



Diffusion MRI Analysis

Sonia Pujol, Ph.D.

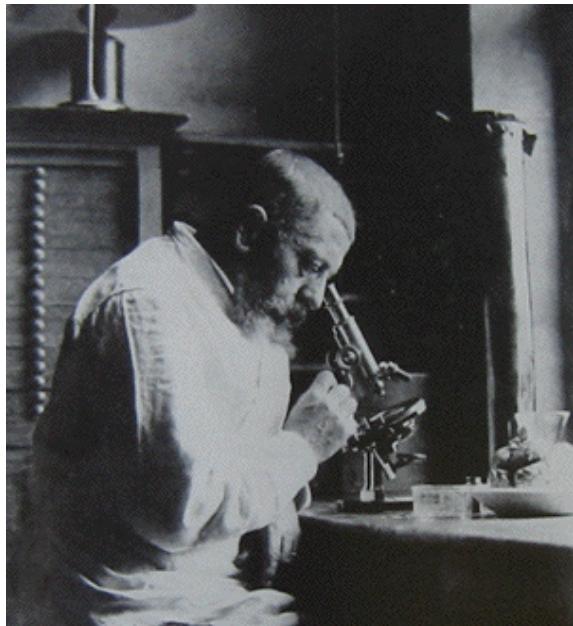
Surgical Planning Laboratory
Brigham and Women's Hospital
Harvard Medical School

Brain Anatomy



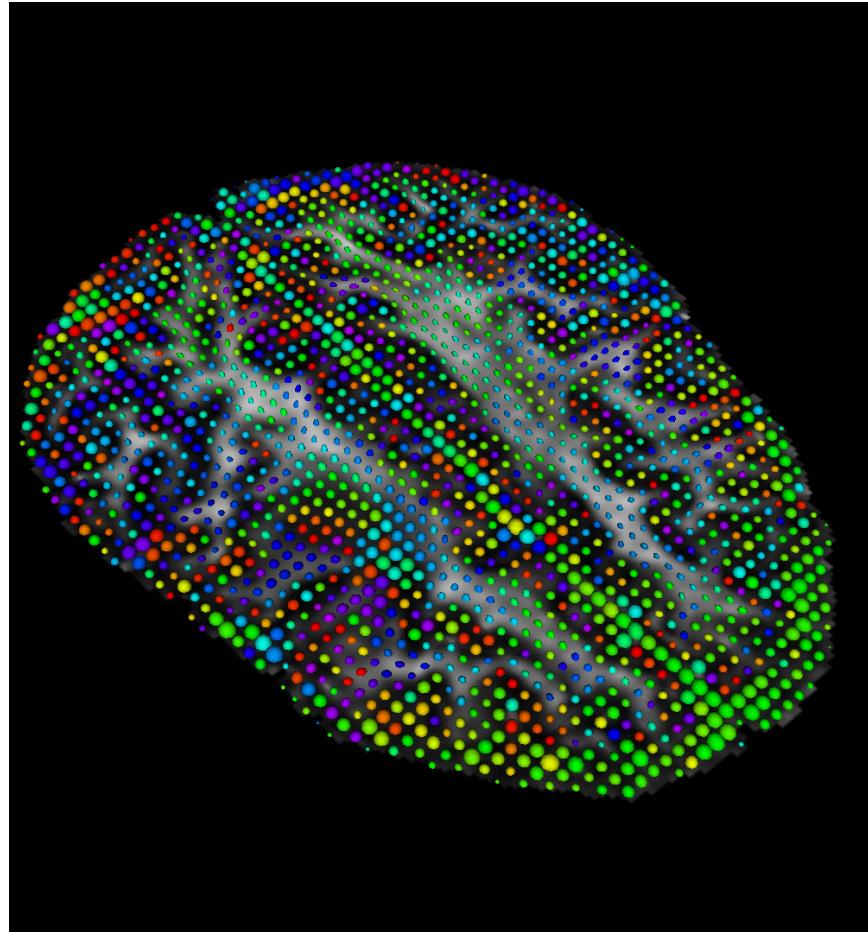
- White matter ~45% of the brain
- Myelinated nerve fibers (~ 10 μm axon diameter)

White Matter Exploration



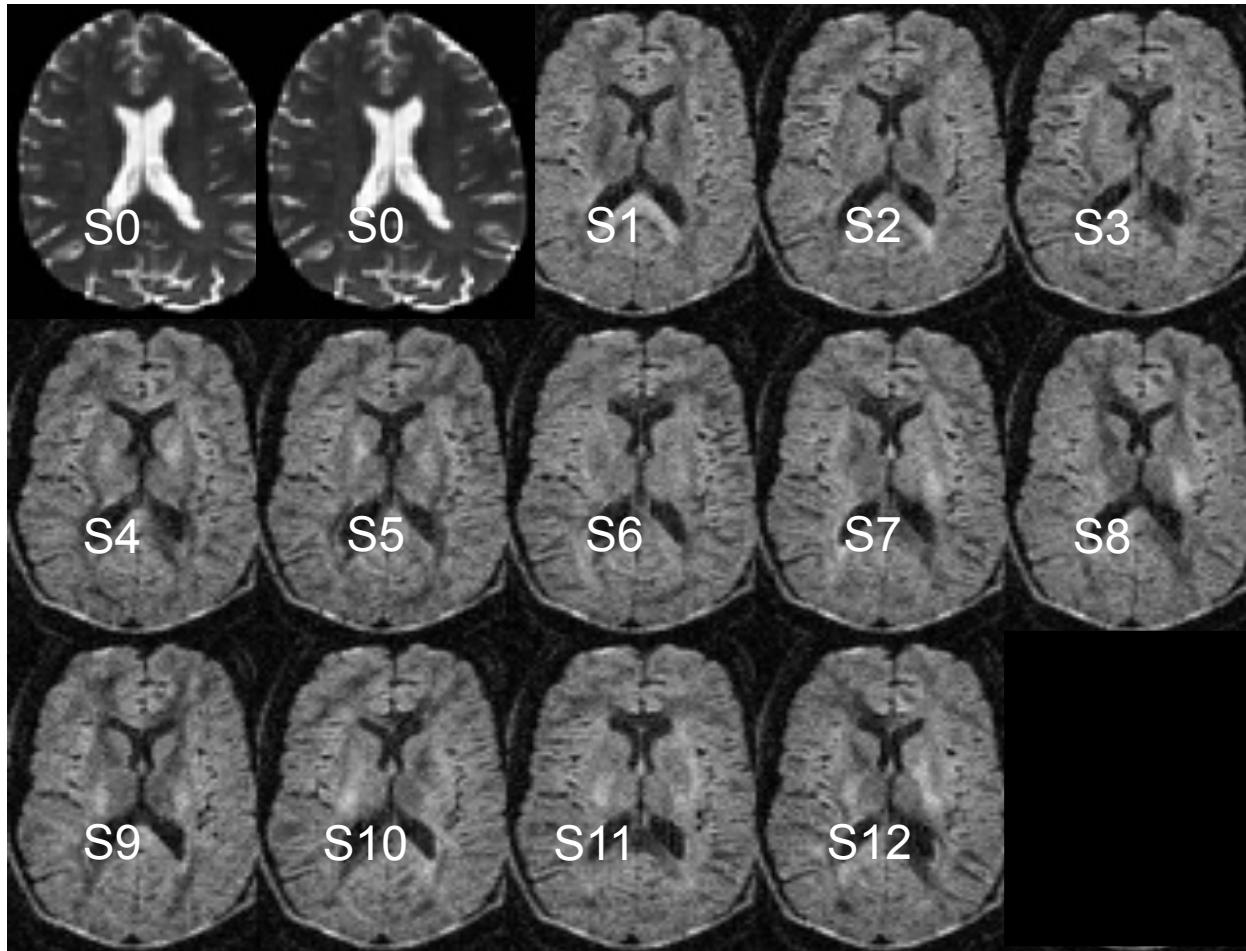
Jules Joseph and Augusta Dejerine (*Anatomie des centres nerveux* (Paris, 1890-1901)): Neuroanatomy atlas based on myelin stained preparation

Diffusion Tensor Imaging (DTI)



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

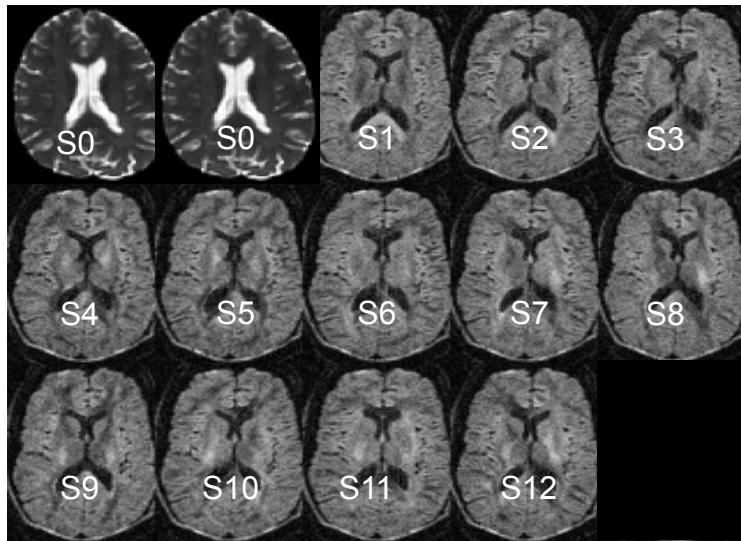
Diffusion Weighted Imaging (DWI)



In this example, the DWI scan was acquired with 12 diffusion sensitizing gradient directions (S1-S12) and 2 non-diffusion sensitizing gradients (S0)

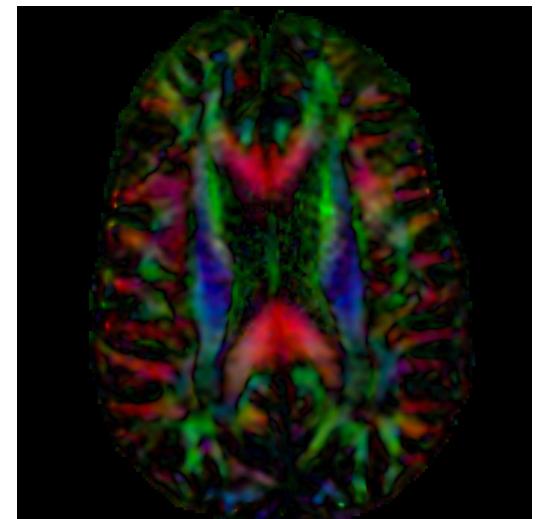
From DWI to DTI

DWI



DWI dataset

DTI



DTI dataset



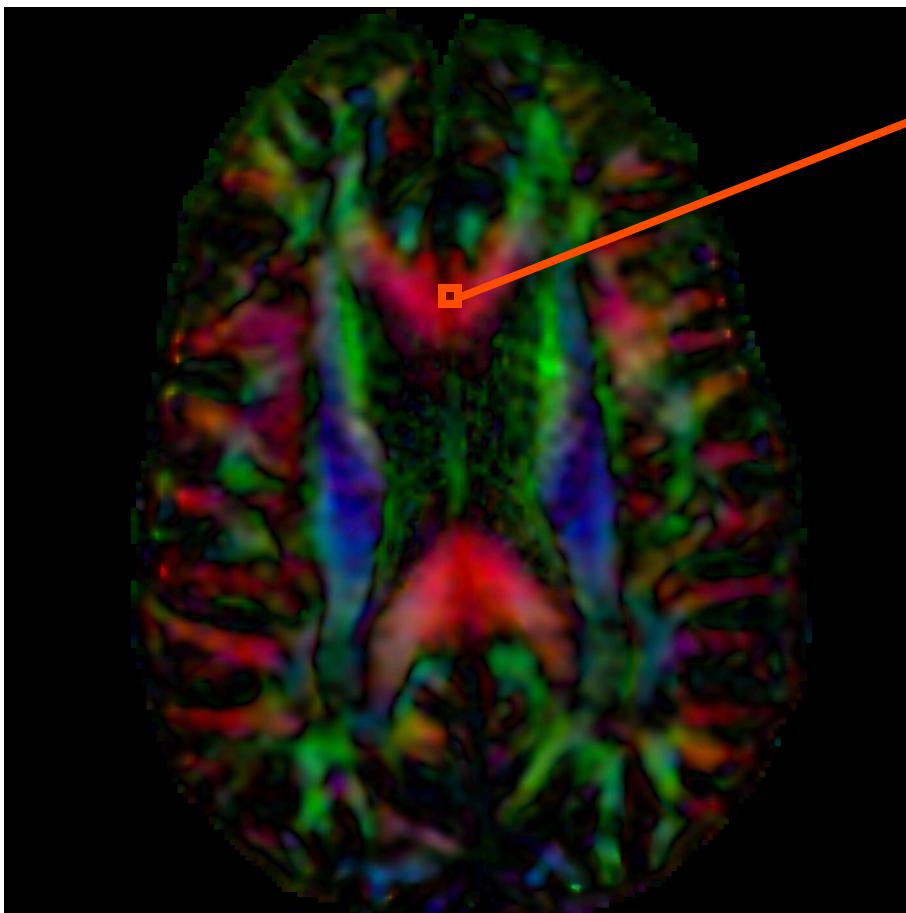
$$S_i = S_0 e^{-b \hat{g}^T \underline{D} \hat{g}_i}$$

Stejskal-Tanner (1965)



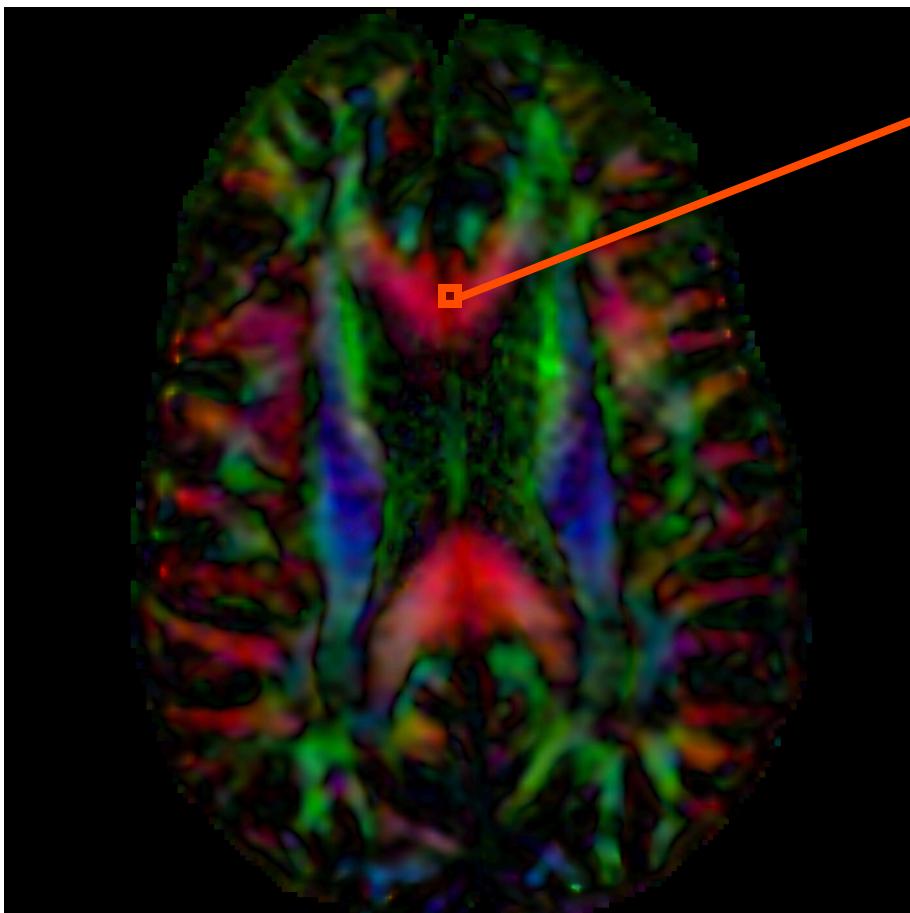
*S_i: DWI volume acquired with
ith gradient
S₀: Baseline volume*

Diffusion Tensor Imaging



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

Diffusion Tensor Imaging

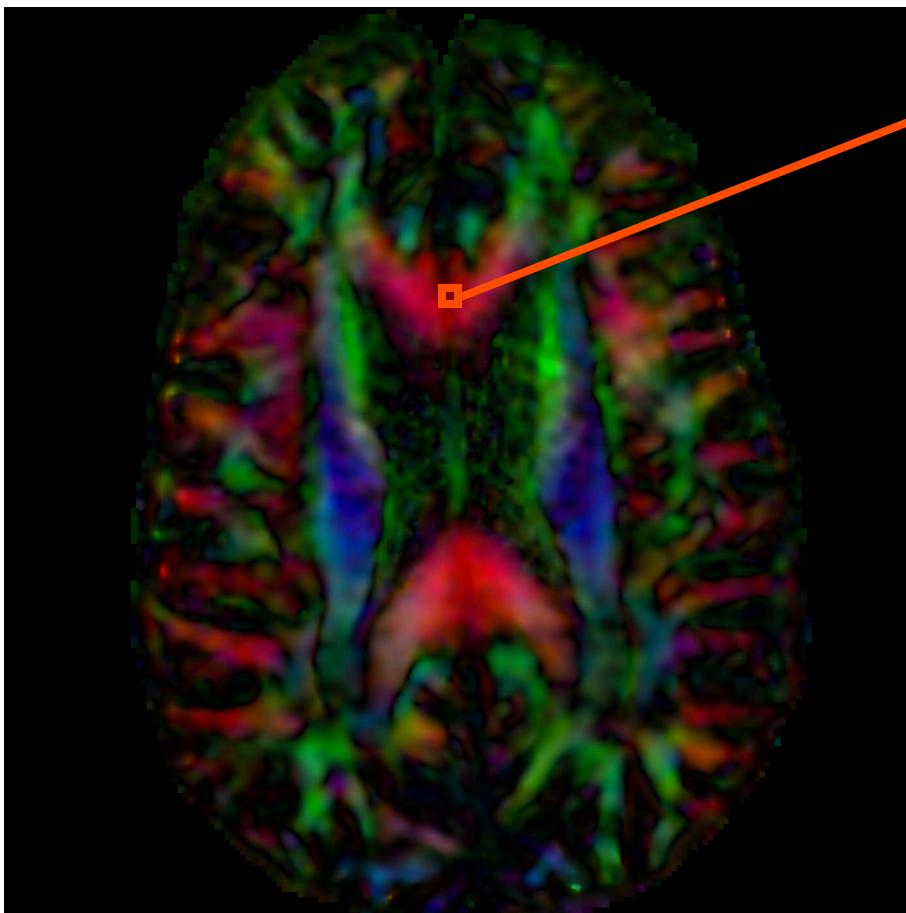


$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$

↓

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

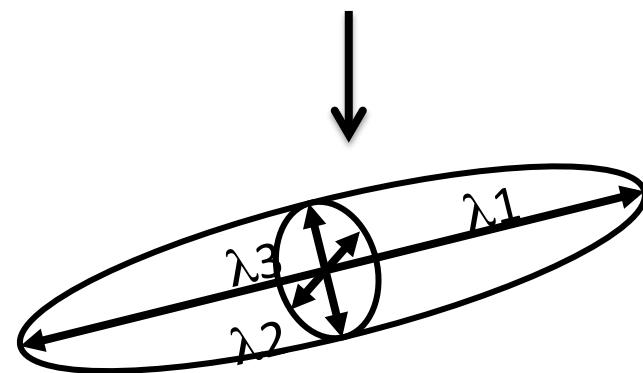
Diffusion Tensor Imaging



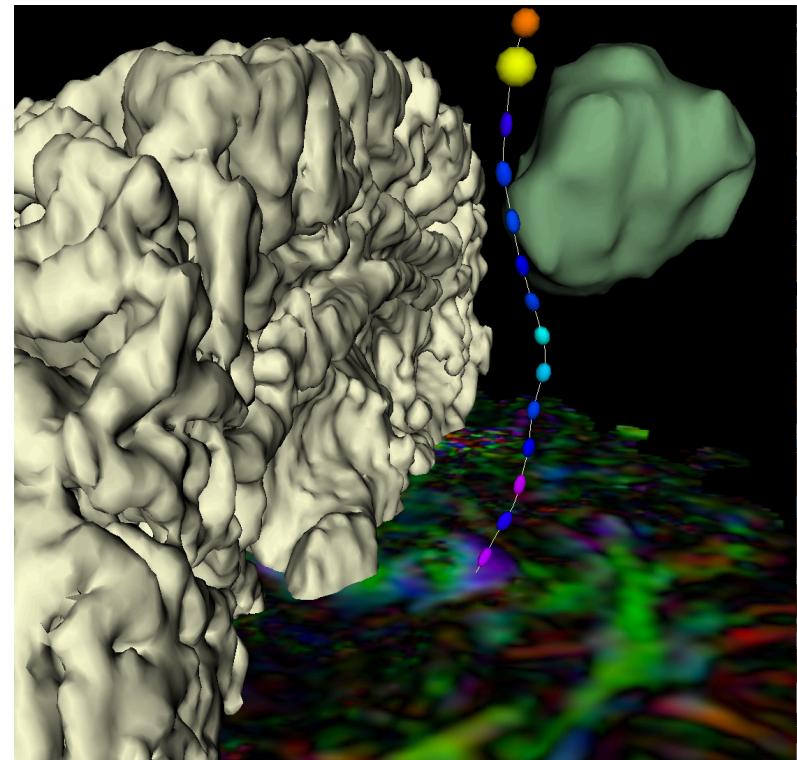
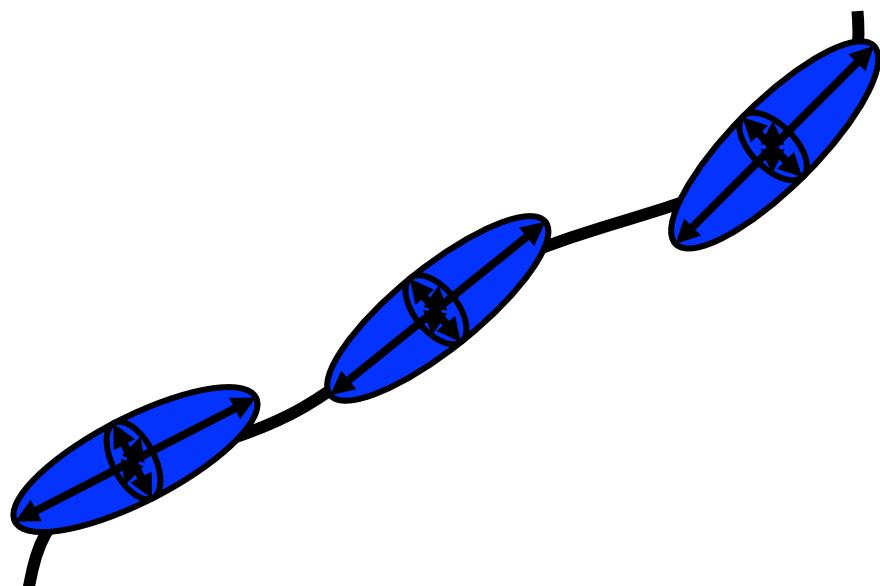
$$S_i = S_0 e^{-b \hat{g}^T \underline{D} \hat{g}_i}$$

↓

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

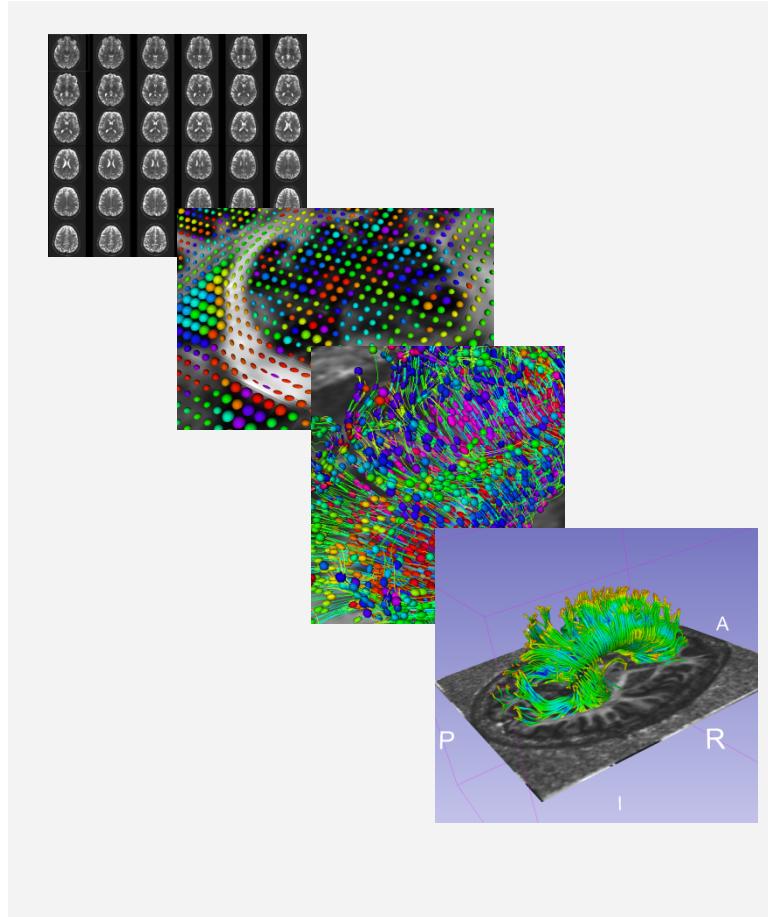


Tractography



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

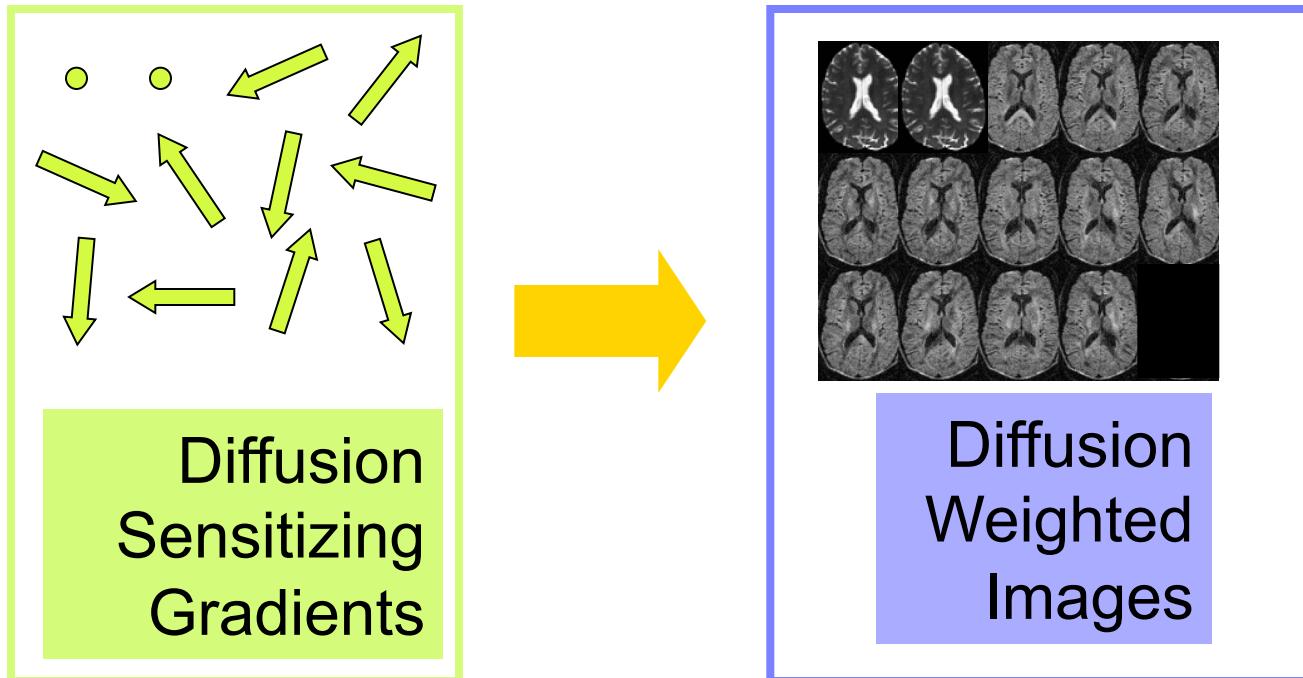
Tutorial Outline



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

Tutorial Dataset

The tutorial dataset is a Diffusion Weighted MR scan of the brain acquired with 41 diffusion sensitizing gradient directions and 7 baseline.



Tutorial Software

The tutorial was created using the 3D Slicer (Version 4.5) available at:

<http://download.slicer.org>

Please note that the **Diffusion Weighted Volume Masking** module has been updated in 2016. In this tutorial, we use a Slicer nightly build (Slicer4.5.0-2016-02-23). If you plan to use the Diffusion Weighted Volume Mask module, we recommend you download a Slicer nightly build version posterior to 02-23-2016.

Disclaimer

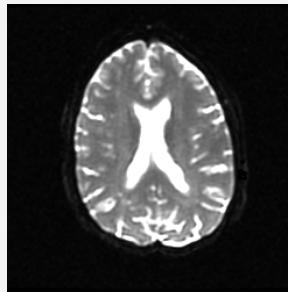
It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules. Slicer is a tool for research, and is not FDA approved.

Learning Objectives

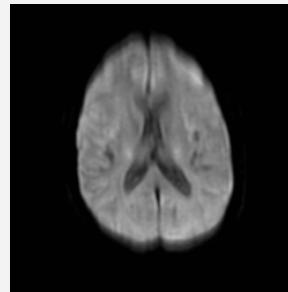
Following this tutorial, you'll be able to

- 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

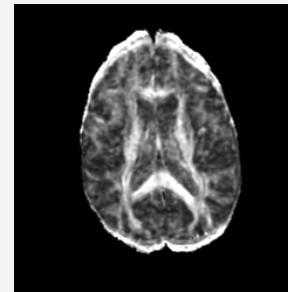
MR Diffusion Analysis Pipeline



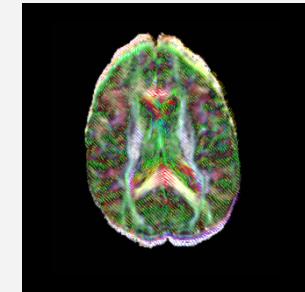
DWI
Acquisition



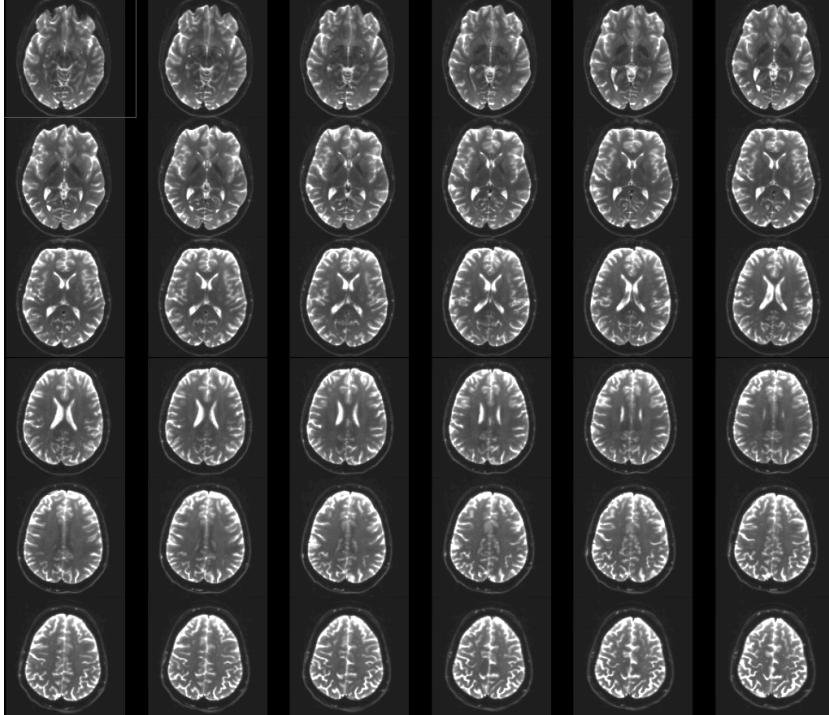
Tensor
Calculation



Scalar
Maps

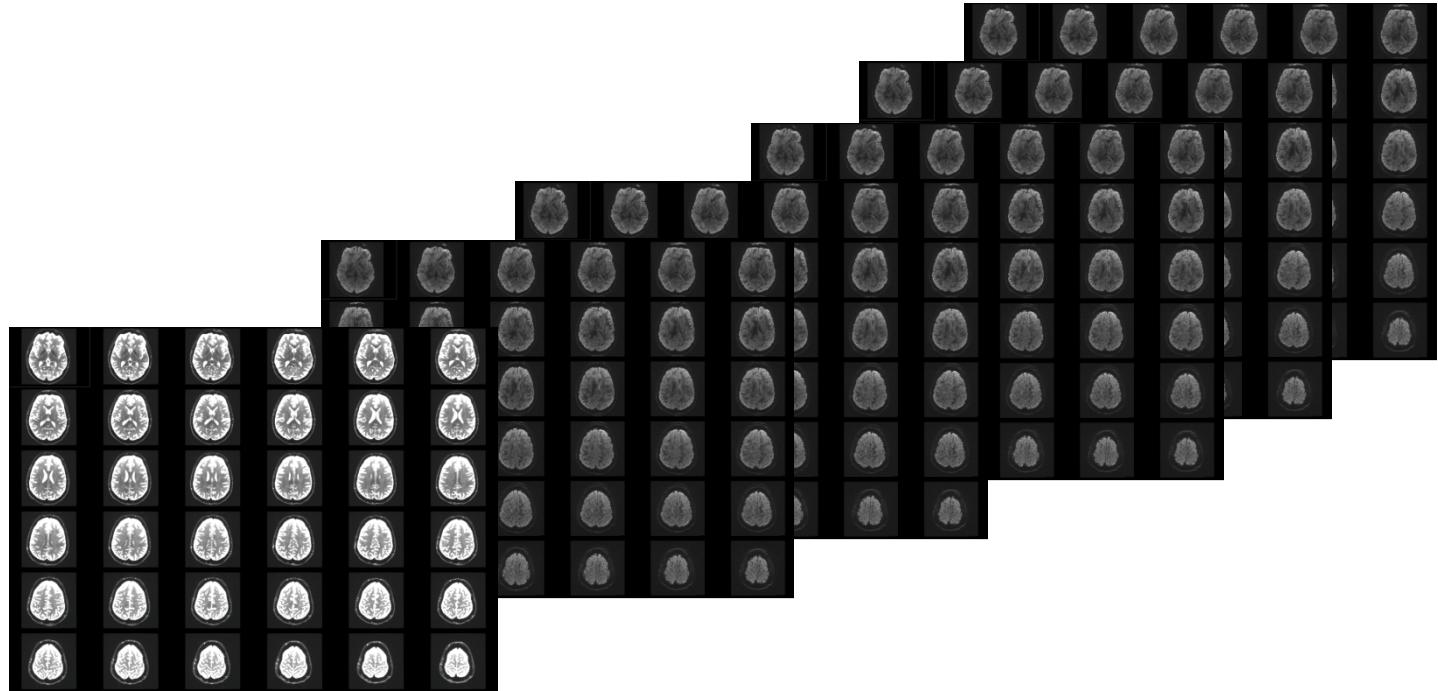


3D
Visualization



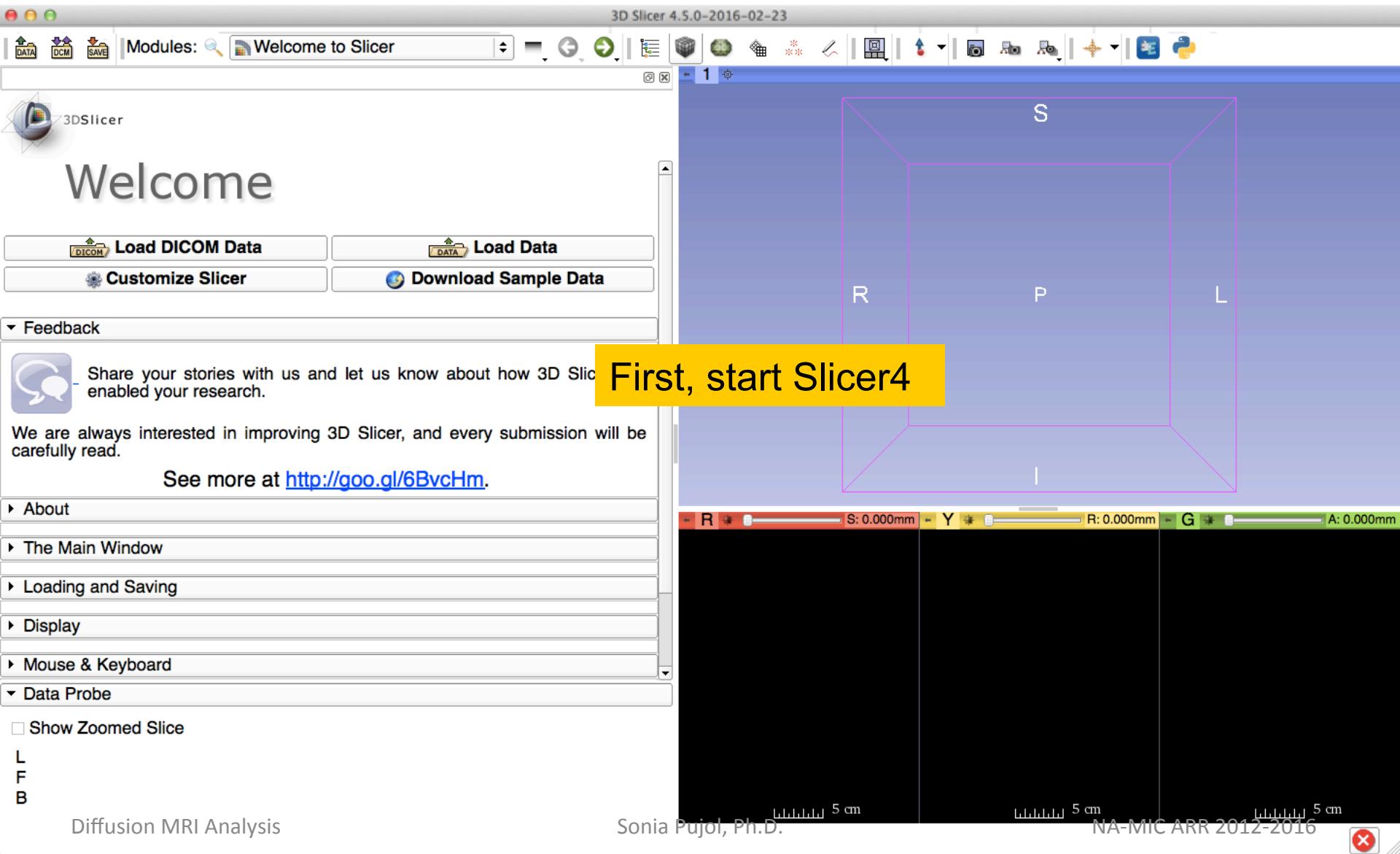
Part 1: From DWI images to Tensors

Understanding the DWI Dataset

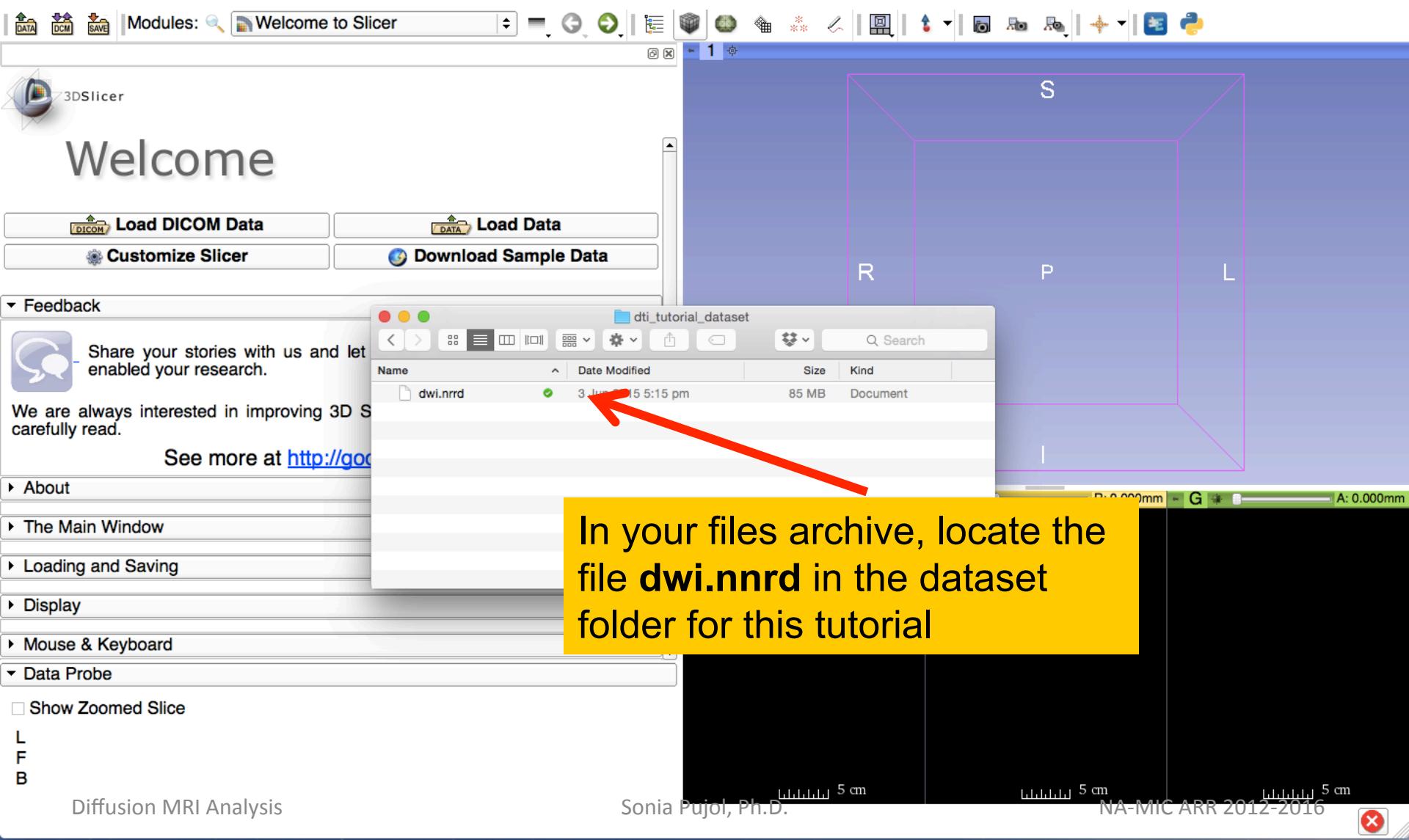


The Diffusion Weighted Imaging (DWI) dataset is composed of 48 volumes acquired with 41 different diffusion-sensitizing gradient directions, and 7 baseline image acquired without diffusion weighting.

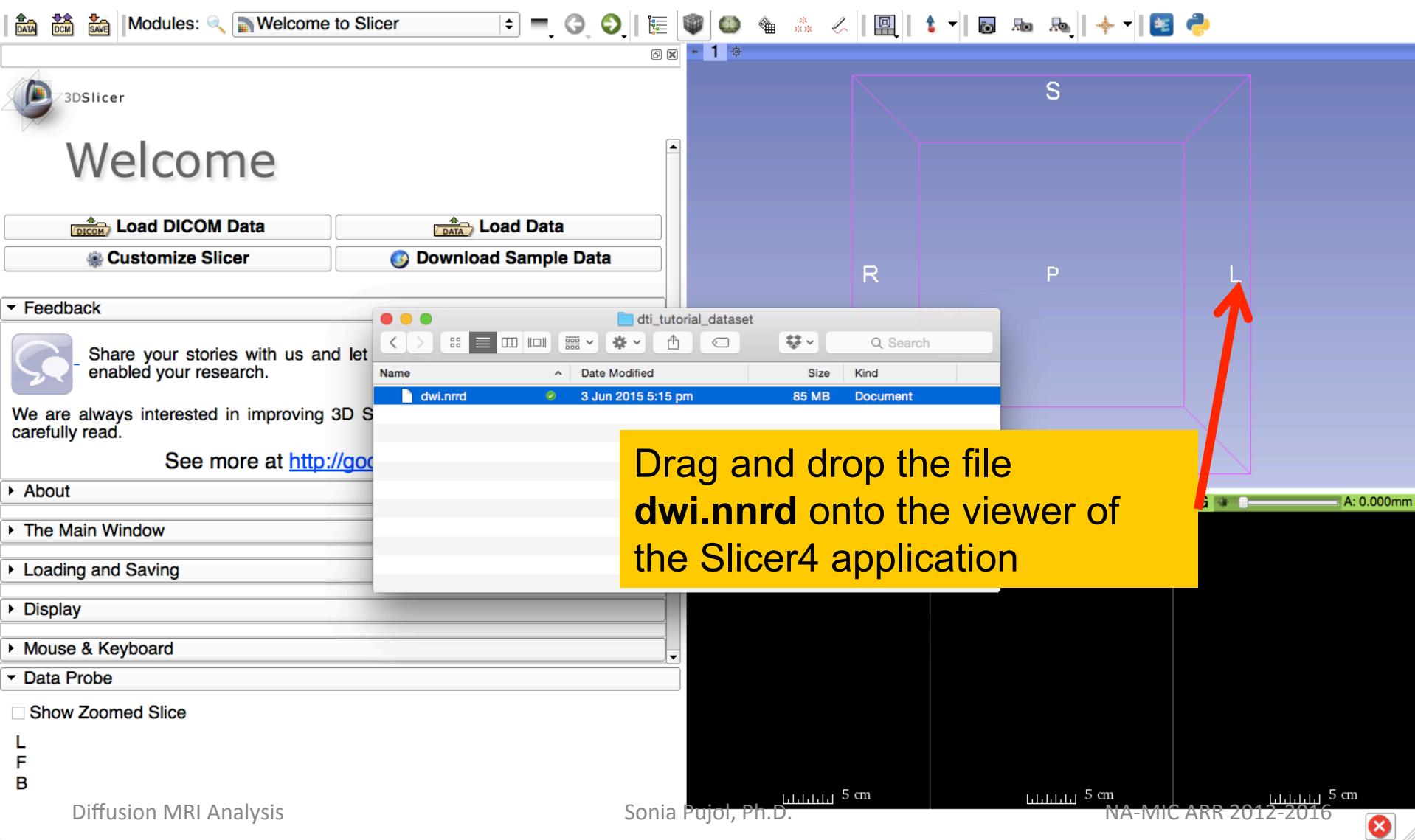
Loading the DWI Dataset



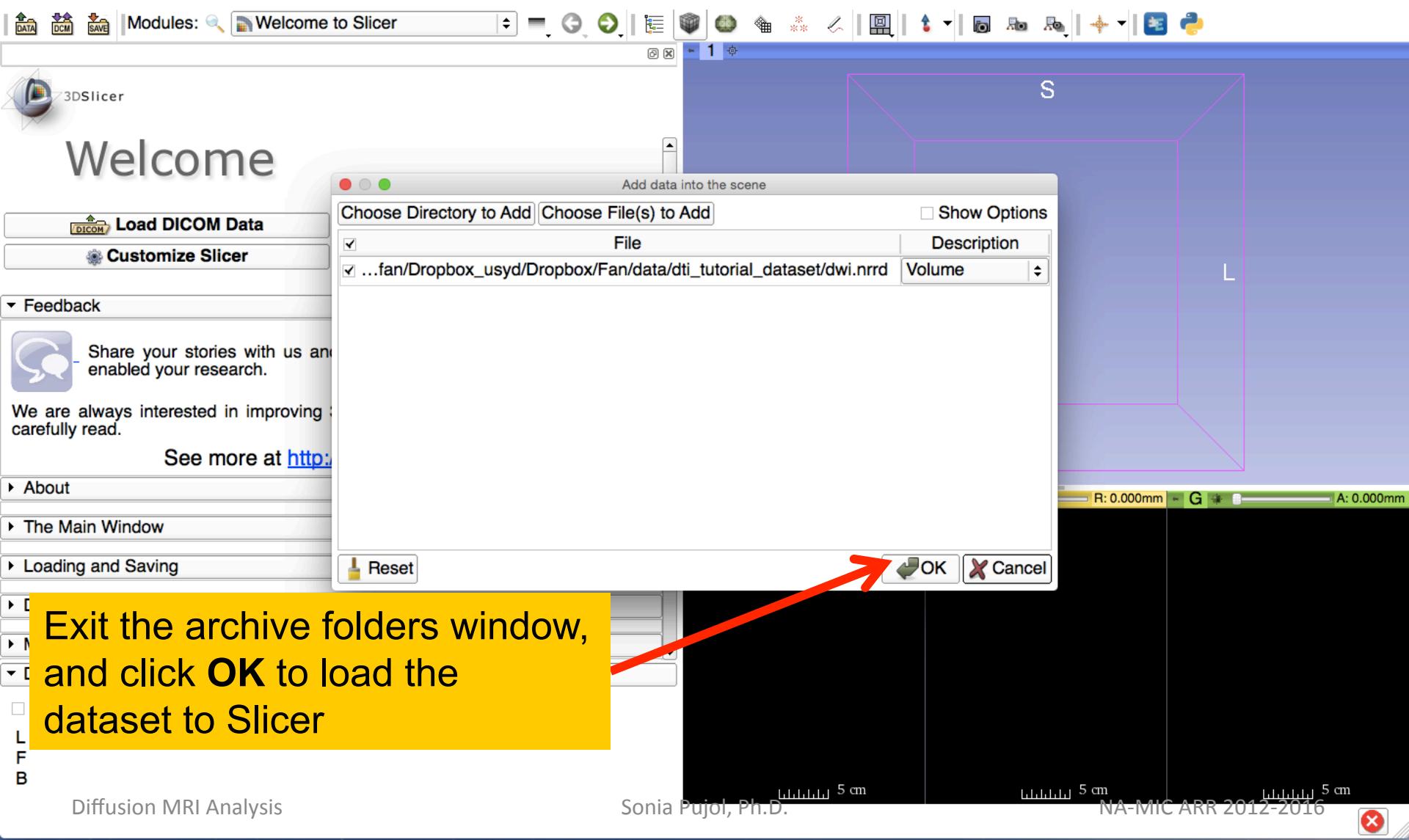
Loading the DWI Dataset



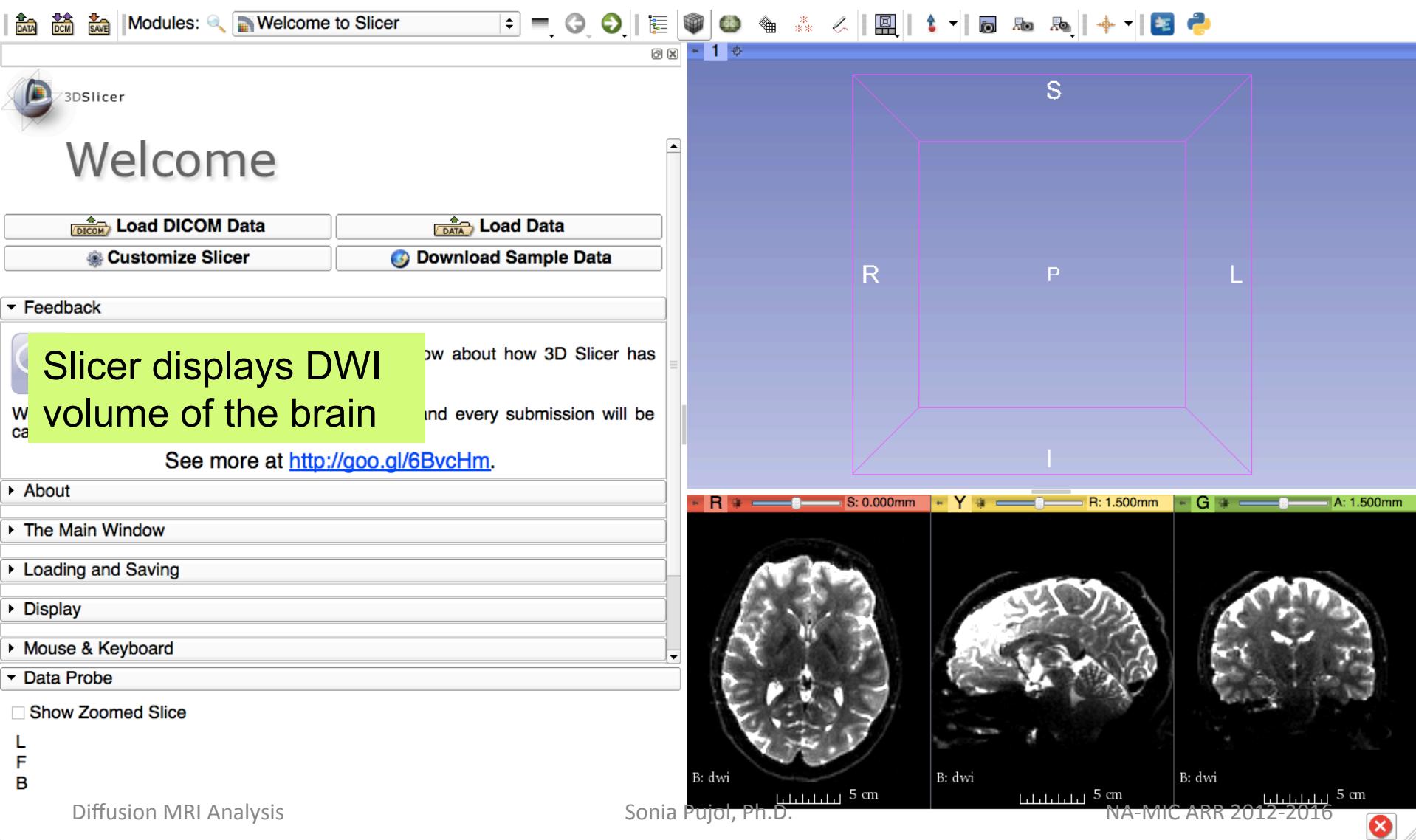
Loading the DWI Dataset



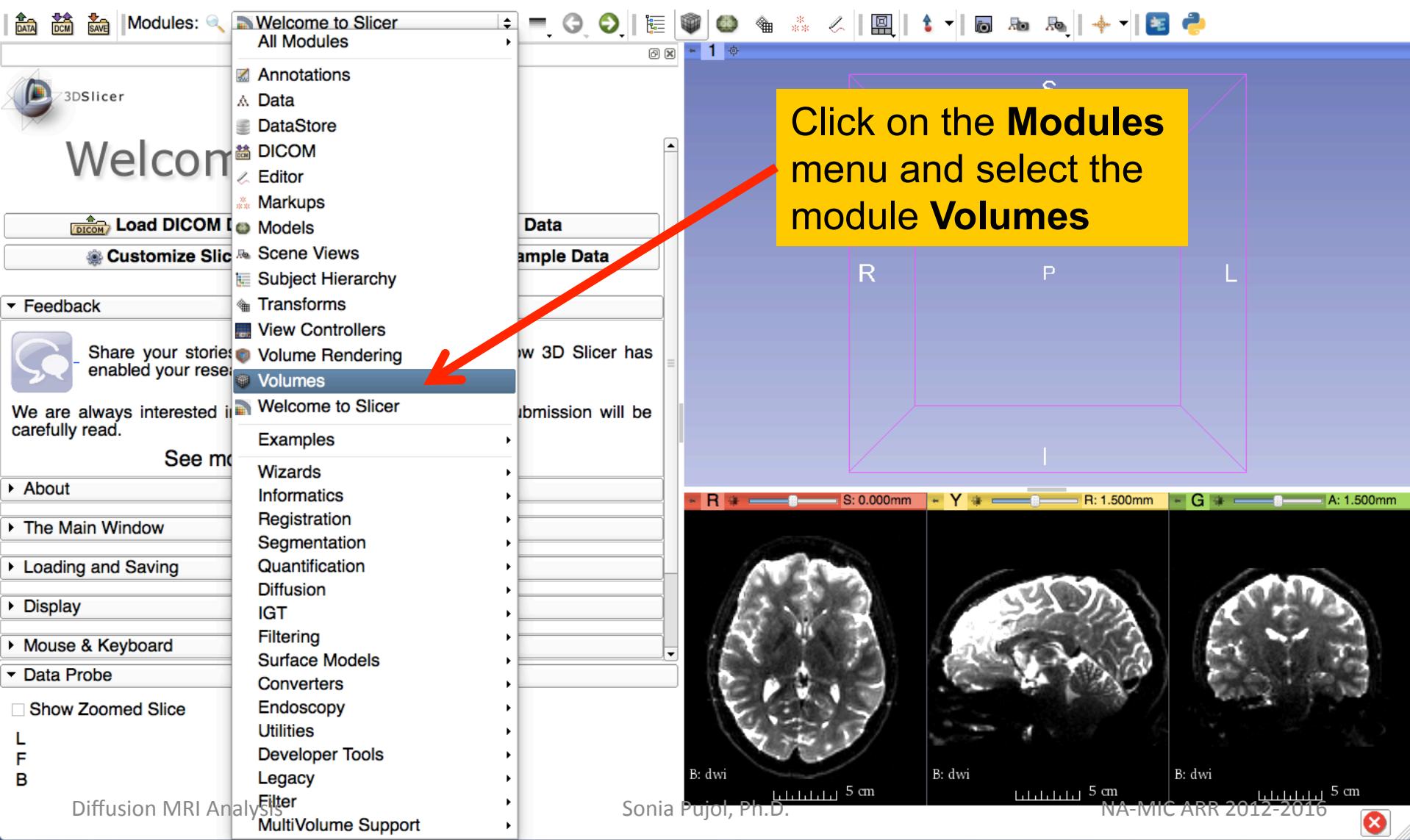
Loading the DWI Dataset



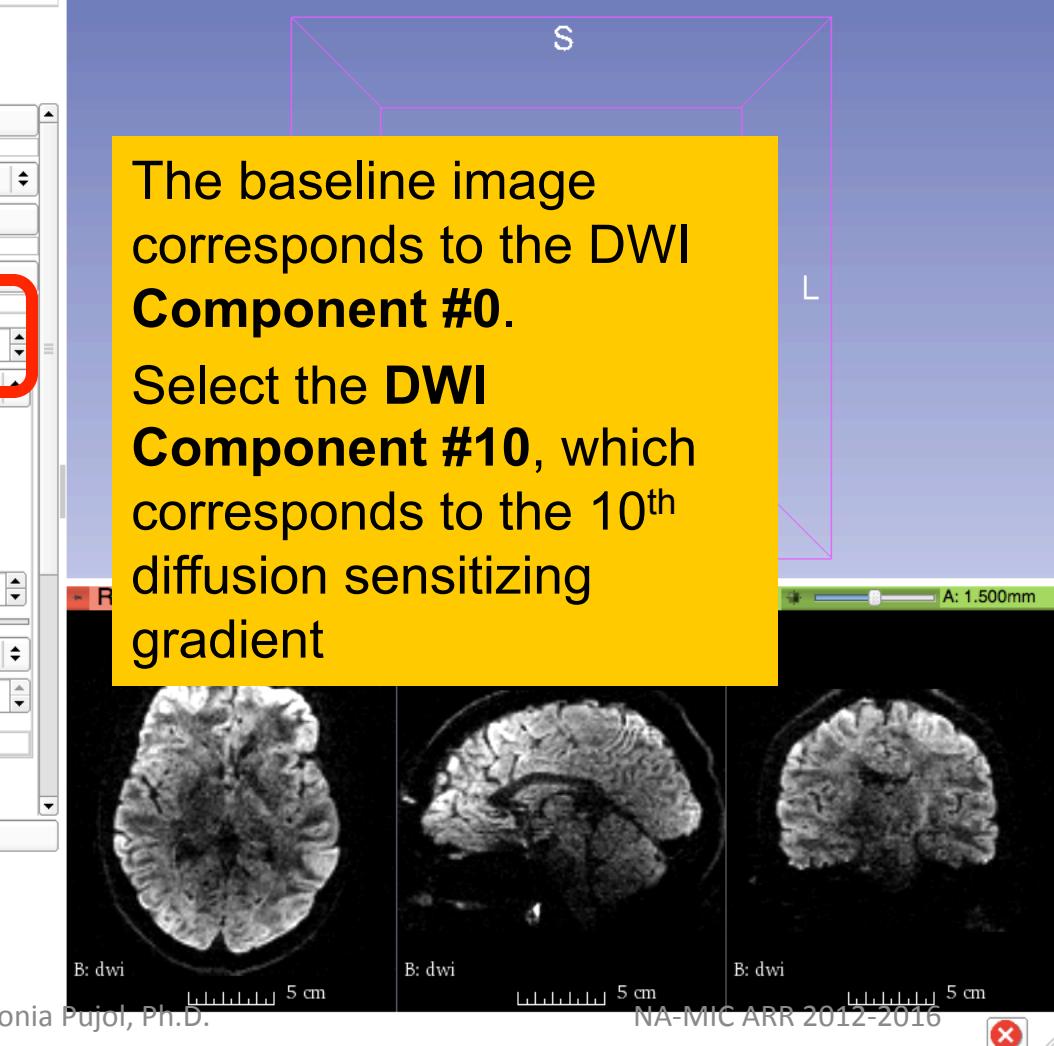
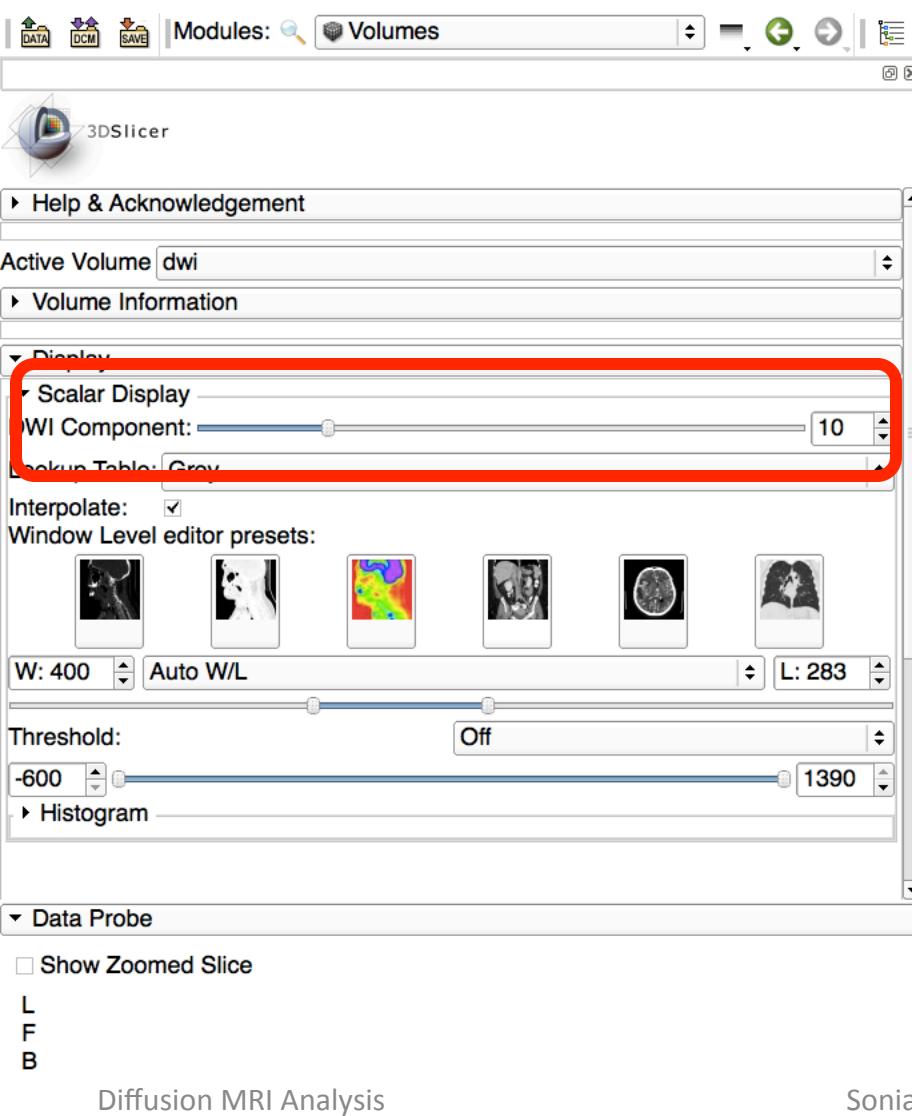
Loading the DWI Dataset



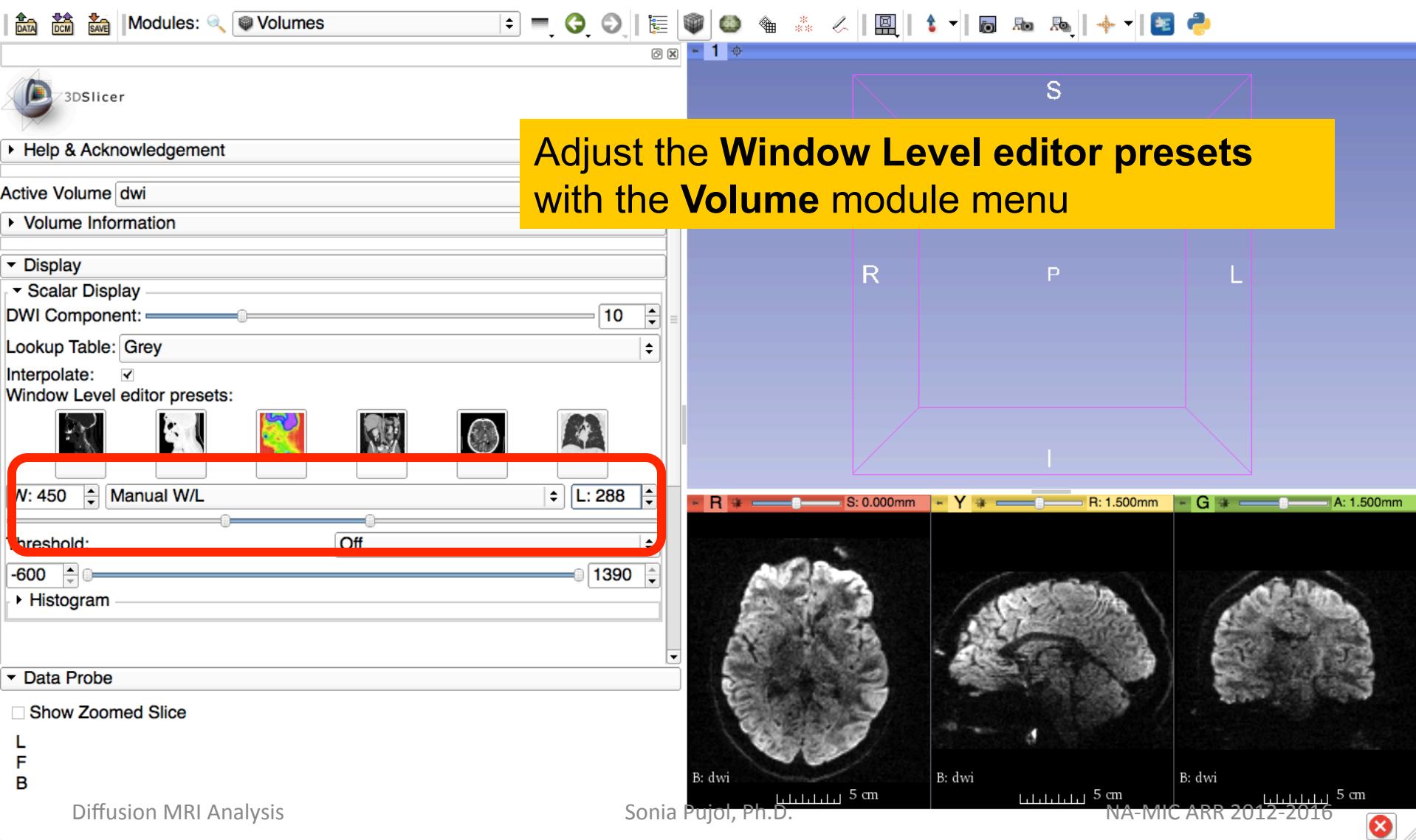
Loading the DWI Dataset



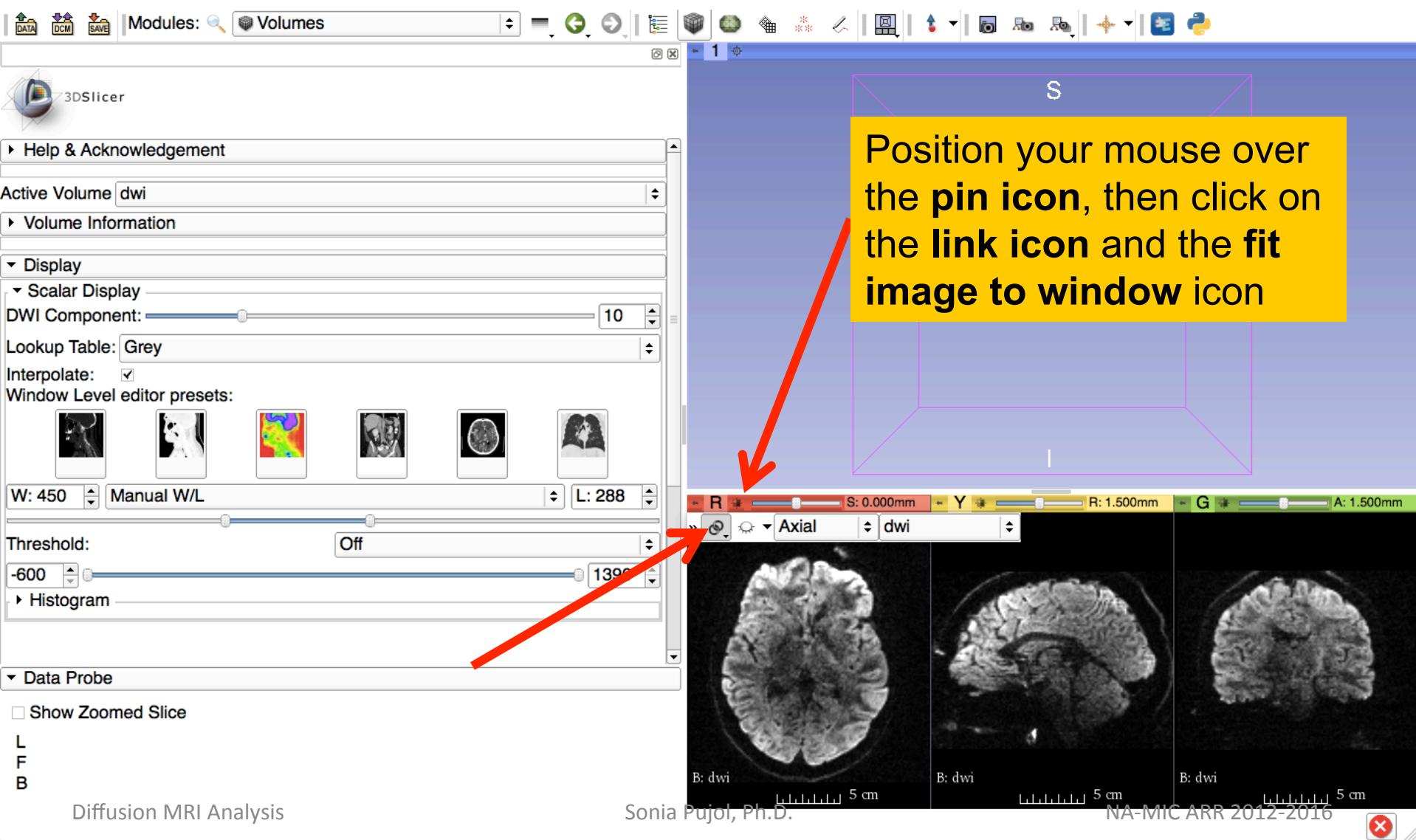
Loading the DWI Dataset



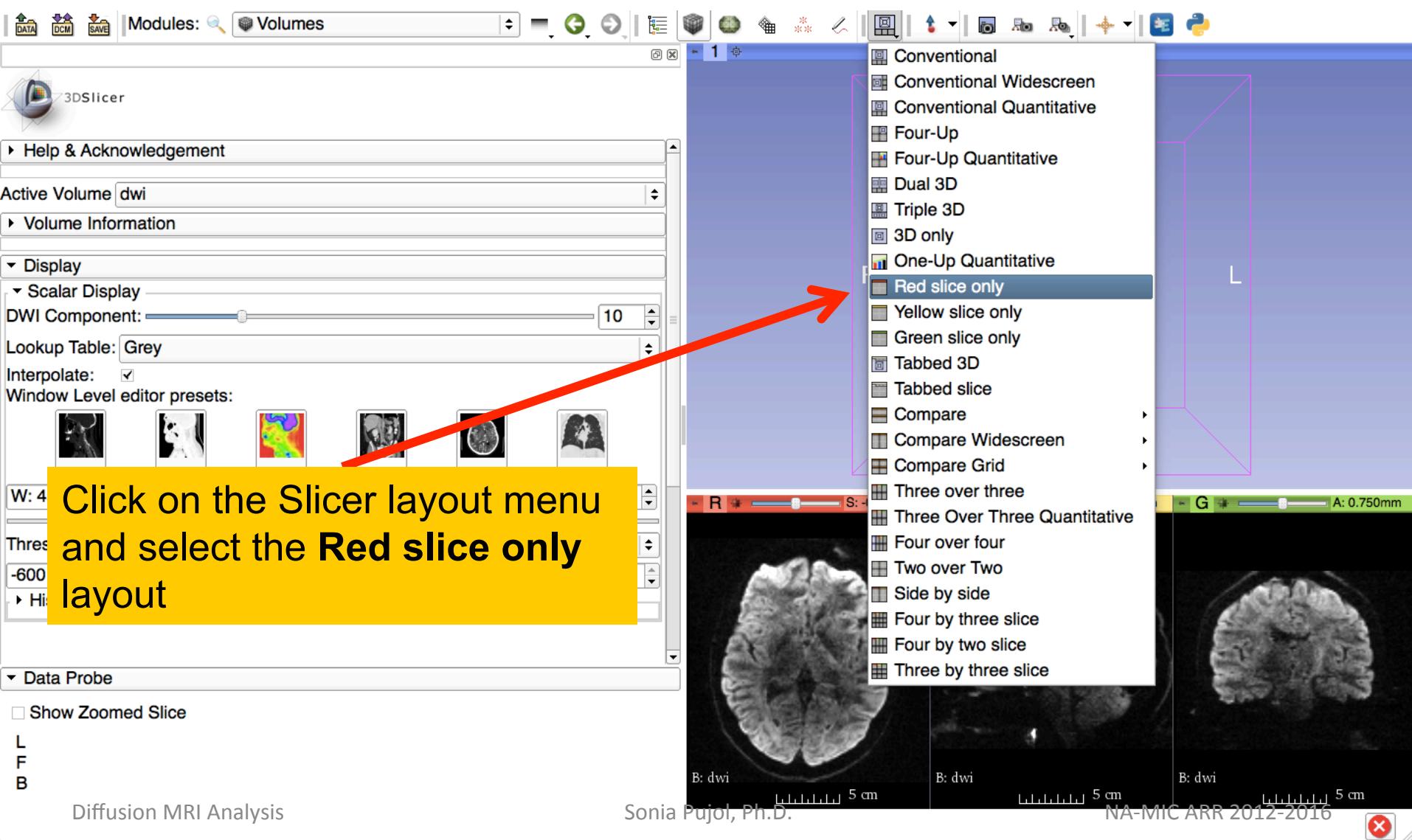
Loading the DWI Dataset



Loading the DWI Dataset

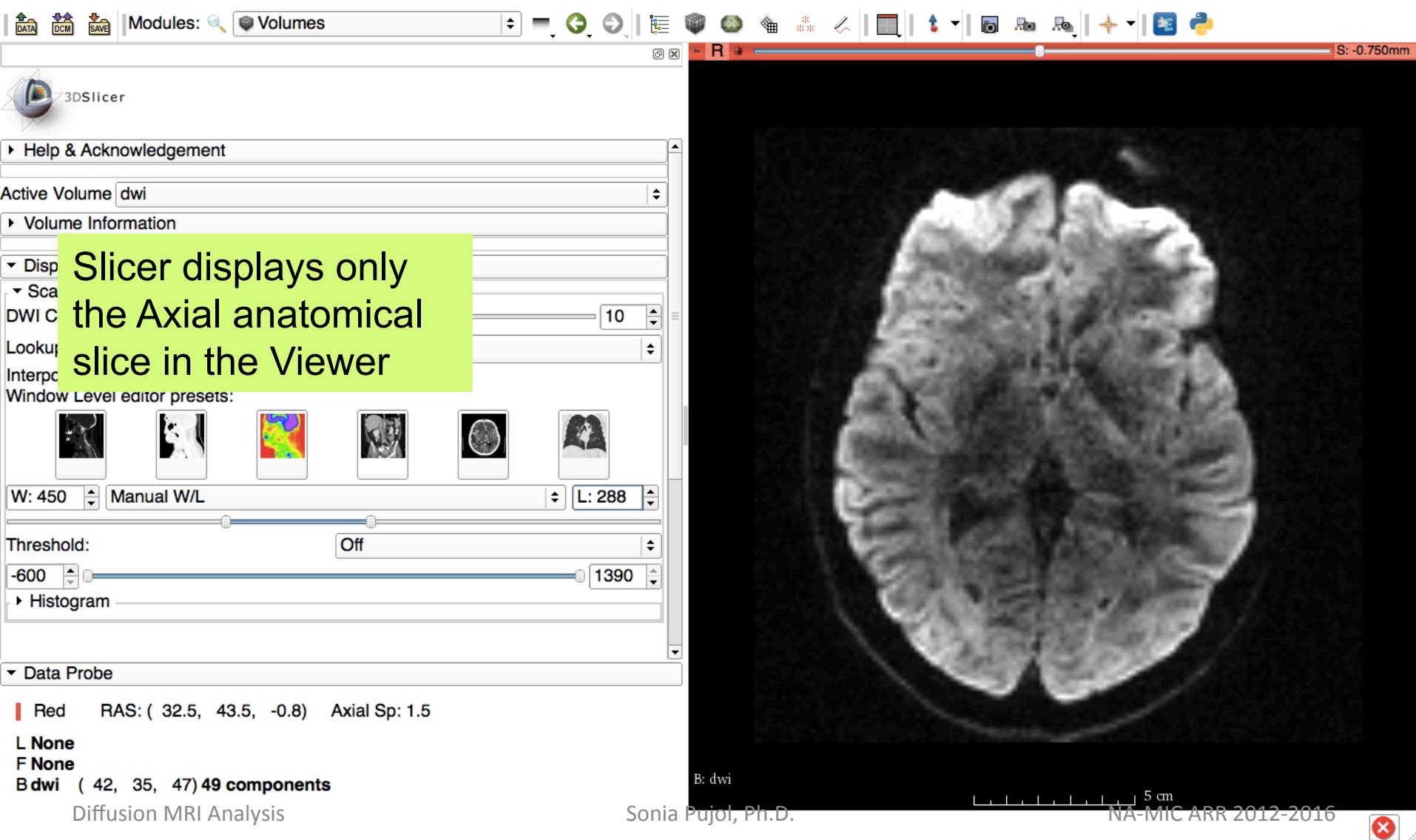


Loading the DWI Dataset

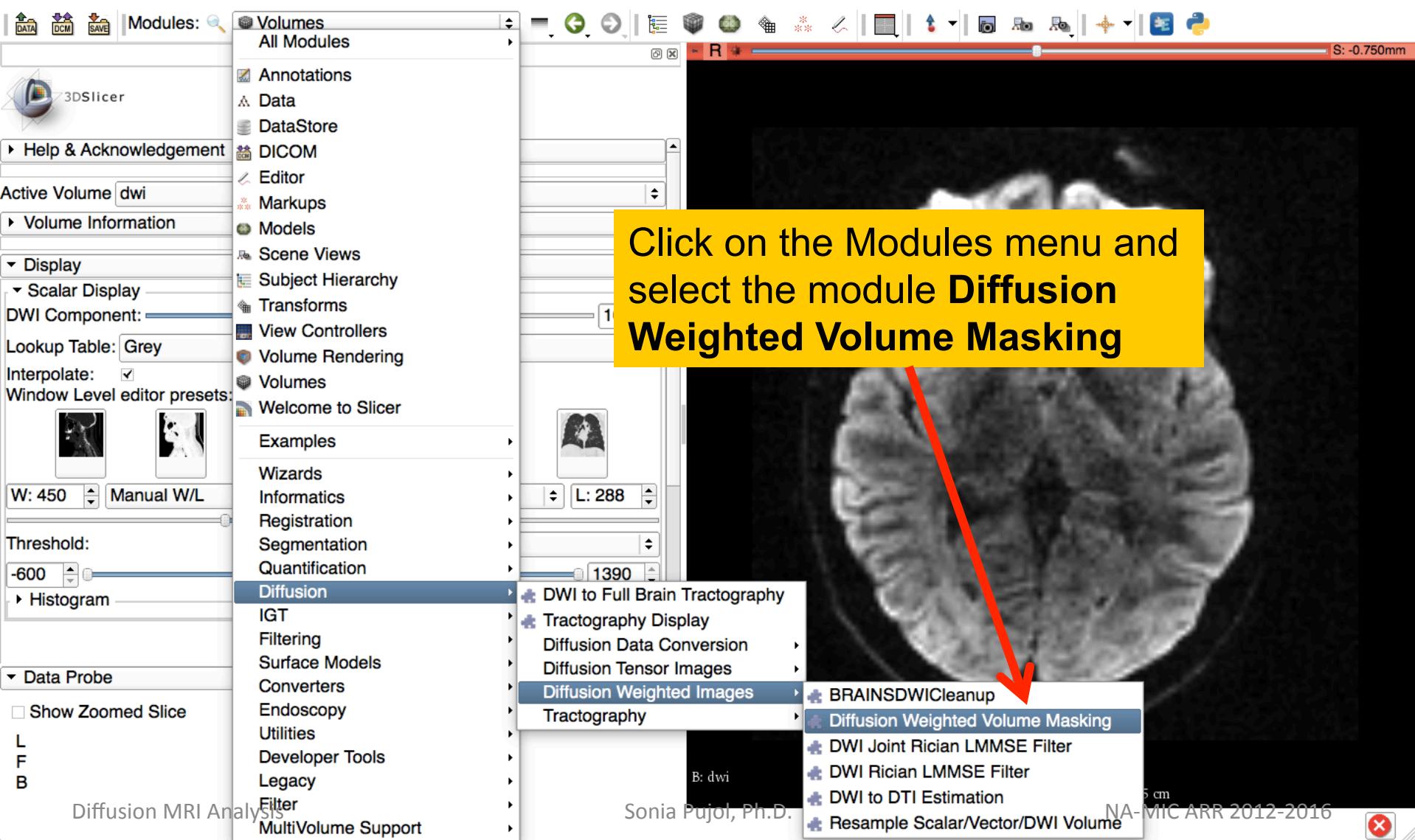


Click on the Slicer layout menu
and select the **Red slice only**
layout

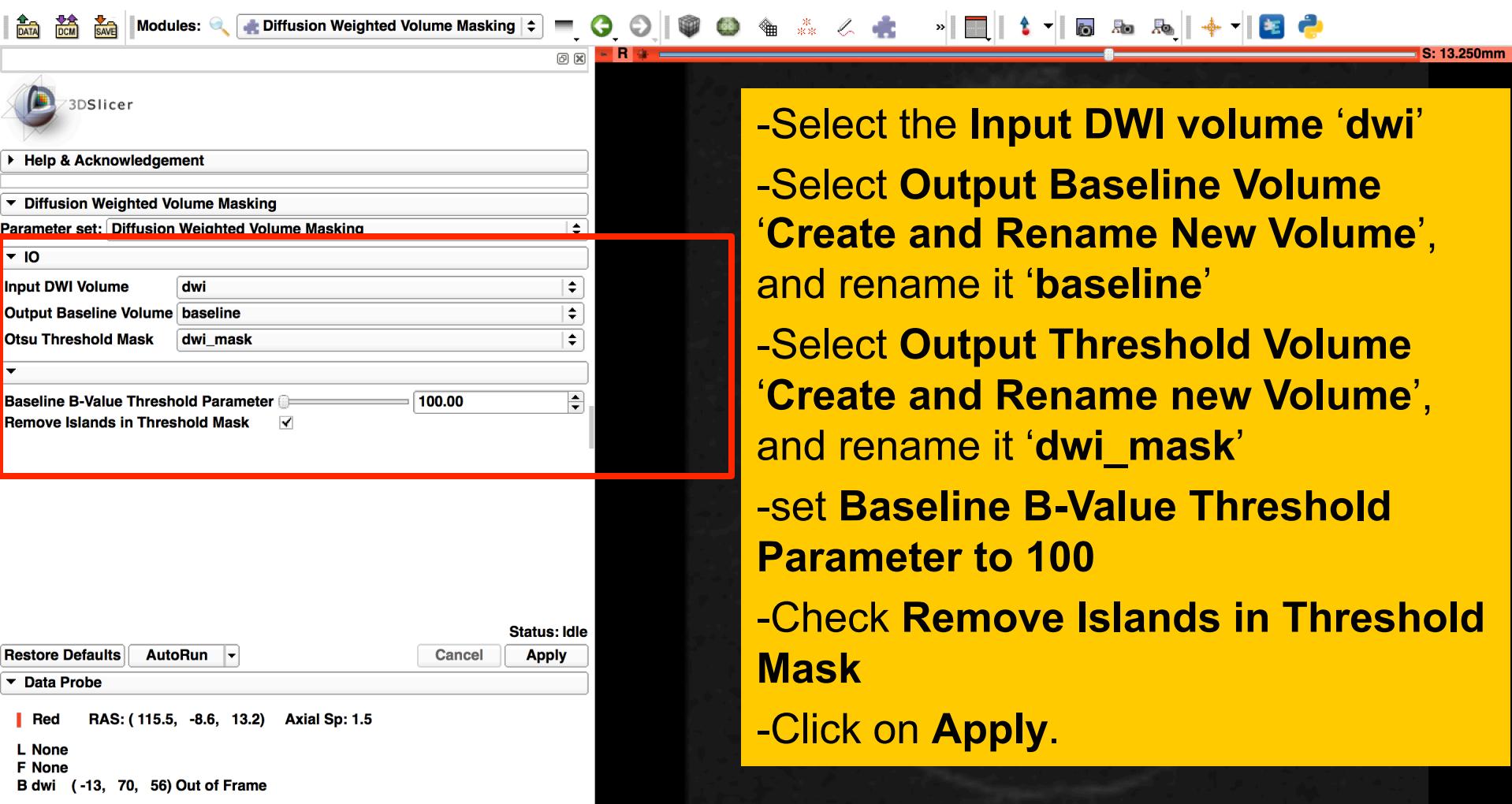
Loading the DWI Dataset



Creating a brain mask

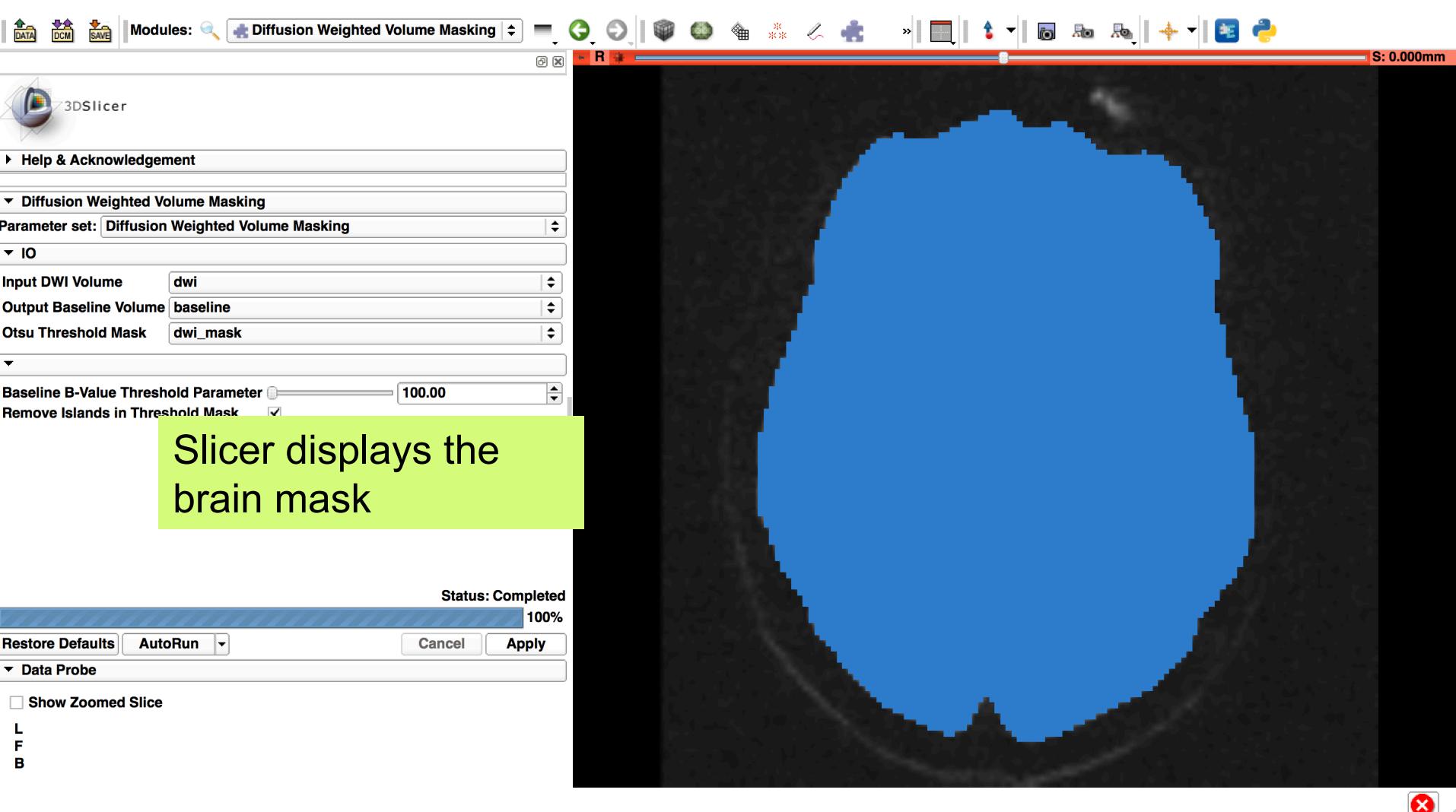


Creating a brain mask

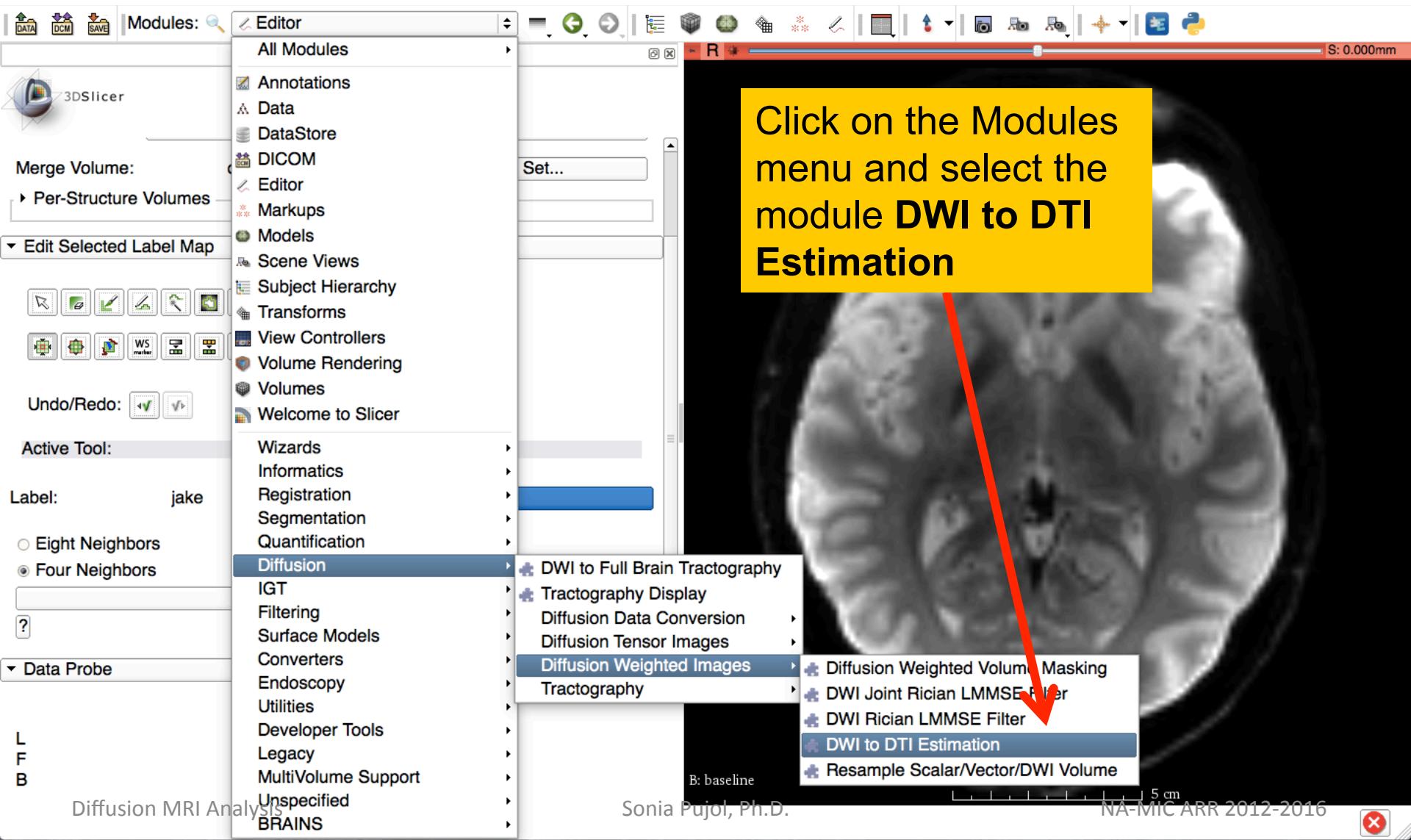


Note: This version of the Diffusion Weighted Volume Masking module is available in the Slicer4.5 nightly build posterior to Feb.23, 2016

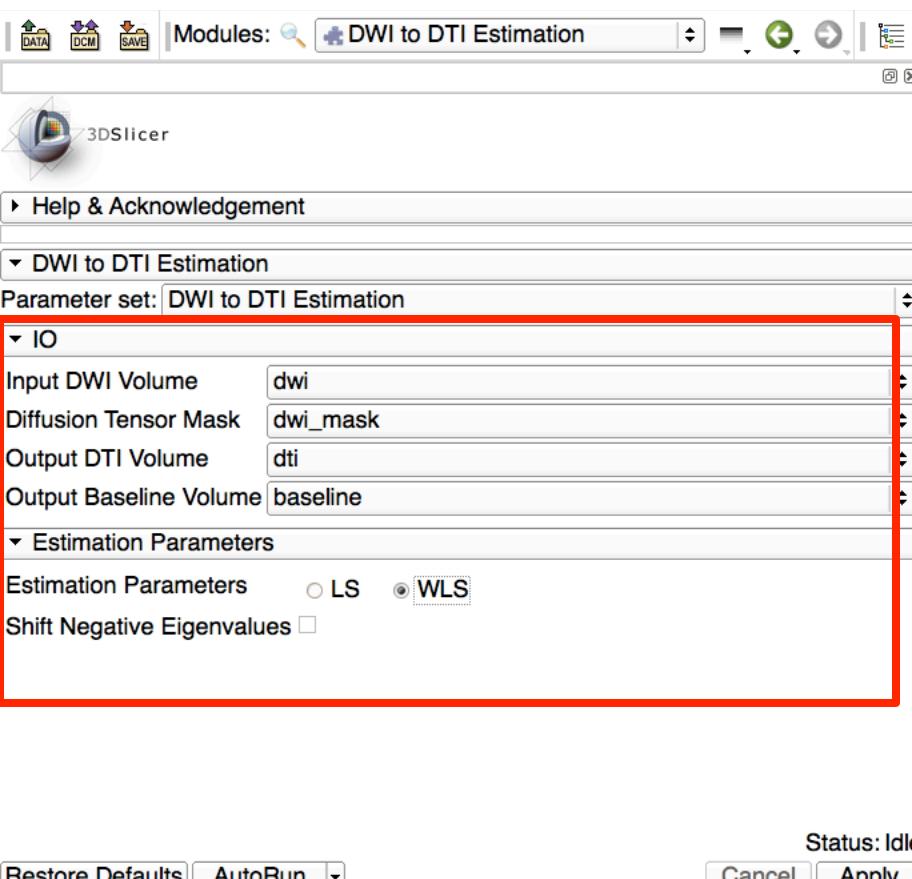
Creating a brain mask



Estimating the tensor



Estimating the tensor



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

- Set the **Input DWI volume** to 'dwi'
- Set the **Diffusion Tensor Mask** to '**dwi_mask**'
- Select **Output DTI Volume 'Create and Rename New Volume'**, and rename it '**dti**'
- Set **Output Baseline Volume** to '**baseline**'
- Select the **Estimation Parameters 'WLS'** (Weighted Least Squares) and click on **Apply**.

Estimating the tensor

Position your mouse over the **pin icon** and select the volume **dti**

3DSlicer

Modules: DWI to DTI Estimation

Parameter set: DWI

IO

Input DWI Volume: dwi

Diffusion Tensor Mask: dwi_mask

Output DTI Volume: dti

Output Baseline Volume: baseline

Estimation Parameters: LS (radio button)

Shift Negative Eigenvalues:

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

Data Probe

L F B

Diffusion MRI Analysis

Axial

None
dwi
Output Baseline Volume
baseline
dwi_mask
dti (selected)
Rename cu DiffusionTensorVolume

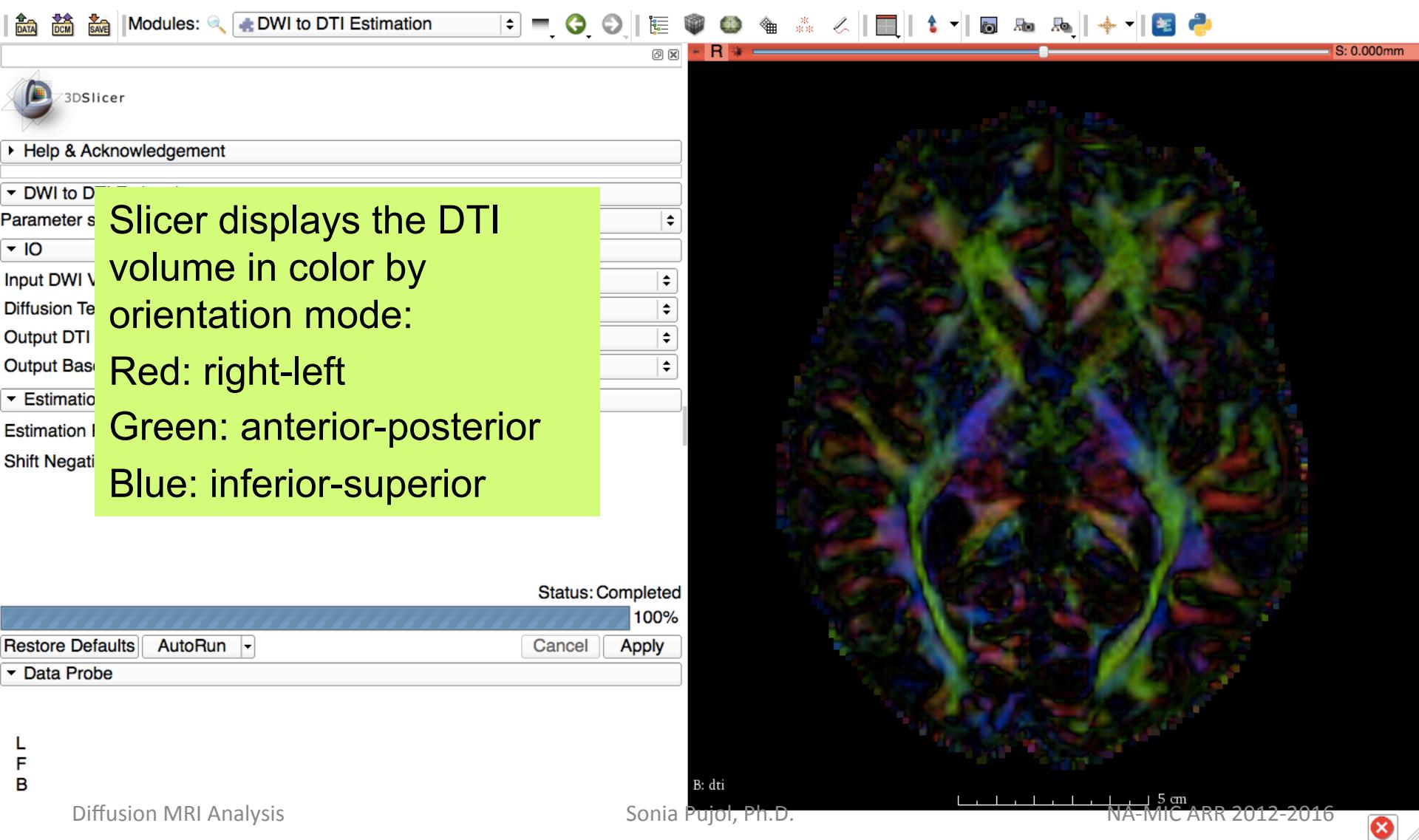
B: baseline

5 cm

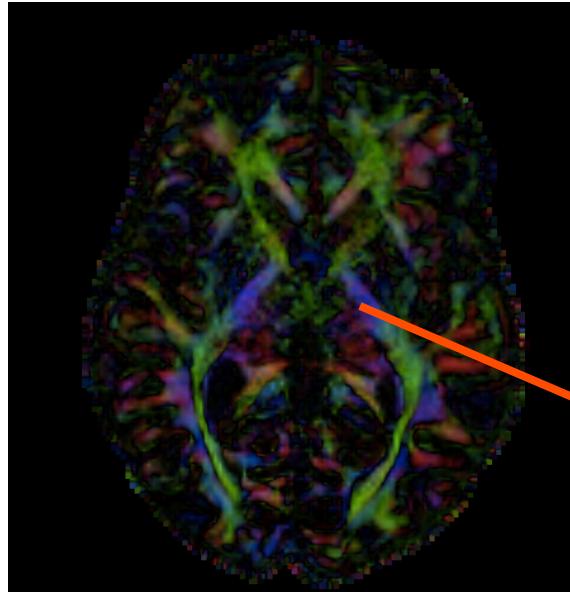
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NA-MIC ARR 2012-2016

Exploring the DWI Dataset



Diffusion Tensor Data



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

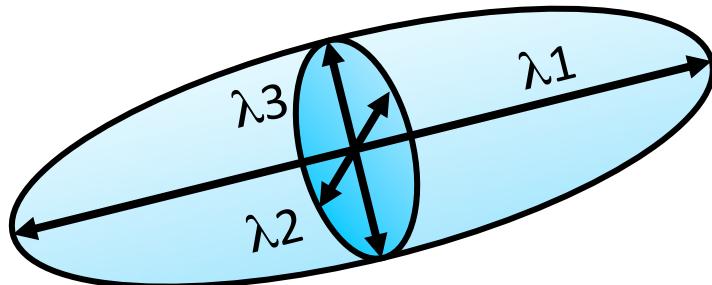
Stejskal-Tanner equation (1965)

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

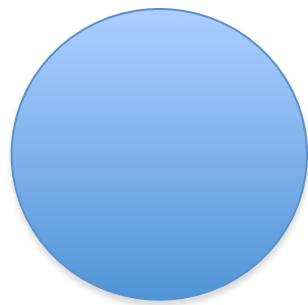
The diffusion tensor \underline{D} in the voxel (I,J,K) is a 3×3 symmetric matrix.

Diffusion Tensor

- The diffusion tensor \underline{D} in each voxel can be visualized as a diffusion ellipsoid, with the eigenvectors indicating the directions of the principal axes, and the ellipsoidal proportional to the square root of the eigenvalues defining the
- 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.

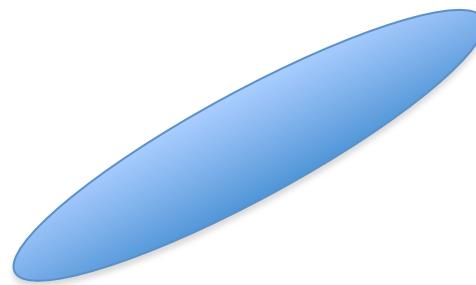


Diffusion Tensor Shape



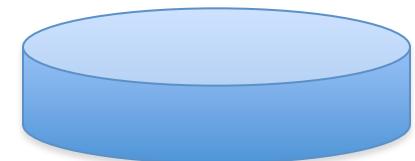
$$\lambda_1 = \lambda_2 = \lambda_3$$

Isotropic media
(Cerebrospinal
Fluid, gray matter)



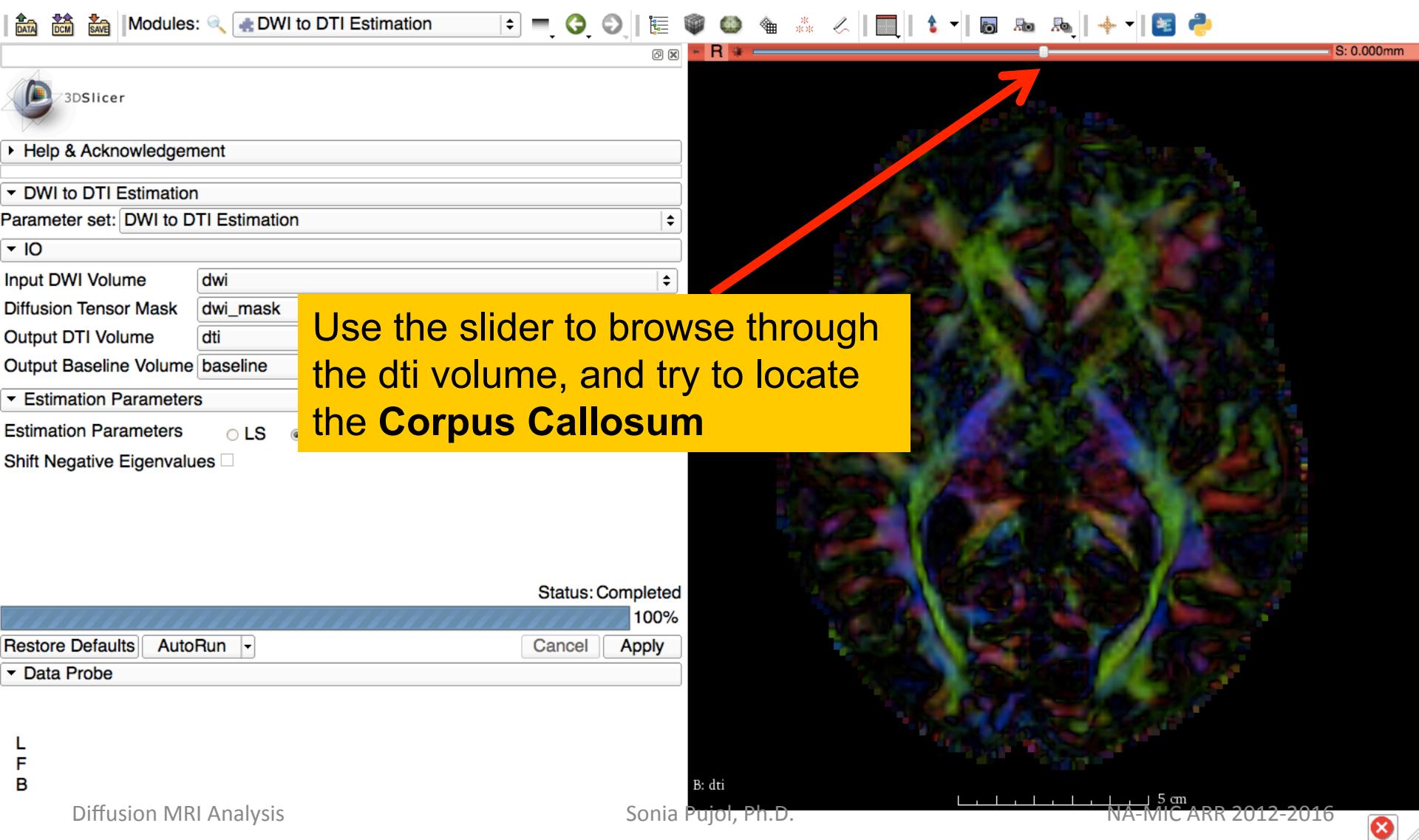
$$\lambda_1 >> \lambda_2, \lambda_3$$

Anisotropic media
(white matter)



$$\lambda_1 \sim \lambda_2 >> \lambda_3$$

Exploring the DWI Dataset



Corpus Callosum

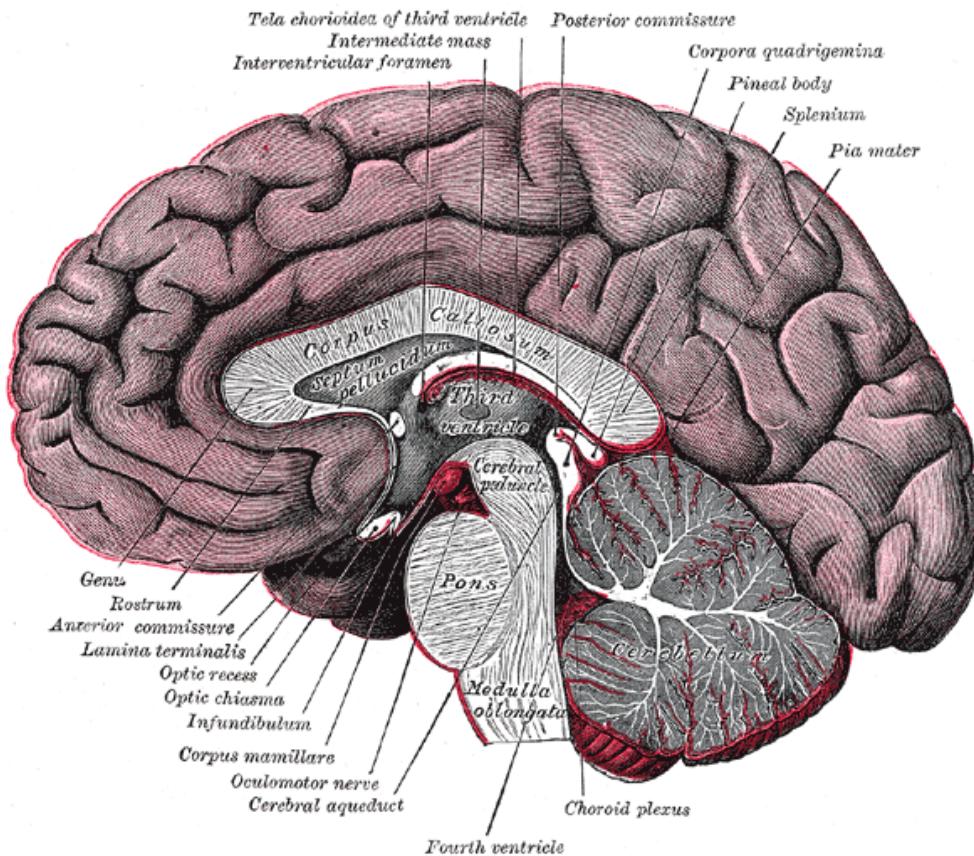


Image from Gray's Anatomy

Diffusion MRI Analysis

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NA-MIC ARR 2012-2014

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

Corpus Callosum

3DSlicer

Modules: DWI to DTI Estimation S: 19.000mm

Help & Acknowledgement

DWI to DTI Estimation

Parameter set: DWI to DTI Estimation

IO

Input DWI Volume dwi

Diffusion Tensor Mask dwi_mask

Output DTI Volume dti

Output Baseline Volume baseline

Estimation Parameters LS WLS

Shift Negative Eigenvalues

Image Courtesy of Dr. Alexandra Golby, Brigham and Women's Hospital, Boston, MA..

Status: Completed 100%

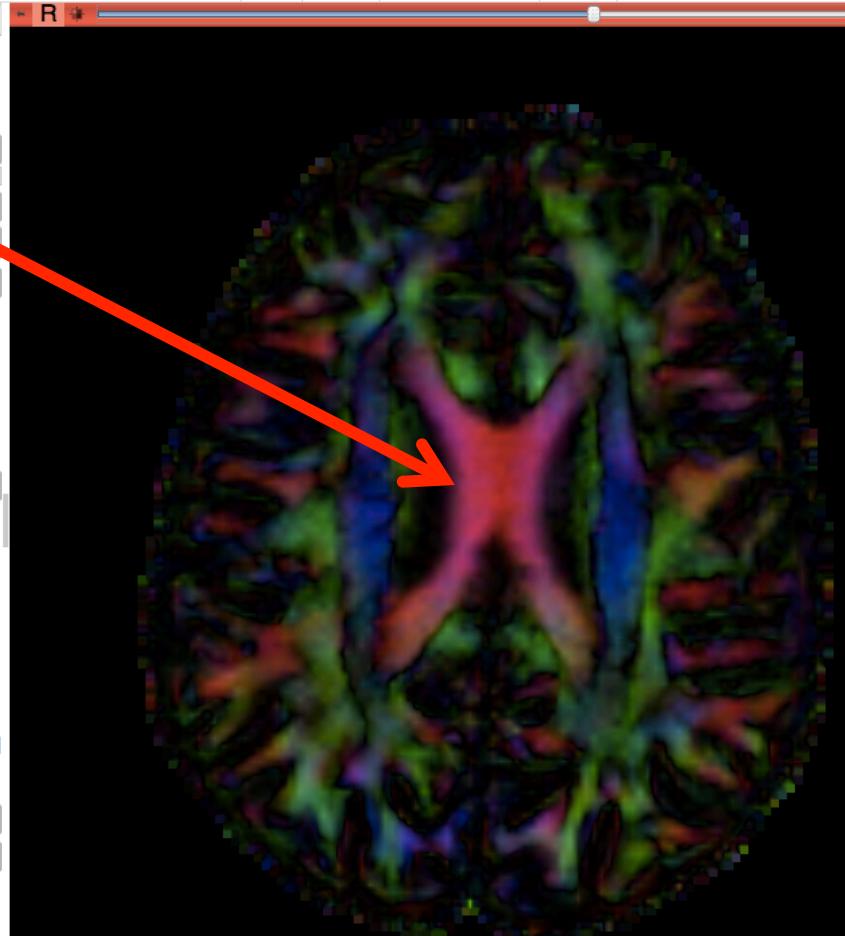
Restore Defaults AutoRun Cancel Apply

Data Probe

L F B

Diffusion MRI Analysis

Corpus Callosum



A red arrow points from the text "Corpus Callosum" in the 3DSlicer interface to the central white matter tract in the brain scan, which is color-coded in red to indicate high FA (anisotropy) and thus high fiber density.

R

B: dti

5 cm

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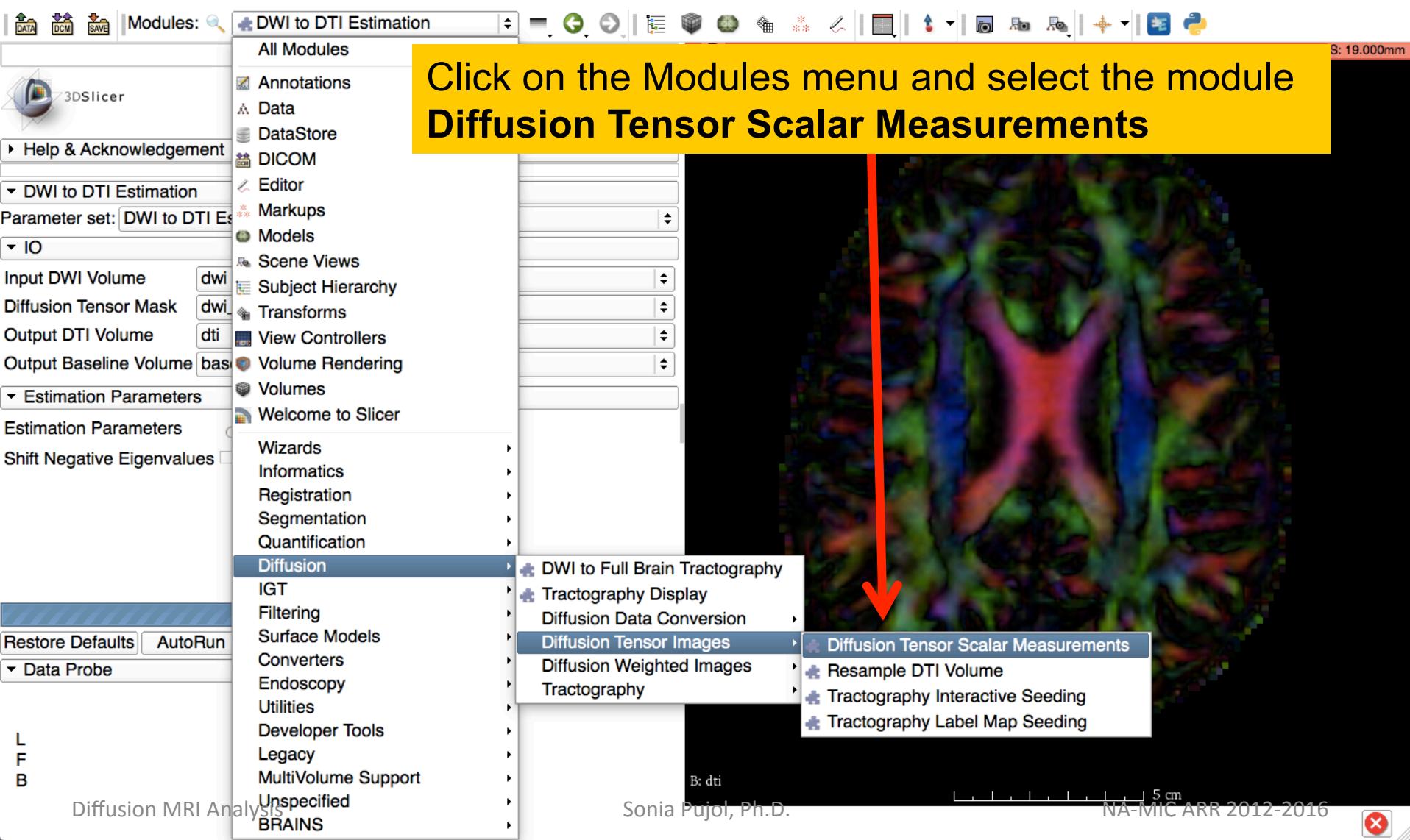
NA-MIC ARR 2012-2016

Characterizing the Size of the tensor: Trace

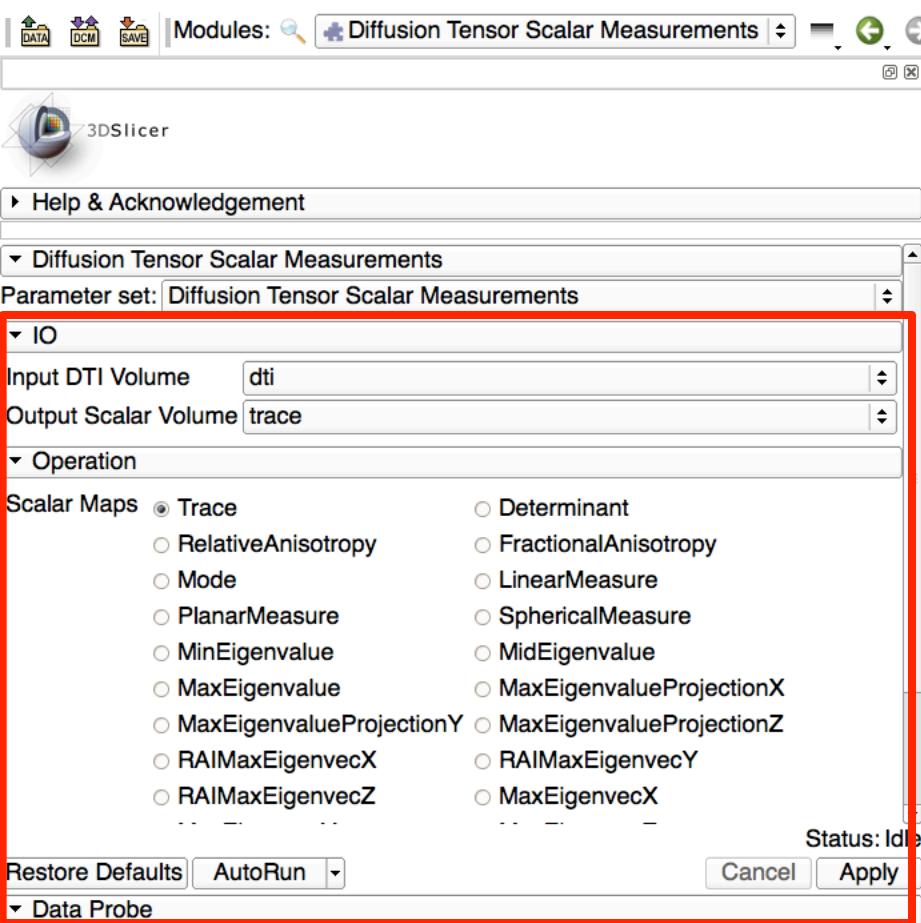
$$\text{Trace}(D) = \lambda_1 + \lambda_2 + \lambda_3$$

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

Trace



Trace



Type in the following information in the IO menu:

- select the Operation '**Trace**'
- set **Input DTI Volume** to '**dti**'
- select **Output Scalar Volume**
- Create and Rename new Volume** and rename it '**trace**'
- click on **Apply** to calculate the trace map of the tensor volume

Trace

The trace image appears in the red viewer

L
F
B

Diffusion MRI Analysis

Modules: Diffusion Tensor Scalar Measurements

R S: 0.000mm

3DSlicer

Help & Acknowledgement

Diffusion Tensor Scalar Measurements

Parameters

Input Data

Output Scalar Volume: trace

Operation

Scalar Maps:

- Trace
- Determinant
- RelativeAnisotropy
- FractionalAnisotropy
- Mode
- LinearMeasure
- PlanarMeasure
- SphericalMeasure
- MinEigenvalue
- MidEigenvalue
- MaxEigenvalue
- MaxEigenvalueProjectionX
- MaxEigenvalueProjectionY
- MaxEigenvalueProjectionZ
- RAIMaxEigenvecX
- RAIMaxEigenvecY

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

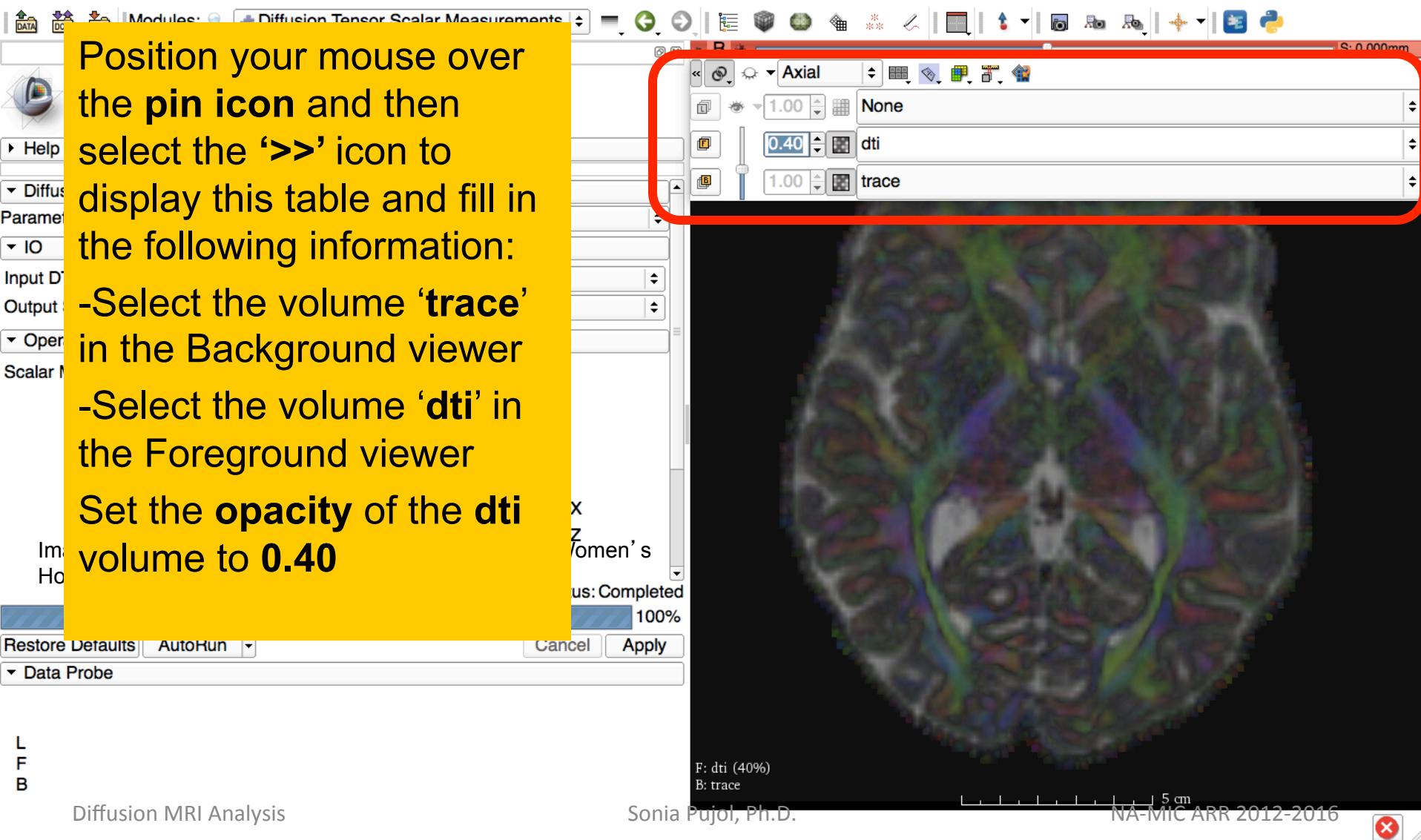
Data Probe

B: trace

5 cm

NA-MIC ARR 2012-2016

Trace



Trace

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

Parameter set: Diffusion Tensor Scalar Measurements

▼ IO

Input DTI Volume dti

Output Scalar Volume trace

▼ Operation

- Scalar Maps Trace Determinant
 RelativeAnisotropy FractionalAnisotropy
 Mode LinearMeasure
 PlanarMeasure SphericalMeasure
 MinEigenvalue MidEigenvalue
 MaxEigenvalue MaxEigenvalueProjectionX
 MaxEigenvalueProjectionY MaxEigenvalueProjectionZ
 RAIMaxEigenvecX RAIMaxEigenvecY

Status: Completed

100%

Restore Defaults AutoRun

Cancel Apply

▼ Data Probe

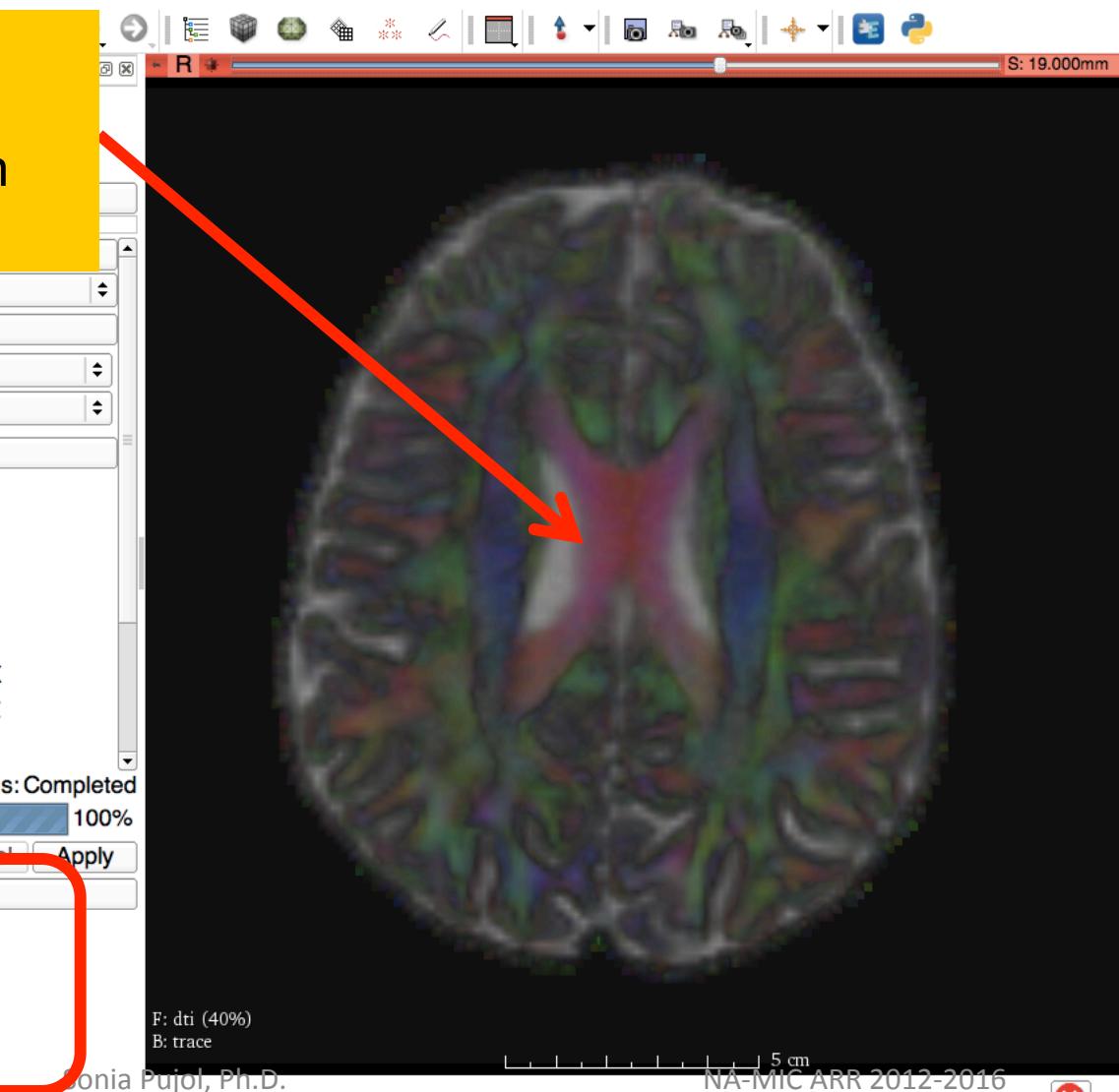
Red RAS: (6.2, 6.7, 19.0) Axial Sp: 1.5

L None

F dti (60, 60, 60) ColorOrientation 0

B trace (60, 60, 60) 0.002111

Diffusion MRI Analysis



Trace

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

Input DTI Volume dti
Output Scalar Volume trace

Operation

Scalar Maps Trace Determinant
 RelativeAnisotropy FractionalAnisotropy
 Mode LinearMeasure
 PlanarMeasure SphericalMeasure
 MinEigenvalue MidEigenvalue
 MaxEigenvalue MaxEigenvalueProjectionX
 MaxEigenvalueProjectionY MaxEigenvalueProjectionZ
 RAIMaxEigenvecX RAIMaxEigenvecY

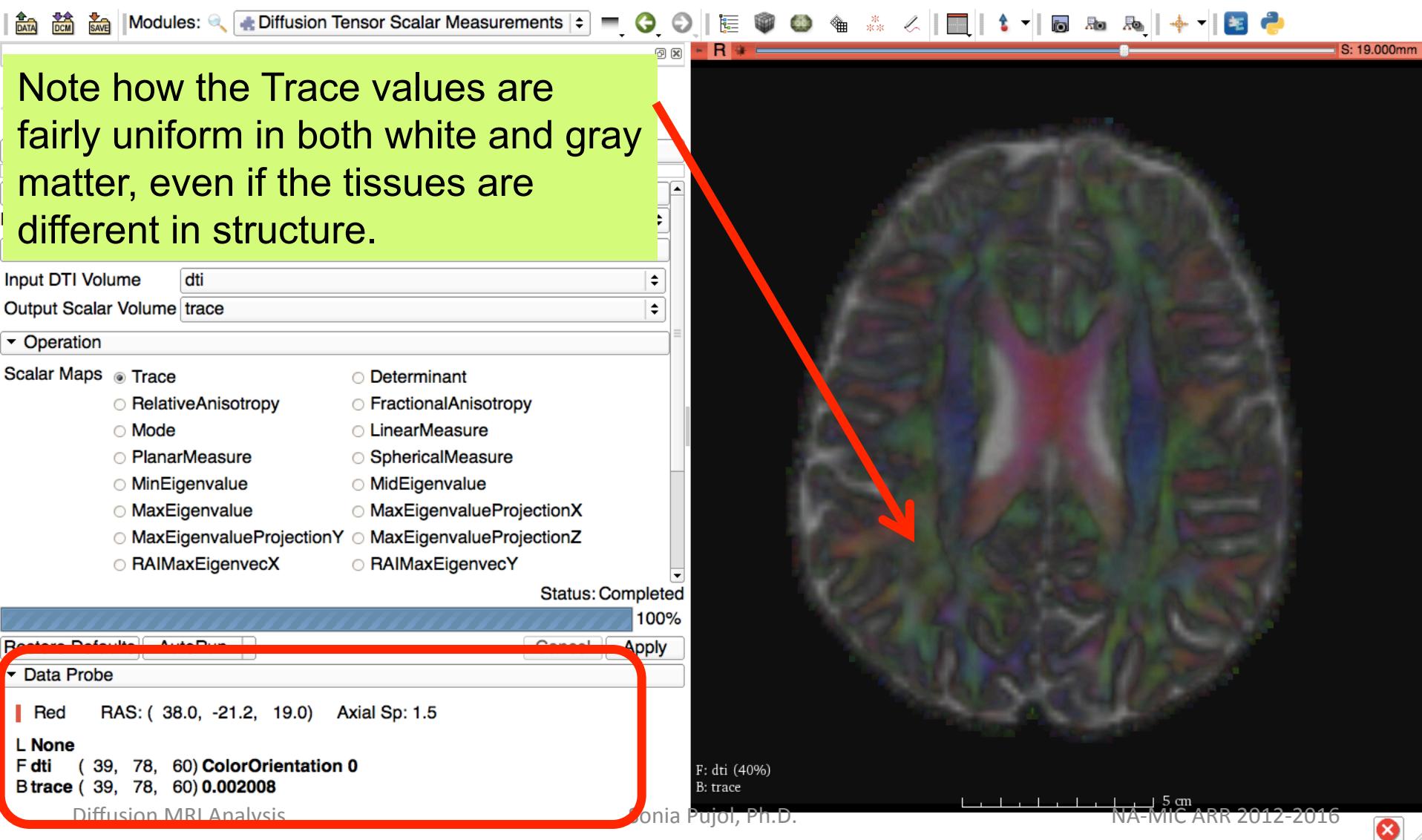
Status: Completed 100%

Data Probe

Red RAS: (38.0, -21.2, 19.0) Axial Sp: 1.5

L None
F dti (39, 78, 60) ColorOrientation 0
B trace (39, 78, 60) 0.002008

Diffusion MRI Analysis



R S: 19.000mm

F: dti (40%)
B: trace

5 cm

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Scalar Maps: Fractional Anisotropy

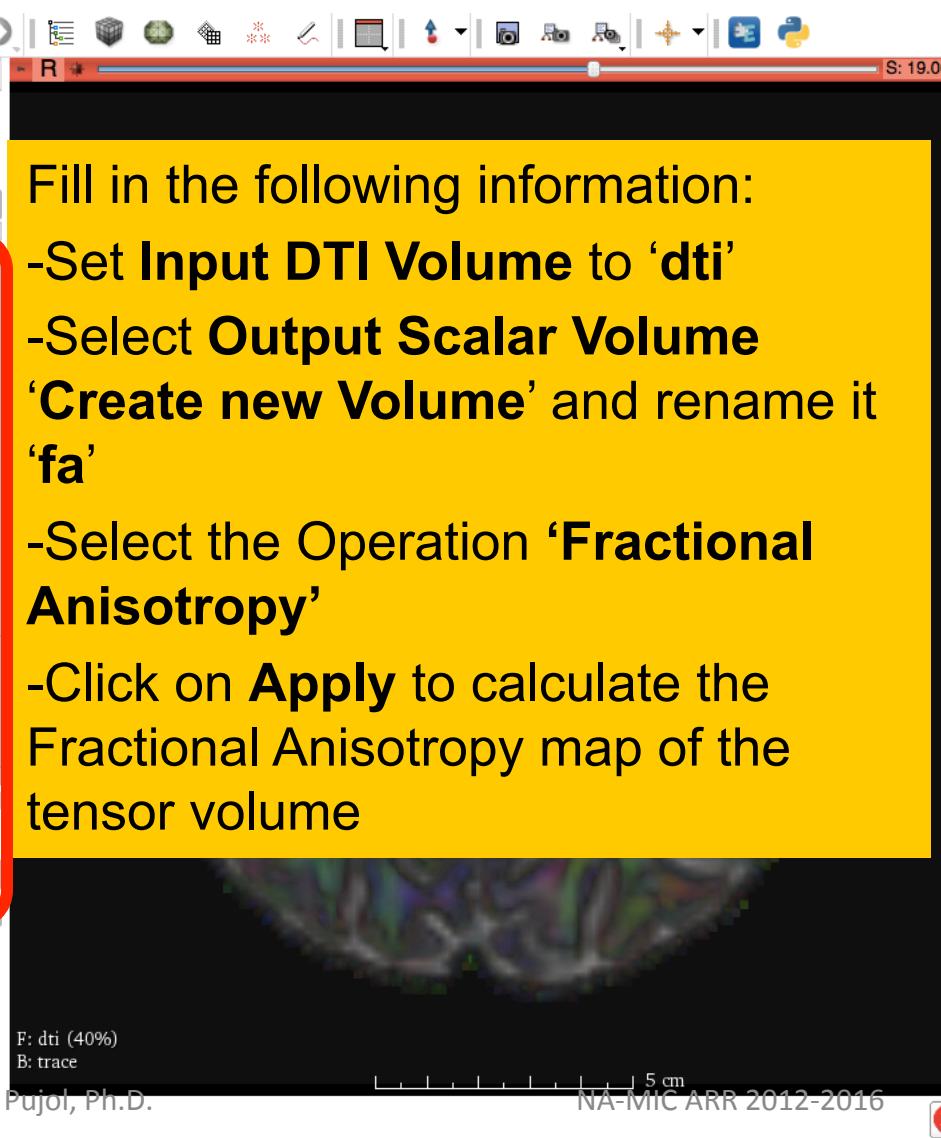
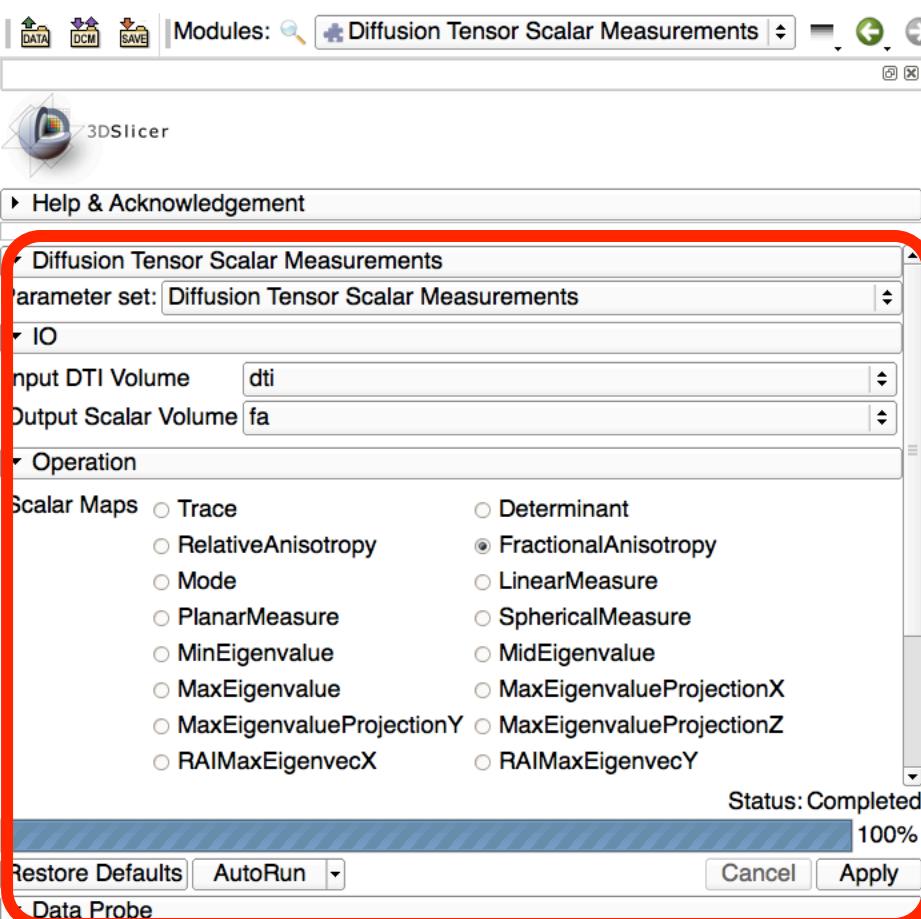
$$FA(D) = \frac{\sqrt{(\lambda_1 - \lambda_2)^2 + (\lambda_1 - \lambda_3)^2 + (\lambda_2 - \lambda_3)^2}}{\sqrt{2} \sqrt{\lambda_1^2 + \lambda_2^2 + \lambda_3^2}}$$

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

Fractional Anisotropy

Fill in the following information:

- Set **Input DTI Volume** to ‘**dti**’
- Select **Output Scalar Volume** ‘**Create new Volume**’ and rename it ‘**fa**’
- Select the Operation ‘**Fractional Anisotropy**’
- Click on **Apply** to calculate the Fractional Anisotropy map of the tensor volume



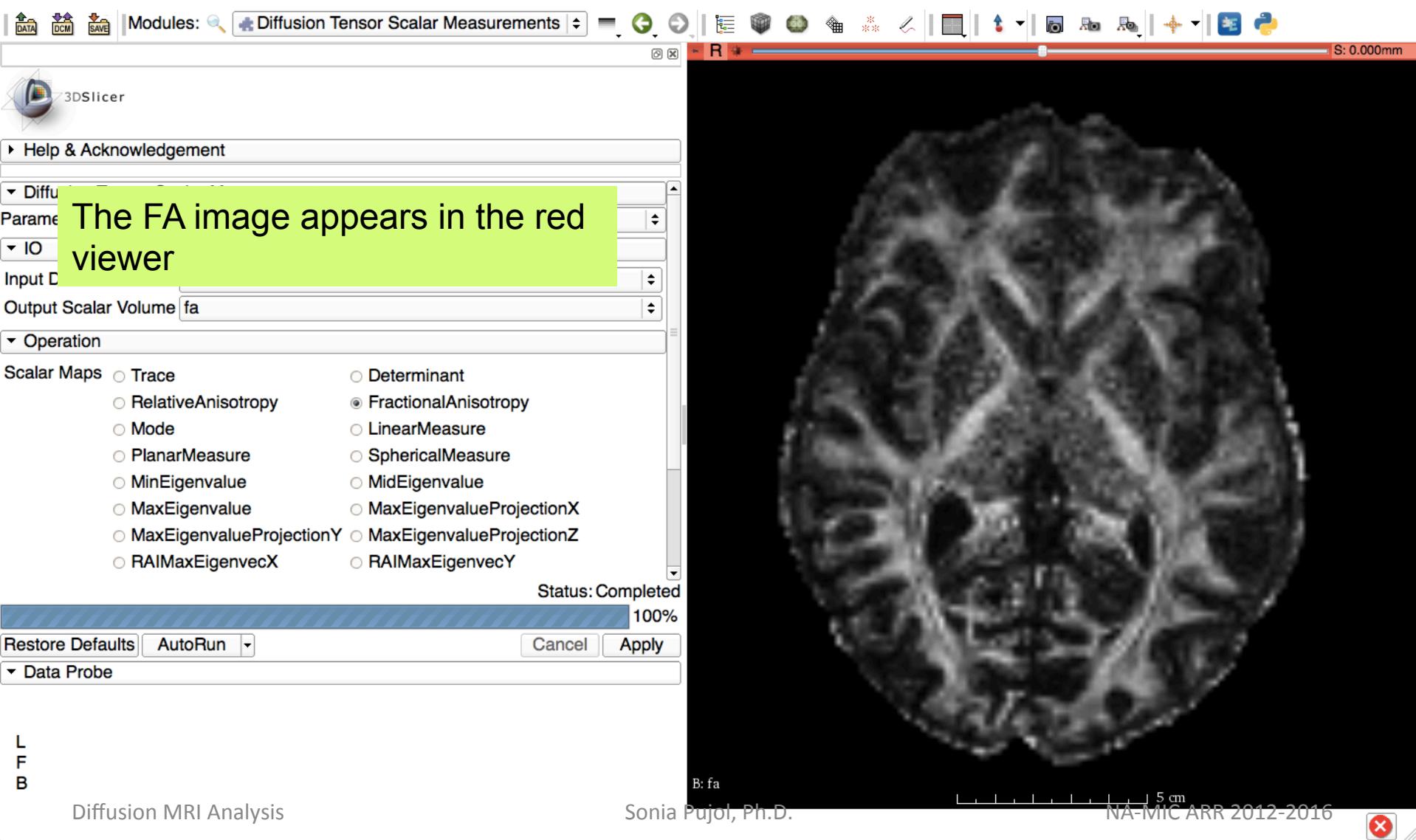
L
F
B

Diffusion MRI Analysis

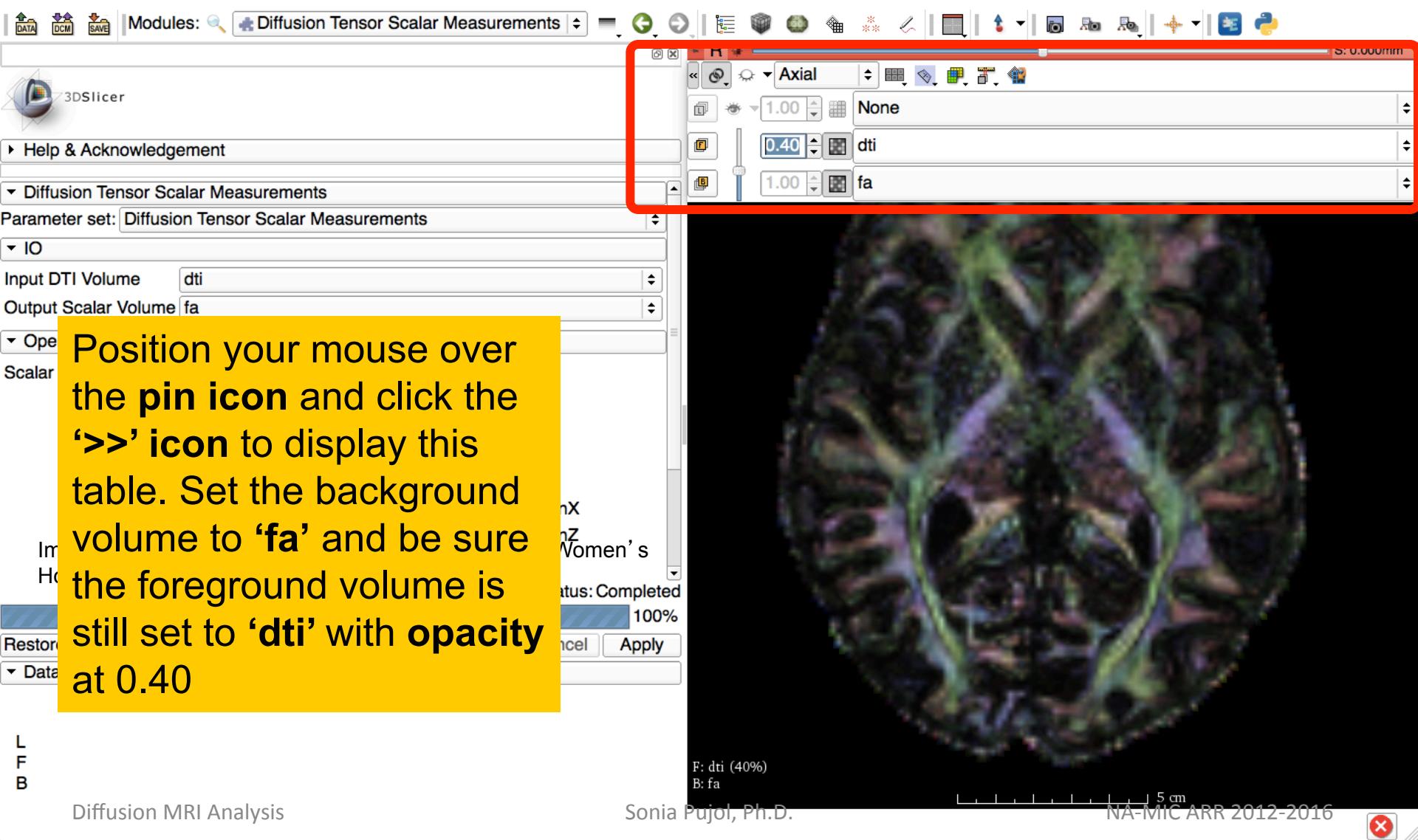
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Fractional Anisotropy



Fractional Anisotropy



Fractional Anisotropy

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

Output Scalar Volume fa

Operation

Scalar Maps

- Trace
- Determinant
- FractionalAnisotropy
- RelativeAnisotropy
- Mode
- LinearMeasure
- PlanarMeasure
- SphericalMeasure
- MinEigenvalue
- MidEigenvalue
- MaxEigenvalue
- MaxEigenvalueProjectionX
- MaxEigenvalueProjectionY
- MaxEigenvalueProjectionZ
- RAIMaxEigenvecX
- RAIMaxEigenvecY

Status: Completed 100%

Buttons: Defaults AutoRun Cancel Apply

Data Probe

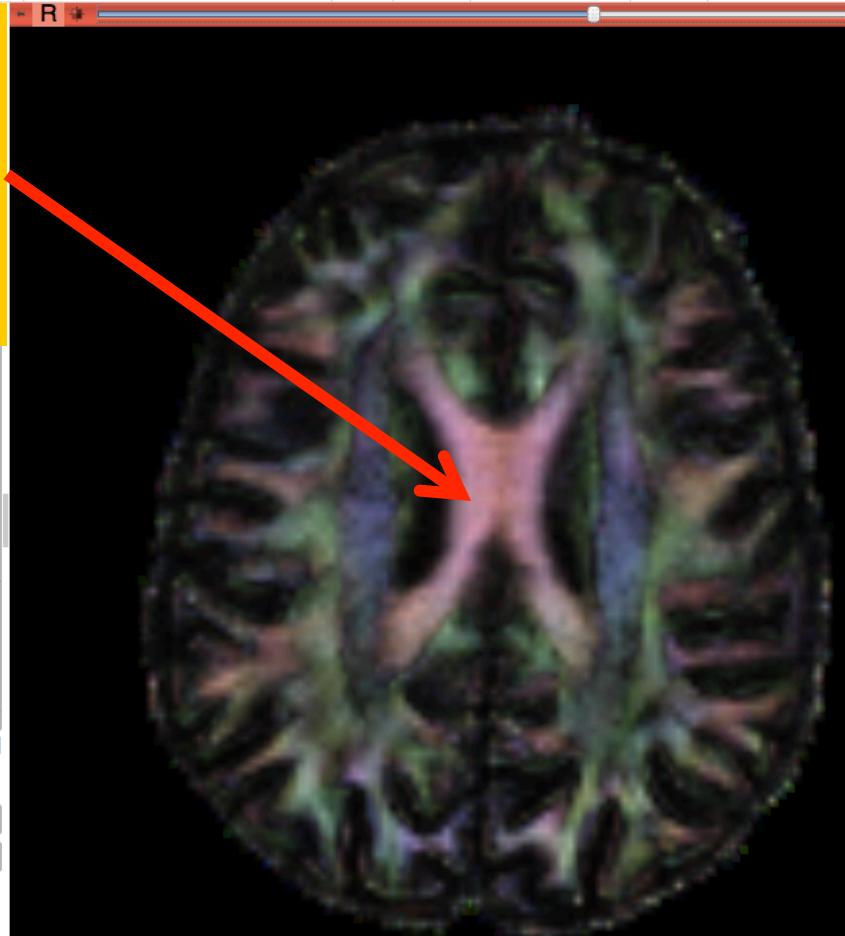
Red RAS: (7.7, 8.8, 19.0) Axial Sp: 1.5

L None

F dti (59, 58, 60) ColorOrientation 0

B fa (59, 58, 60) 0.890284

Diffusion MRI Analysis



R S: 19.000mm

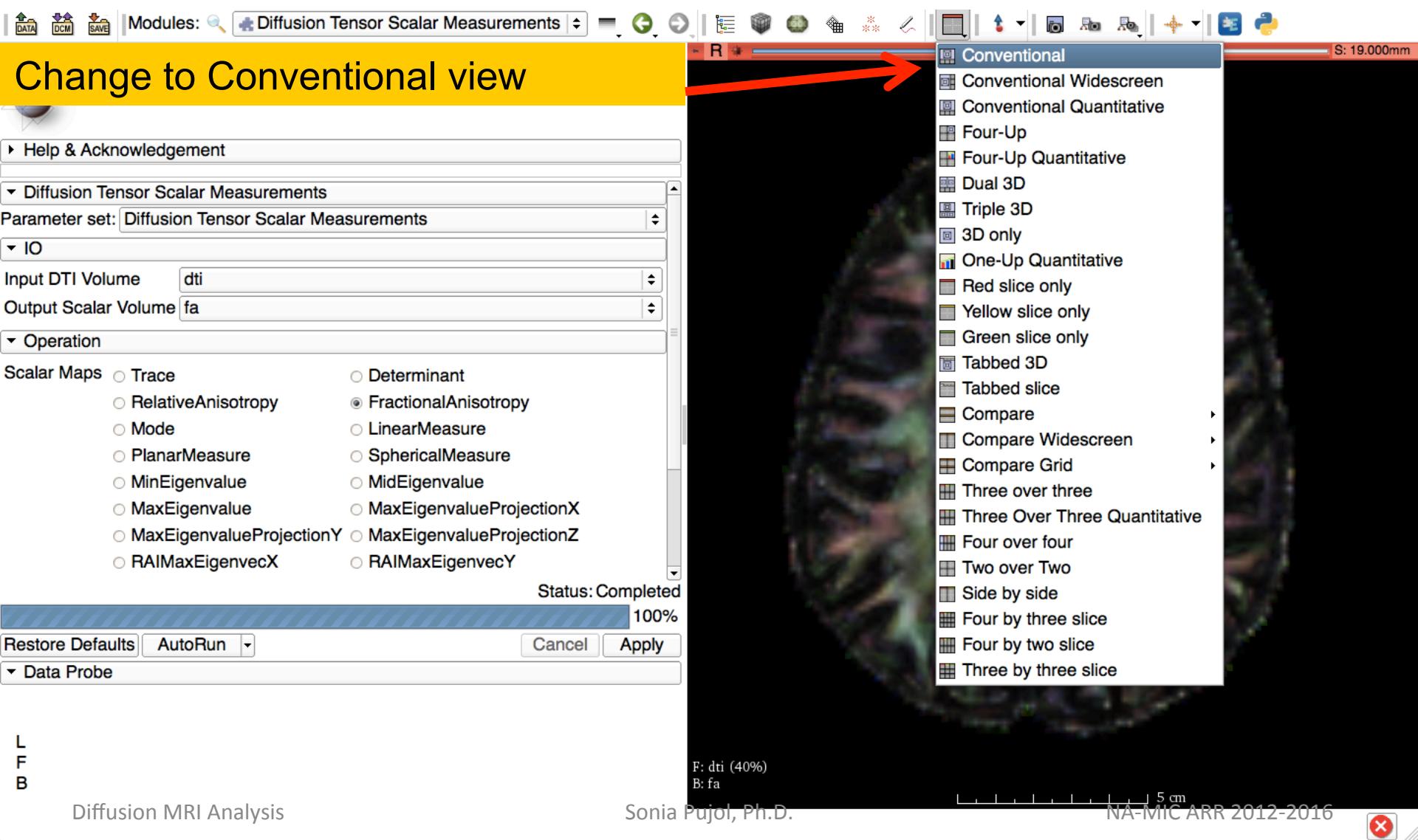
F: dti (40%)
B: fa

5 cm

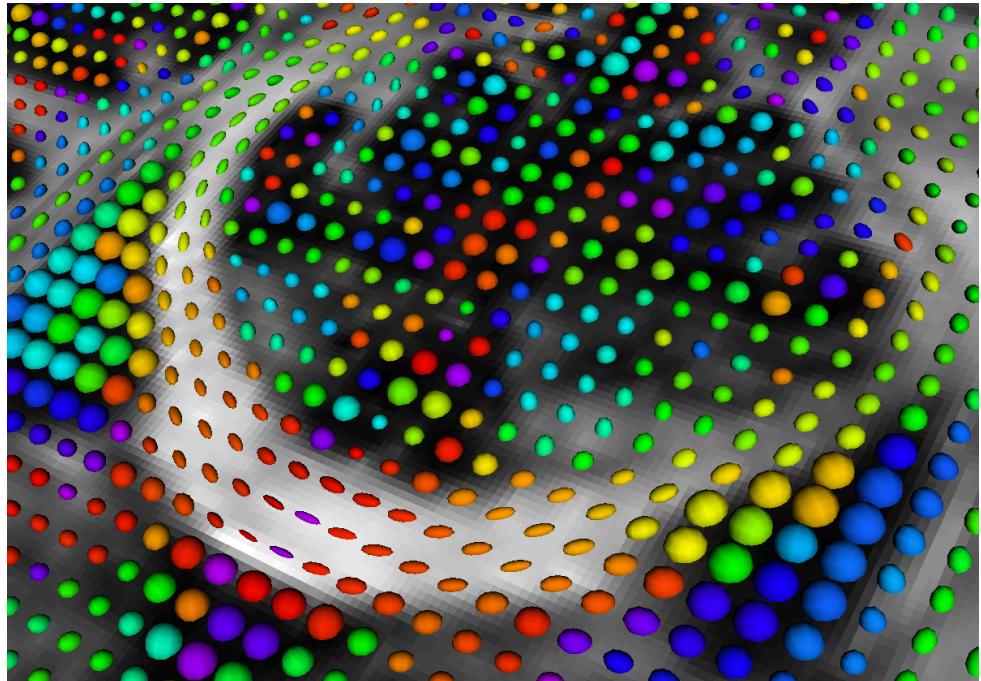
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Fractional Anisotropy

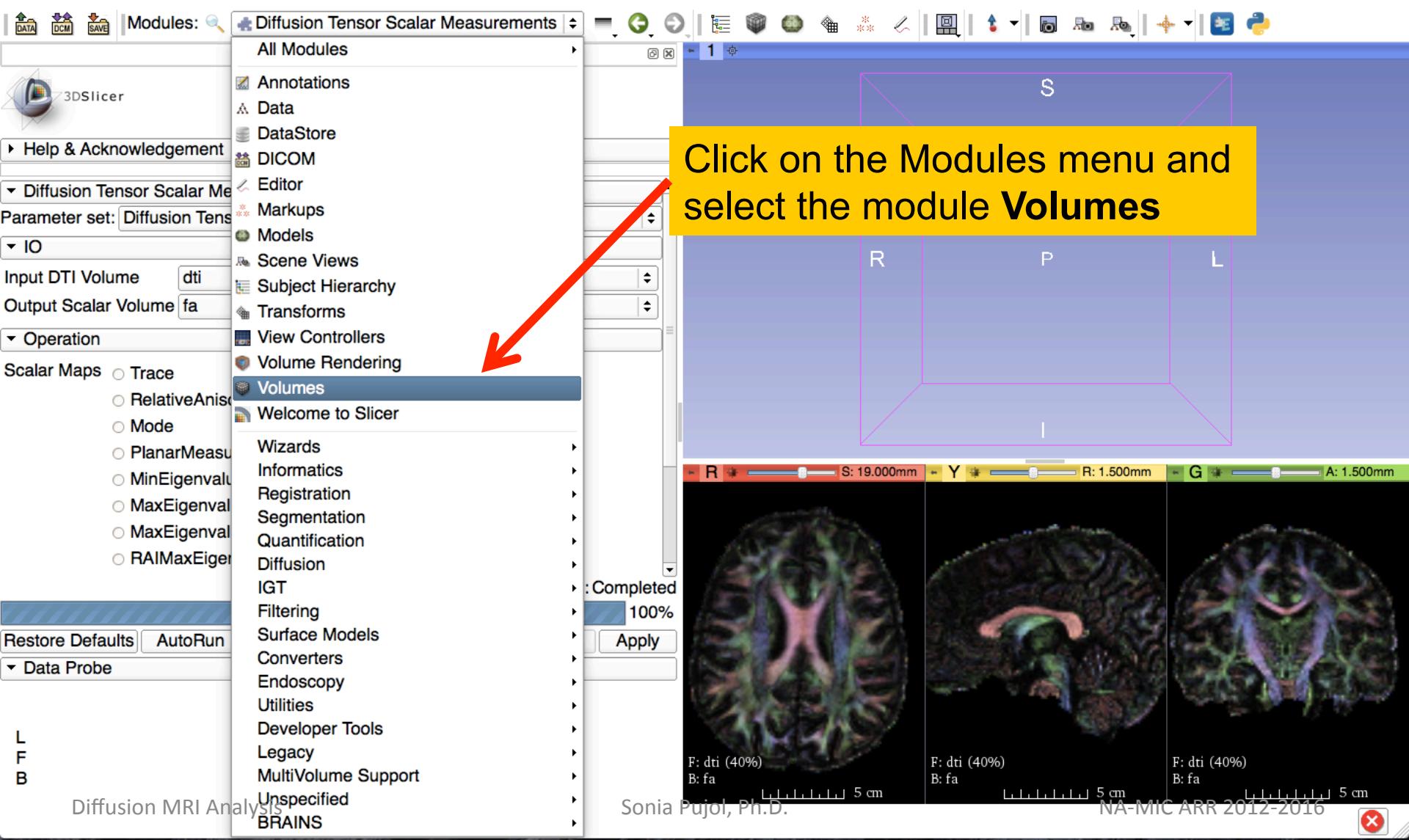


L
F
B

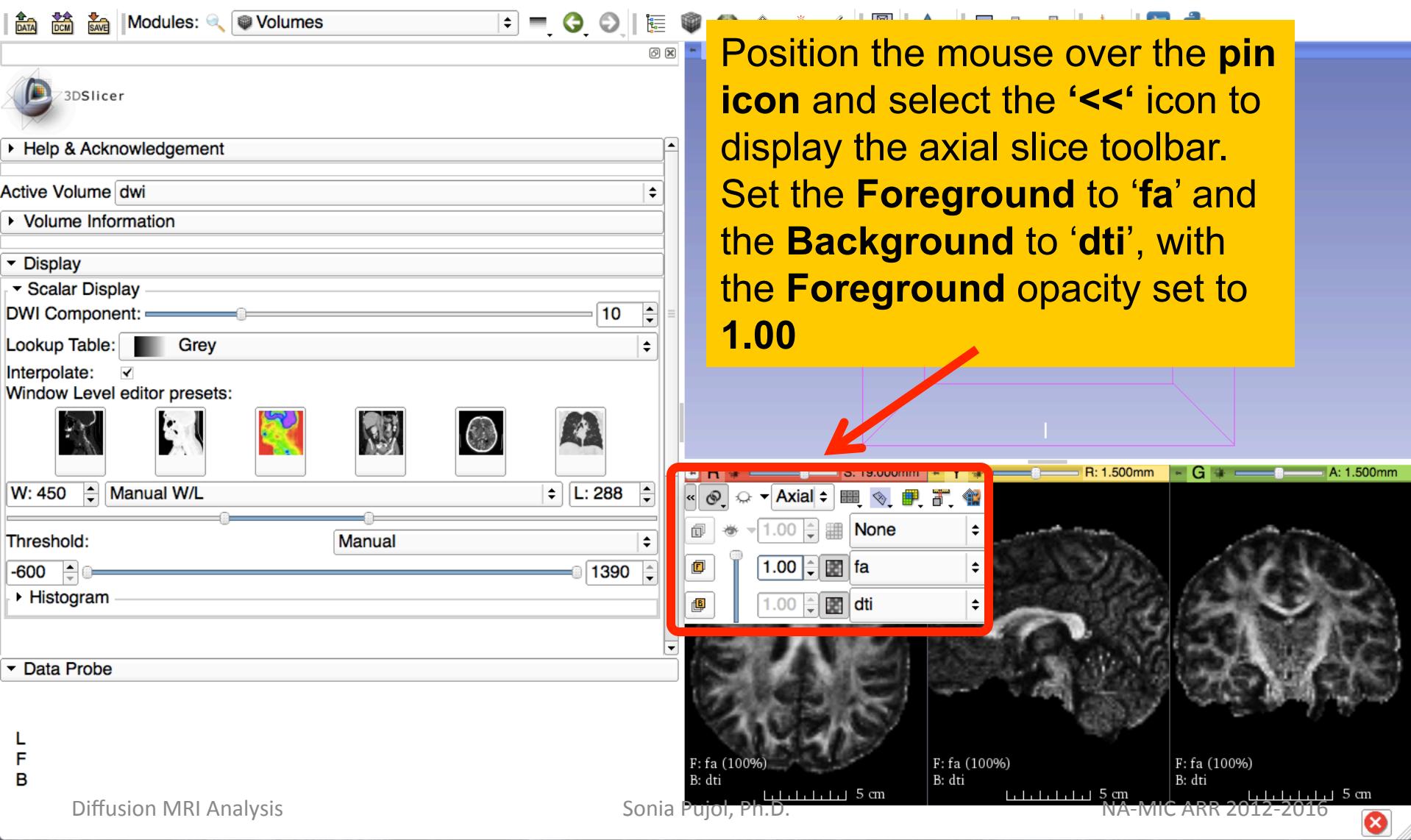


Part 2: Visualizing the tensor data

3D Visualization: Glyphs



3D Visualization: Glyphs



3D Visualization: Glyphs

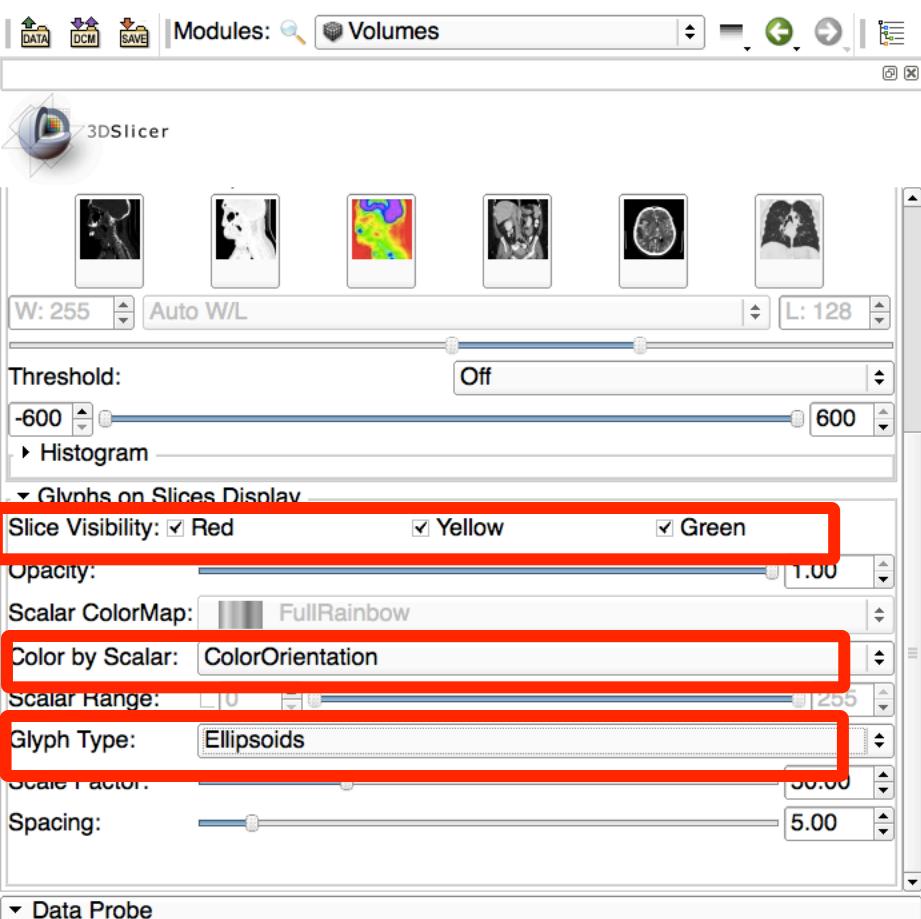
The screenshot shows the 3D Slicer interface with several panels:

- Top Bar:** Modules: Volumes, with various tool icons.
- Left Panel (Controls):**
 - Help & Acknowledgement
 - Active Volume: dti (highlighted by a red box)
 - Volume Information
 - Display
 - Scalar Display
 - Scalar Mode: ColorOrientation (highlighted by a red box)
 - Lookup Table: Grey
 - Interpolate: checked
 - Window Level editor presets: includes grayscale and color-coded preset icons.
 - W: 255, L: 128
 - Threshold: Off, -600 to 600
 - Histogram
 - Glyphs on Slices Display
 - Slice Visibility: Red (unchecked), Yellow (unchecked), Green (unchecked)
 - Data Probe
- Right Panel (Visualizations):**
 - A 3D volume rendering of a brain with a pink wireframe cube overlaid, labeled with 'S' at the top.
 - Three 2D axial slices below the 3D view, each labeled with 'F: fa (100%)' and 'B: dti'. The slices are labeled R, Y, and G from left to right, corresponding to the color bars above them.
 - Scale bars indicate 5 cm for each slice.
 - Credit: Sonia Pujol, Ph.D.
 - Conference: NA-MIC ARR 2012-2016

Text Overlay:

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

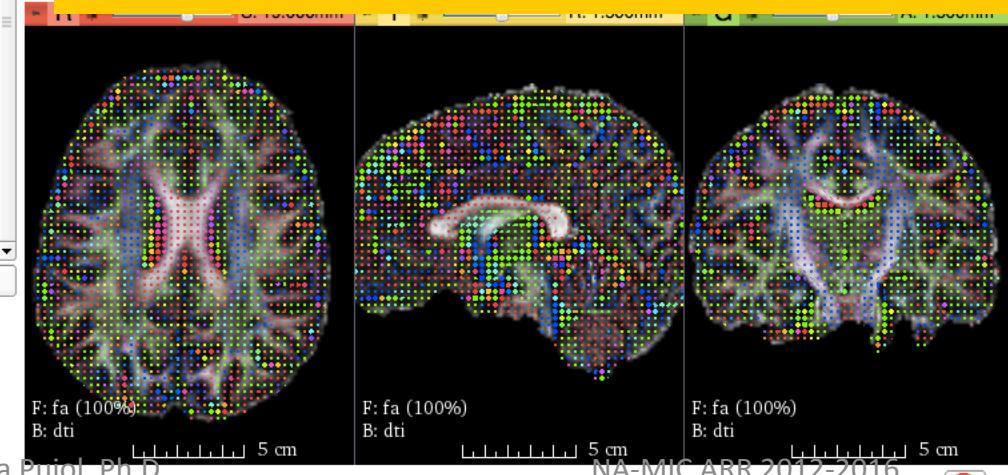
3D Visualization: Glyphs



Scroll down the module panel and:
-Check off the option for **Red, Yellow, and Green Slice Visibility**

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

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

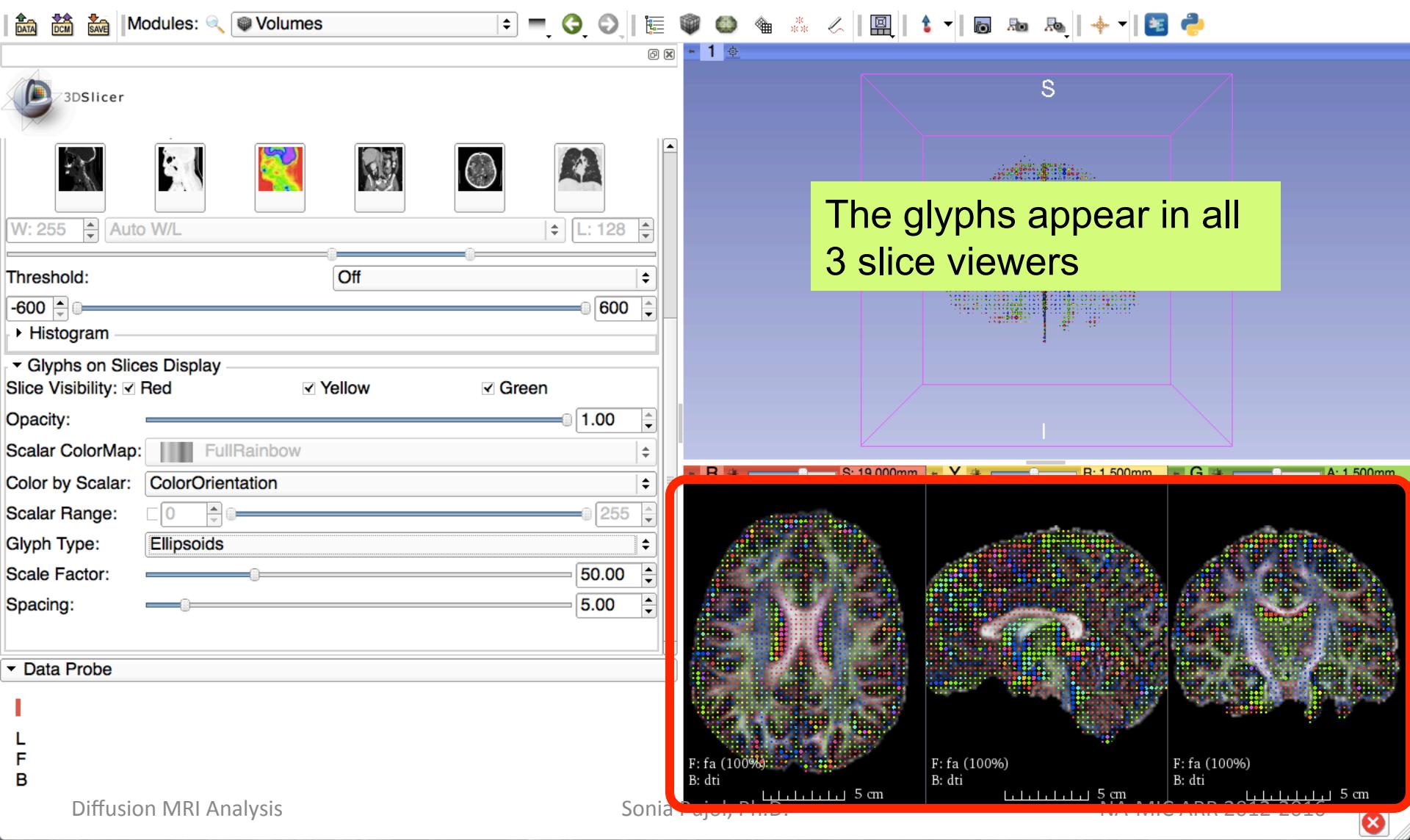


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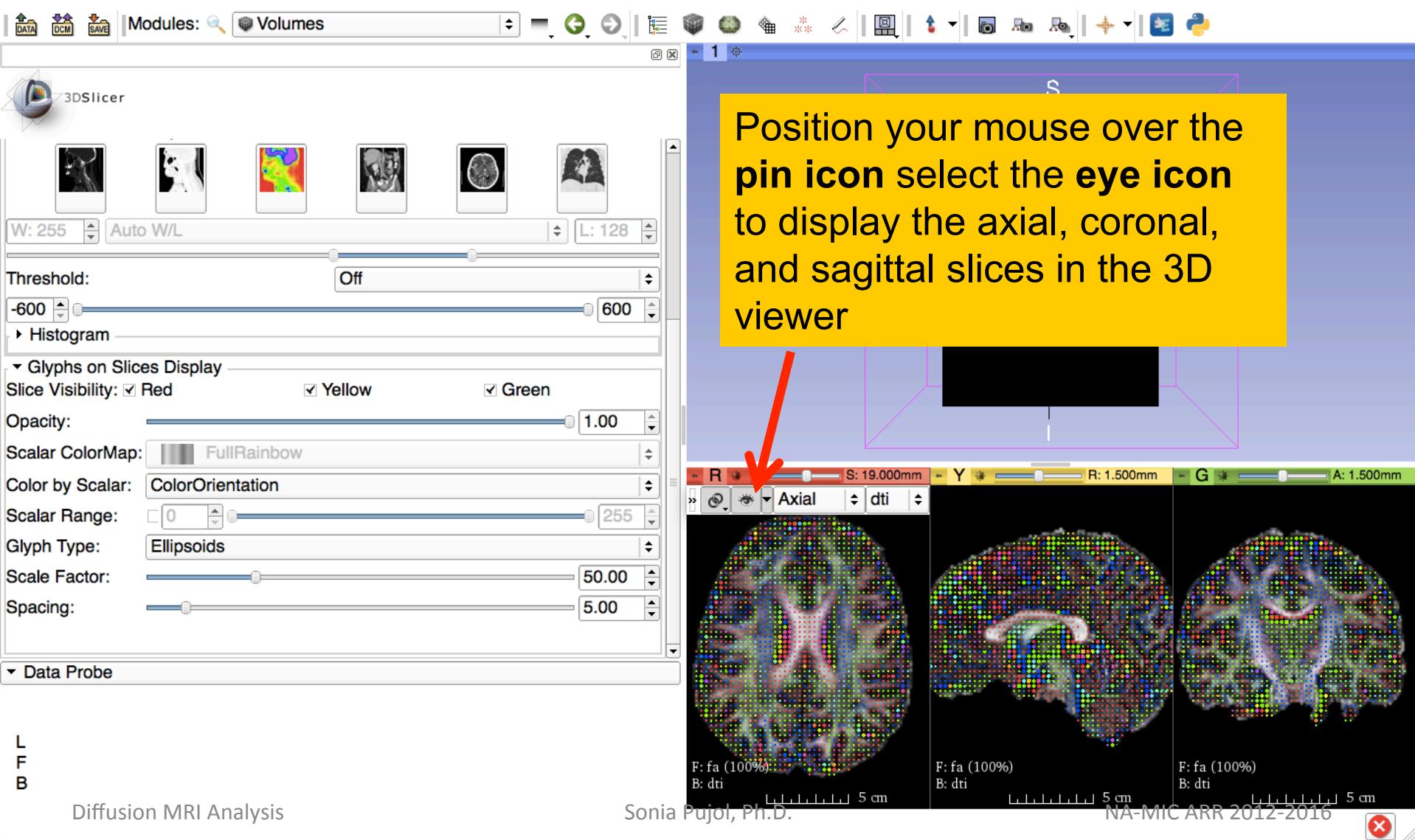
Diffusion MRI Analysis

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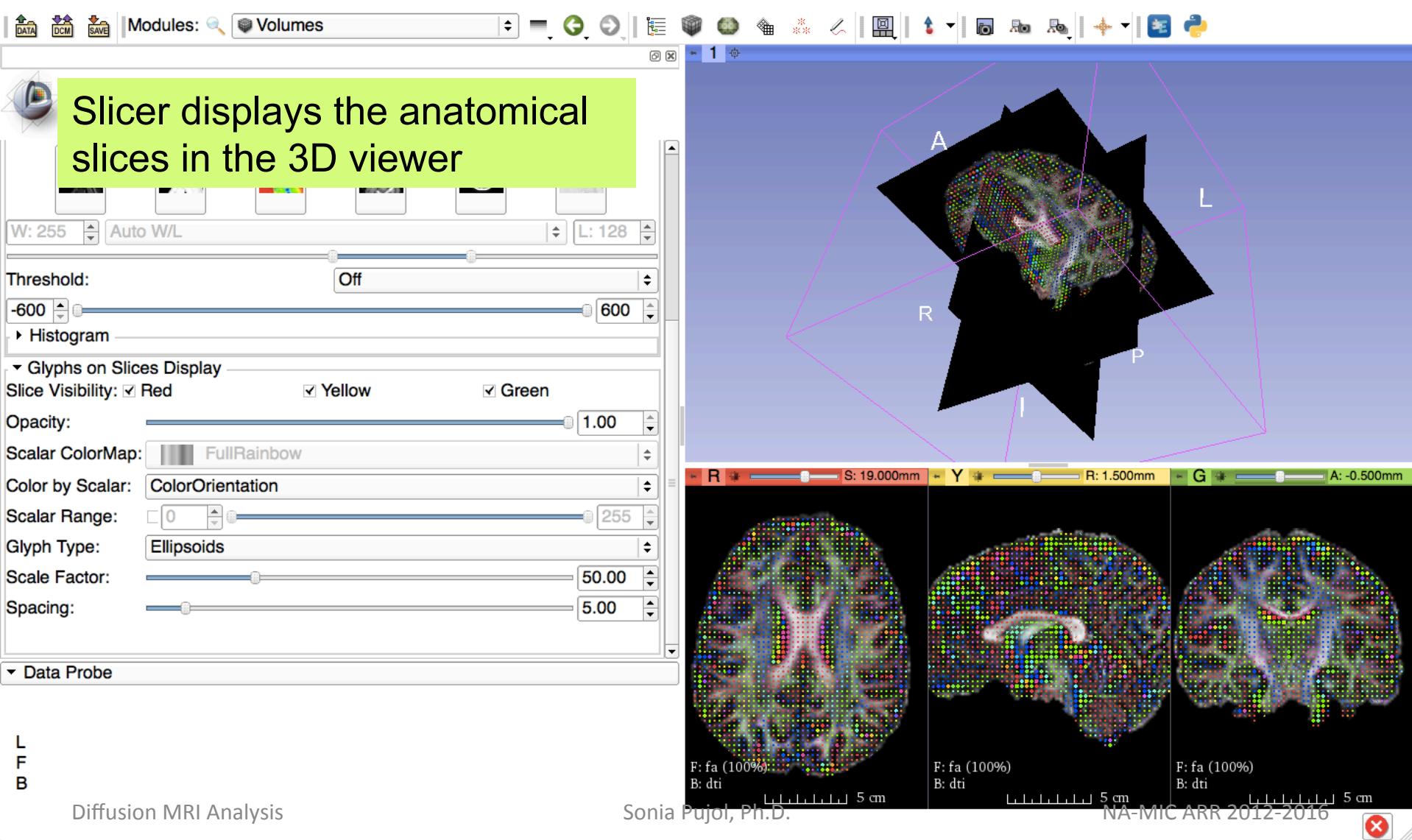
3D Visualization: Glyphs



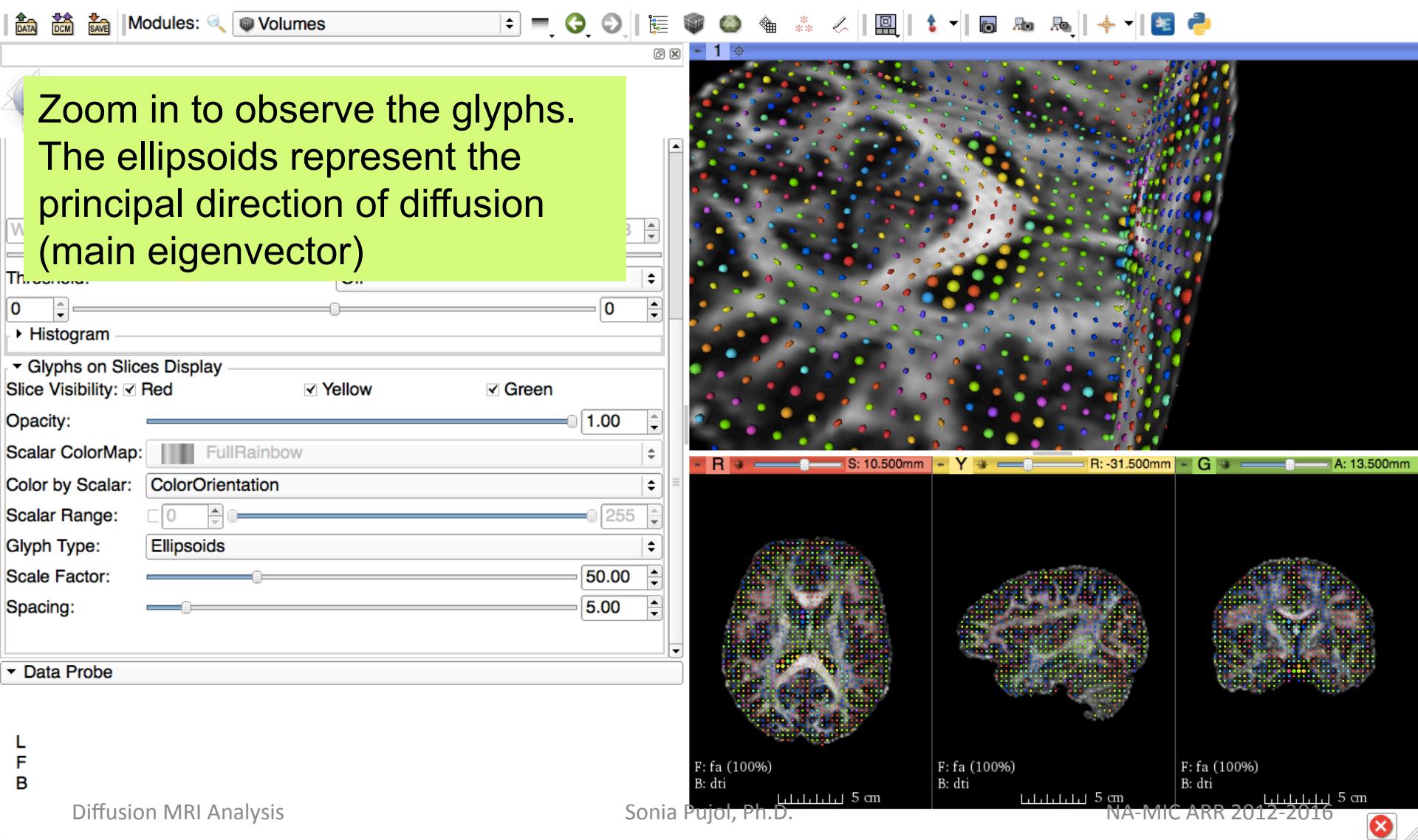
3D Visualization: Glyphs



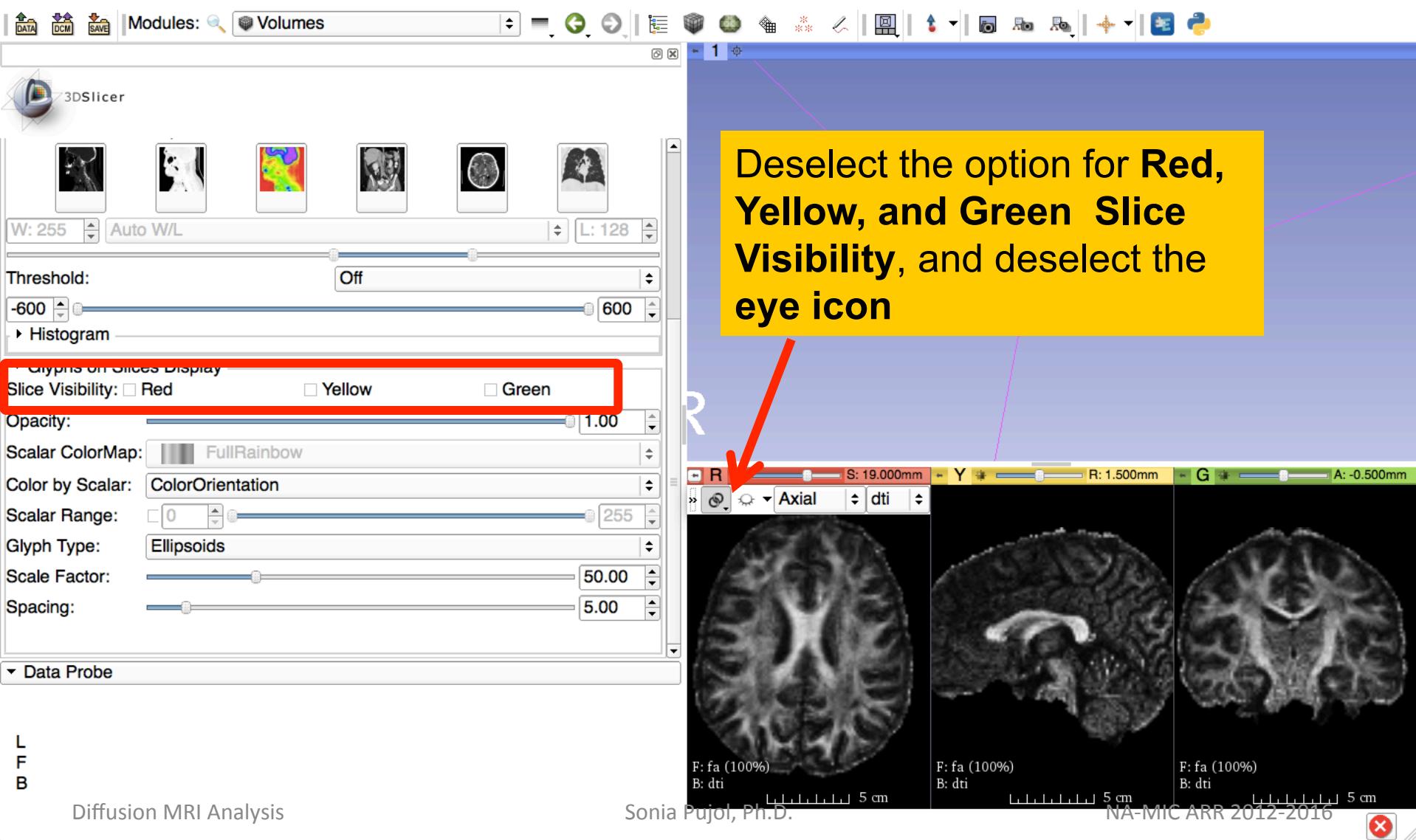
3D Visualization: Glyphs



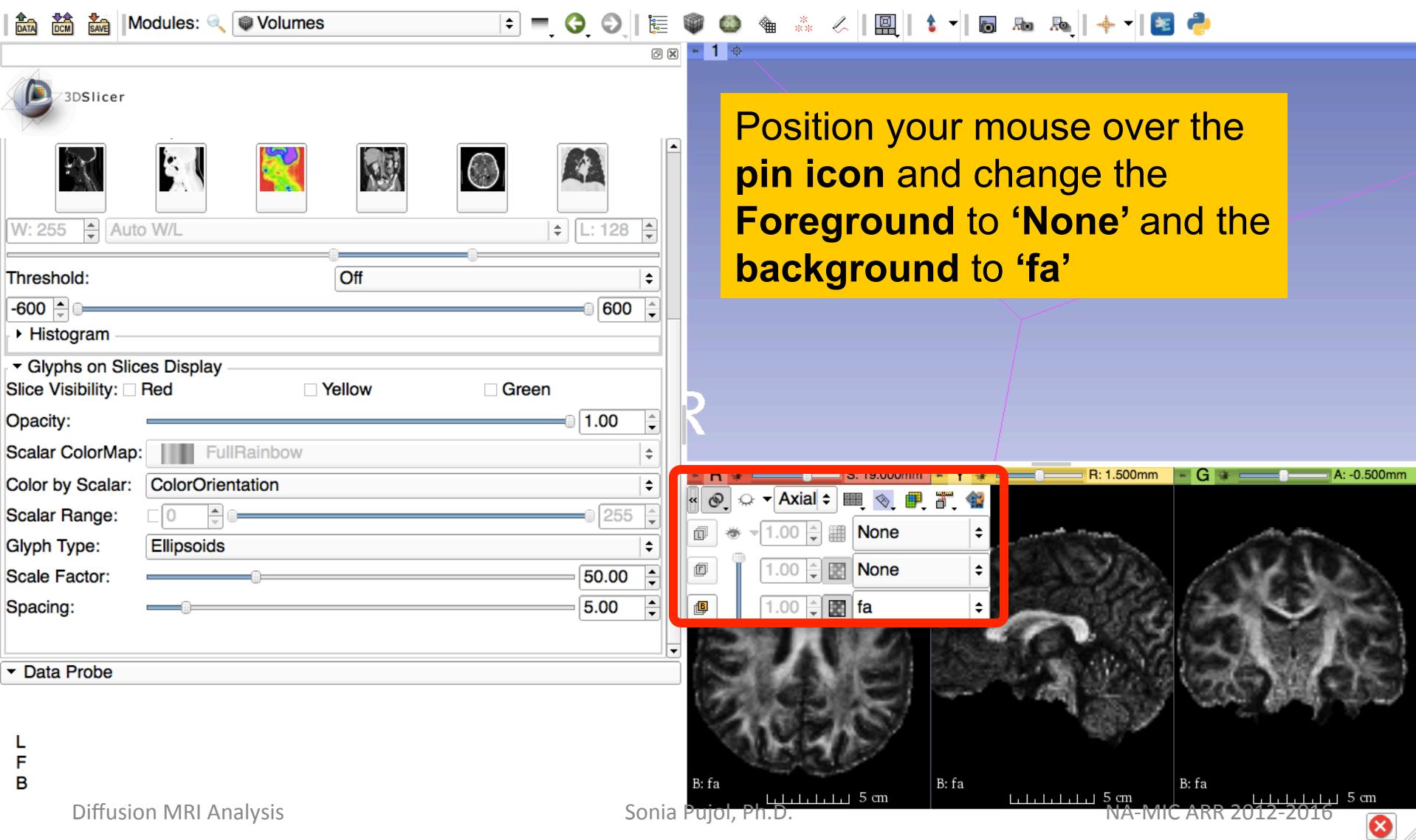
3D Visualization: Glyphs

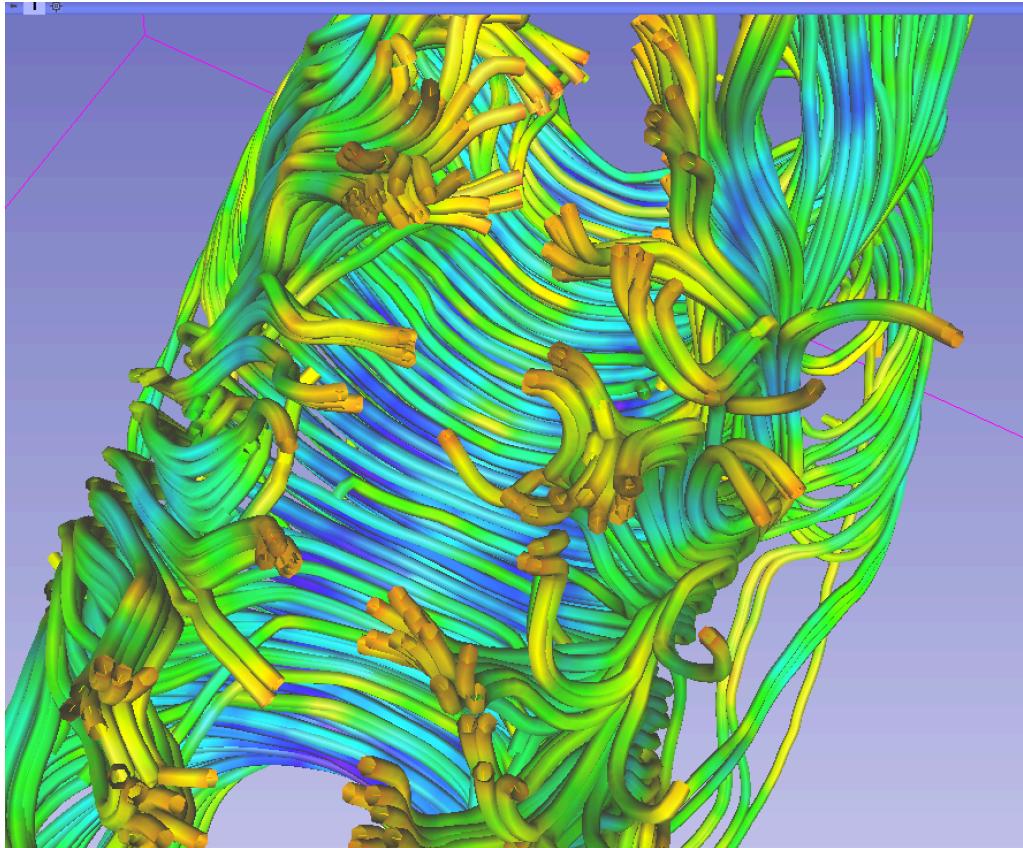


Diffusion MRI tractography



Diffusion MRI tractography



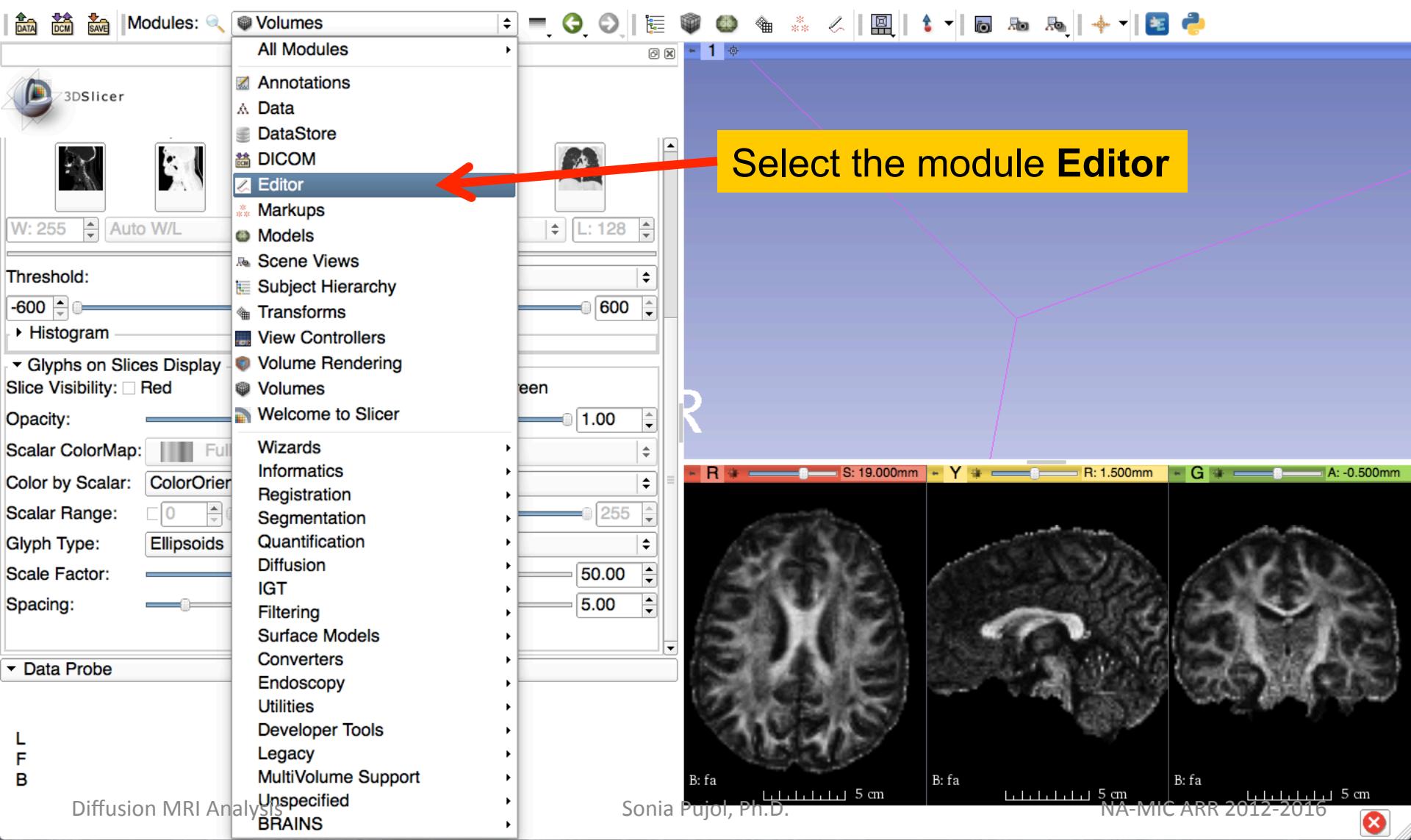


Part 3: From tensors to tracts

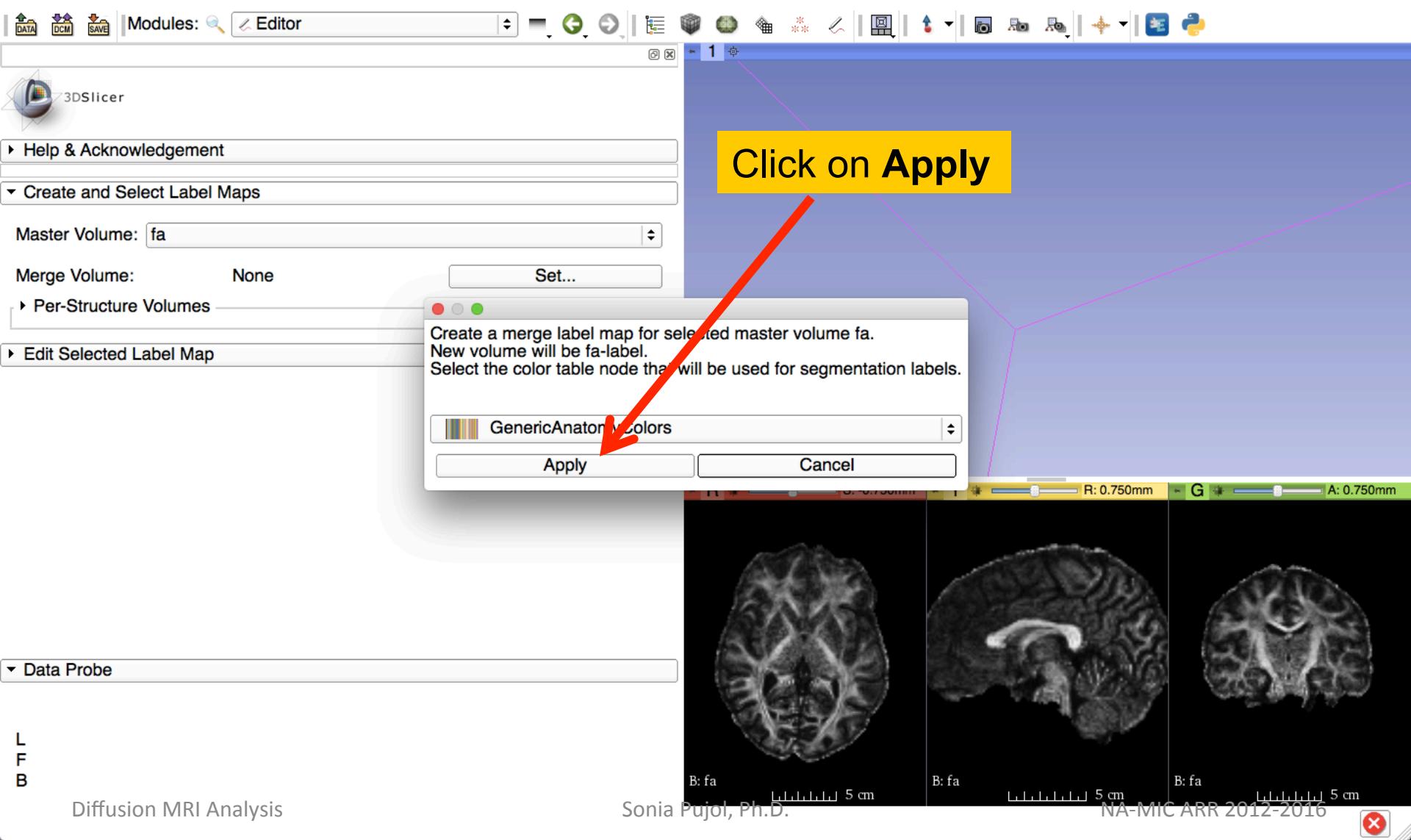
DTI tractography

- Definition of a region of interest (ROI) for seeding tract in an FA map (Editor module)
- Single-tensor tractography (Tractography Interactive Seeding module)
- Fiducial-seeding tractography (Tractography Interactive Seeding module)

Diffusion MRI tractography



Diffusion MRI tractography



Diffusion MRI tractography

Select the **Yellow slice only** layout

Master Volume: fa

Merge Volume: fa-label Set...

Per-Structure Volumes

Edit Selected Label Map

Tools: various icons for selection, segmentation, and measurement.

Undo/Redo:

Active Tool: DefaultTool

Label: tissue 1

Data Probe

L F B

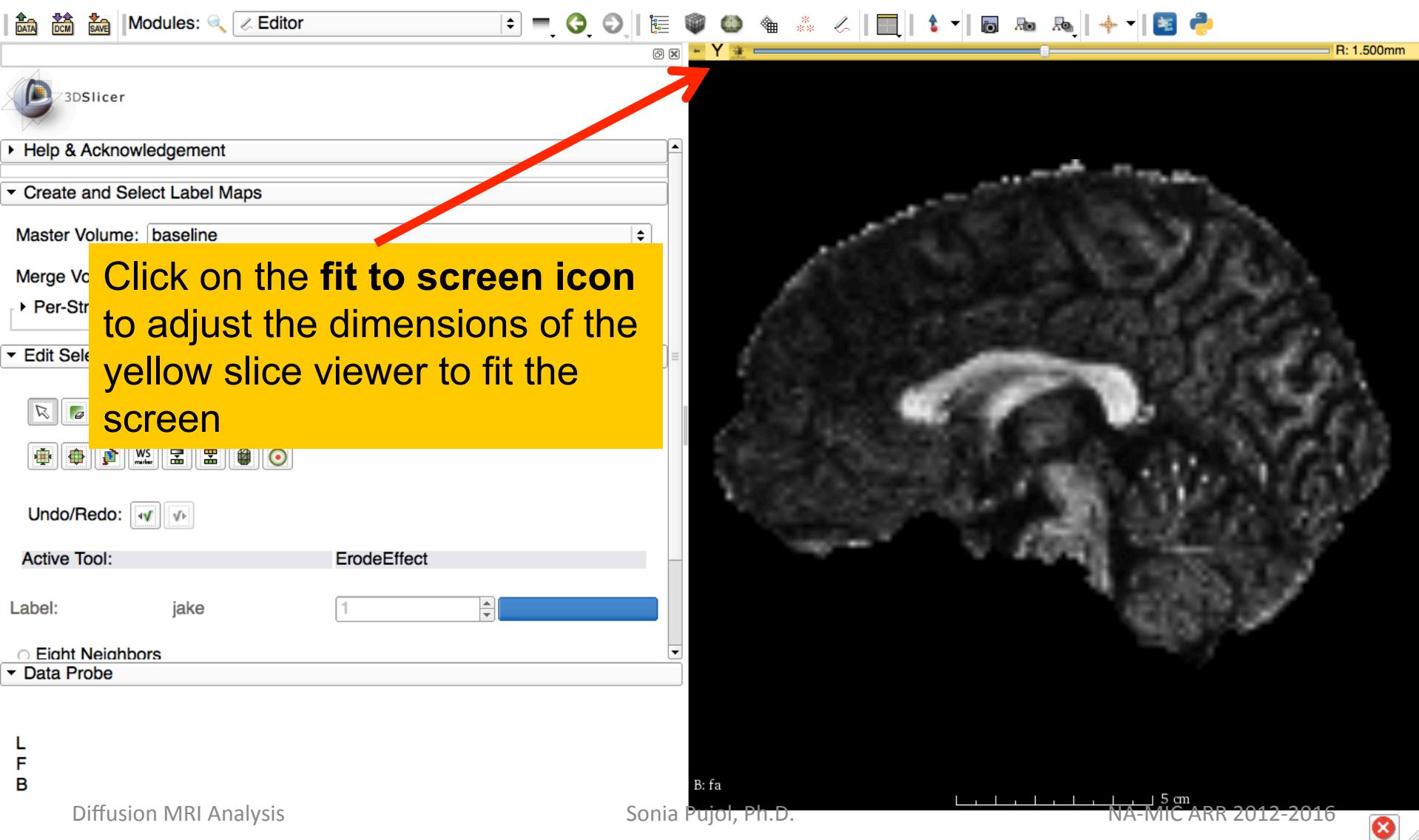
Modules: Editor

Layout Options (Right-click context menu):

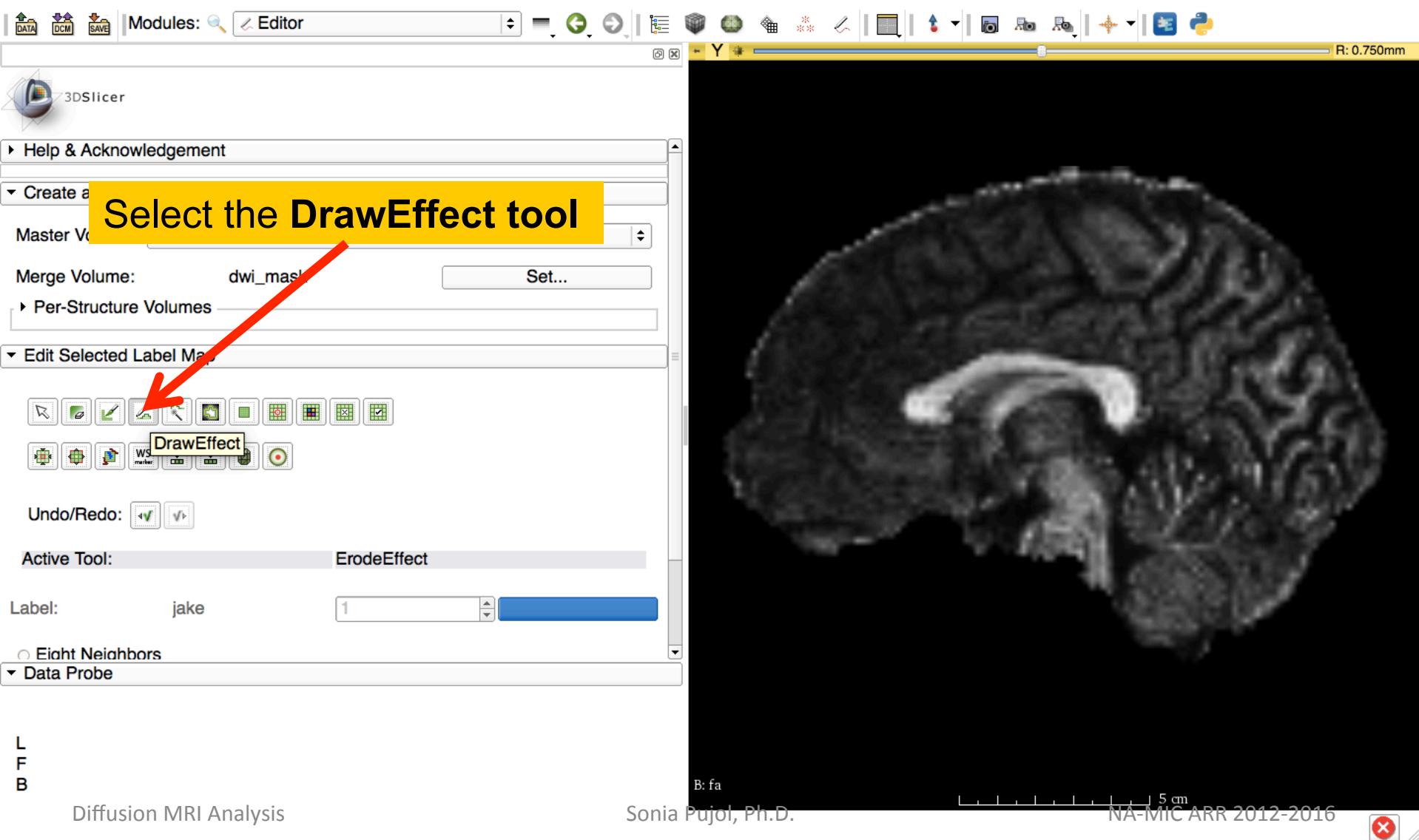
- Conventional
- Conventional Widescreen
- Conventional Quantitative
- Four-Up
- Four-Up Quantitative
- Dual 3D
- Triple 3D
- 3D only
- One-Up Quantitative
- Red slice only
- Yellow slice only** (selected)
- Green slice only
- Tabbed 3D
- Tabbed slice
- Compare
- Compare Widescreen
- Compare Grid
- Three over three
- Three Over Three Quantitative
- Four over four
- Two over Two
- Side by side
- Four by three slice
- Four by two slice
- Three by three slice

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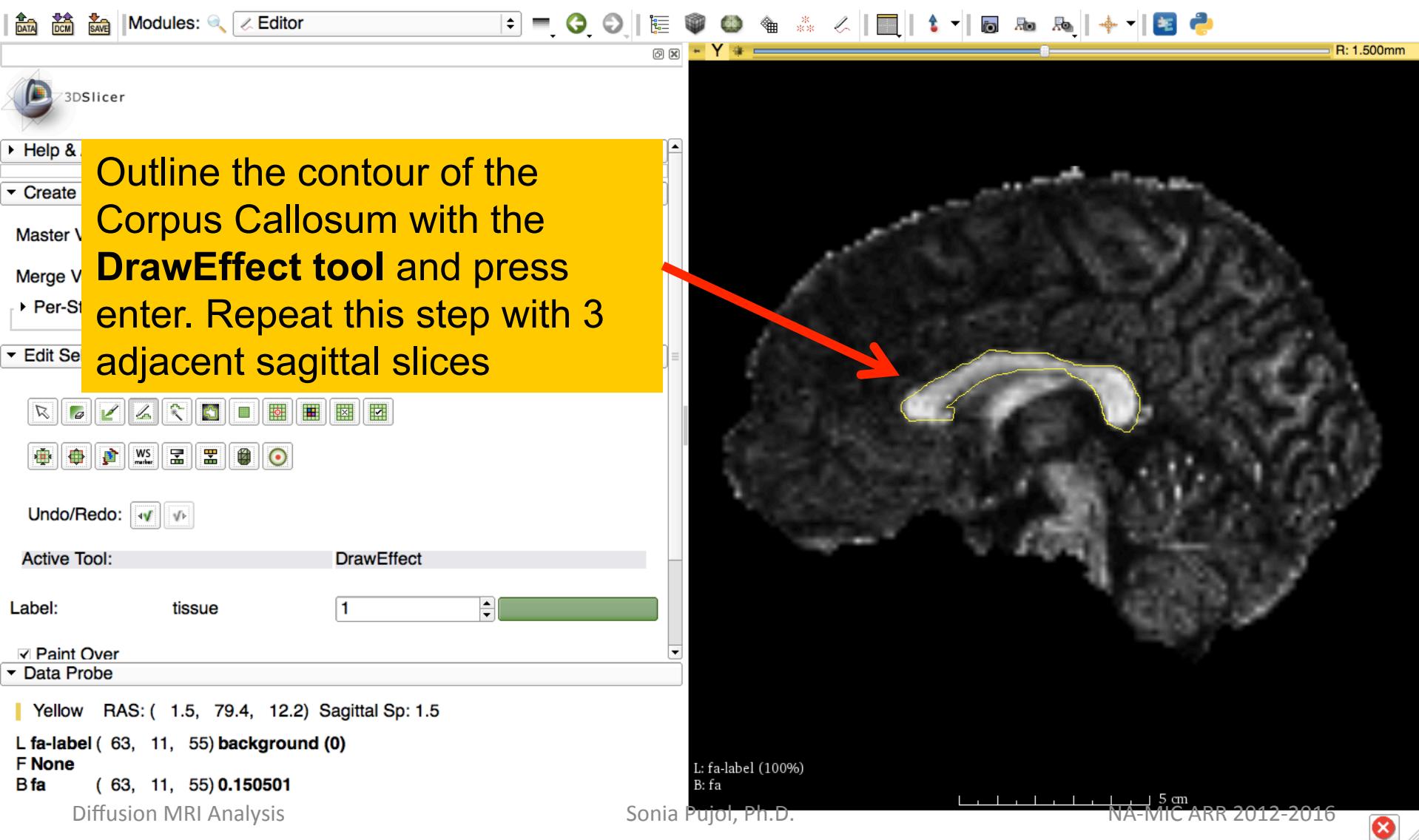
Diffusion MRI tractography



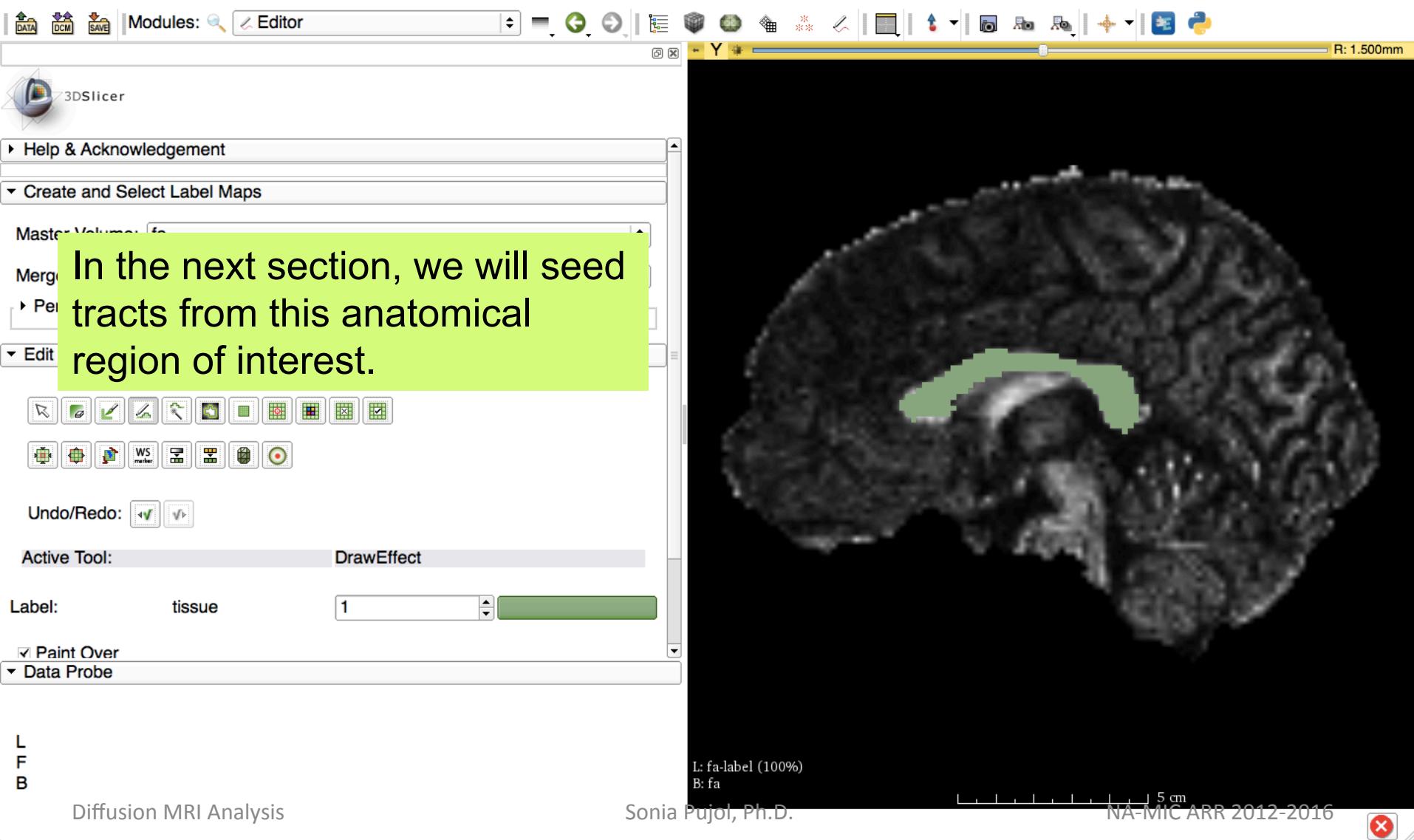
Diffusion MRI tractography



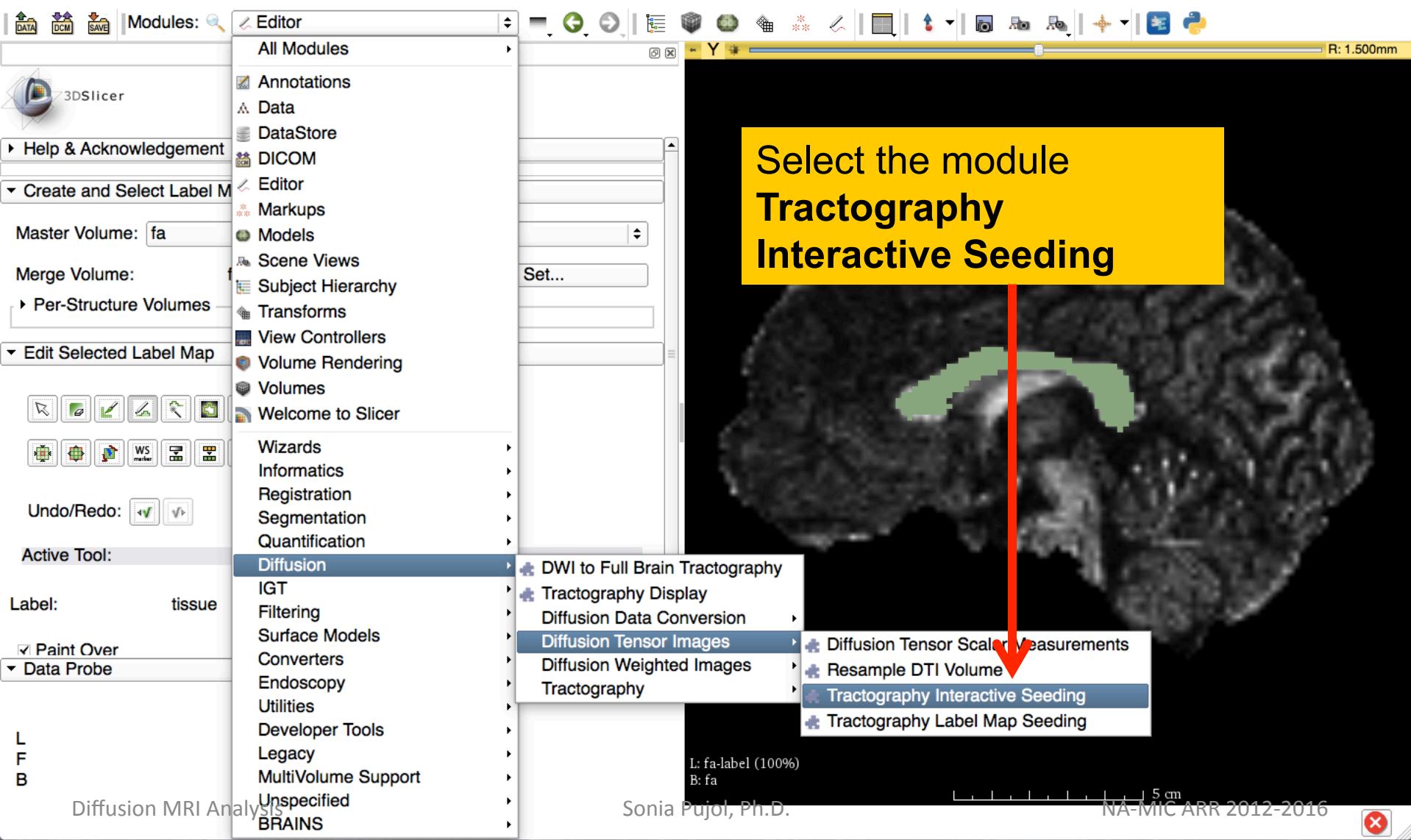
Diffusion MRI tractography



Diffusion MRI tractography



Diffusion MRI tractography



Labelmap Seeding: Step1: I/O

Change to **Conventional** view

R: 1.500mm

Conventional

- Conventional Widescreen
- Conventional Quantitative
- Four-Up
- Four-Up Quantitative
- Dual 3D
- Triple 3D
- 3D only
- One-Up Quantitative
- Red slice only
- Yellow slice only
- Green slice only
- Tabbed 3D
- Tabbed slice
- Compare
- Compare Widescreen
- Compare Grid
- Three over three
- Three Over Three Quantitative
- Four over four
- Two over Two
- Side by side
- Four by three slice
- Four by two slice
- Three by three slice

- Set the **Input DTI Volume** to 'dti'
- Set the **Input Label Map** to 'fa-label'
- Set **Output Fiber Bundle** to 'Create and Rename New Fiber Bundle' and rename it 'corpusCallosum'
- Uncheck **Enable Seeding Tracks**

L
F
B

Diffusion MRI Analysis

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Labelmap Seeding: Step 2: Seeding parameters

The screenshot shows the 3DSlicer interface with the 'Tractography Interactive Seeding' module selected. On the left, the 'Tractography Seeding Parameters' panel is open, displaying various seeding options and tractography parameters. A red box highlights the 'Use index Space' checkbox and the 'Maximum Path Length' slider. Another red box highlights the 'Stopping Criteria' dropdown set to 'Fractional Anisotropy', the 'Stopping Value' slider at 0.15, and the 'Stopping Track Curvature' slider at 0.70. On the right, a 3D brain volume is shown with a green fiber tractography bundle originating from a seed point. The image is labeled with anatomical axes (L/R, A/P, I/S) and a coordinate system (R: 1.500mm, S: 0.000mm, G: 1.500mm).

Select the default Tractography Seeding parameters:

- Check Use index Space
- Stopping Criteria: FractionalAnistropy
- Stopping Value: 0.15

L
F
B

Diffusion MRI Analysis

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Labelmap Seeding: Step 3: Generate Tracts

3DSlicer

Help & Acknowledgement

IO

Parameters FiducialSeedingParameters

Presets Slicer4 Interactive Seeding Defaults

Input DTI Volume dti

Input Fiducials, Model or Label Map fa-label

Output Fiber Bundle corpusCallosum

Enable Seeding Tracts

Label Map Options

Use index Space

Seed Spacing 2.00

Random Grid

Linear Measure Start Threshold 0.30

ROI Label

File Prefix

Data Probe

L
F
B

Diffusion MRI Analysis

Modules: Tractography Interactive Seeding

1

P

A

I

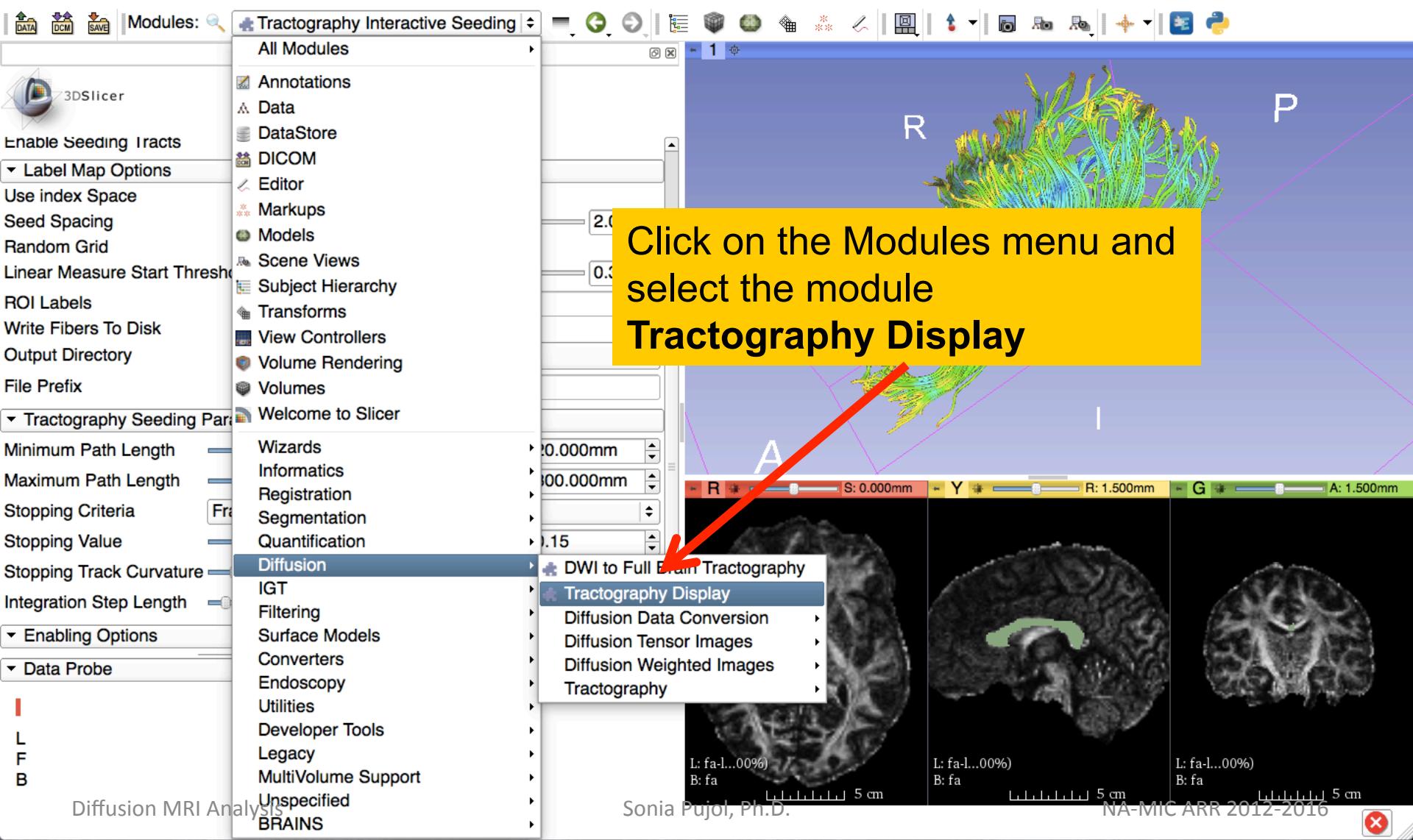
R S: 0.000mm Y: 0.000mm G: 0.000mm A: 1.500mm

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

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Labelmap Seeding: Step 4: Undesirable track removal



Labelmap Seeding: Step 4: Undesirable track removal

3DSlicer

Modules: Tractography Display

Help & Acknowledgement

Simple Display

Solid Tube Color

Name: corpusCallosum

Lines Tubes Tubes Slice

Percentage of Fibers Shown: 100%

Fiber Bundle Selection

ROI for Fiber Selection: ROI Node

Disable ROI Positive ROI Negative ROI

Interactive ROI ROI Visibility

Extract Bundle From ROI: None

Update corpusCallosum From ROI: Confirm update

Enable Interactive Edit

Advanced Display

Data Probe

L F B

Set ROI for Fiber Select to 'ROI node'

R P A

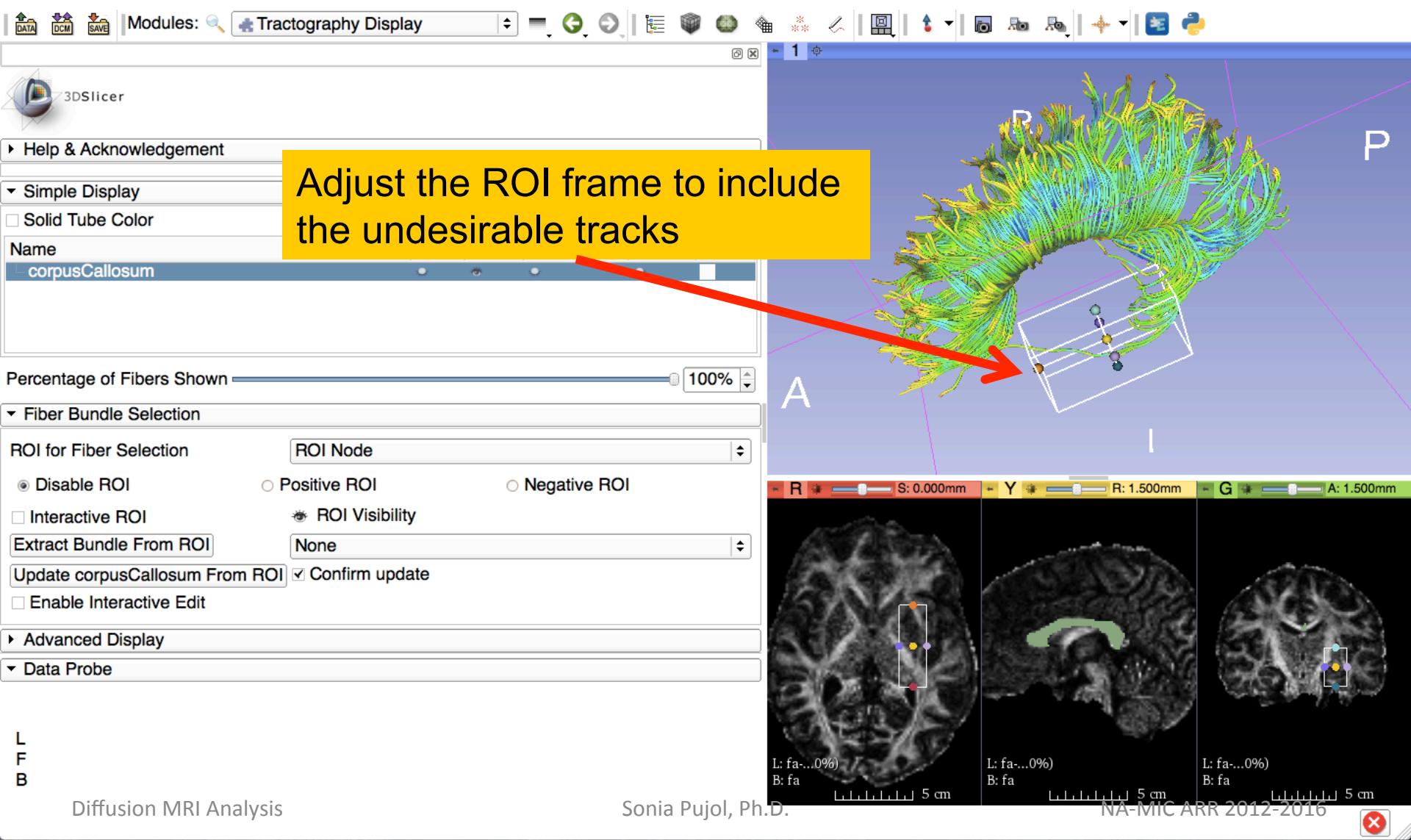
S: 0.000mm Y R: 1.500mm G A: 1.500mm

Diffusion MRI Analysis

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Labelmap Seeding: Step 4: Undesirable track removal



Labelmap Seeding: Step 4: Undesirable track removal

DATA DCM SAVE Modules: Tractography Display

3DSlicer

Help & Acknowledgments Simple Display Solid Tube Color

Name corpusCallosum Lines Tubes Tubes Slice Glyphs Tubes

Percentage of Fibers Shown 100%

Fiber Bundle Selection

ROI for Fiber Selection

Disable ROI Positive ROI Negative ROI

Interactive ROI ROI Visibility

Extract Bundle From ROI None

Update corpusCallosum From ROI Confirm update

Enable Interactive Edit

Advanced Display

Data Probe

L F B

Click on Negative ROI to finish

The image shows the 3DSlicer software interface. On the left, a control panel for 'Tractography Display' includes settings for 'Name' (corpusCallosum), 'Percentage of Fibers Shown' (100%), and 'Fiber Bundle Selection' (set to 'Negative ROI'). A yellow box highlights the 'Negative ROI' button with the instruction 'Click on Negative ROI to finish'. A red arrow points from this text to the 'Negative ROI' button. On the right, a 3D brain model displays colored tracts (yellow, green, blue) representing fiber bundles. A white rectangular ROI is overlaid on the brain, with a red arrow pointing to its center. Below the 3D view are three 2D axial slices of the brain, each showing a small white ROI. The bottom right corner contains the text 'NA-MIC ARR 2012-2016'.

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Diffusion MRI Analysis

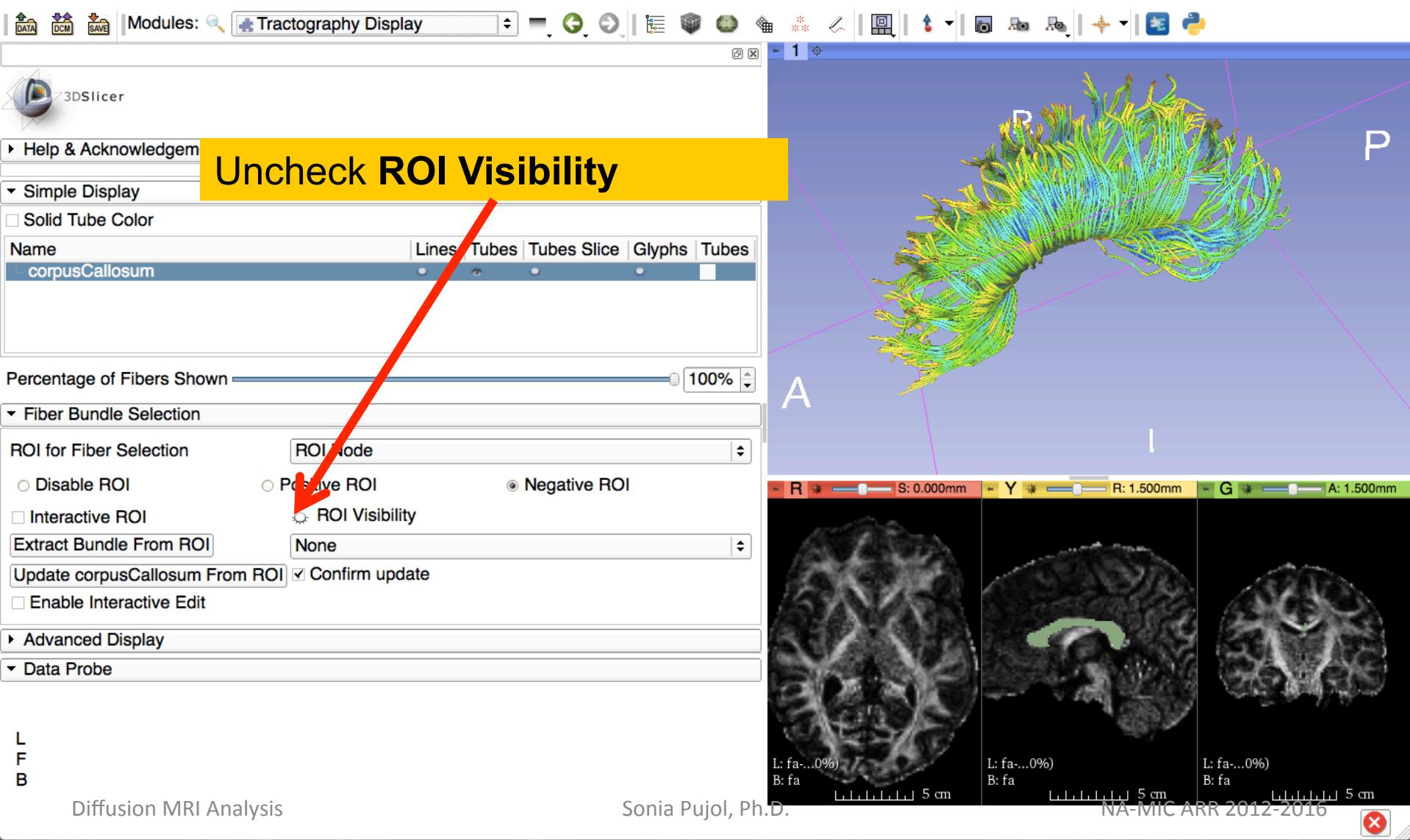
R S: 0.00mm Y R: 1.500mm G A: 1.500mm

L: fa...0% B: fa L: fa...0% B: fa L: fa...0% B: fa

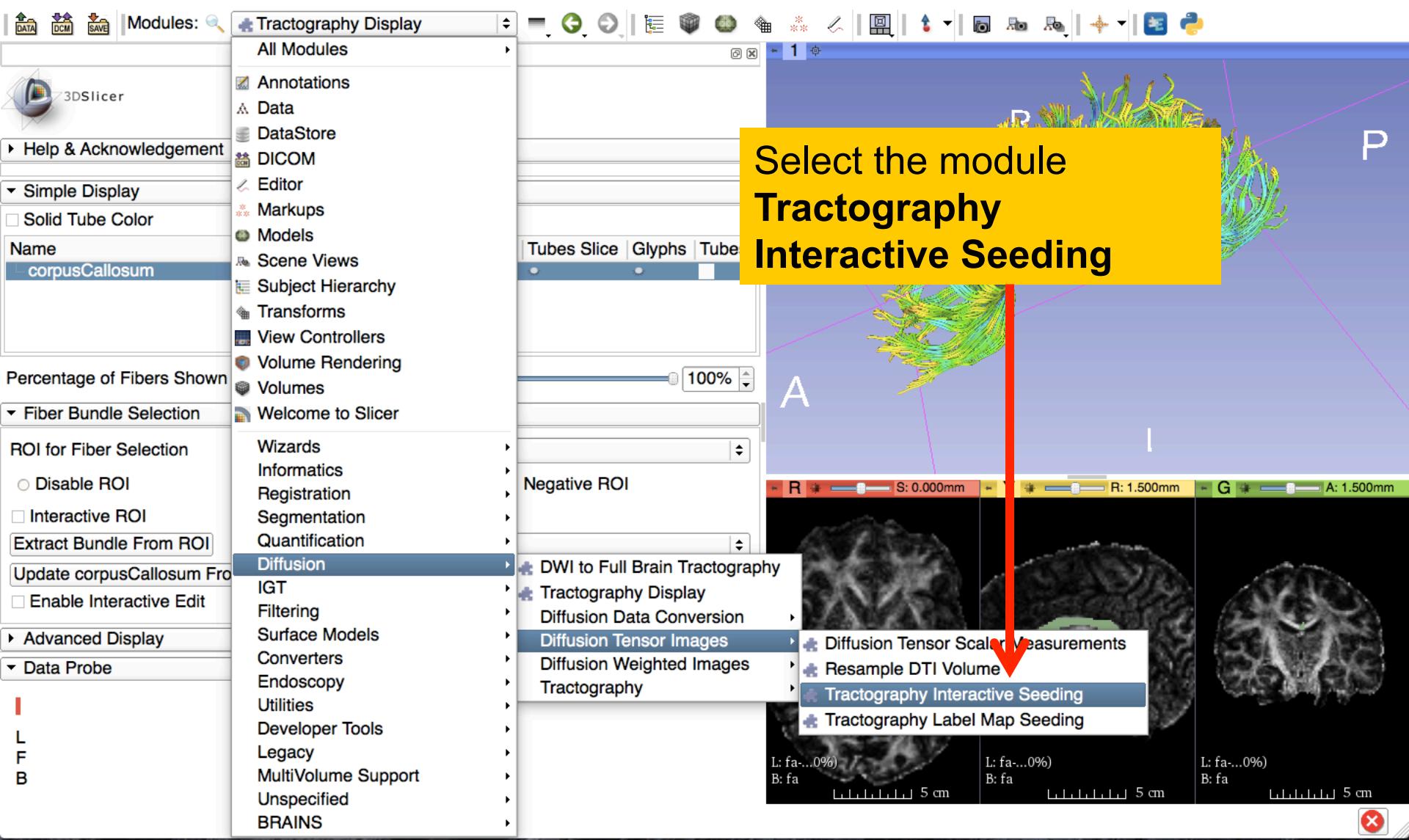
5 cm 5 cm 5 cm

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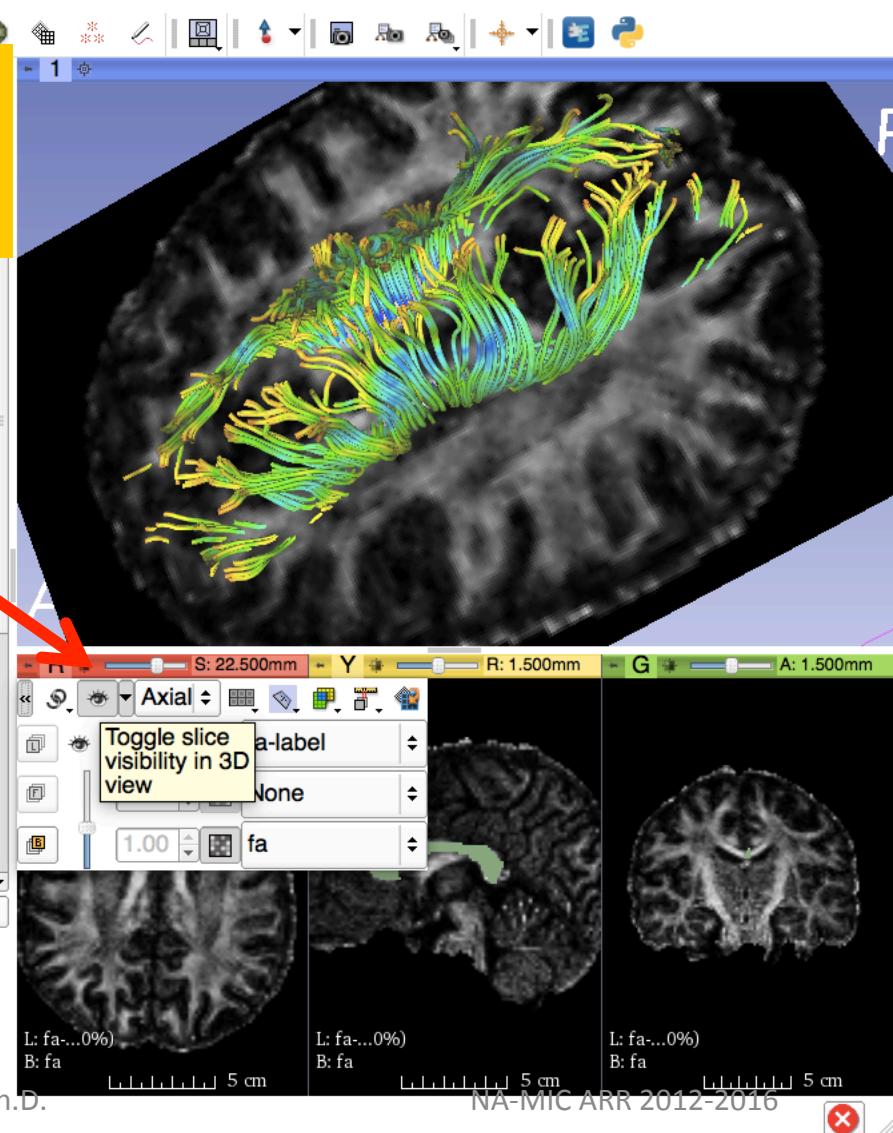
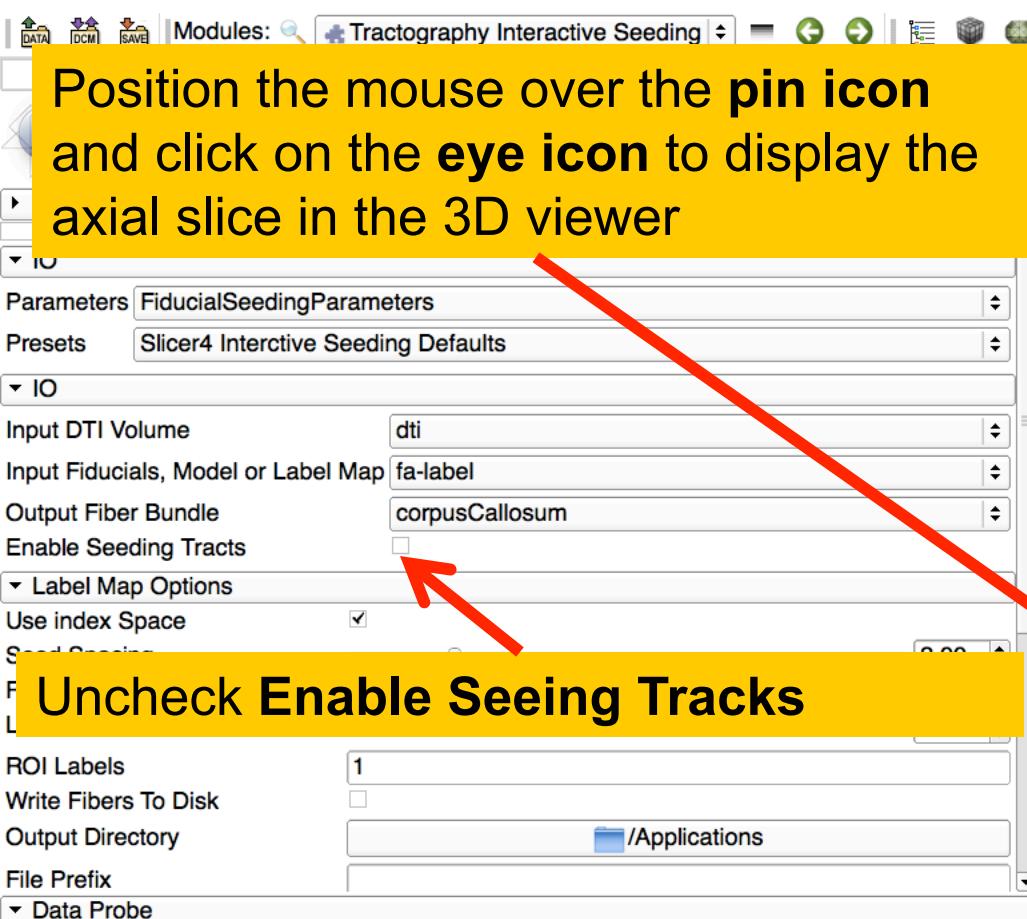
Labelmap Seeding: Step 4: Undesirable track removal



Labelmap Seeding: Tracts



Tractography Results



Fiducial Seeding

DATA DCM SAVE Modules: Tractography Interactive Seeding

All Modules

- Annotations
- Data
- DataStore
- DICOM
- Editor
- Markups**
- Models
- Scene Views
- Subject Hierarchy
- Transforms
- View Controllers
- Volume Rendering
- Volumes
- Welcome to Slicer

Wizards

Informatics

Registration

Segmentation

Quantification

Diffusion

IGT

Filtering

Surface Models

Converters

Endoscopy

Utilities

Developer Tools

Legacy

MultiVolume Support

Unspecified

BRAINS

3DSlicer

Help & Acknowledgement

IO

Parameters FiducialSeeding

Presets Slicer4 Interactive

Input DTI Volume

Input Fiducials, Model or Label

Output Fiber Bundle

Enable Seeding Tracts

Label Map Options

Use index Space

Seed Spacing

Random Grid

Linear Measure Start Threshold

ROI Labels

Write Fibers To Disk

Output Directory

File Prefix

Data Probe

L
F
B

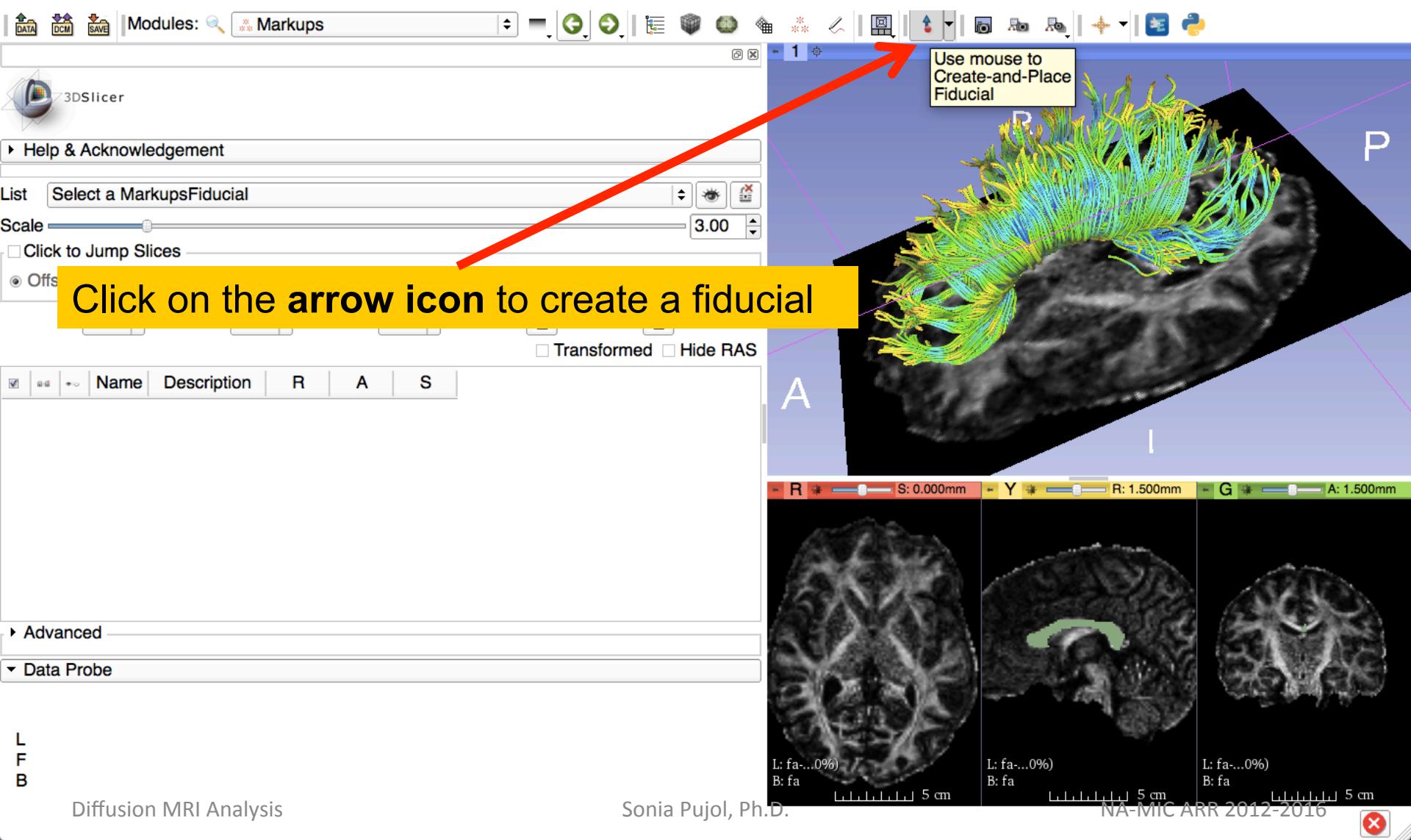
Diffusion MRI Analysis

Select the module **Markups**

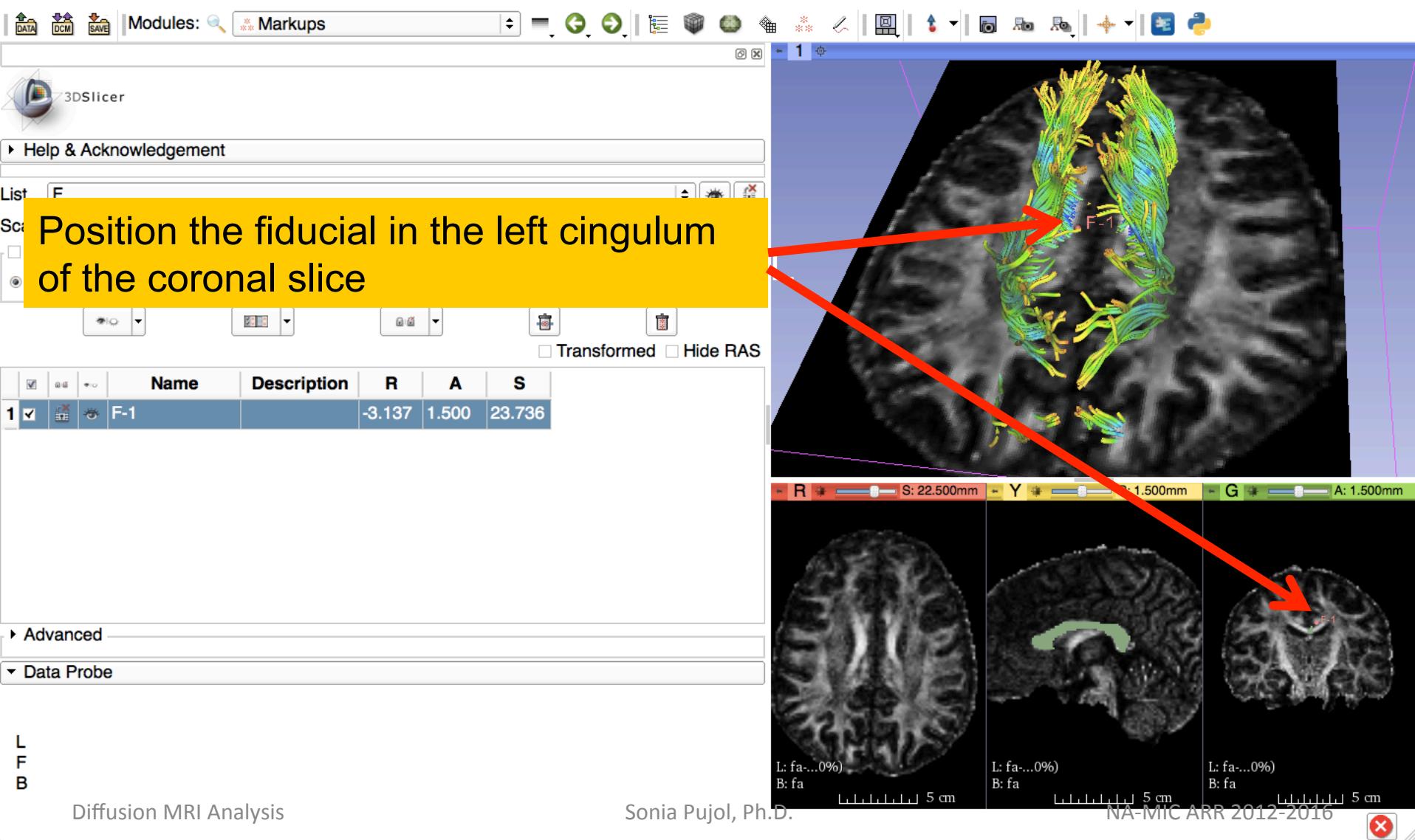
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Fiducial Seeding



Fiducial Seeding



Fiducial Seeding

Double click on the fiducial and change the name to **LeftCingulum**

The screenshot shows the 3D Slicer interface. On the left, a table lists a single fiducial entry:

| | Name | Description | R | A | S |
|---|--------------|-------------|--------|-------|--------|
| 1 | LeftCingulum | | -3.137 | 1.500 | 23.736 |

A red arrow points from the 'Description' column to the text 'Double click on the fiducial and change the name to **LeftCingulum**'. Another red arrow points from the 'LeftCingulum' label in the table to the corresponding label on the brain segmentation. A third red arrow points from the 'LeftCingulum' label in the table to the same label in the bottom right brain slice.

3DSlicer

Help & Acknowledgement

Transformed Hide RAS

Advanced

Data Probe

L F B

Diffusion MRI Analysis

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Fiducial Seeding

Select the module **Tractography Interactive Seeding**

Set the Input DTI volume to '**dti**'
Set the Input **Fiducials, Model or Label Map** to '**F**'
Select the Output Fiber Bundle 'Create New Fiber Bundle' and rename it '**Cingulum**'
Check **Enable Seeing Tracks**

3DSlicer

DATA DCM SAVE Modules: Tractography Interactive Seeding

Help & Acknowledgement

IO

Parameters FiducialSeedingParameters

Presets Slicer4 Interctive Seeding Defaults

Input DTI Volume dti

Input Fiducials, Model or Label Map F

Output Fiber Bundle Cingulum

Enable Seeding Tracts

Seed Placement Options

Fiducial Region Size 2.50mm

Fiducial Seeding Step Size 1.00mm

Seed Selected Fiducials

Max Number of Seeds 100

Data Probe

L F B

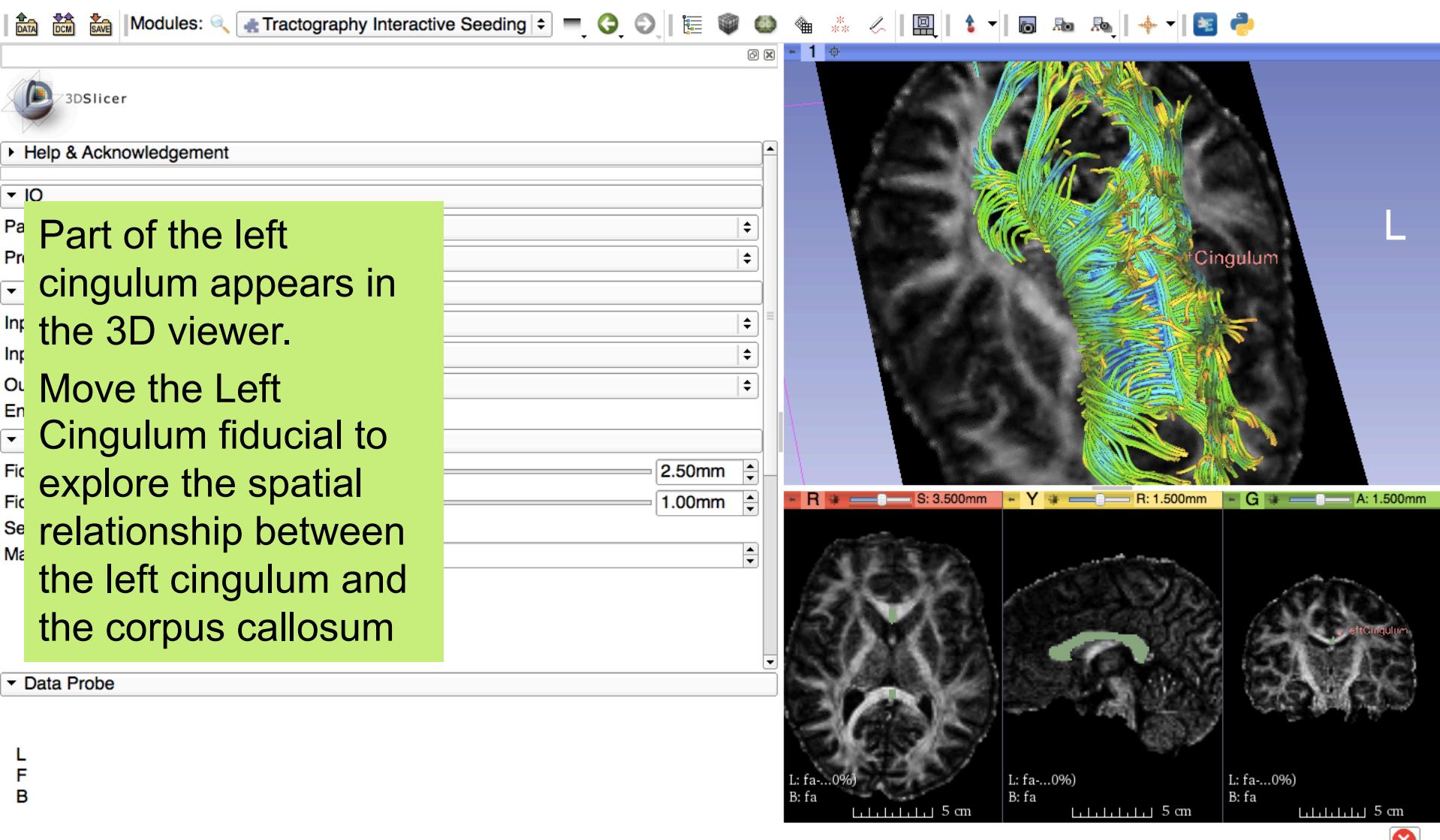
Diffusion MRI Analysis

B: fa 5 cm B: fa 5 cm B: fa 5 cm

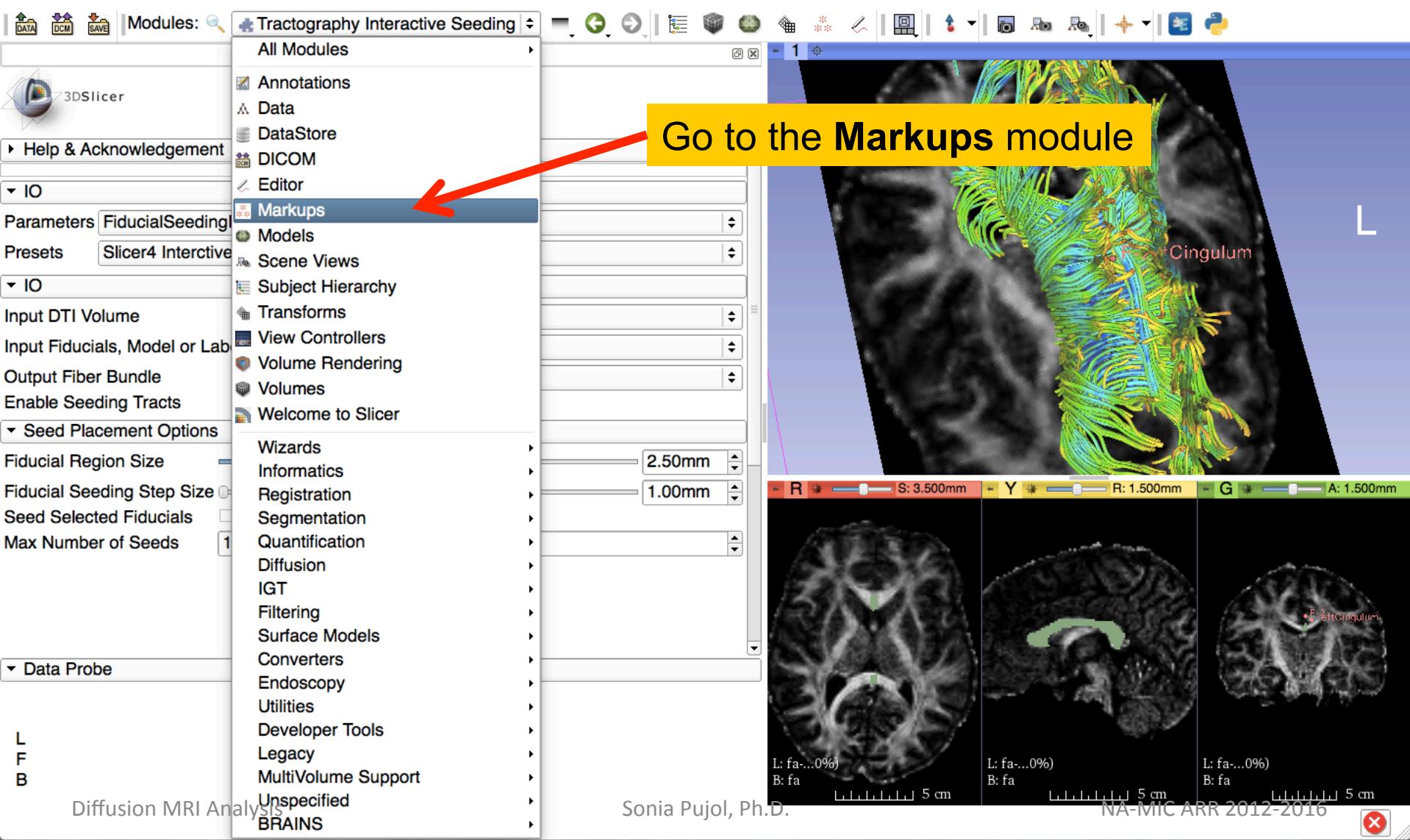
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Fiducial Seeding



Fiducial Seeding



Fiducial Seeding

The screenshot shows the 3DSlicer software interface for diffusion MRI analysis. The top menu bar includes modules like DATA, DCM, and SAVE, and MARKUPS. The main window displays a 3D brain volume with colored tracts representing white matter fibers. A red arrow points from the text instructions to the 'RightCingulum' entry in the list table. Another red arrow points from the text instructions to the 3D brain visualization.

3DSlicer

Help & Acknowledgement

List F

Scale 3.00

Click to Jump Slices

Offset Centered Show Slice Intersections

Transformed Hide RAS

| | Name | Description | R | A | S |
|---|---------------|-------------|--------|-------|---|
| 1 | LeftCingulum | | -4.691 | 1.500 | |
| 2 | RightCingulum | | 10.057 | 1.500 | |

Advanced

Data Probe

L
F
B

Double click on the Name and change it to **RightCingulum**

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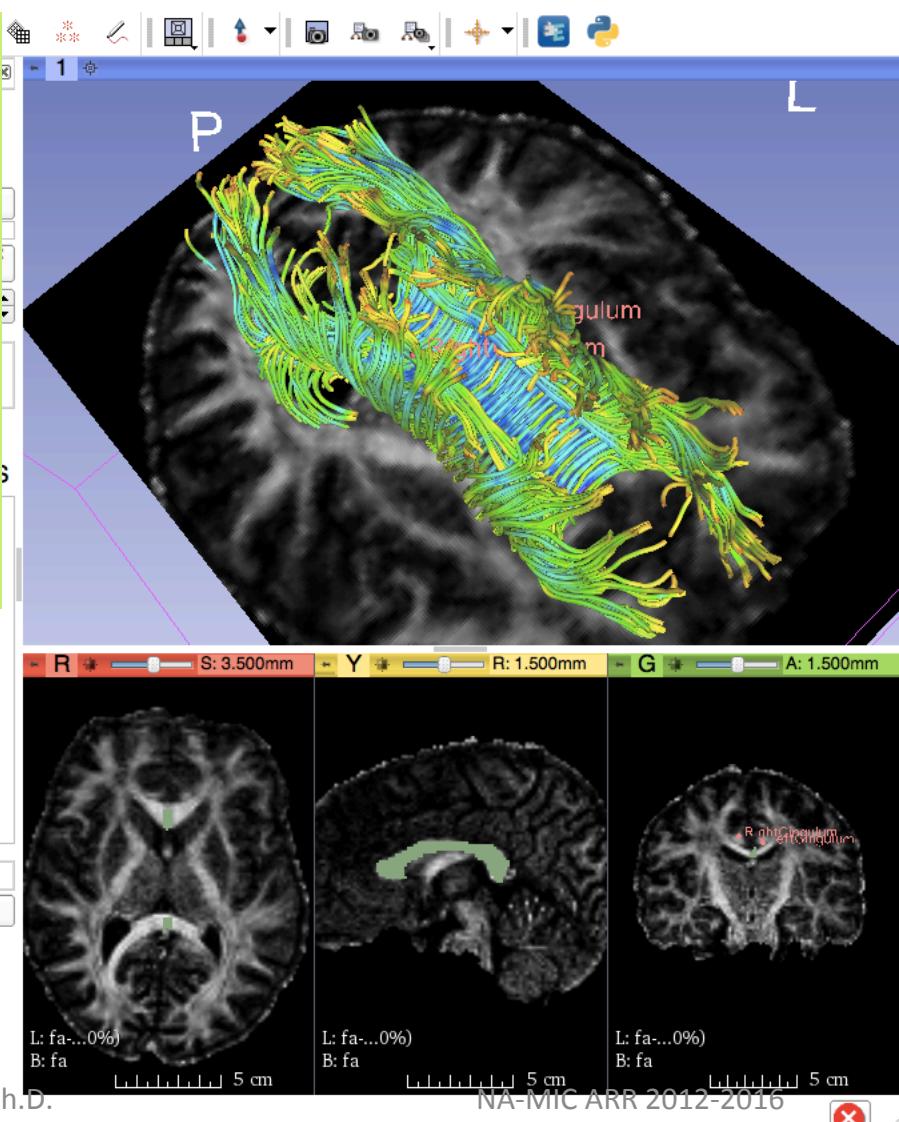
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Fiducial Seeding

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

| | Name | Description |
|---|---------------|-------------|
| 1 | LeftCingulum | |
| 2 | RightCingulum | |



Fiducial Seeding

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

The screenshot shows the 3DSlicer interface. On the left, a table lists three fiducials: LeftCingulum, RightCingulum, and F-3. The F-3 entry has a red arrow pointing to it from the yellow callout box. The main window displays a 3D brain model with colored tracts (green, blue, yellow) and a red arrow pointing to the F-3 fiducial. Below the 3D viewer are three 2D axial slices showing the brain. The bottom right corner contains the text "NA-MIC ARR 2012-2016".

| | Name | Description | R | A | S |
|---|---------------|-------------|--------|--------|--------|
| 1 | LeftCingulum | | -4.691 | 1.500 | 24.513 |
| 2 | RightCingulum | | 9.301 | 1.500 | 27.622 |
| 3 | F-3 | | 36.616 | -6.073 | -5.171 |

Advanced

Data Probe

L
F
B

Diffusion MRI Analysis

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Fiducial Seeding

3DSlicer

Help & Acknowledgement

List F

Scale 3.00

Click to Jump Slices

Offset Centered Show Slice Intersections

Transformed Hide RAS

| | Name | Description | R | A | S |
|---|---------------|-------------|--------|-------|--------|
| 1 | LeftCingulum | | -4.691 | 1.500 | 24.513 |
| 2 | RightCingulum | | 9.301 | 1.500 | 27.622 |
| 3 | | | | | -6.937 |

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

Advanced

Data Probe

L F B

Diffusion MRI Analysis

1 P L

R S: -16.500mm Y R: 1.500mm G A: 1.500mm

L: fa...% B: fa 5 cm

L: fa...% B: fa 5 cm

L: fa...% B: fa 5 cm

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Tractography ‘on-the-fly’

The screenshot shows the 3DSlicer interface with various modules and tools. On the left, a table lists three fiducial points: LeftCingulum, RightCingulum, and F-3. The main window displays a 3D brain volume with colored tracts (green, blue, yellow) representing white matter pathways. A green callout box contains the text: "The Fiducial Seeding functionality allows you to do tractography ‘on-the-fly’ to explore white matter structures interactively". Below the main window, two axial MRI slices show the seeding points. The bottom right corner features the text "NA-MIC ARR 2012-2016".

3DSlicer

Help & Acknowledgement

List F

Scale 3.00

Click to Jump Slices

Offset Centered Show Slice Intersections

Transformed Hide RAS

| | Name | Description | R | A | S |
|---|---------------|-------------|--------|--------|--------|
| 1 | LeftCingulum | | -4.691 | 1.500 | 24.513 |
| 2 | RightCingulum | | 9.301 | 1.500 | 27.622 |
| 3 | F-3 | | 35.306 | -3.916 | -5.110 |

Advanced

Data Probe

L
F
B

Diffusion MRI Analysis

P L

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

nm G A: 1.500mm

L: fa...0% B: fa 5 cm

L: fa...0% B: fa 5 cm

L: fa...0% B: fa 5 cm

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DTI Analysis

3DSlicer

DATA DCM SAVE Modules: Data

Help & Acknowledgement

Display & Modify Scene

Nodes

- Scene
- View1
- Red
- Yellow
- Green
- Default Scene Camera
- dwi
- baseline
- dwi_mask
- dti
- fa
- trace
- fa-label
- All Annotations
- ROI Node
- ROI List
- corpusCallosum
- F
- Cingulum

Scene Model: Transform

Display MRML ID's

Show Hidden nodes

Data Probe

L F B

Volume

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

P L

R S: -16.500mm Y R: 1.500mm G A: 1.500mm

L: fa...0% B: fa 5 cm

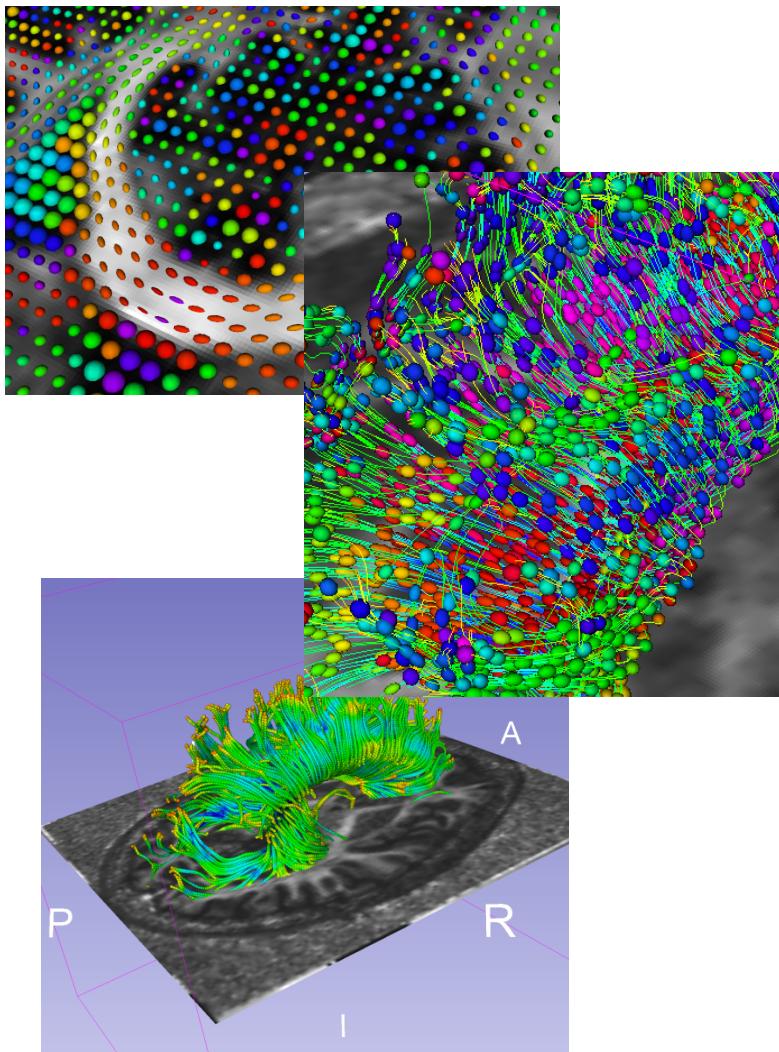
L: fa...0% B: fa 5 cm

L: fa...0% B: fa 5 cm

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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 3D architecture of the brain white matter.

Acknowledgments



- Neuroimage Analysis Center (NAC)
NIH P41RR013218
- National Alliance for Medical Image Computing (NA-MIC)
NIH U54EB005149
- Martin Styner, Ph.D., University of North Carolina at Chapel Hill
- Fan Zhang, MSc., University of Sydney