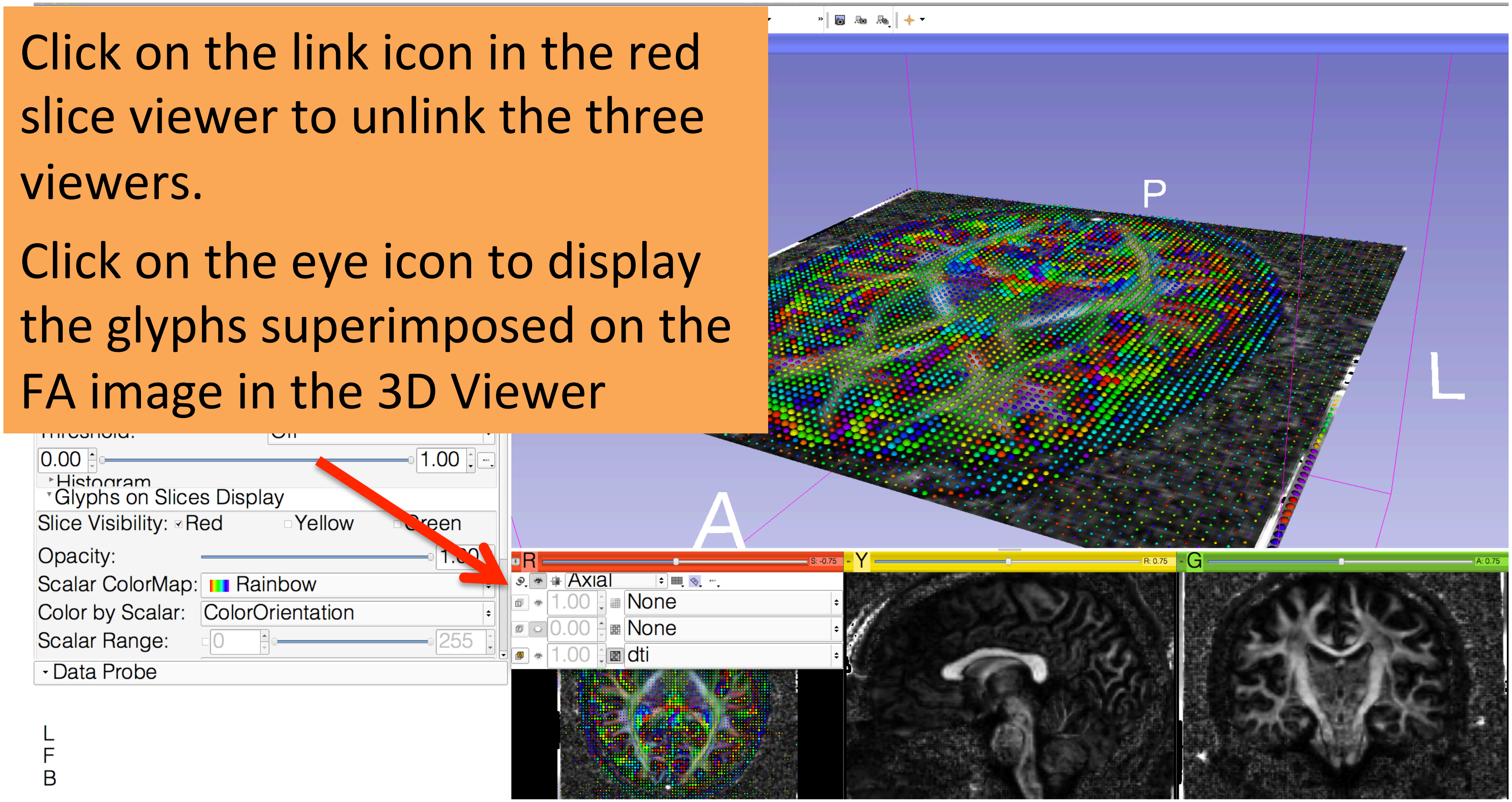
Color by Scalar: ColorOrientation

Scalar Range: 0 – 255

Data Probe

The Glyphs appear in the red slice viewer

3D Visualization: Glyphs



Click on the link icon in the red slice viewer to unlink the three viewers.

Click on the eye icon to display the glyphs superimposed on the FA image in the 3D Viewer

0.00 – 1.00

Histogram

Glyphs on Slices Display

Slice Visibility: ☑ Red ☐ Yellow ☐ Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Color by Scalar: ColorOrientation

Scalar Range: 0 – 255

Data Probe

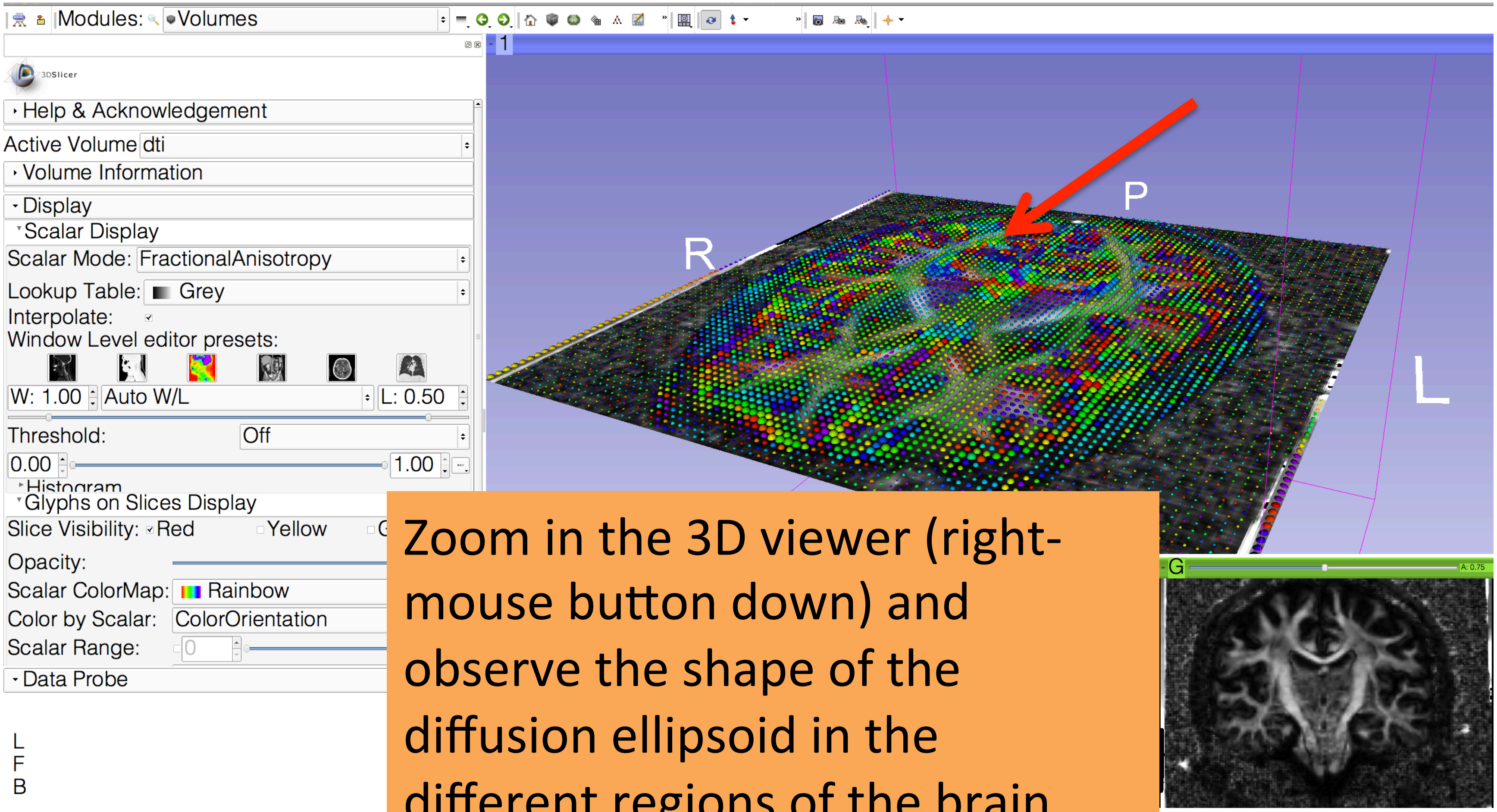
Axial

1.00 None

0.00 None

1.00 dti

3D Visualization: Glyphs



Modules: Volumes

Active Volume: dti

Scalar Mode: FractionalAnisotropy

Lookup Table: Grey

Interpolate: ☑

W: 1.00 Auto W/L L: 0.50

Threshold: Off

0.00 1.00

Slice Visibility: ☑ Red ☐ Yellow

Scalar ColorMap: Rainbow

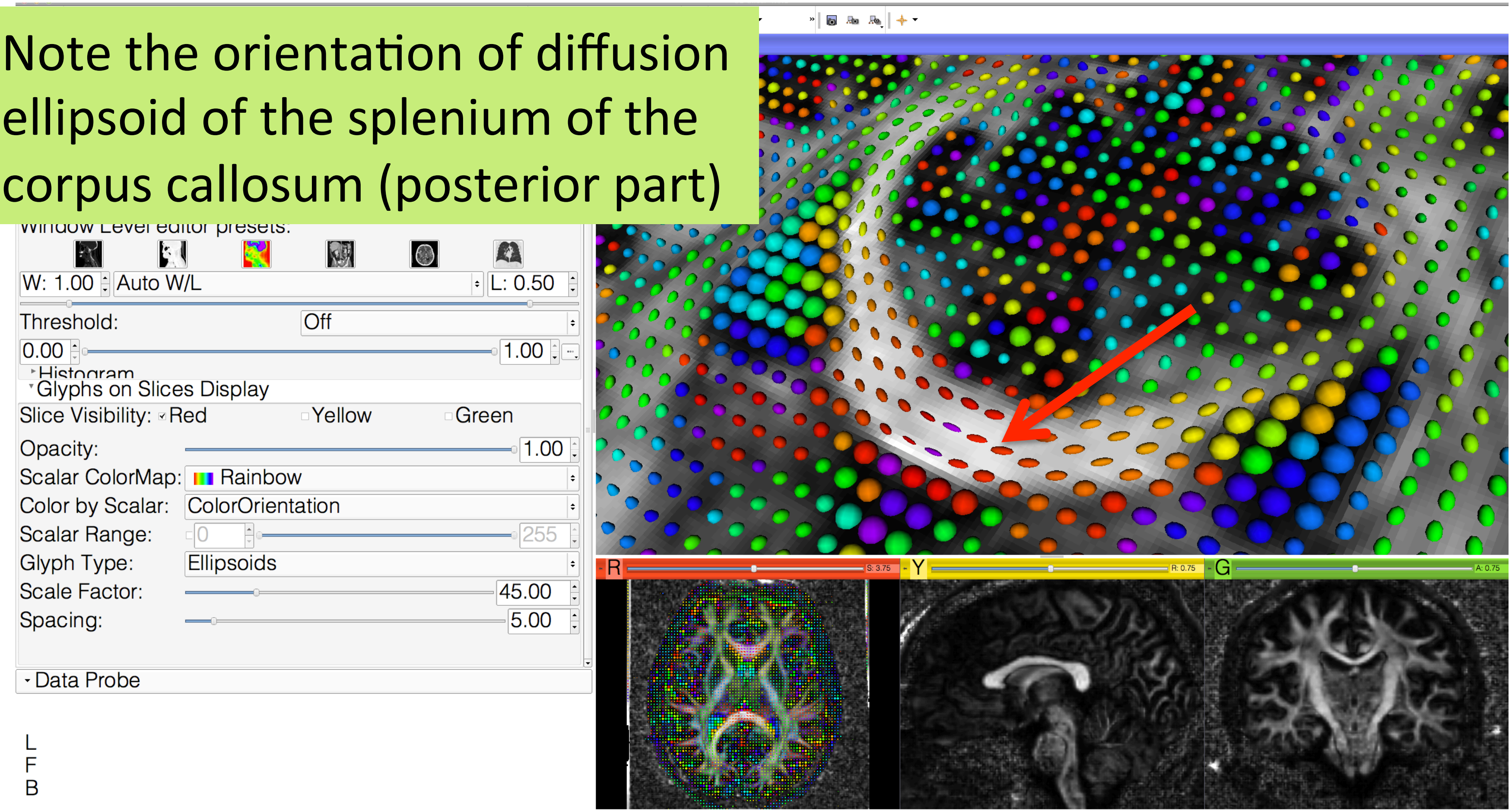
Color by Scalar: ColorOrientation

Scalar Range: 0

Zoom in the 3D viewer (right-mouse button down) and observe the shape of the diffusion ellipsoid in the different regions of the brain

3D Visualization: Glyphs

Note the orientation of diffusion ellipsoid of the splenium of the corpus callosum (posterior part)



Window Level editor presets:

W: 1.00 Auto W/L L: 0.50

Threshold: Off

0.00 1.00

Histogram

Glyphs on Slices Display

Slice Visibility: ☑ Red ☐ Yellow ☐ Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Color by Scalar: ColorOrientation

Scalar Range: 0 255

Glyph Type: Ellipsoids

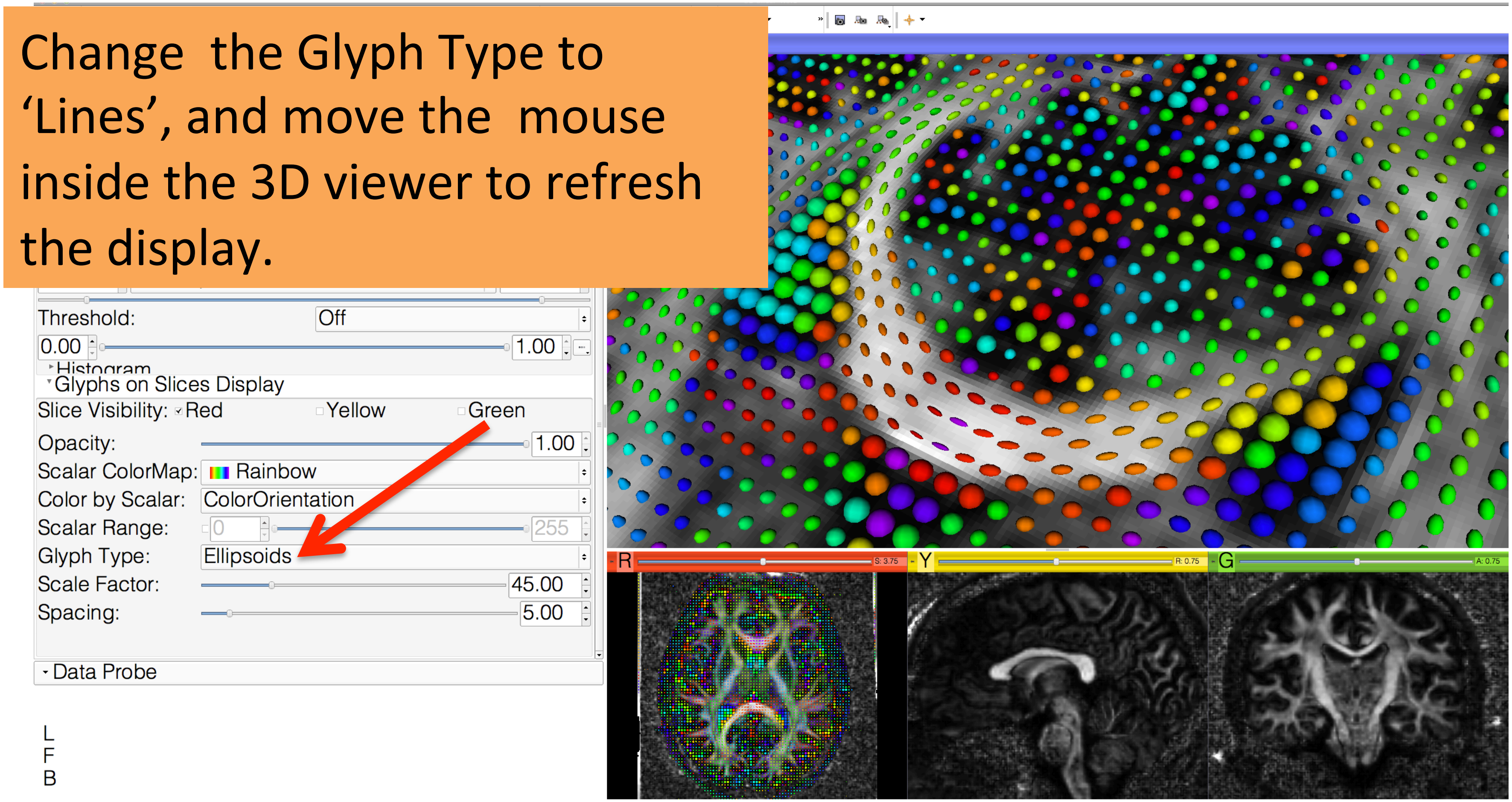
Scale Factor: 45.00

Spacing: 5.00

Data Probe

3D Visualization: Glyphs

Change the Glyph Type to ‘Lines’, and move the mouse inside the 3D viewer to refresh the display.



Threshold: Off

0.00 … 1.00

Histogram

Glyphs on Slices Display

Slice Visibility: ☑ Red ☐ Yellow ☐ Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Color by Scalar: ColorOrientation

Scalar Range: 0 … 255

Glyph Type: Ellipsoids

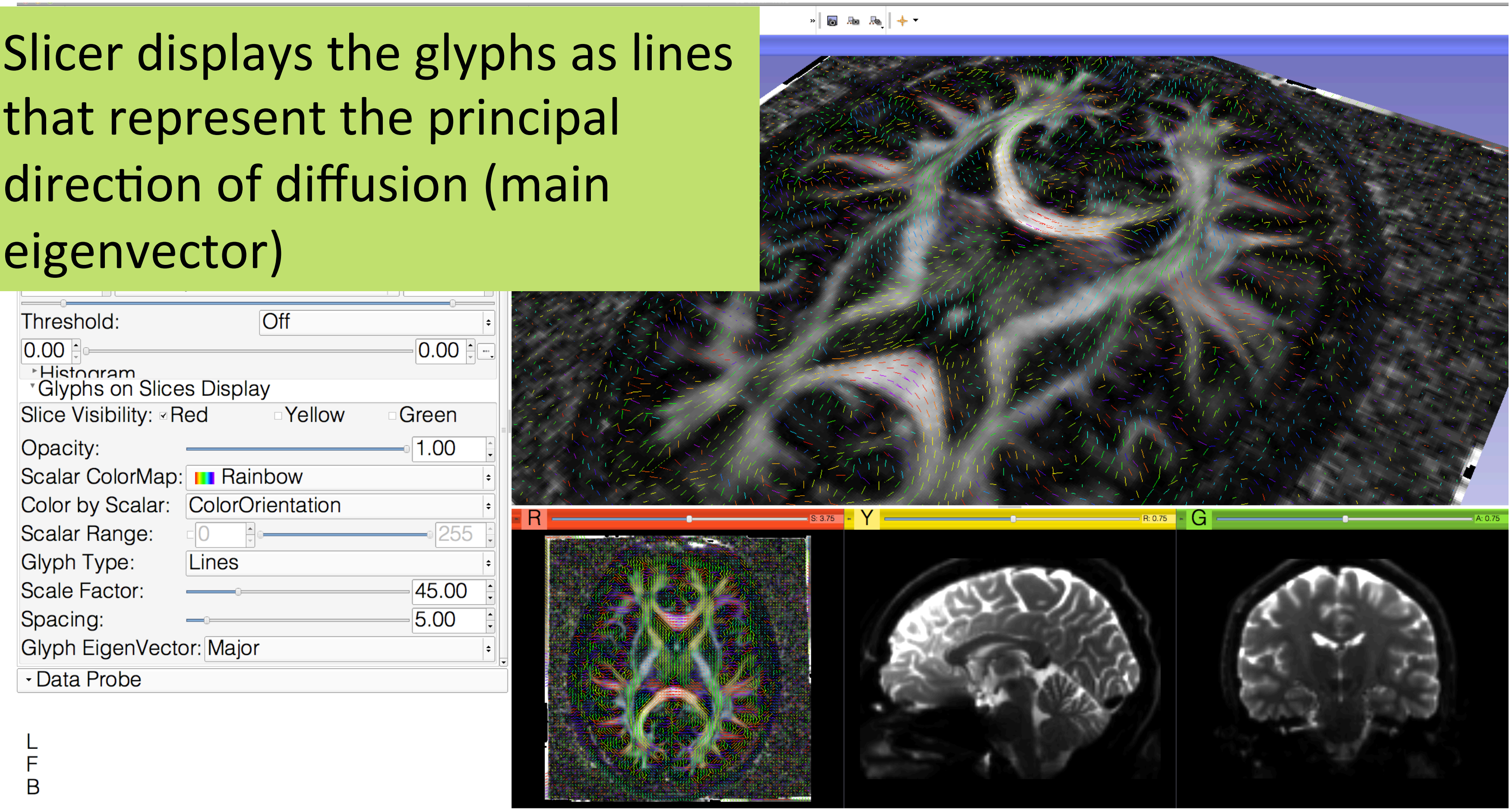
Scale Factor: 45.00

Spacing: 5.00

Data Probe

3D Visualization: Glyphs

Slicer displays the glyphs as lines that represent the principal direction of diffusion (main eigenvector)



Threshold: Off

0.00 — 0.00

Histogram

Glyphs on Slices Display

Slice Visibility: ☑ Red ☐ Yellow ☐ Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Color by Scalar: ColorOrientation

Scalar Range: 0 — 255

Glyph Type: Lines

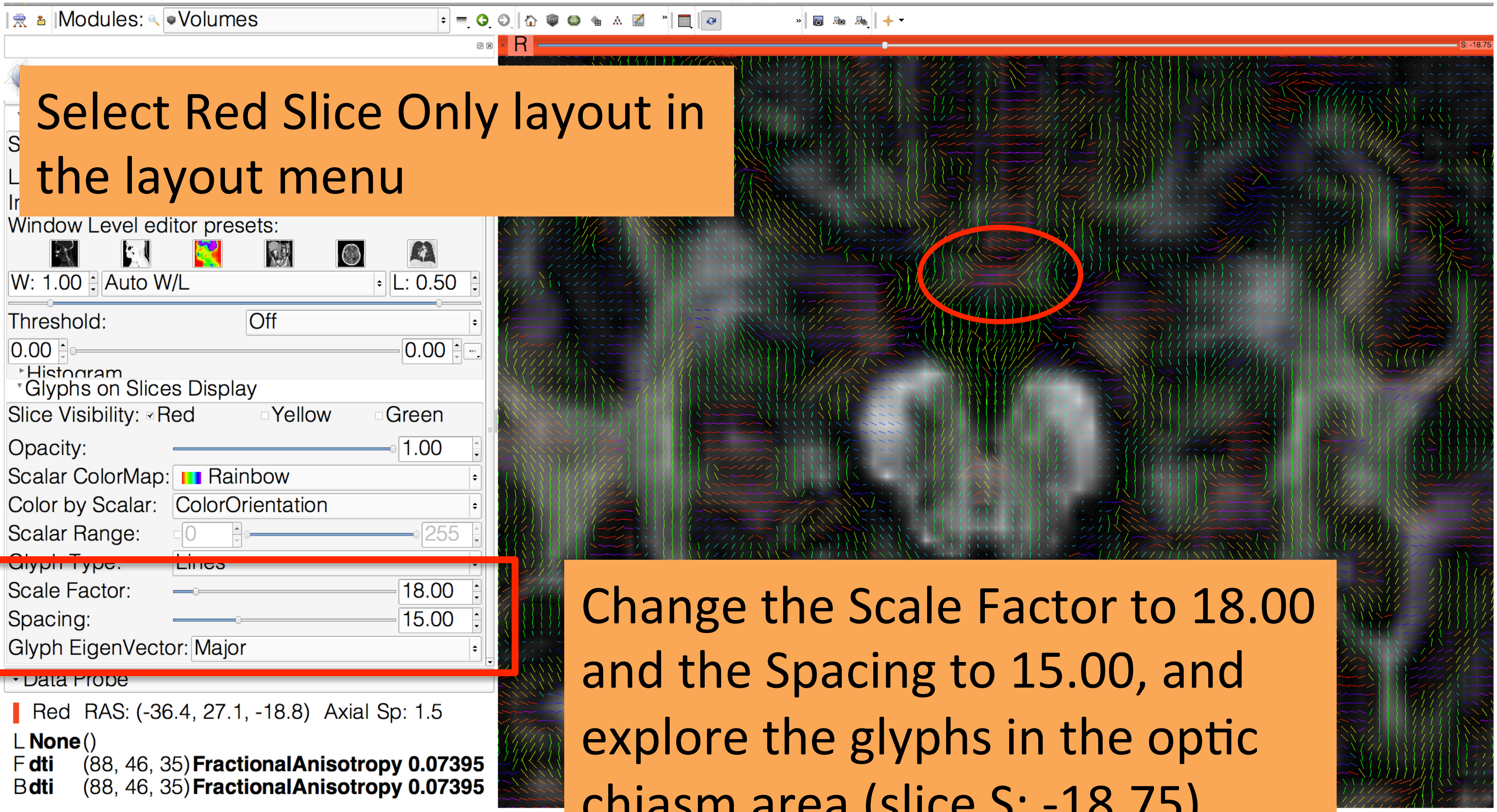
Scale Factor: 45.00

Spacing: 5.00

Glyph EigenVector: Major

Data Probe

3D Visualization: Glyphs



Select Red Slice Only layout in the layout menu

Window Level editor presets:

W: 1.00 Auto W/L L: 0.50

Threshold: Off

0.00 0.00

Glyphs on Slices Display

Slice Visibility: ☑ Red ☐ Yellow ☐ Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Color by Scalar: ColorOrientation

Scalar Range: 0 255

Glyph Type: Lines

Scale Factor: 18.00

Spacing: 15.00

Glyph EigenVector: Major

Red RAS: (-36.4, 27.1, -18.8) Axial Sp: 1.5

L **None** ()

F **dti** (88, 46, 35) **FractionalAnisotropy 0.07395**

B **dti** (88, 46, 35) **FractionalAnisotropy 0.07395**

Change the Scale Factor to 18.00 and the Spacing to 15.00, and explore the glyphs in the optic chiasm area (slice S: -18.75)

Optic Chiasm

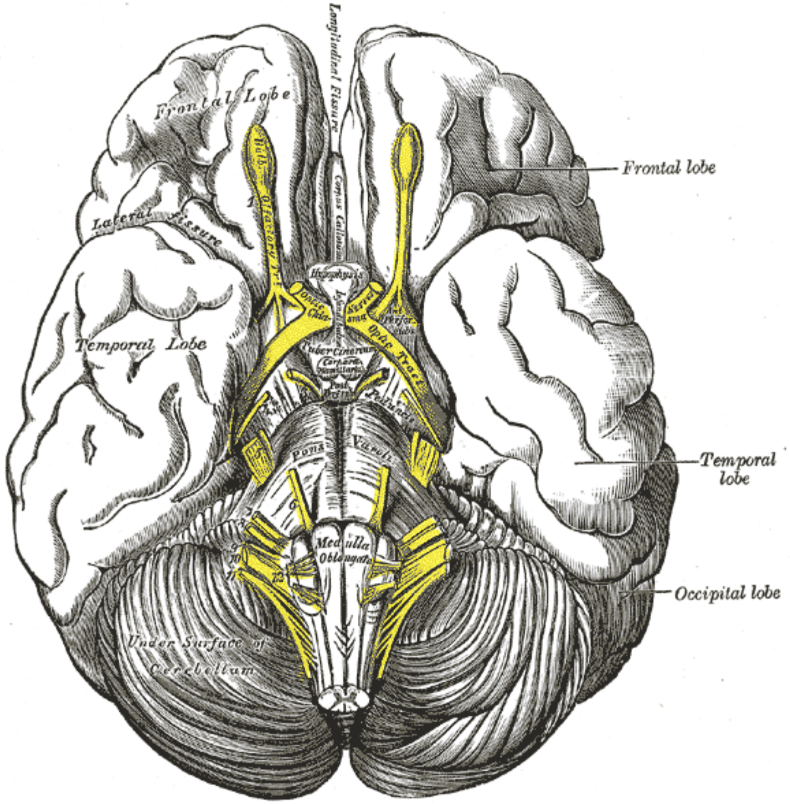
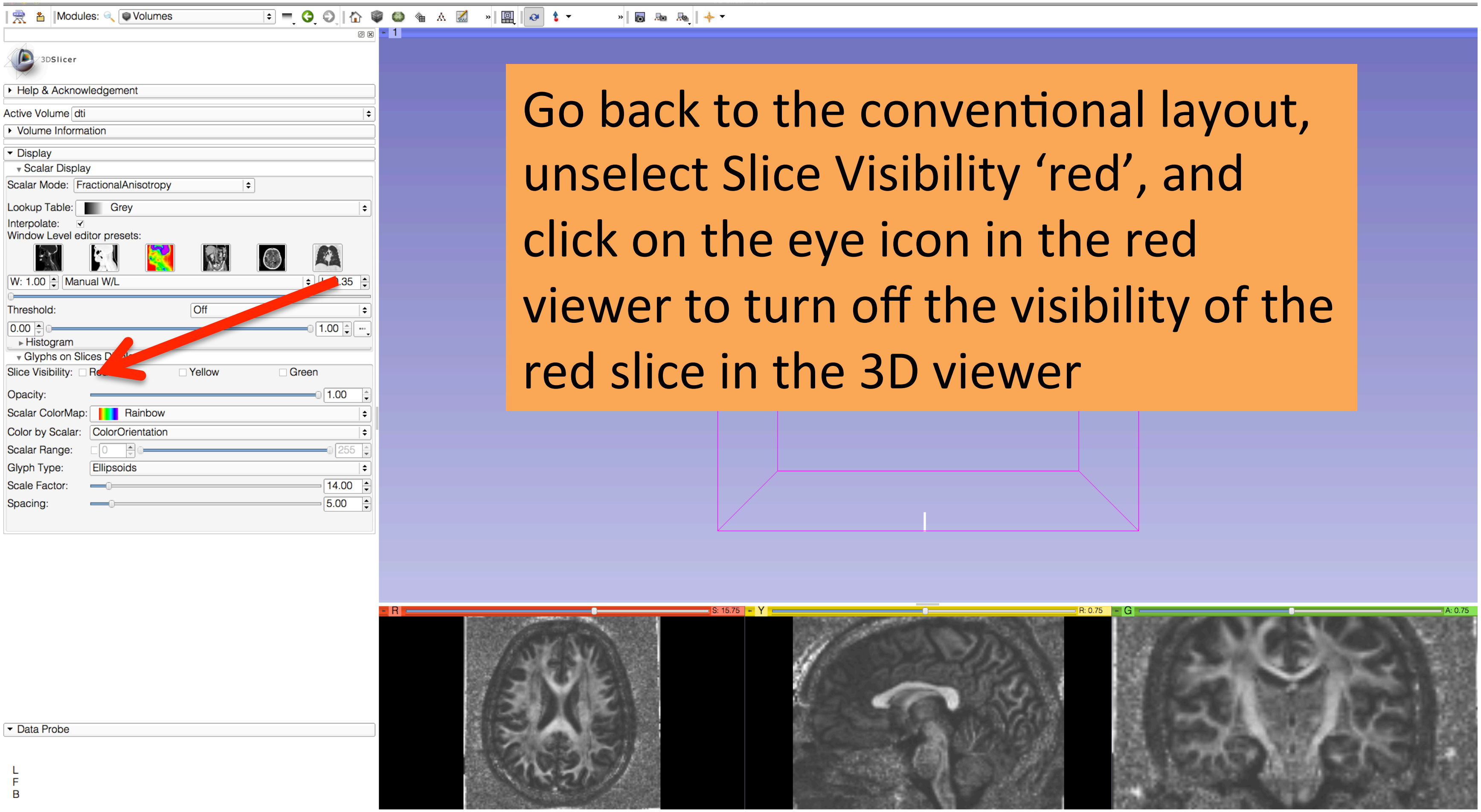


Image from Gray's Anatomy

The optic chiasm corresponds to the part of the brain where the optic nerves cross.

3D Visualization: Glyphs



Active Volume: dti

Scalar Mode: FractionalAnisotropy

Lookup Table: Grey

Interpolate: ☑

W: 1.00 Manual W/L

Threshold: Off

0.00 1.00

Slice Visibility: ☐ Re ☐ Yellow ☐ Green

Opacity: 1.00

Scalar ColorMap: Rainbow

Color by Scalar: ColorOrientation

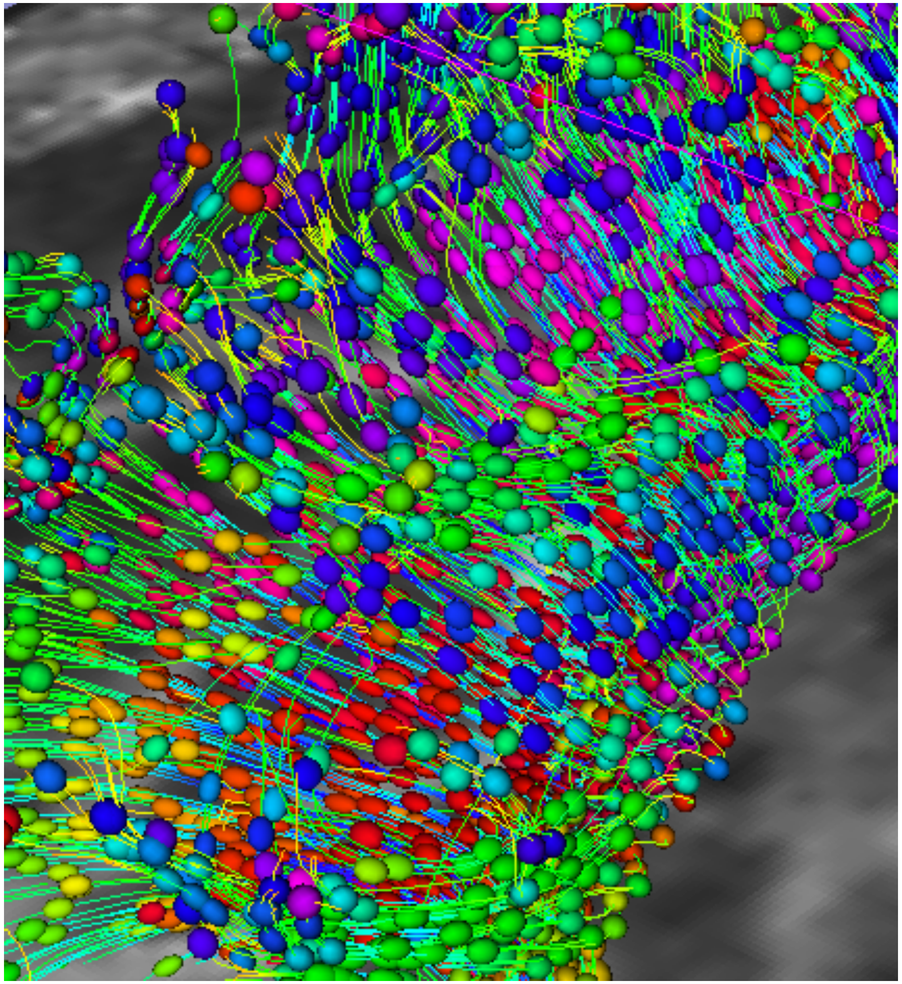
Scalar Range: 0 255

Glyph Type: Ellipsoids

Scale Factor: 14.00

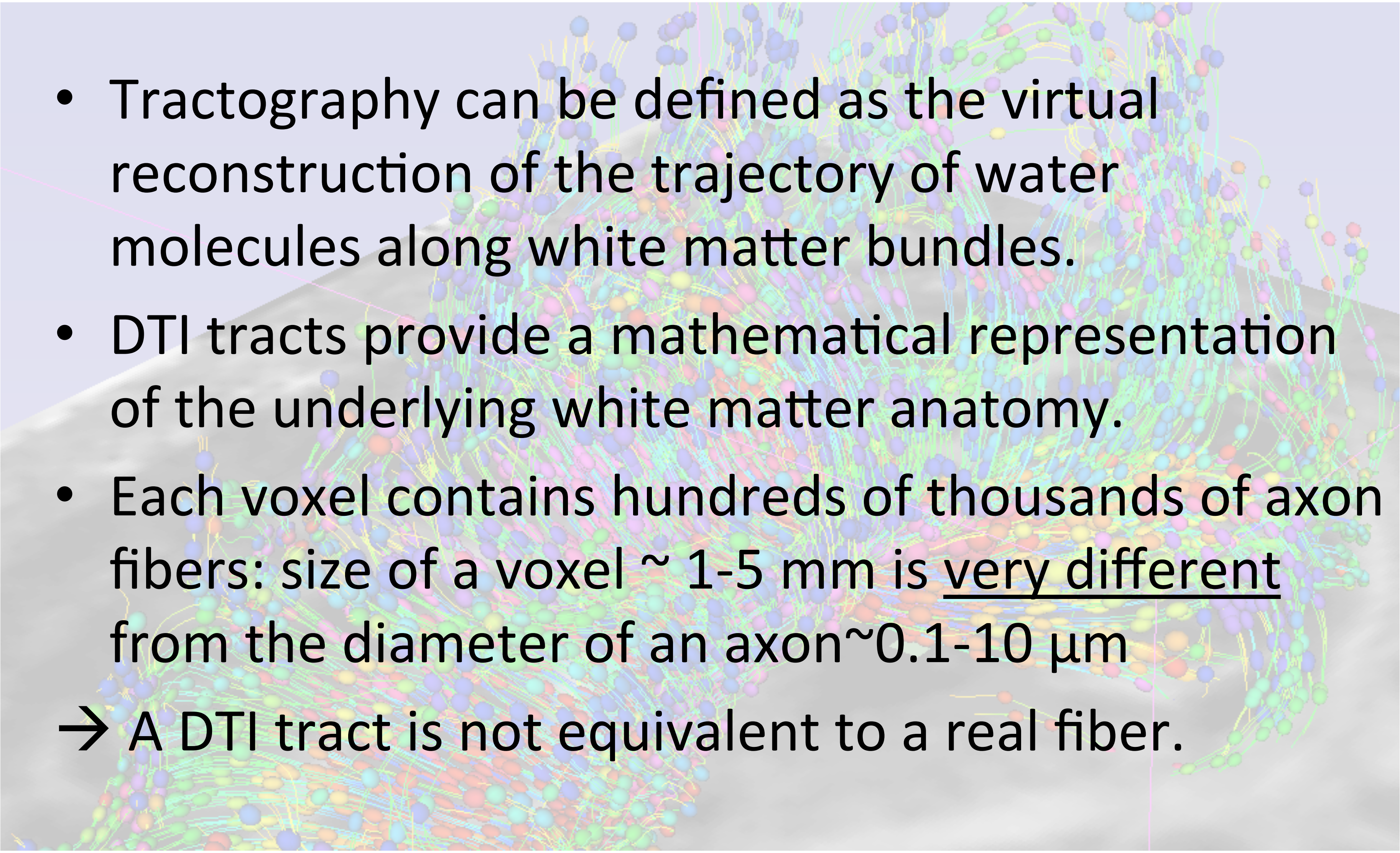
Spacing: 5.00

Go back to the conventional layout, unselect Slice Visibility 'red', and click on the eye icon in the red viewer to turn off the visibility of the red slice in the 3D viewer



Part 3:
From tensors to tracts

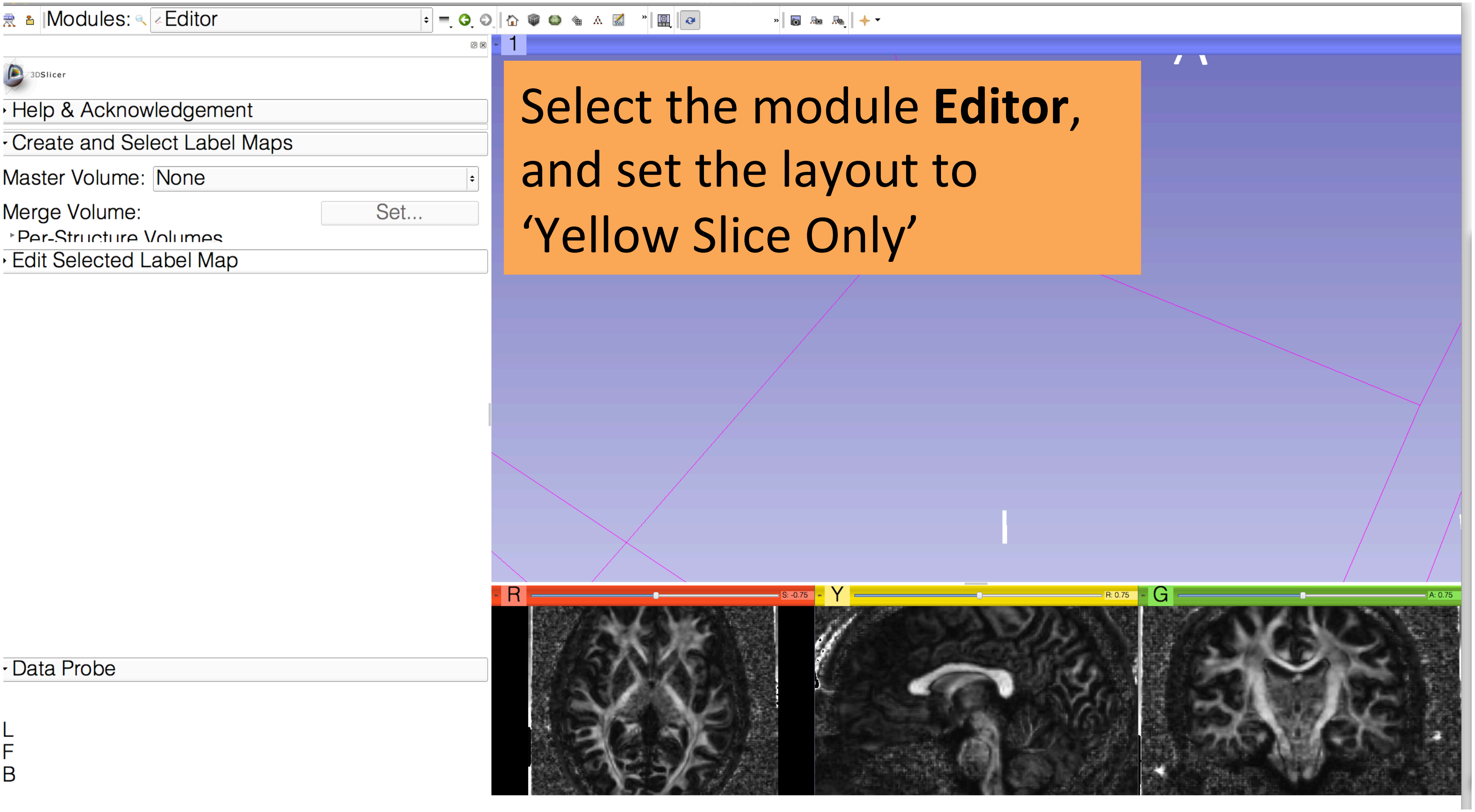
Diffusion MRI tractography



- Tractography can be defined as the virtual reconstruction of the trajectory of water molecules along white matter bundles.
- DTI tracts provide a mathematical representation of the underlying white matter anatomy.
- Each voxel contains hundreds of thousands of axon fibers: size of a voxel ~ 1-5 mm is <u>very different</u> from the diameter of an axon~0.1-10 µm

→ A DTI tract is not equivalent to a real fiber.

Tractography Seeding: ROI definition

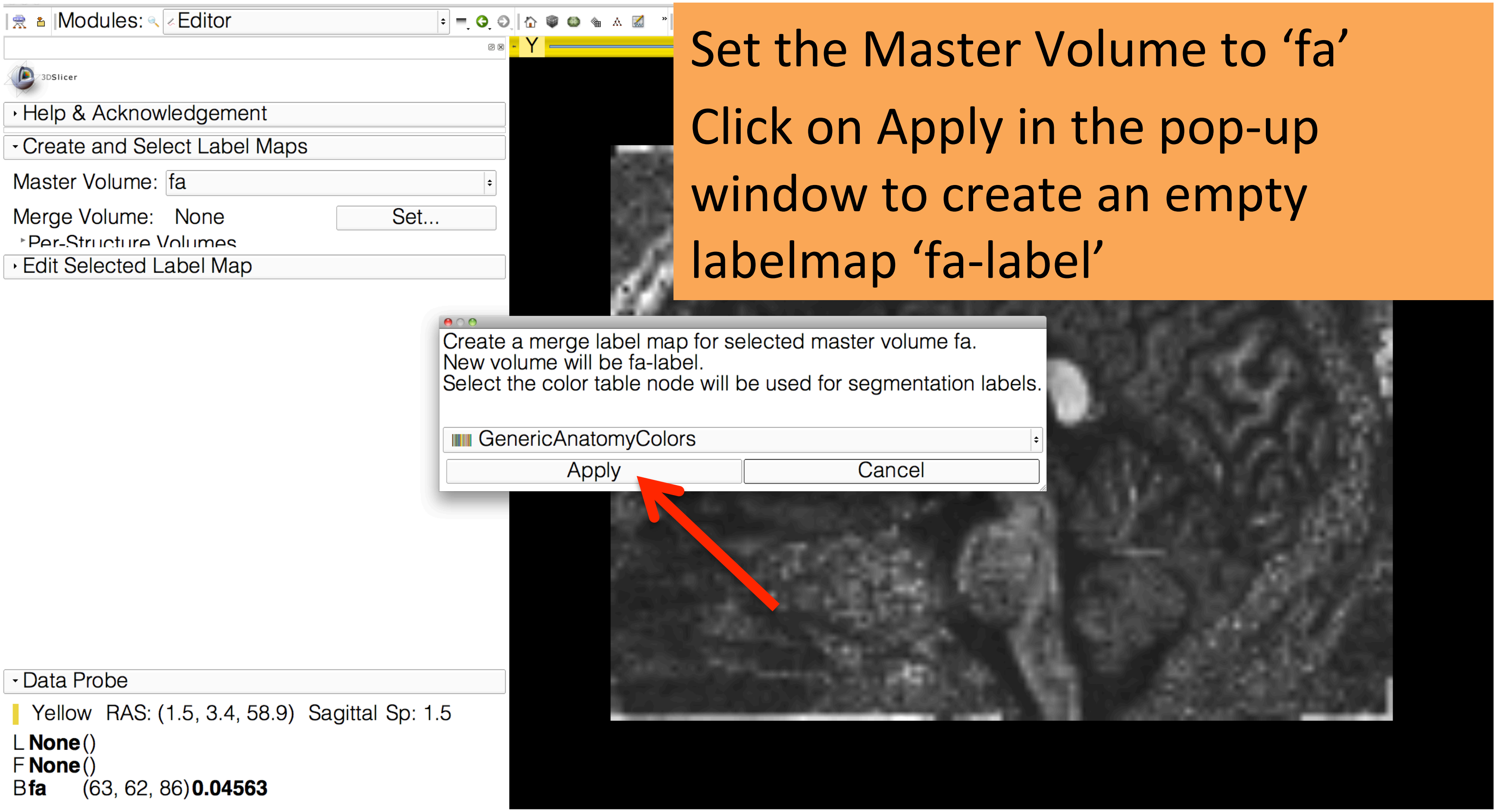


Modules: Editor

Master Volume: None

Select the module **Editor**, and set the layout to ‘Yellow Slice Only’

ROI Definition



Set the Master Volume to ‘fa’

Click on Apply in the pop-up window to create an empty labelmap ‘fa-label’

Master Volume: fa

Merge Volume: None

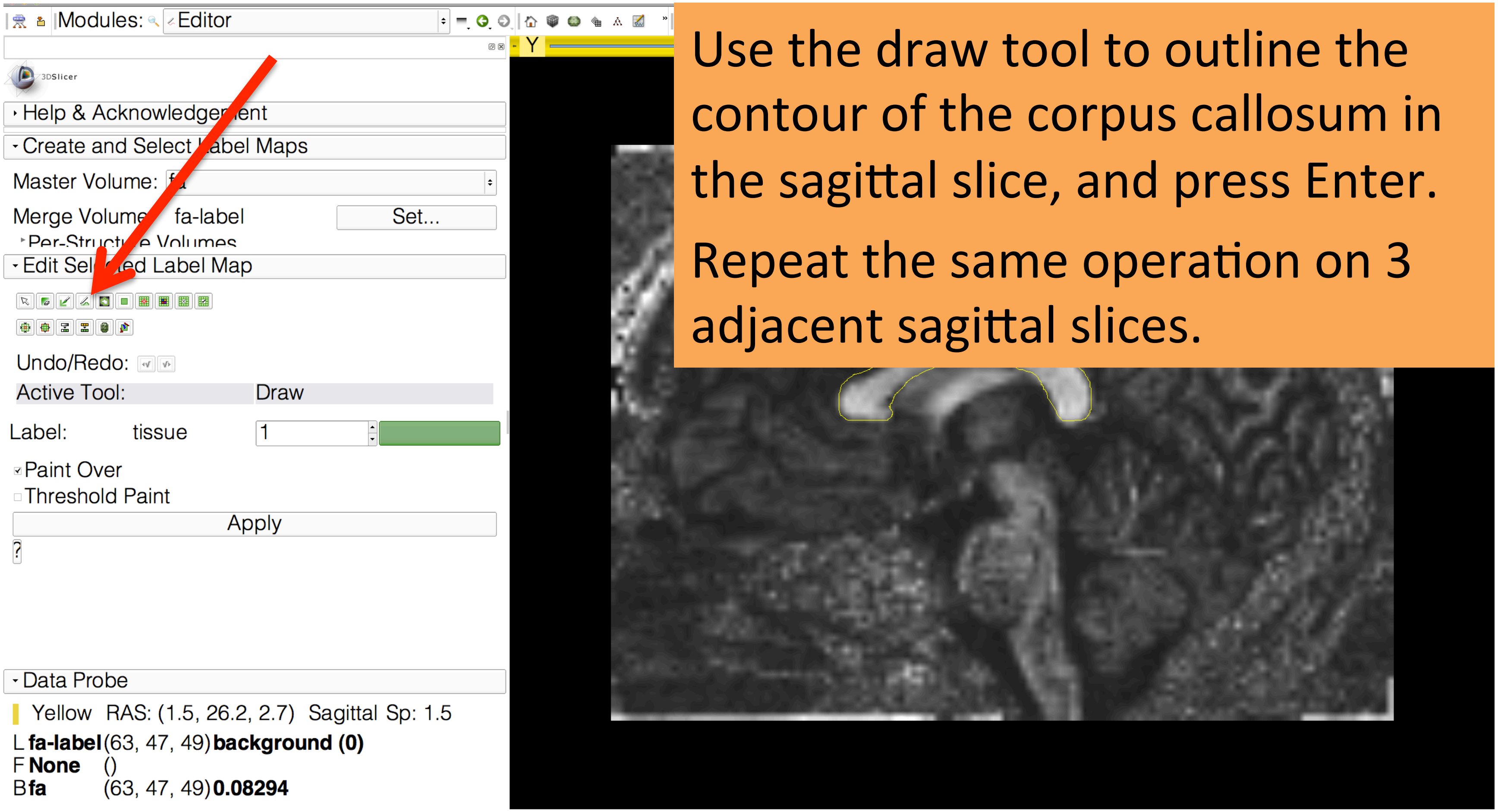
Create a merge label map for selected master volume fa.
New volume will be fa-label.
Select the color table node will be used for segmentation labels.

GenericAnatomyColors

Yellow RAS: (1.5, 3.4, 58.9) Sagittal Sp: 1.5

L **None** ()
F **None** ()
B **fa** (63, 62, 86) **0.04563**

ROI Drawing



Modules: Editor

Master Volume: fa

Merge Volume: fa-label

Undo/Redo:

Active Tool: Draw

Label: tissue 1

☑ Paint Over

☐ Threshold Paint

Yellow RAS: (1.5, 26.2, 2.7) Sagittal Sp: 1.5

L **fa-label** (63, 47, 49) **background (0)**

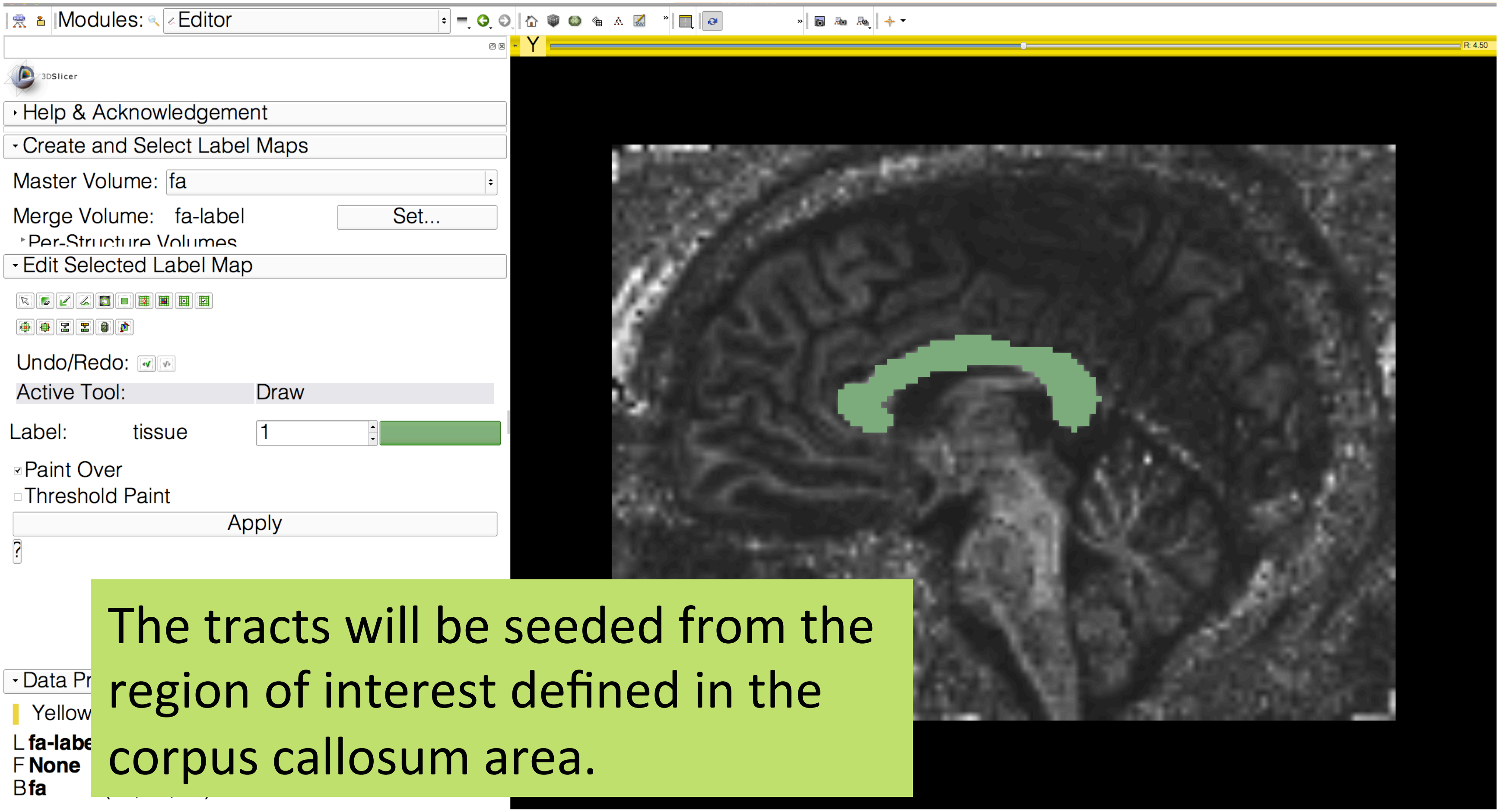
F **None** ()

B **fa** (63, 47, 49) **0.08294**

Use the draw tool to outline the contour of the corpus callosum in the sagittal slice, and press Enter.

Repeat the same operation on 3 adjacent sagittal slices.

ROI Drawing



Modules: Editor

Master Volume: fa

Merge Volume: fa-label

Undo/Redo:

Active Tool: Draw

Label: tissue 1

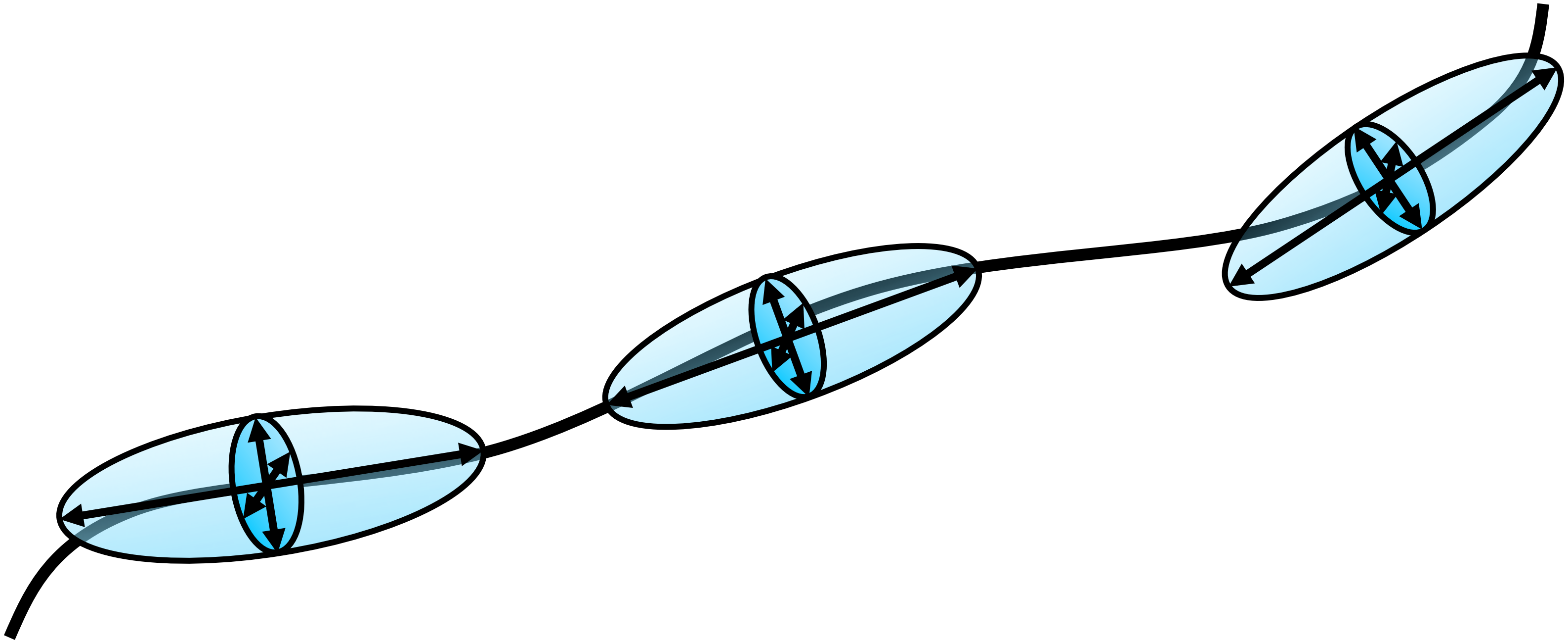
☑ Paint Over

☐ Threshold Paint

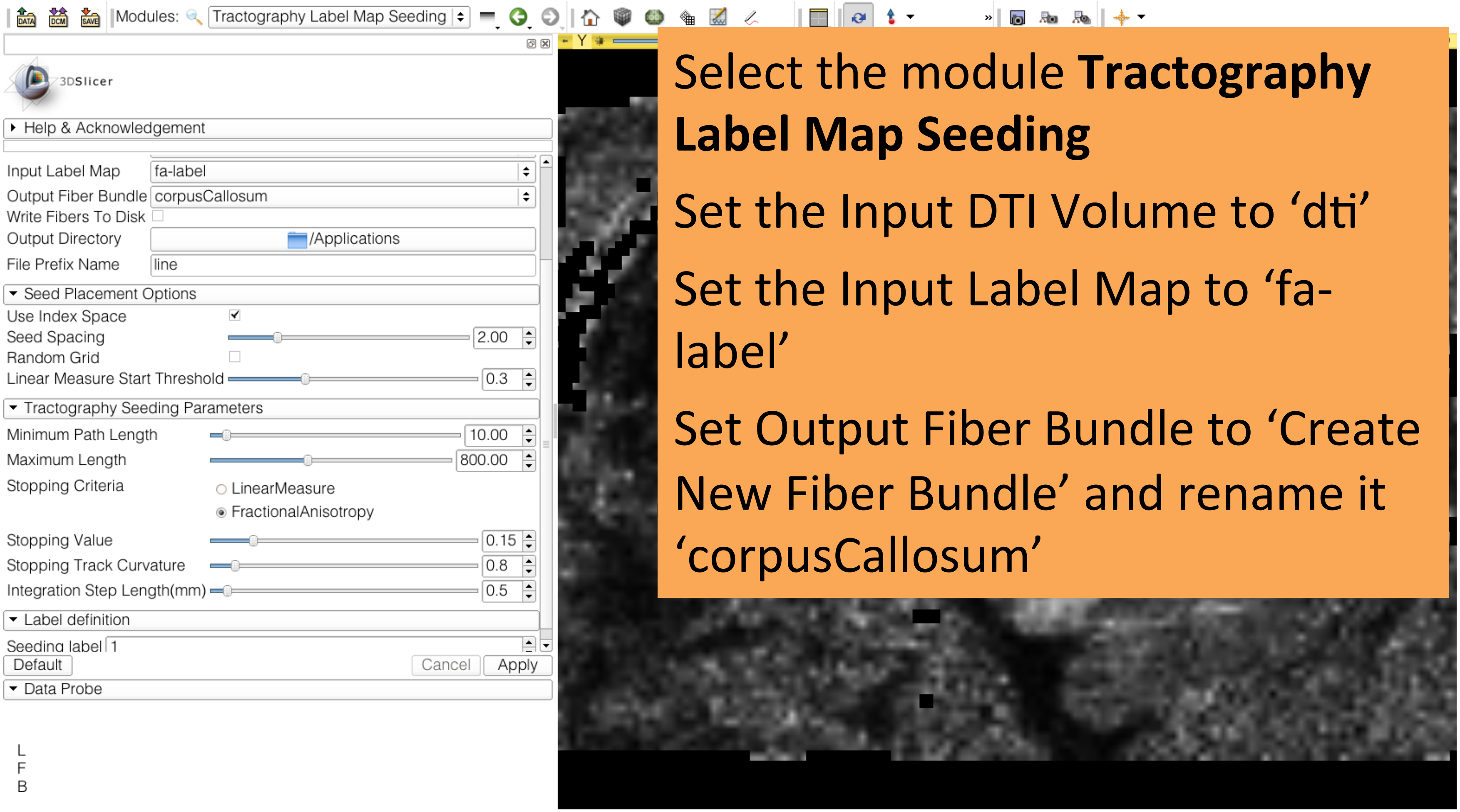
The tracts will be seeded from the region of interest defined in the corpus callosum area.

Streamline tractography

Underlying Assumption: the orientation of the fibers is collinear with the direction of the principal eigenvector



Labelmap Seeding: I/O



Modules: Tractography Label Map Seeding

Input Label Map: fa-label
Output Fiber Bundle: corpusCallosum
Write Fibers To Disk: ☐
Output Directory: /Applications
File Prefix Name: line

Seed Placement Options
Use Index Space: ☑
Seed Spacing: 2.00
Random Grid: ☐
Linear Measure Start Threshold: 0.3

Tractography Seeding Parameters
Minimum Path Length: 10.00
Maximum Length: 800.00
Stopping Criteria: ○ LinearMeasure ● FractionalAnisotropy
Stopping Value: 0.15
Stopping Track Curvature: 0.8
Integration Step Length(mm): 0.5

Label definition
Seeding label: 1

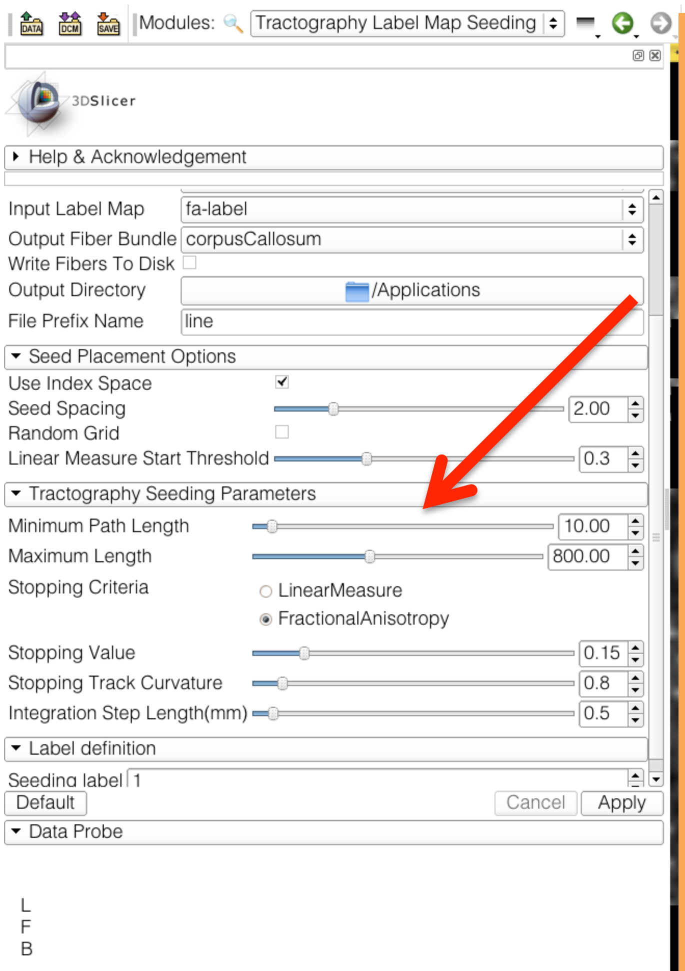
Select the module **Tractography Label Map Seeding**

Set the Input DTI Volume to 'dti'

Set the Input Label Map to 'fa-label'

Set Output Fiber Bundle to 'Create New Fiber Bundle' and rename it 'corpusCallosum'

Labelmap Seeding: parameters



Input Label Map: fa-label

Output Fiber Bundle: corpusCallosum

Write Fibers To Disk ☐

Output Directory: /Applications

File Prefix Name: line

Seed Placement Options

Use Index Space ☑

Seed Spacing: 2.00

Random Grid ☐

Linear Measure Start Threshold: 0.3

Tractography Seeding Parameters

Minimum Path Length: 10.00

Maximum Length: 800.00

Stopping Criteria: ○ LinearMeasure ● FractionalAnisotropy

Stopping Value: 0.15

Stopping Track Curvature: 0.8

Integration Step Length(mm): 0.5

Label definition

Seeding label: 1

Select the Seed Placement Options to 'Use Index Space'.

Select Stopping Mode 'Fractional Anisotropy'

Select the default tractography Seeding parameters:

-Minimum length: 10 mm

-Maximum length: 800 mm

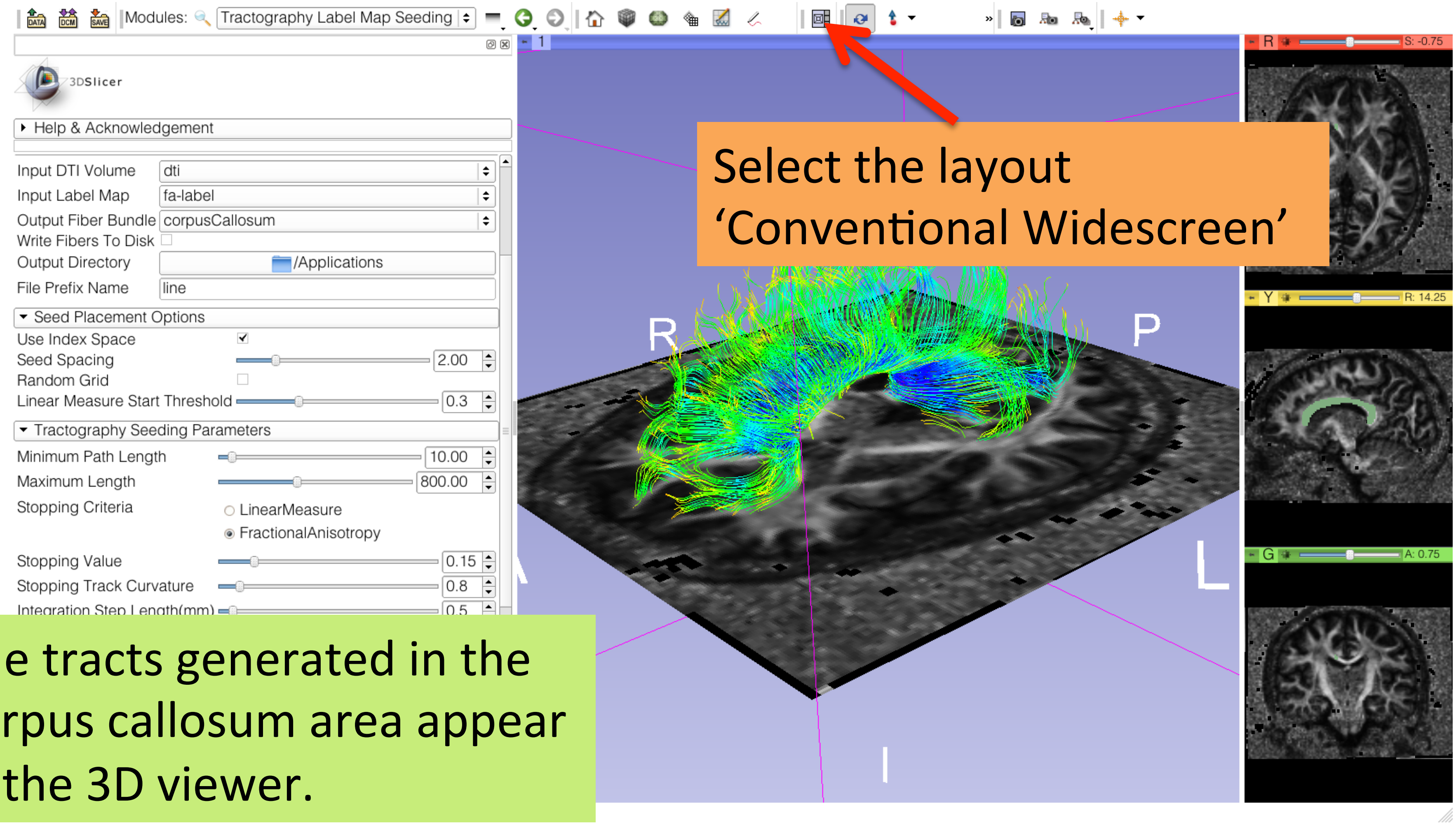
-Stopping value: 0.15

-Stopping track curvature: 0.8

-Integration step length: 0.5 mm

Click on **Apply**

Labelmap Seeding: Tracts



Modules: Tractography Label Map Seeding

Help & Acknowledgement

Input DTI Volume: dti
Input Label Map: fa-label
Output Fiber Bundle: corpusCallosum
Write Fibers To Disk ☐
Output Directory: /Applications
File Prefix Name: line

Seed Placement Options

Use Index Space ☑
Seed Spacing: 2.00
Random Grid ☐
Linear Measure Start Threshold: 0.3

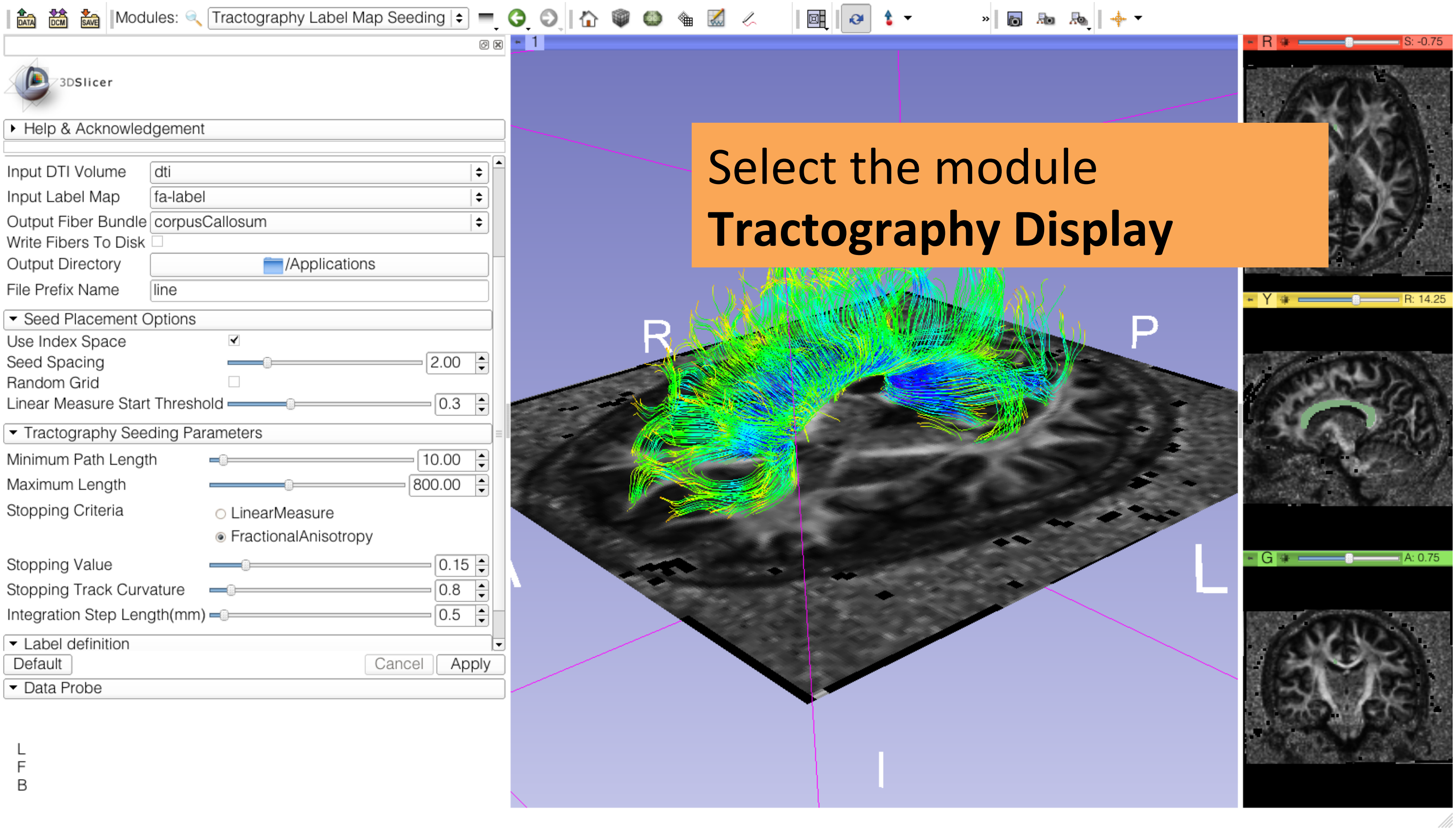
Tractography Seeding Parameters

Minimum Path Length: 10.00
Maximum Length: 800.00
Stopping Criteria: ○ LinearMeasure ● FractionalAnisotropy
Stopping Value: 0.15
Stopping Track Curvature: 0.8
Integration Step Length(mm): 0.5

Select the layout ‘Conventional Widescreen’

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

Labelmap Seeding: Tracts



Select the module **Tractography Display**

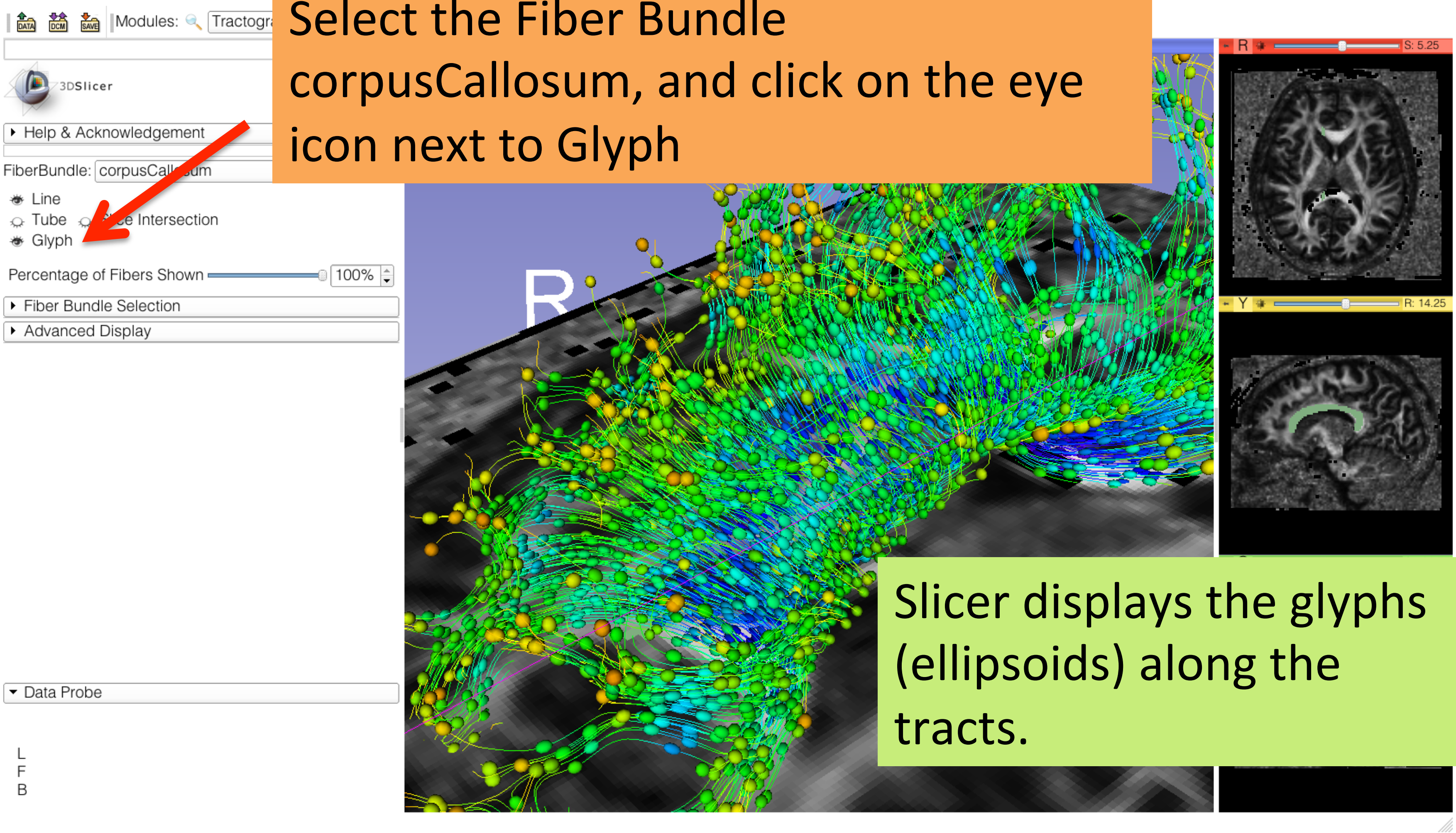
Modules: Tractography Label Map Seeding

Input DTI Volume: dti
Input Label Map: fa-label
Output Fiber Bundle: corpusCallosum
Write Fibers To Disk: ☐
Output Directory: /Applications
File Prefix Name: line

Seed Placement Options
Use Index Space: ☑
Seed Spacing: 2.00
Random Grid: ☐
Linear Measure Start Threshold: 0.3

Tractography Seeding Parameters
Minimum Path Length: 10.00
Maximum Length: 800.00
Stopping Criteria: ○ LinearMeasure ● FractionalAnisotropy
Stopping Value: 0.15
Stopping Track Curvature: 0.8
Integration Step Length(mm): 0.5

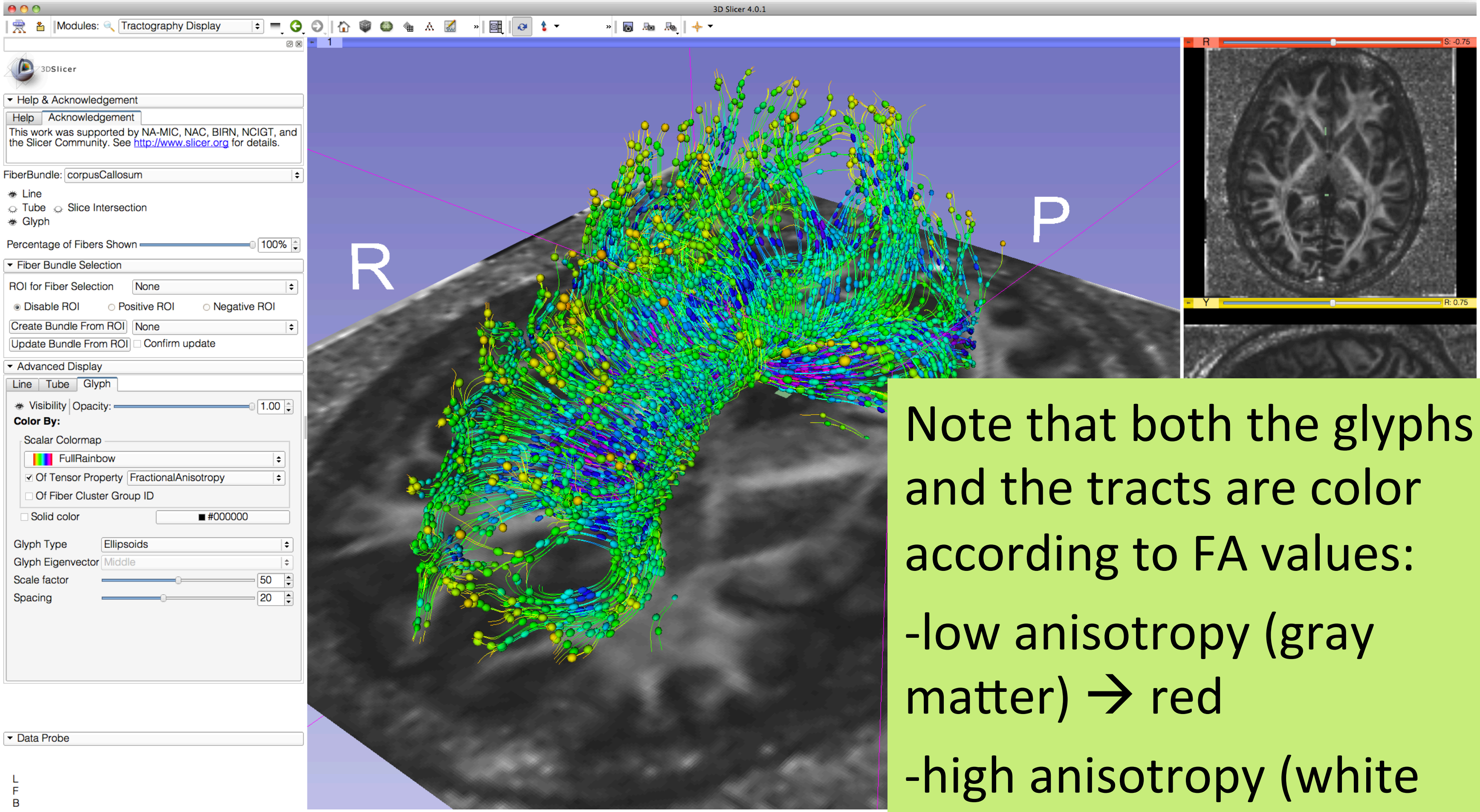
Tractography Results



Select the Fiber Bundle corpusCallosum, and click on the eye icon next to Glyph

Slicer displays the glyphs (ellipsoids) along the tracts.

Tractography Results



Modules: Tractography Display

Help & Acknowledgement

Help | Acknowledgement

This work was supported by NA-MIC, NAC, BIRN, NCIGT, and the Slicer Community. See http://www.slicer.org for details.

FiberBundle: corpusCallosum

Line
Tube
Slice Intersection
Glyph

Percentage of Fibers Shown 100%

Fiber Bundle Selection

ROI for Fiber Selection: None

● Disable ROI ○ Positive ROI ○ Negative ROI

Create Bundle From ROI: None

Update Bundle From ROI ☐ Confirm update

Advanced Display

Line | Tube | Glyph

Visibility | Opacity: 1.00

Color By:

Scalar Colormap

FullRainbow

☑ Of Tensor Property FractionalAnisotropy

☐ Of Fiber Cluster Group ID

☐ Solid color #000000

Glyph Type: Ellipsoids

Glyph Eigenvector: Middle

Scale factor: 50

Spacing: 20

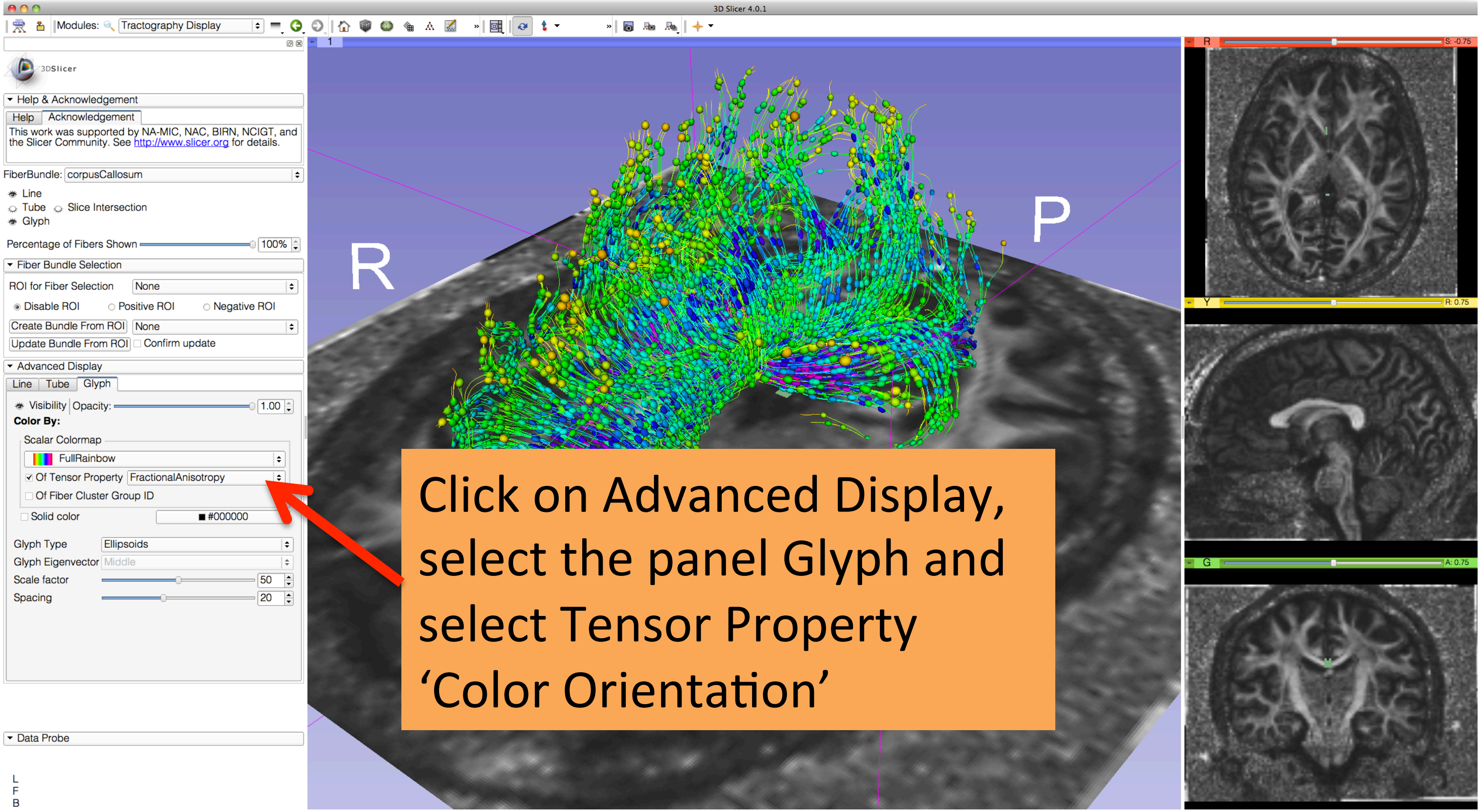
Data Probe

Note that both the glyphs and the tracts are color according to FA values:

-low anisotropy (gray matter) → red

-high anisotropy (white matter) → blue

Tractography Results



3D Slicer 4.0.1

Modules: Tractography Display

Help & Acknowledgement

Help | Acknowledgement

This work was supported by NA-MIC, NAC, BIRN, NCIGT, and the Slicer Community. See http://www.slicer.org for details.

FiberBundle: corpusCallosum

● Line
○ Tube ○ Slice Intersection
● Glyph

Percentage of Fibers Shown 100%

Fiber Bundle Selection

ROI for Fiber Selection: None

● Disable ROI ○ Positive ROI ○ Negative ROI

Create Bundle From ROI: None

Update Bundle From ROI ☐ Confirm update

Advanced Display

Line | Tube | Glyph

● Visibility Opacity: 1.00

Color By:

Scalar Colormap: FullRainbow

☑ Of Tensor Property: FractionalAnisotropy

☐ Of Fiber Cluster Group ID

☐ Solid color: #000000

Glyph Type: Ellipsoids

Glyph Eigenvector: Middle

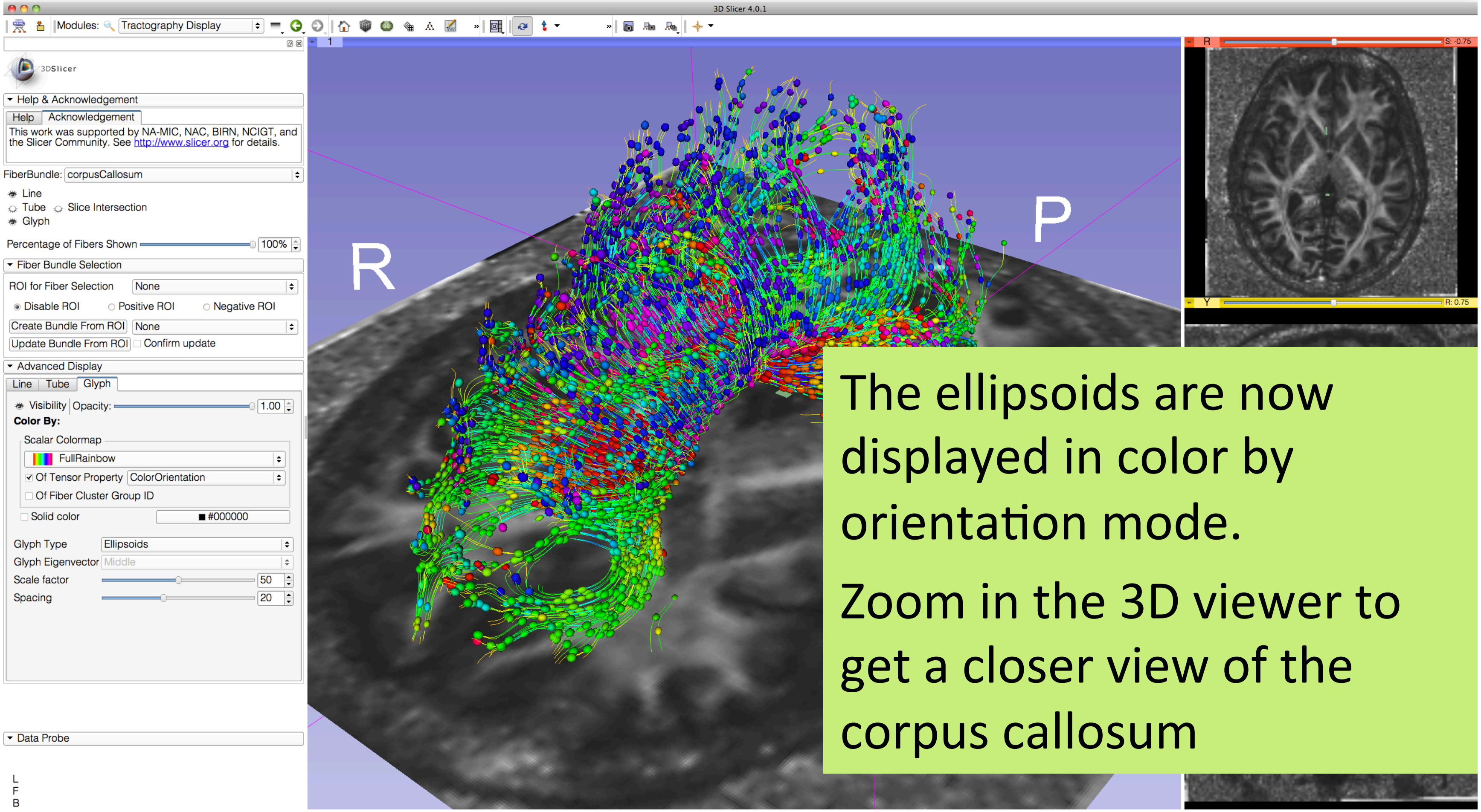
Scale factor: 50

Spacing: 20

Data Probe

Click on Advanced Display, select the panel Glyph and select Tensor Property 'Color Orientation'

Tractography Results



3D Slicer 4.0.1

Modules: Tractography Display

Help & Acknowledgement

This work was supported by NA-MIC, NAC, BIRN, NCIGT, and the Slicer Community. See http://www.slicer.org for details.

FiberBundle: corpusCallosum

Percentage of Fibers Shown: 100%

ROI for Fiber Selection: None

● Disable ROI ○ Positive ROI ○ Negative ROI

Create Bundle From ROI: None

Update Bundle From ROI ☐ Confirm update

Visibility Opacity: 1.00

Color By:

Scalar Colormap: FullRainbow

☑ Of Tensor Property: ColorOrientation

☐ Of Fiber Cluster Group ID

☐ Solid color: #000000

Glyph Type: Ellipsoids

Glyph Eigenvector: Middle

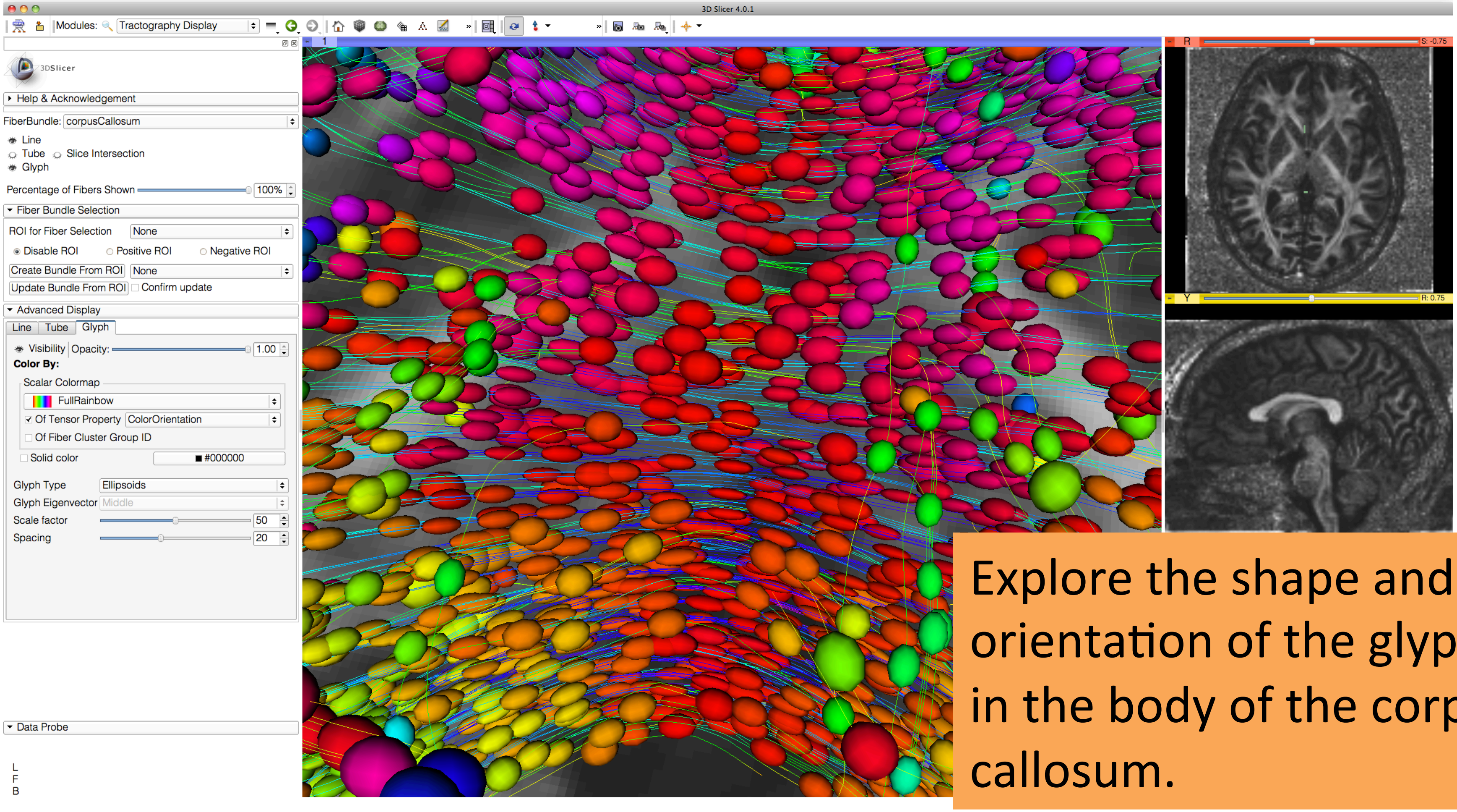
Scale factor: 50

Spacing: 20

The ellipsoids are now displayed in color by orientation mode.

Zoom in the 3D viewer to get a closer view of the corpus callosum

Tractography Results



Modules: Tractography Display

Help & Acknowledgement

FiberBundle: corpusCallosum

Line
Tube
Slice Intersection
Glyph

Percentage of Fibers Shown: 100%

Fiber Bundle Selection

ROI for Fiber Selection: None

● Disable ROI ○ Positive ROI ○ Negative ROI

Create Bundle From ROI: None

Update Bundle From ROI ☐ Confirm update

Advanced Display

Line | Tube | Glyph

Visibility | Opacity: 1.00

Color By:

Scalar Colormap: FullRainbow

☑ Of Tensor Property: ColorOrientation

☐ Of Fiber Cluster Group ID

☐ Solid color: #000000

Glyph Type: Ellipsoids

Glyph Eigenvector: Middle

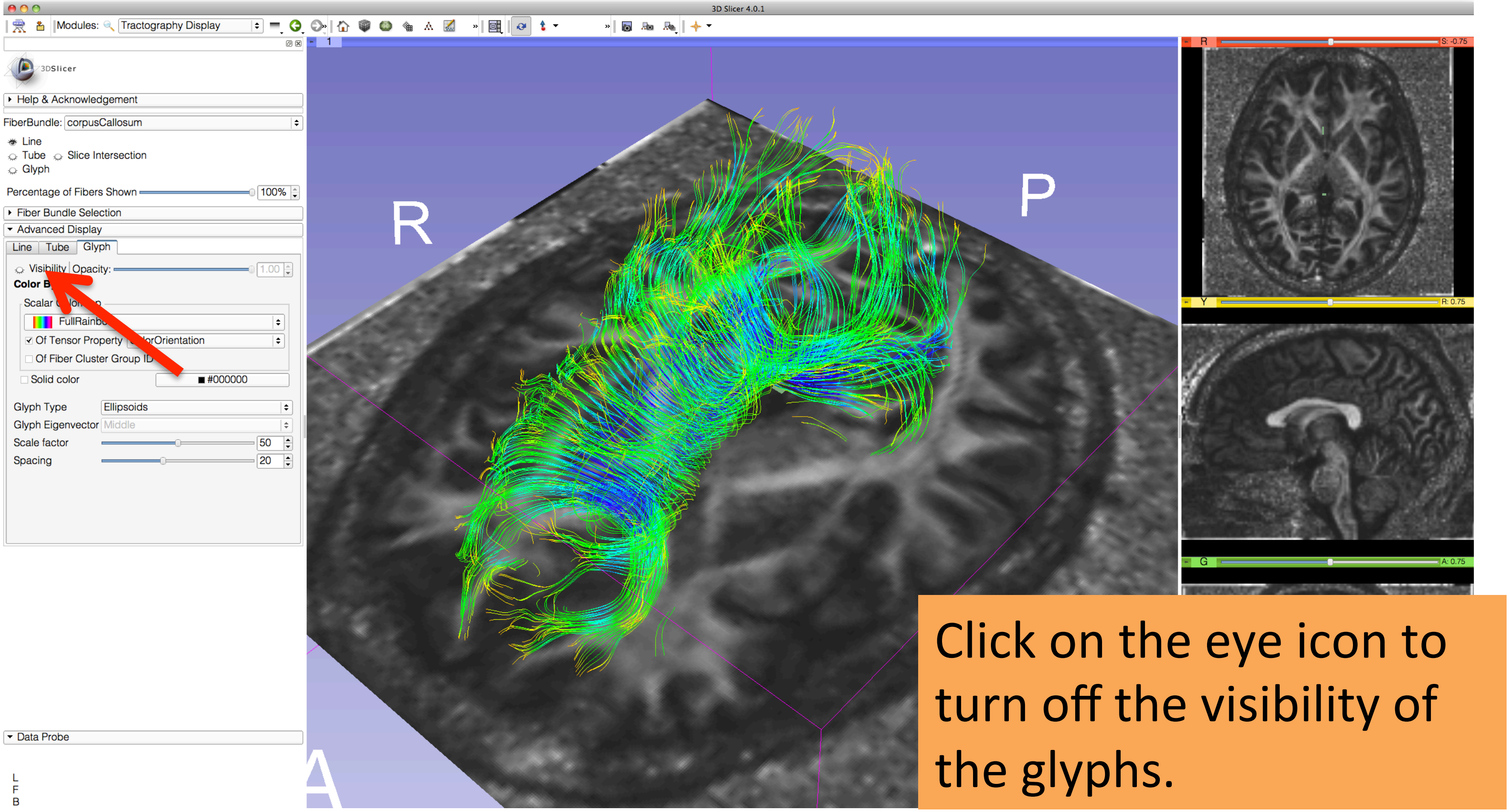
Scale factor: 50

Spacing: 20

Data Probe

Explore the shape and orientation of the glyphs in the body of the corpus callosum.

Tractography Results



FiberBundle: corpusCallosum

Percentage of Fibers Shown 100%

Opacity: 1.00

Of Tensor Property: ColorOrientation

Solid color #000000

Glyph Type Ellipsoids

Glyph Eigenvector Middle

Scale factor 50

Spacing 20

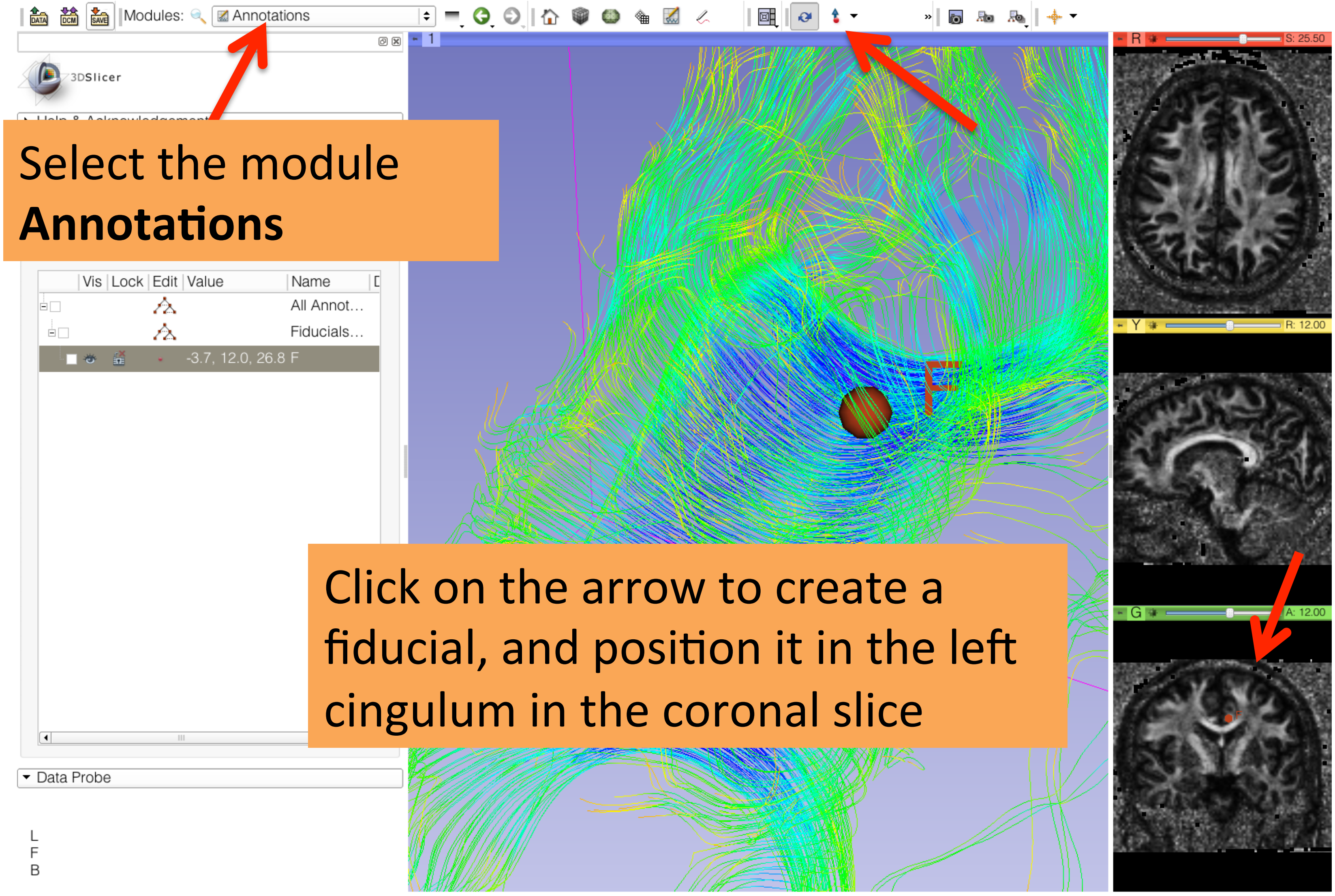
S: -0.75

R: 0.75

A: 0.75

Click on the eye icon to turn off the visibility of the glyphs.

Fiducial Seeding

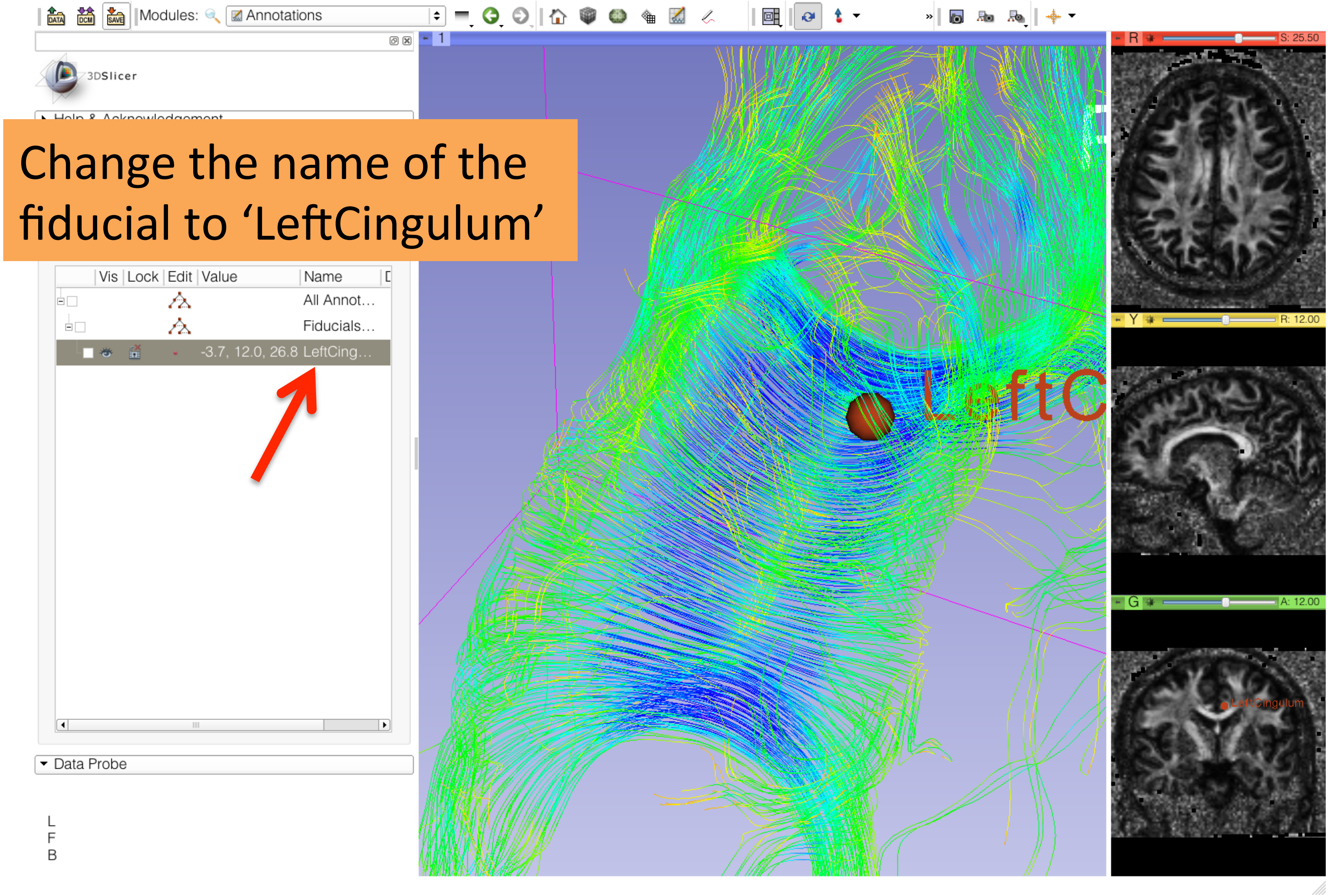


Vis	Lock	Edit	Value	Name
				All Annot...
				Fiducials...
			-3.7, 12.0, 26.8 F	

Select the module **Annotations**

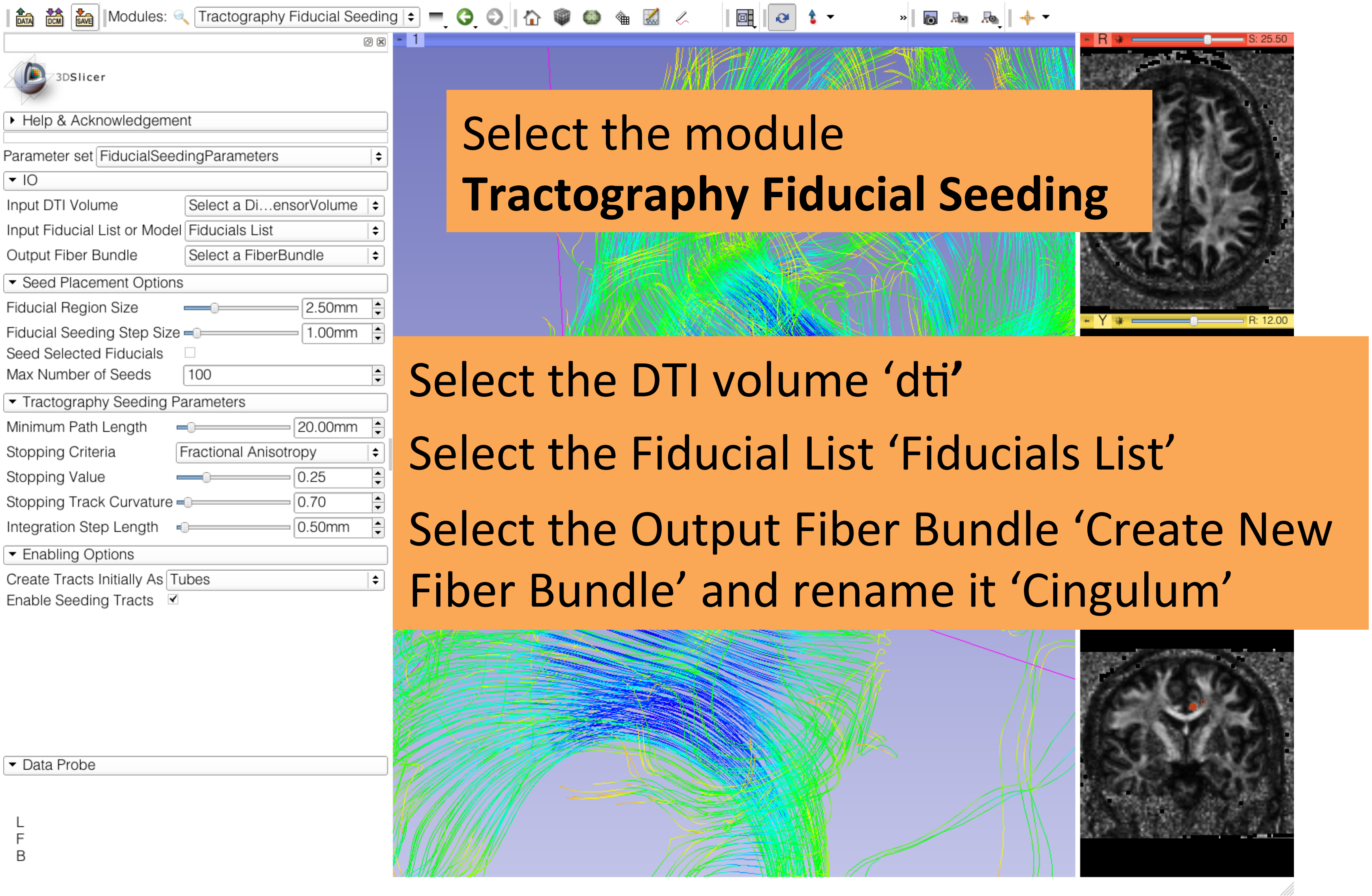
Click on the arrow to create a fiducial, and position it in the left cingulum in the coronal slice

Fiducial Seeding



Change the name of the fiducial to 'LeftCingulum'

Fiducial Seeding



Parameter set FiducialSeedingParameters

IO
Input DTI Volume: Select a Di…ensorVolume
Input Fiducial List or Model: Fiducials List
Output Fiber Bundle: Select a FiberBundle

Seed Placement Options
Fiducial Region Size: 2.50mm
Fiducial Seeding Step Size: 1.00mm
Seed Selected Fiducials ☐
Max Number of Seeds: 100

Tractography Seeding Parameters
Minimum Path Length: 20.00mm
Stopping Criteria: Fractional Anisotropy
Stopping Value: 0.25
Stopping Track Curvature: 0.70
Integration Step Length: 0.50mm

Enabling Options
Create Tracts Initially As: Tubes
Enable Seeding Tracts ☑

Data Probe

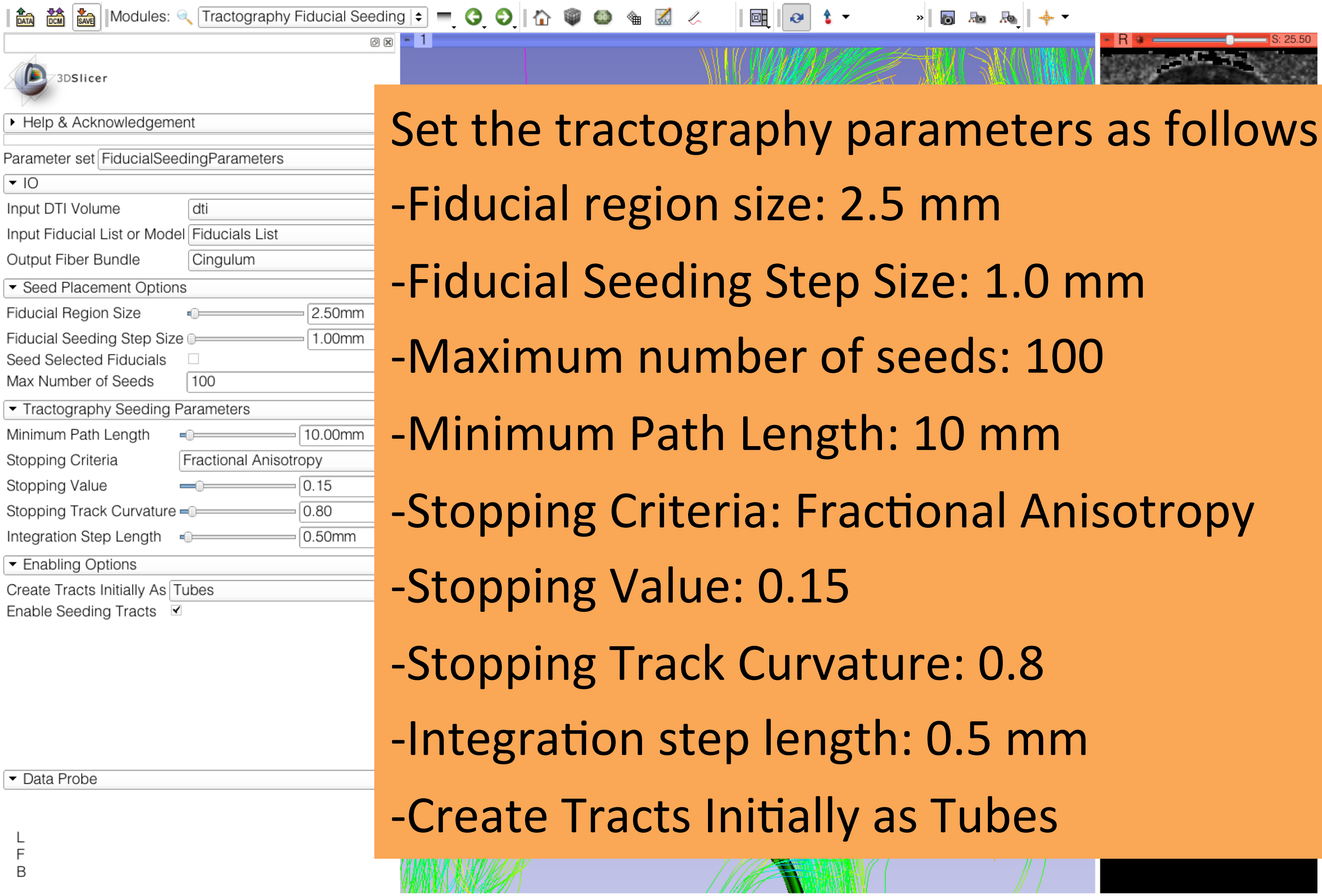
Select the module
Tractography Fiducial Seeding

Select the DTI volume ‘dti’

Select the Fiducial List ‘Fiducials List’

Select the Output Fiber Bundle ‘Create New Fiber Bundle’ and rename it ‘Cingulum’

Fiducial Seeding



Modules: Tractography Fiducial Seeding

Help & Acknowledgement

Parameter set FiducialSeedingParameters

IO

Input DTI Volume	dti
Input Fiducial List or Model	Fiducials List
Output Fiber Bundle	Cingulum

Seed Placement Options

Fiducial Region Size	2.50mm
Fiducial Seeding Step Size	1.00mm
Seed Selected Fiducials	☐
Max Number of Seeds	100

Tractography Seeding Parameters

Minimum Path Length	10.00mm
Stopping Criteria	Fractional Anisotropy
Stopping Value	0.15
Stopping Track Curvature	0.80
Integration Step Length	0.50mm

Enabling Options

Create Tracts Initially As	Tubes
Enable Seeding Tracts	☑

Data Probe

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

-Stopping Criteria: Fractional Anisotropy

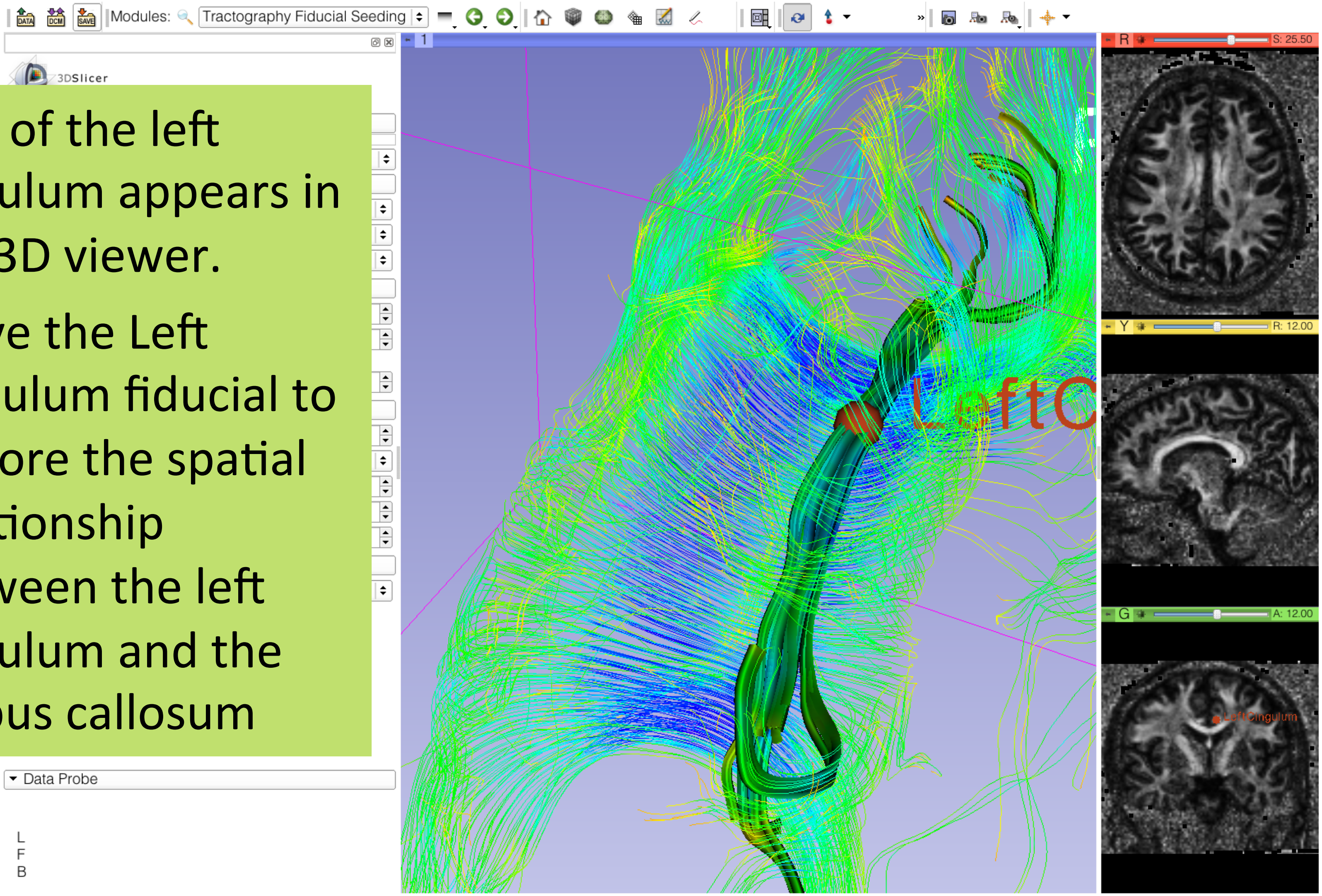
-Stopping Value: 0.15

-Stopping Track Curvature: 0.8

-Integration step length: 0.5 mm

-Create Tracts Initially as Tubes

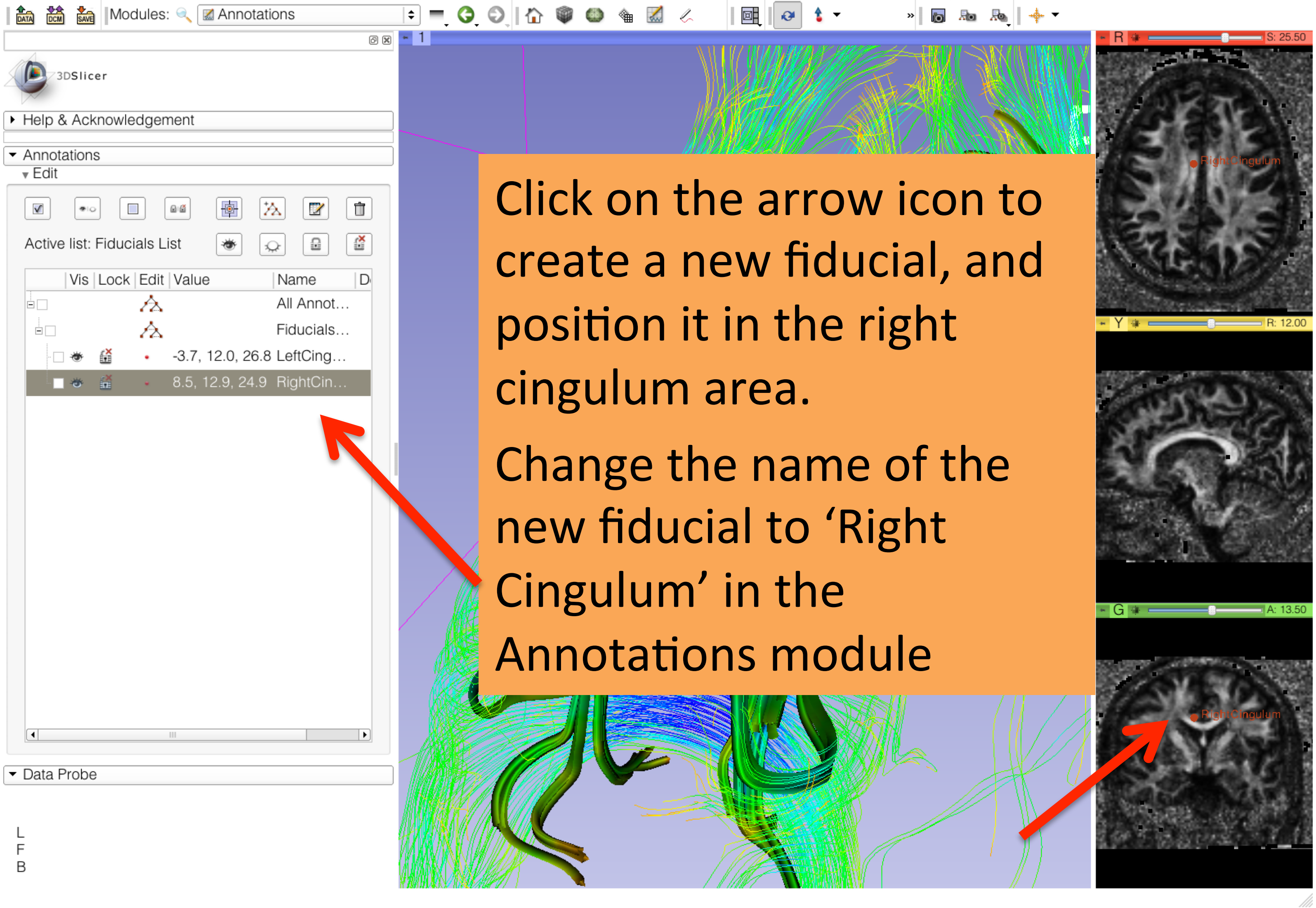
Fiducial Seeding



Part of the left cingulum appears in the 3D viewer.

Move the Left Cingulum fiducial to explore the spatial relationship between the left cingulum and the corpus callosum

Fiducial Seeding



Modules: Annotations

Active list: Fiducials List

Vis	Lock	Edit	Value	Name	D
				All Annot…	
				Fiducials…	
			-3.7, 12.0, 26.8	LeftCing…	
			8.5, 12.9, 24.9	RightCin…	

S: 25.50

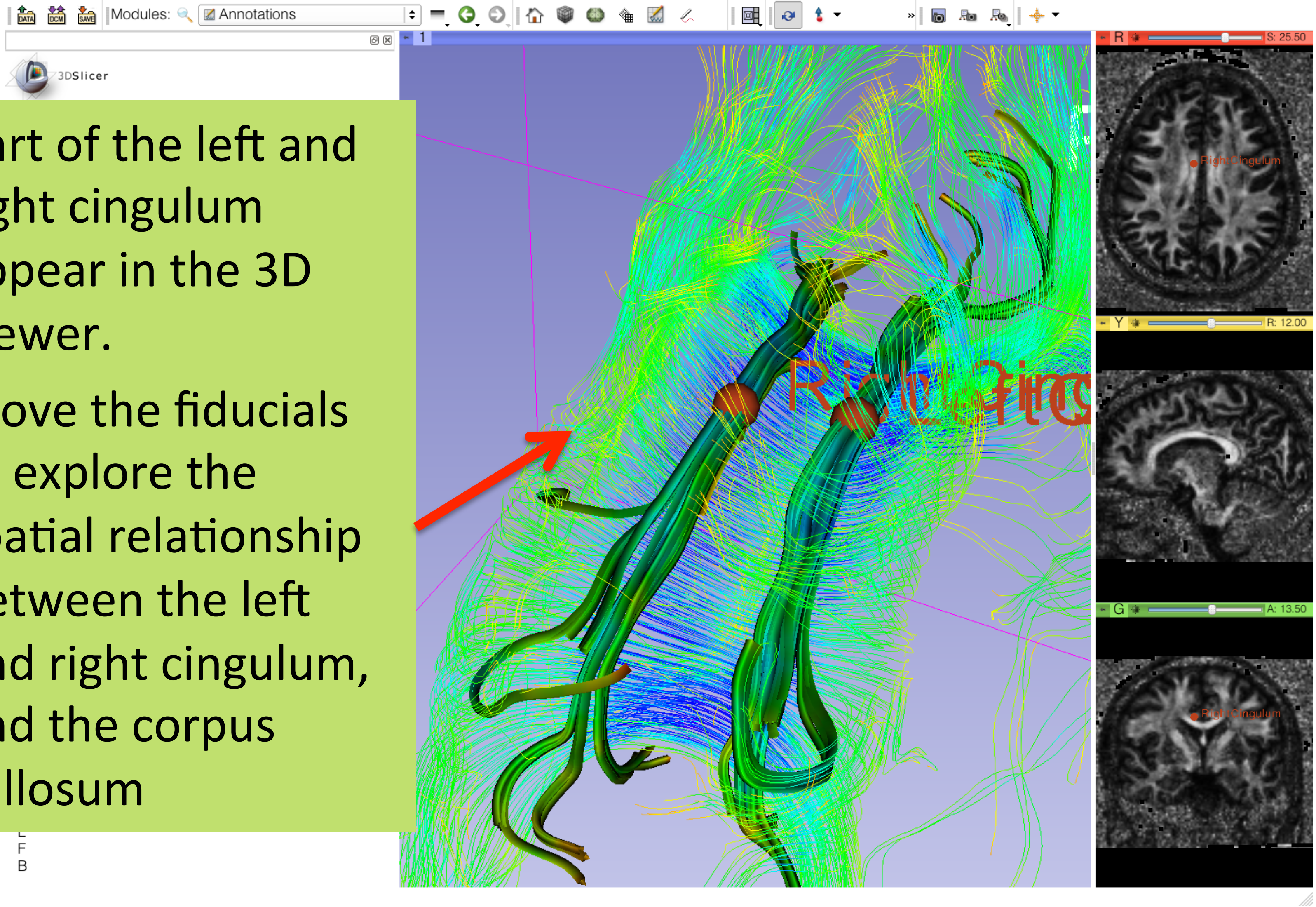
R: 12.00

A: 13.50

Click on the arrow icon to create a new fiducial, and position it in the right cingulum area.

Change the name of the new fiducial to 'Right Cingulum' in the Annotations module

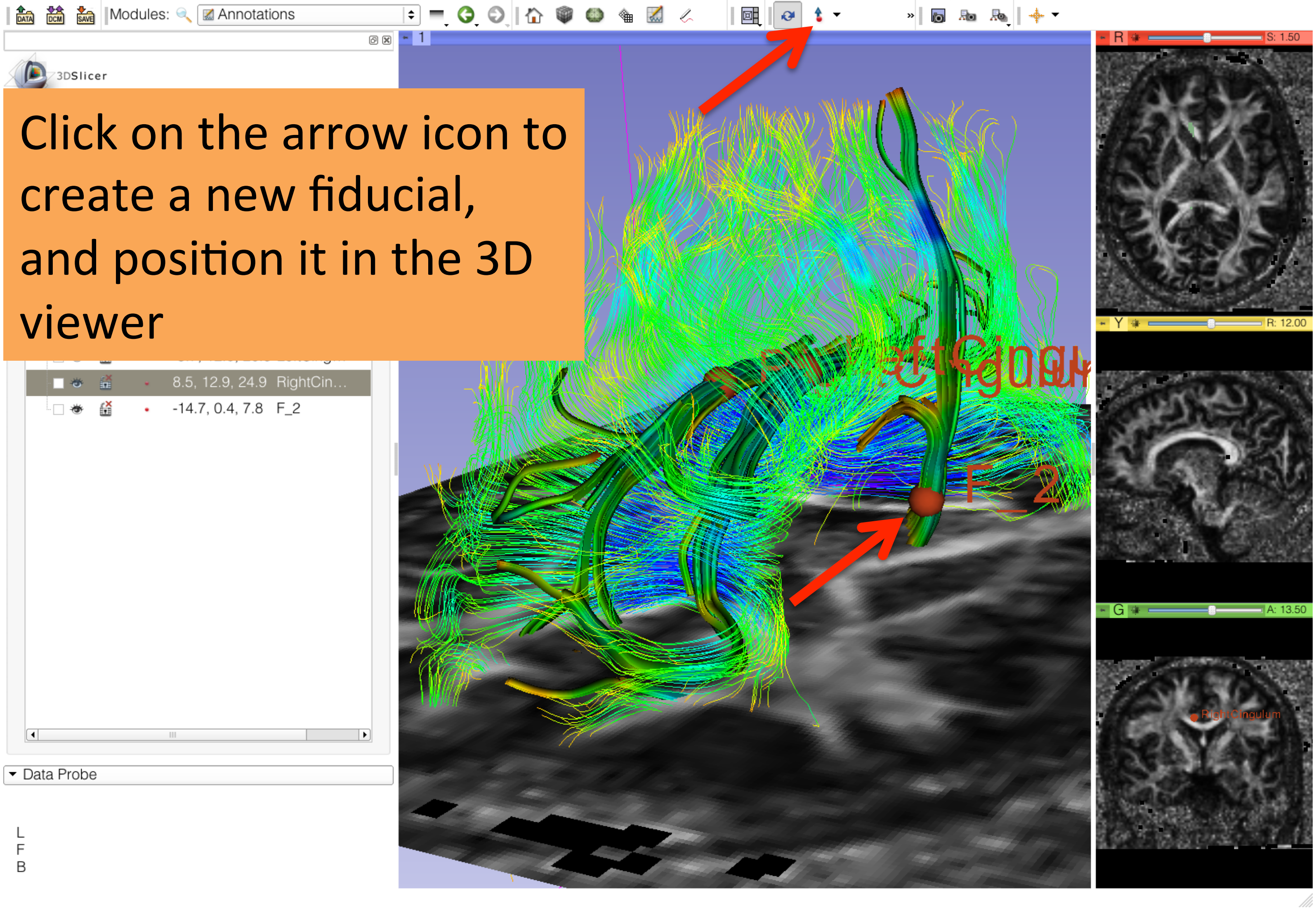
Fiducial Seeding



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

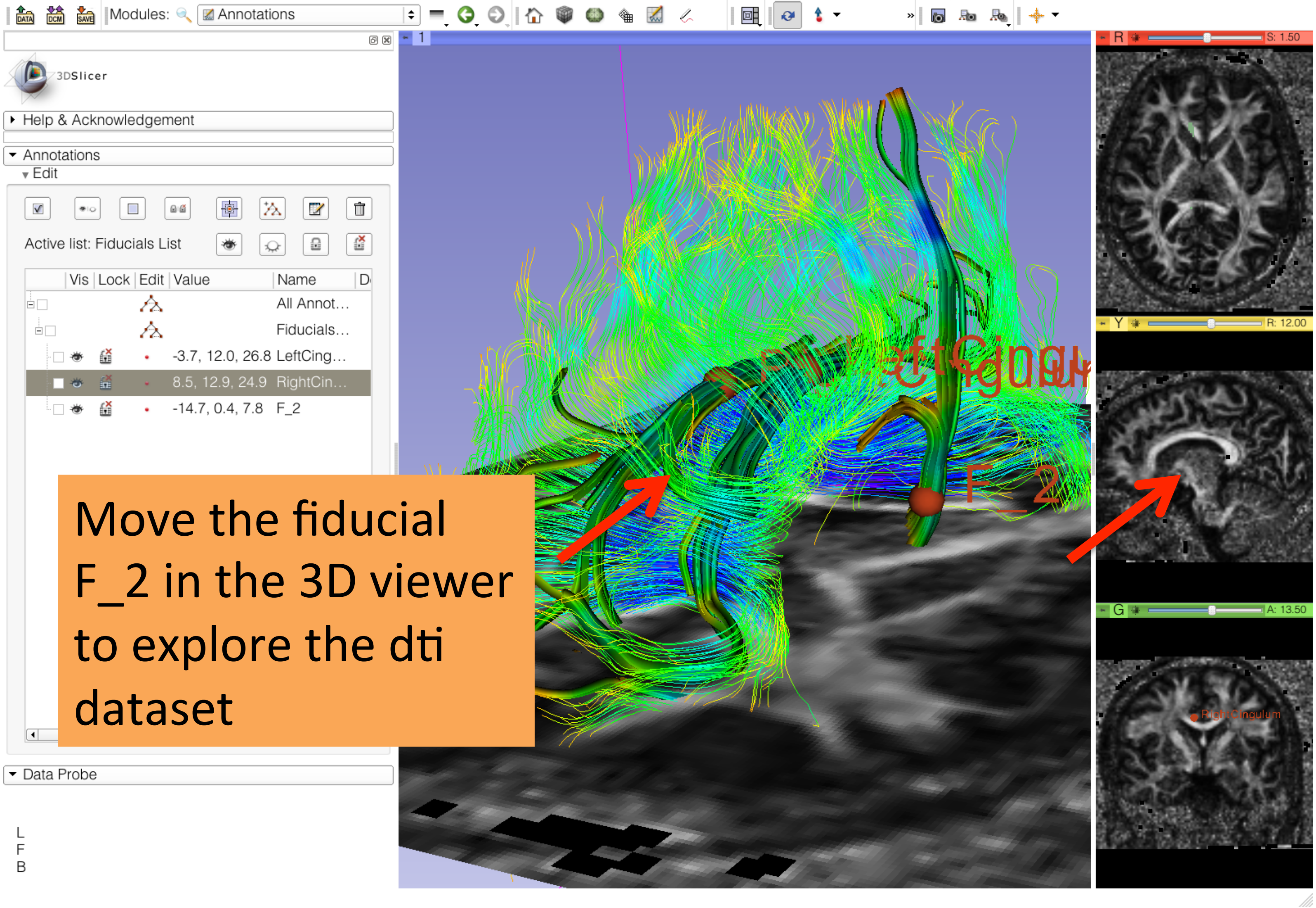


Click on the arrow icon to create a new fiducial, and position it in the 3D viewer

8.5, 12.9, 24.9 RightCin…

-14.7, 0.4, 7.8 F_2

Fiducial Seeding

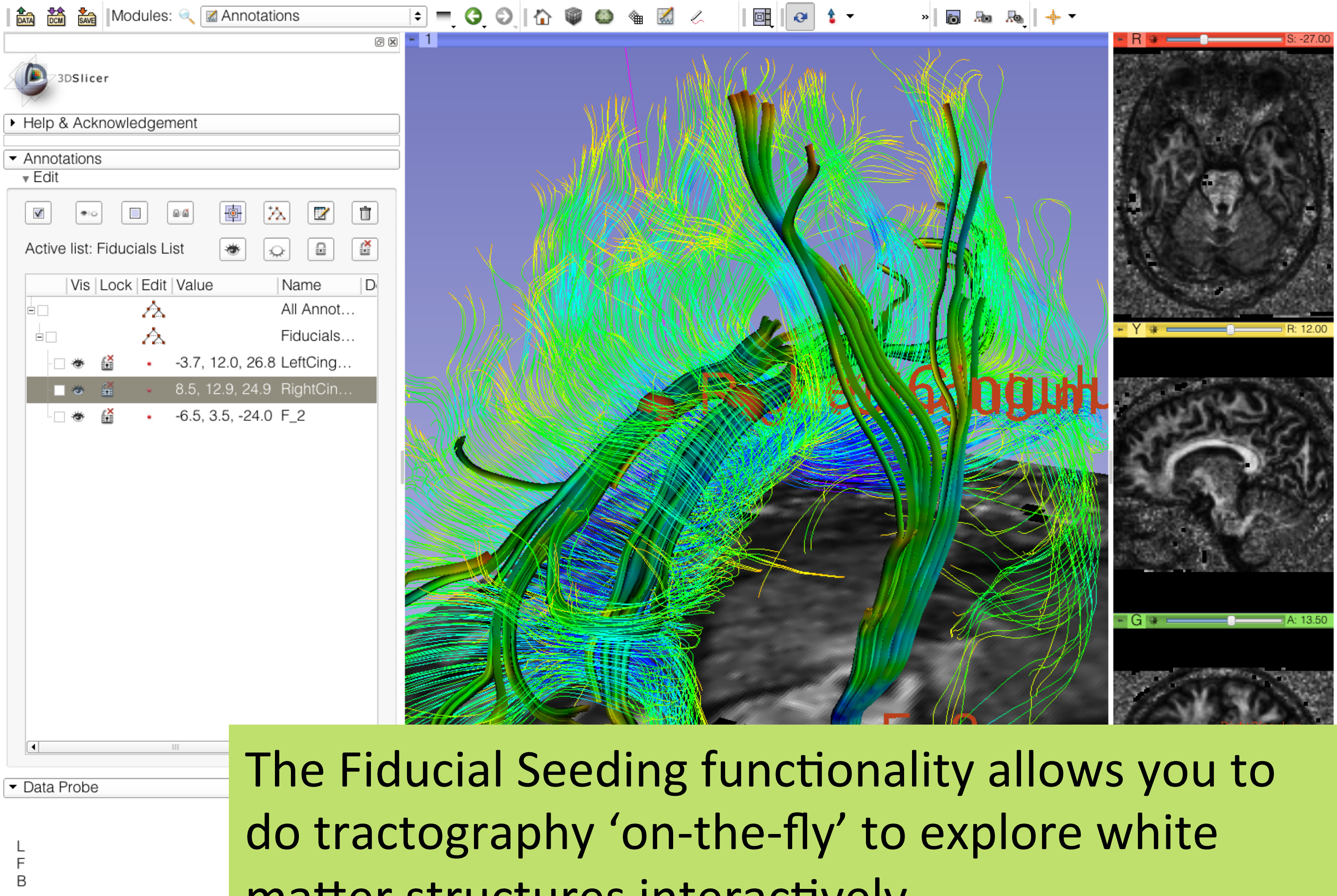


Active list: Fiducials List

Vis	Lock	Edit	Value	Name	D
				All Annot…	
				Fiducials…	
			-3.7, 12.0, 26.8	LeftCing…	
			8.5, 12.9, 24.9	RightCin…	
			-14.7, 0.4, 7.8	F_2	

Move the fiducial F_2 in the 3D viewer to explore the dti dataset

Tractography ‘on-the-fly’

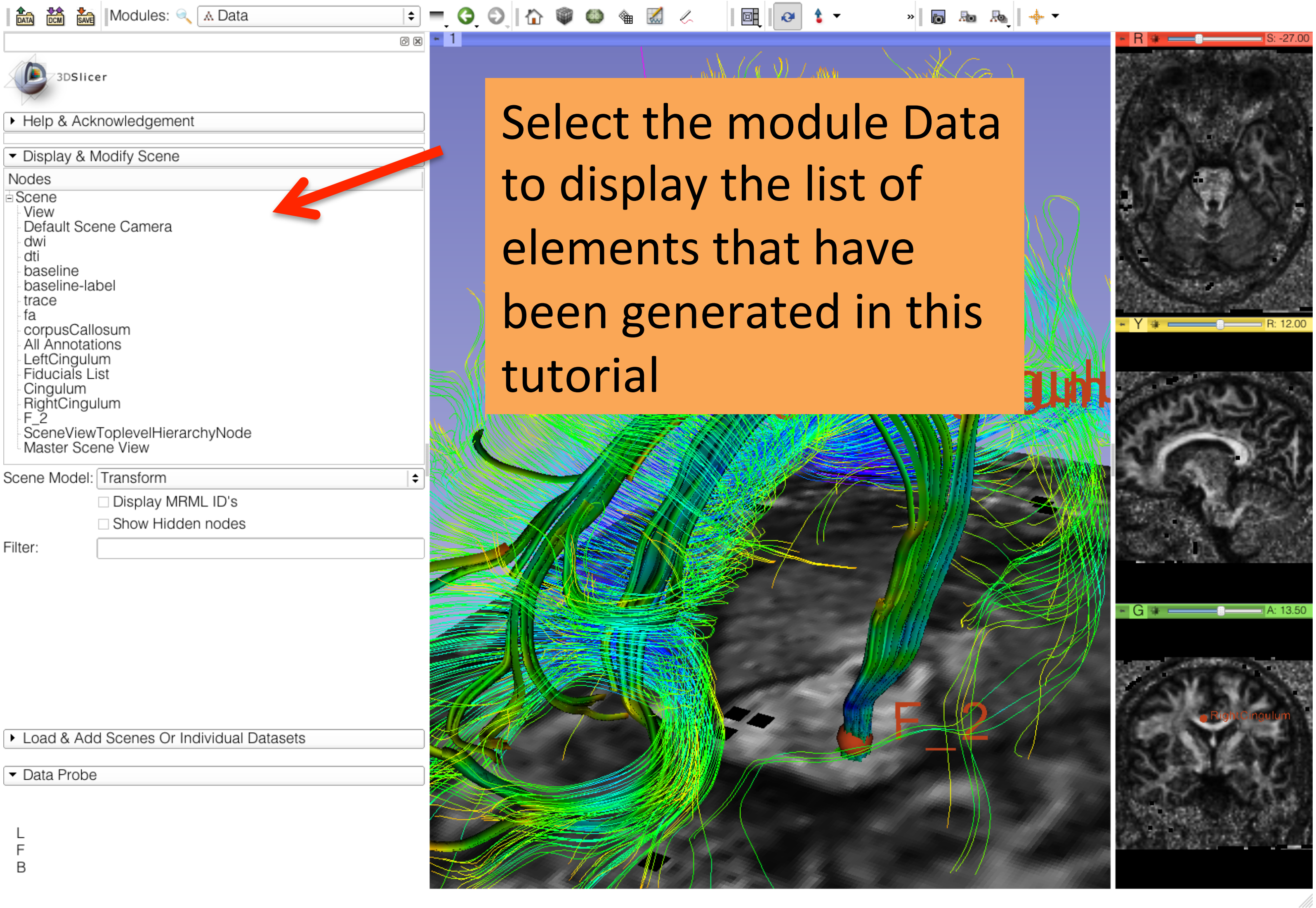


Active list: Fiducials List

	Vis	Lock	Edit	Value	Name	D
☐					All Annot…	
☐					Fiducials…	
☐				-3.7, 12.0, 26.8	LeftCing…	
☐				8.5, 12.9, 24.9	RightCin…	
☐				-6.5, 3.5, -24.0	F_2	

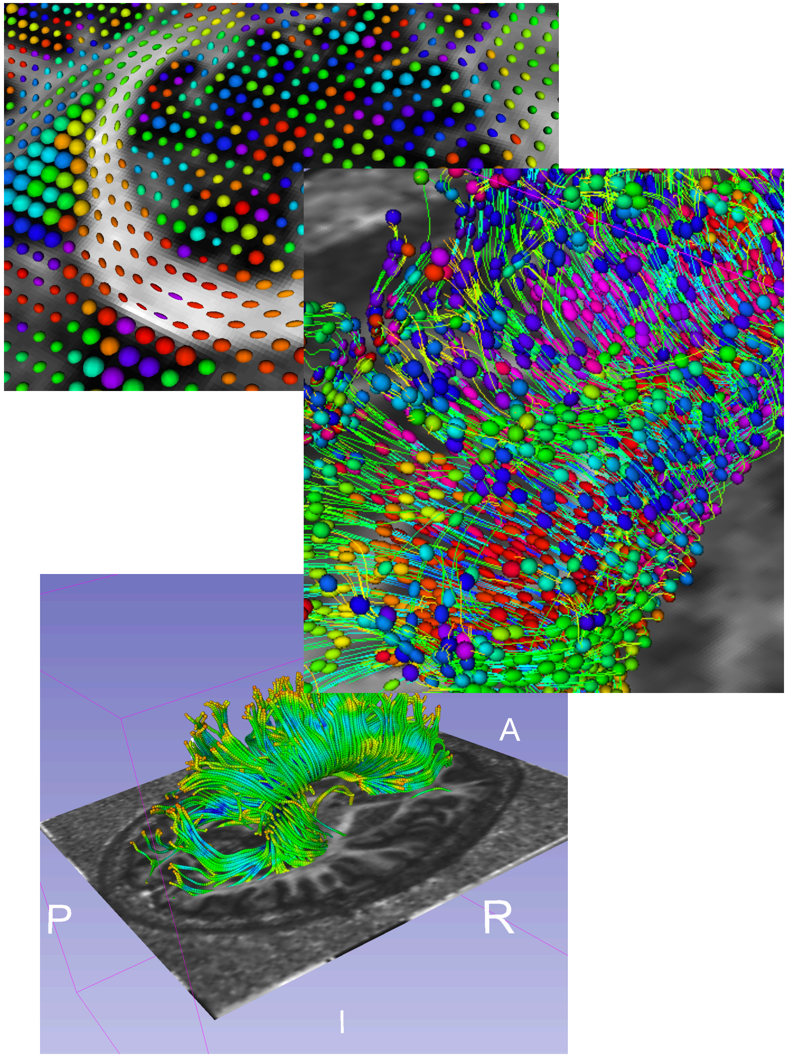
The Fiducial Seeding functionality allows you to do tractography ‘on-the-fly’ to explore white matter structures interactively

DTI Analysis



Select the module Data to display the list of elements that have been generated in this tutorial

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.

Acknowledgments

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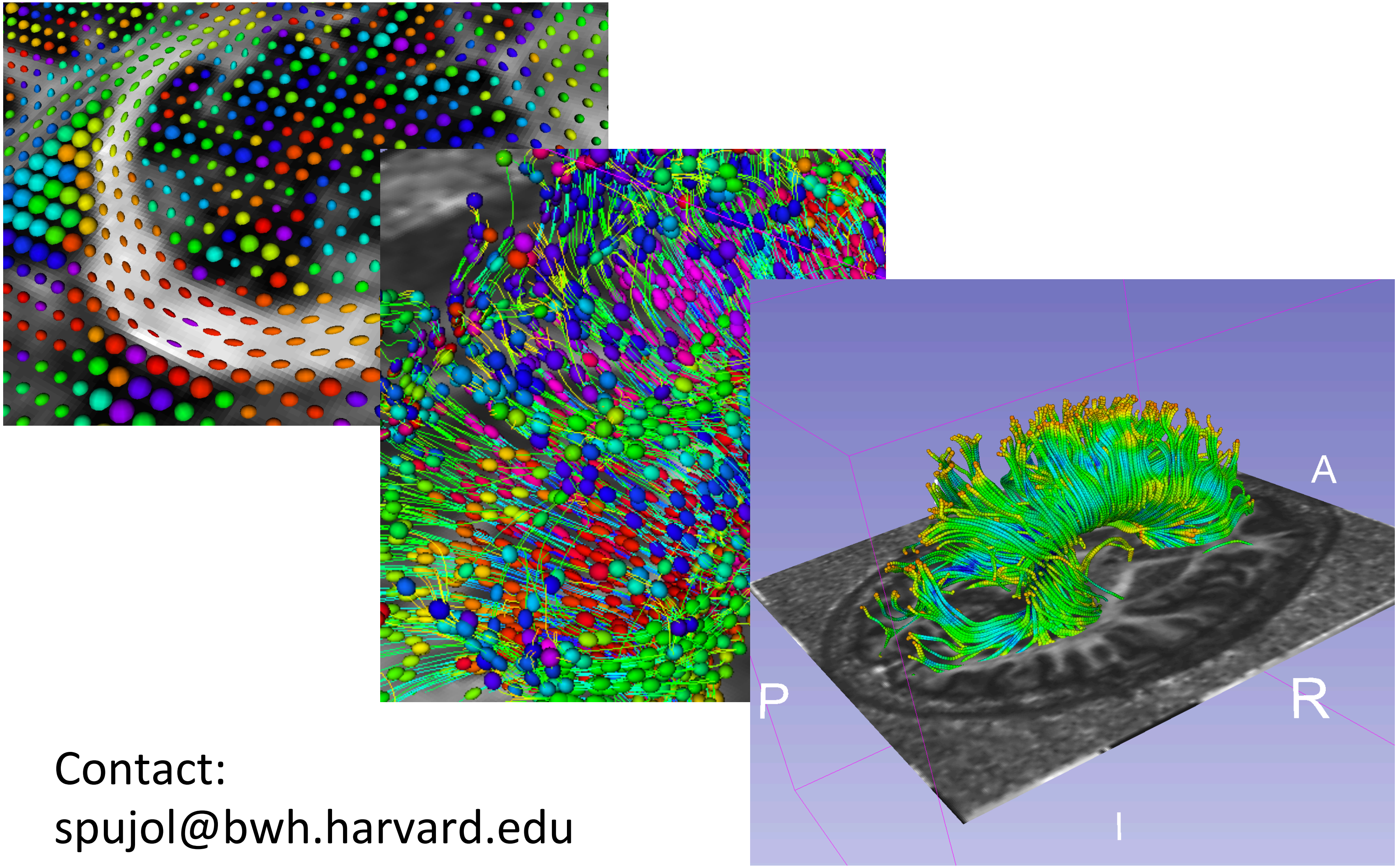

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