



# Diffusion MRI Analysis

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# Brain Anatomy



- White matter ~45% of the brain
- Myelinated nerve fibers (~ 10  $\mu\text{m}$  axon diameter)

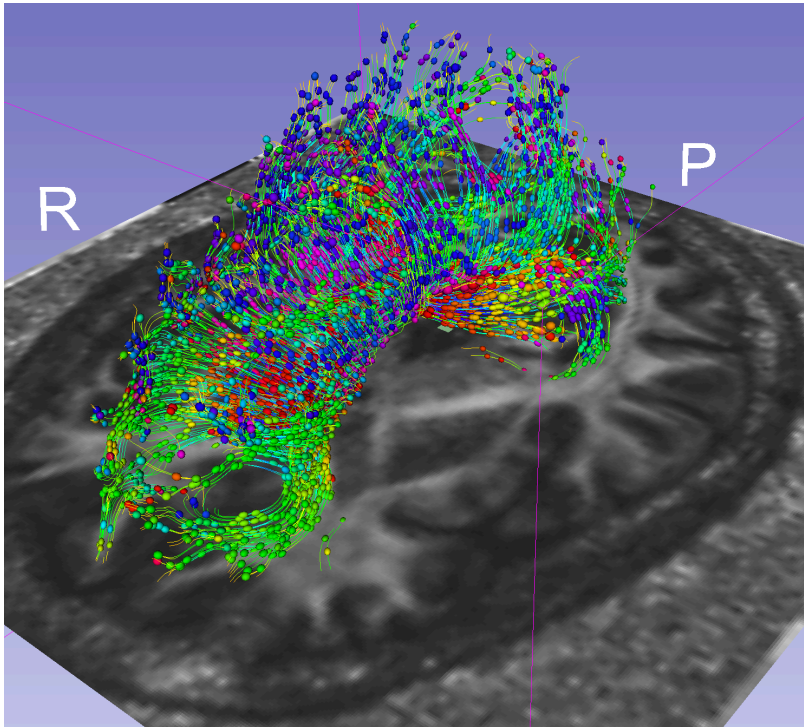


# White Matter Exploration



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

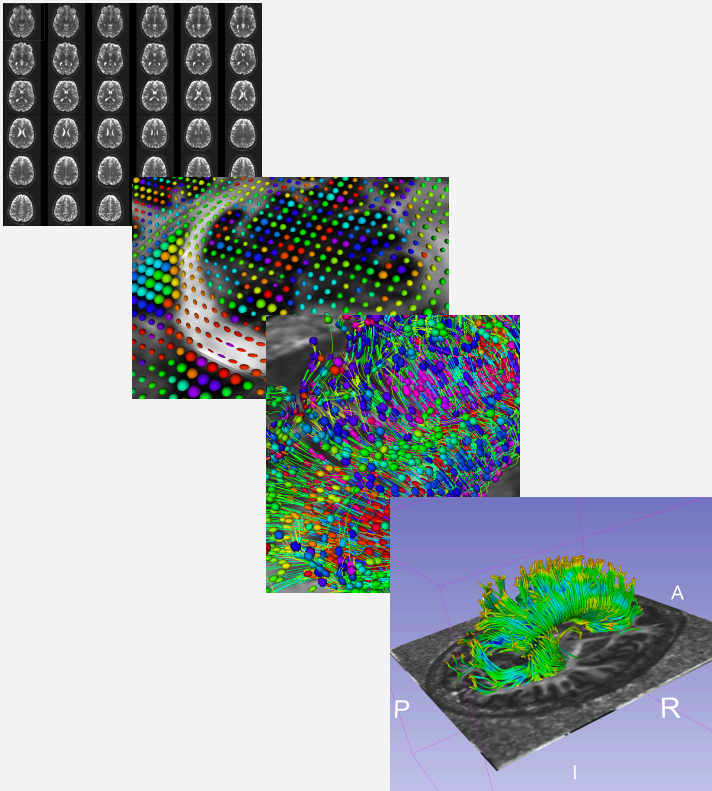
# White Matter Exploration



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

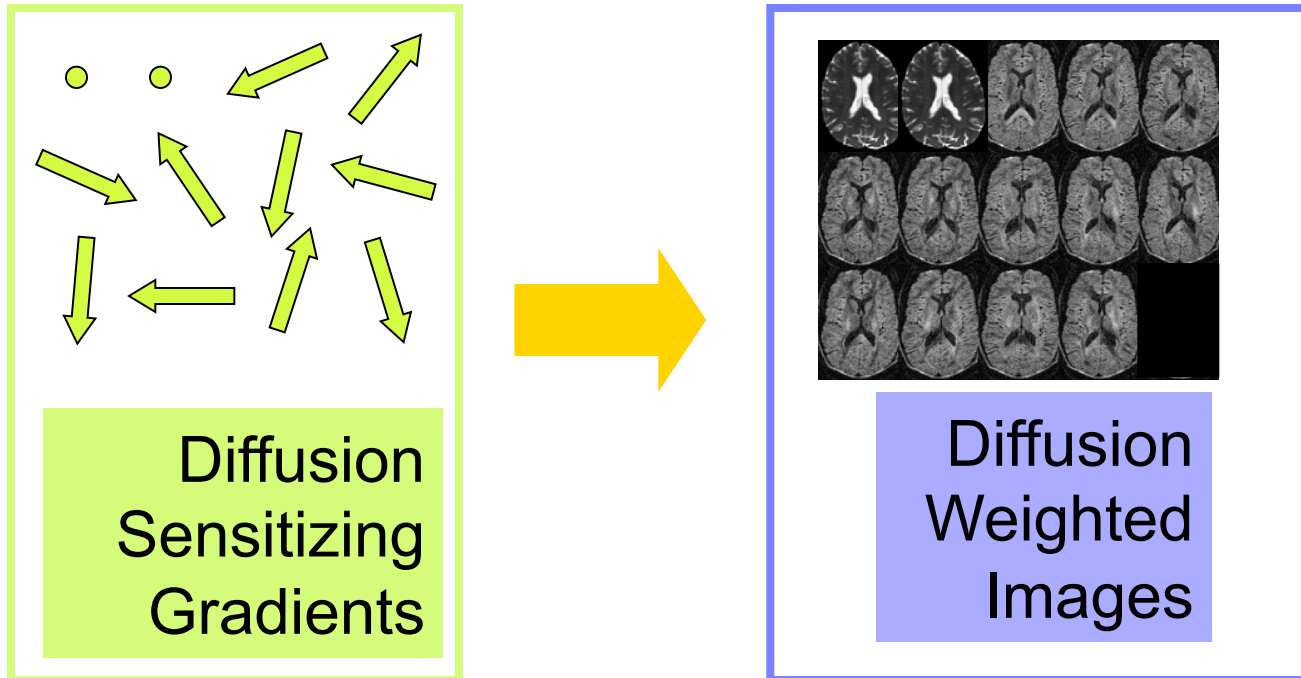
# Tutorial Outline

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.



The dataset is available on the Slicer Training Compendium ([www.slicer.org](http://www.slicer.org))

# Tutorial software



The screenshot shows the 3DSlicer website homepage. At the top left is the 3DSlicer logo, a stylized sphere with a grid. To its right is the text "3DSlicer" and a description: "A multi-platform, free and open source software package for visualization and medical image computing". A search bar is located to the right of the description. Below the description are four buttons: "Download", "Tutorials", "Reference", and "Feedback".

On the left side, there is a "Slicer Wiki" section with a "Download" button and a list of links: "About Slicer" (Introduction, Acknowledgments, Contact Us), "Resources" (For Users, For Developers, Commercial Use, NCIA, Publication DB, Image Gallery, Slicer Community, Source Code, Licensing, Mailing Lists, Web Archive).

The main content area features three columns of images illustrating the software's capabilities: "Powerful processing." (showing MRI slices with a green region), "Streamlined interface." (showing a 3D model of a brain), and "Extensible platform." (showing a 3D model of a hand). Below these images is a large banner for "3D Slicer version 4.0" with the website URL "www.slicer.org".

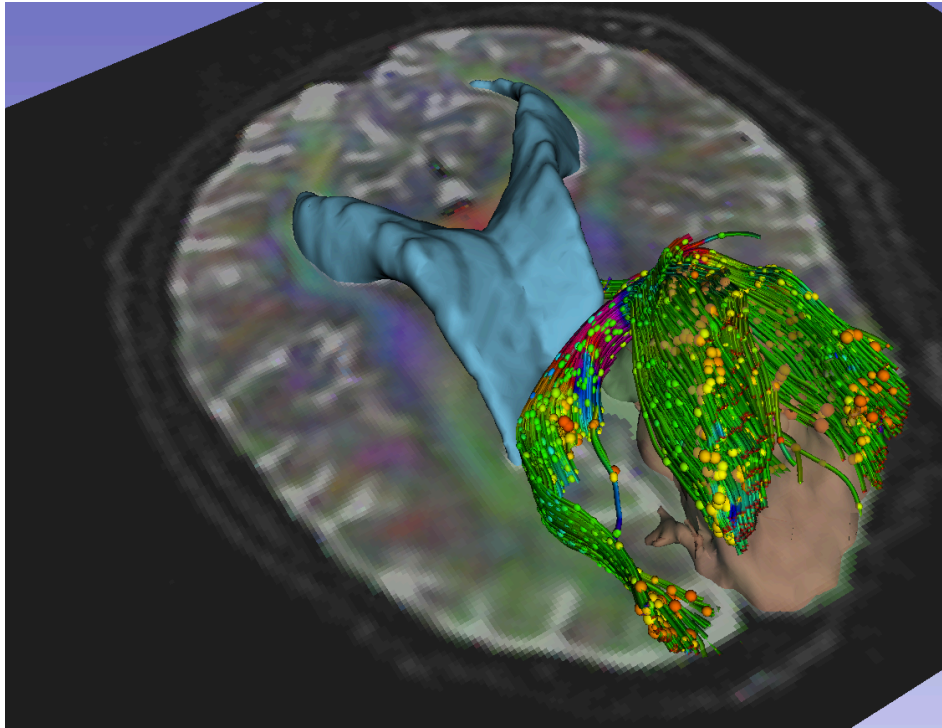
At the bottom of the page, there is a footer with copyright information: "Content of this site is Copyright 2012 BWH and 3D Slicer contributors, unless otherwise noted. Contact webmaster@bwh.harvard.edu for questions about the use of this site's content. See here for more information about the web infrastructure."

The tutorial uses the 3DSlicer version 4.1 software available at [www.slicer.org](http://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

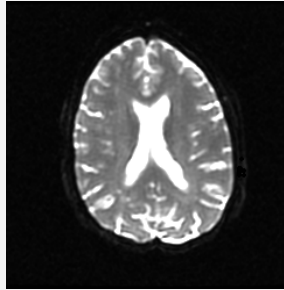
# Learning Objectives

Following this tutorial, you'll be able to

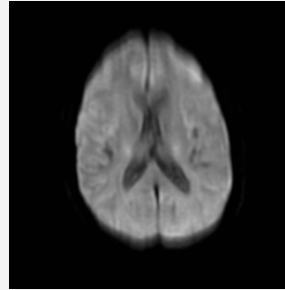
- 1) Estimate a tensor volume from a set of Diffusion Weighted Images
- 2) Understand the shape and size of the diffusion ellipsoid
- 3) Reconstruct DTI tracts from a pre-defined region of interest
- 4) Interactively visualize DTI tracts seeded from a fiducial



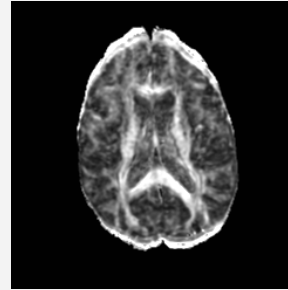
# MR Diffusion Analysis Pipeline



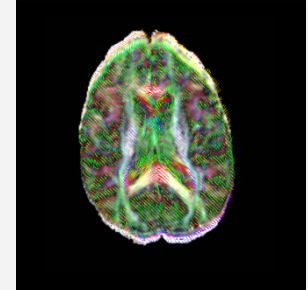
DWI  
Acquisition



Tensor  
Calculation

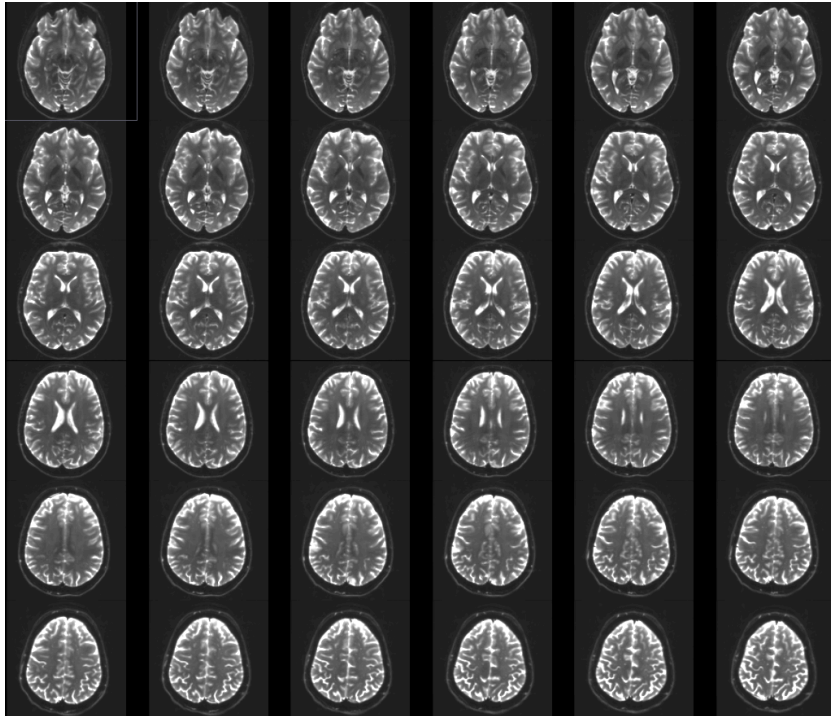


Scalar  
Maps



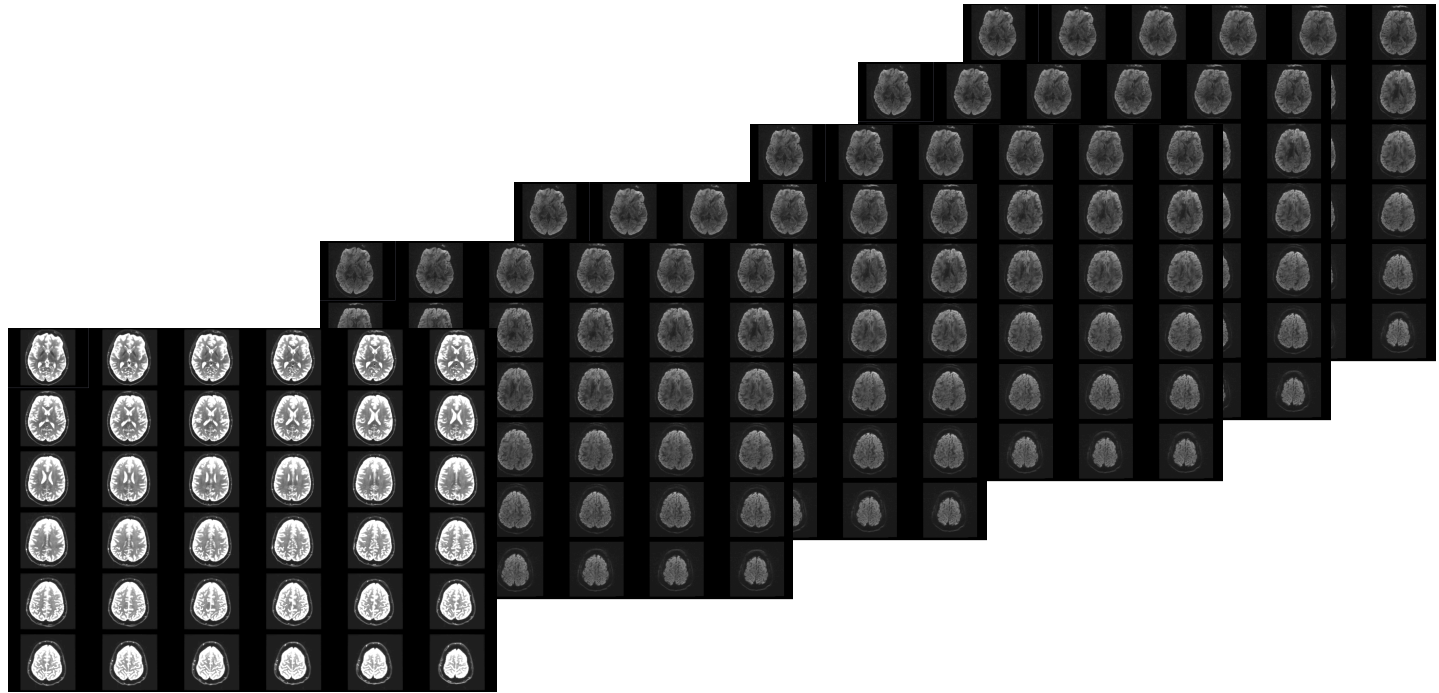
3D  
Visualization





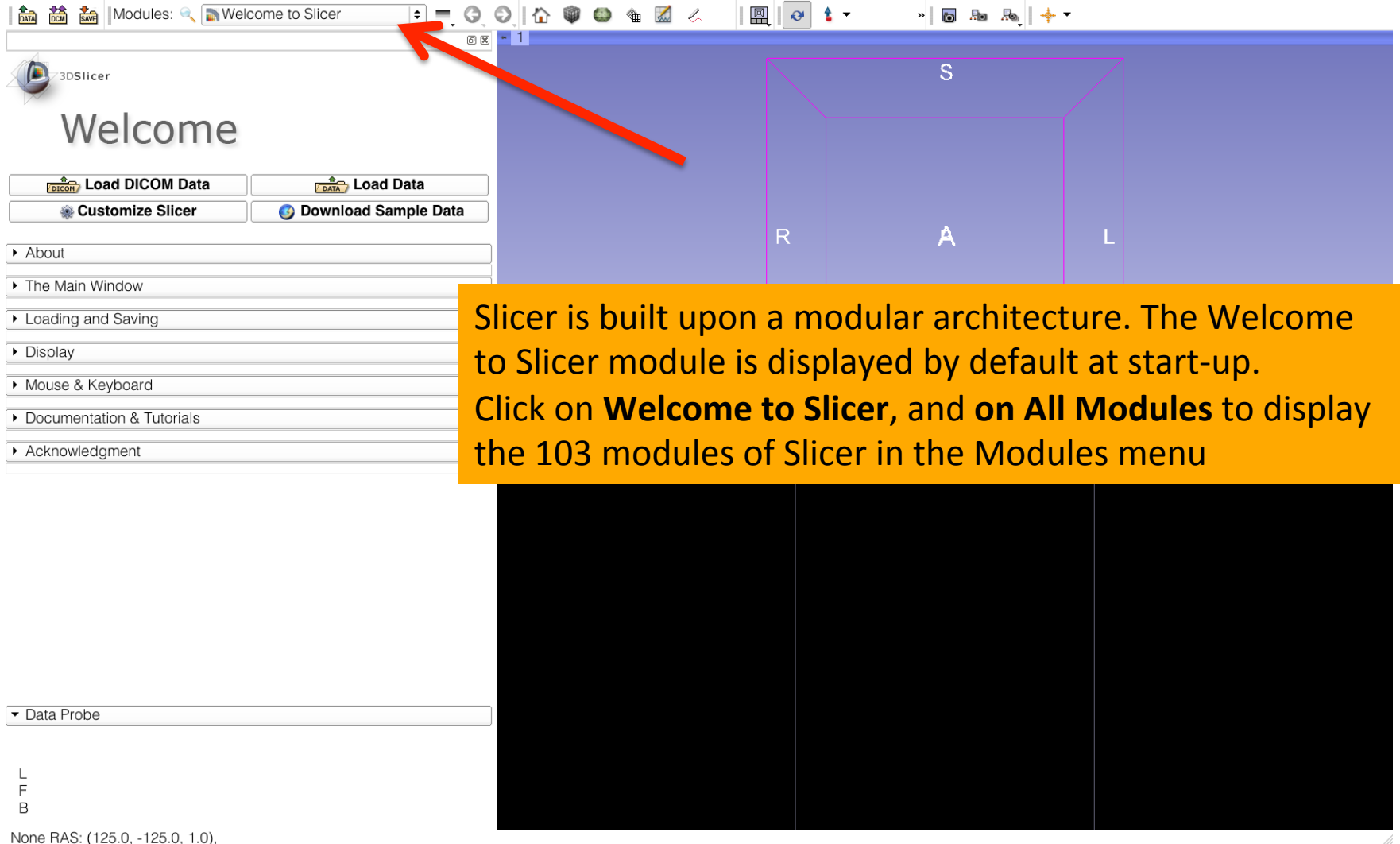
# Part 1: From DWI images to Tensors

# Understanding the DWI dataset

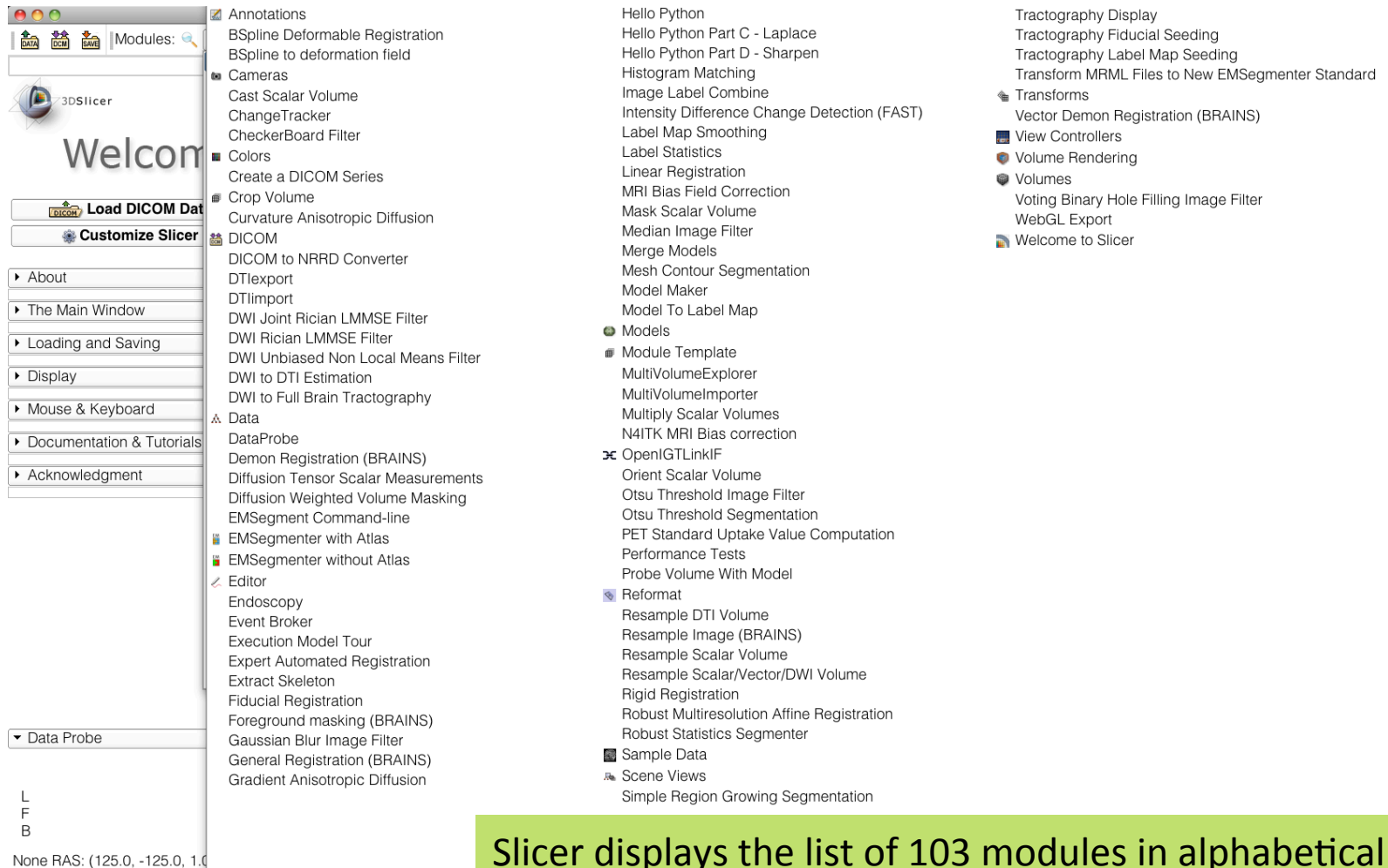


The Diffusion Weighted Imaging (DWI) dataset is composed of 1 volume acquired without diffusion-sensitizing gradient, and 41 volumes acquired with 41 different diffusion-sensitizing gradient directions.

# Start the Slicer Software

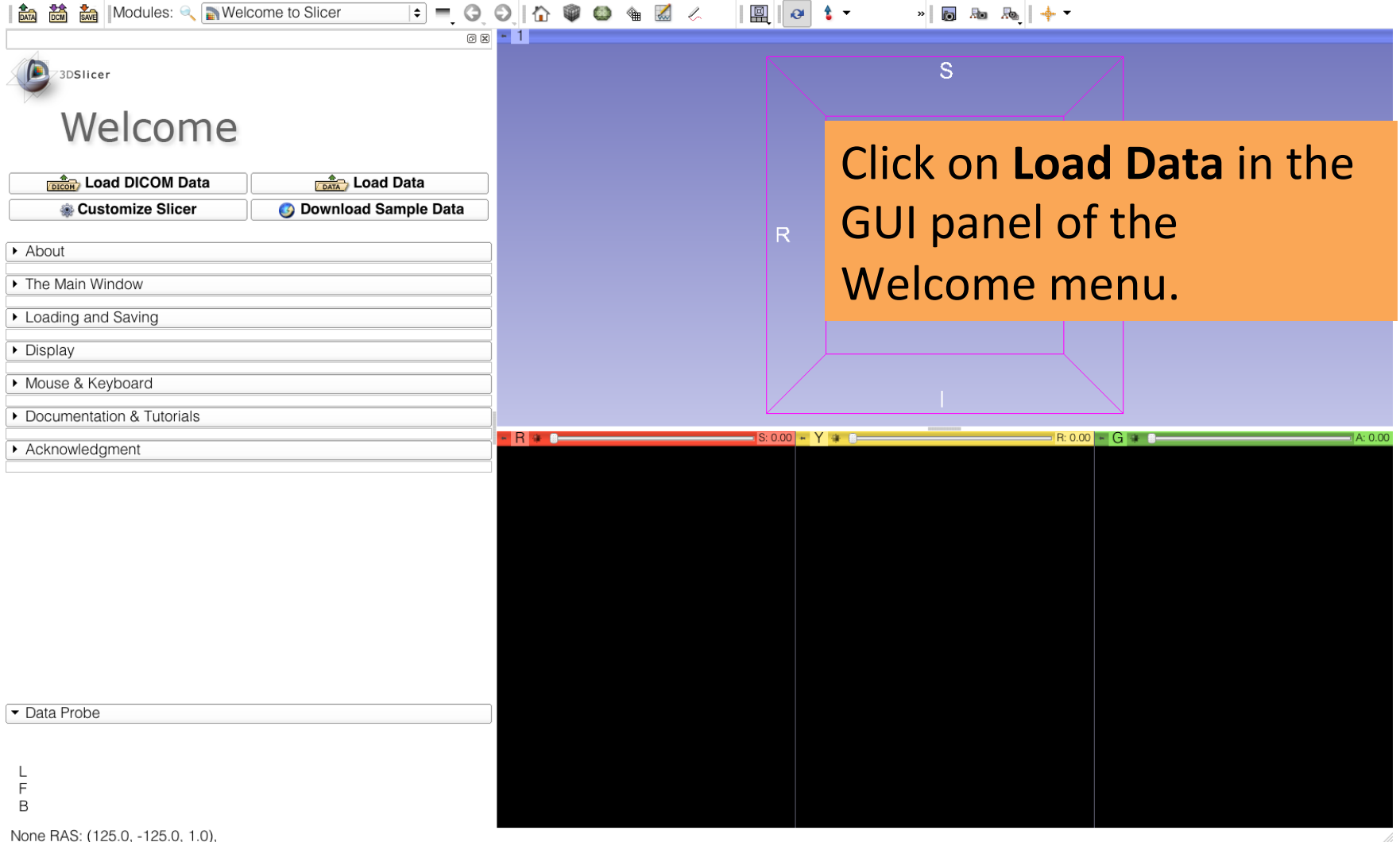


# Start the Slicer software

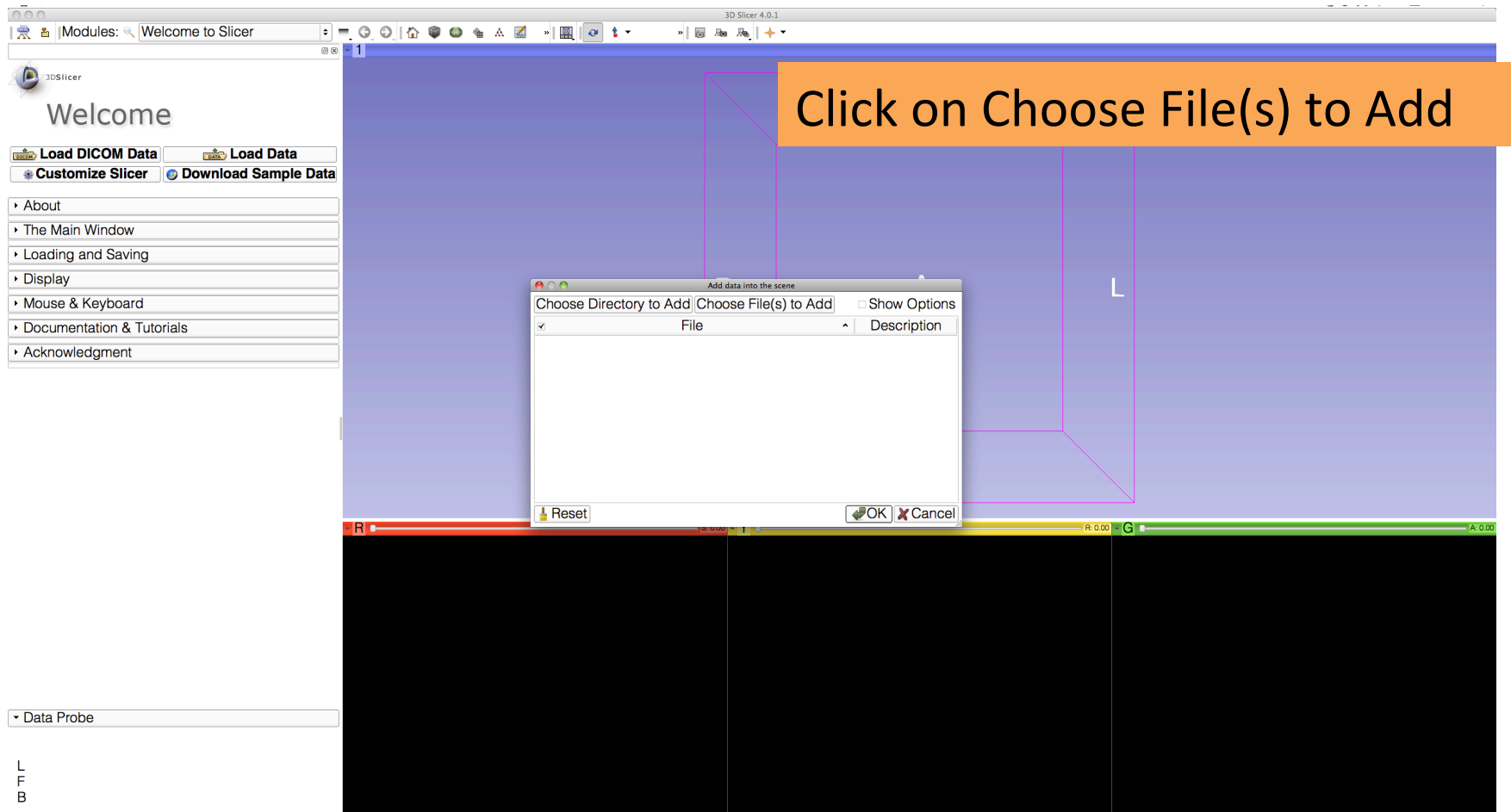


Slicer displays the list of 103 modules in alphabetical order.

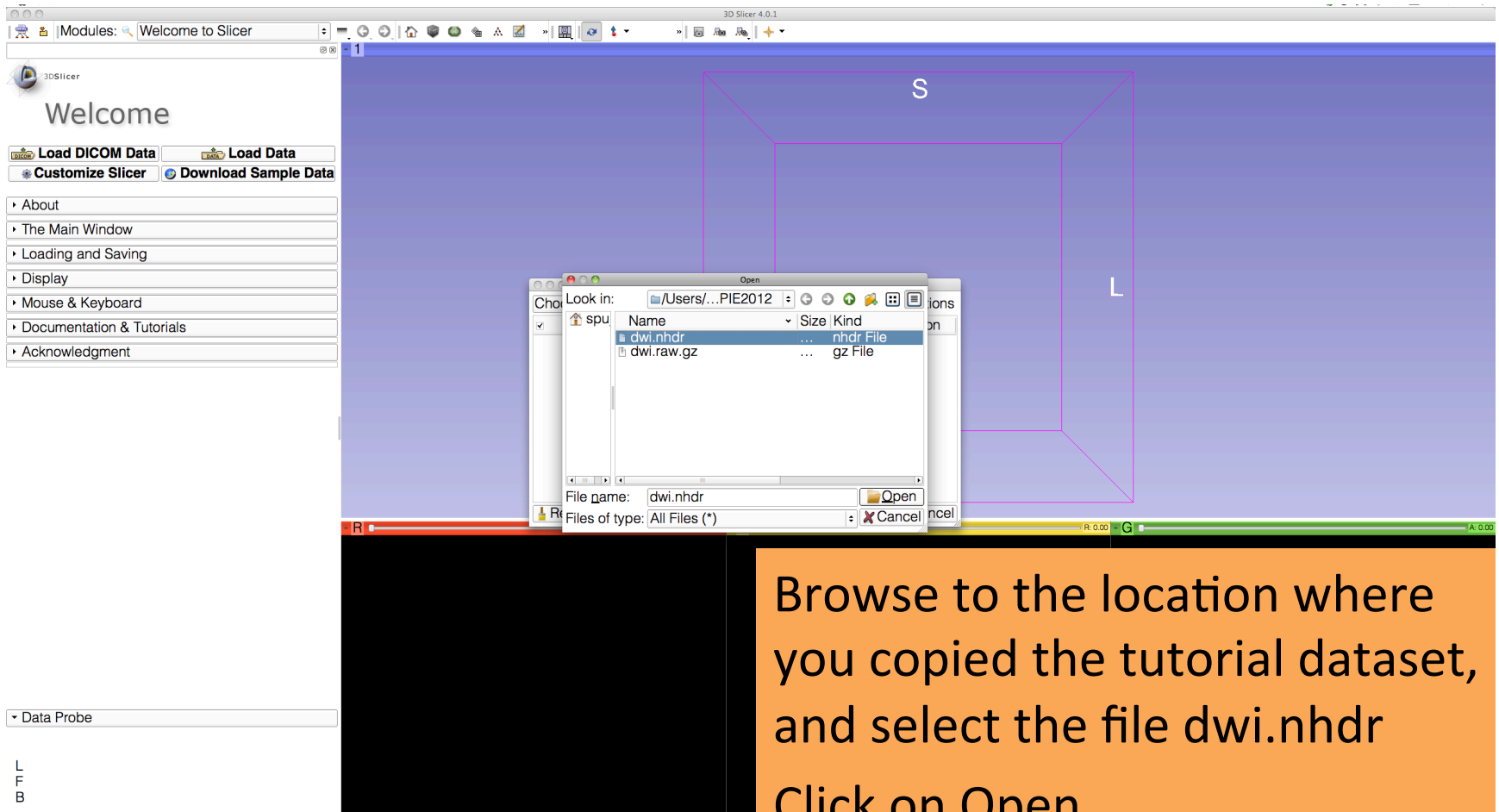
# Loading the DWI dataset



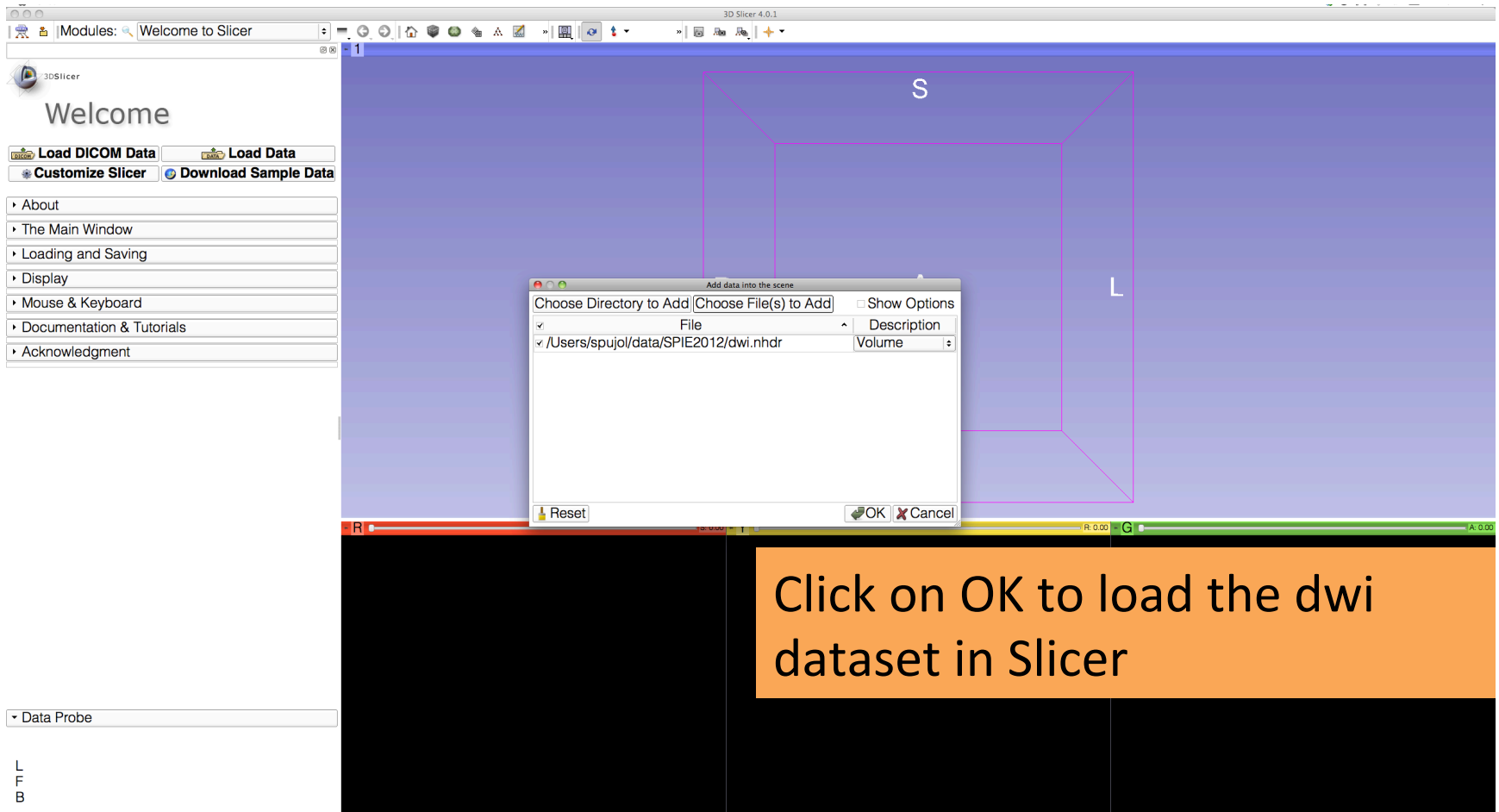
# Loading the DWI dataset



# Loading the DWI dataset

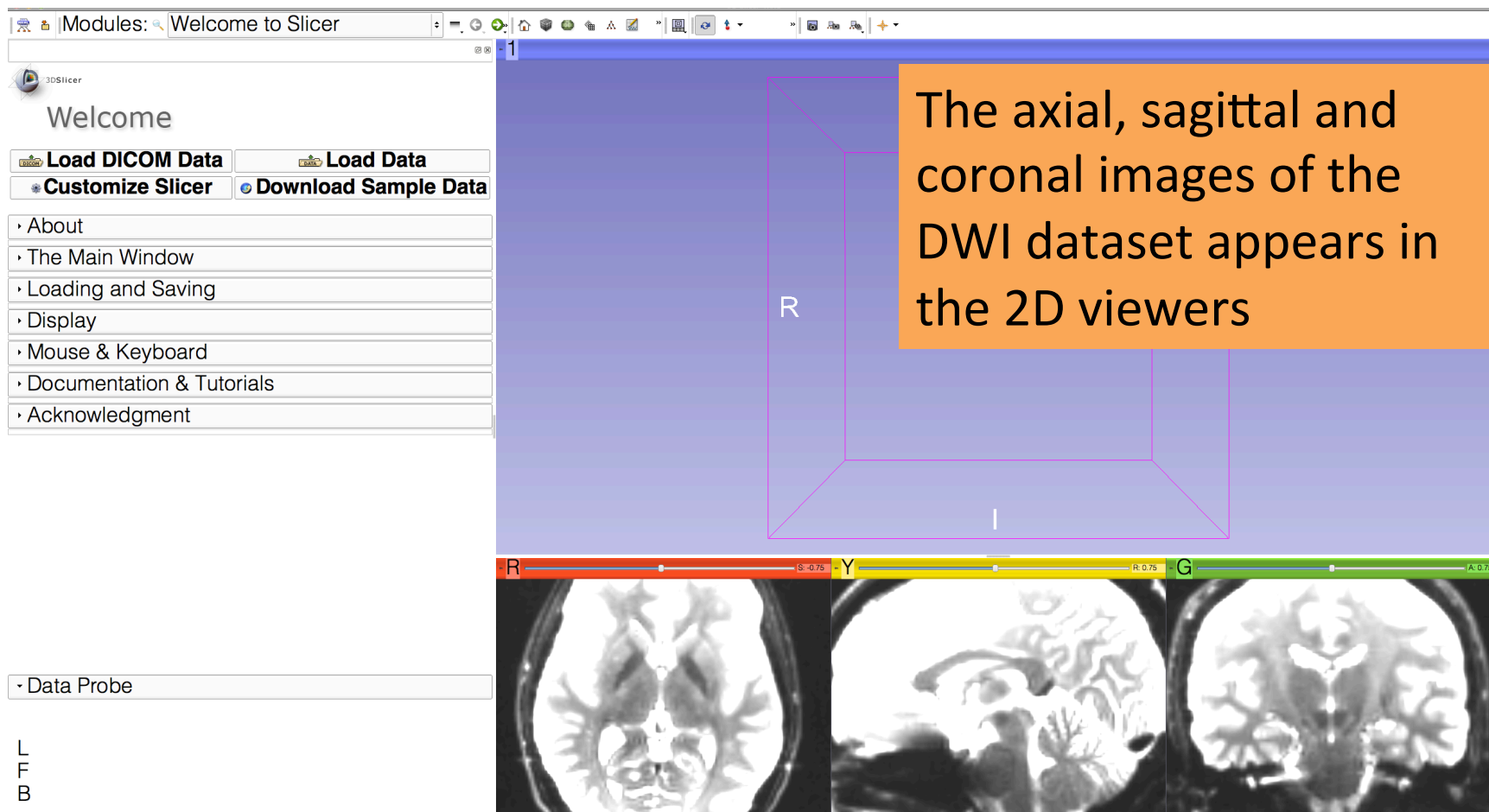


# Loading the DWI dataset





# Loading the DWI dataset



# Adjusting Window and Level

The screenshot shows the 3D Slicer software interface. The 'Volumes' module is selected in the top menu. The left sidebar contains various settings for the active volume 'dwi'. A red arrow points to the 'Threshold' slider, which is currently set to 'Off' with a range from 0.00 to 4040.00. The 'W/L' (Window/Level) settings are set to 'Auto W/L' with a window width of 532 and a level of 272. The main 3D view shows a brain slice with a purple wireframe box and a white 'R' label. Below the 3D view are three 2D image thumbnails labeled R, Y, and G. An orange text box on the right contains the following text:

Select the module Volumes from the modules menu.  
Adjust the window and display of the baseline image using the W/L slider

L  
F  
B

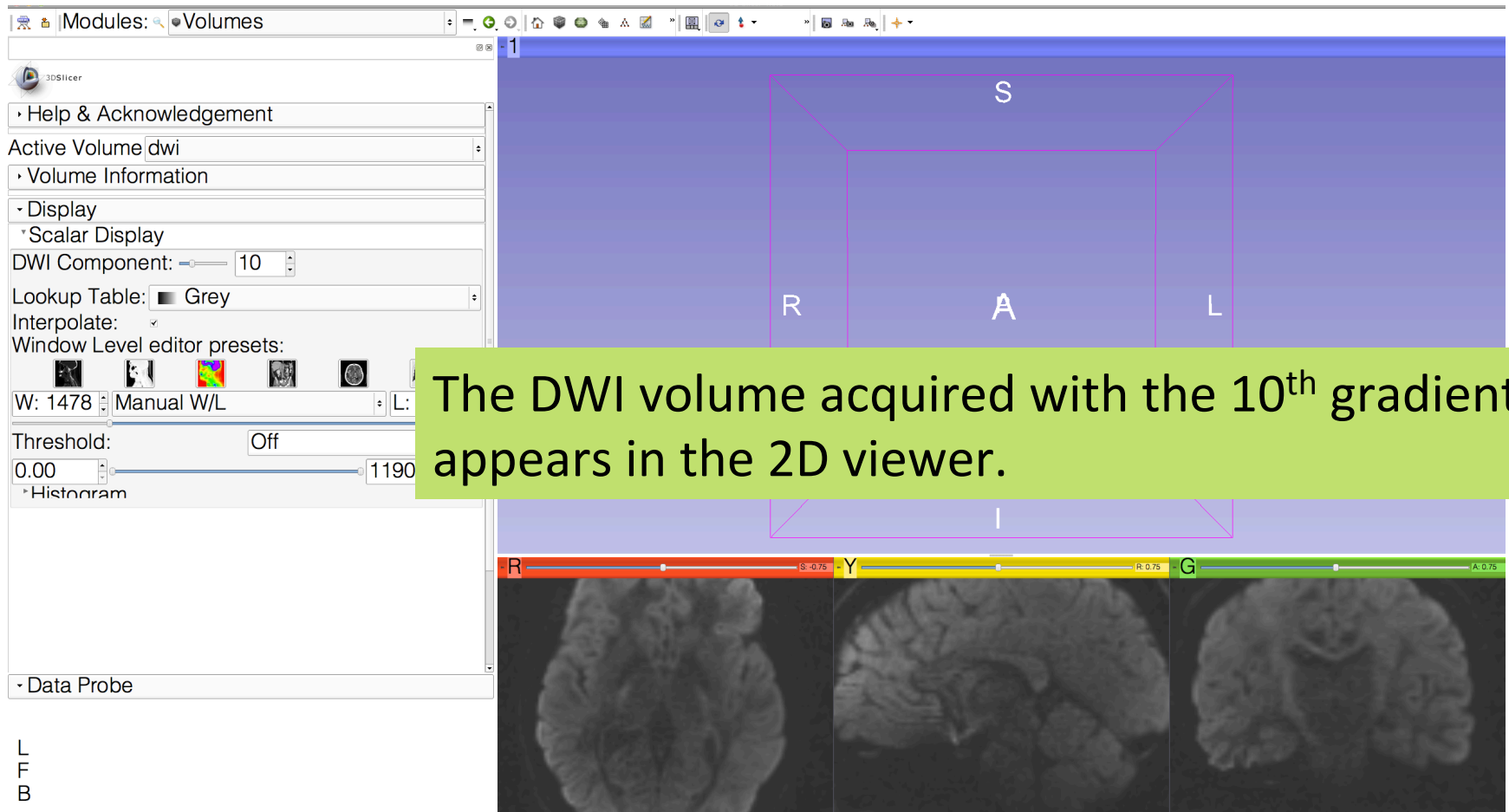
# Exploring the DWI dataset

The screenshot shows the 3D Slicer software interface. The 'Volumes' module is active. In the 'Display' section, 'Scalar Display' is selected, and the 'DWI Component' is set to 0. A red arrow points to this dropdown menu. Below it, the 'Lookup Table' is set to 'Grey'. The 'Window Level editor' shows 'W: 1478' and 'L: 529'. The 'Histogram' section is visible at the bottom. On the right, an orange text box contains instructions: 'The baseline image corresponds to the DWI Component #0. Select the DWI component #10, which corresponds to the 10<sup>th</sup> diffusion sensitizing gradient'. A purple box labeled 'R' is drawn around the 'DWI Component' dropdown. At the bottom, three brain slices are shown in axial, sagittal, and coronal views, with color-coded axes: R (Red), Y (Yellow), G (Green), and A (Blue).

The baseline image corresponds to the DWI Component #0.

Select the DWI component #10, which corresponds to the 10<sup>th</sup> diffusion sensitizing gradient

# Exploring the DWI dataset



# Exploring the DWI dataset

The screenshot shows the 3D Slicer software interface. The top menu bar includes 'Modules' and 'Volumes'. The left sidebar contains the following sections:

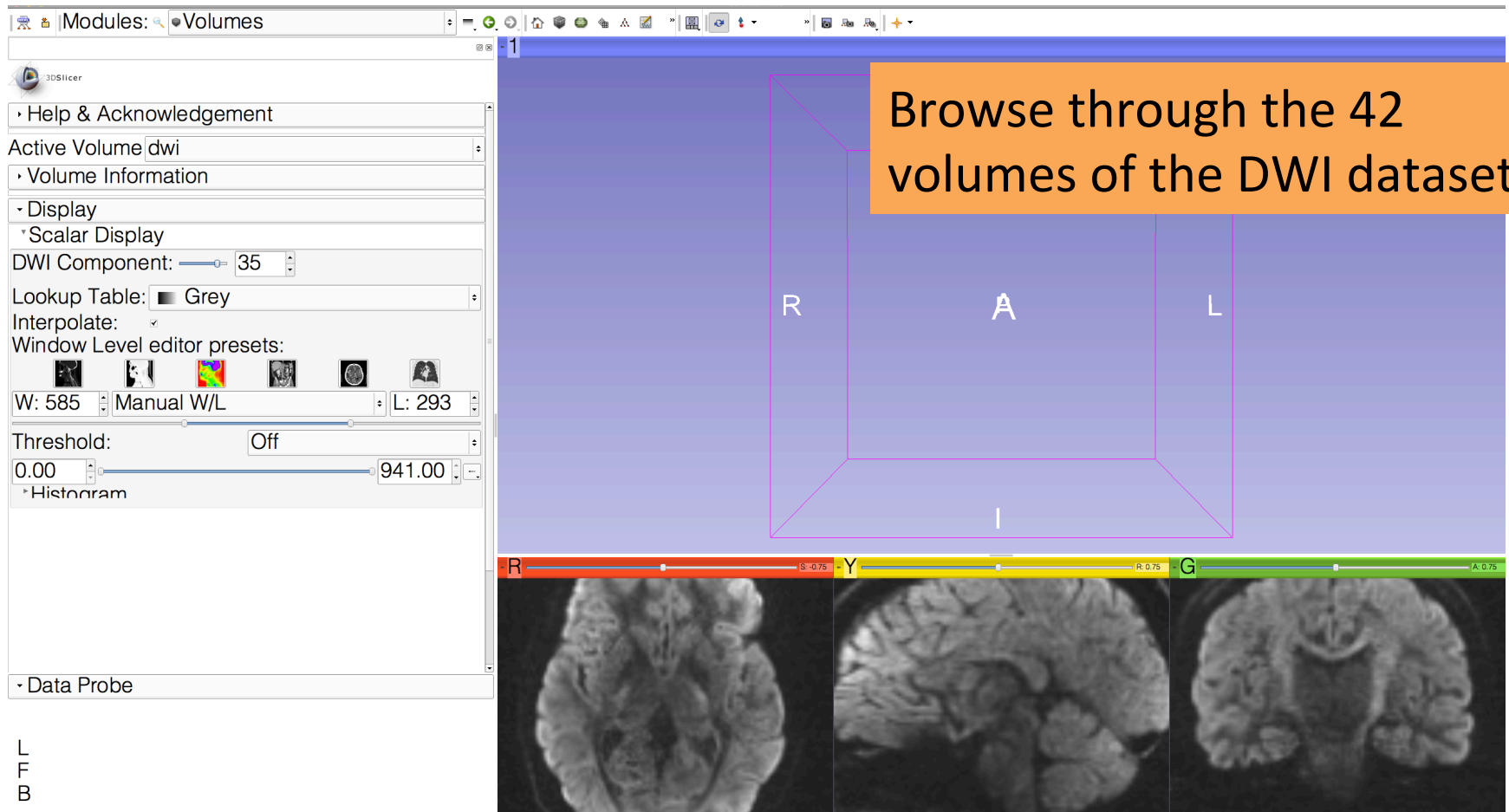
- Help & Acknowledgement
- Active Volume: dwi
- Volume Information
- Display
  - Scalar Display
  - DWI Component: 10
  - Lookup Table: Grey
  - Interpolate: checked
  - Window Level editor presets: [Icons]
  - W: 585 | Manual W/L | L: 400
  - Threshold: Off (indicated by a red arrow)
  - 0.00 | 1190.00
  - Histogram
- Data Probe

The central 3D view shows a purple volume with a white wireframe box. The axes are labeled R (Right), A (Anterior), L (Left), and I (Inferior). An orange callout box contains the text: "Adjust the window and display of the baseline image using the W/L slider".

At the bottom, there are three axial slices with color-coded axes: R (Red), Y (Yellow), and G (Green). The slices show brain tissue in grayscale.

L  
F  
B

# Exploring the DWI dataset



L  
F  
B

# Exploring the DWI dataset

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'.

L  
F  
B

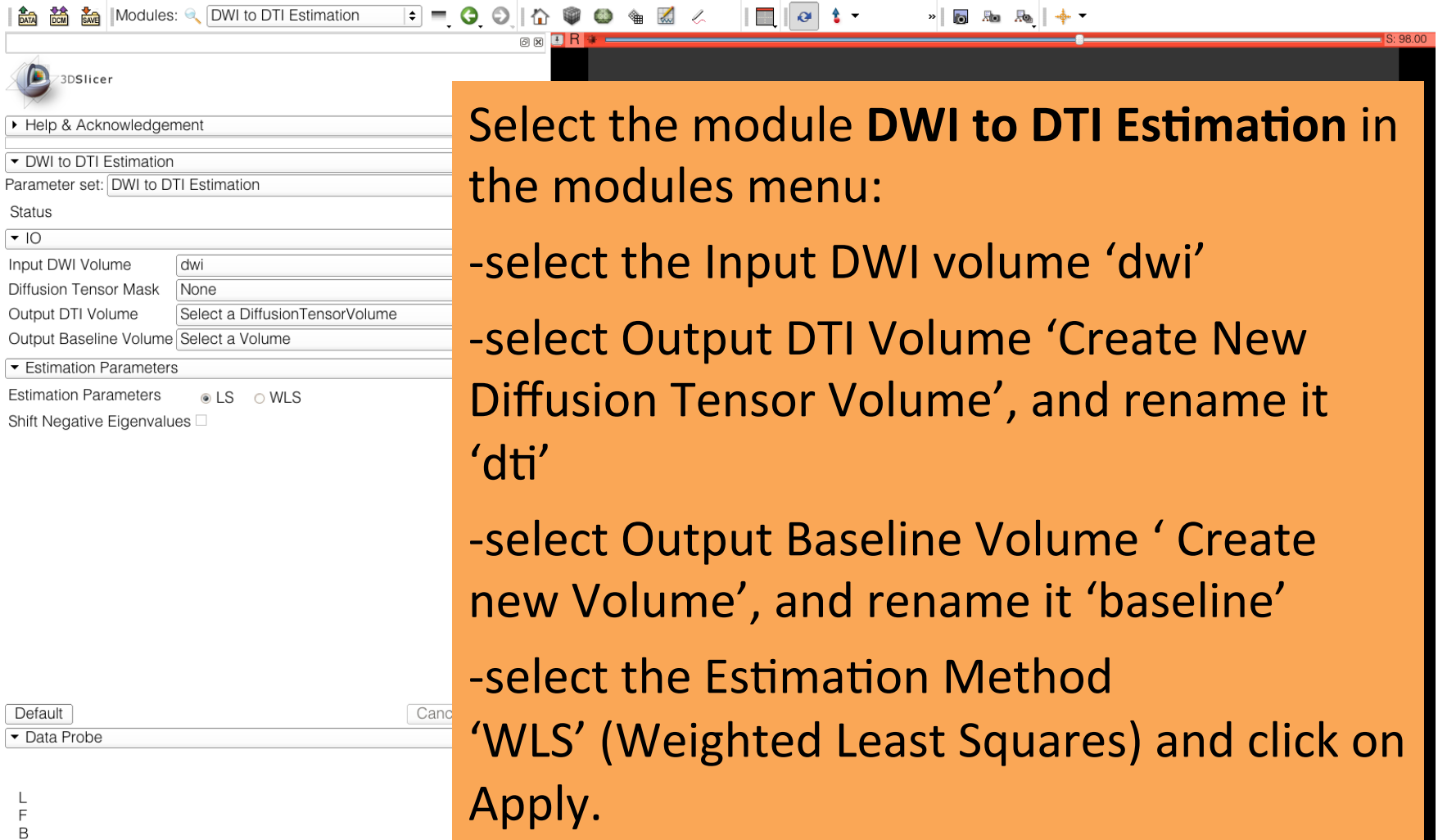
# Exploring the DWI dataset

The screenshot shows the 3D Slicer 4.0.1 interface. The top toolbar contains various icons for navigation and viewing. A red arrow points to the 'R' icon, which represents the 'Red Slice Only' layout. An orange callout box with white text says: "Select the 'Red Slice Only' Layout from the viewing menu". The main window displays a grayscale axial DWI brain scan. On the left, the 'Volumes' panel is open, showing settings for the active volume 'dwi', including 'DWI Component: 10', 'Look up Table: Grey', and 'Threshold: Off'. The 'Data Probe' panel is also visible at the bottom left.

L  
F  
B



# Diffusion Tensor Estimation



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

3DSlicer

Help & Acknowledgement

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

Default

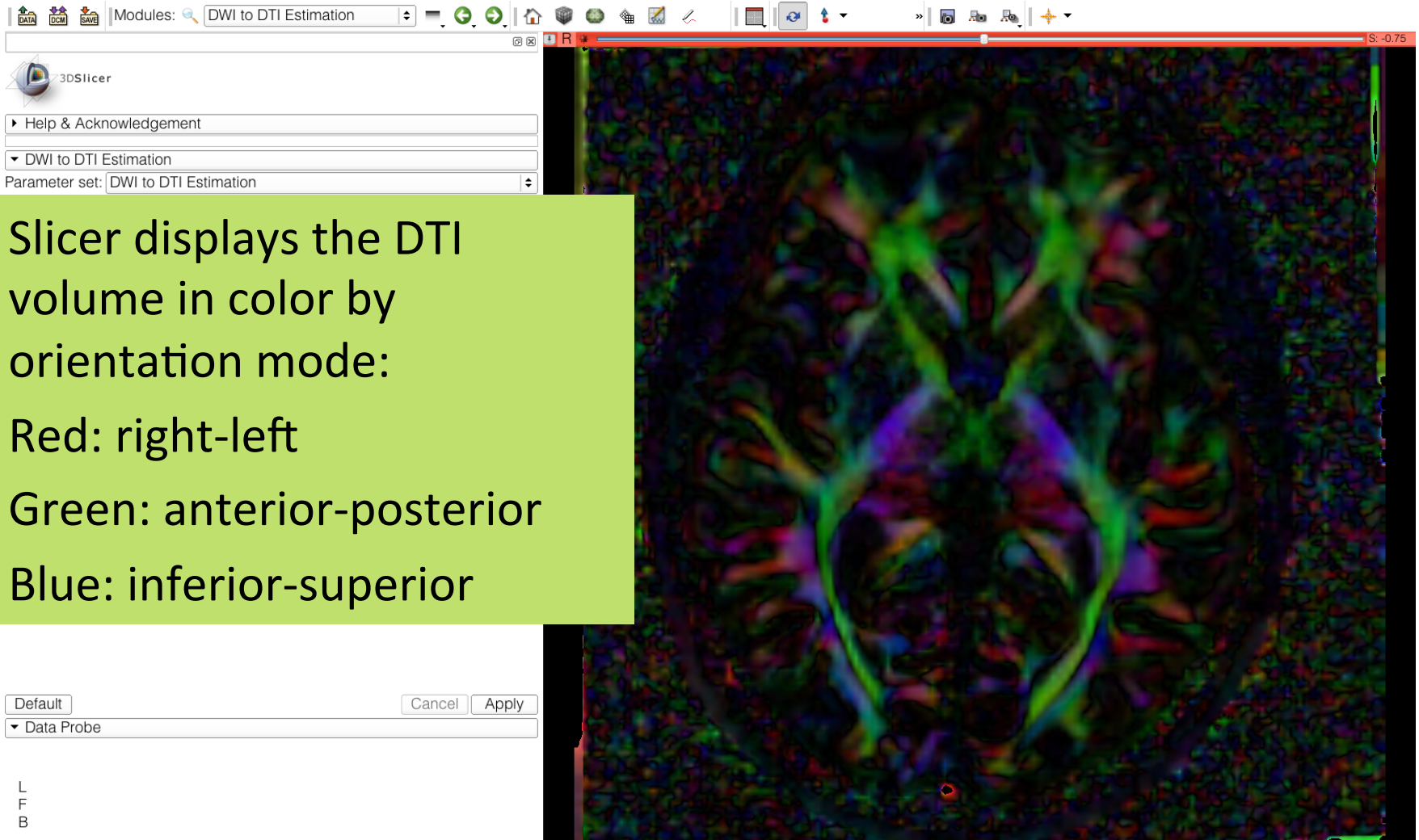
Cancel Apply

Data Probe

L  
F  
B

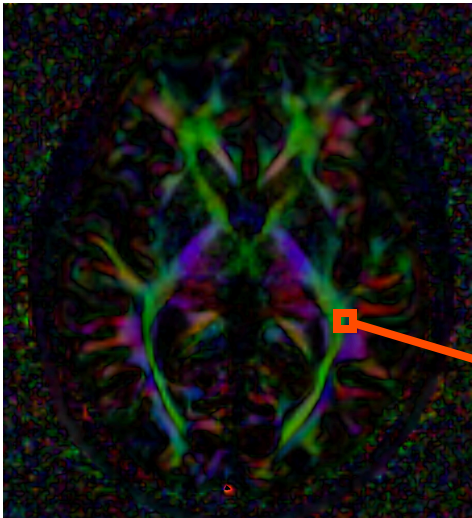
Select the volume 'dti' in the red viewer

# Diffusion Tensor Estimation



Slicer displays the DTI volume in color by orientation mode:  
Red: right-left  
Green: anterior-posterior  
Blue: inferior-superior

# Diffusion Tensor Data



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

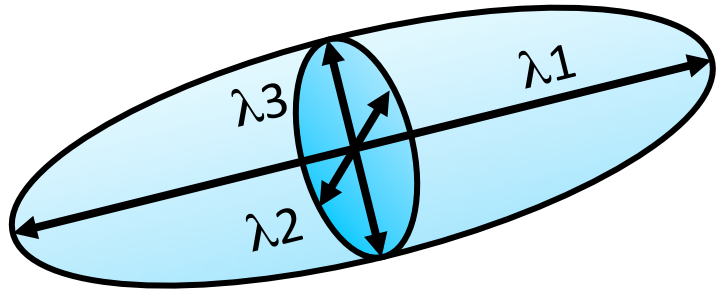
Stejskal-Tanner equation (1965)

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

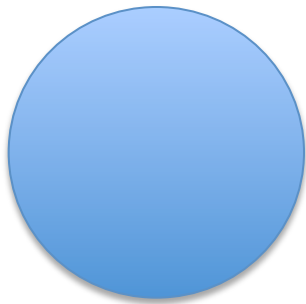
The diffusion tensor  $\underline{\mathbf{D}}$  in the voxel (I,J,K) is a 3x3 symmetric matrix.

# 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  $\lambda_1$ ,  $\lambda_2$ ,  $\lambda_3$  to characterize the size and shape of the diffusion tensor.

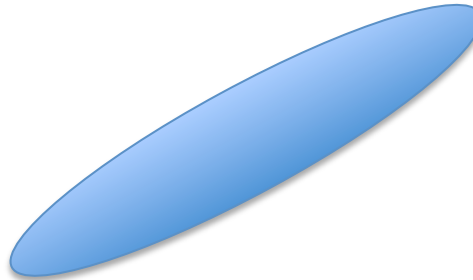


# Diffusion Tensor Shape



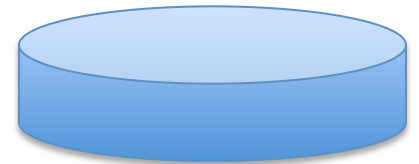
$$\lambda_1 = \lambda_2 = \lambda_3$$

Isotropic media  
(CSF, gray matter)



$$\lambda_1 \gg \lambda_2, \lambda_3$$

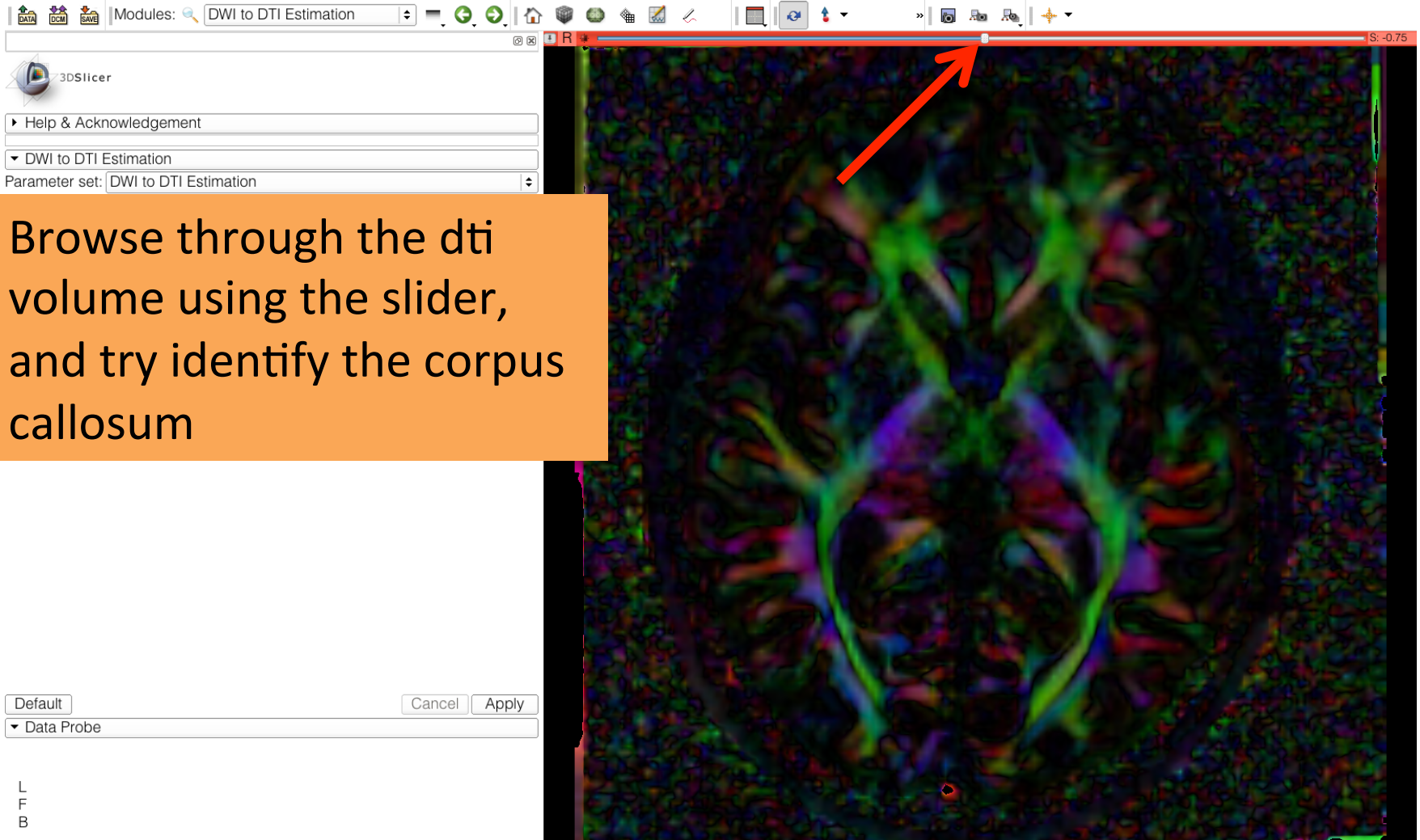
Anisotropic media  
(white matter)



$$\lambda_1 \sim \lambda_2 \gg \lambda_3$$



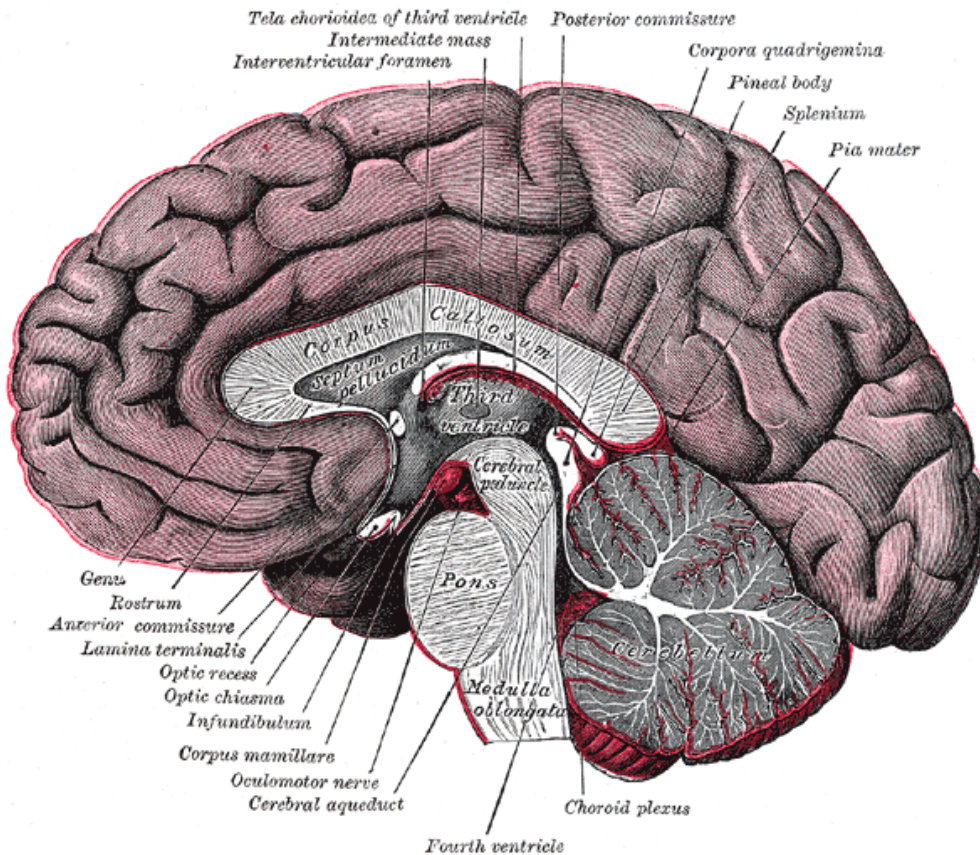
# Exploring the Diffusion Tensor Data



The screenshot shows the 3DSlicer interface with the 'DWI to DTI Estimation' module active. The main view displays a colorful DTI volume. A red arrow points to a slider control at the top of the view, used for navigating through the DTI volume. The interface includes a top toolbar, a left sidebar with a menu, and a bottom panel with 'Default', 'Data Probe', 'Cancel', and 'Apply' buttons. The text 'L F B' is visible in the bottom left corner.

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

The image shows the 3DSlicer software interface. On the left, the 'DWI to DTI Estimation' module is active. The 'IO' section shows the following settings:

- Input DWI Volume: dwi
- Diffusion Tensor Mask: None
- Output DTI Volume: dti
- Output Baseline Volume: baseline

The 'Estimation Parameters' section shows:

- Estimation Parameters:  LS  WLS
- Shift Negative Eigenvalues:

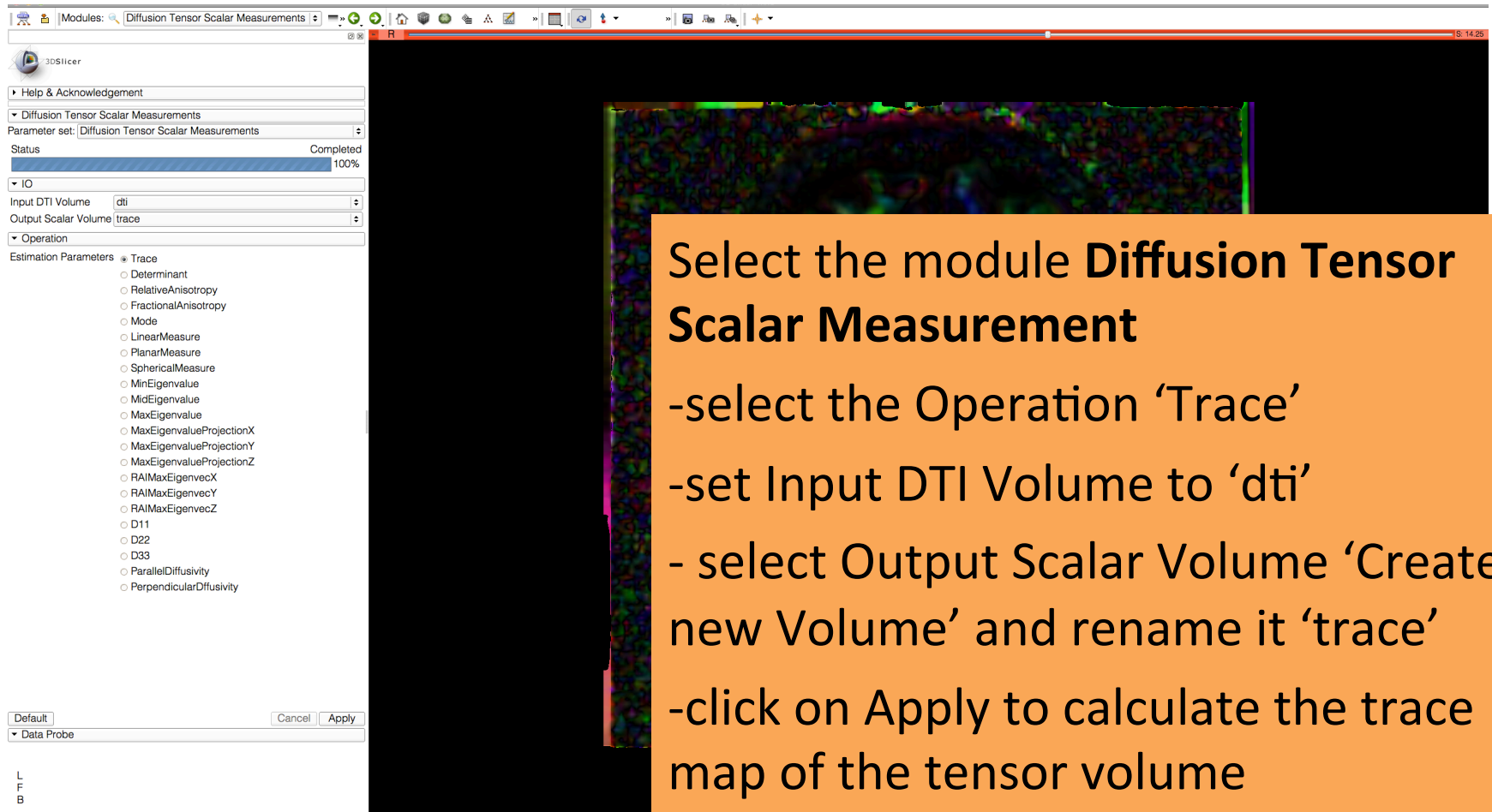
Buttons for 'Default', 'Cancel', and 'Apply' are visible at the bottom of the parameter panel. A green box with the text 'Corpus Callosum' and a red arrow points to the central white structure in the brain scan on the right. The brain scan is a color-coded DTI map showing white matter tracts in various colors (red, green, blue, purple) against a dark background. The text 'R' is visible in the top right corner of the scan area, indicating the right side of the brain.

# Characterizing the Size of the tensor: Trace

$$\text{Trace}(D) = \lambda_1 + \lambda_2 + \lambda_3$$

- 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



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

3DSlicer

Diffusion Tensor Scalar Measurements

Parameter set: Diffusion Tensor Scalar Measurements

Status Completed 100%

IO

Input DTI Volume dti

Output Scalar Volume trace

Operation

- LinearMeasure
- PlanarMeasure
- SphericalMeasure
- MinEigenvalue
- MidEigenvalue
- MaxEigenvalue
- MaxEigenvalueProjectionX
- MaxEigenvalueProjectionY
- MaxEigenvalueProjectionZ
- RAIMaxEigenvecX

Default Cancel Apply

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

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

Estimation Parameters

- Trace
- Determinant
- RelativeAnisotropy
- FractionalAnisotropy
- Mode
- LinearMeasure
- PlanarMeasure
- SphericalMeasure

Default

Data Prob

L  
F  
B

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

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%

Input DTI Volume: dti  
Output Scalar Volume: trace

1.00 None  
0.40 dti  
1.00 trace

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.

Default Cancel Apply

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



# Trace

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

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%

MaxEigenvalueProjectionX  
MaxEigenvalueProjectionY  
MaxEigenvalueProjectionZ  
RAIMaxEigenvecX

Default Cancel Apply

Data Probe

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




L None ()

F dti (57, 48, 60) ColorOrientation 0

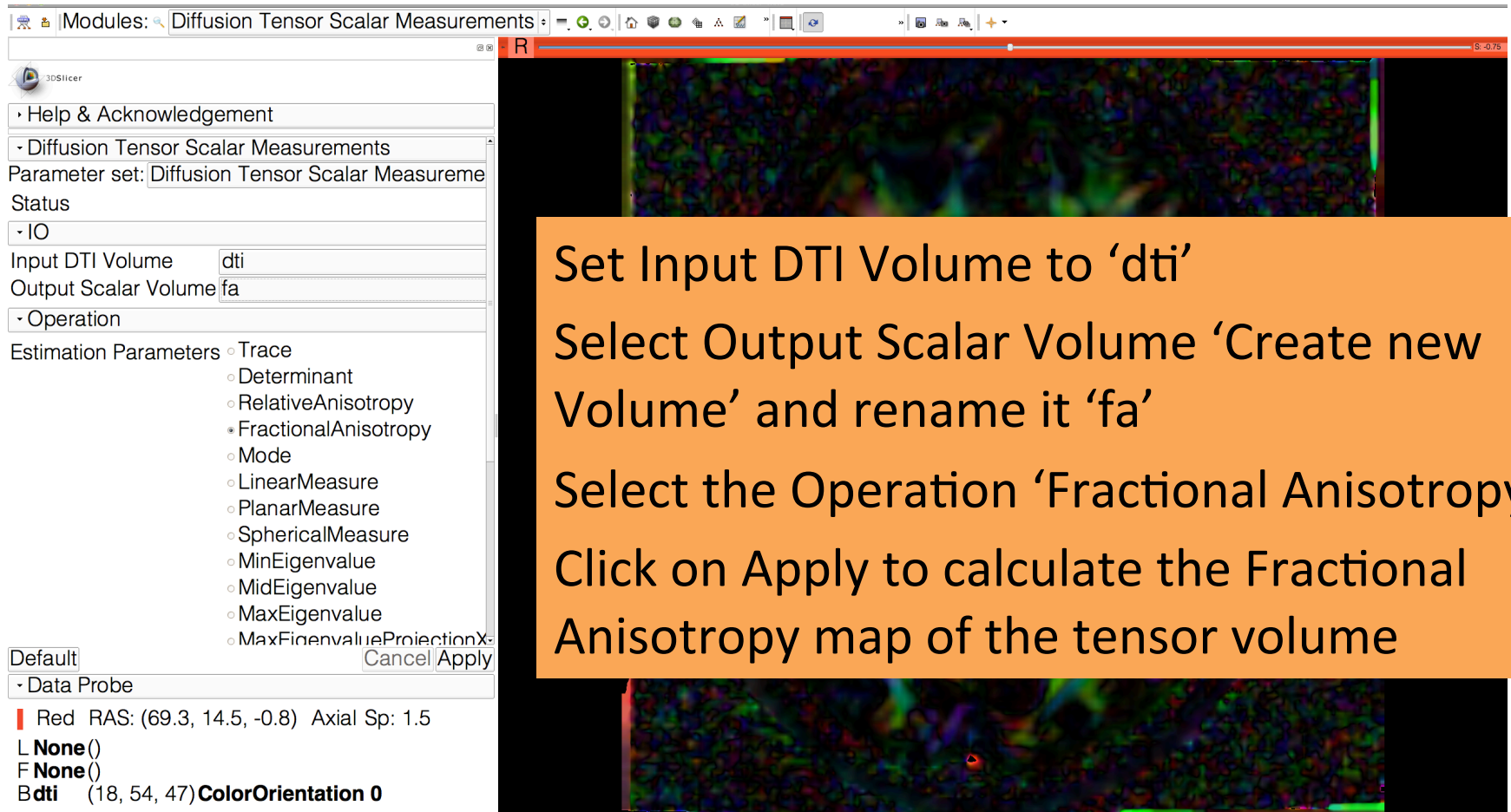
B trace (57, 48, 60) 0.002243

# 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: 

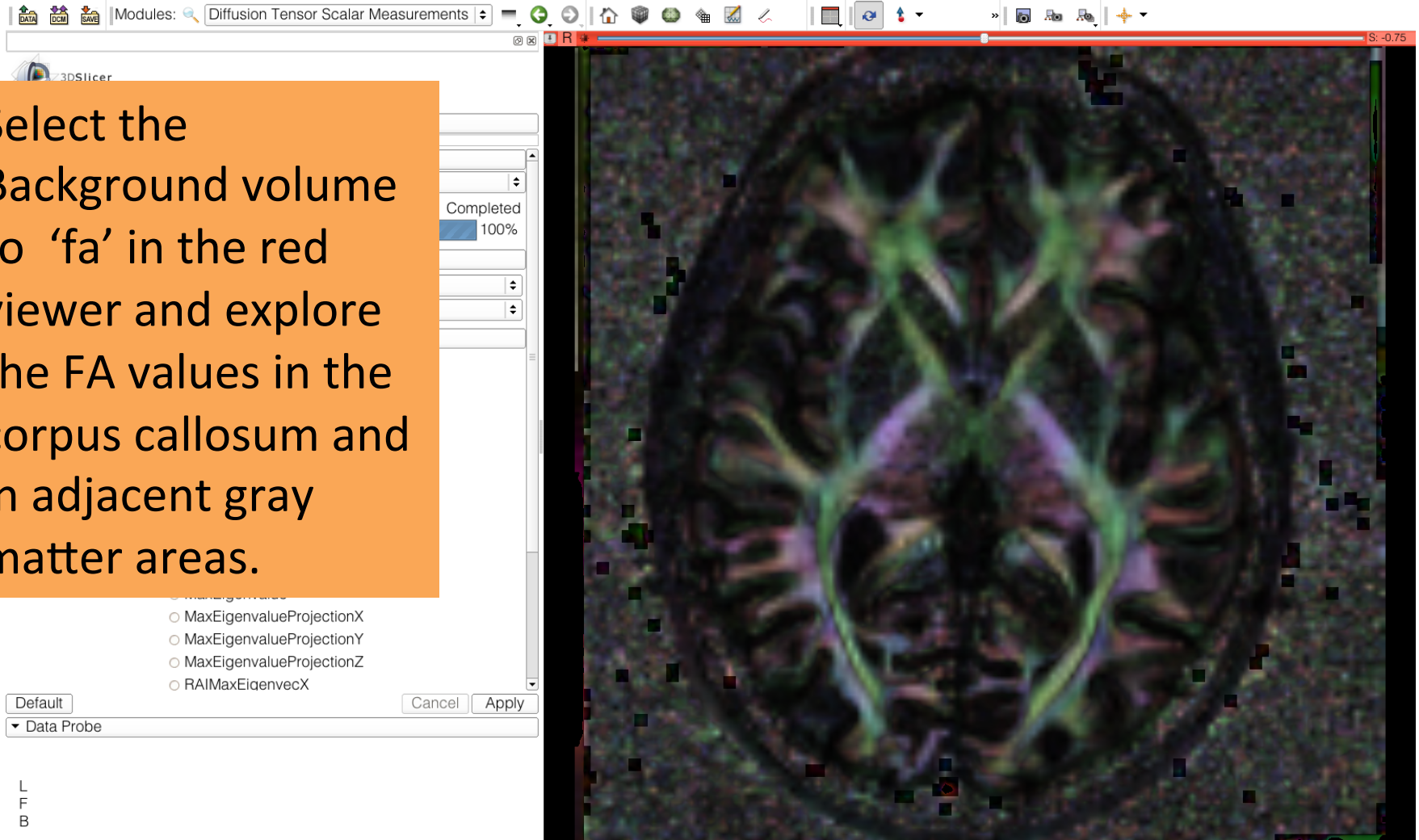
# Characterizing the Shape of the tensor: Fractional Anisotropy



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

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

The screenshot shows the 3D Slicer 4.0.1 interface. The 'Diffusion Tensor Scalar Measurements' panel is open, displaying a list of parameters with radio buttons. The 'Data Probe' section shows the current selection: 'Red RAS: (7.2, 25.4, 15.8) Axial Sp: 1.5'. Below this, a table lists the data for 'dti' and 'fa' at the selected location:

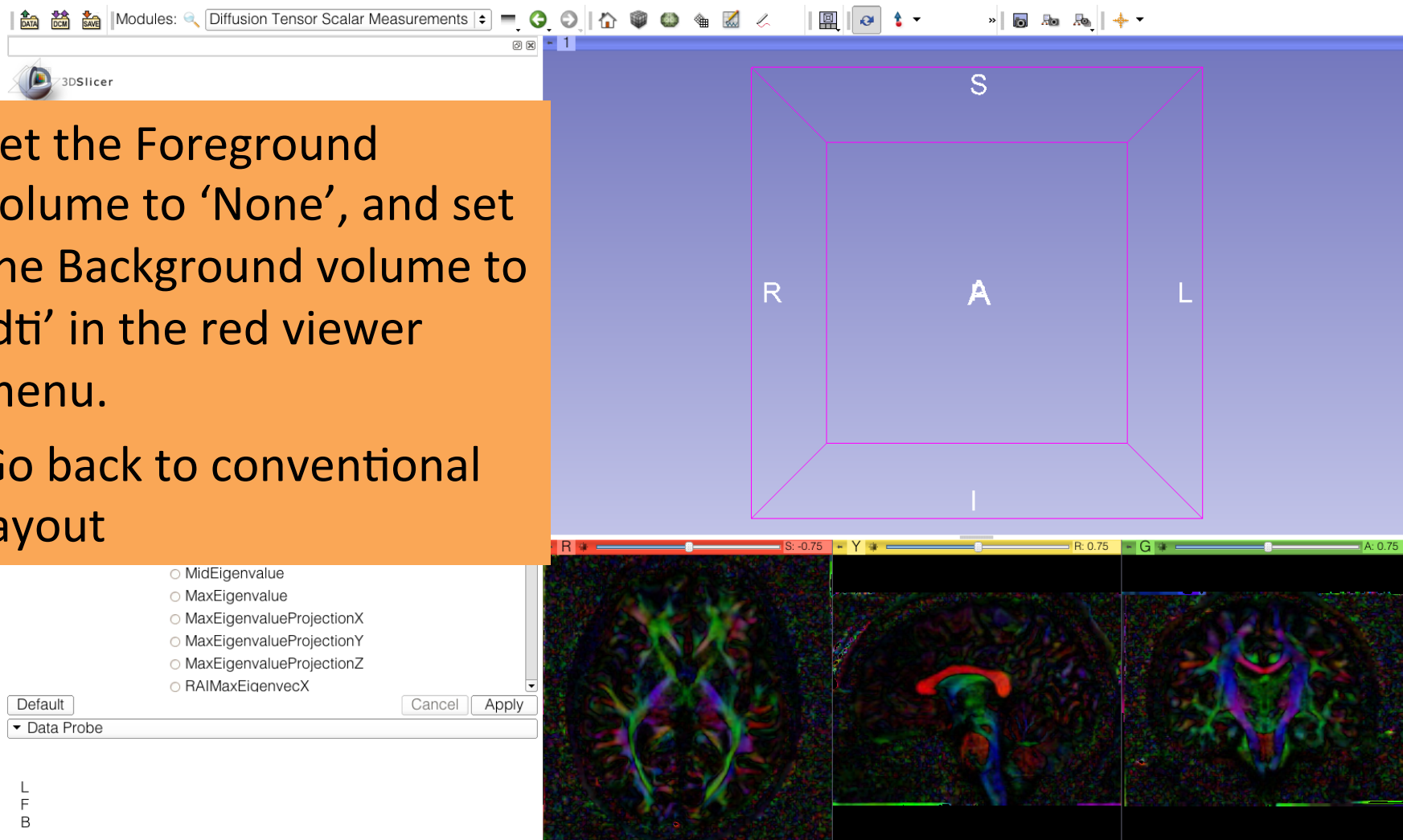
dti	(59, 47, 58)	ColorOrientation 0
fa	(59, 47, 58)	0.8329

The main window displays an axial brain MRI slice with a color-coded FA map. A red arrow points to a white matter region, indicating high FA values.

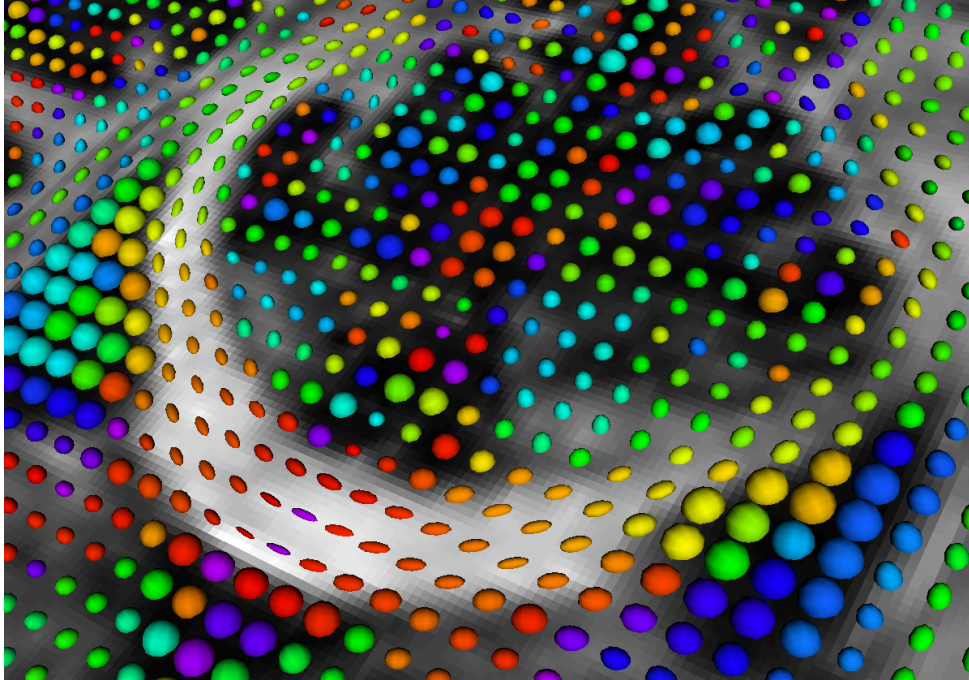
# Fractional Anisotropy

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

Go back to conventional layout

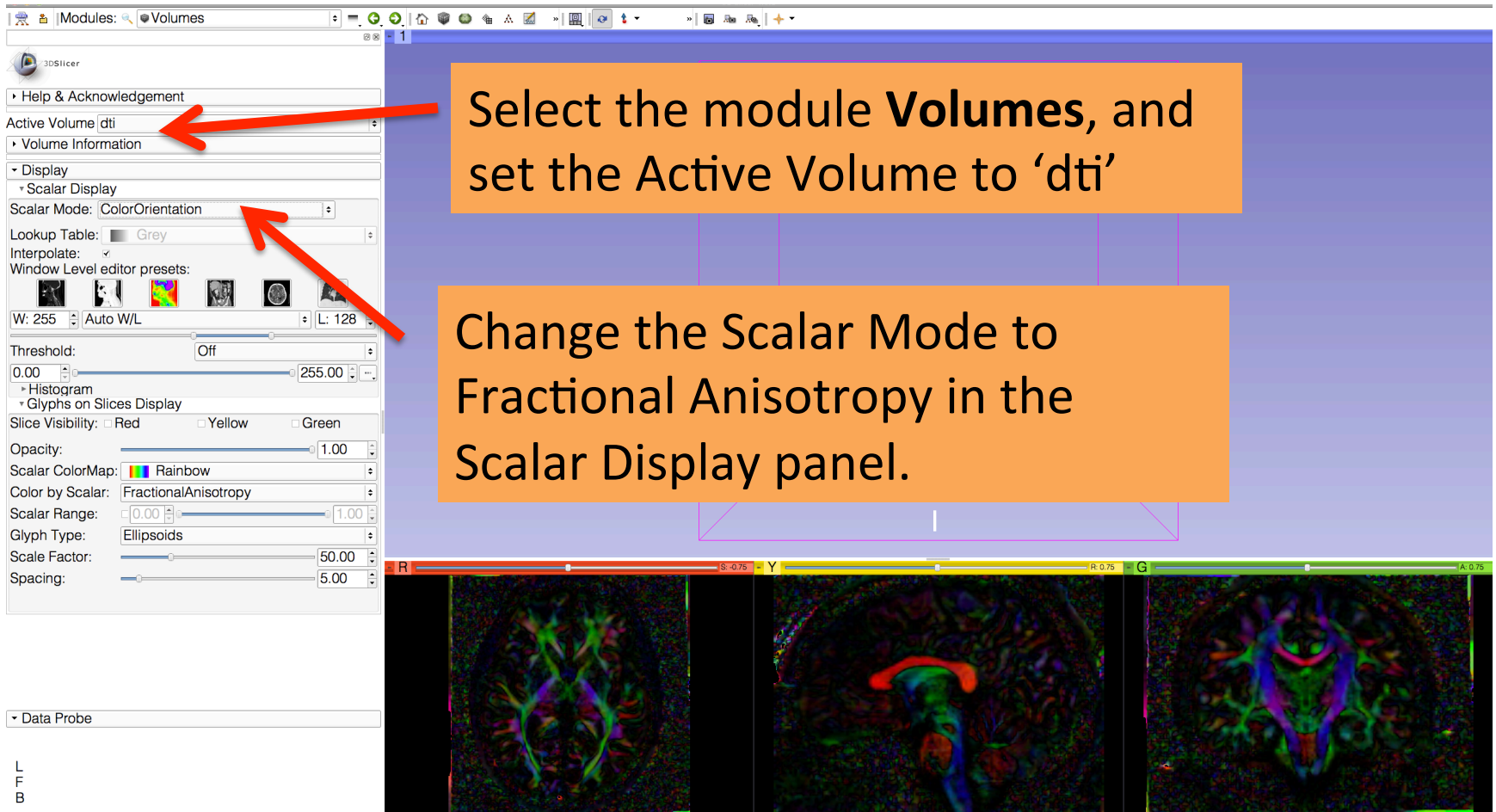






## Part 2: Visualizing the tensor data

# 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.

W: 255 Auto W/L L: 128

Threshold: Off 0.00 255.00

Color by Scalar: FractionalAnisotropy

Scalar Range: 0.00 1.00

Glyph Type: Ellipsoids

Scale Factor: 50.00

Spacing: 5.00

R 0.75 Y 0.75 G 0.75

L  
F  
B

# 3D Visualization: Glyphs

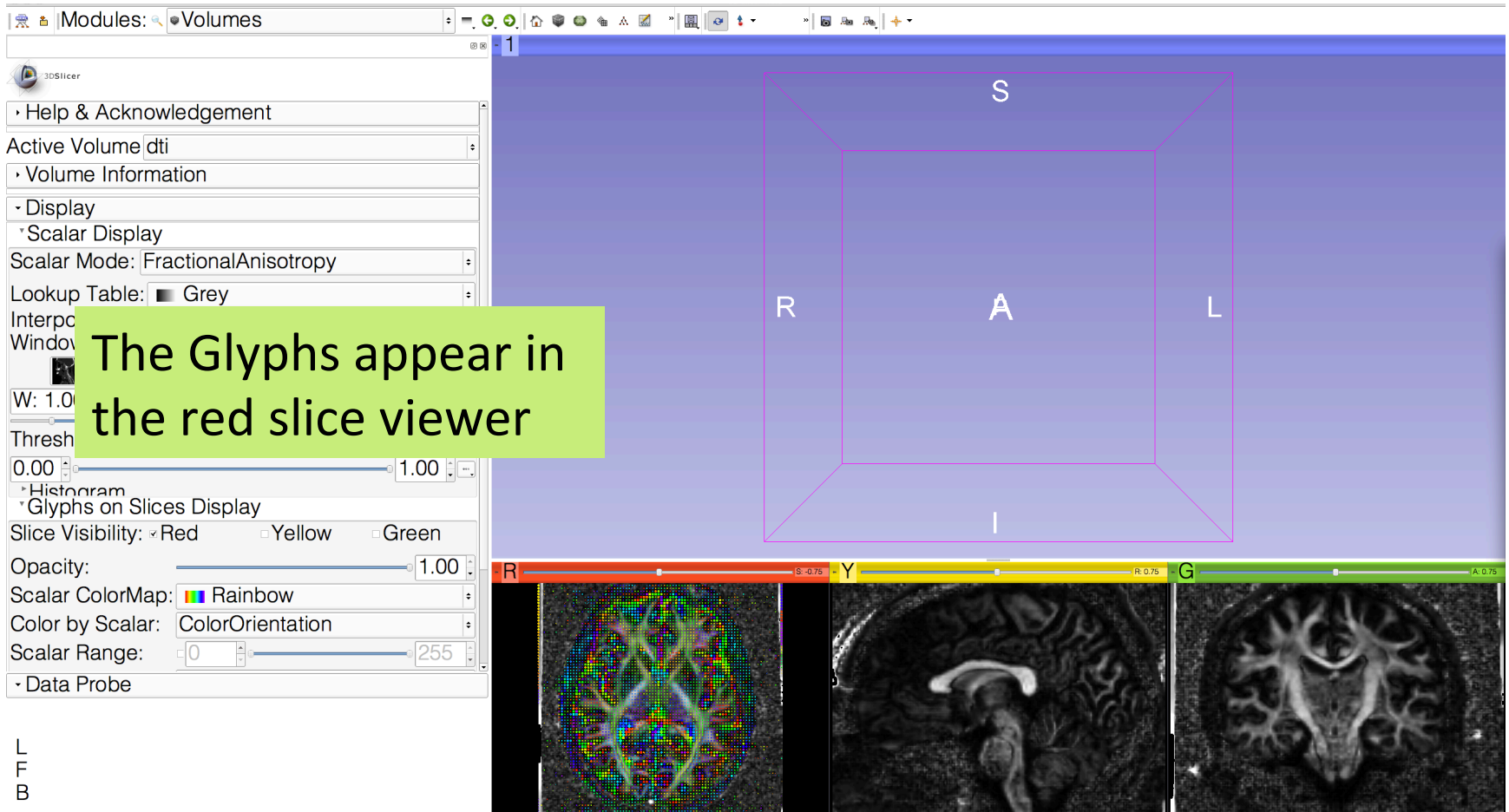
The image shows the 3D Slicer software interface. The top toolbar includes 'Modules: Volumes' and various icons. On the left, a sidebar contains the 'Display' section. Below it is the 'Window Level editor' with 'Auto W/L' selected and a red arrow pointing to it. At the bottom left, the 'Glyphs on Slices Display' panel is highlighted with a red box, showing 'Color by Scalar' set to 'FractionalAnisotrop' and 'Slice Visibility' checked for 'Red'. The main view shows three orthogonal slices (R, A, L) with a 3D brain model. At the bottom left, the letters 'L', 'F', and 'B' are stacked vertically.

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’ ‘

L  
F  
B

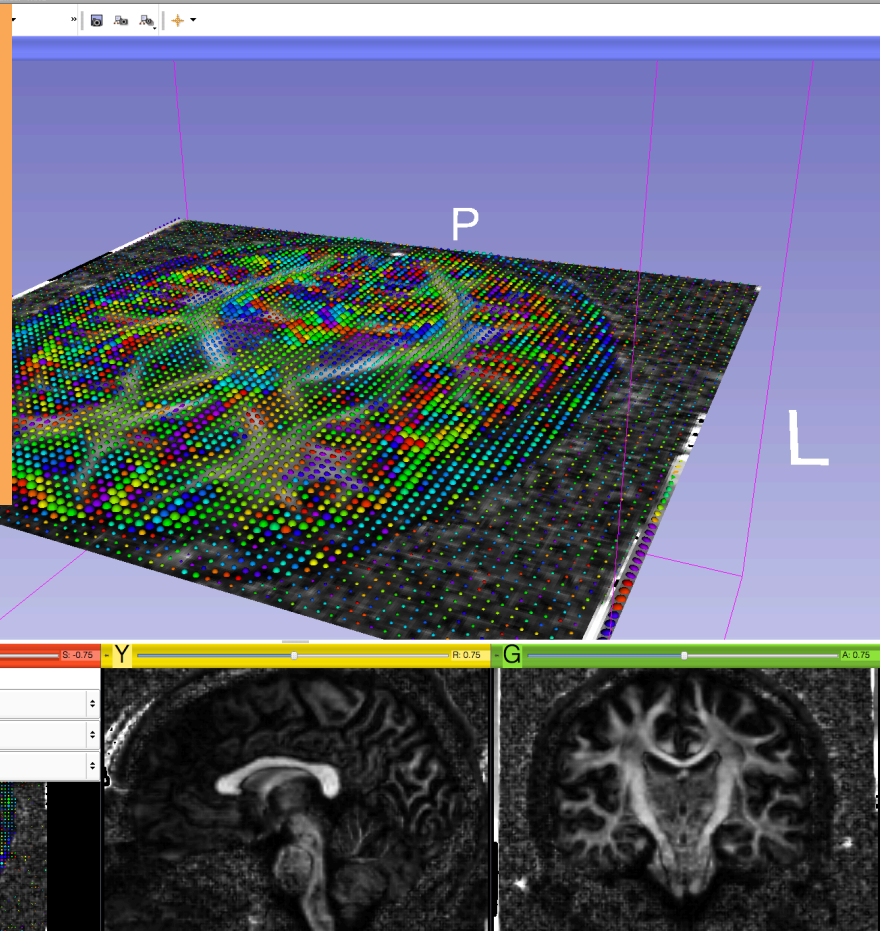
# 3D Visualization: Glyphs



# 3D Visualization: Glyphs

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

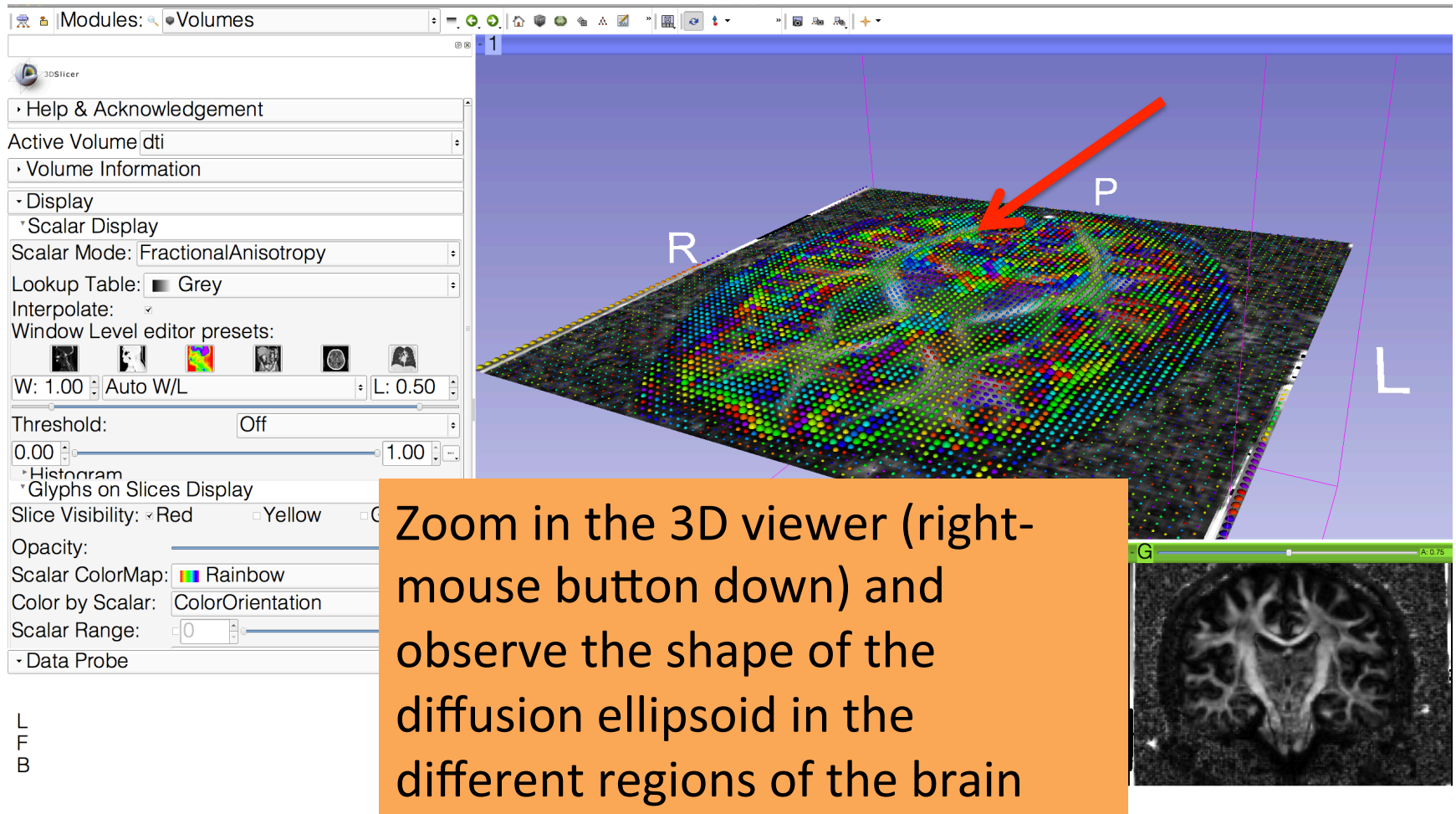
Click on the eye icon to display the glyphs superimposed on the FA image in the 3D Viewer



L  
F  
B



# 3D Visualization: Glyphs



# 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

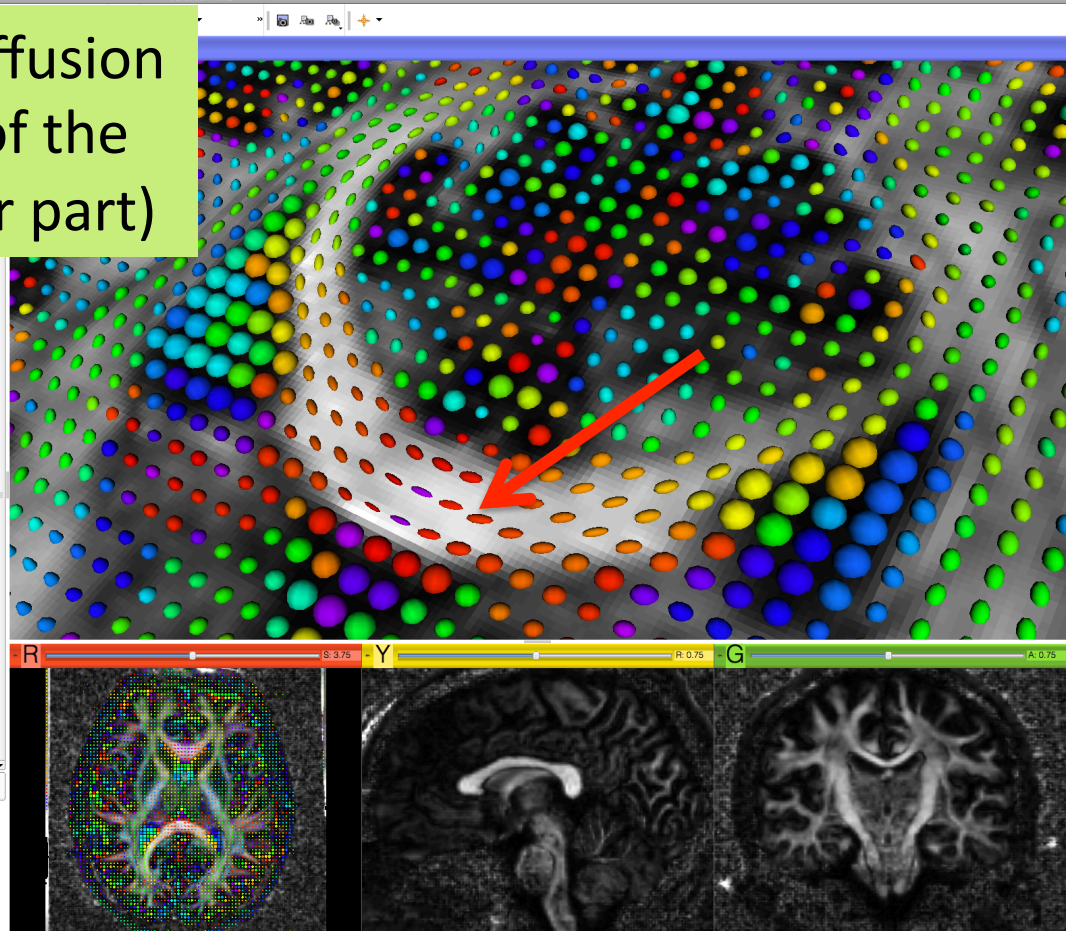
Scalar Range: 0 | 255

Glyph Type: Ellipsoids

Scale Factor: 45.00

Spacing: 5.00

- Data Probe



L  
F  
B

# 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

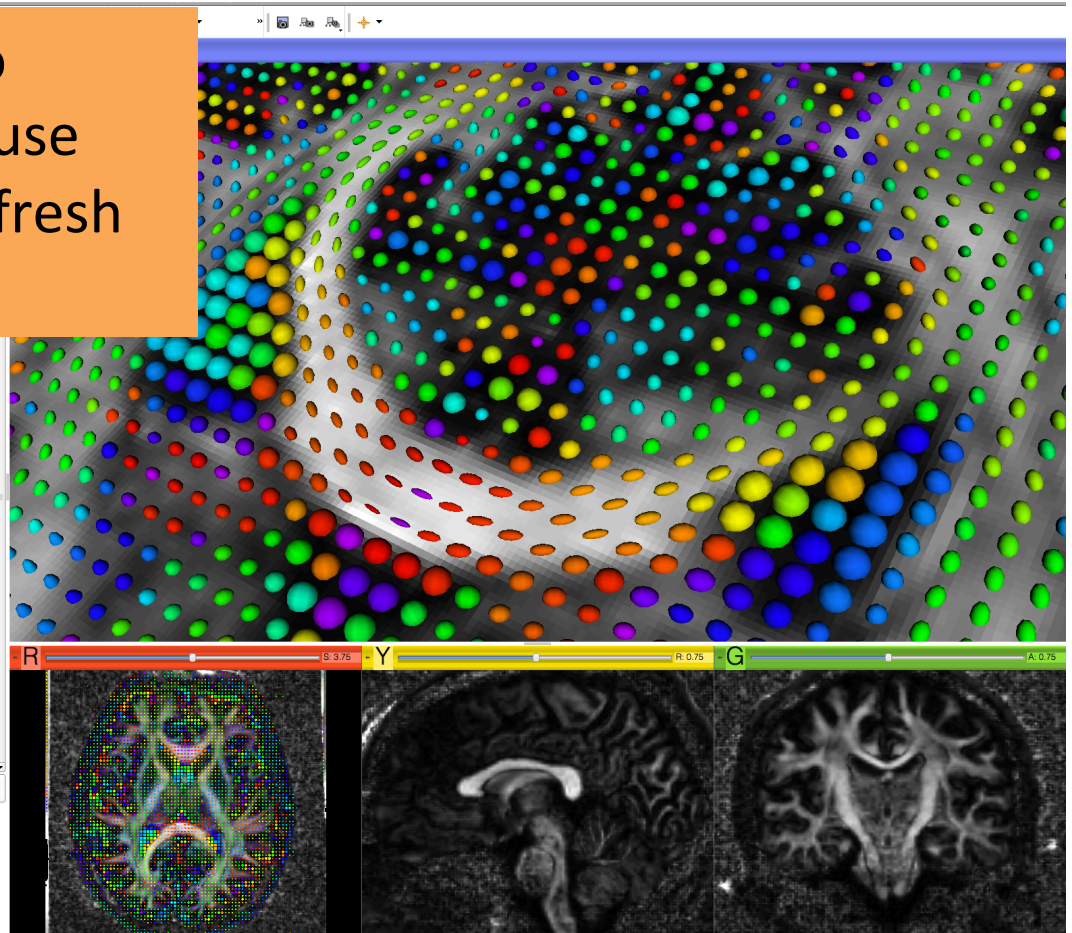
Scalar Range:  0  255

Glyph Type:  Ellipsoids

Scale Factor:  45.00

Spacing:  5.00

Data Probe

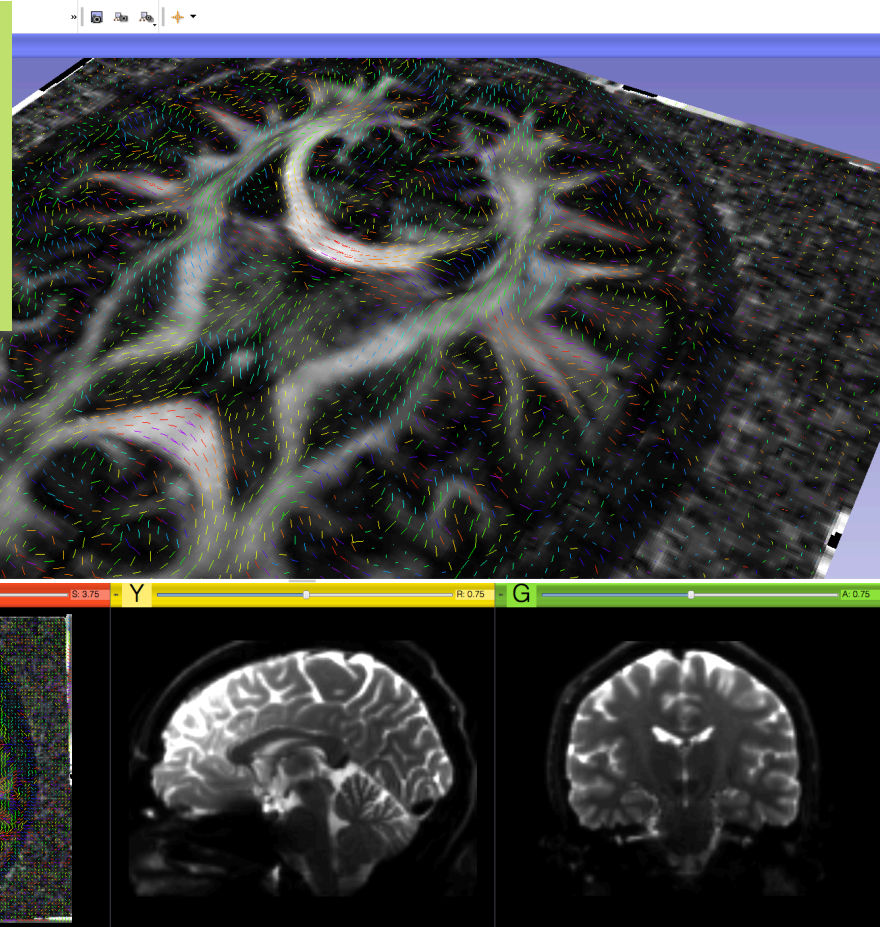


L  
F  
B



# 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

L  
F  
B

# 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

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: 18.00

Spacing: 15.00

Glyph EigenVector: Major

Data Probe

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

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

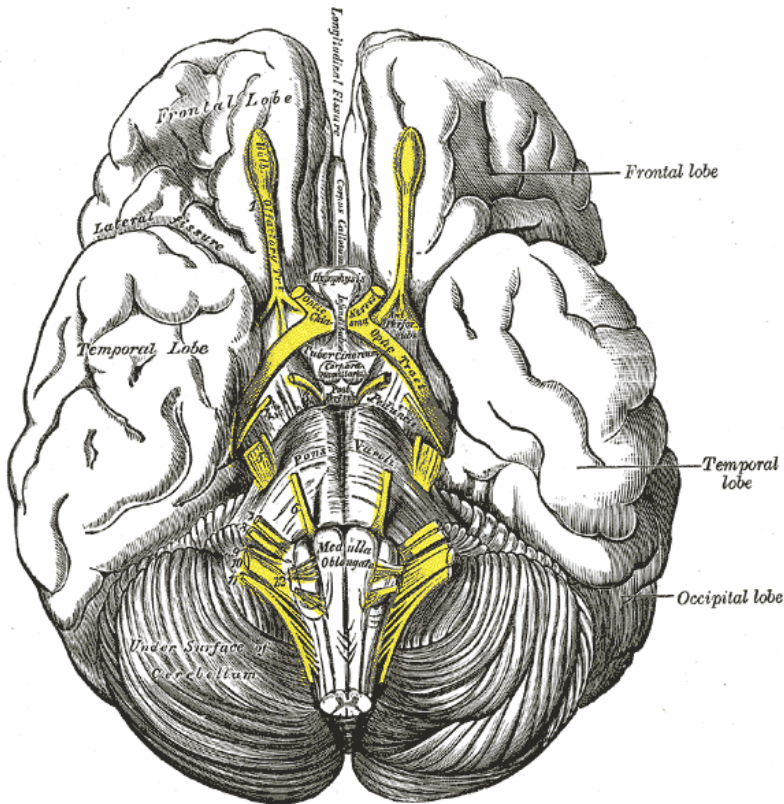
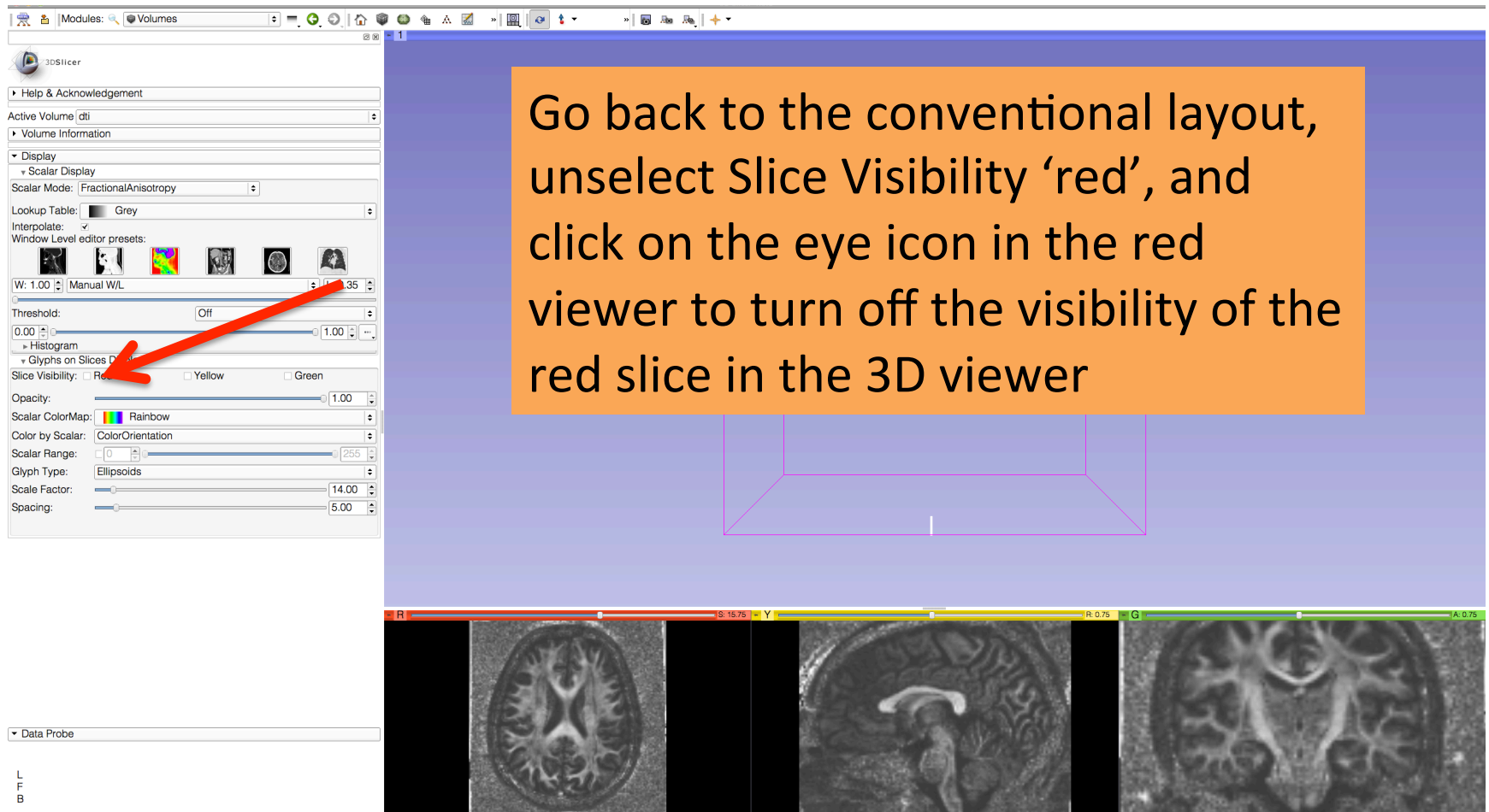


Image from Gray's Anatomy

# 3D Visualization: Glyphs



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

3D Slicer

Modules: Volumes

Active Volume: dti

Volume Information

Display

Scalar Display

Scalar Mode: FractionalAnisotropy

Lookup Table: Grey

Interpolate:

Window Level editor presets:

W: 1.00 Manual W/L: 0.35

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: 14.00

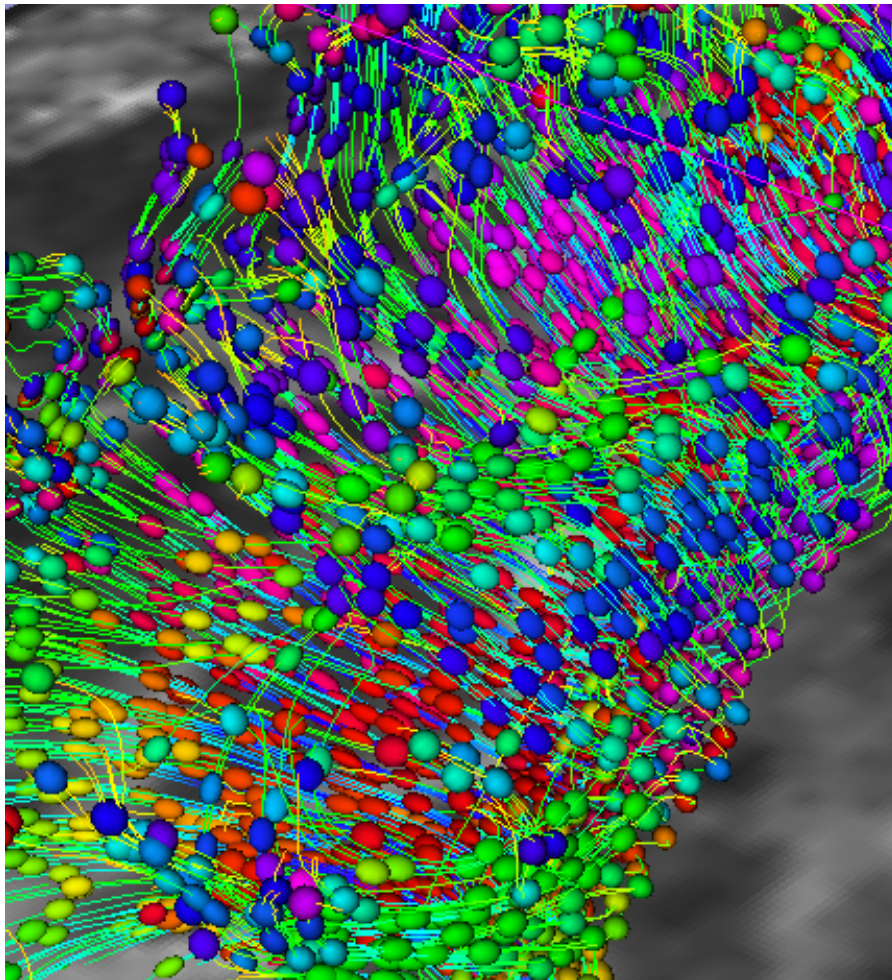
Spacing: 5.00

Data Probe

L  
F  
B

R S Y R G A



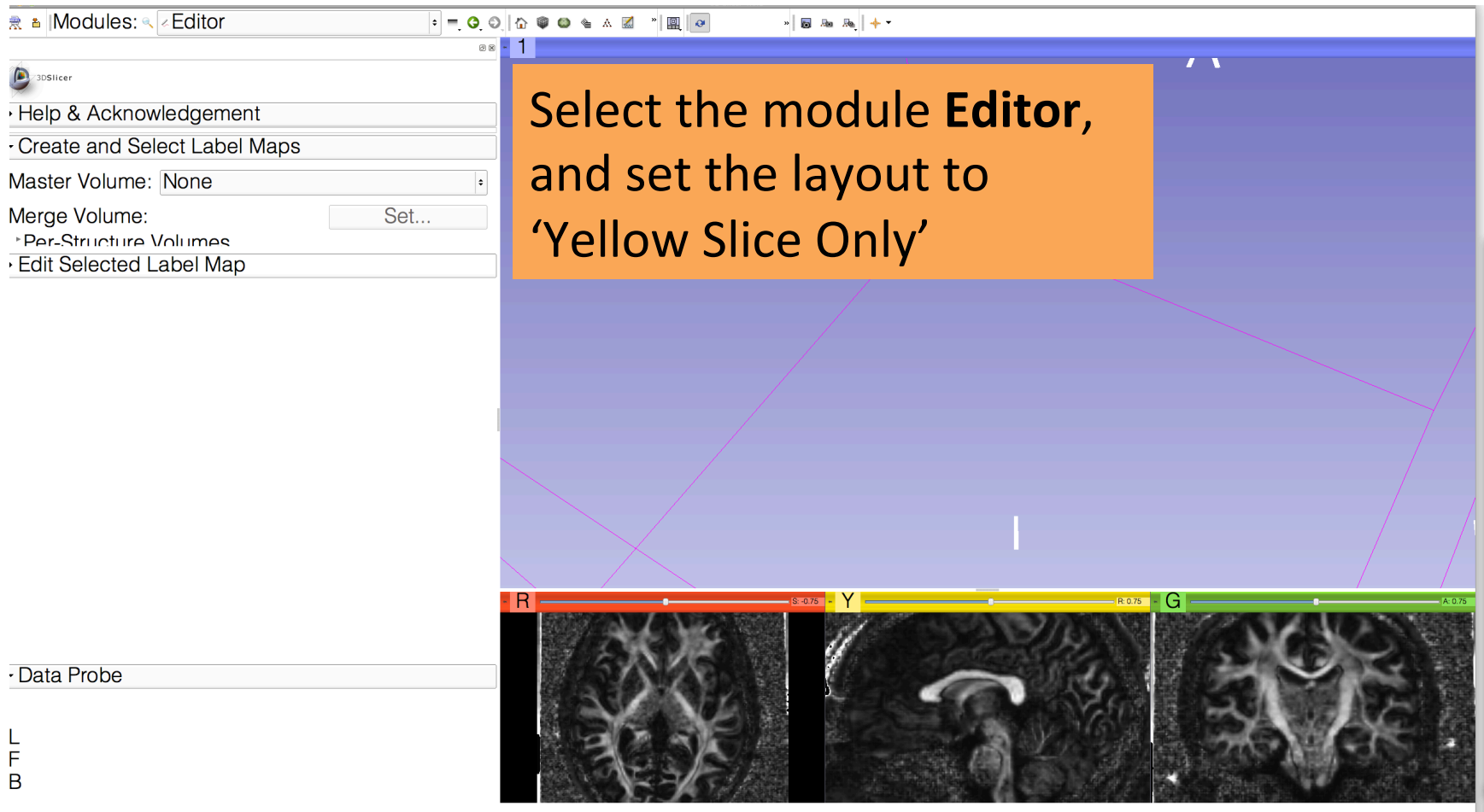


## Part 3: From tensors to tracts

# Diffusion MRI tractography

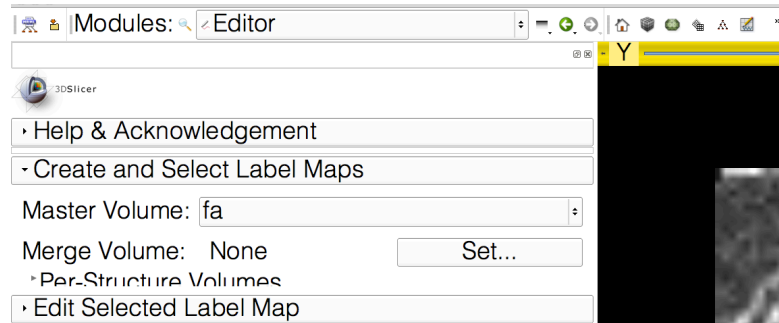
- Tractography can be defined as the virtual reconstruction of the trajectory of water molecules along white matter bundles.
  - DTI tracts provide a mathematical representation of the underlying white matter anatomy.
  - Each voxel contains hundreds of thousands of axon fibers: size of a voxel  $\sim 1\text{-}5\text{ mm}$  is very different from the diameter of an axon  $\sim 0.1\text{-}10\ \mu\text{m}$
- A DTI tract is not equivalent to a real fiber.

# Tractography Seeding: ROI definition

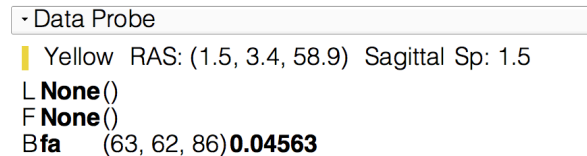
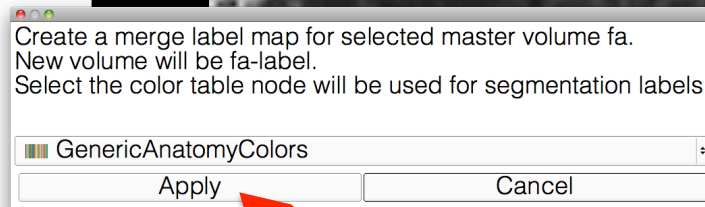




# ROI Definition

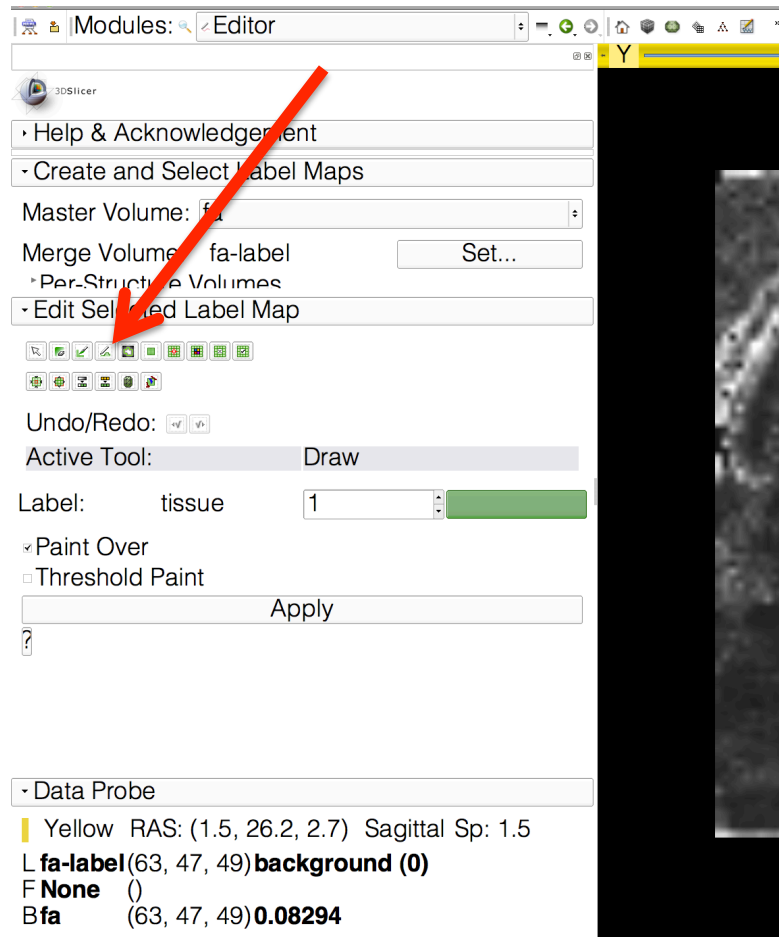


Set the Master Volume to 'fa'  
Click on Apply in the pop-up window to create an empty labelmap 'fa-label'





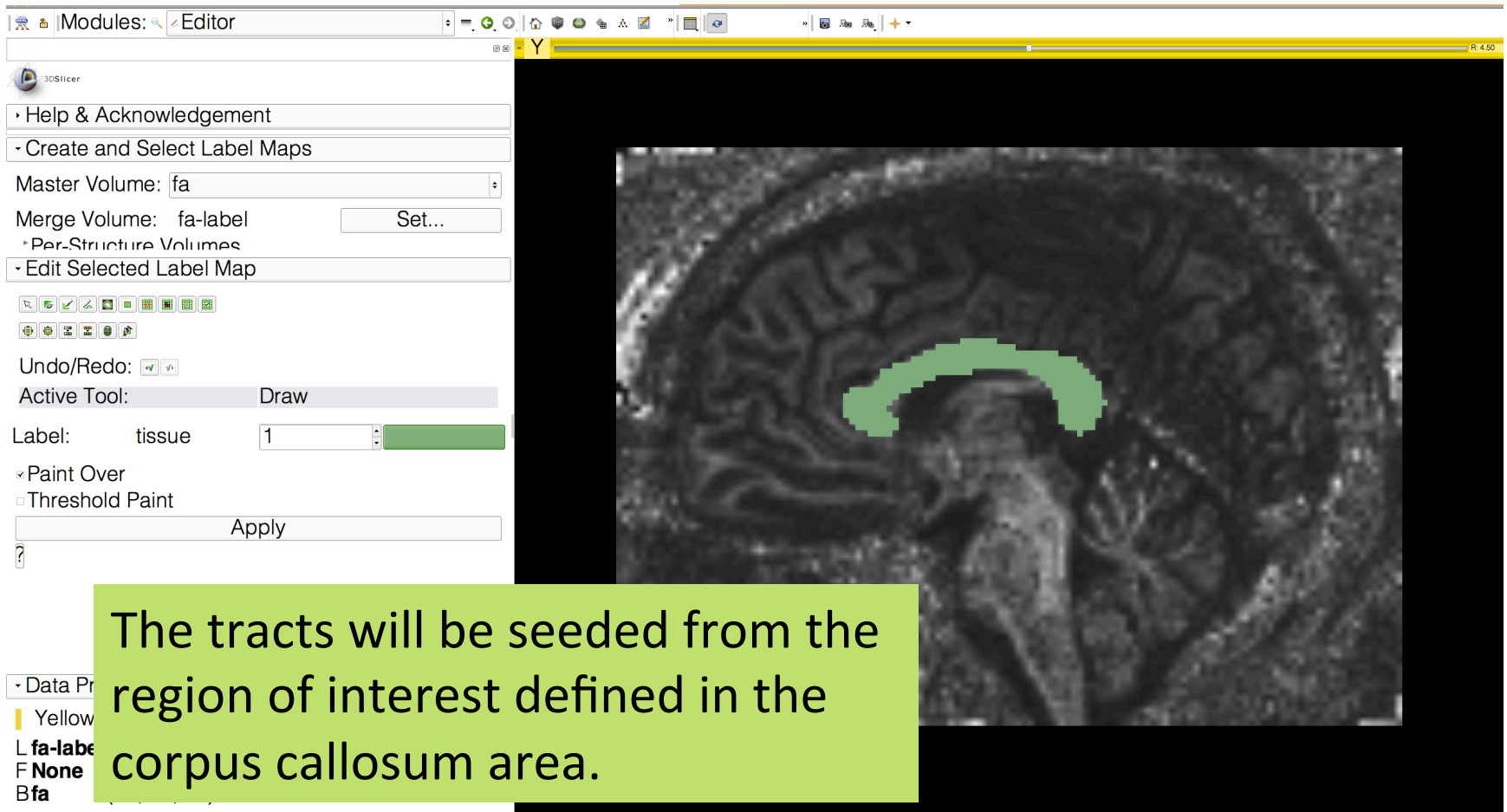
# ROI Drawing



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.



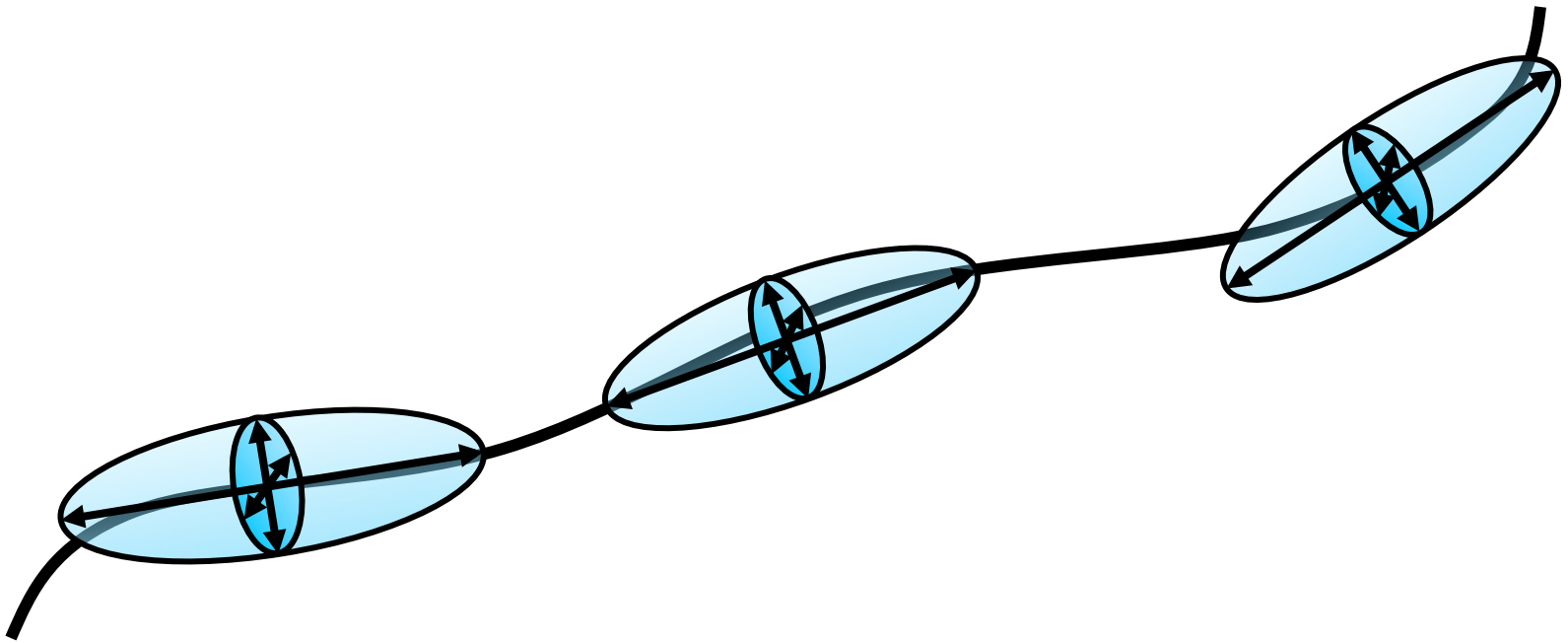
# ROI Drawing



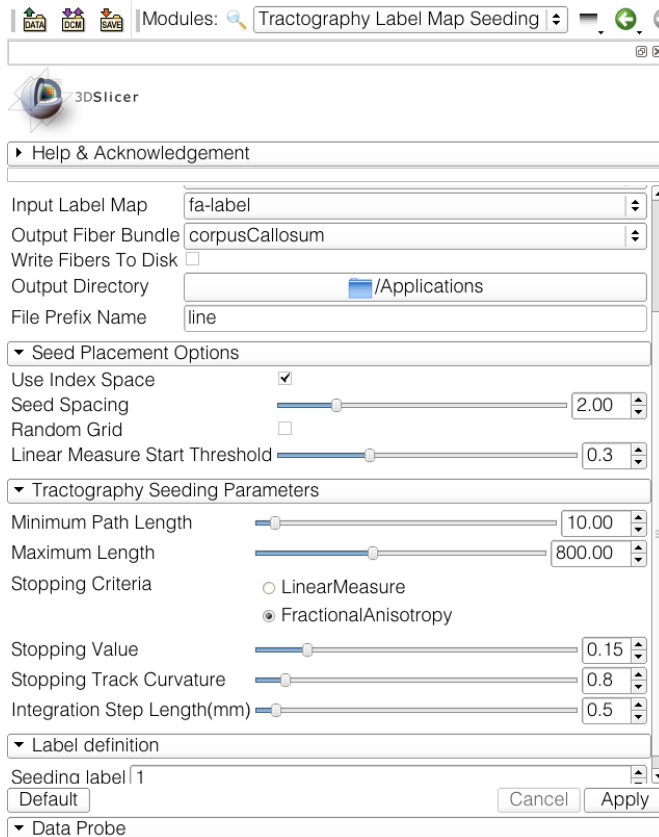
The screenshot shows the 3D Slicer software interface. The top menu bar includes 'Modules' and 'Editor'. The left sidebar contains a 'Help & Acknowledgement' section, a 'Create and Select Label Maps' section with 'Master Volume: fa' and 'Merge Volume: fa-label', and an 'Edit Selected Label Map' section. The 'Edit Selected Label Map' section includes a toolbar with various drawing tools, 'Undo/Redo' buttons, and an 'Active Tool: Draw' dropdown. Below this, the 'Label: tissue' is set to '1' with a green color swatch. There are also checkboxes for 'Paint Over' and 'Threshold Paint', and an 'Apply' button. The main view shows a grayscale axial MRI slice of a brain with a green, semi-circular region of interest (ROI) drawn over the corpus callosum area. A green text box is overlaid on the bottom left of the image, containing the text: '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



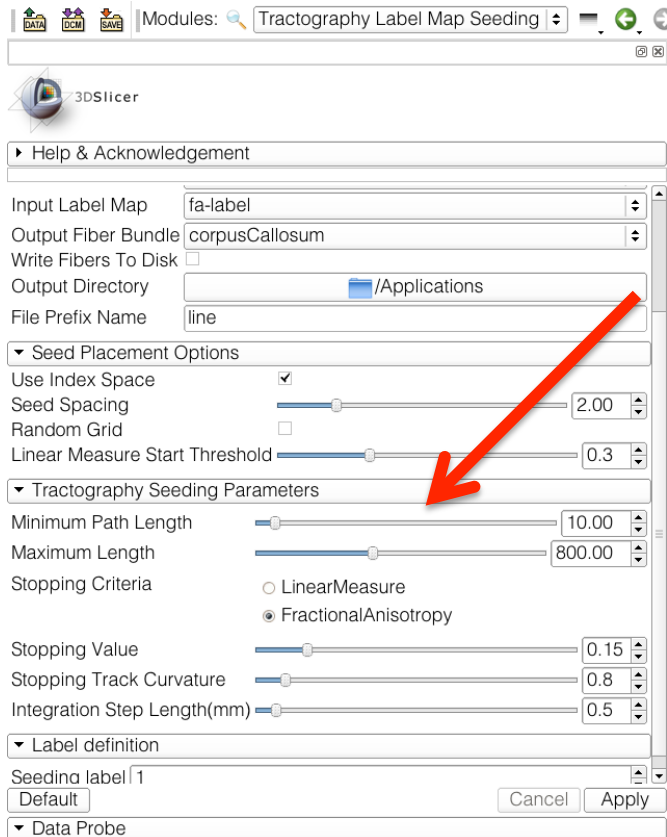
Select the module **Tractography Label Map Seeding**

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'

L  
F  
B

# Labelmap Seeding: parameters



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

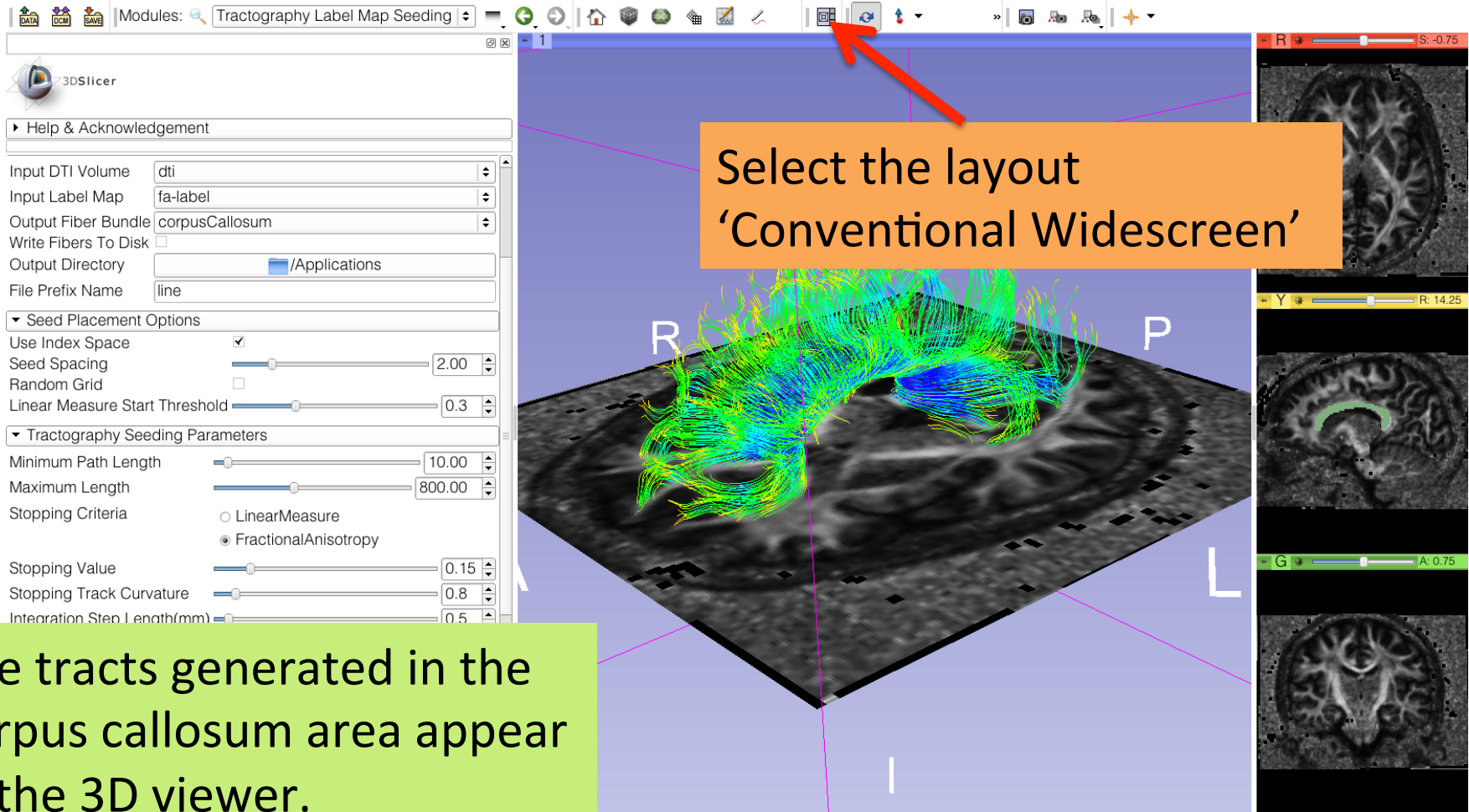
-Stopping value: 0.15

-Stopping track curvature: 0.8

-Integration step length: 0.5 mm

Click on **Apply**

# Labelmap Seeding: Tracts



# Labelmap Seeding: Tracts

The screenshot displays the 3DSlicer software interface. On the left, the 'Tractography Label Map Seeding' module is active, showing various configuration options:

- 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

**Label definition:** Default

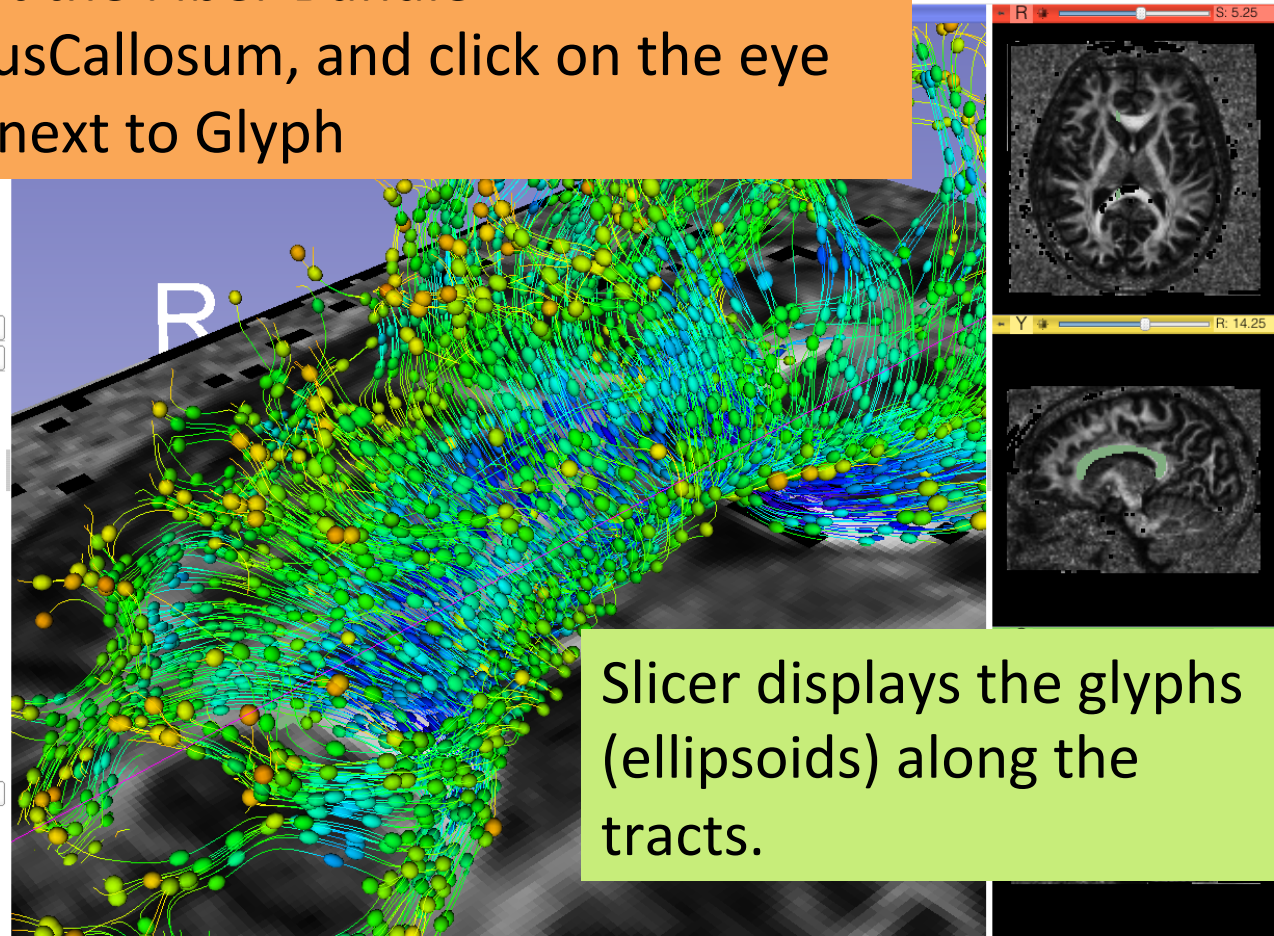
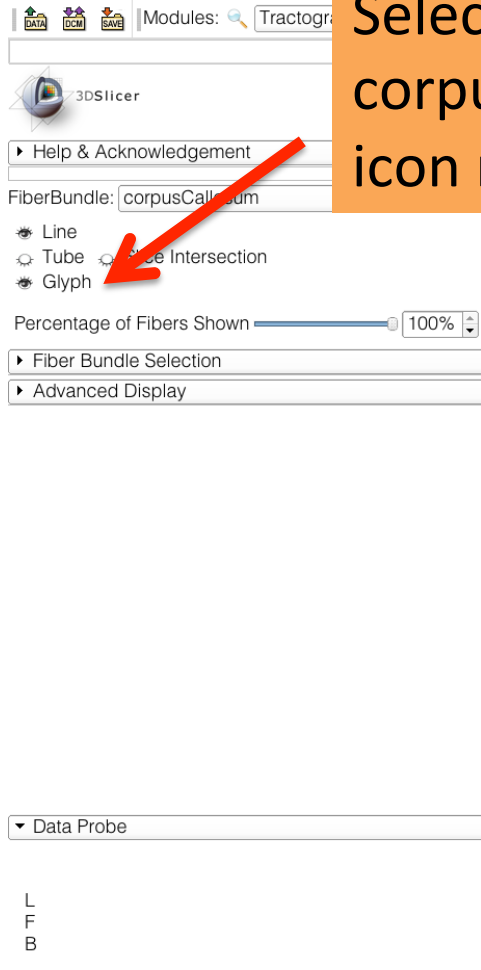
**Data Probe:** (Buttons: Cancel, Apply)

The main 3D view shows a brain slice with a bundle of tracts colored in a gradient from blue to green. The axes are labeled R (Right), P (Posterior), L (Left), and I (Inferior). An orange callout box with the text 'Select the module Tractography Display' points to the 3D view. On the right, a vertical stack of three axial brain slices is shown, with the top slice labeled 'R' and 'S: -0.75', the middle slice labeled 'Y' and 'R: 14.25', and the bottom slice labeled 'G' and 'A: 0.75'.



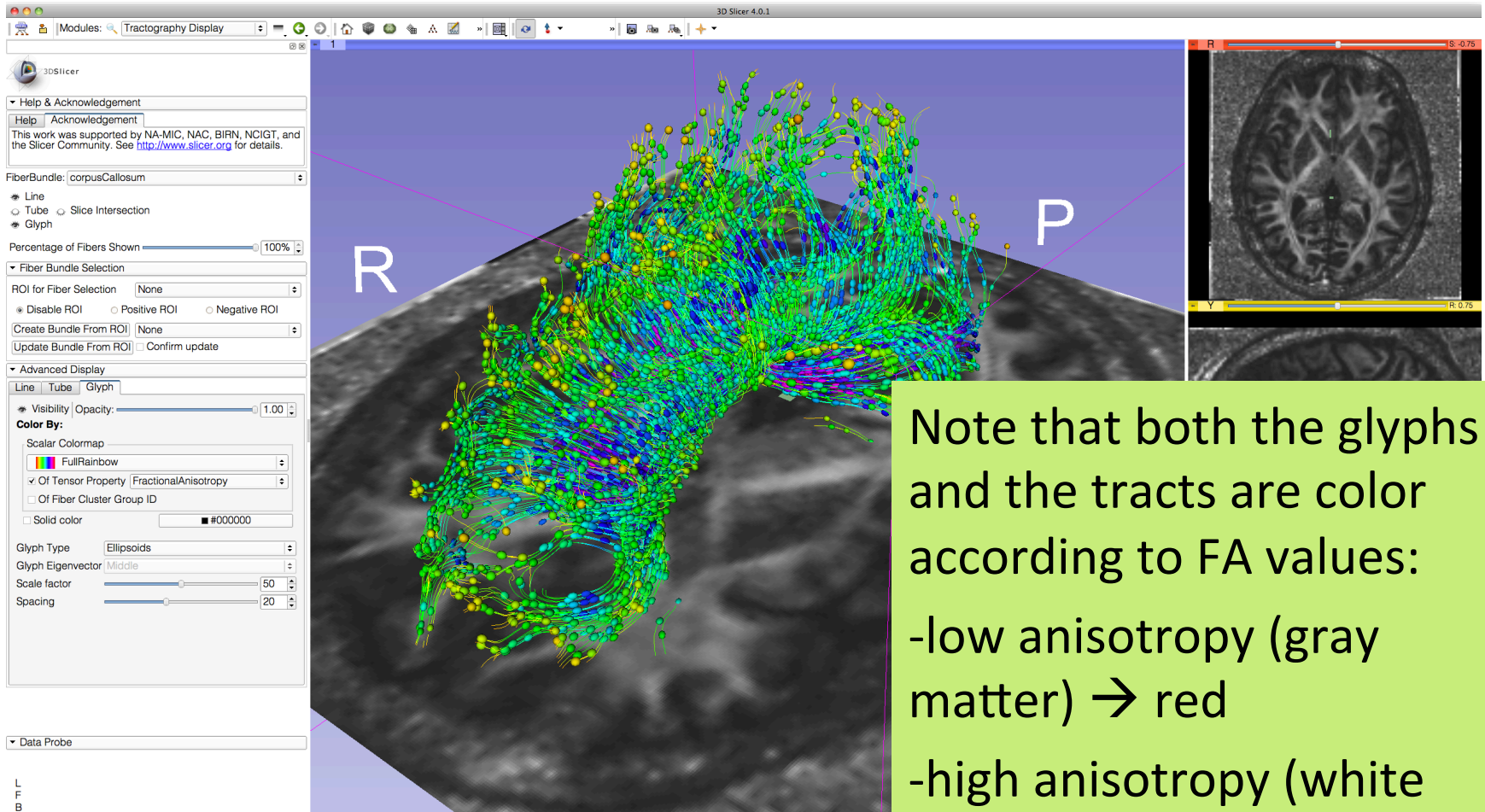
# Tractography Results

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



Slicer displays the glyphs (ellipsoids) along the tracts.

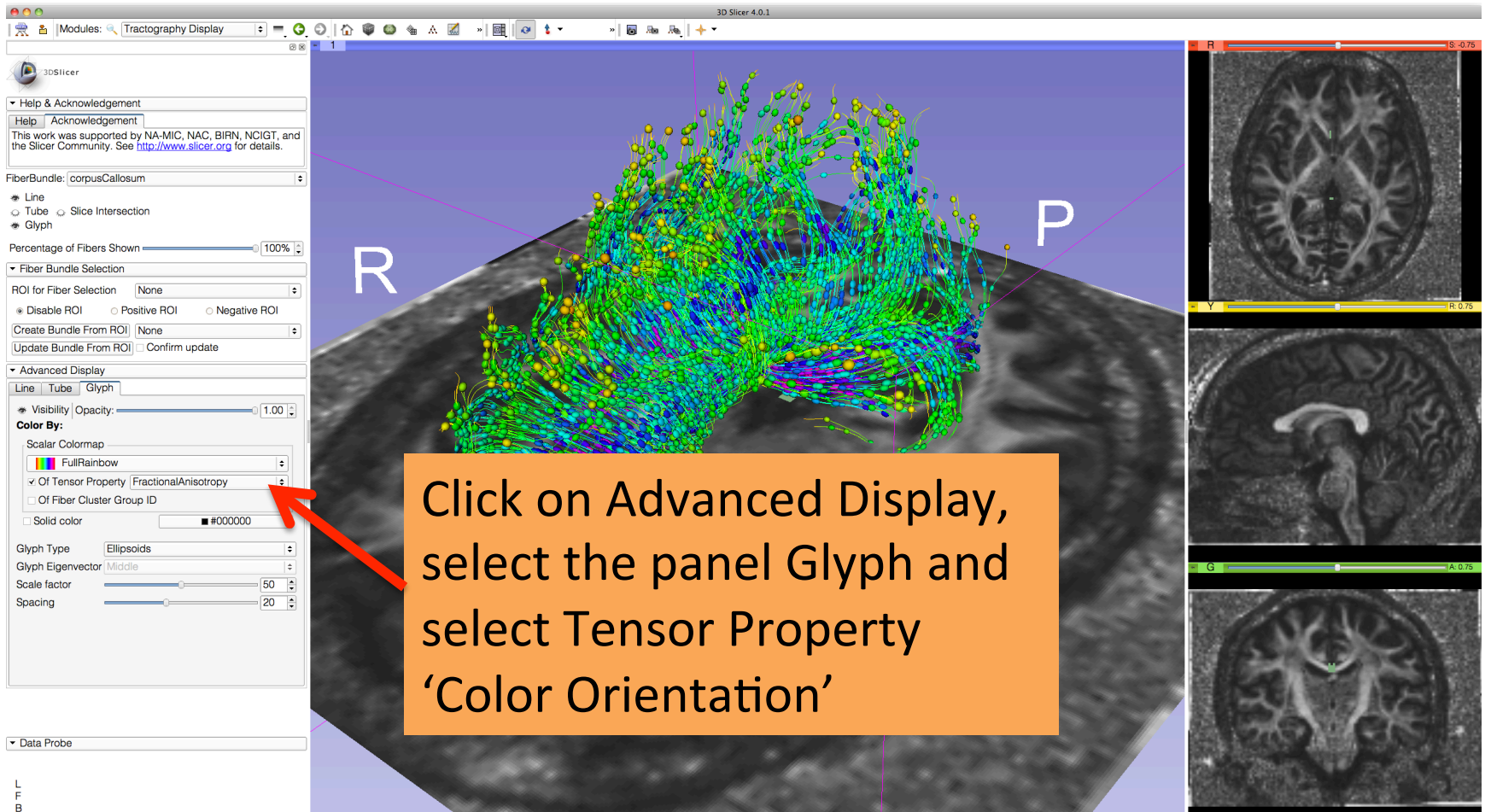
# Tractography Results



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

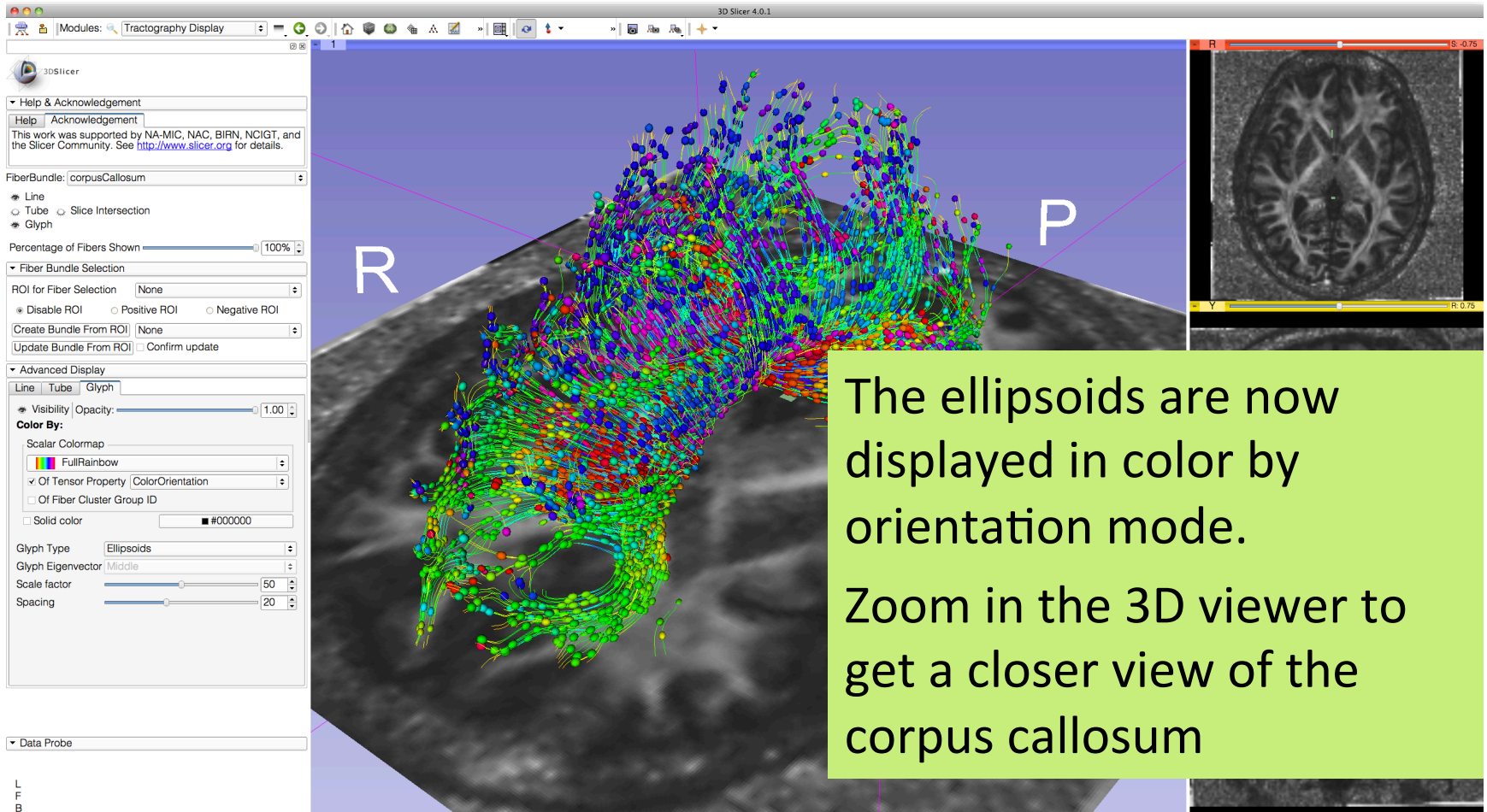
- low anisotropy (gray matter) → red
- high anisotropy (white matter) → blue

# Tractography Results





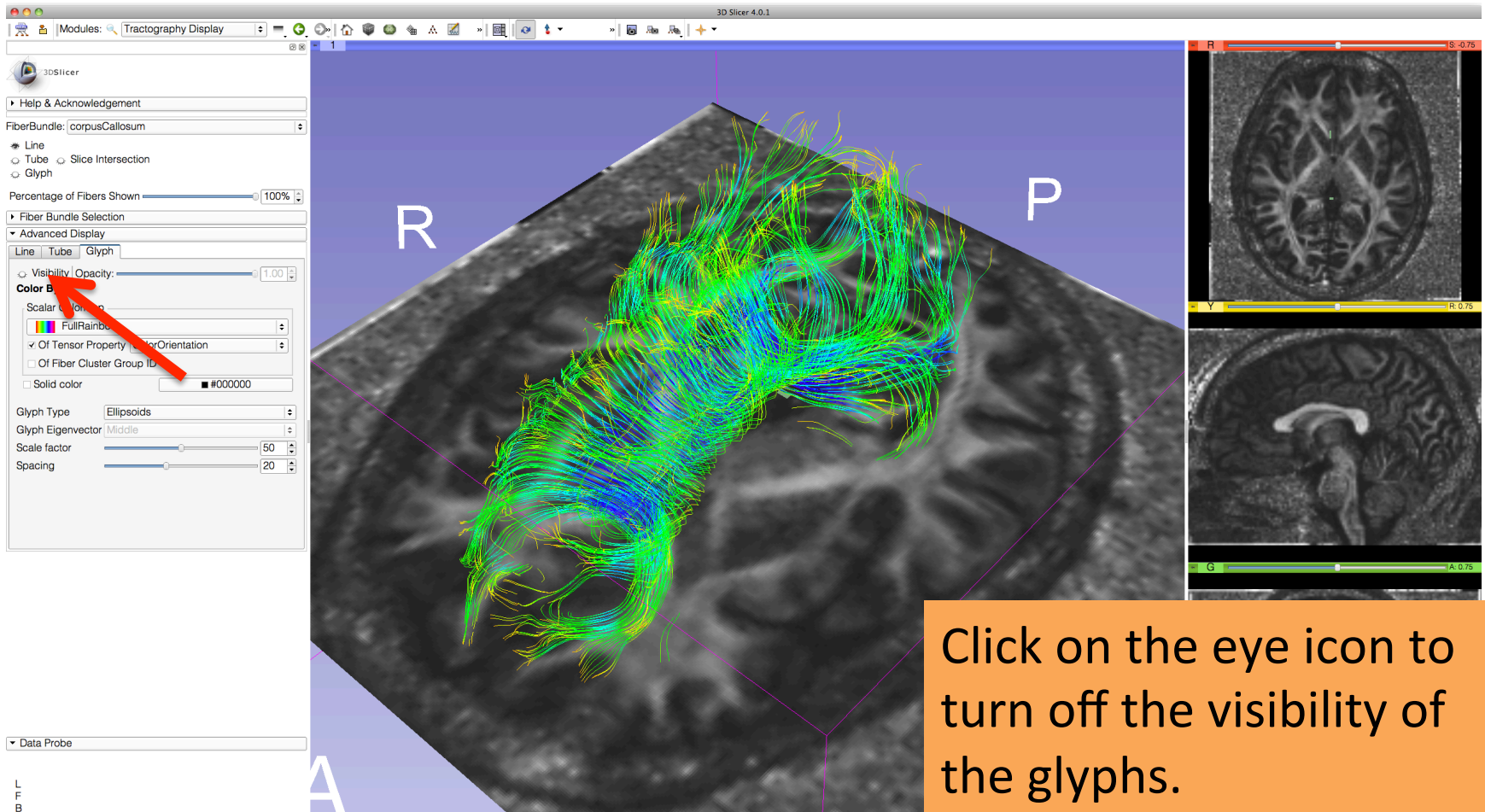
# Tractography Results



# Tractography Results

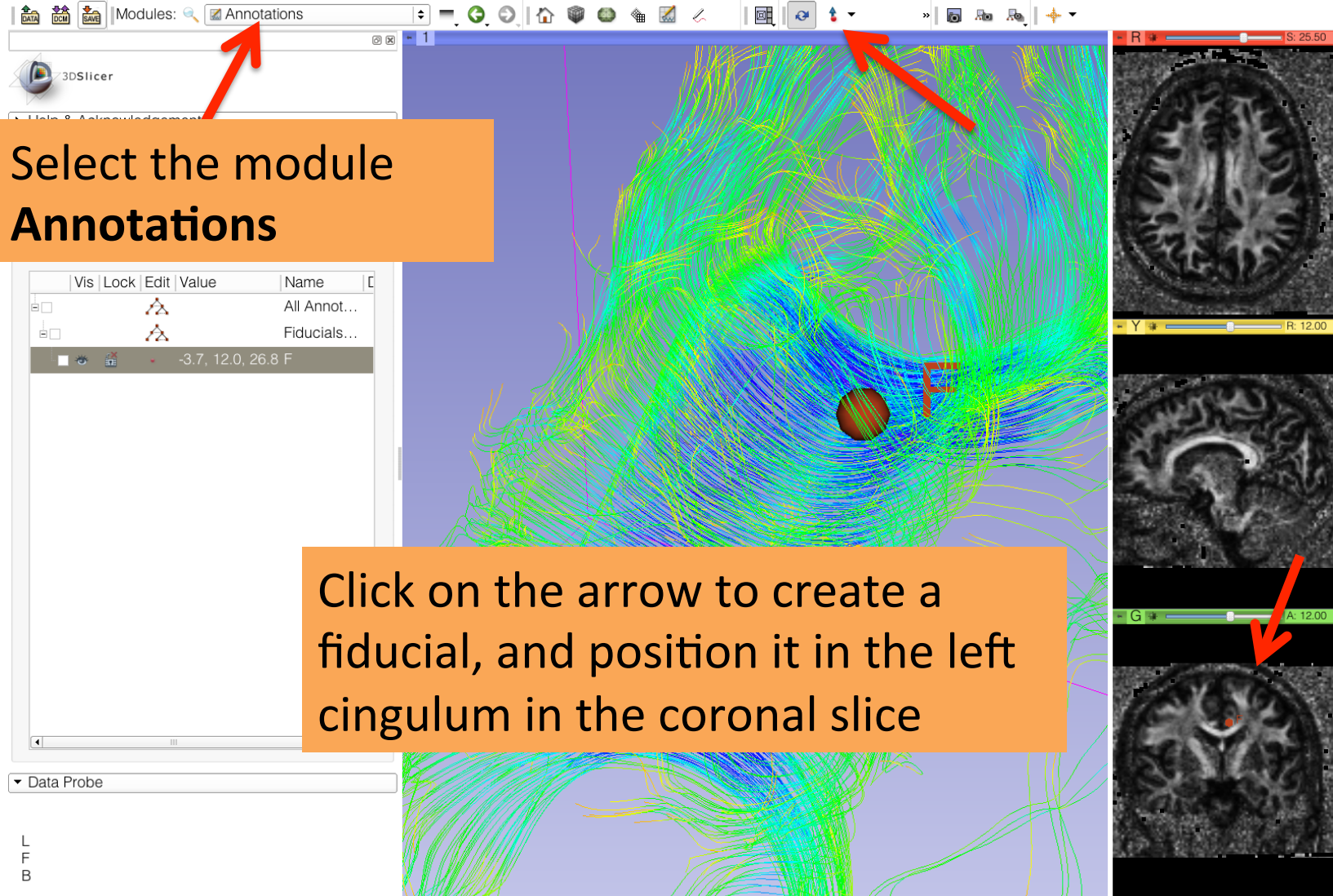


# Tractography Results





# Fiducial Seeding





# Fiducial Seeding

Change the name of the fiducial to 'LeftCingulum'

The screenshot displays the 3D Slicer interface. The top toolbar includes icons for Data, DICOM, SAVE, and various navigation tools. The 'Annotations' module is active. On the left, a table lists annotations:

Vis	Lock	Edit	Value	Name
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		All Annot...
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		Fiducials...
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	-3.7, 12.0, 26.8	LeftCing...

A red arrow points to the 'LeftCing...' entry. The main 3D view shows a brain with a dense network of multi-colored fibers. A red sphere is placed on the brain, labeled 'LeftC'. The right panel shows three orthogonal MRI slices: axial (top), sagittal (middle), and coronal (bottom). The coronal slice has a red dot labeled 'LeftCingulum'.

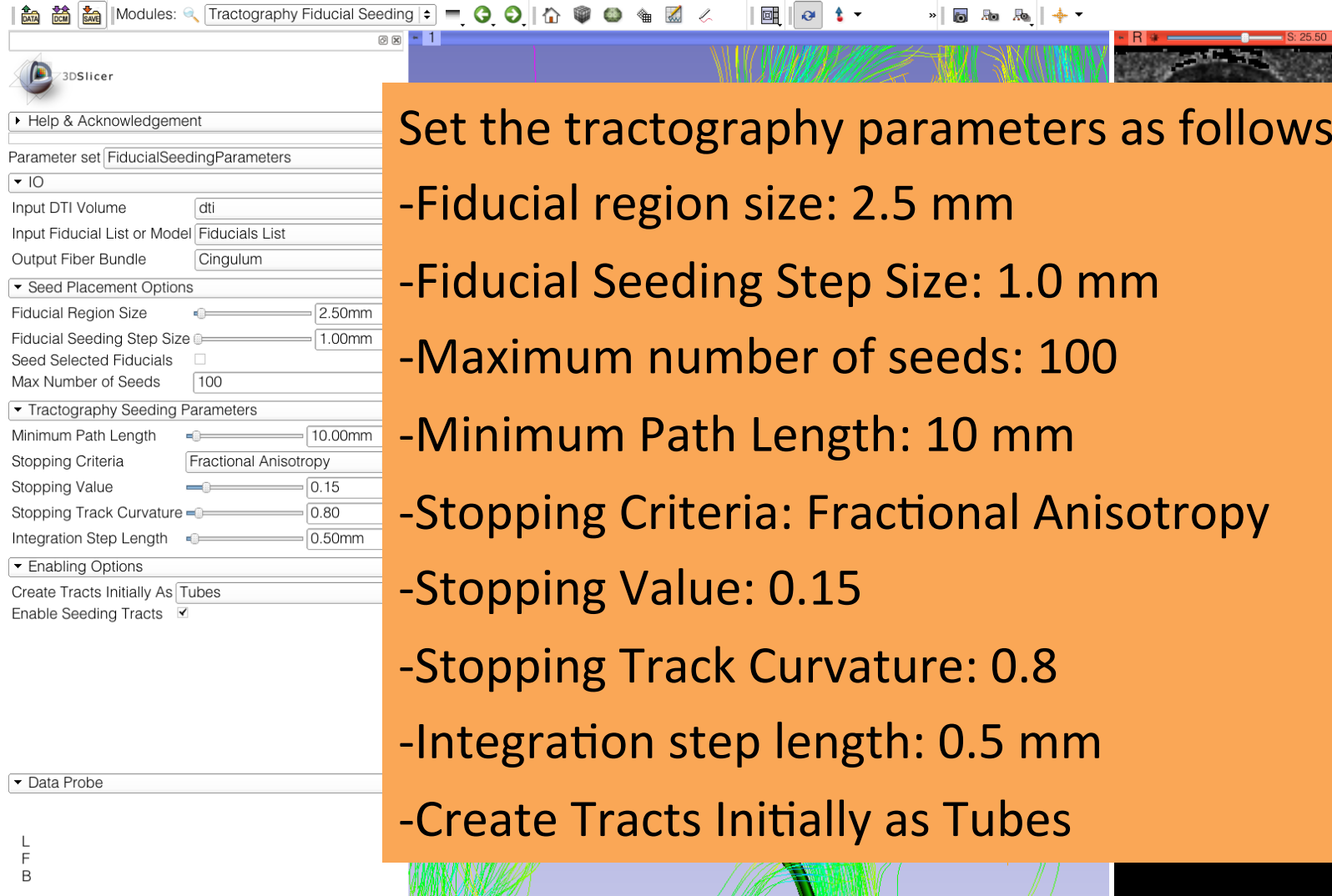
# Fiducial Seeding

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'

L  
F  
B

# Fiducial Seeding



3DSlicer

Modules: Tractography Fiducial Seeding

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

L  
F  
B

R S: 25.50

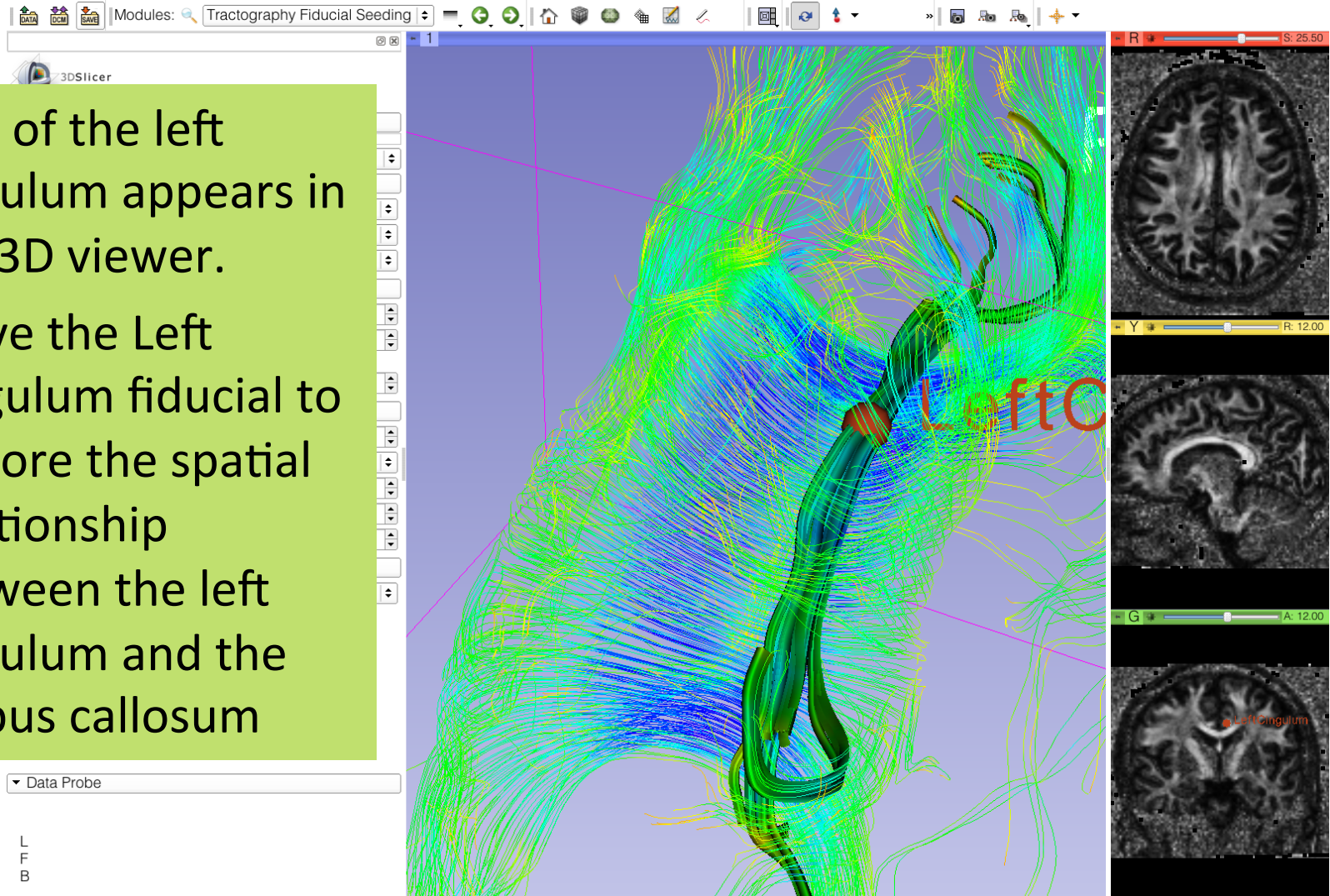
Set the tractography parameters as follows:

- 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

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

Vis	Lock	Edit	Value	Name	D
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		All Annot...	
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		Fiducials...	
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	-3.7, 12.0, 26.8	LeftCing...	
<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	8.5, 12.9, 24.9	RightCin...	

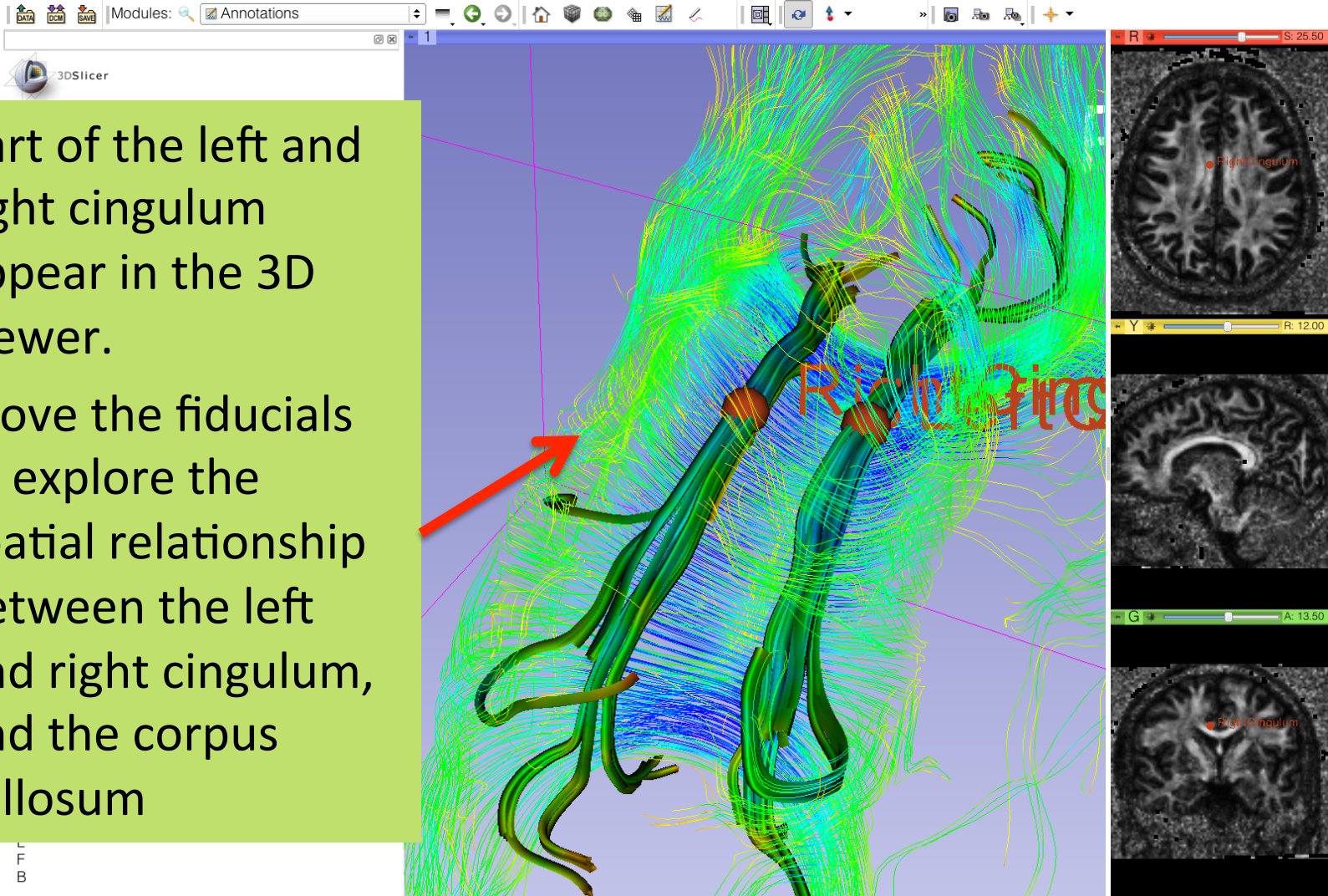
L  
F  
B



# 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

Data Probe

L  
F  
B

RightCinulum

S: 1.50  
R: 12.00  
A: 13.50

# Fiducial Seeding

3DSlicer

Annotations

Active list: Fiducials List

Vis	Lock	Edit	Value	Name	D
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		All Annot...	
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>		Fiducials...	
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	-3.7, 12.0, 26.8	LeftCing...	
<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	8.5, 12.9, 24.9	RightCin...	
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	-14.7, 0.4, 7.8	F_2	

Move the fiducial F\_2 in the 3D viewer to explore the dti dataset

R S: 1.50

Y R: 12.00

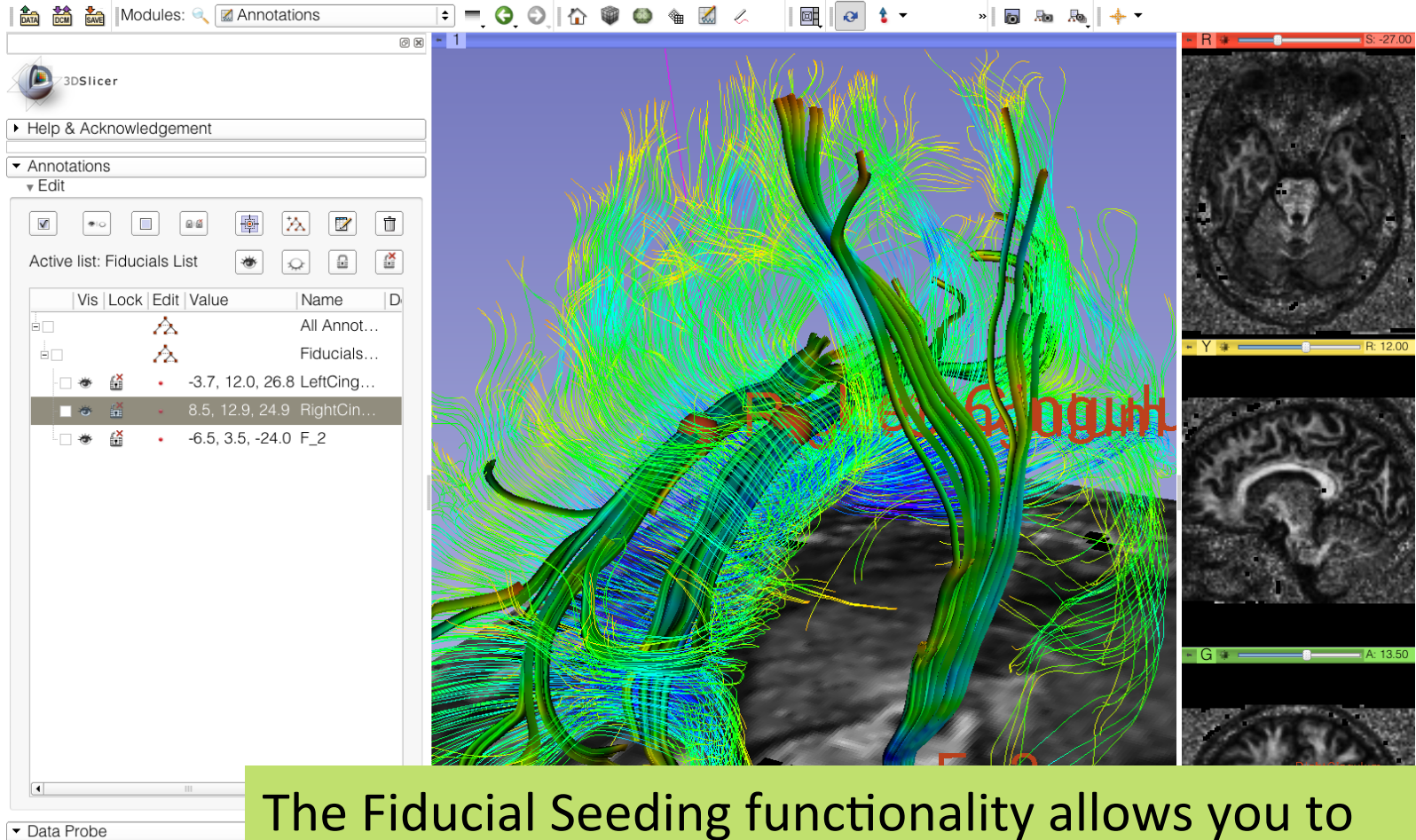
G A: 13.50

RightCingulum

L  
F  
B



# Tractography 'on-the-fly'



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

3DSlicer

Modules: Data

Help & Acknowledgement

Display & Modify Scene

Nodes

- Scene
  - View
    - Default Scene Camera
    - dwi
    - dti
    - baseline
    - baseline-label
    - trace
    - fa
    - corpusCallosum
    - All Annotations
    - LeftCingulum
    - Fiducials List
    - Cingulum
    - RightCingulum
    - F\_2
    - SceneViewToplevelHierarchyNode
    - Master Scene View

Scene Model: Transform

- Display MRML ID's
- Show Hidden nodes

Filter:

Load & Add Scenes Or Individual Datasets

Data Probe

L  
F  
B

R S: -27.00

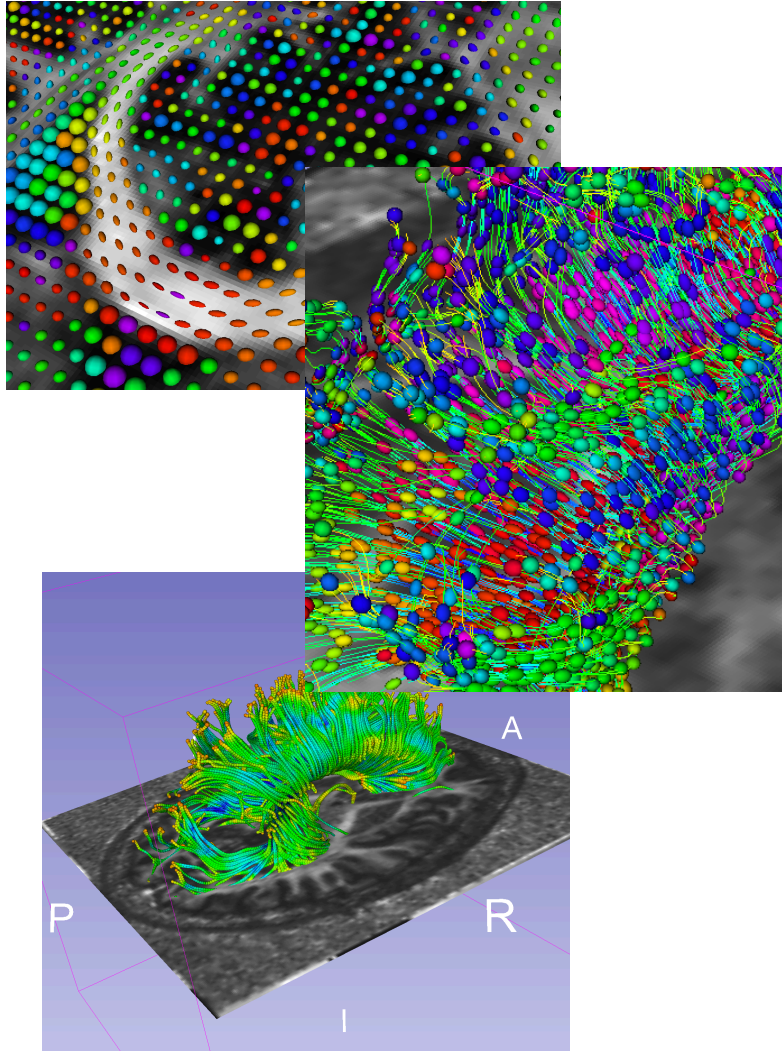
Y R: 12.00

G A: 13.50

RightCingulum

F\_2

# 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

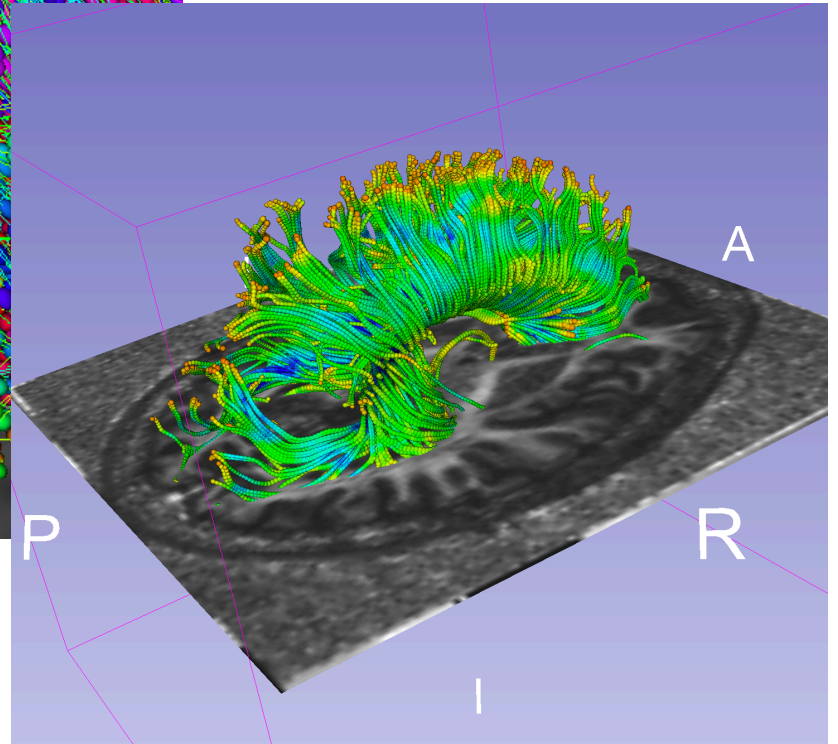
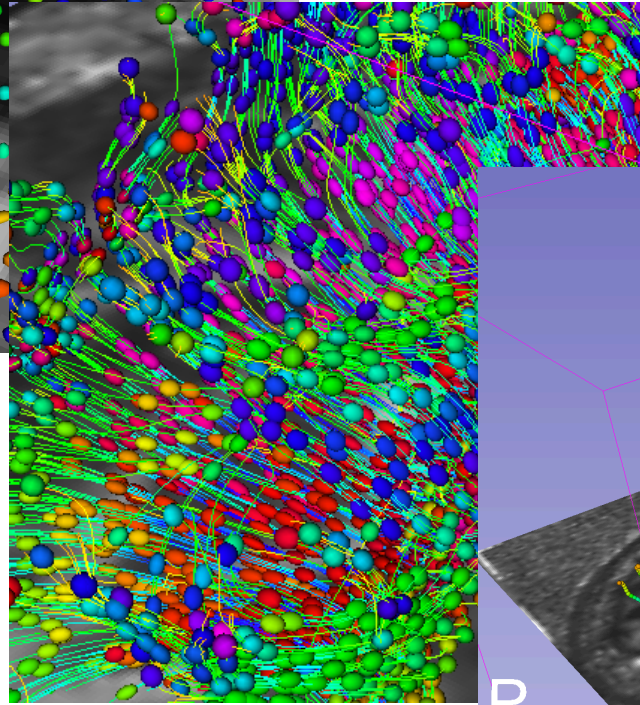
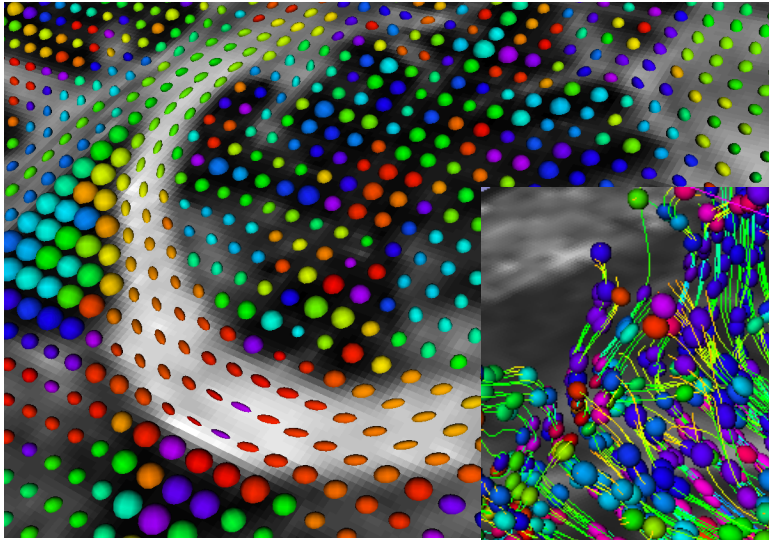


National Alliance for Medical Image Computing  
NIH U54EB005149



Neuroimage Analysis Center  
NIH P41RR013218





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# Slicer Community

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[slicer-devel@bwh.harvard.edu](mailto:slicer-devel@bwh.harvard.edu)