



Diffusion MRI Analysis: from images to tracts

Sonia Pujol, Ph.D.

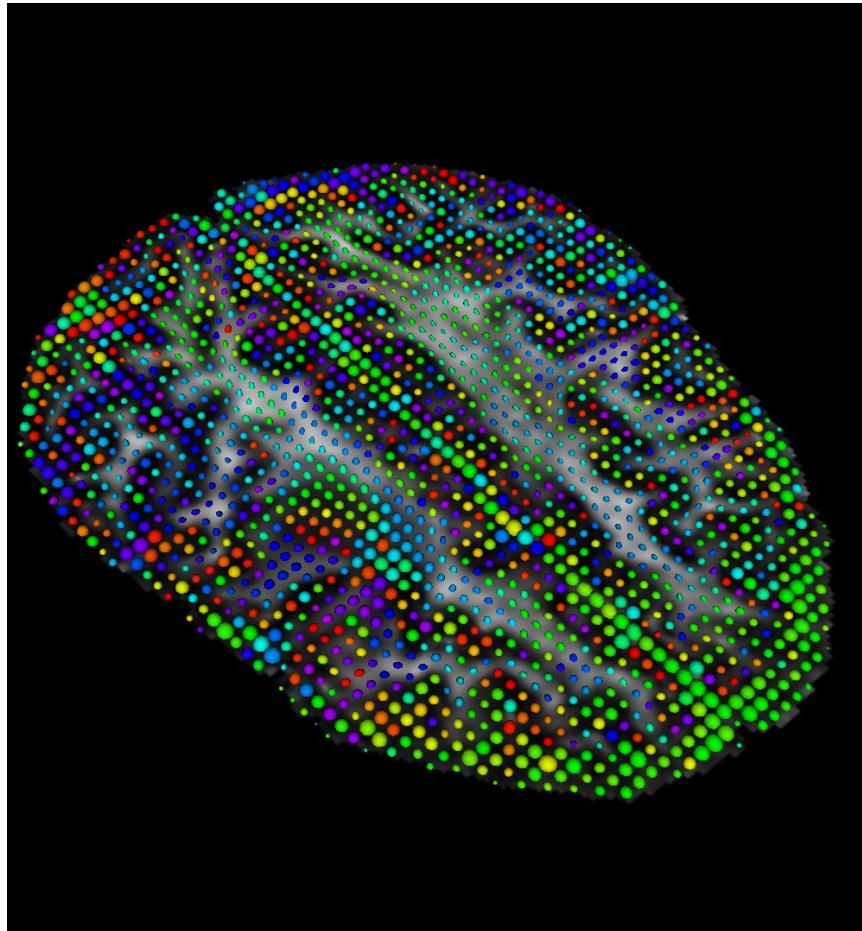
Surgical Planning Laboratory
Harvard University

Brain Anatomy



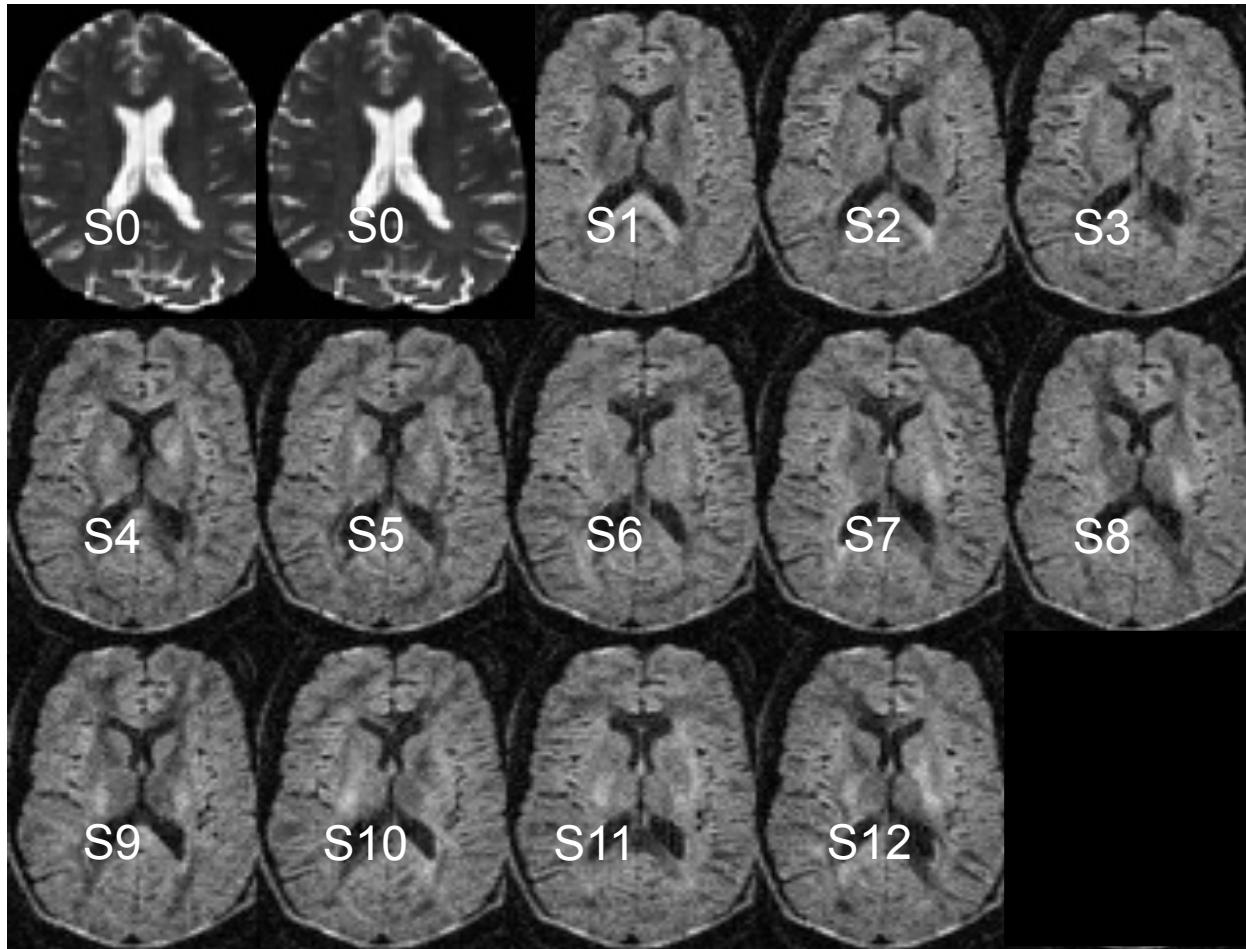
- White matter represents 45% of the brain, and is composed of myelinated nerve fibers

Diffusion MR Imaging



- 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

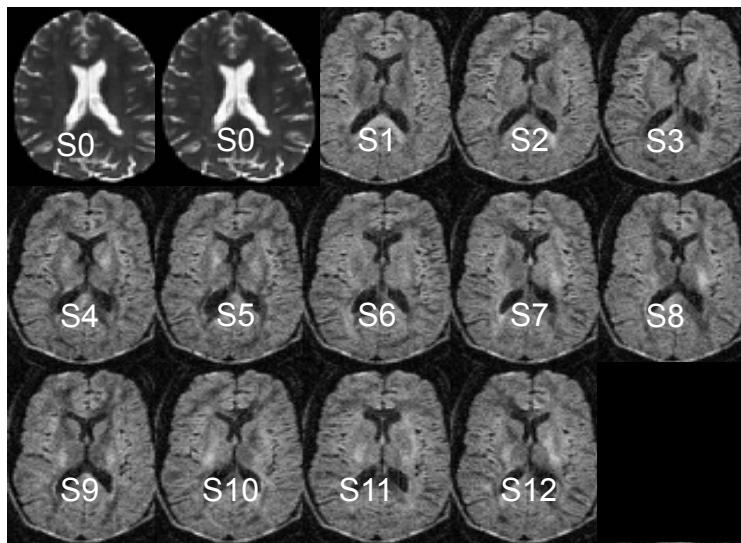
Diffusion Weighted Imaging (DWI)



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

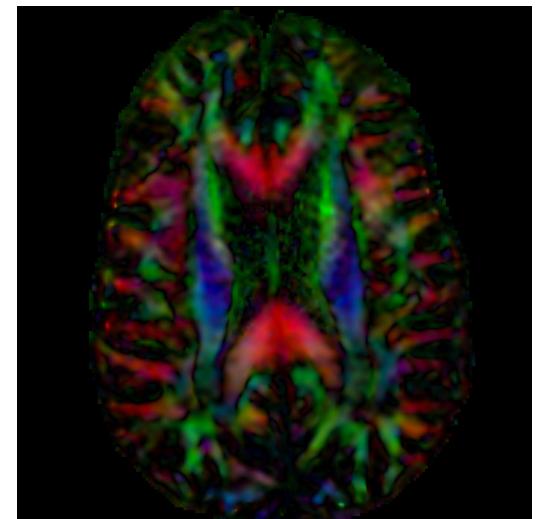
From DWI to DTI

DWI



DWI dataset acquired with
12 gradients and 2
baselines

DTI



DTI dataset

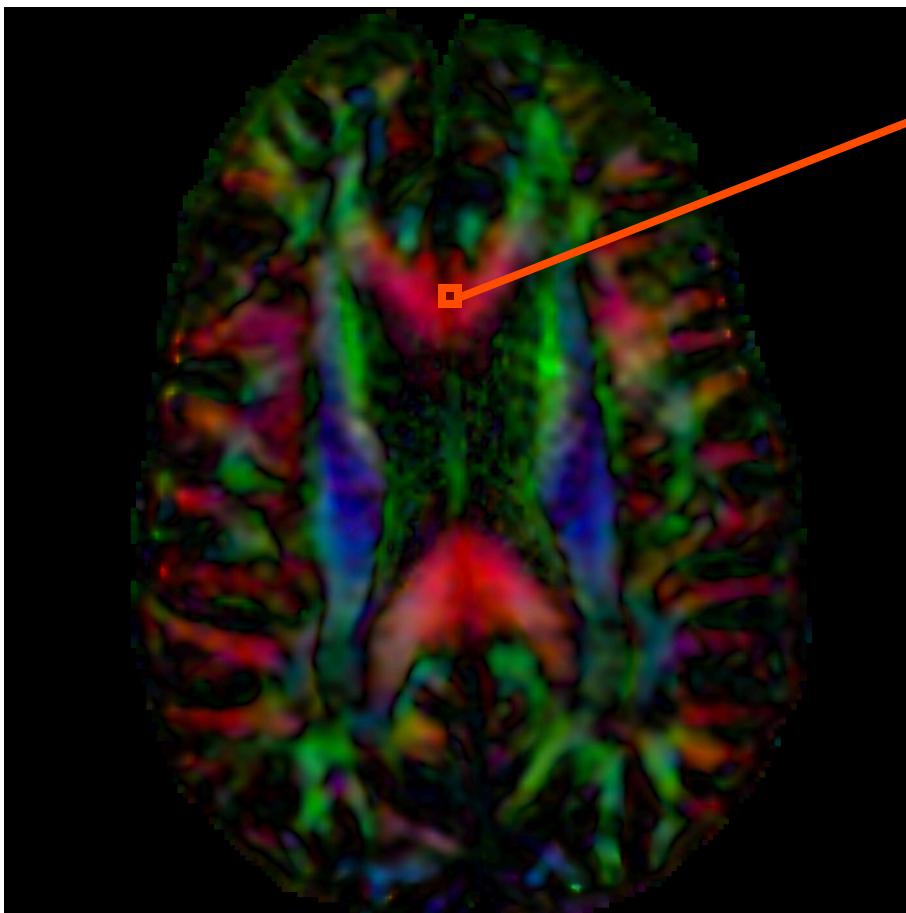


$$S_i = S_0 e^{-b \hat{g}^T \underline{D} \hat{g}_i}$$

Stejskal-Tanner (1965)

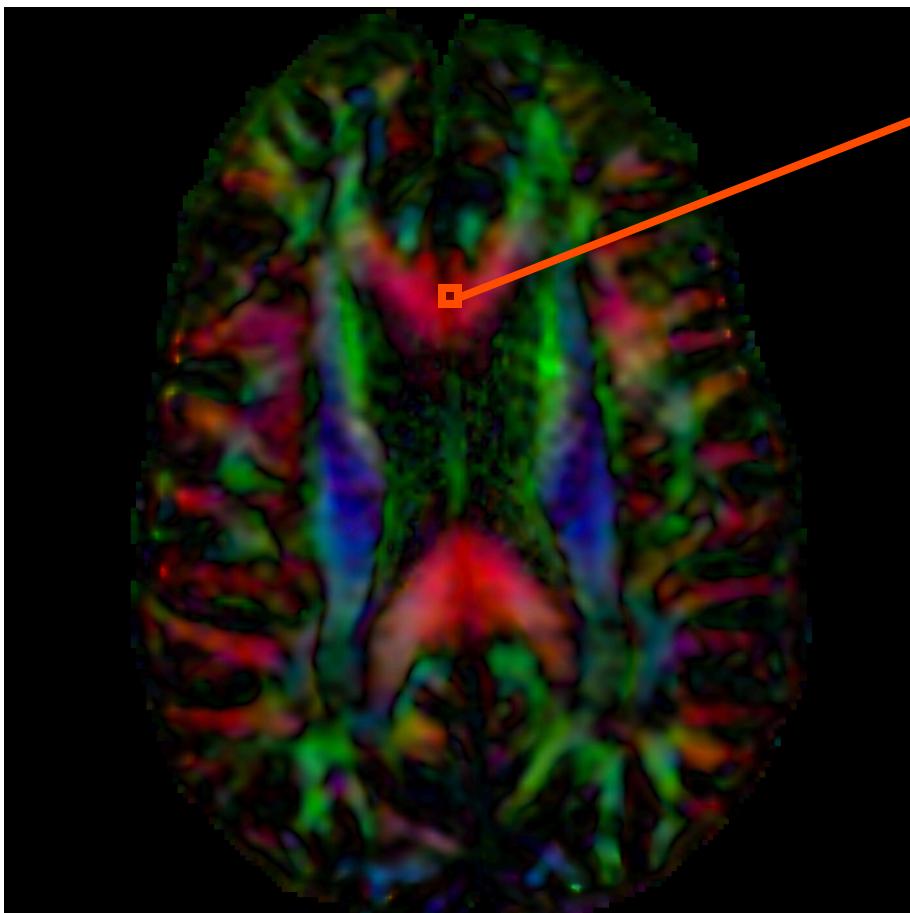
*S_i: DWI volume acquired with
ith gradient
S₀: Baseline volume*

Diffusion Tensor Imaging



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

Diffusion Tensor Imaging

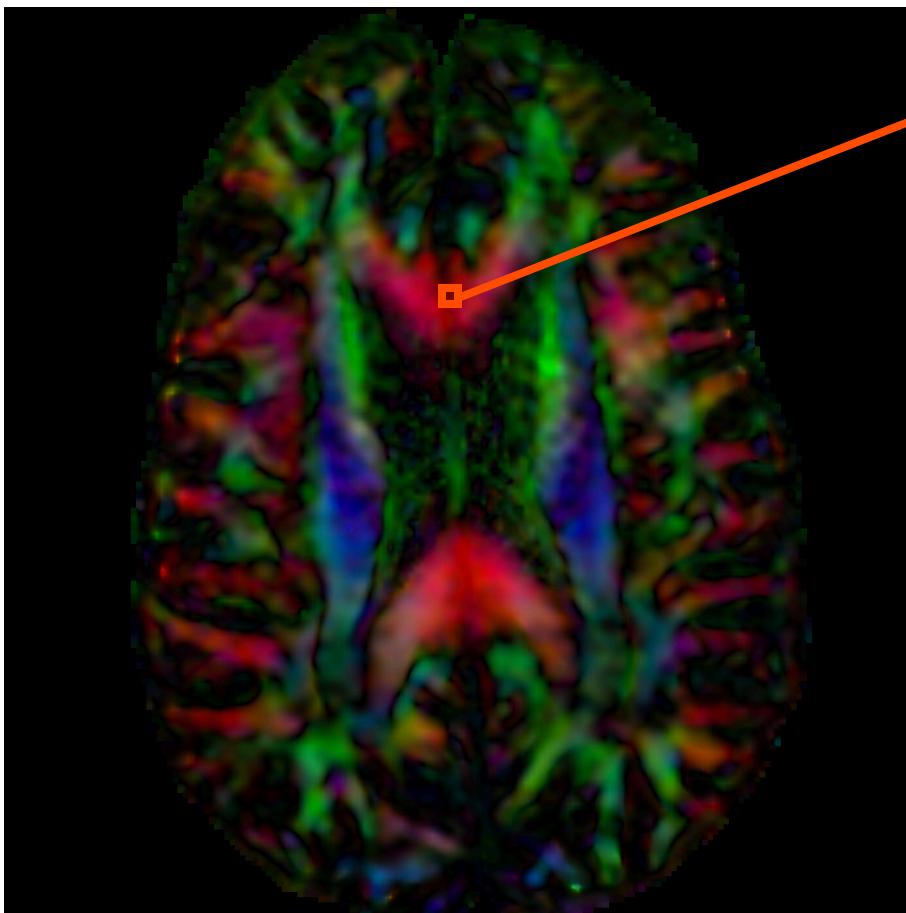


$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$

↓

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

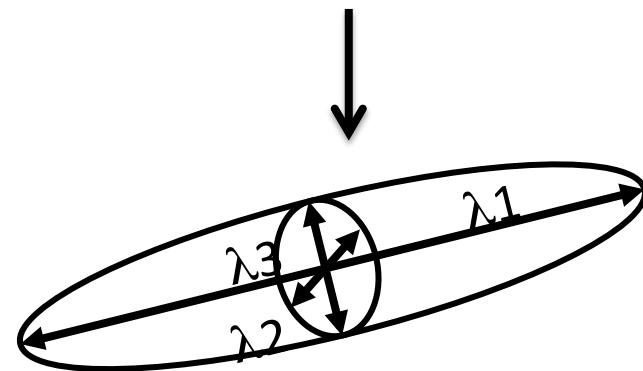
Diffusion Tensor Imaging



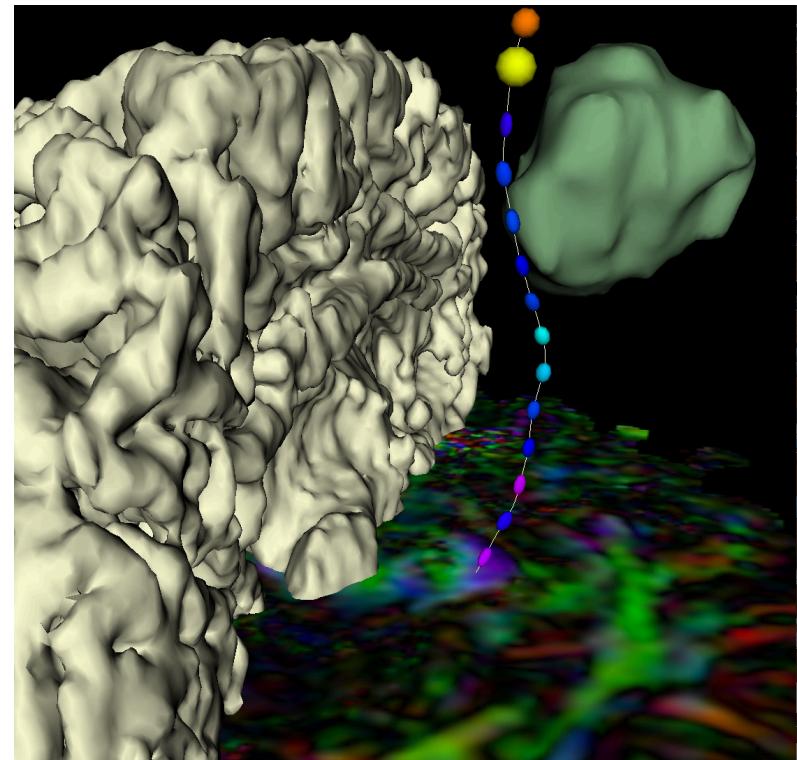
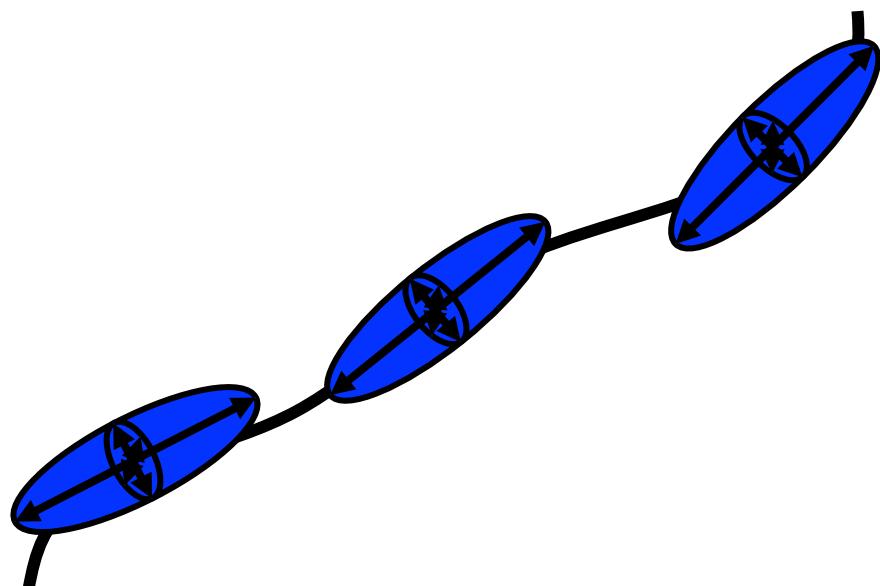
$$S_i = S_0 e^{-b \hat{g}^T \underline{D} \hat{g}_i}$$

↓

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

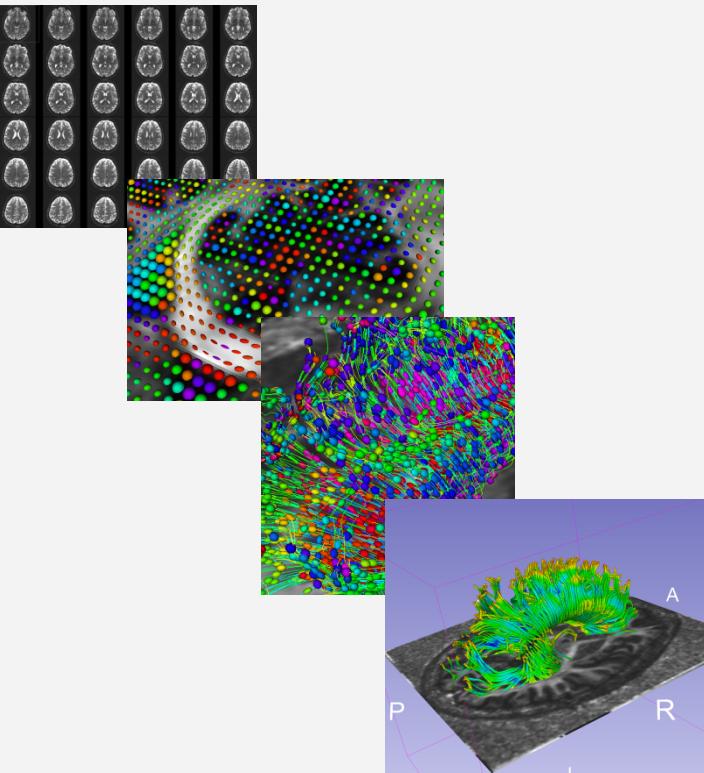


Tractography



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

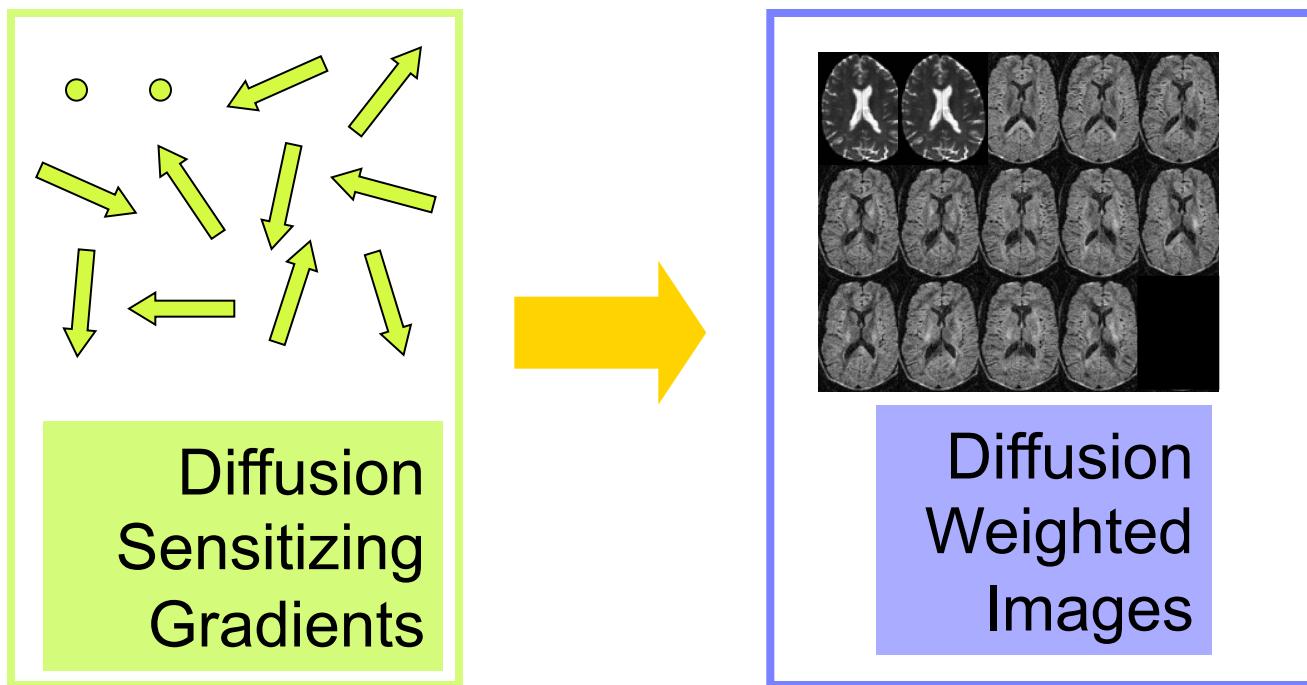
Tutorial Outline



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

Tutorial Dataset

The tutorial dataset is a Diffusion Weighted MR scan of the brain acquired with 41 gradient directions and one baseline (Data source: UNC Chapel Hill)



Tutorial Software

The tutorial uses the 3D Slicer (Version 4.4.0r24272) software available at

[http://www.na-mic.org/Wiki/index.php/
3DSlicer_4.4_r24272](http://www.na-mic.org/Wiki/index.php/3DSlicer_4.4_r24272)

Disclaimer

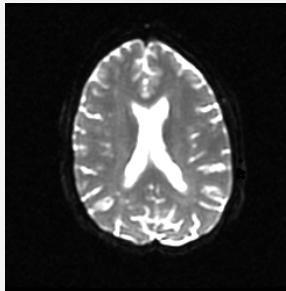
It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules. Slicer is a tool for research, and is not FDA approved.

Learning Objectives

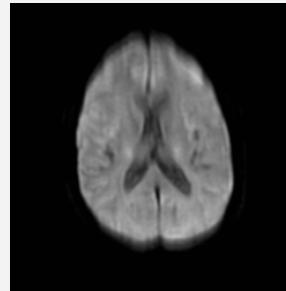
Following this tutorial, you'll be able to

- 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

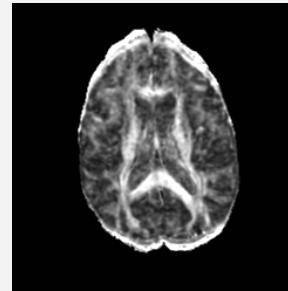
MR Diffusion Analysis Pipeline



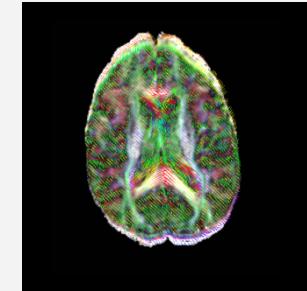
DWI
Acquisition



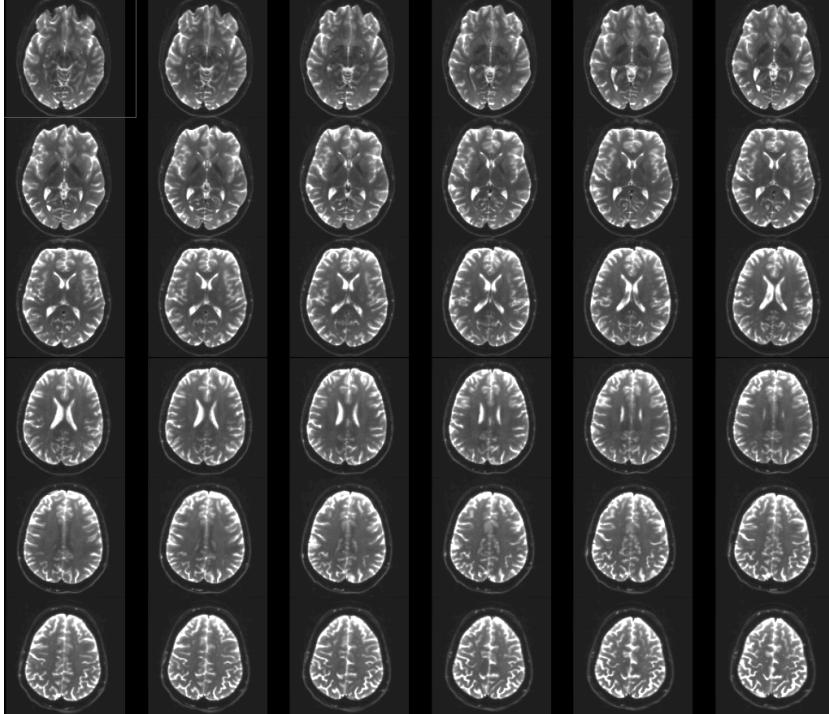
Tensor
Calculation



Scalar
Maps

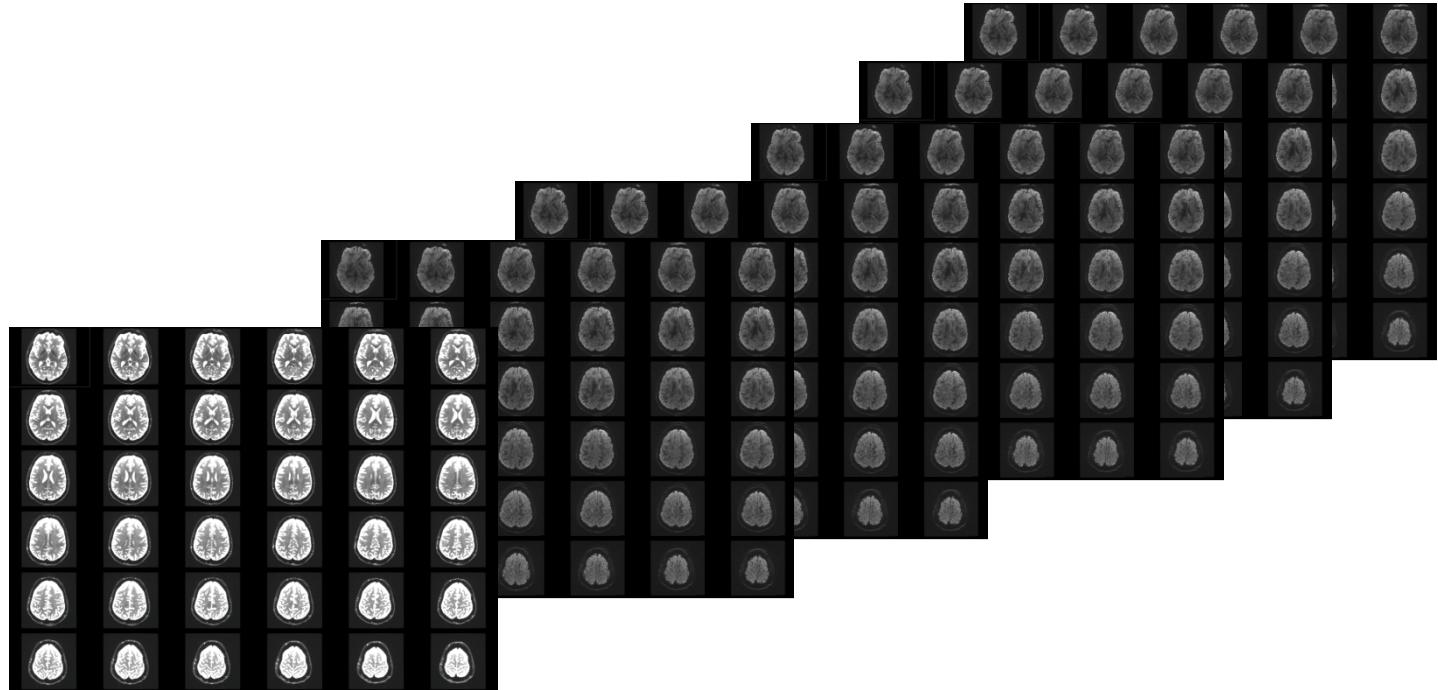


3D
Visualization



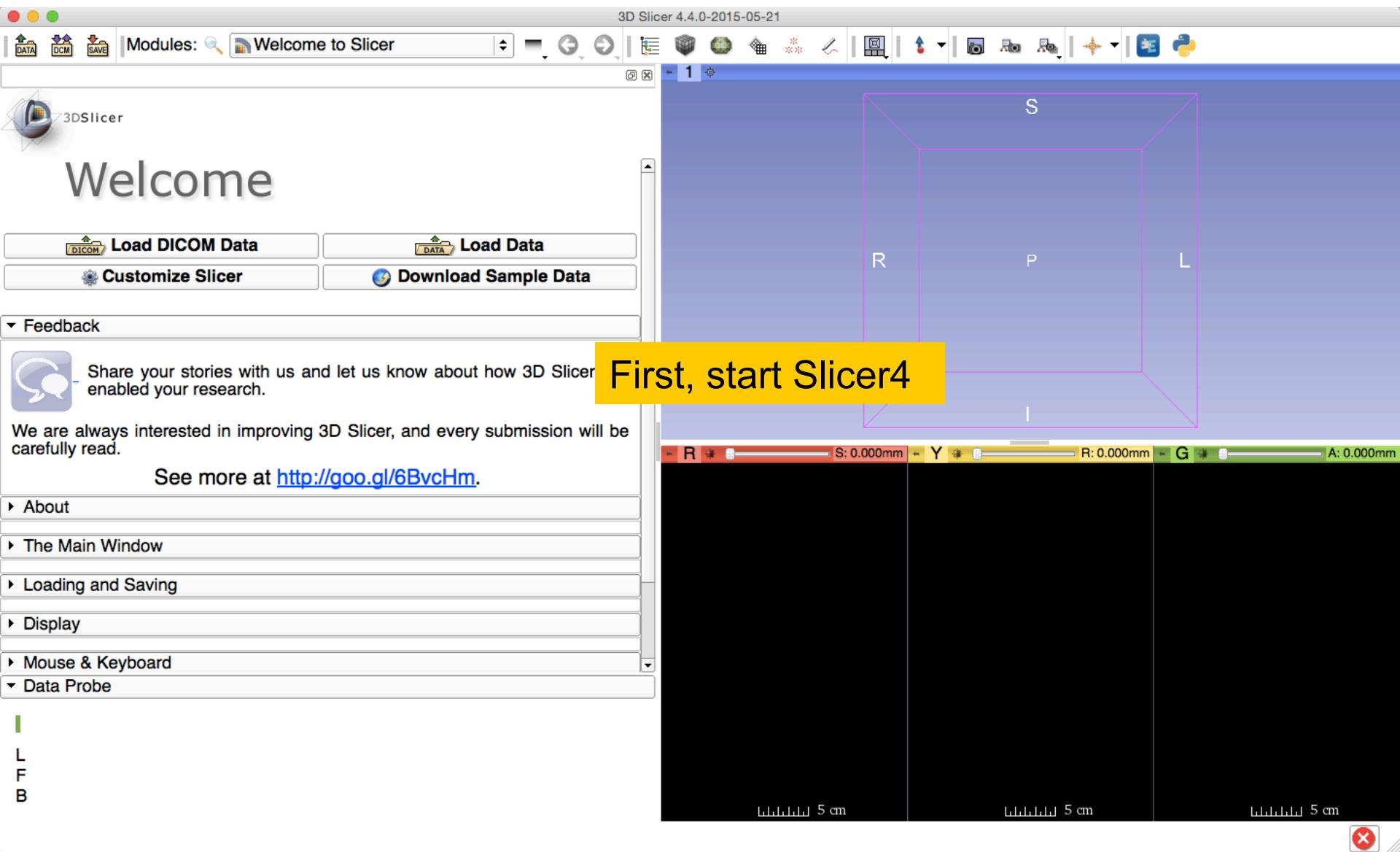
Part 1: From DWI images to Tensors

Understanding the DWI Dataset

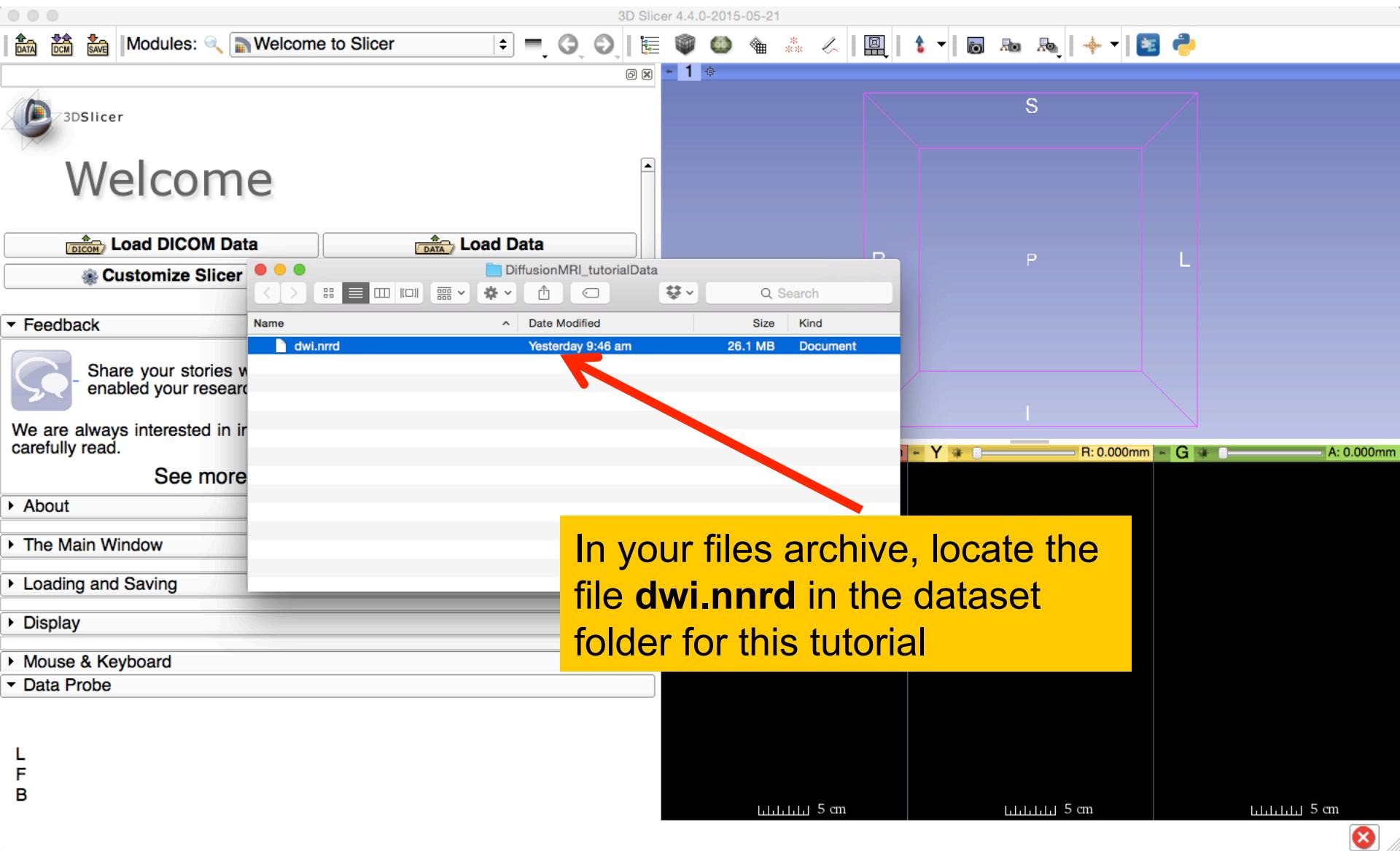


The Diffusion Weighted Imaging (DWI) dataset is composed of a set of volumes acquired with 42 diffusion-sensitizing gradient directions, and 7 baseline image acquired without diffusion weighting.

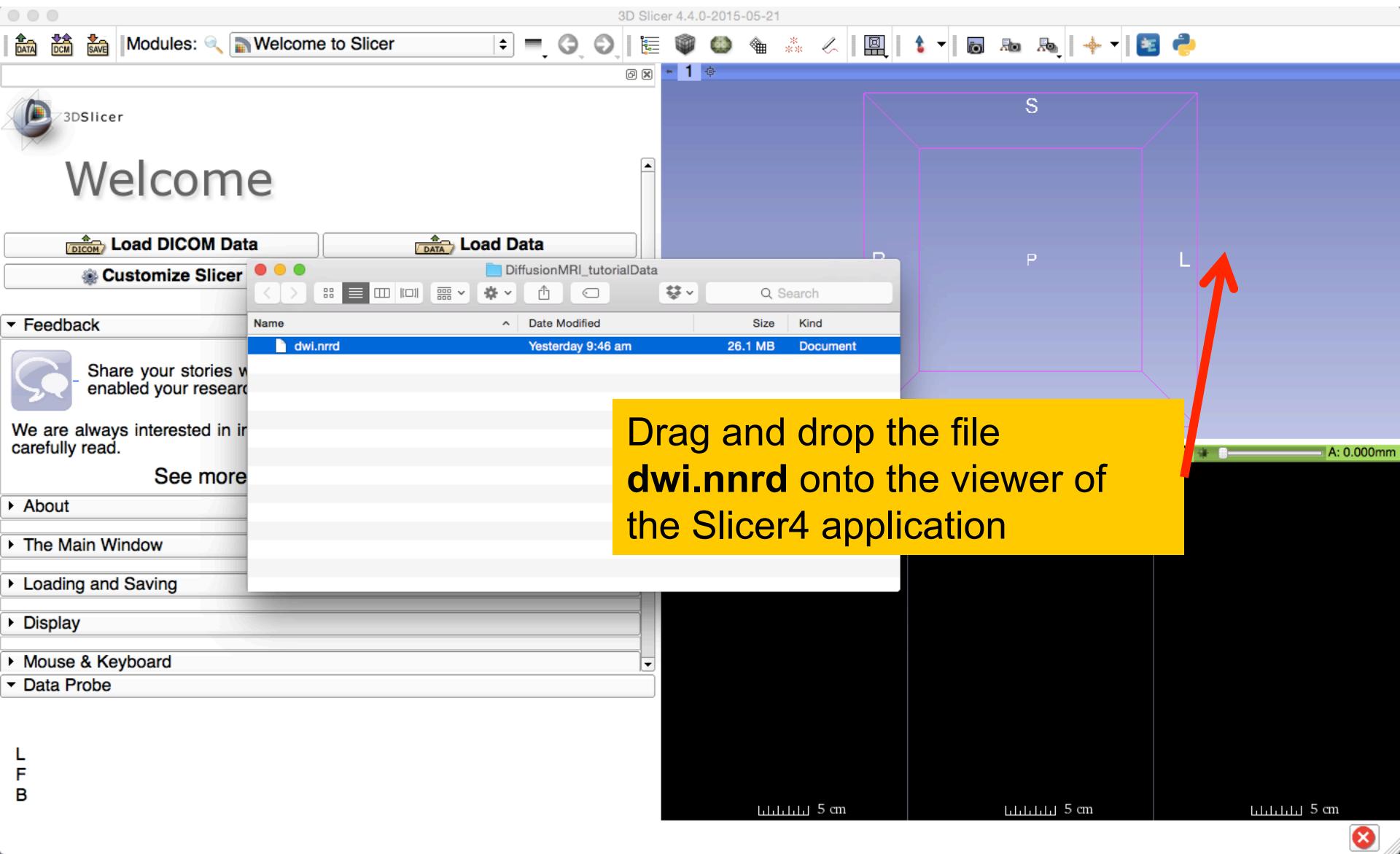
Loading the DWI Dataset



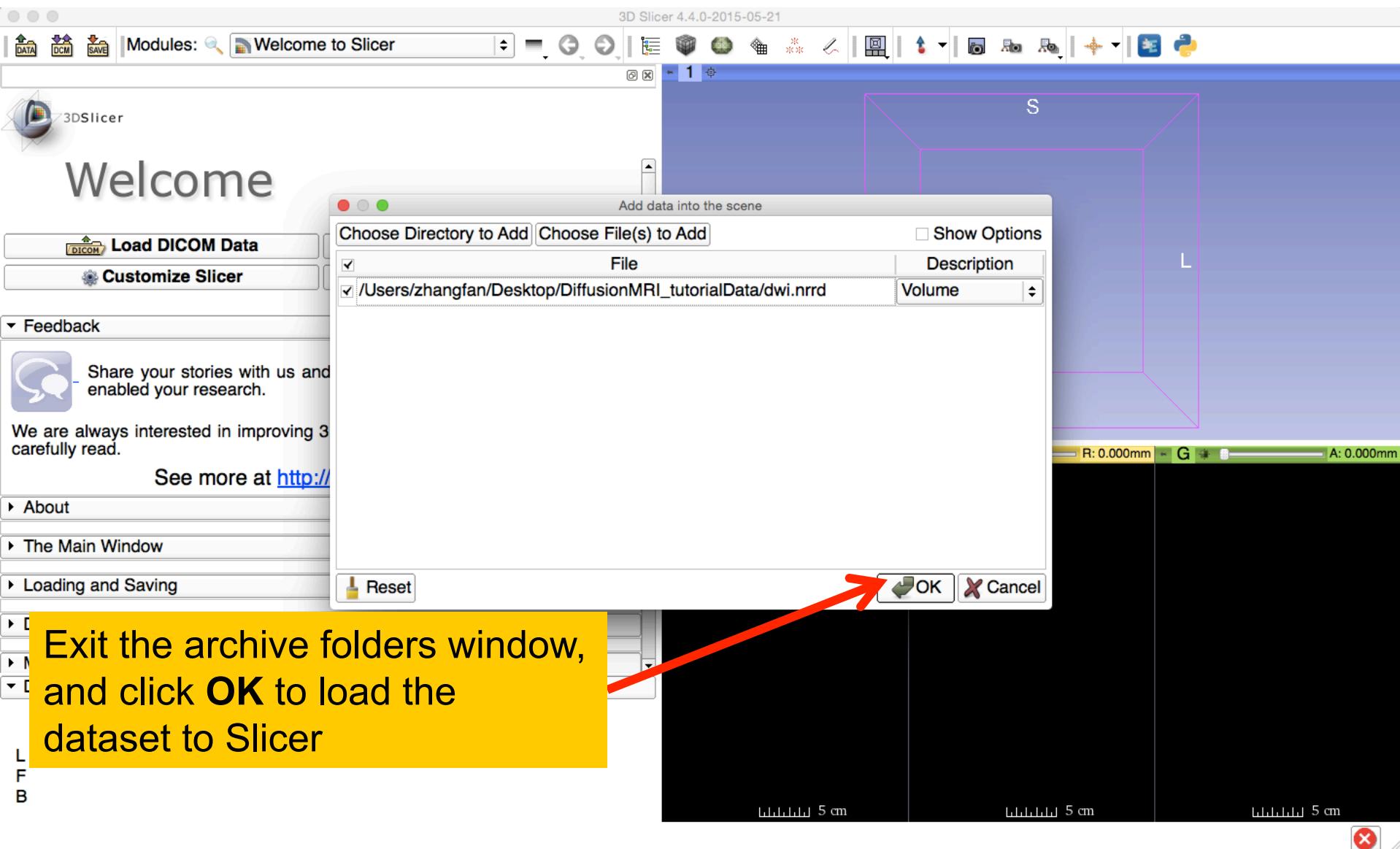
Loading the DWI Dataset



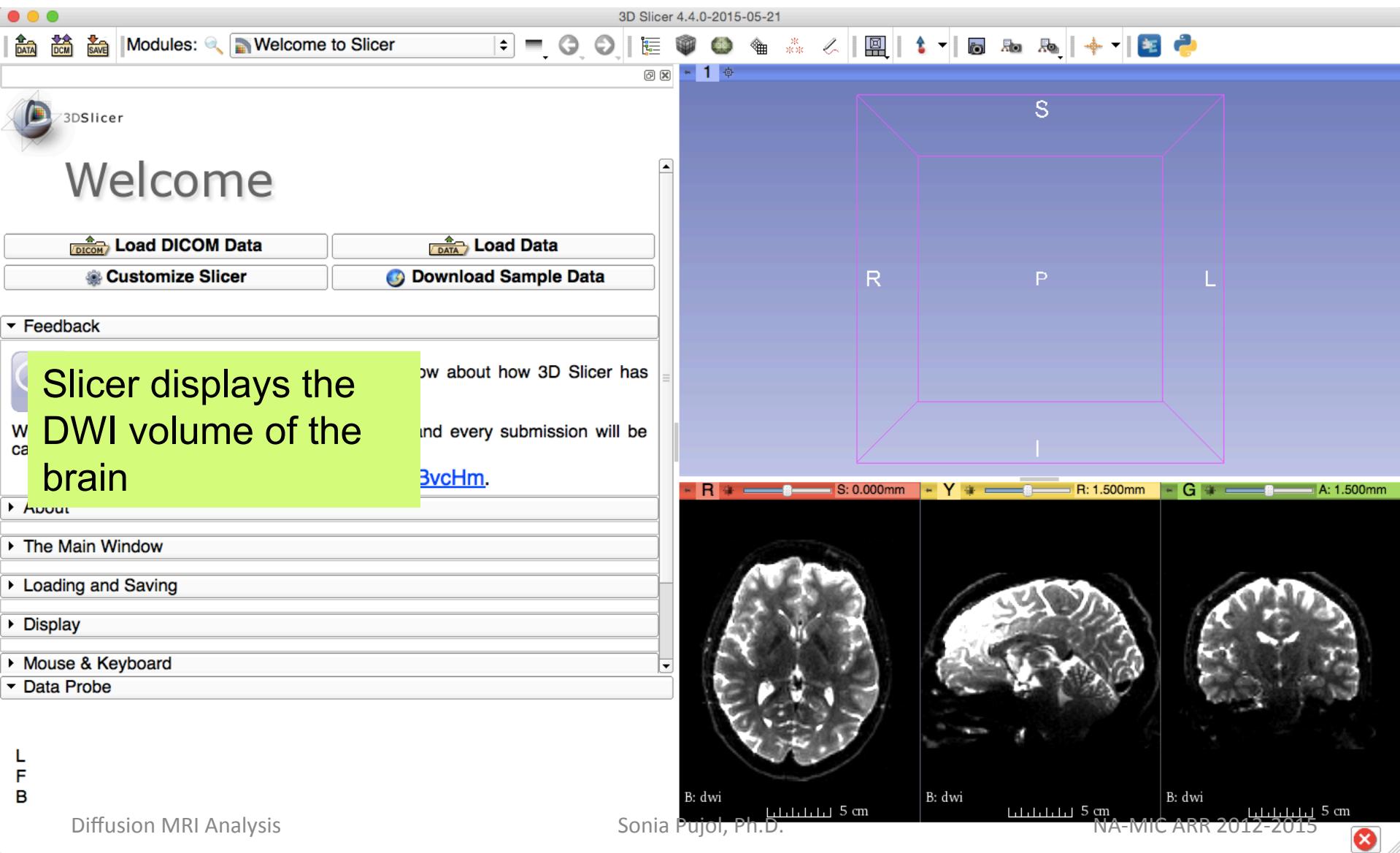
Loading the DWI Dataset



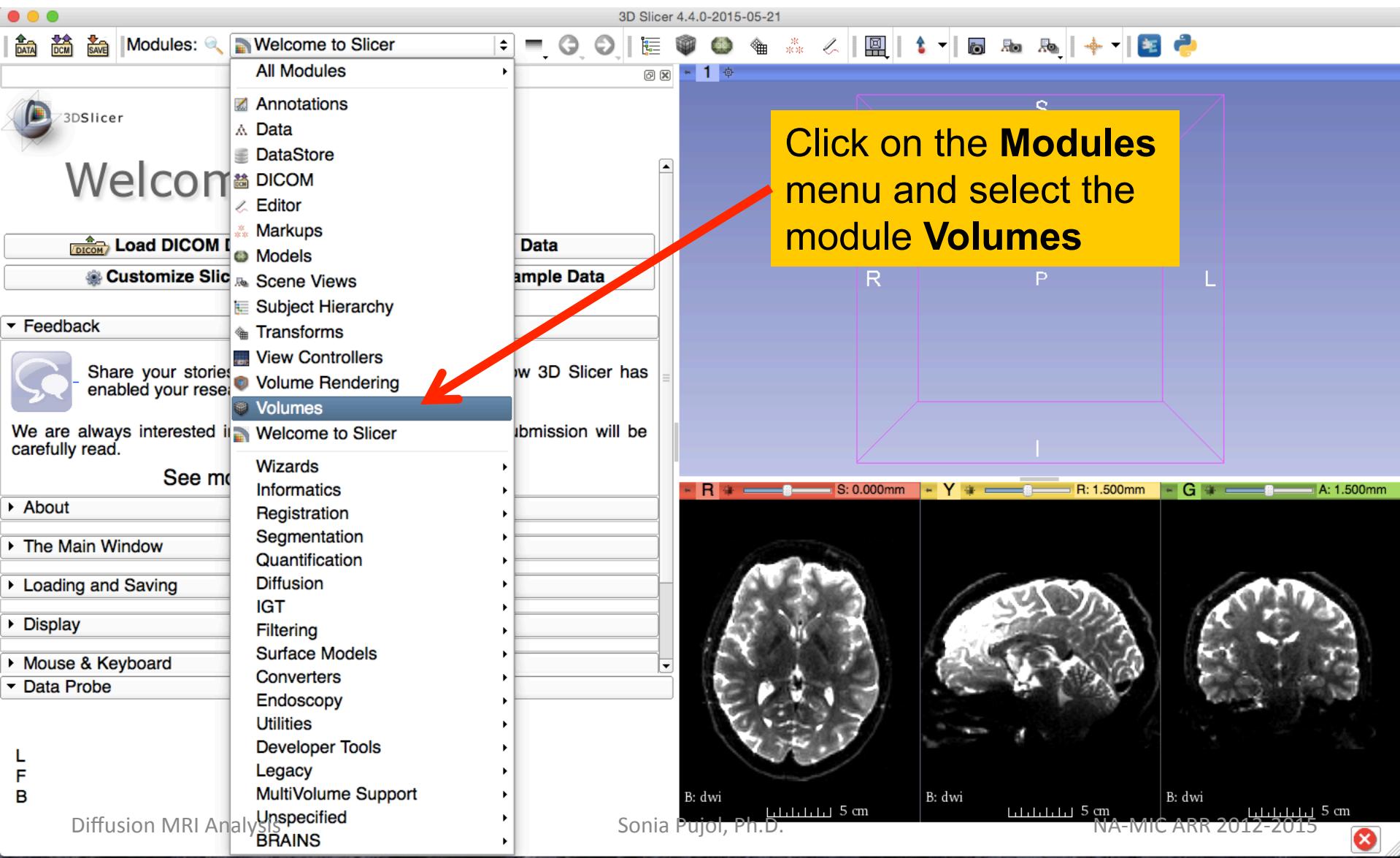
Loading the DWI Dataset



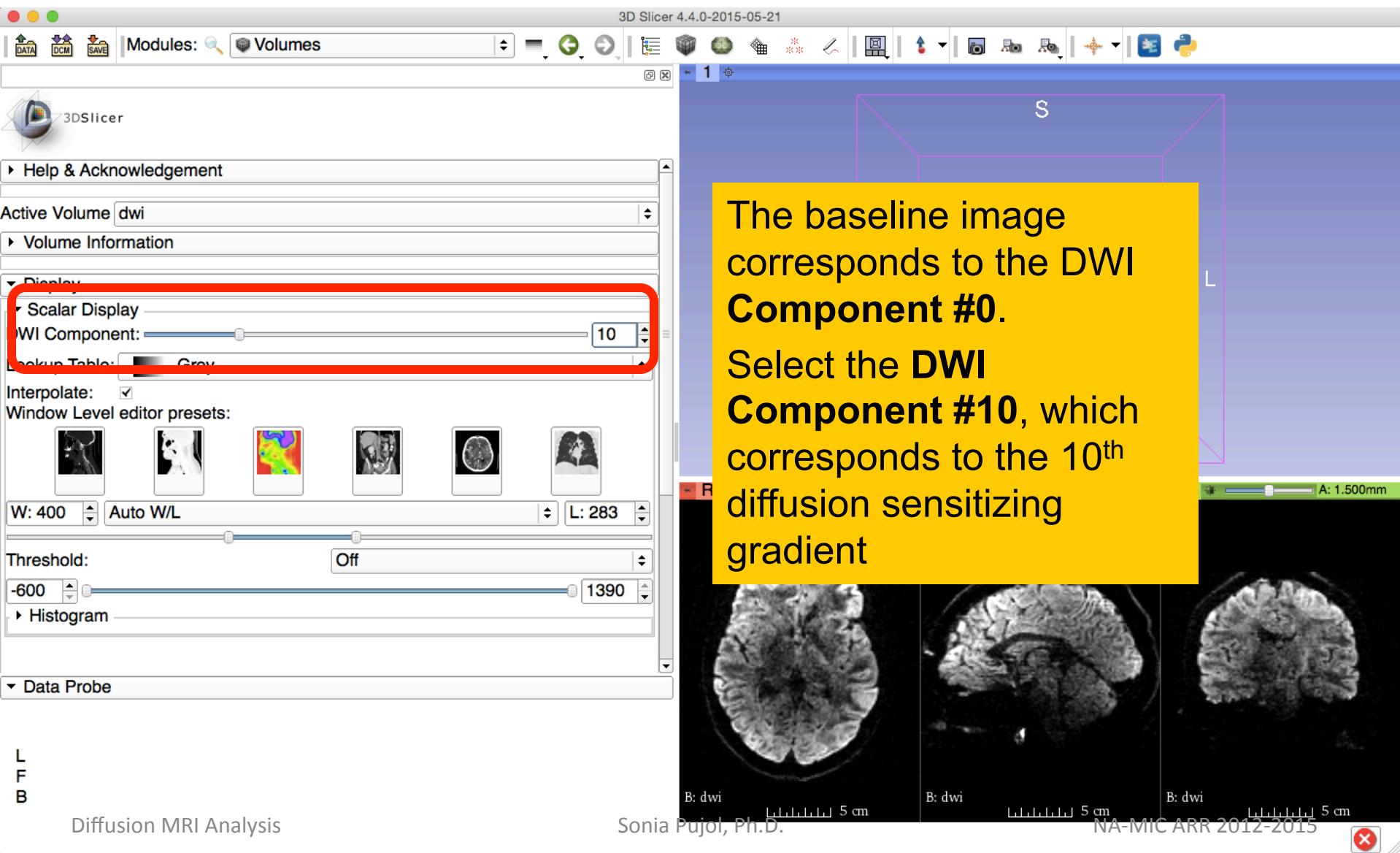
Loading the DWI Dataset



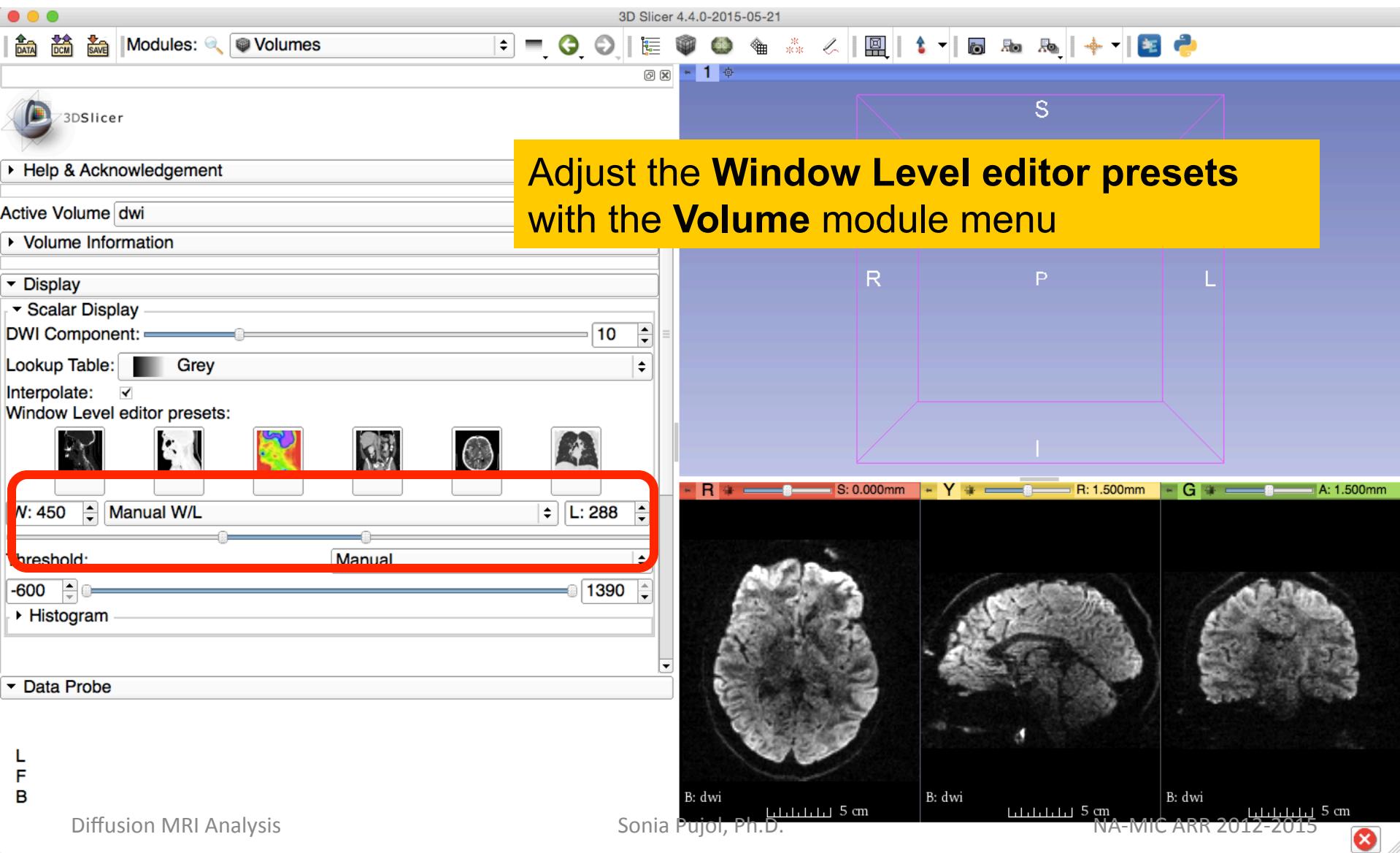
Loading the DWI Dataset



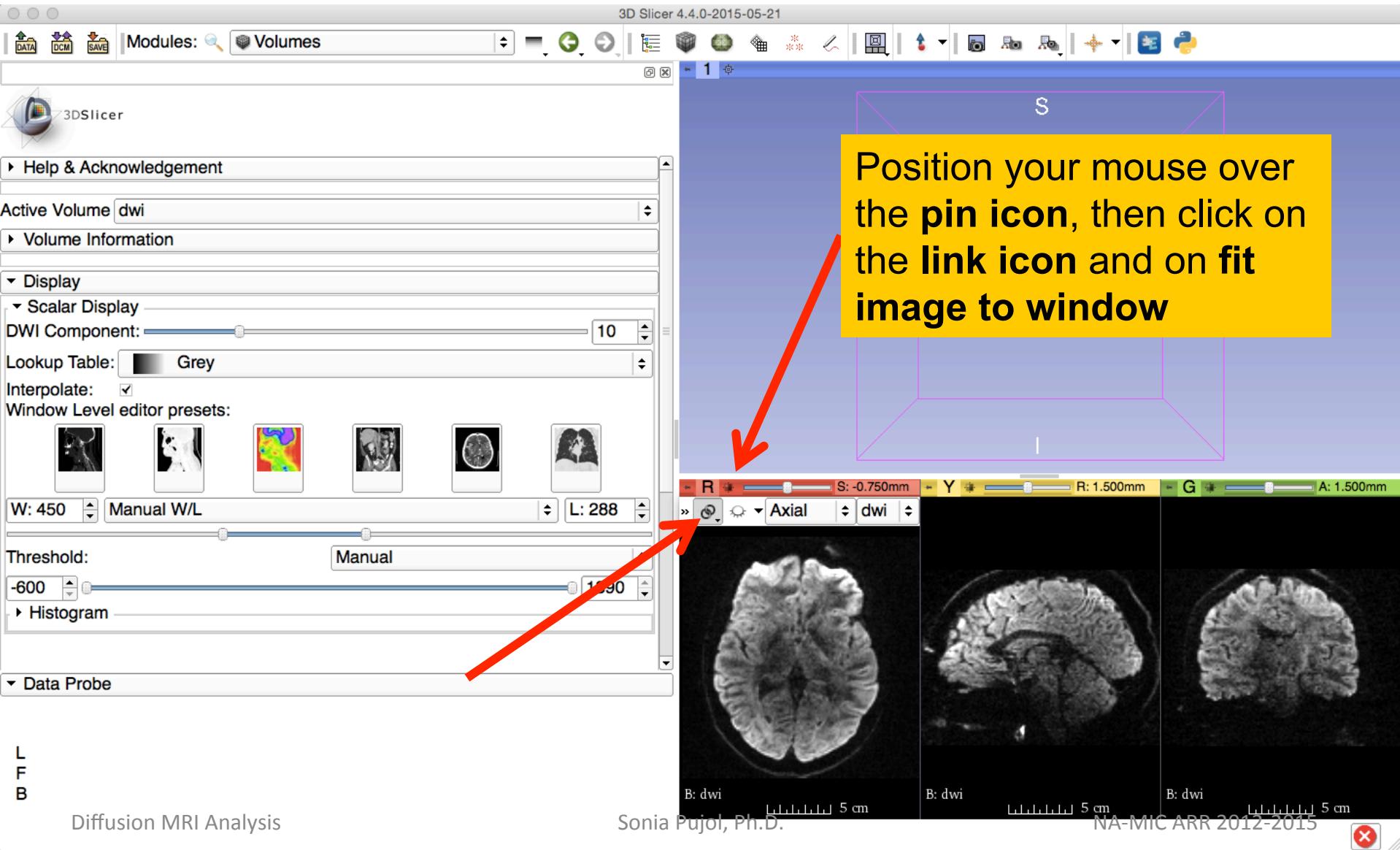
Loading the DWI Dataset



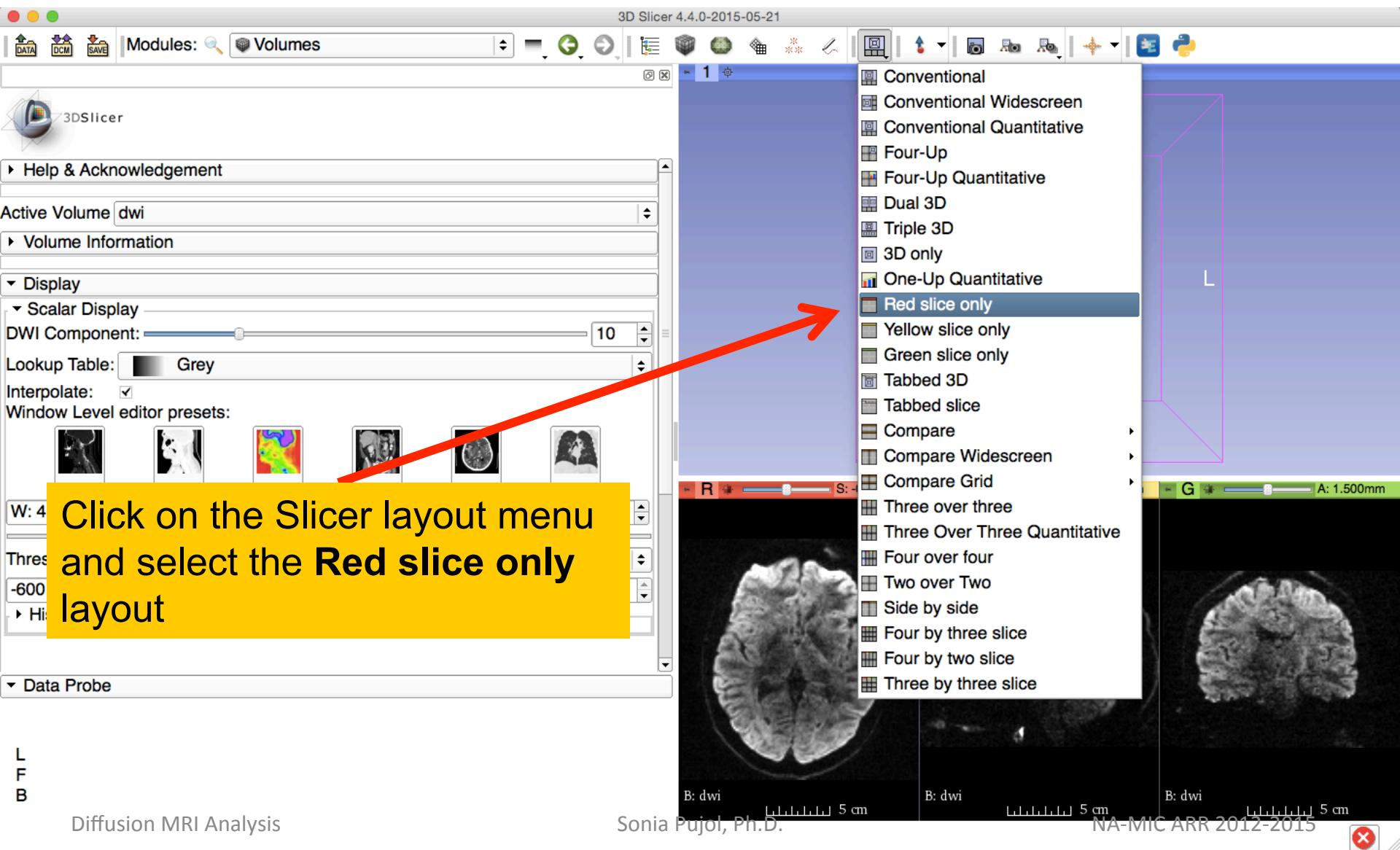
Loading the DWI Dataset



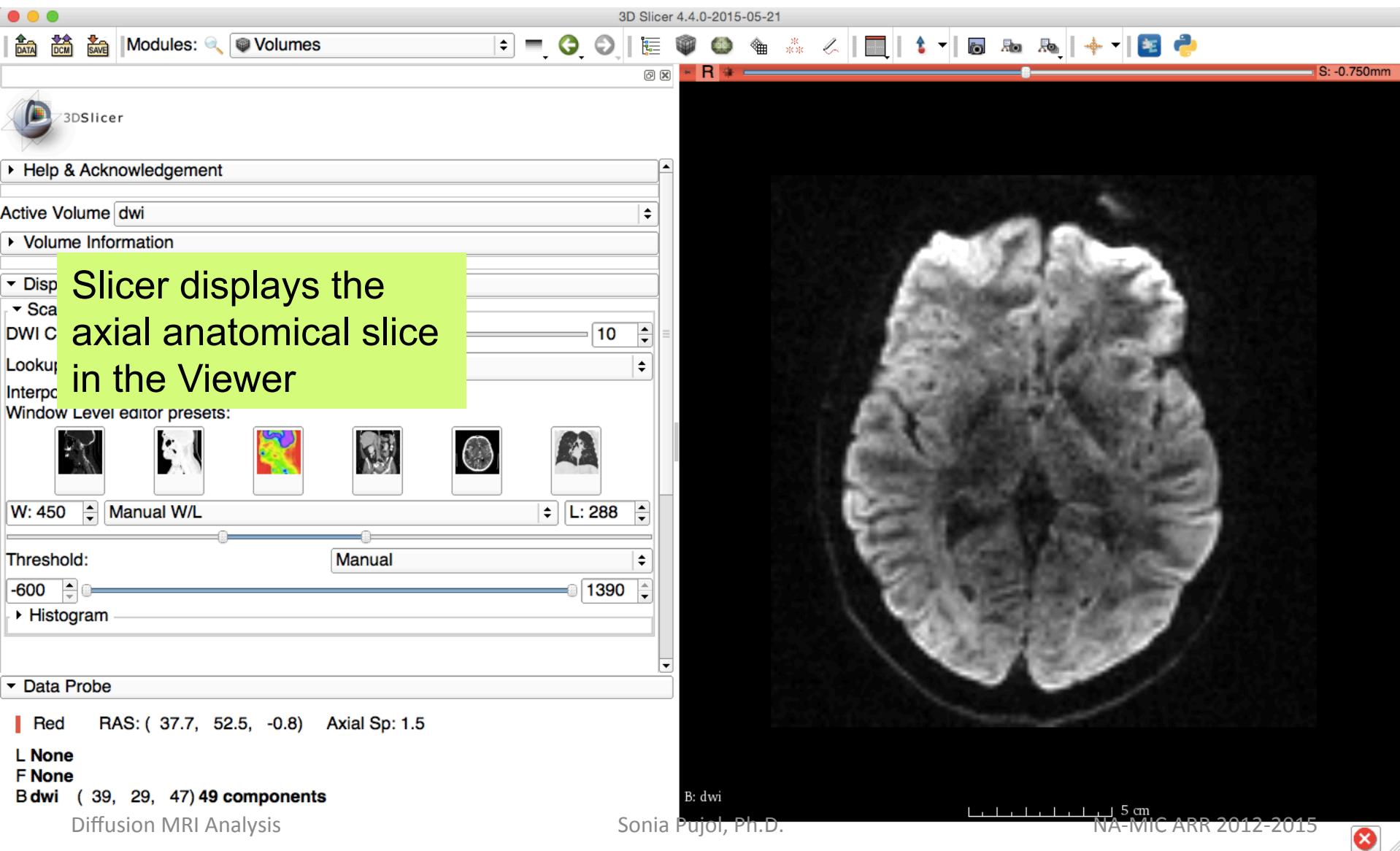
Loading the DWI Dataset



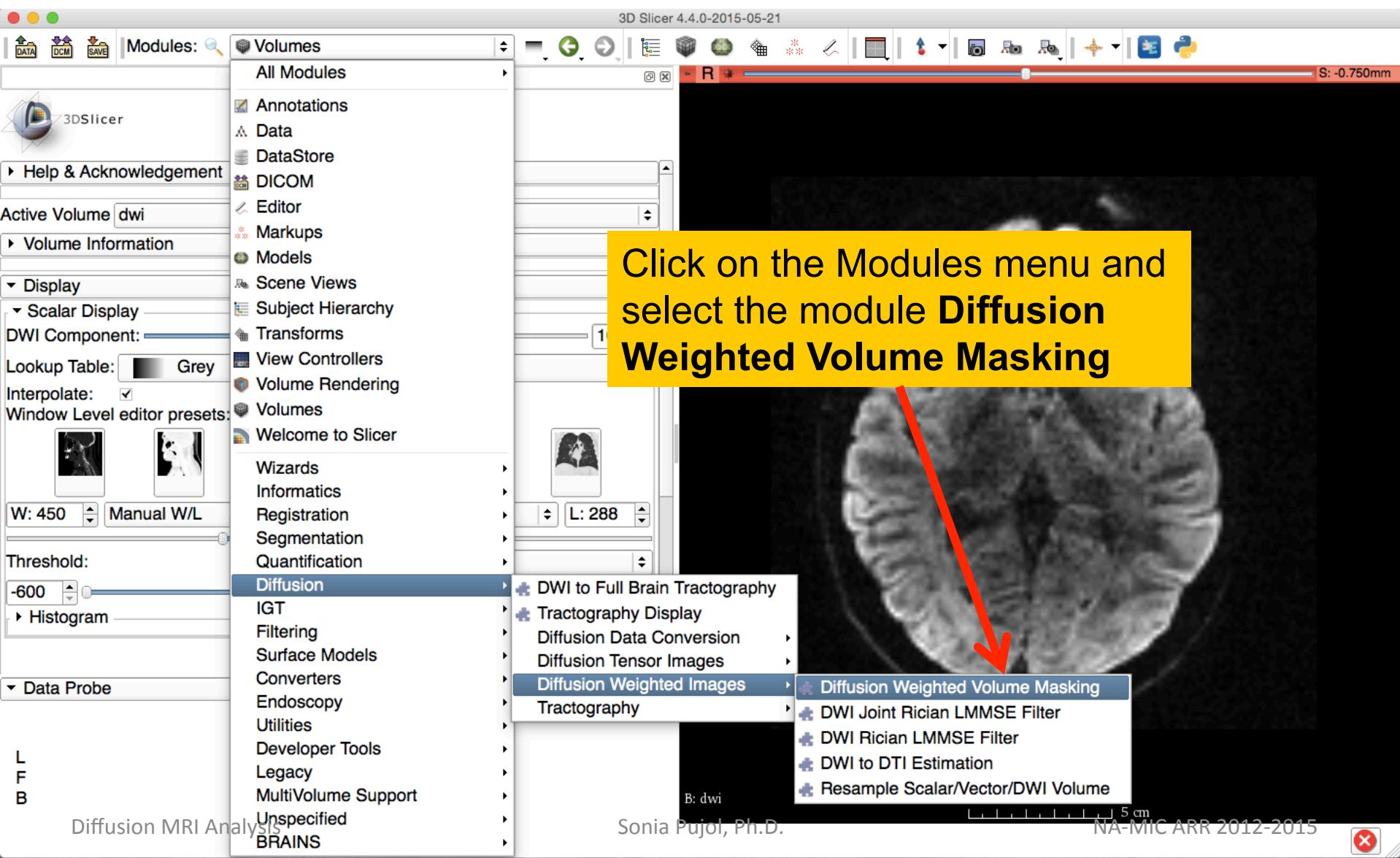
Loading the DWI Dataset



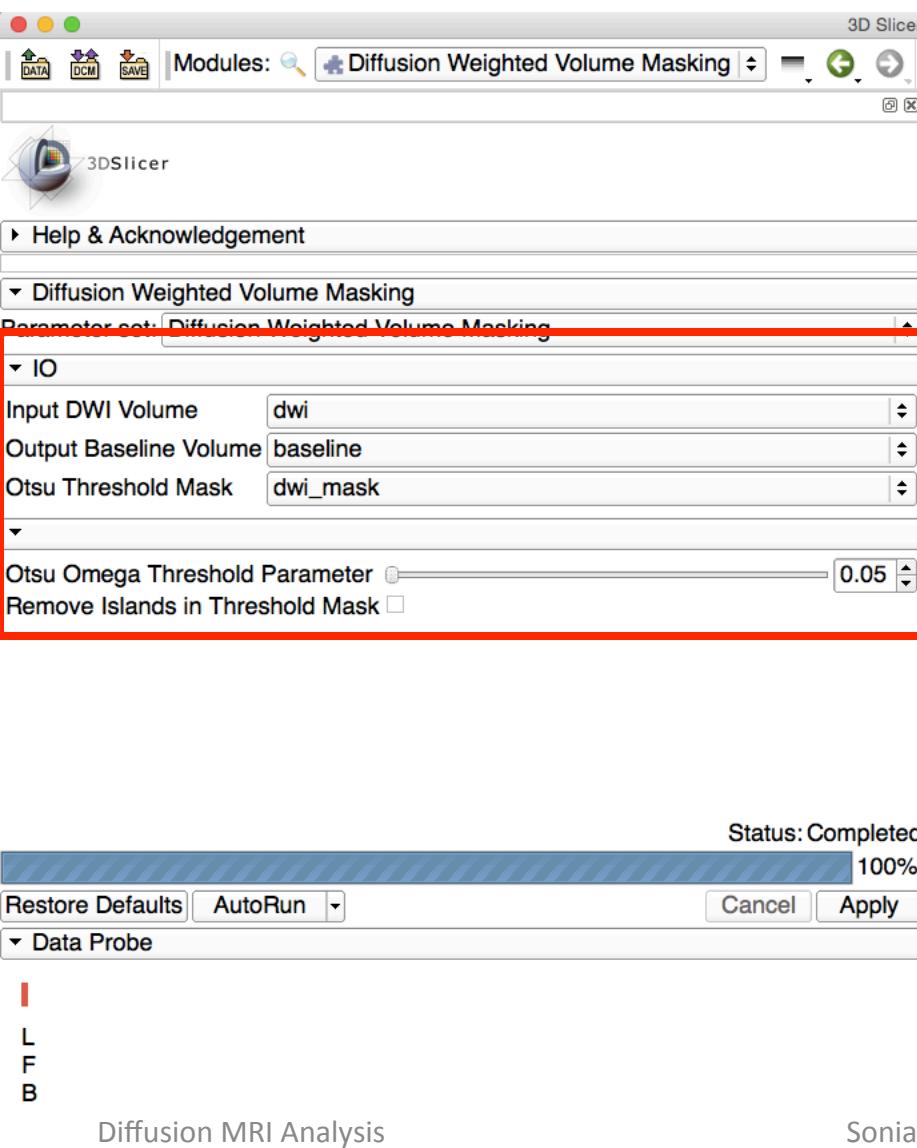
Loading the DWI Dataset



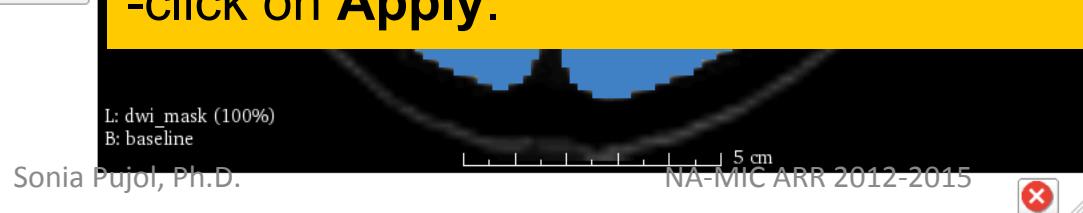
Creating a brain mask



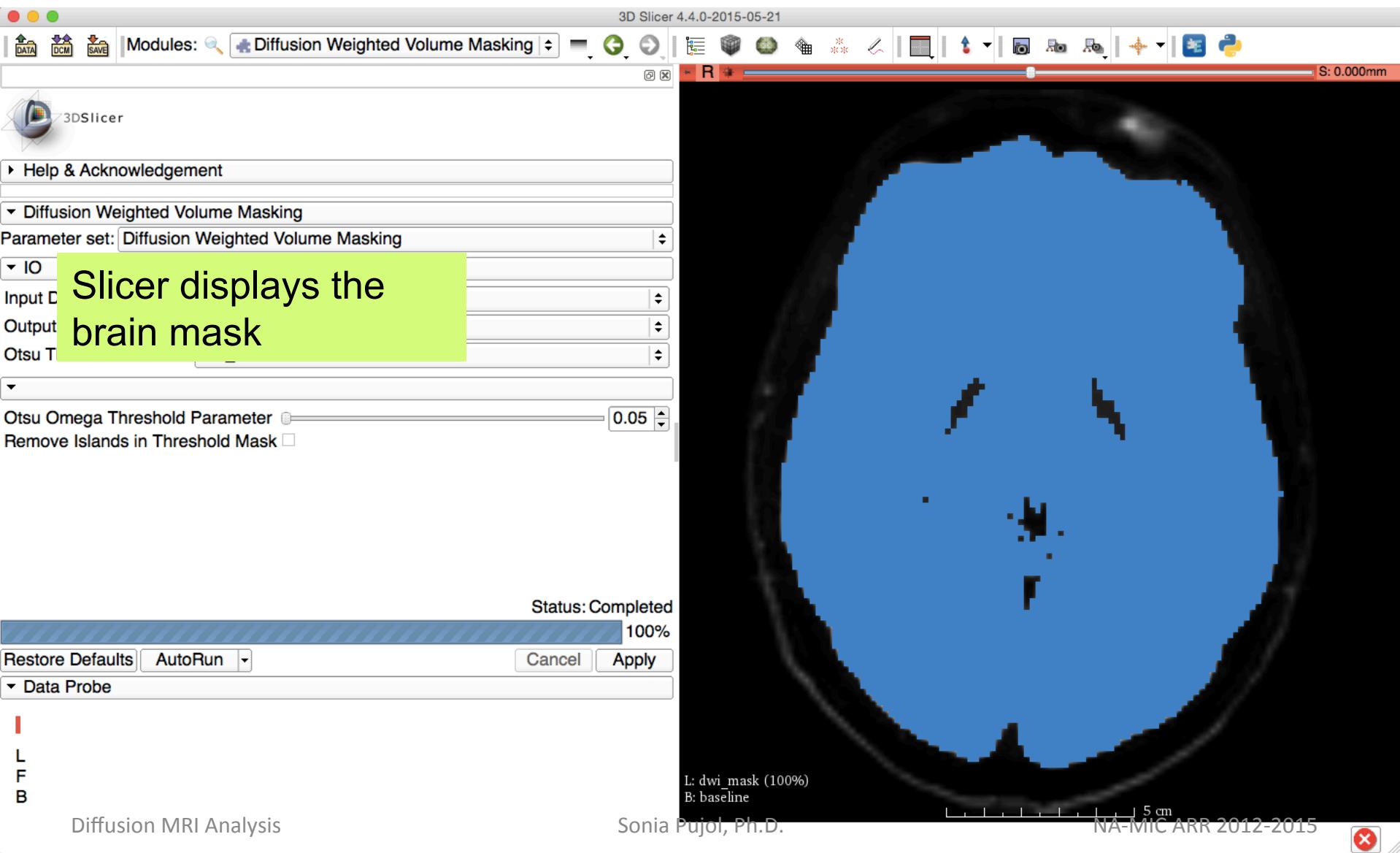
Creating a brain mask



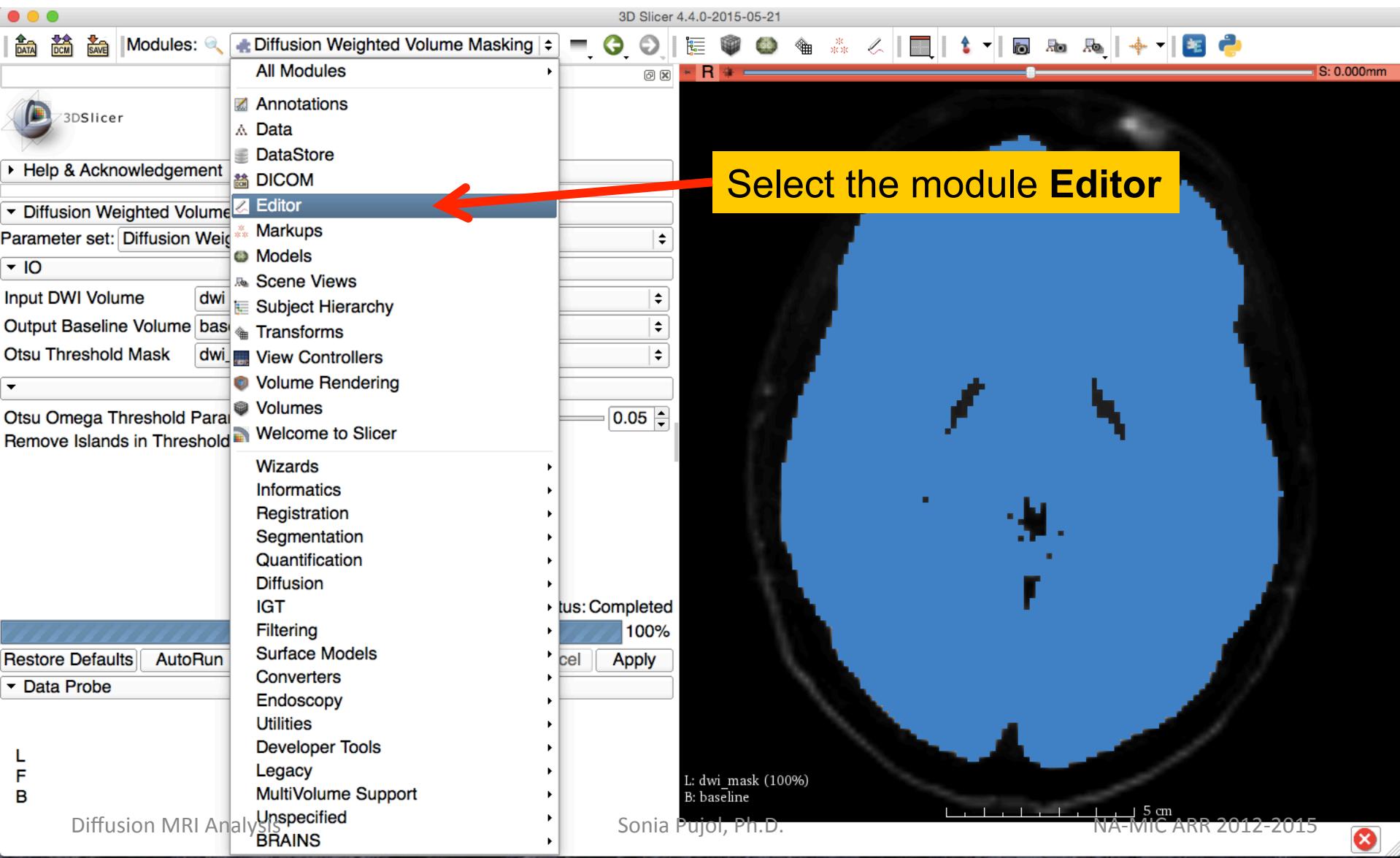
- select the **Input DWI volume 'dwi'**
- select **Output Baseline Volume**
'Create and Rename New Volume',
and rename it **'baseline'**
- select **Output Threshold Volume**
'Create and Rename new Volume',
and rename it **'dwi_mask'**
- uncheck **Remove Islands in Threshold Mask**
- set **Otsu Omega Threshold Parameter 'WLS'** to **0.05**
- click on **Apply**.



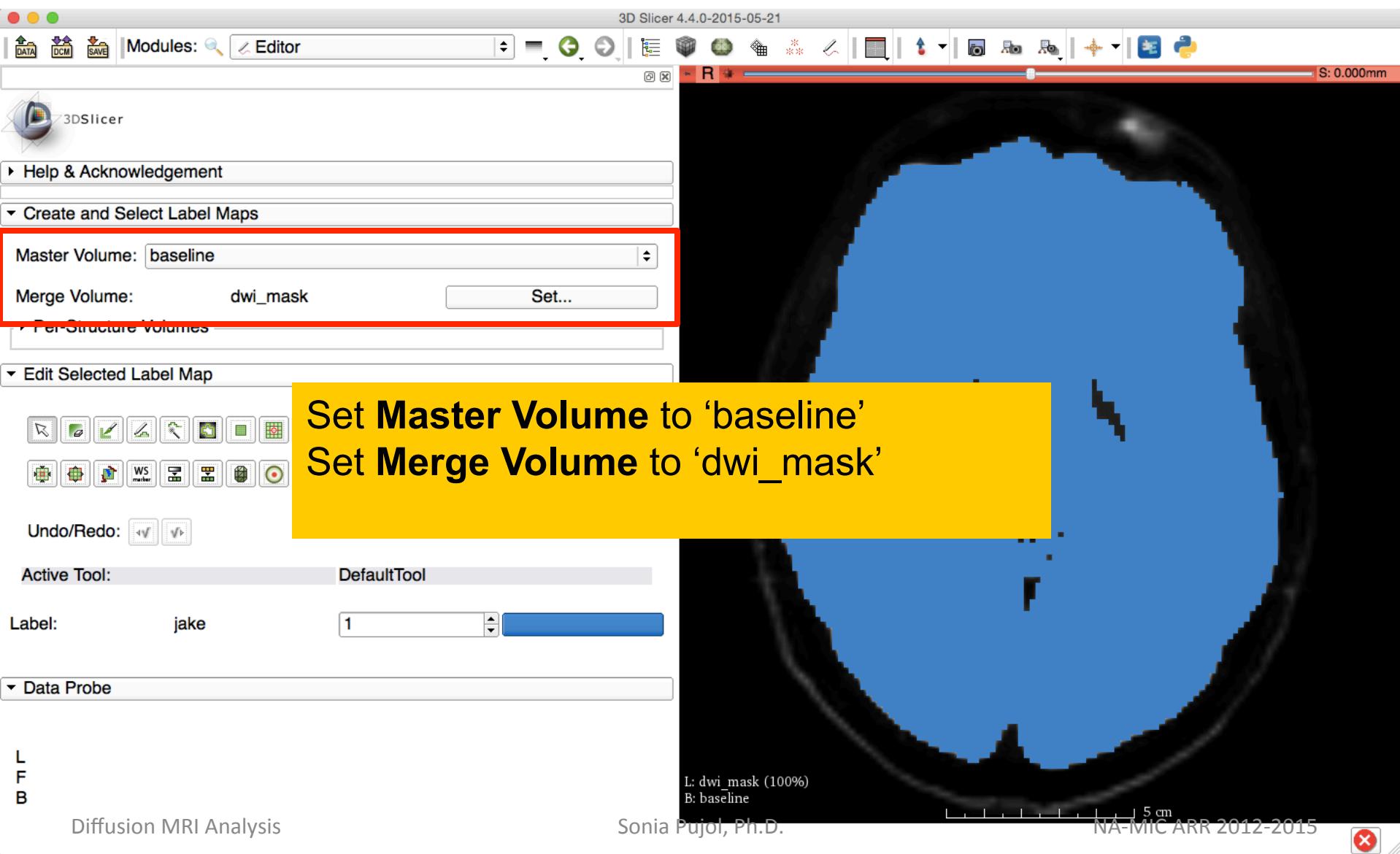
Creating a brain mask



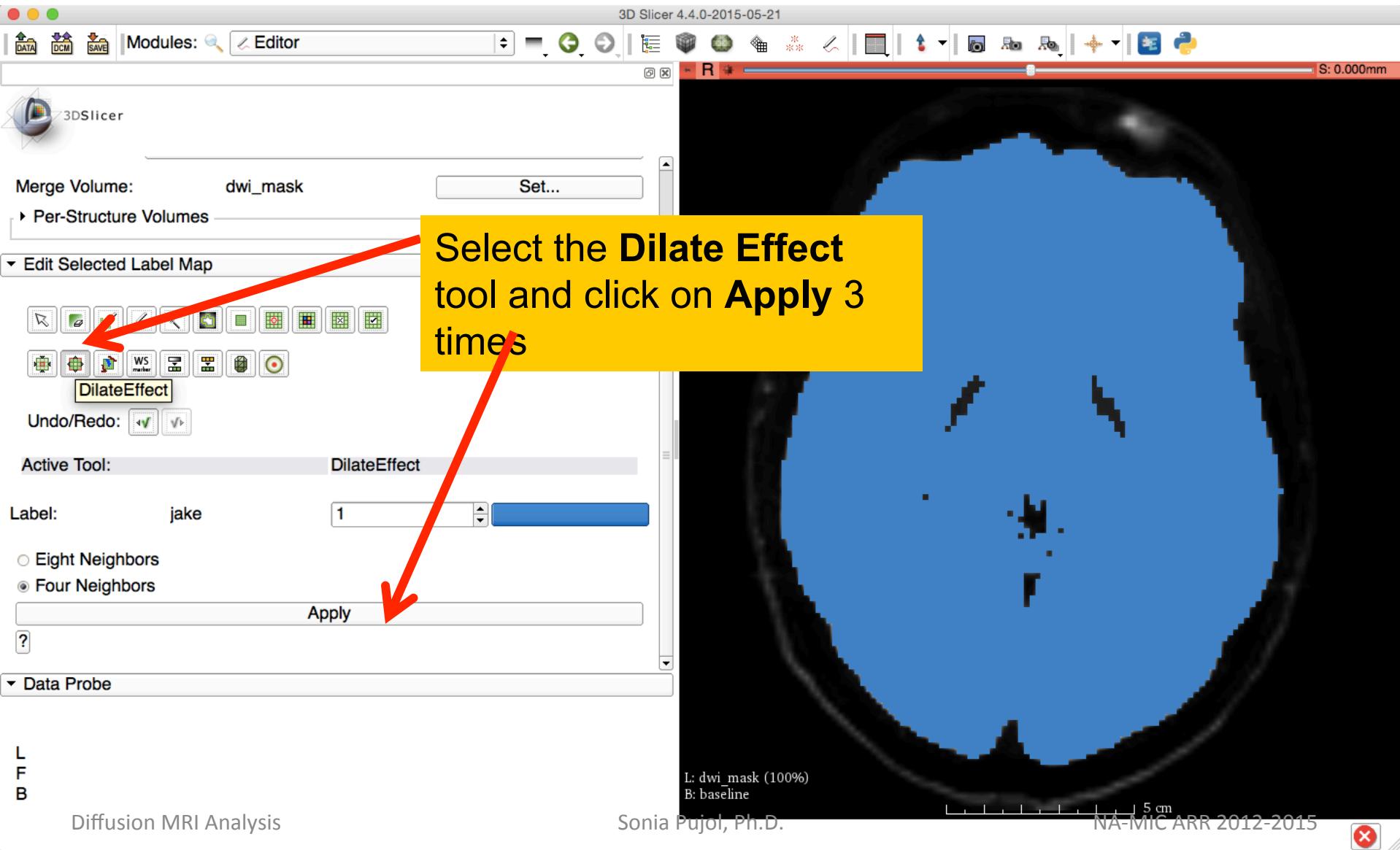
Creating a brain mask



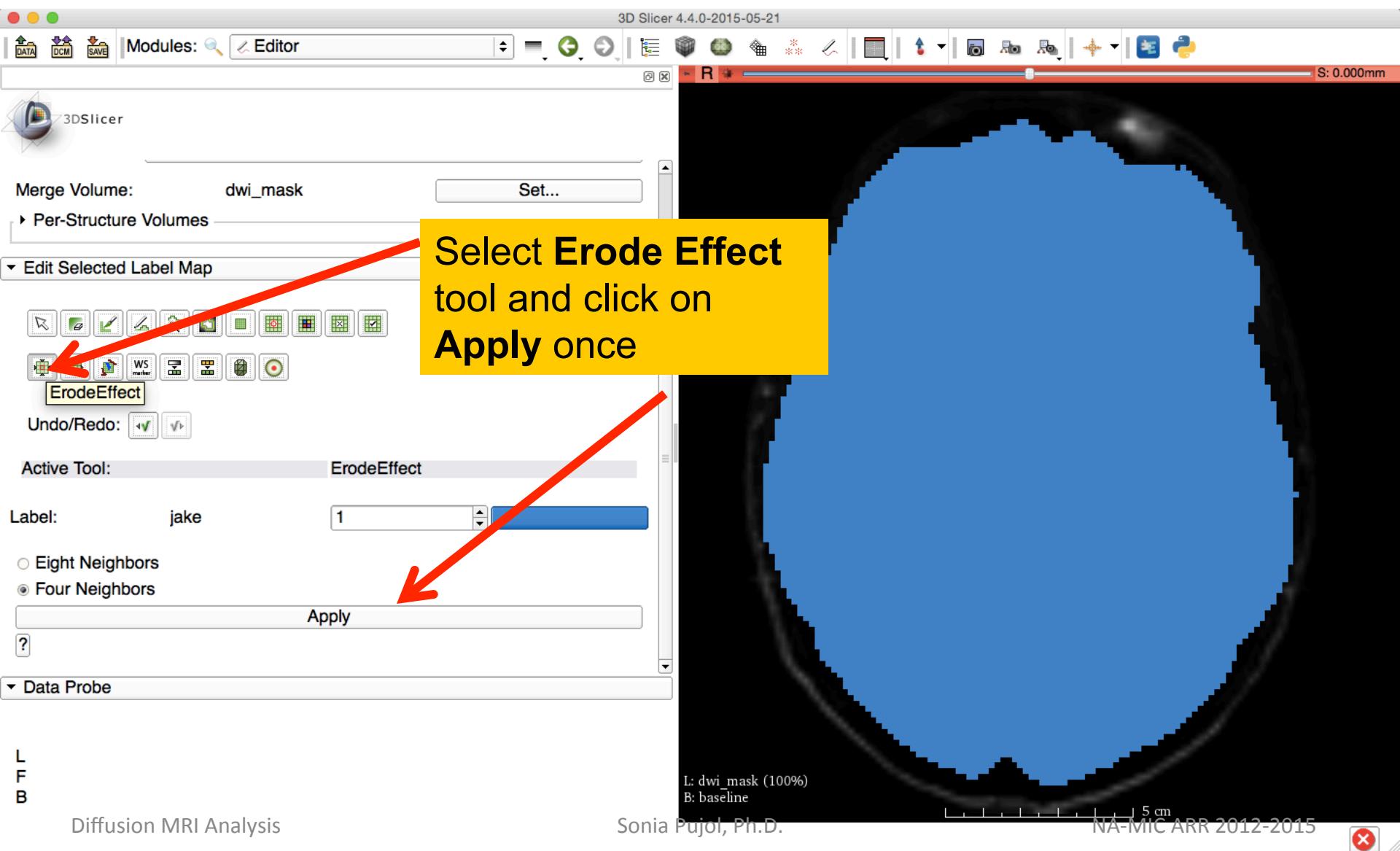
Creating a brain mask



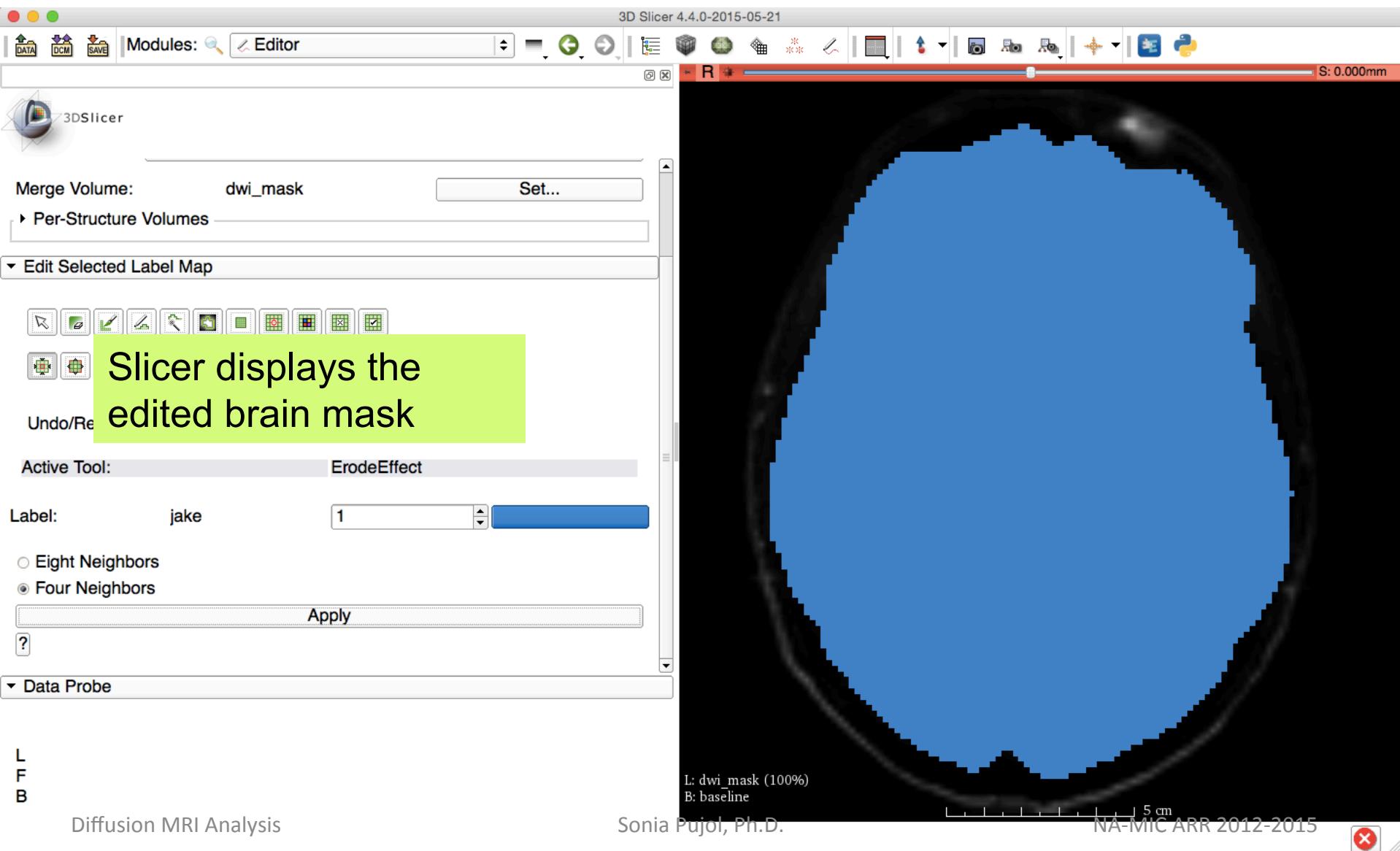
Creating a brain mask



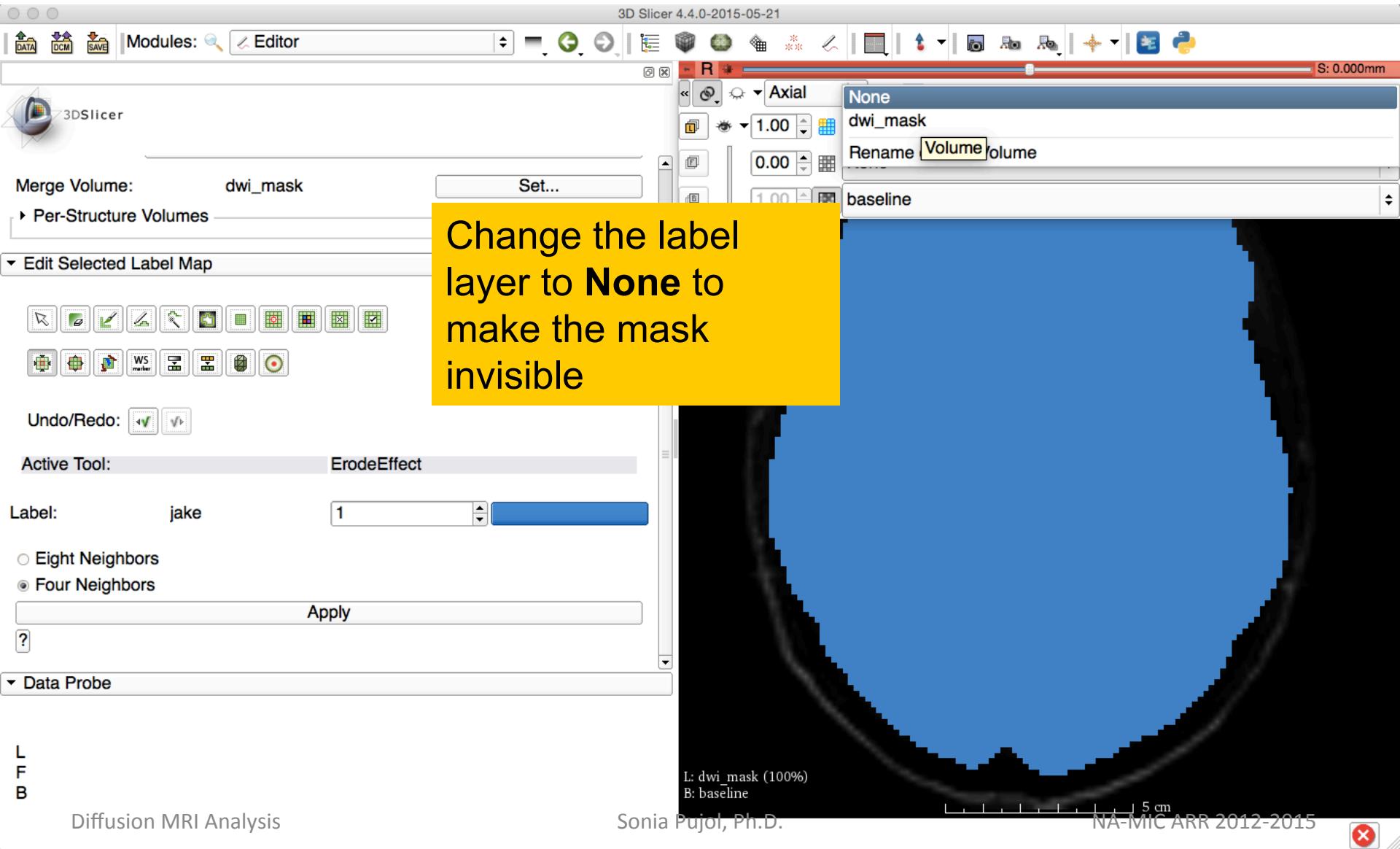
Creating a brain mask



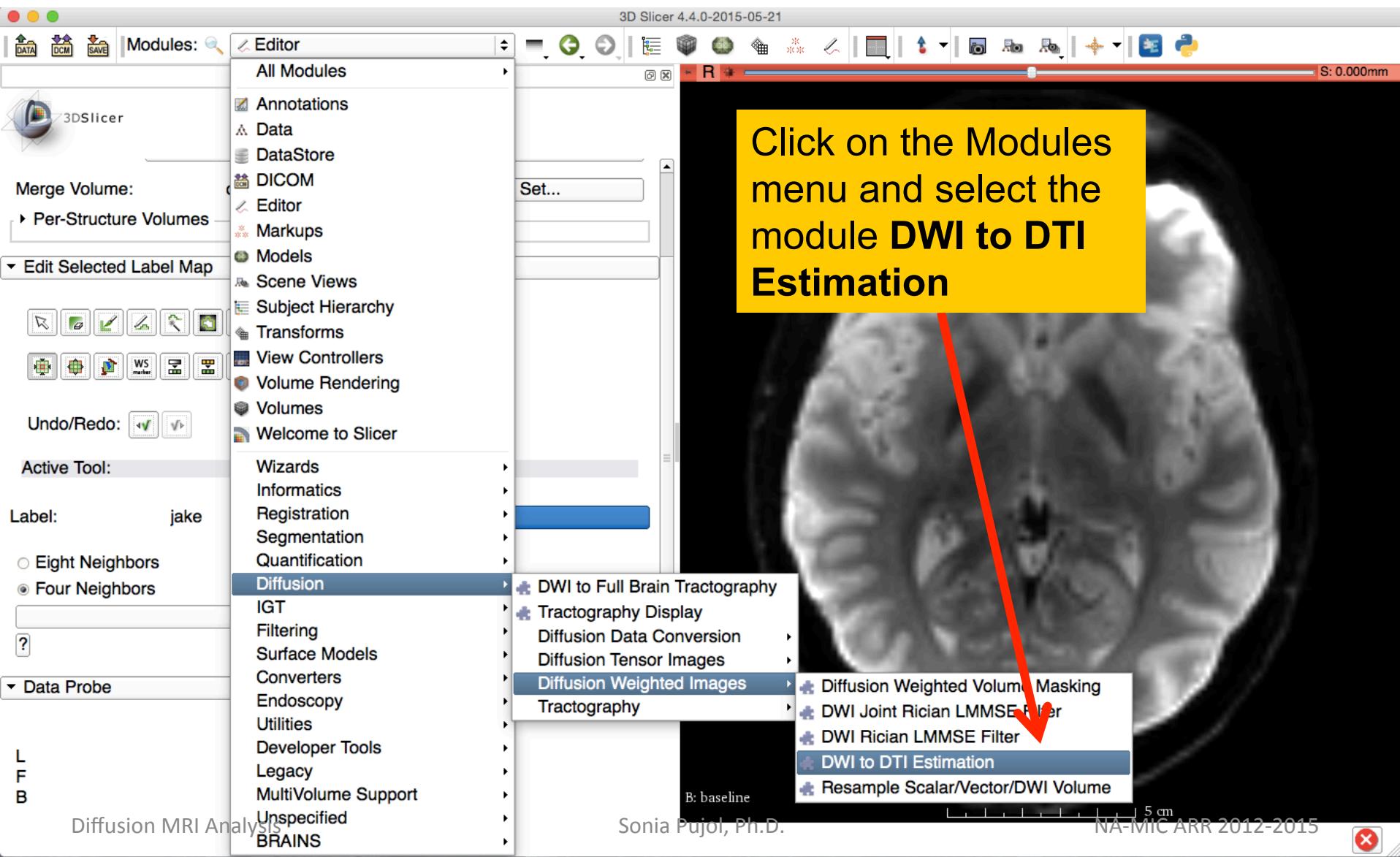
Creating a brain mask



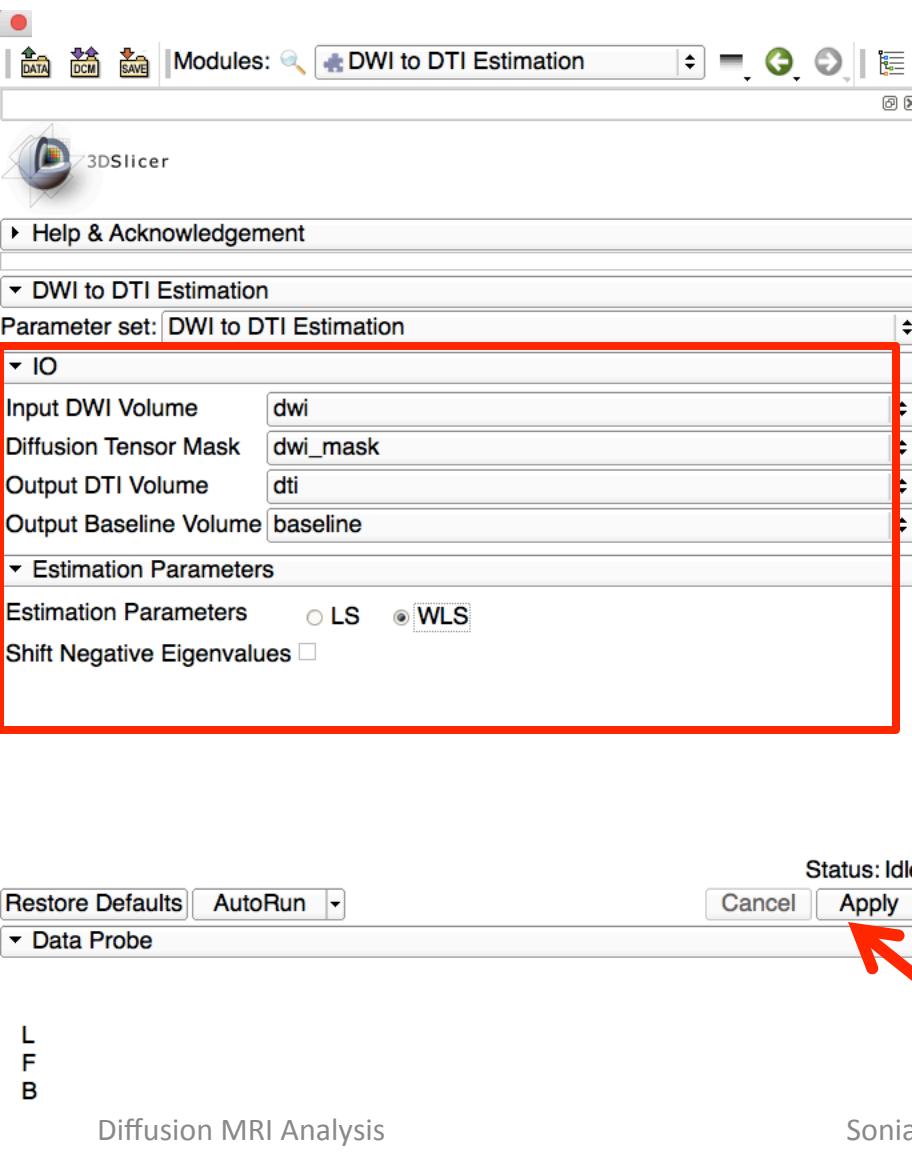
Creating a brain mask



Estimating the tensor



Estimating the tensor



The screenshot shows the 3DSlicer interface with the 'DWI to DTI Estimation' module selected in the modules menu. A red box highlights the 'IO' parameters section, which includes:

- Input DWI Volume: dwi
- Diffusion Tensor Mask: dwi_mask
- Output DTI Volume: dti
- Output Baseline Volume: baseline

A red arrow points to the 'Apply' button at the bottom right of the module panel.

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**.

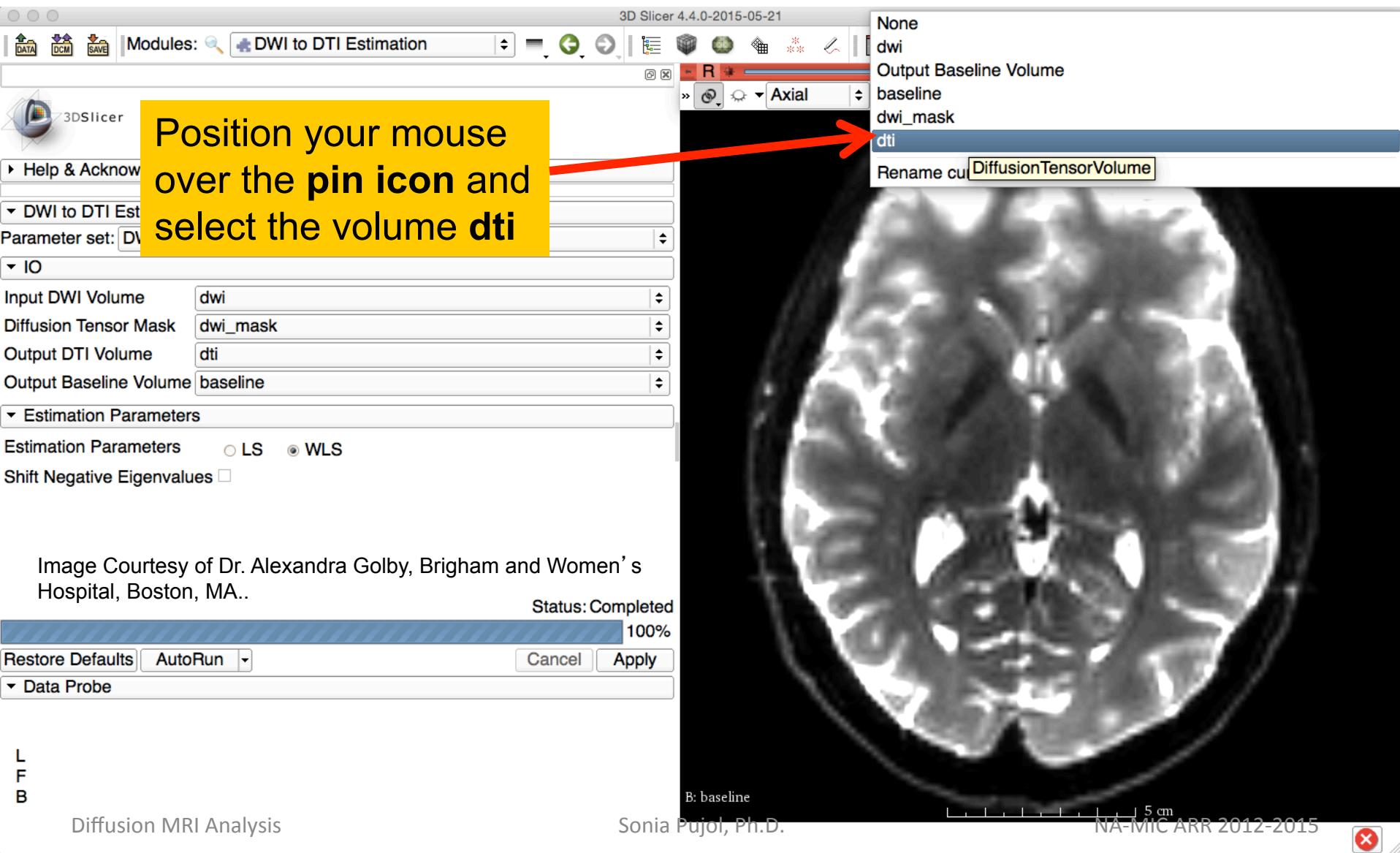
L
F
B

Diffusion MRI Analysis

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NA-MIC ARR 2012-2015

Estimating the tensor



Exploring the DWI Dataset

Slicer displays the DTI volume in color by orientation mode:

- Red: right-left
- Green: anterior-posterior
- Blue: inferior-superior

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

L F B

Diffusion MRI Analysis

3D Slicer 4.4.0-2015-05-21

Modules: DWI to DTI Estimation

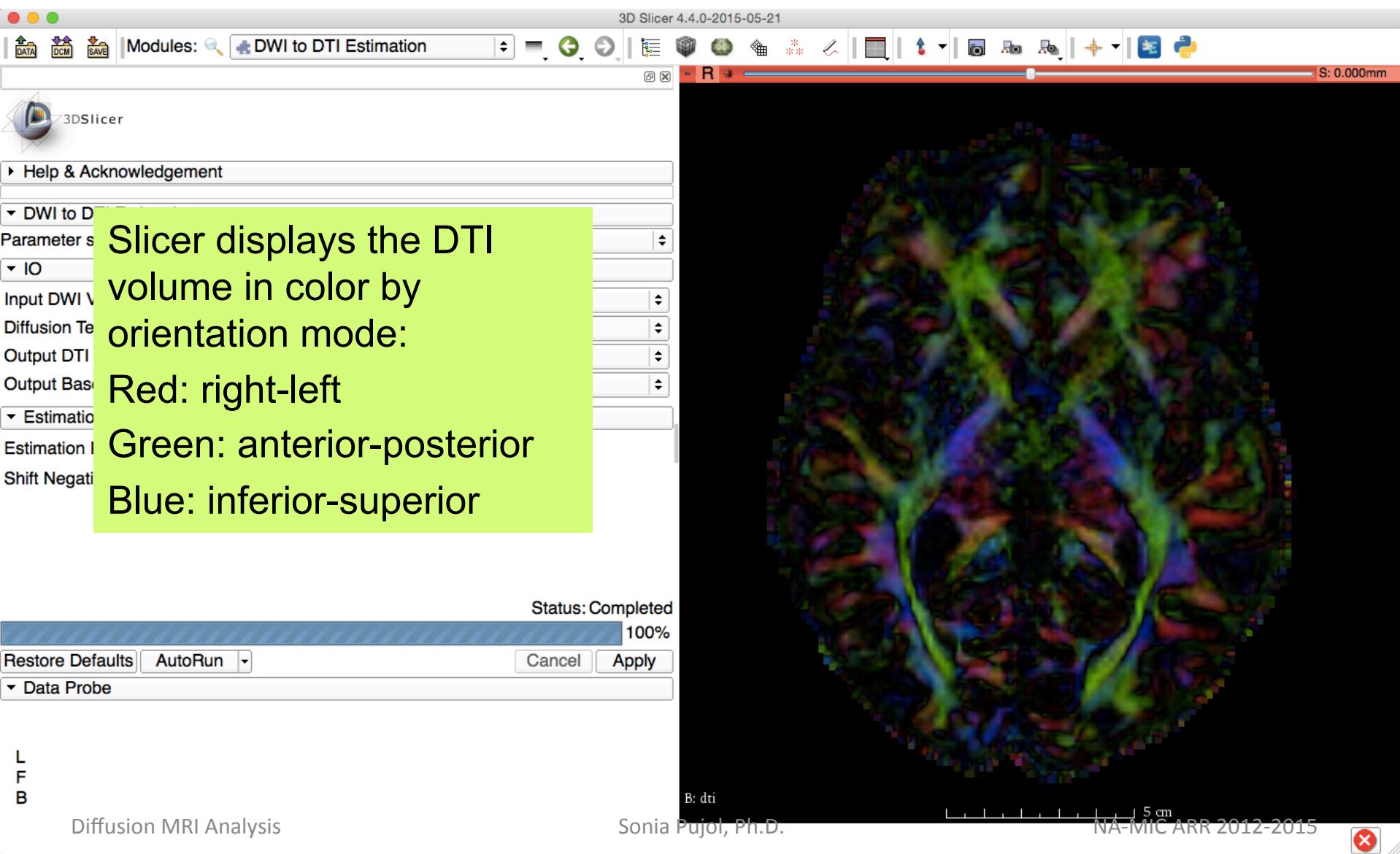
R S: 0.000mm

B: dti

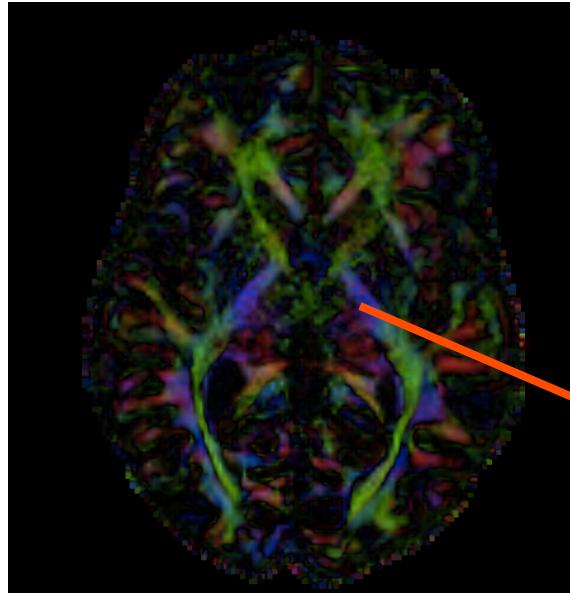
5 cm

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Diffusion Tensor Data



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

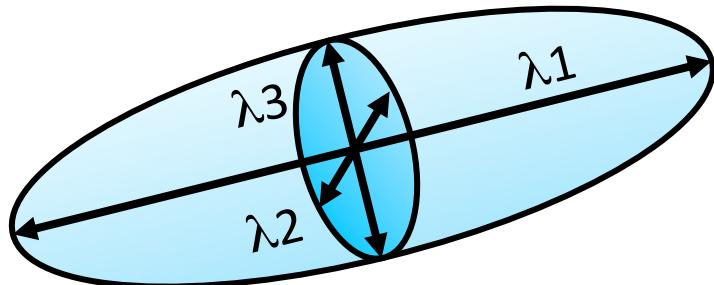
Stejskal-Tanner equation (1965)

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

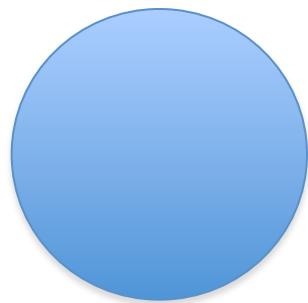
The diffusion tensor \underline{D} in the voxel (I,J,K) is a 3×3 symmetric matrix.

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.

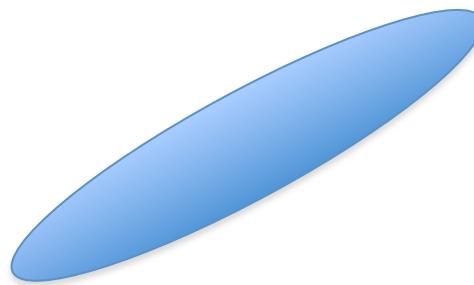


Diffusion Tensor Shape



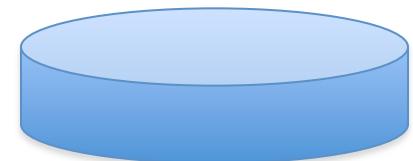
$$\lambda_1 = \lambda_2 = \lambda_3$$

Isotropic media
(Cerebrospinal
Fluid, gray matter)



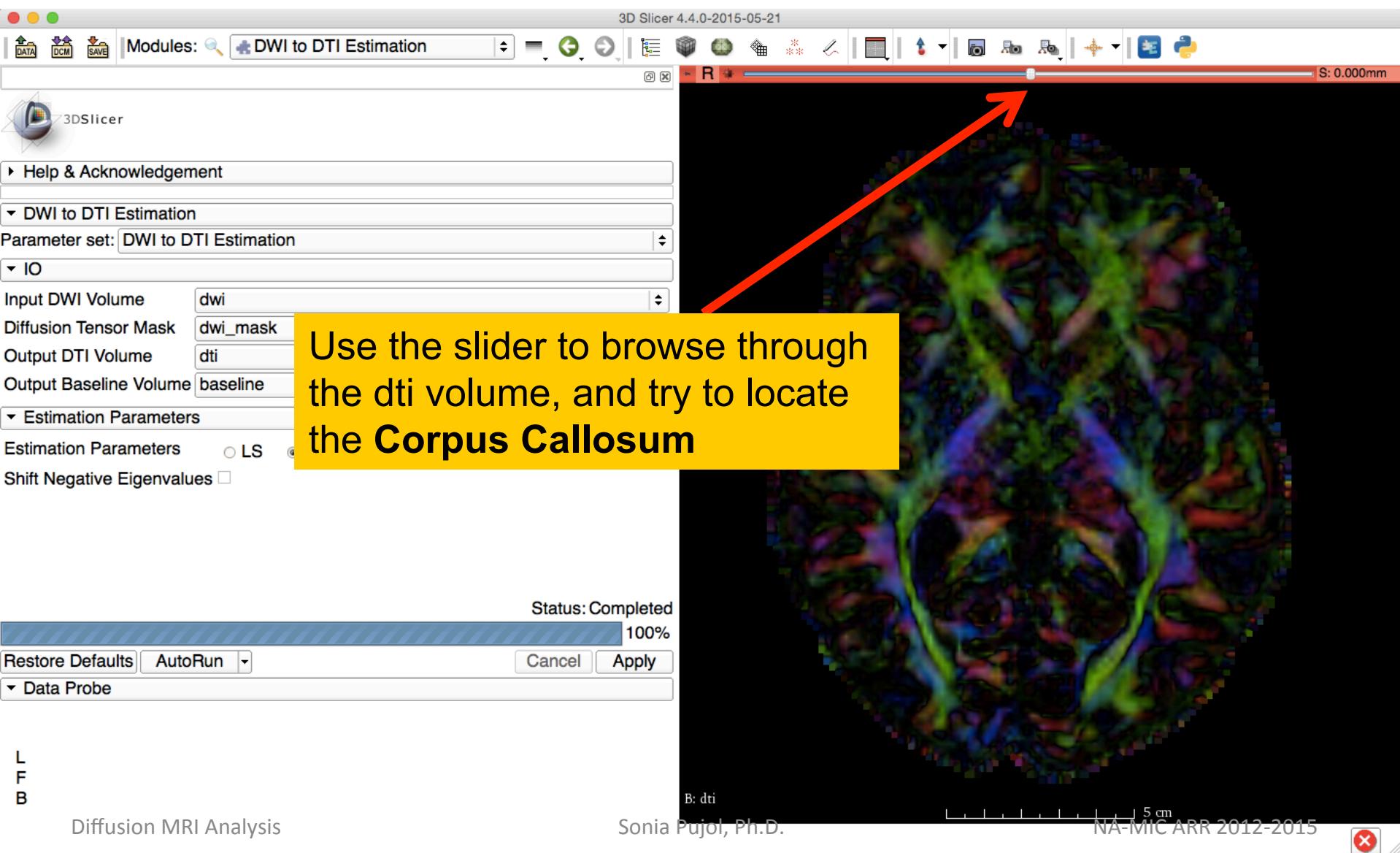
$$\lambda_1 >> \lambda_2, \lambda_3$$

Anisotropic media
(white matter)



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

Exploring the DWI Dataset



Corpus Callosum

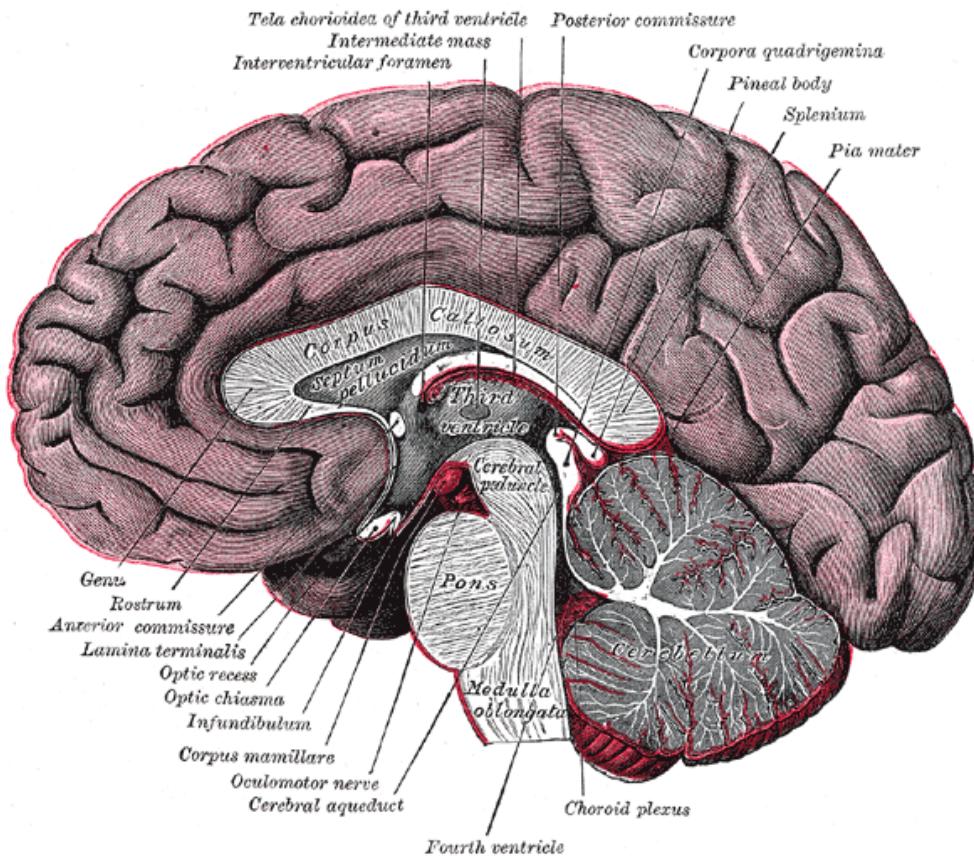


Image from Gray's Anatomy

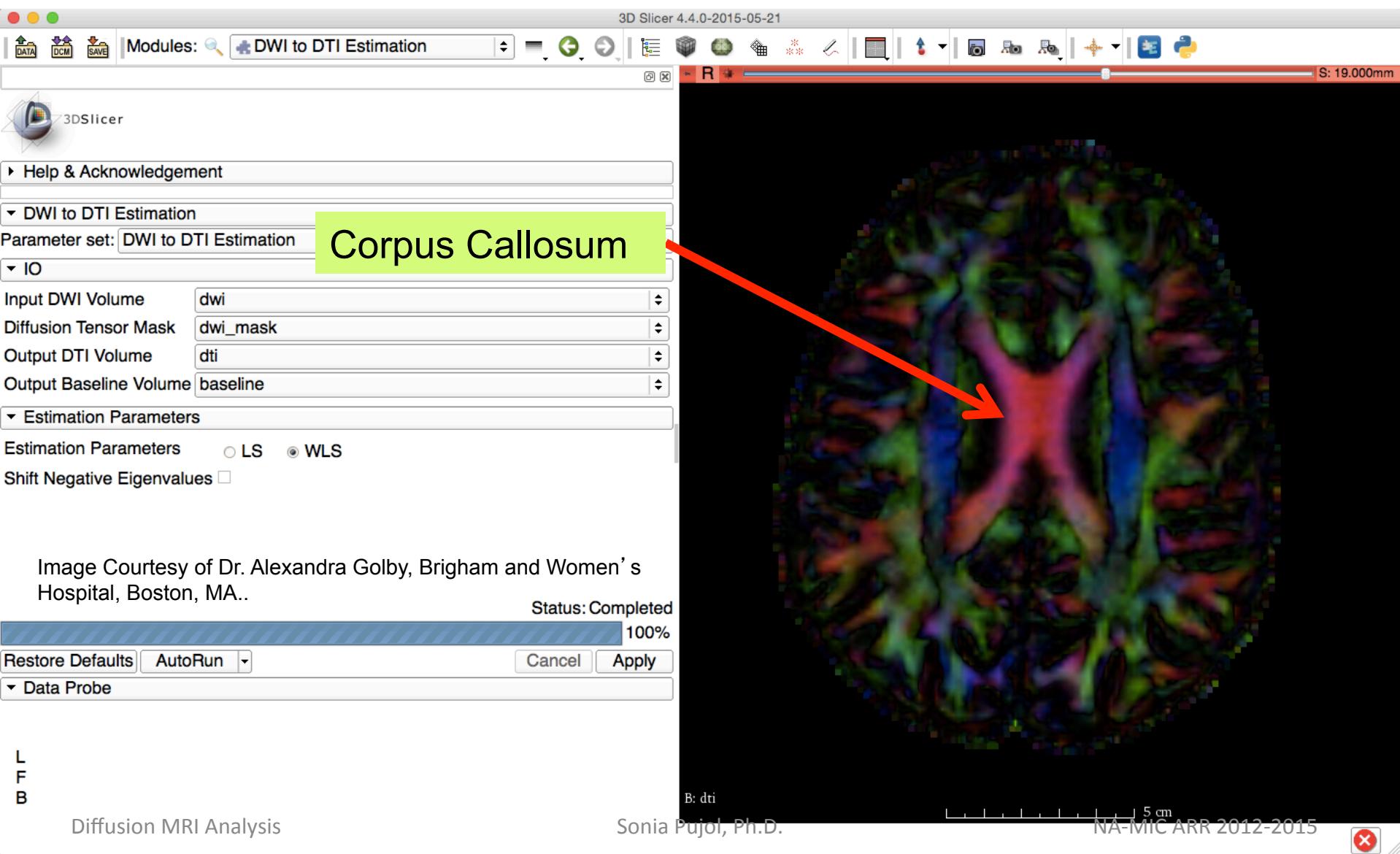
Diffusion MRI Analysis

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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

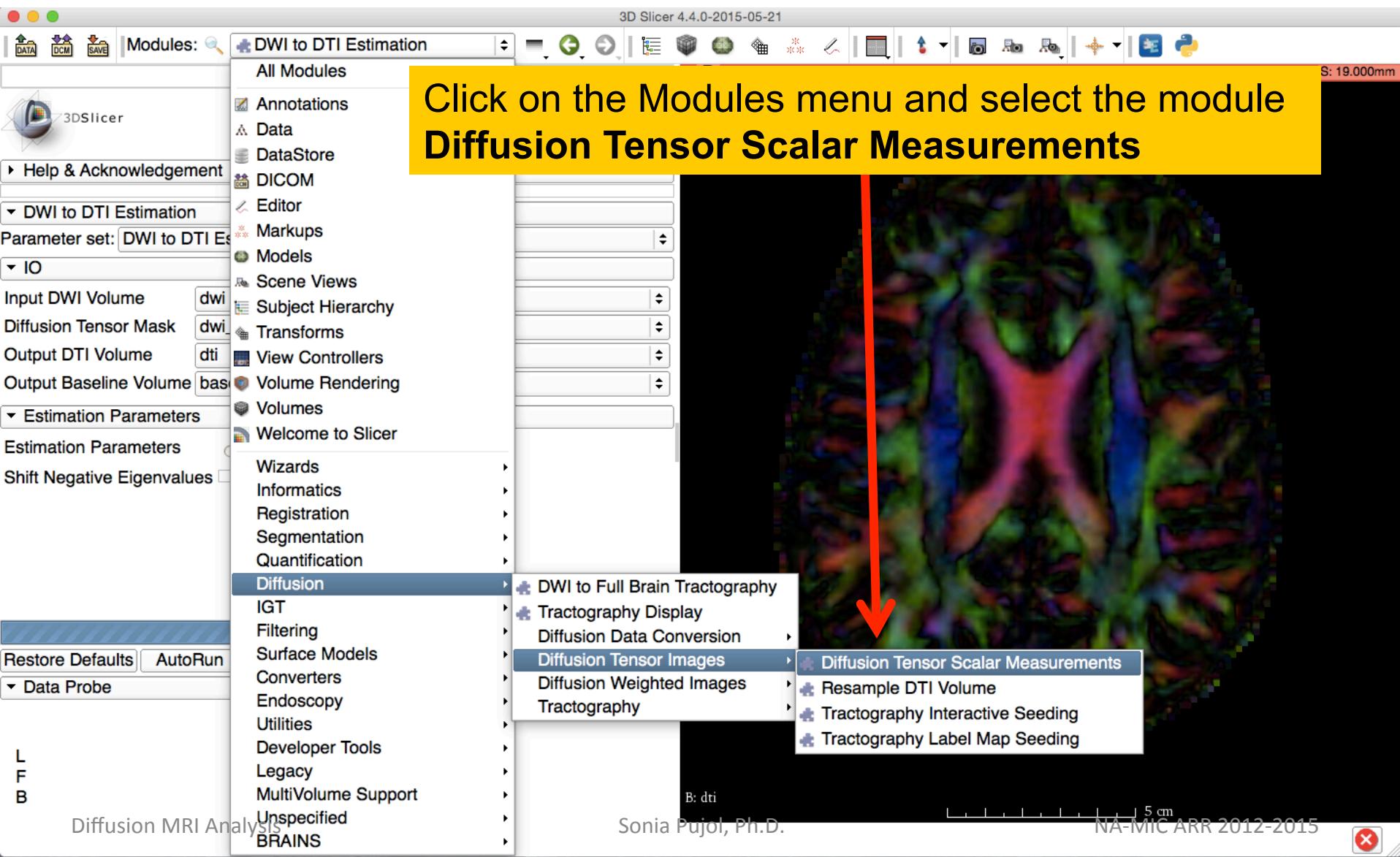


Characterizing the Size of the tensor: Trace

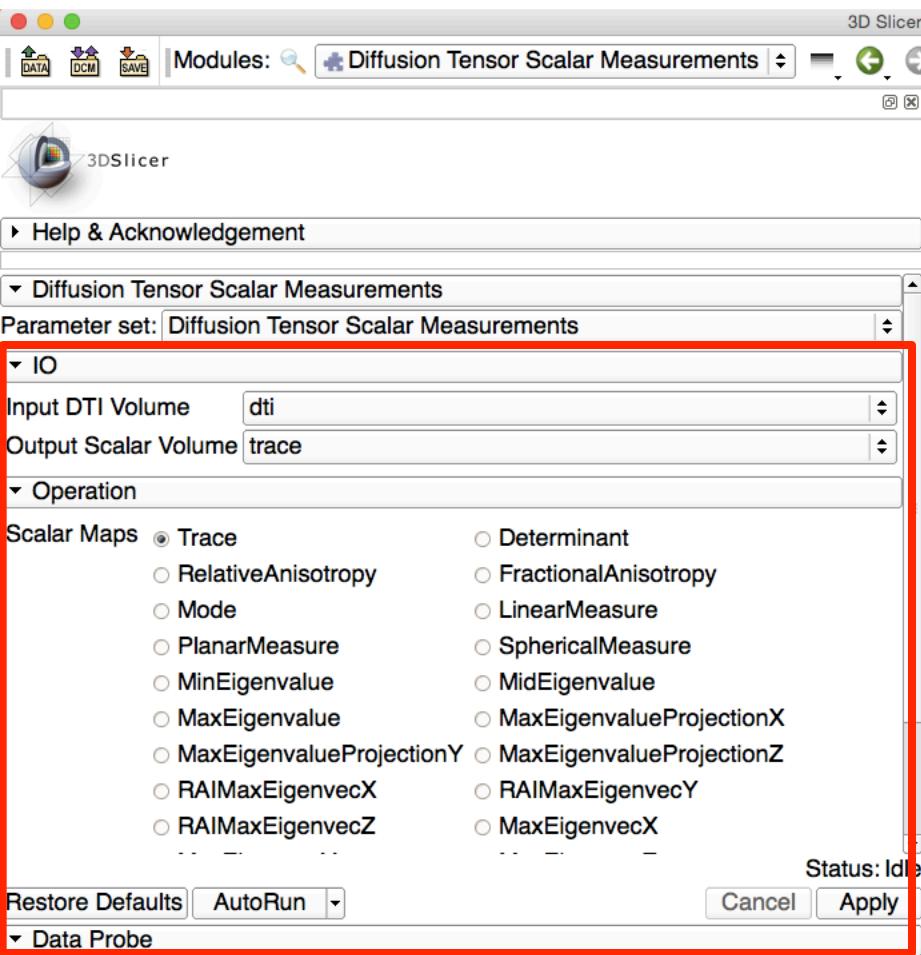
$$\text{Trace}(D) = \lambda_1 + \lambda_2 + \lambda_3$$

- $\text{Trace}(D)$ 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



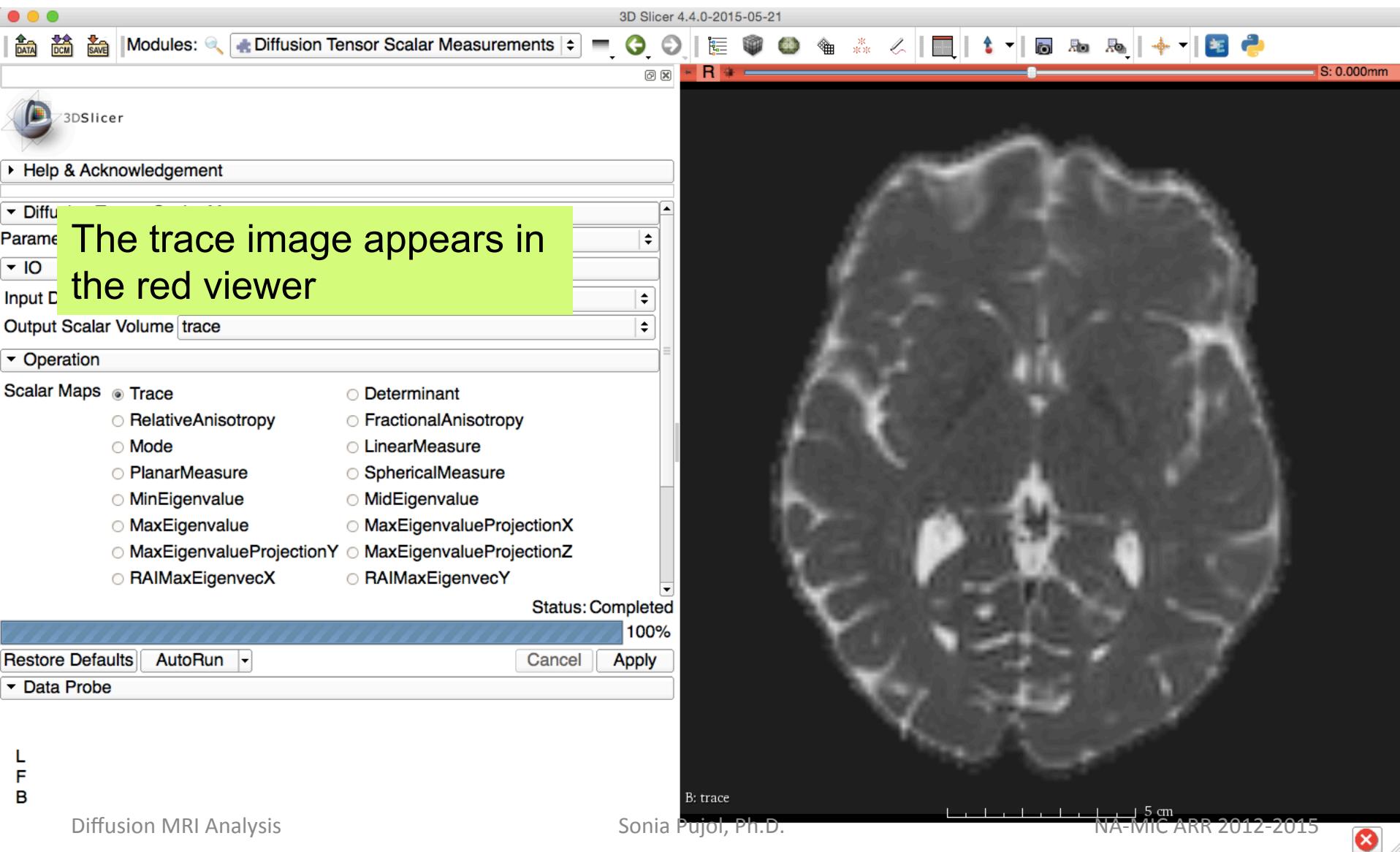
Trace



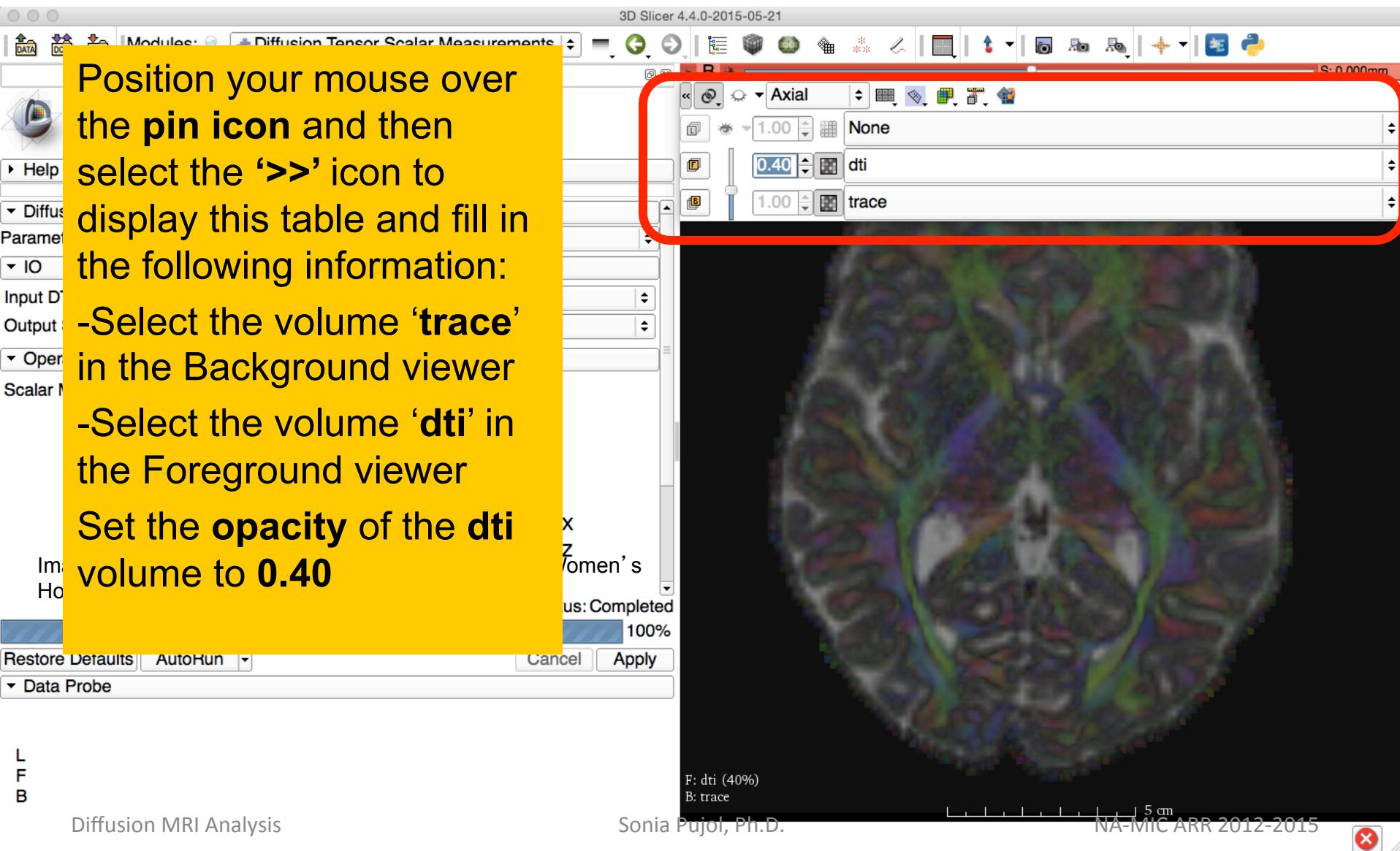
Type in the following information in the IO menu:

- 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



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%

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

R S: 19.000mm

F: dti (40%)
B: trace

5 cm

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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

Scalar Maps

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

Status: Completed 100%

Buttons: Restore Defaults, AutoRun, Cancel, Apply

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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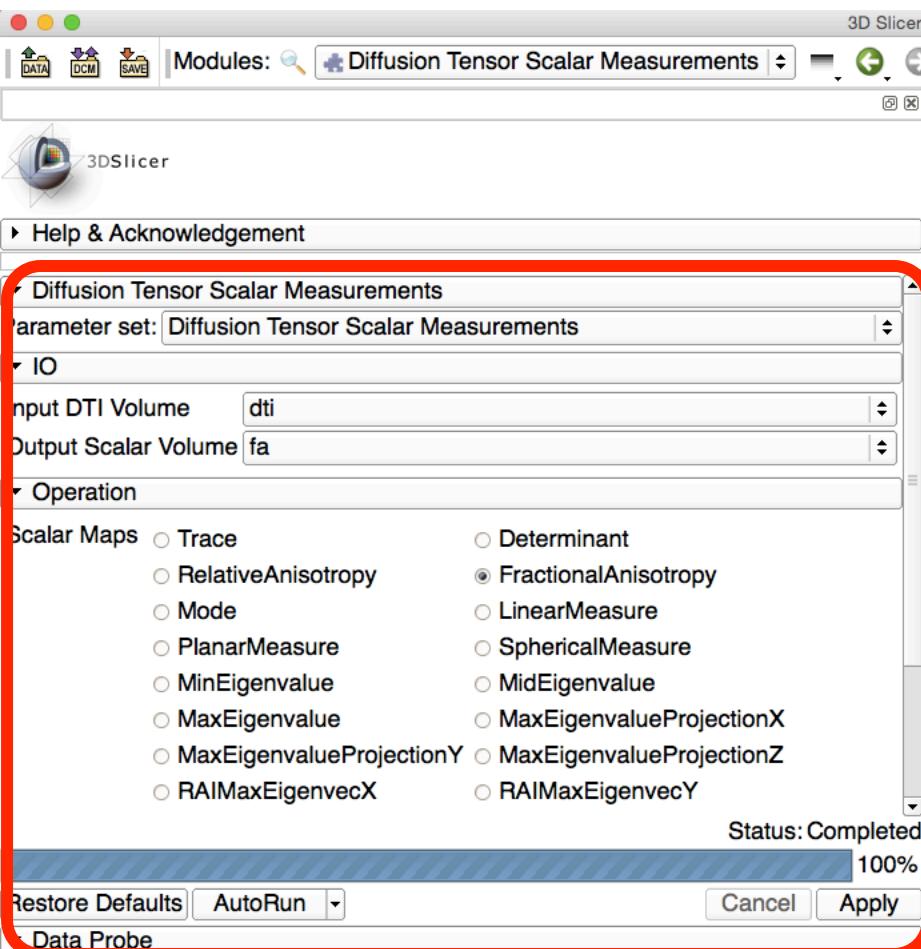
NA-MIC ARR 2012-2015

Scalar Maps: Fractional Anisotropy

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

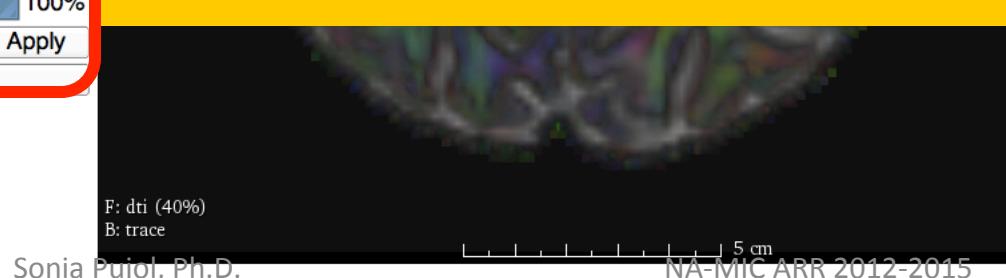
- FA(D) is intrinsic to the tissue and is independent of fiber orientation, and diffusion sensitizing gradient directions
- FA(D) is useful to characterize the shape (degree of ‘out-of-roundness’) of the diffusion ellipsoid
- Low FA:  → High FA: 

Fractional Anisotropy

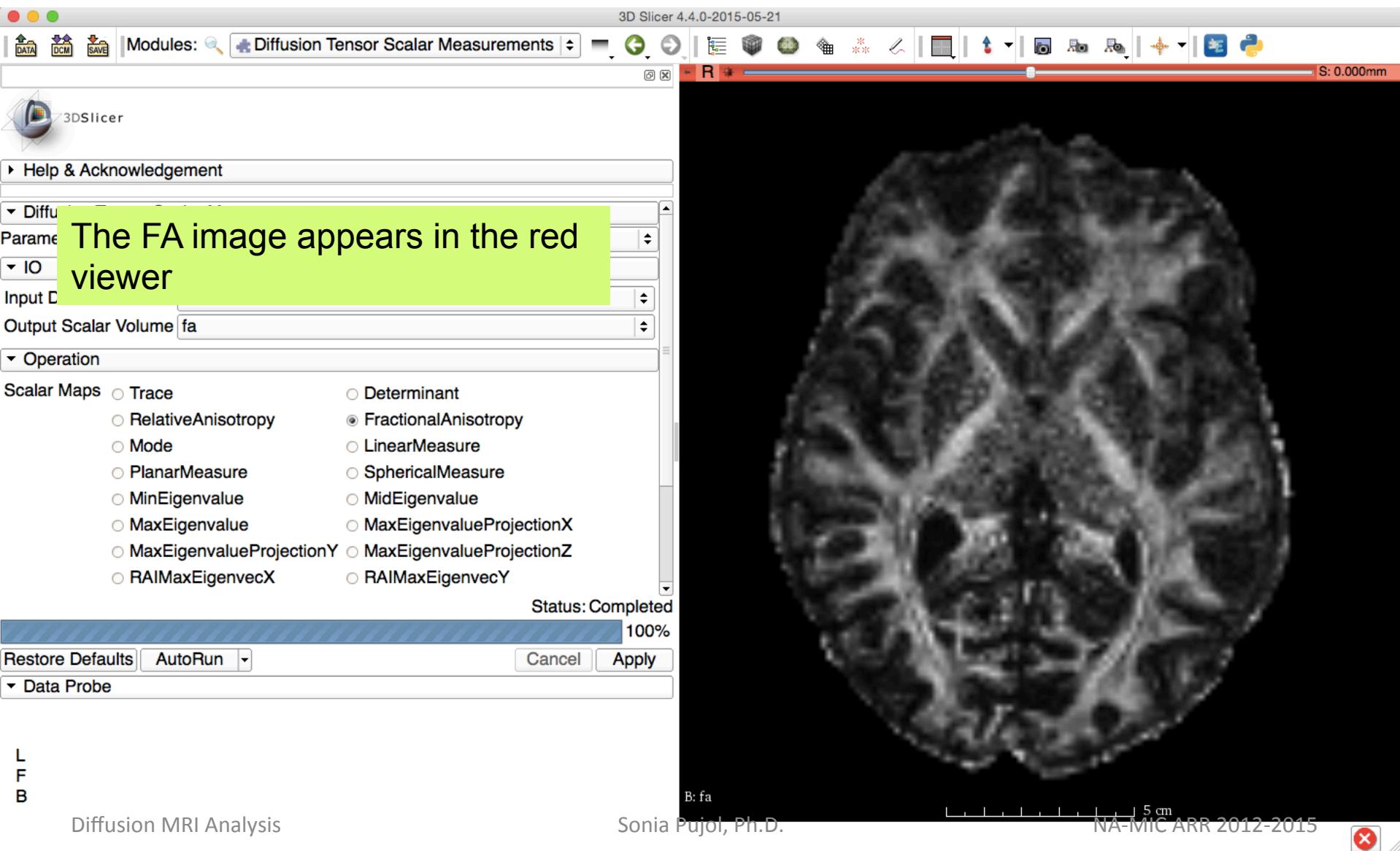


Fill in the following information:

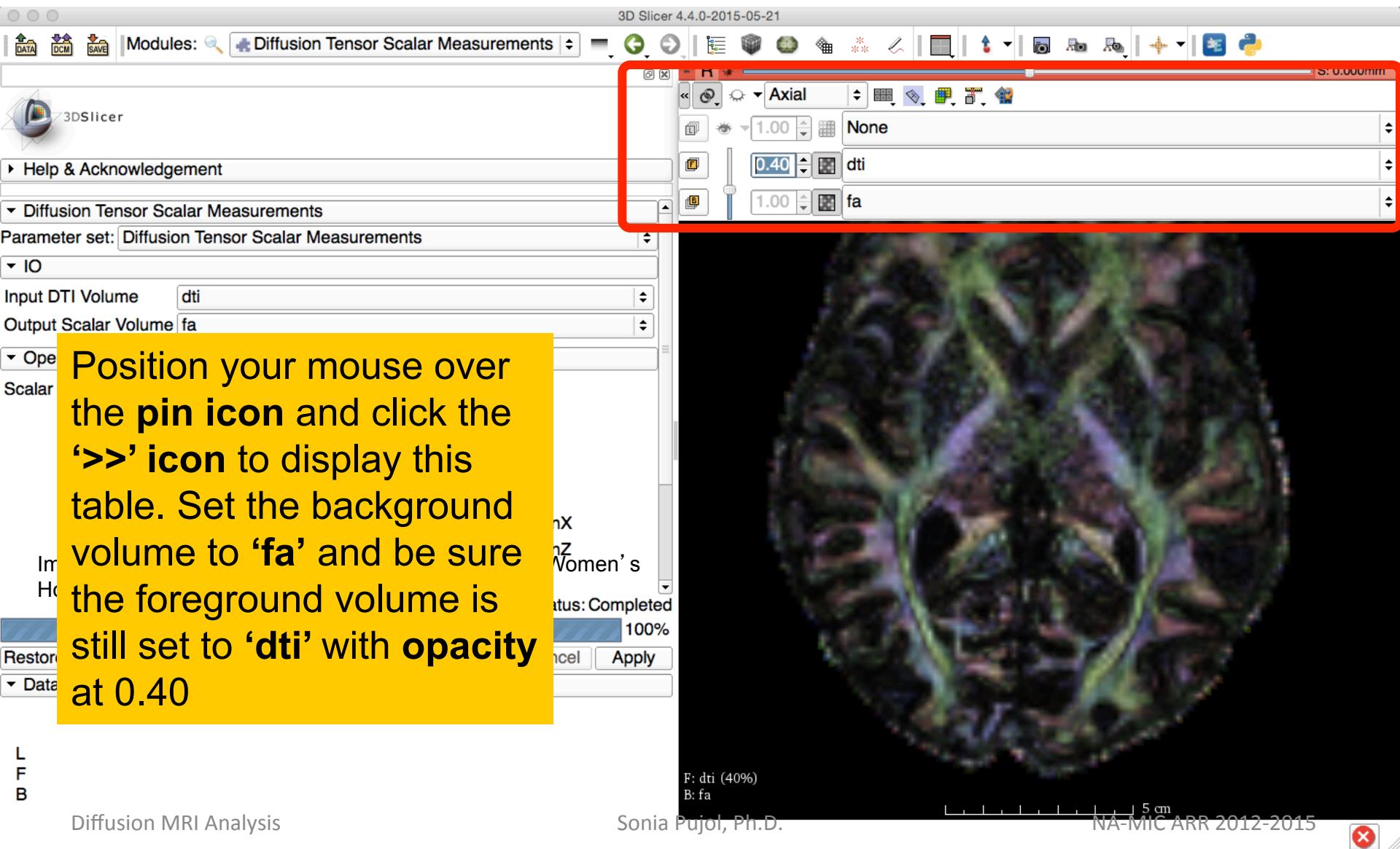
- Set **Input DTI Volume** to 'dti'
- Select **Output Scalar Volume** 'Create new Volume' and rename it 'fa'
- Select the Operation '**Fractional Anisotropy**'
- Click on **Apply** to calculate the Fractional Anisotropy map of the tensor volume



Fractional Anisotropy



Fractional Anisotropy



Fractional Anisotropy

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

Scalar Maps

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

Status: Completed 100%

Buttons: Restore Defaults Auto Run 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

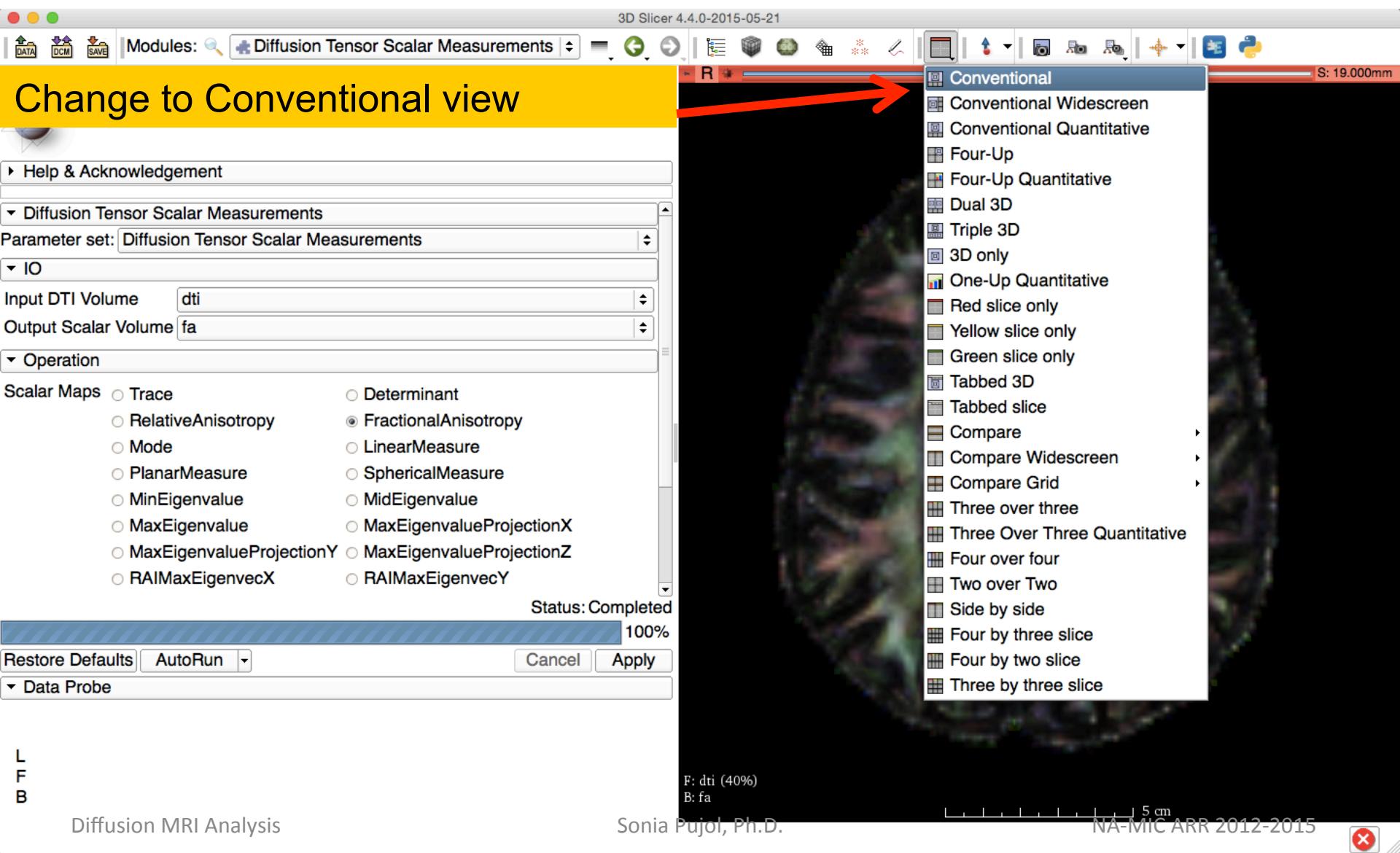
R S: 19.000mm

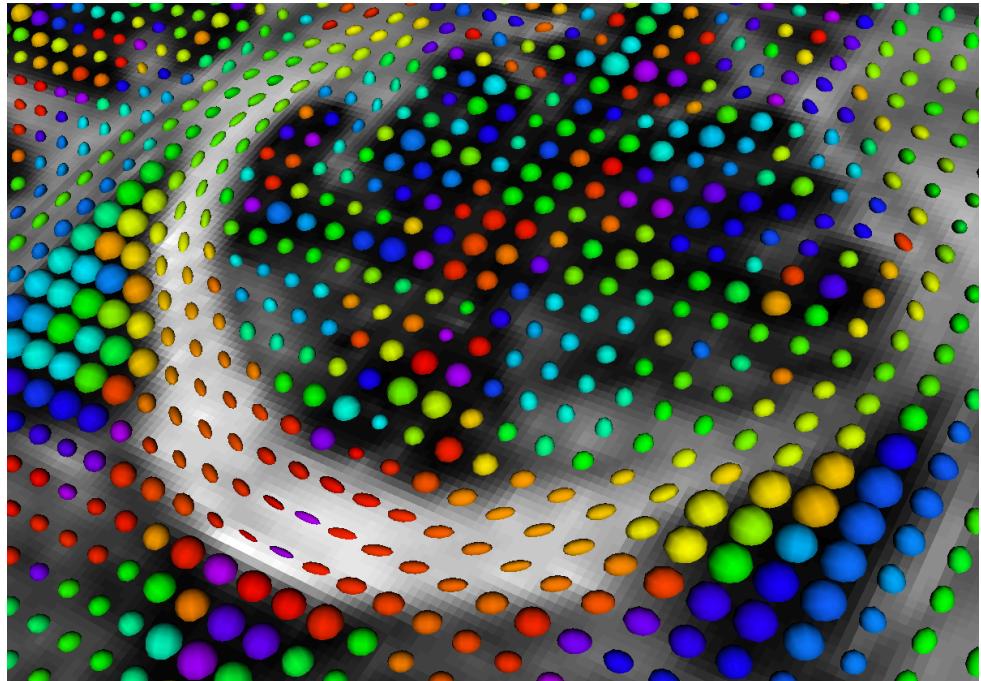
F: dti (40%)
B: fa

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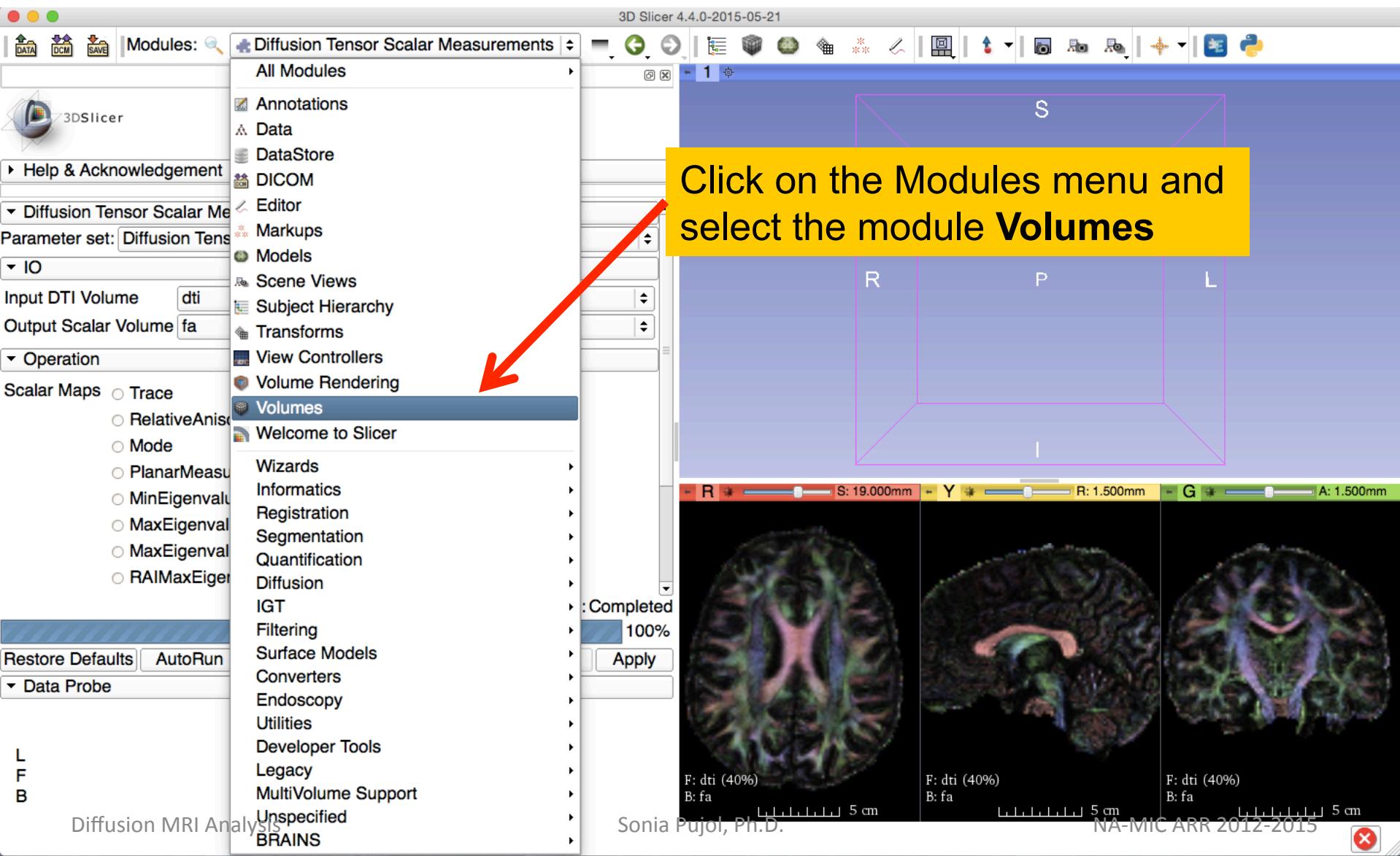
Fractional Anisotropy



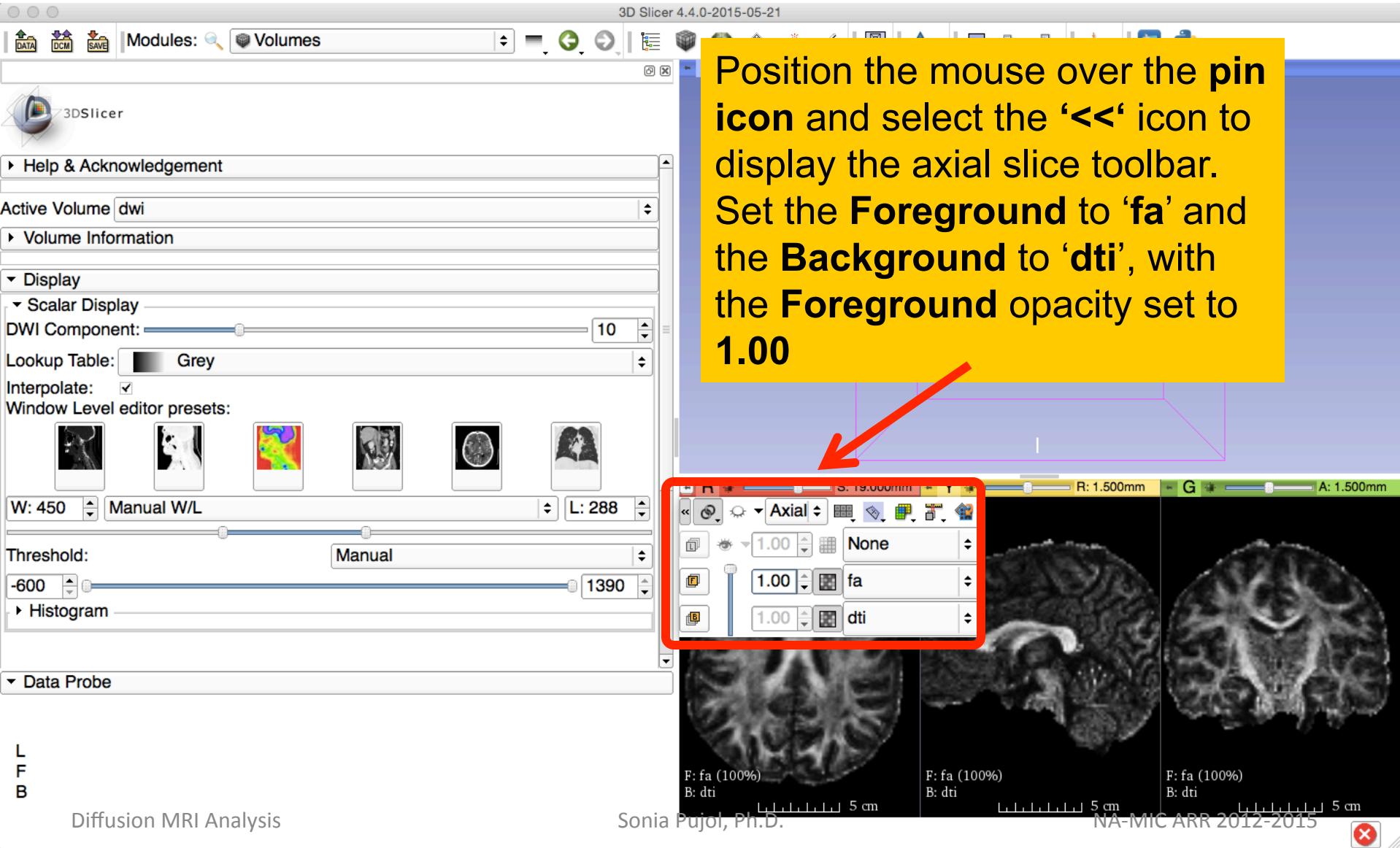


Part 2: Visualizing the tensor data

3D Visualization: Glyphs



3D Visualization: Glyphs



3D Visualization: Glyphs

3D Slicer 4.4.0-2015-05-21

DATA DCM SAVE Modules: Volumes 1

3DSlicer

Help & Acknowledgement

Active Volume: dti

Volume Information

Display

Scalar Display

Scalar Mode: ColorOrientation

Lookup Table: Grey

Interpolate:

Window Level editor presets:

W: 255 L: 128

Threshold: Off

-600 600

Histogram

Glyphs on Slices Display

Slice Visibility: Red Yellow Green

Data Probe

L F B

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

R S: 19.000mm Y R: 1.500mm G A: 1.500mm

F: fa (100%) B: dti 5 cm

F: fa (100%) B: dti 5 cm

F: fa (100%) B: dti 5 cm

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Diffusion MRI Analysis

The screenshot shows the 3D Slicer interface with a brain MRI volume loaded. A pink wireframe cube is overlaid on the image, representing a 3D region of interest. Below the image are three axial slices. A yellow callout box highlights the 'Scalar Mode' setting in the 'Scalar Display' section of the control panel, which is set to 'ColorOrientation'. The control panel also includes settings for 'Active Volume' (set to 'dti'), 'Window Level' (W: 255, L: 128), 'Threshold' (-600 to 600), and 'Glyphs on Slices Display' (slice visibility checkboxes for Red, Yellow, and Green). The bottom of the screen shows the 3D Slicer logo and copyright information.

3D Visualization: Glyphs

3D Slicer 4.4.0-2015-05-21

Modules: Volumes

3DSlicer

W: 255 Auto W/L L: 128

Threshold: Off -600 600

Histogram

Glyphs on Slices Display

Slice Visibility: Red Yellow Green

Opacity: 1.00

Scalar ColorMap: FullRainbow

Color by Scalar: ColorOrientation

Scalar Range: 0 255

Glyph Type: Ellipsoids

Scale Factor: 50.00

Spacing: 5.00

Data Probe

L F B

Diffusion MRI Analysis

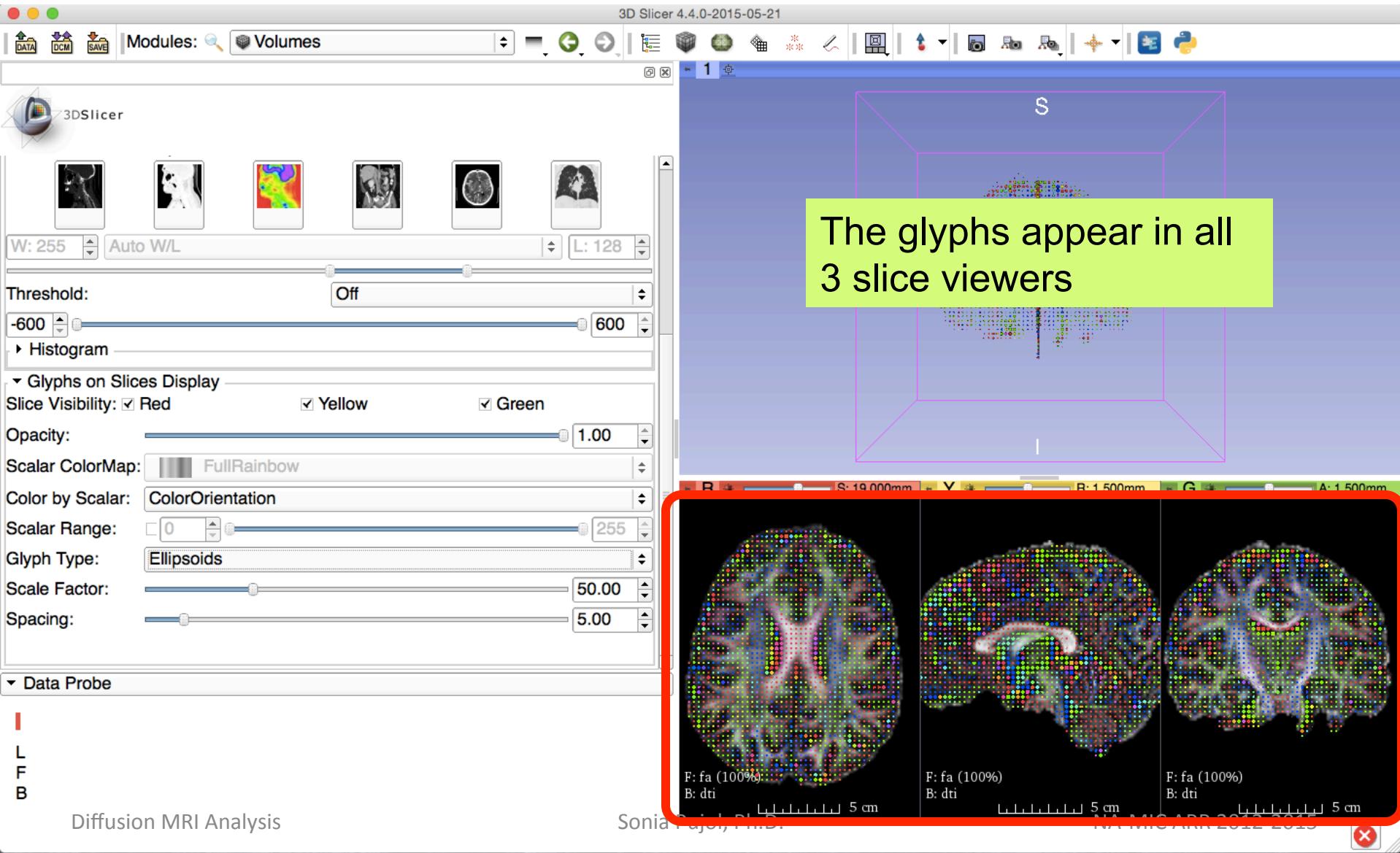
Scroll down the module panel and:

- 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**'

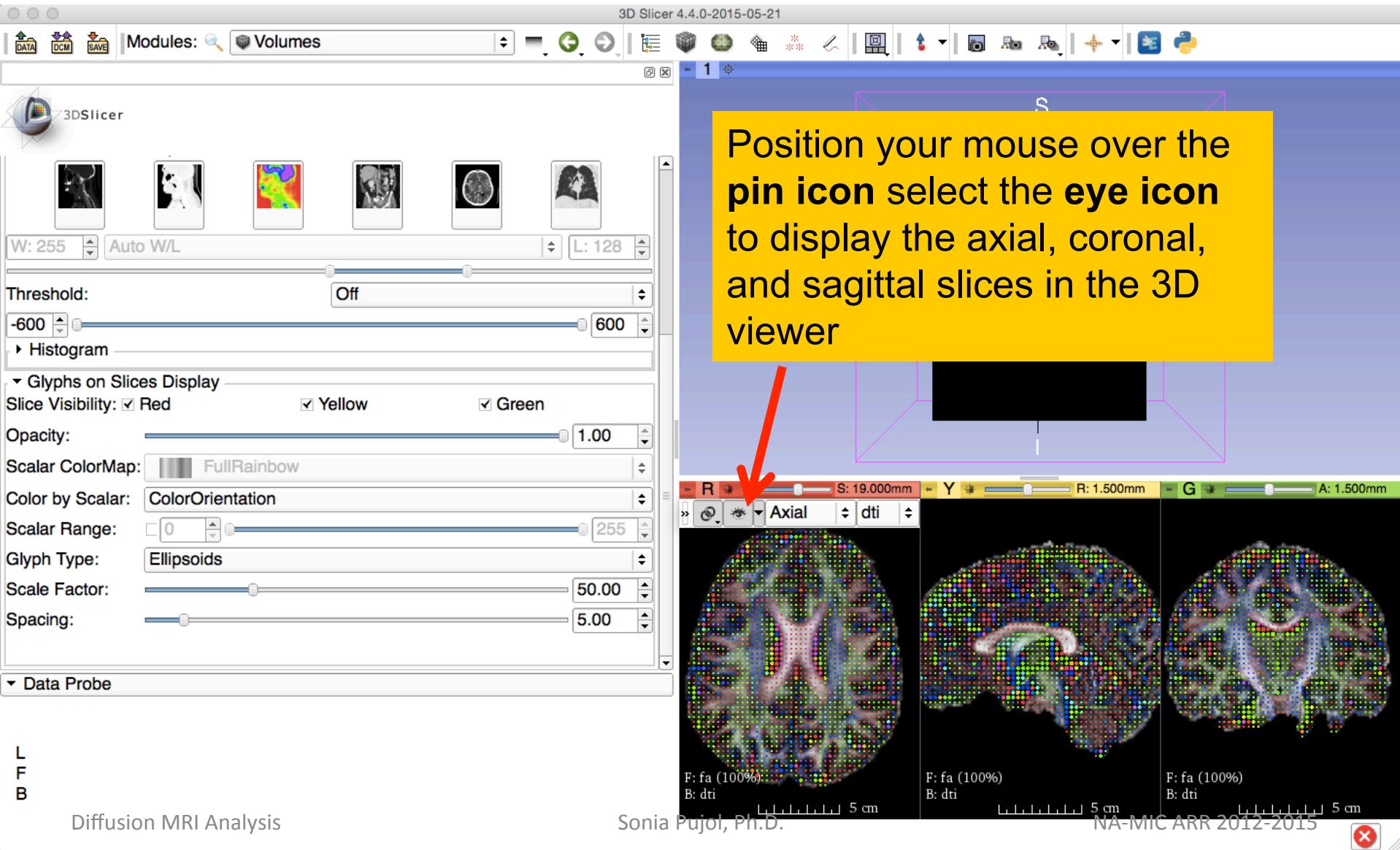
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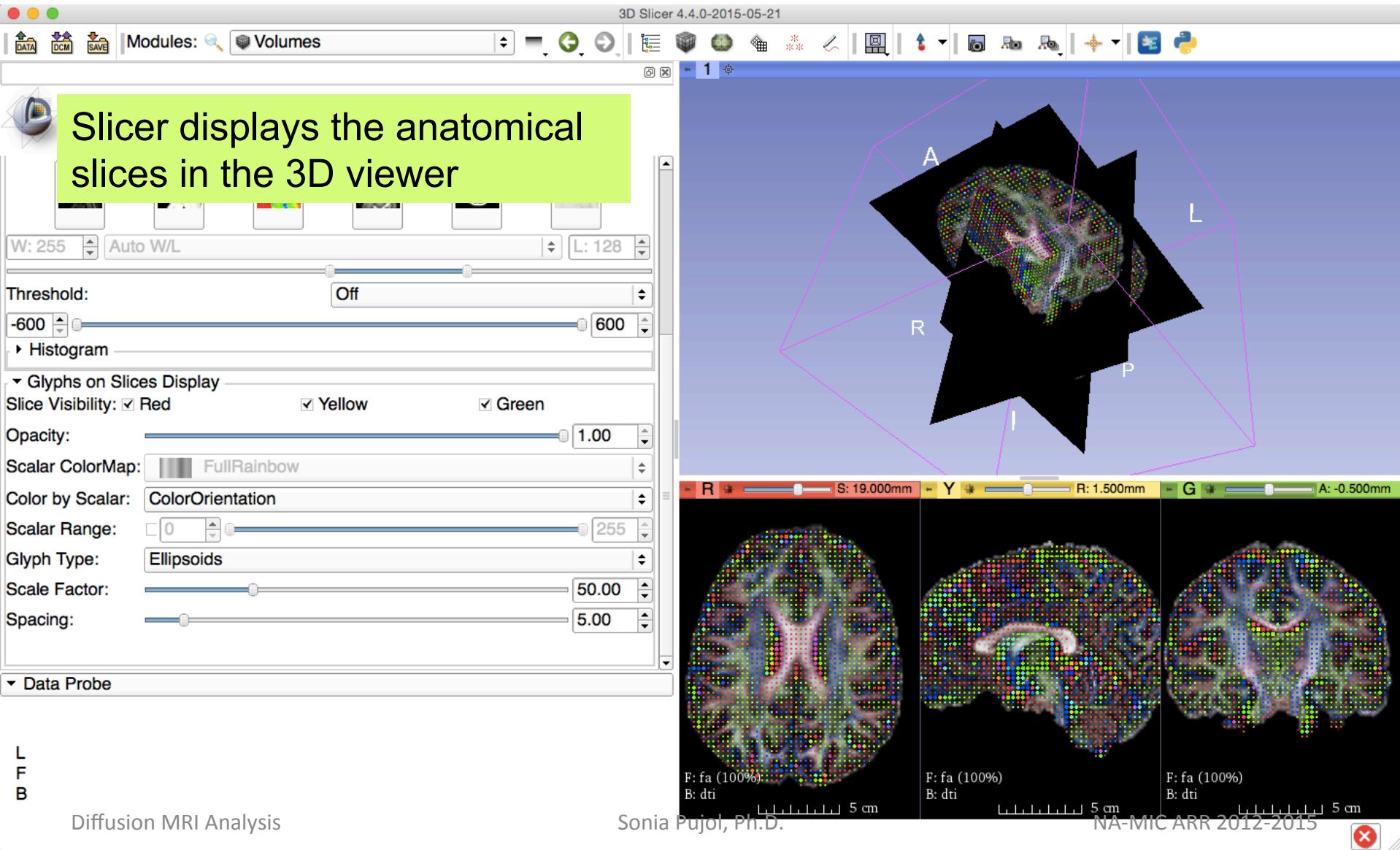
3D Visualization: Glyphs



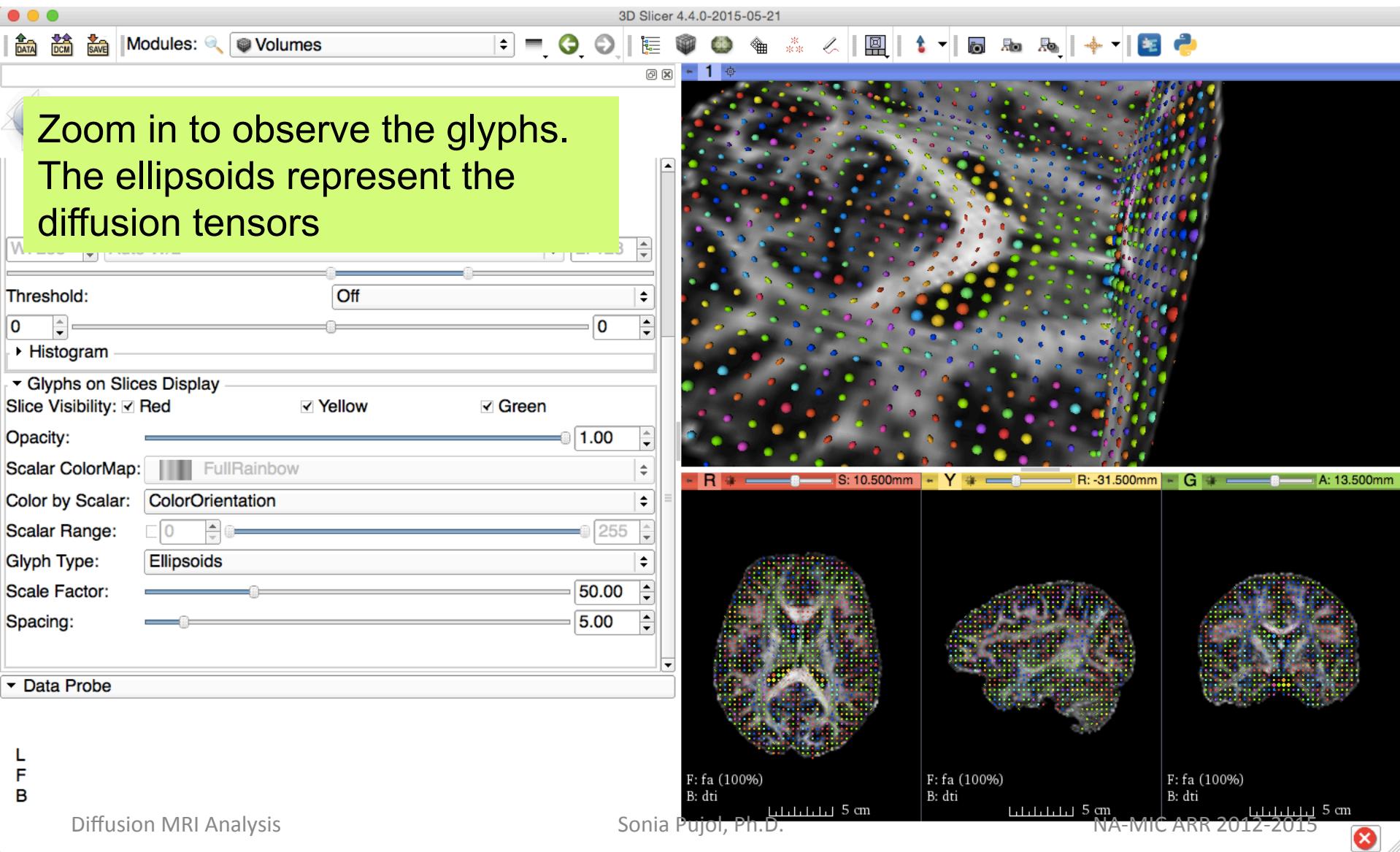
3D Visualization: Glyphs



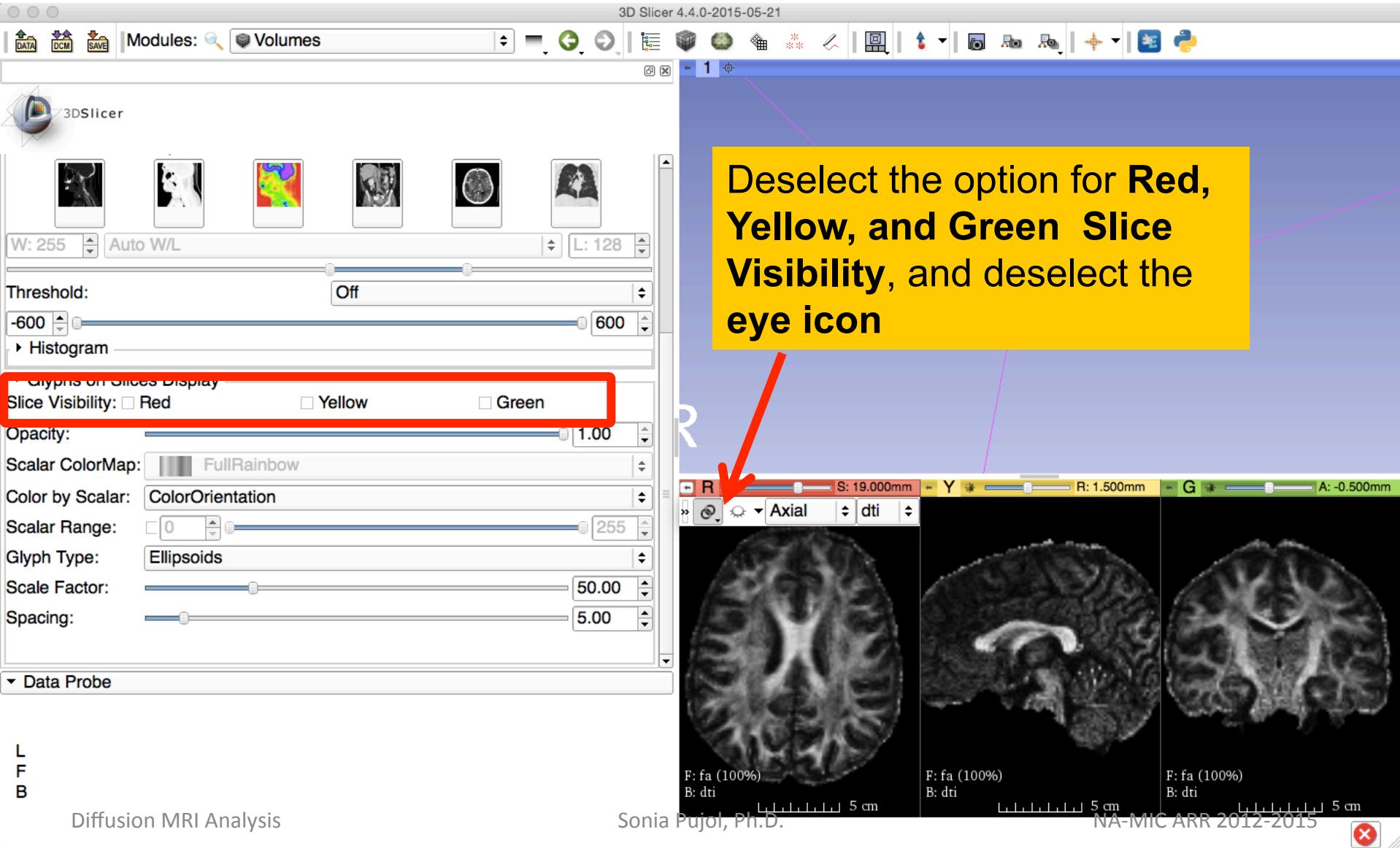
3D Visualization: Glyphs



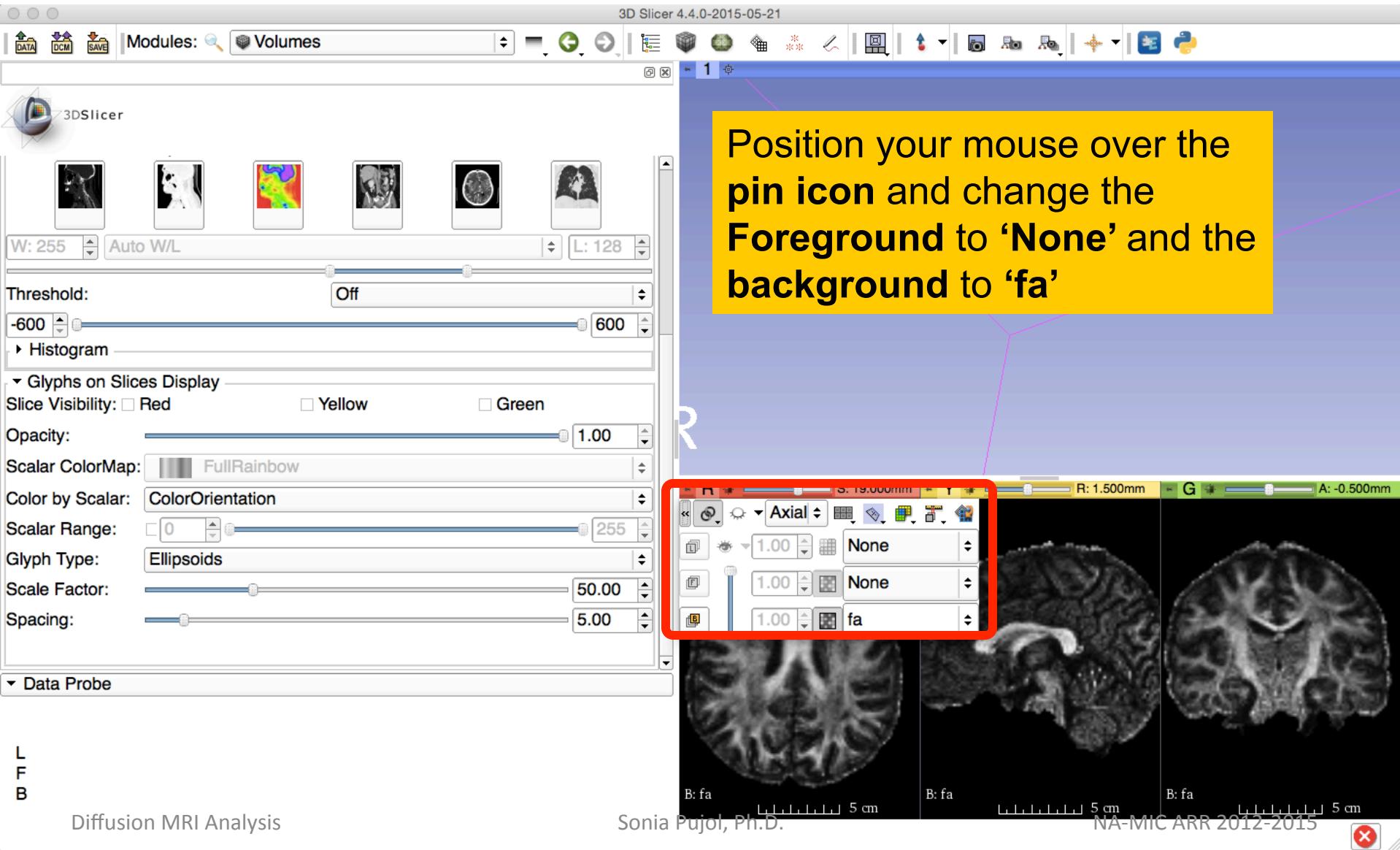
3D Visualization: Glyphs

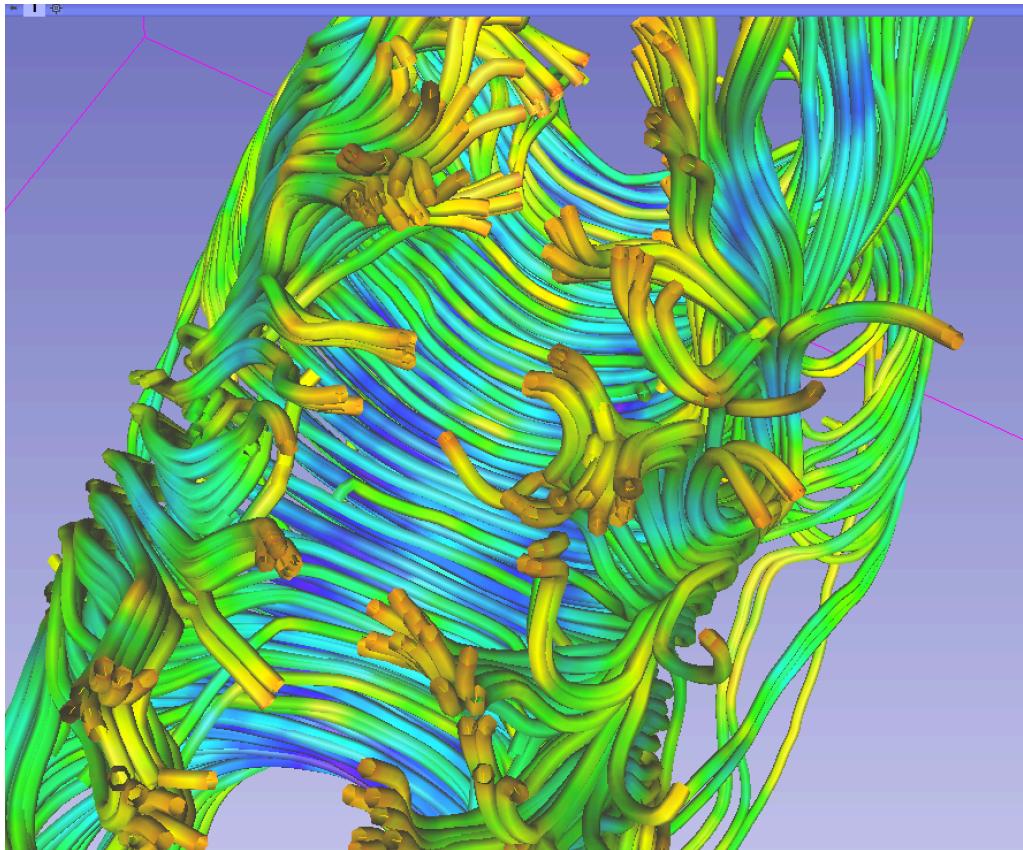


Diffusion MRI tractography



Diffusion MRI tractography



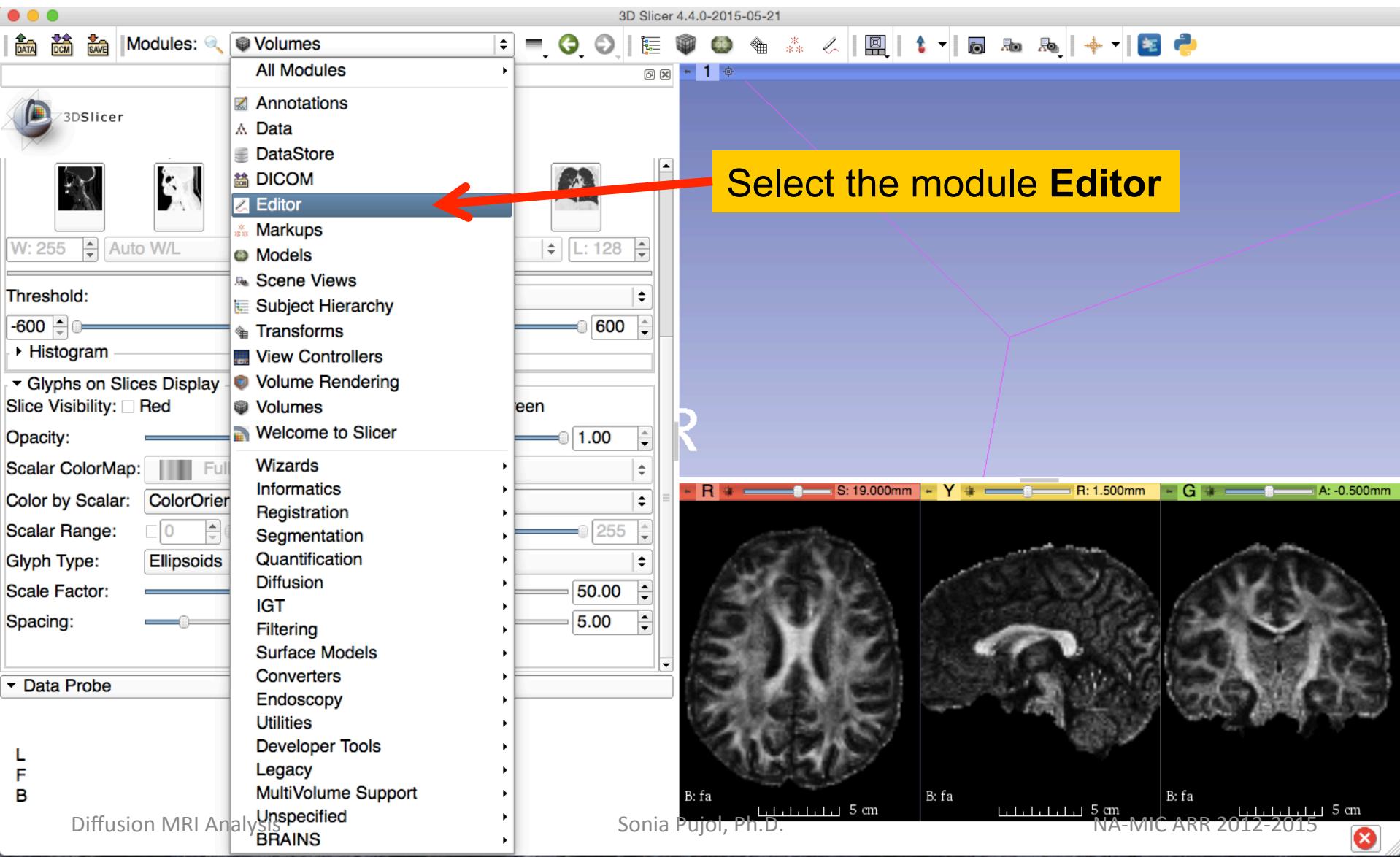


Part 3: From tensors to tracts

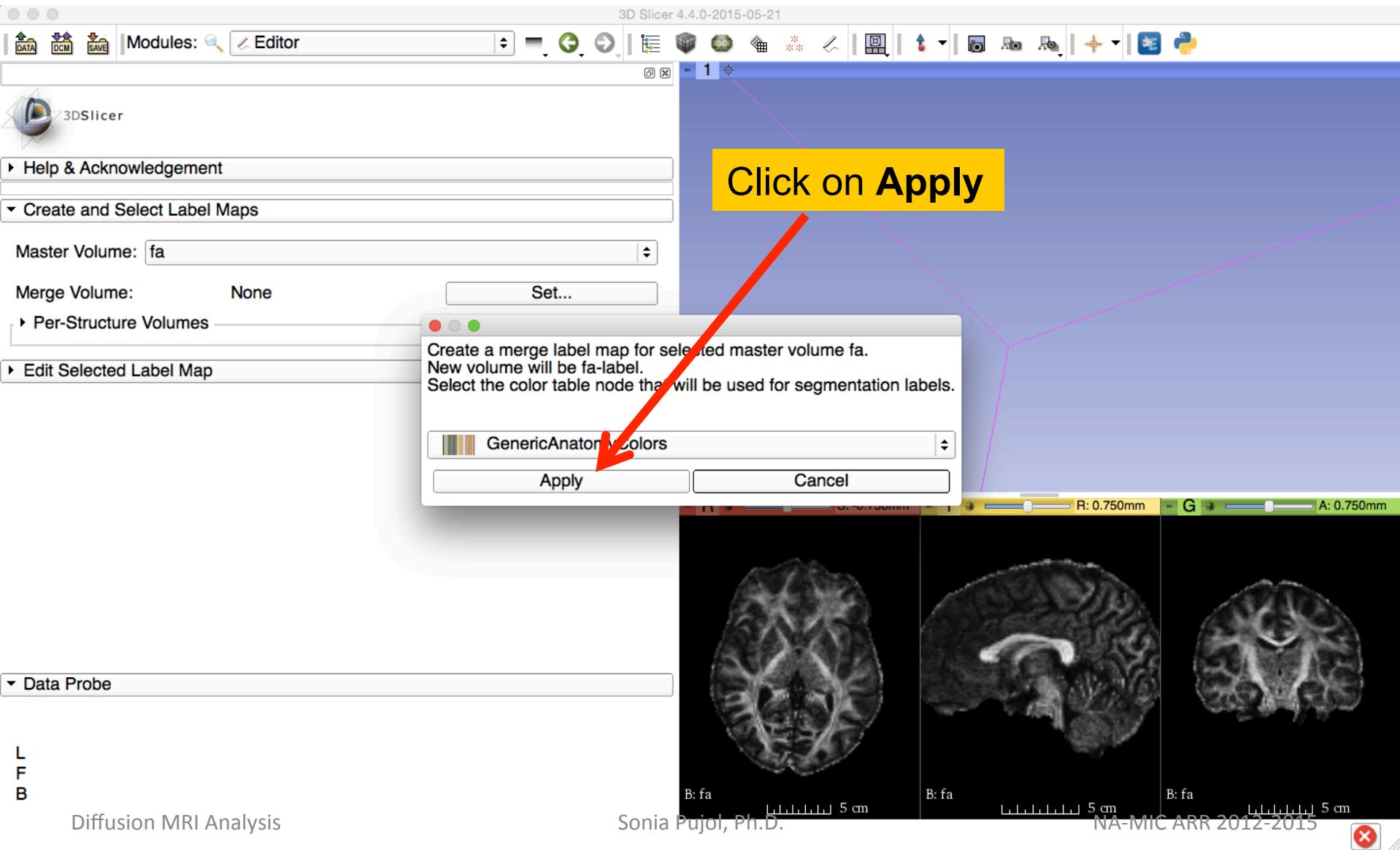
DTI tractography

- 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)

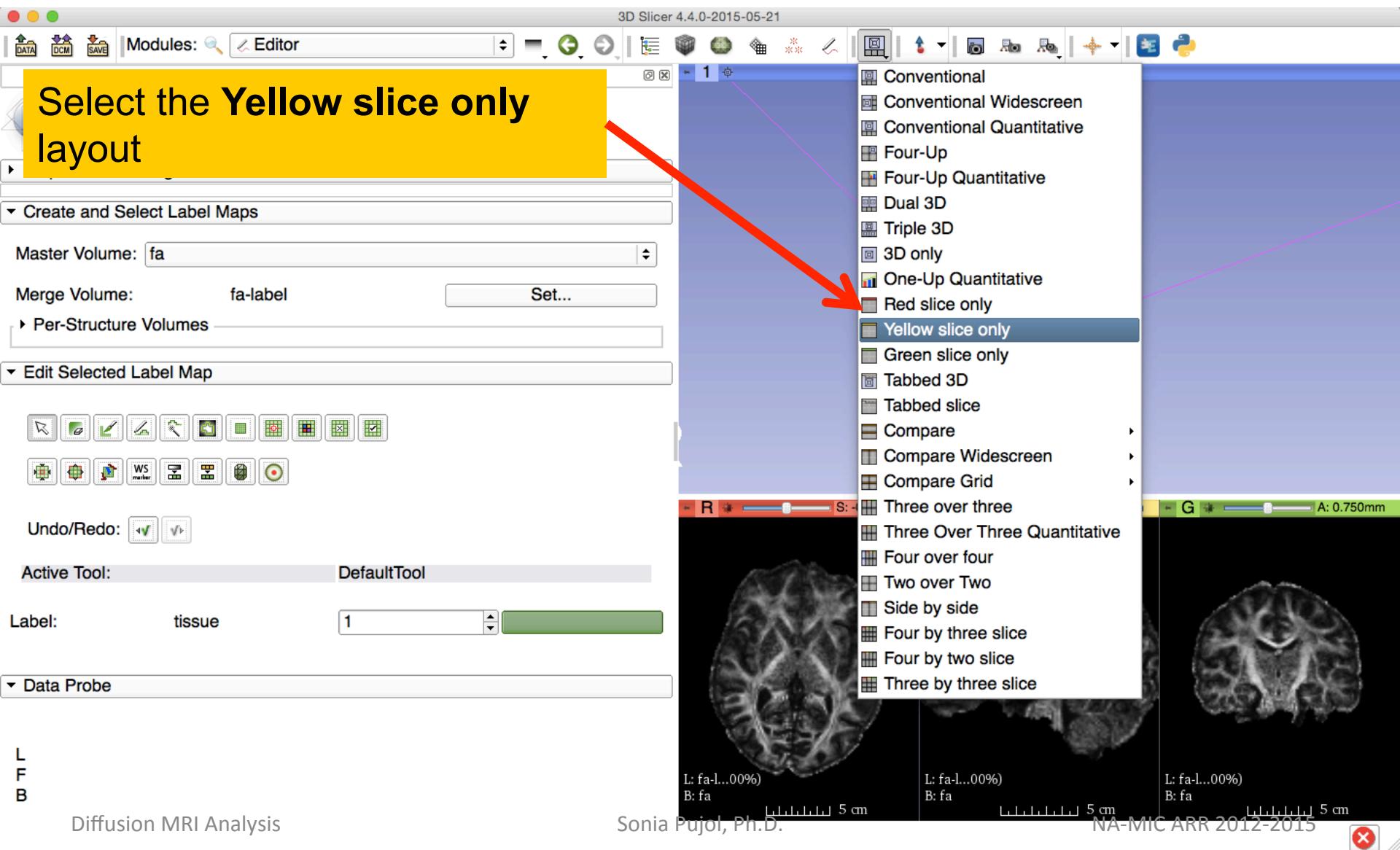
Diffusion MRI tractography



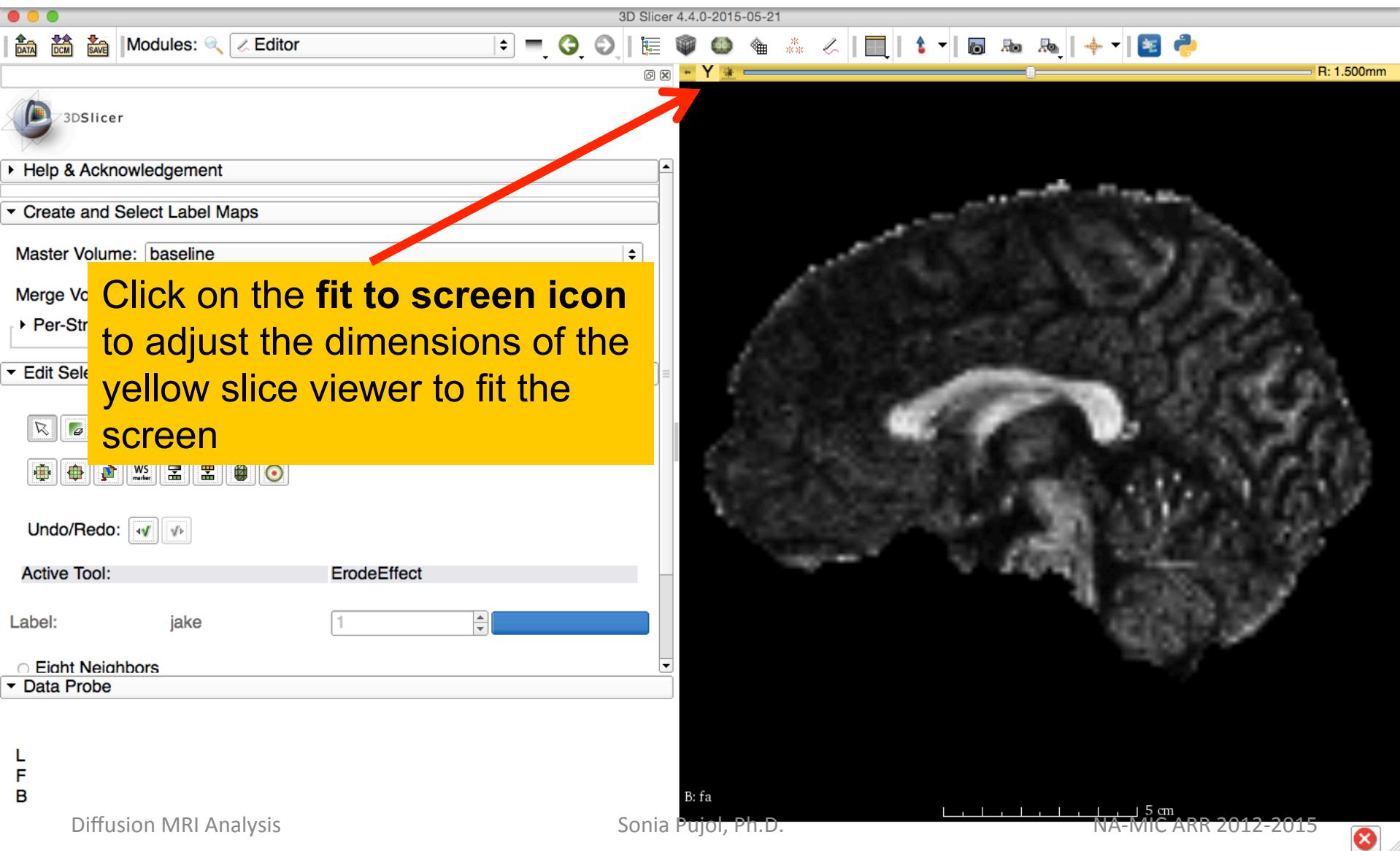
Diffusion MRI tractography



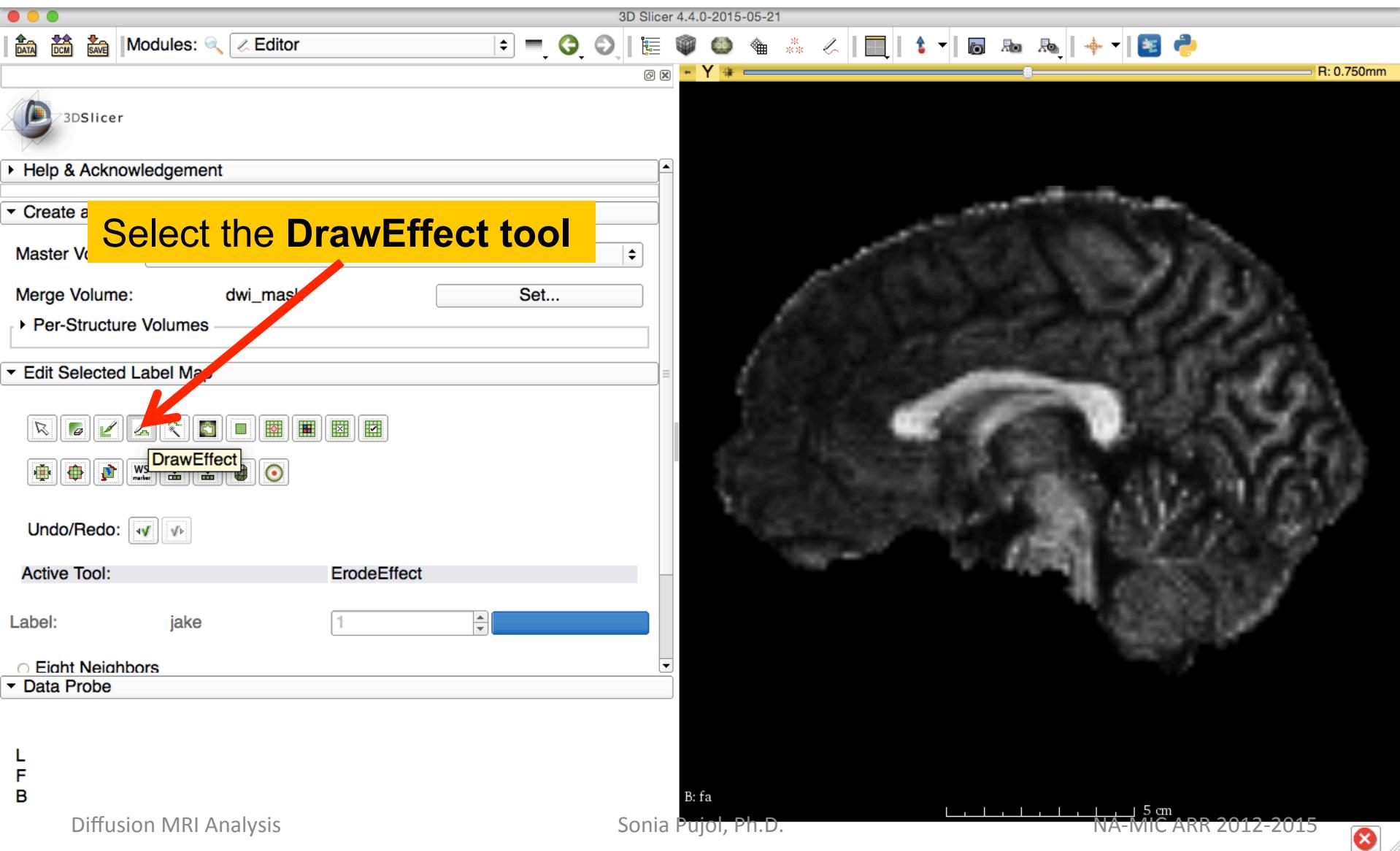
Diffusion MRI tractography



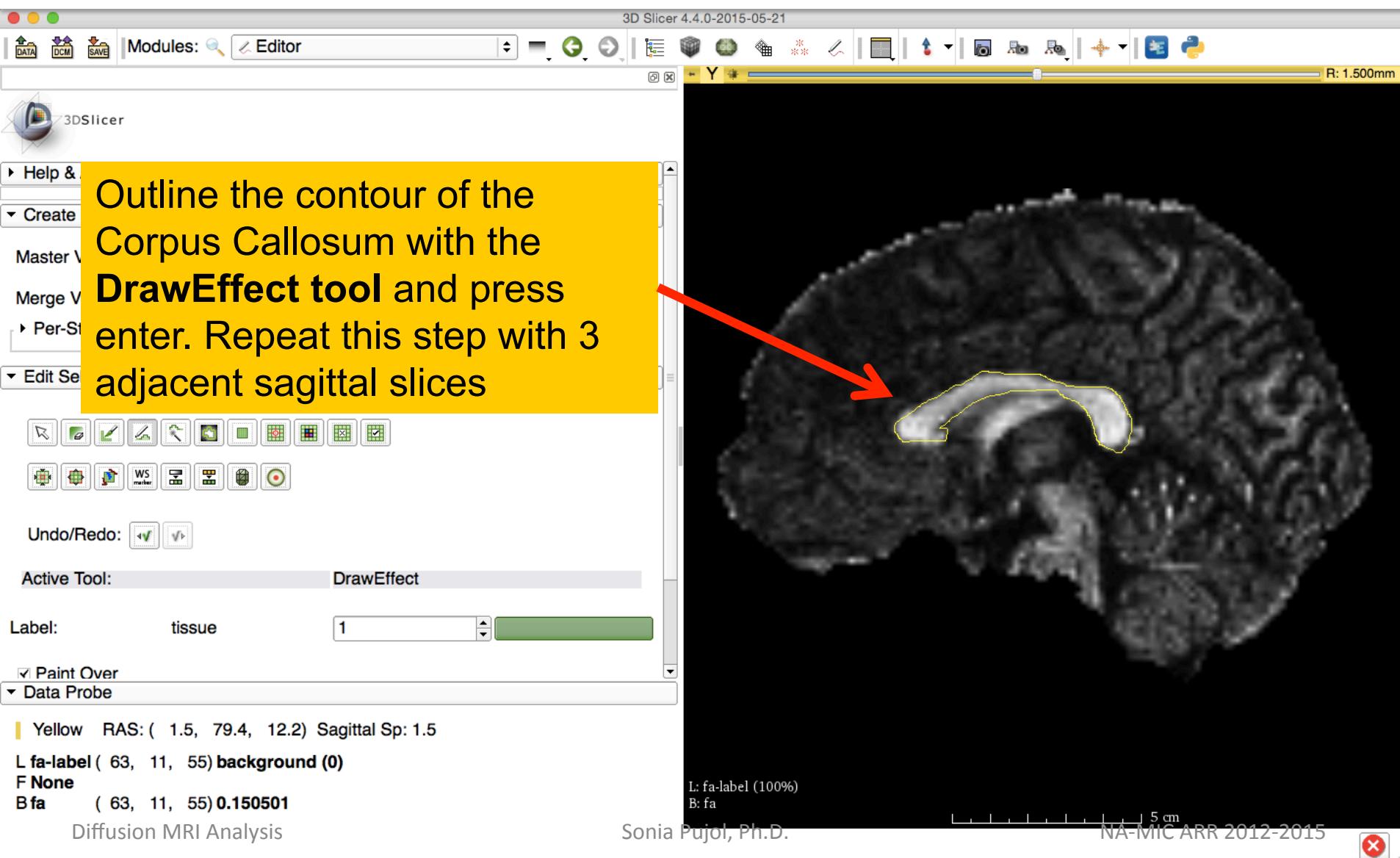
Diffusion MRI tractography



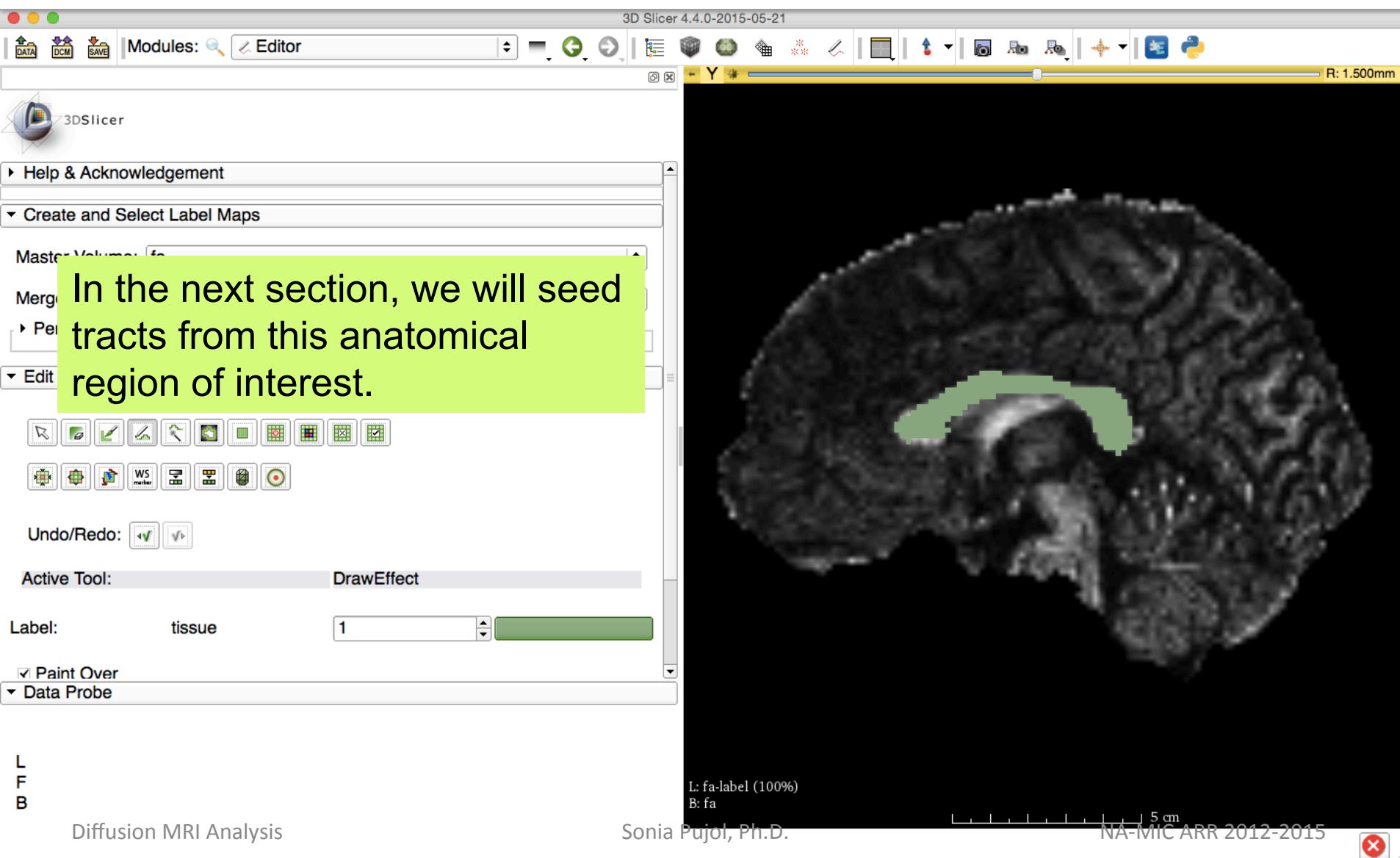
Diffusion MRI tractography



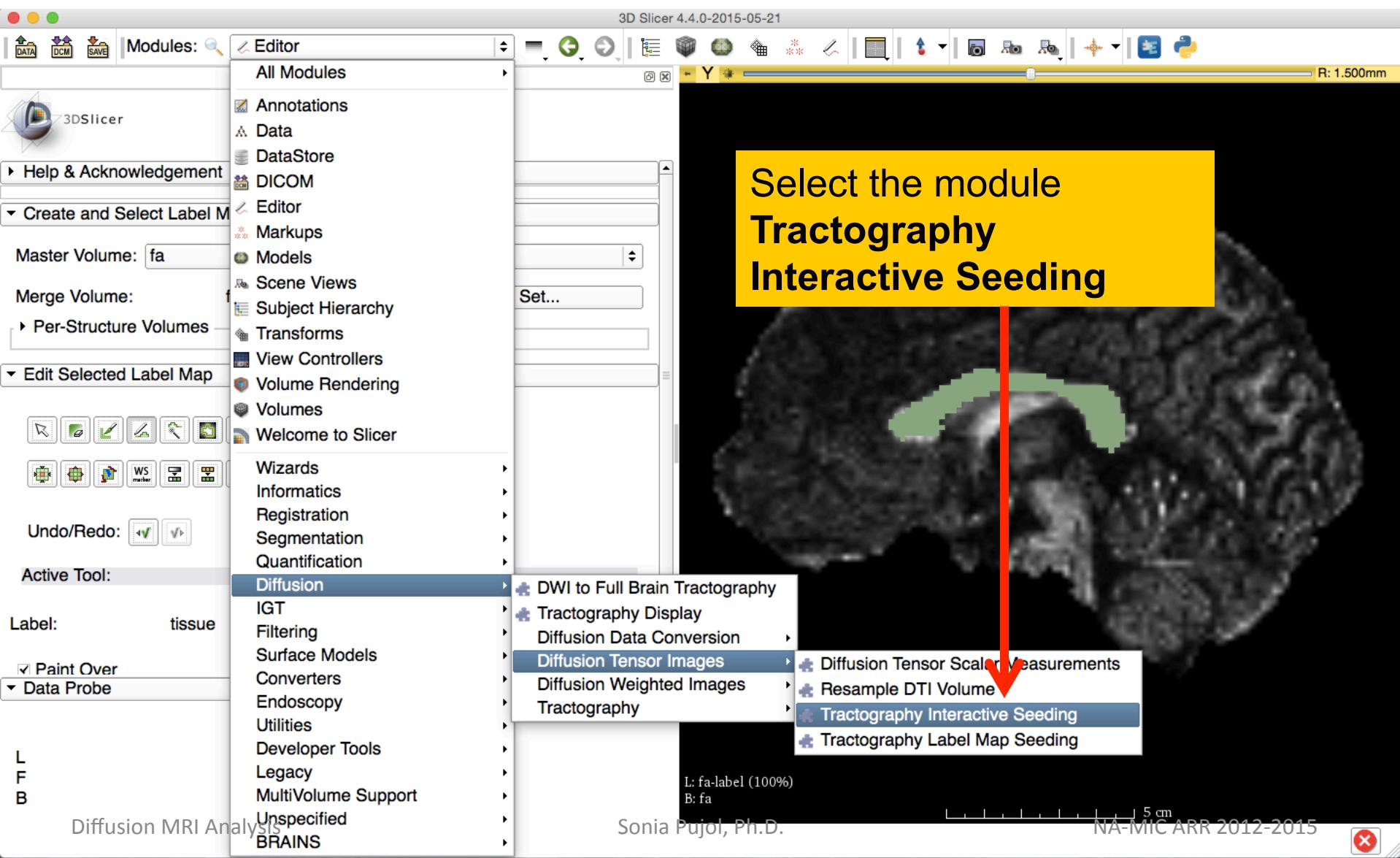
Diffusion MRI tractography



Diffusion MRI tractography



Diffusion MRI tractography



Labelmap Seeding: Step1: I/O

Change to **Conventional** view

R: 1.500mm

3DSlicer

3D Slicer 4.4.0-2015-05-21

Modules: Tractography Interactive Seeding

DATA DCM SAVE

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

Random

Linear

ROI L

Write

Output

File P

Data

L
F
B

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

I (100%)

5 cm

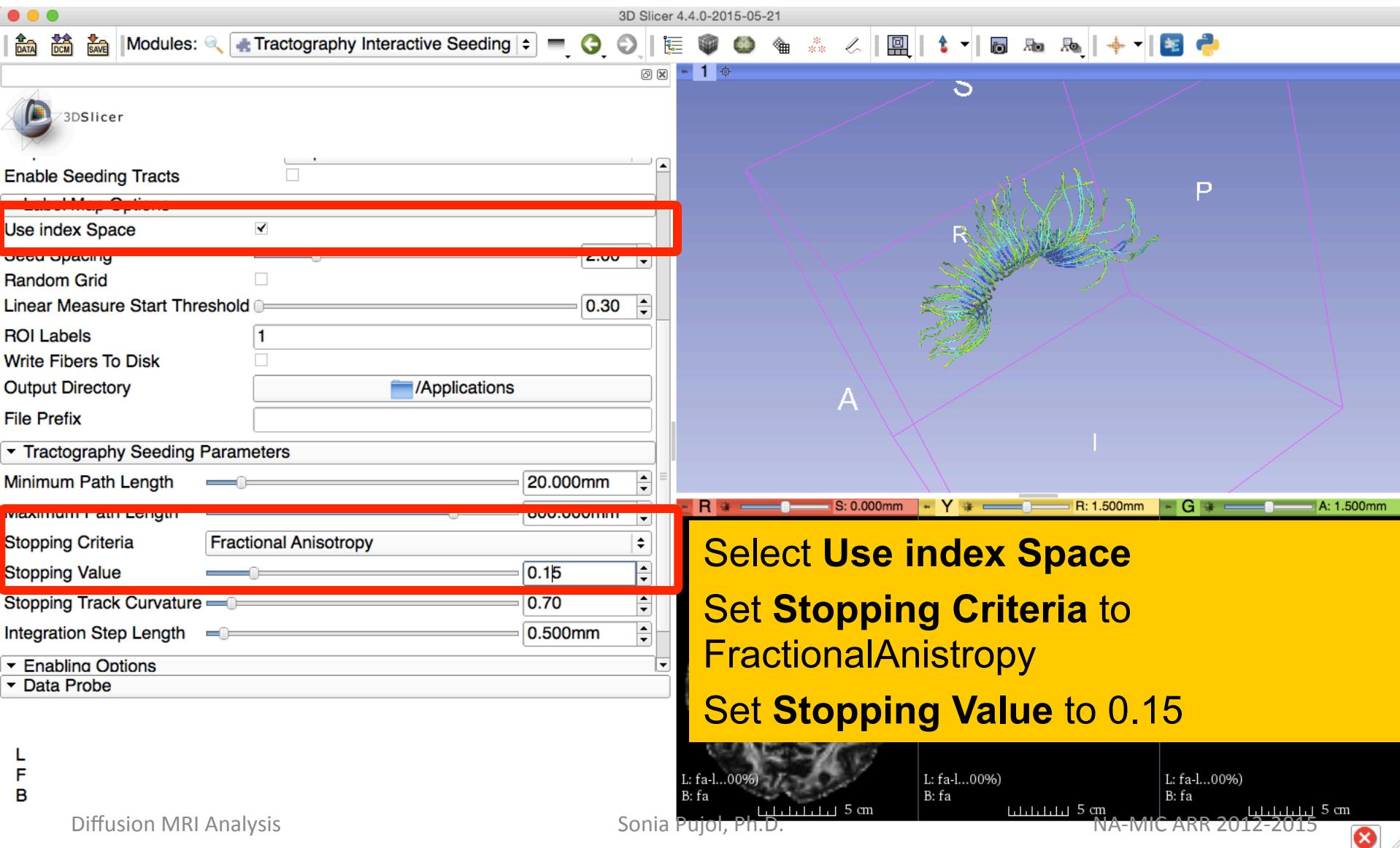
Diffusion MRI Analysis

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- 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

Step 2: Seeding parameters



Step 3: Generate Tracts

3D Slicer 4.4.0-2015-05-21

Modules: Tractography Interactive Seeding

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

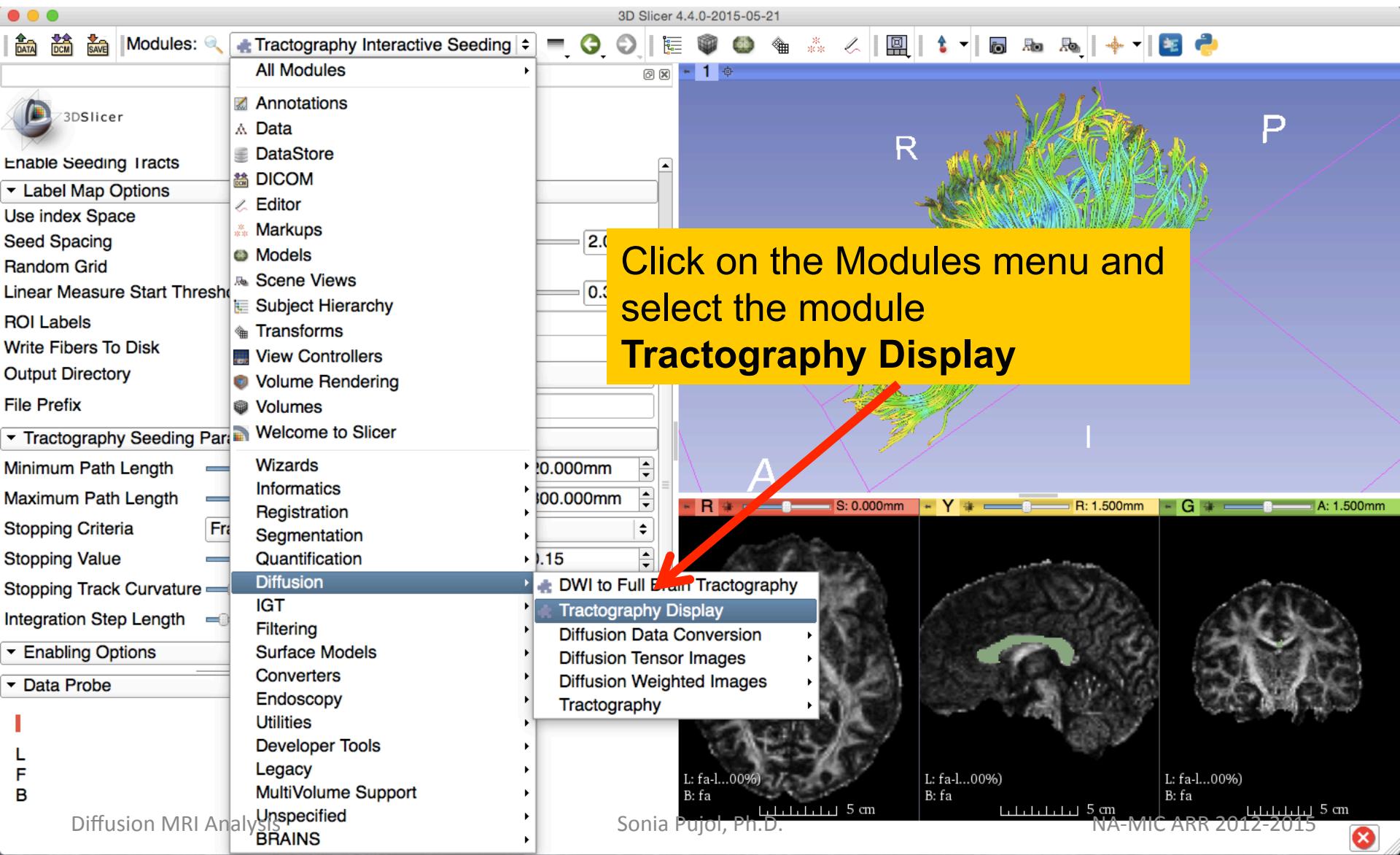
The tracts generated in the corpus callosum area appear in the 3D viewer.

3D viewer showing a brain slice with a green and yellow fiber bundle tract in the corpus callosum area. A red arrow points to the "Enable Seeding Tracts" checkbox in the module parameters. A yellow box contains the text "Check Enable Seeding Tracks". A green box contains the text "The tracts generated in the corpus callosum area appear in the 3D viewer." The 3D viewer interface includes a coordinate system (R, S, A) and a scale bar (5 cm).

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Step 4: Tract editing



Step 4: Tract Editing

3D Slicer 4.4.0-2015-05-21

Modules: Tractography Display

3DSlicer

Help & Acknowledgement

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: ROI Node

Disable ROI (radio button)

Positive ROI (radio button)

Negative ROI (radio button)

ROI Visibility: None

Extract Bundle From ROI

Update corpusCallosum From ROI

Confirm update (checkbox)

Enable Interactive Edit (checkbox)

Advanced Display

Data Probe

L F B

Slicer creates the ROI ROI Node

Select the fiber **corpusCallosum**

In the Fiber Bundle Selection tab, select **ROI for Fiber Selection** to 'Create New'

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

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

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

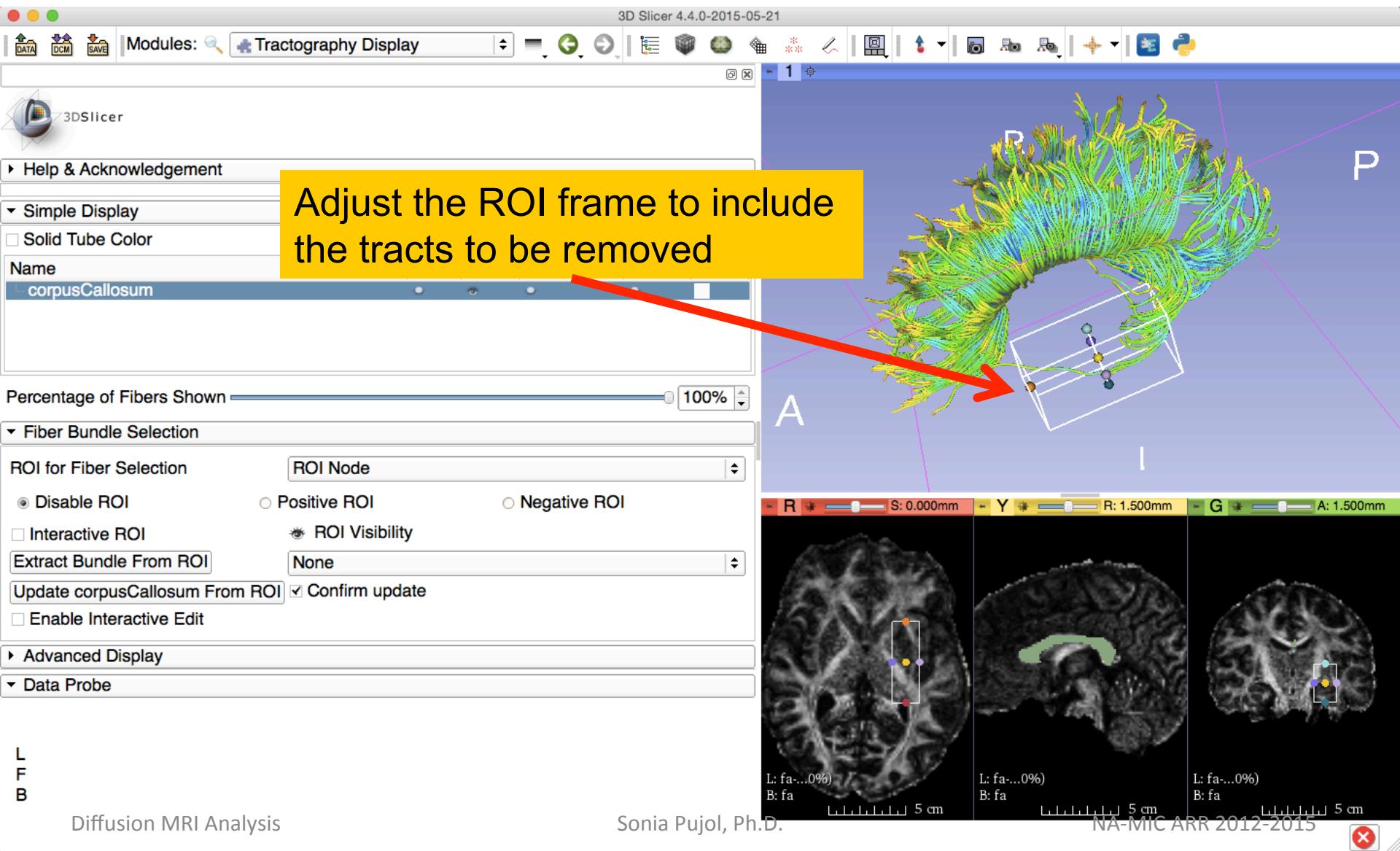
L: fa...% B: fa 5 cm

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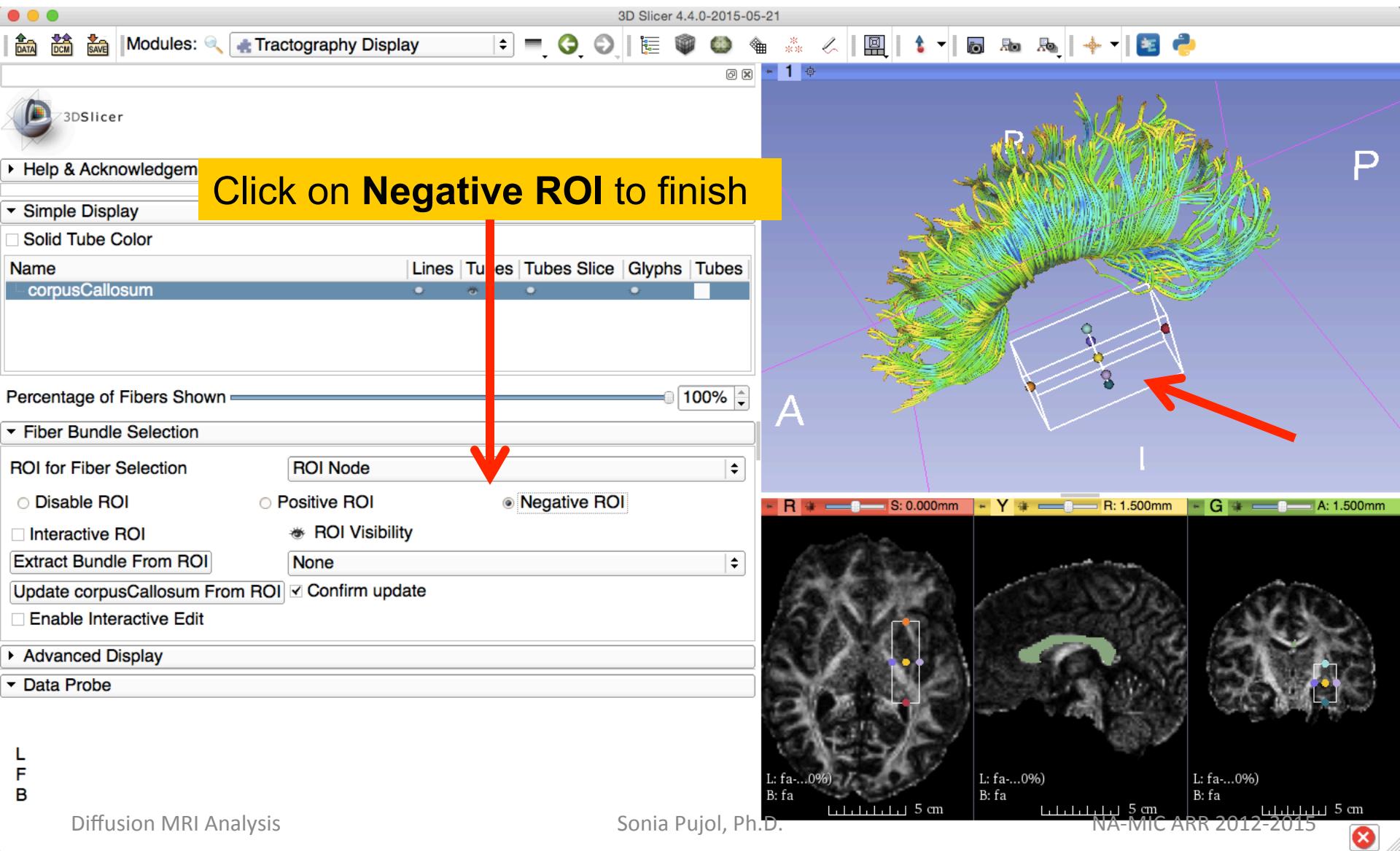
Diffusion MRI Analysis

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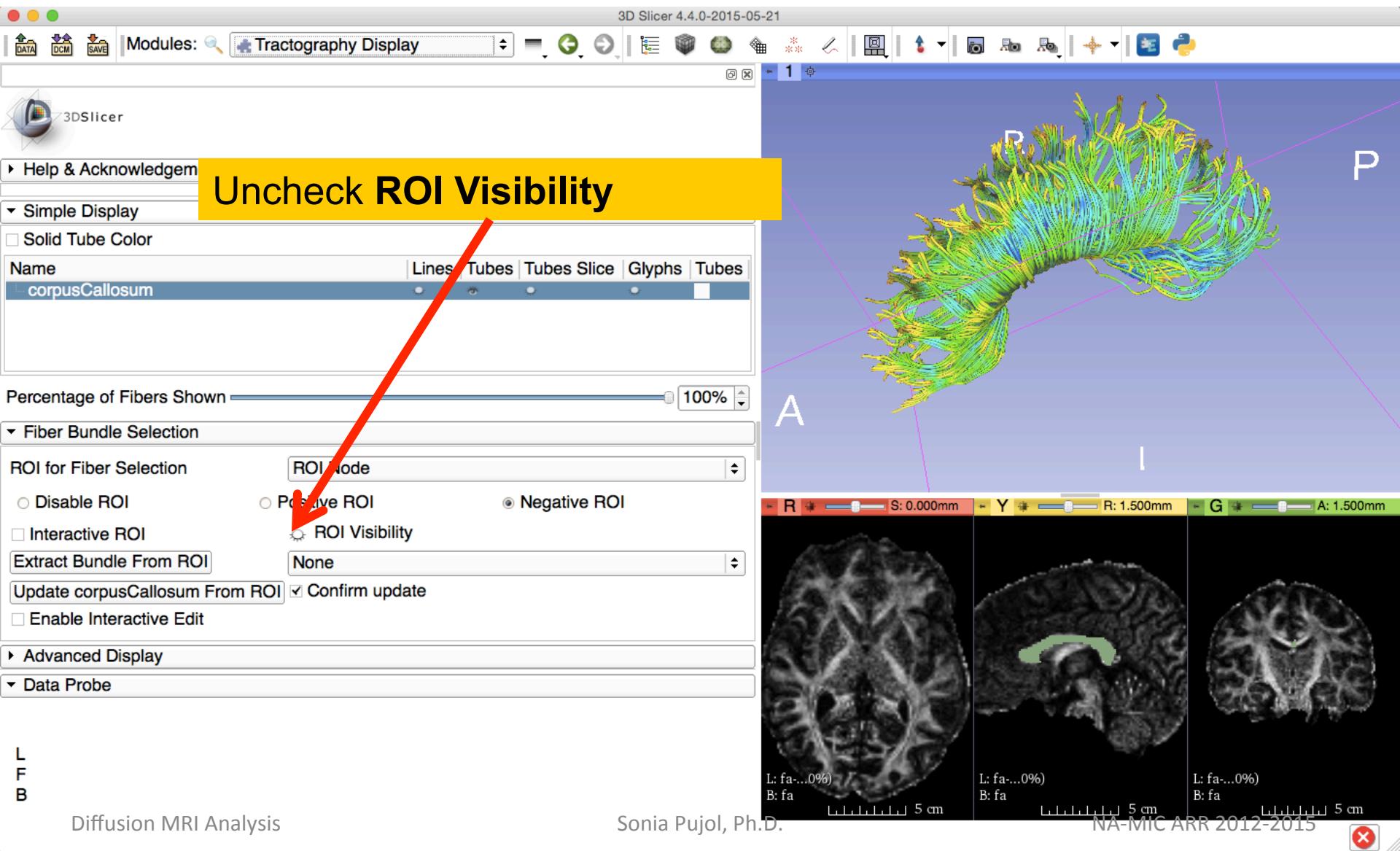
Step 4: Tract Editing



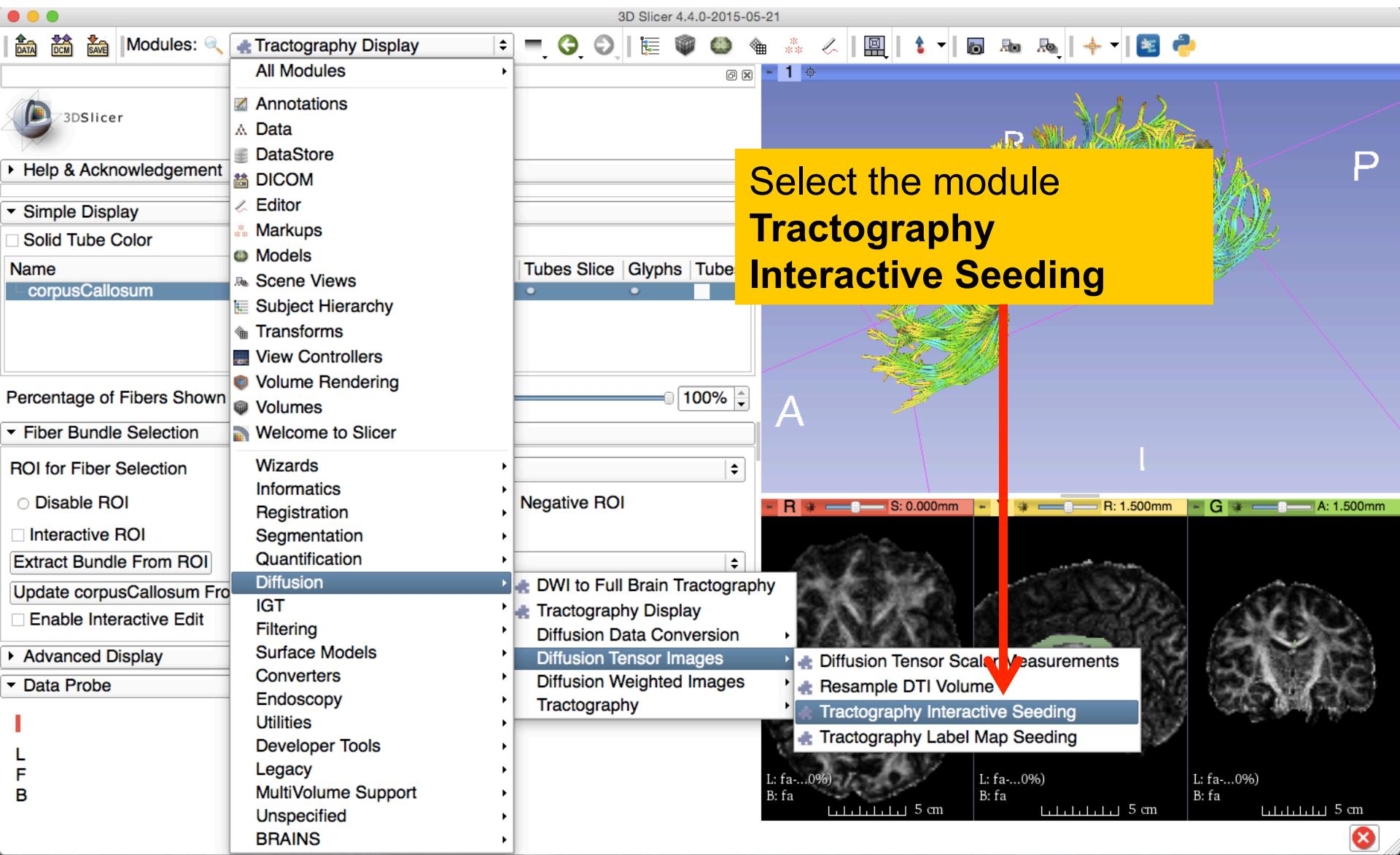
Step 4: Tract Editing



Step 4: Tract Editing



Tractography Interactive Seeding



Tractography Results

Position the mouse over the **pin icon** and click on the **eye icon** to display the axial slice in the 3D viewer

Uncheck **Enable Seeding Tracts**

The screenshot shows the 3D Slicer interface with the following details:

- Top Bar:** Modules: Tractography Interactive Seeding
- Left Panel (Parameters):**
 - Input DTI Volume: dti
 - Input Fiducials, Model or Label Map: fa-label
 - Output Fiber Bundle: corpusCallosum
 - Enable Seeding Tracts: (highlighted with a red arrow)
- Bottom Panel (ROI Labels):**
 - 1
 - /Applications
- 3D Viewer:** Displays a brain with numerous colored tracts (green, yellow, blue) representing fiber bundles.
- Bottom Right (Slice View):** Shows three axial slices of the brain. A tooltip indicates: "Toggle slice visibility in 3D view".
- Bottom Left:** L, F, B labels.
- Bottom Center:** Sonia Pujol, Ph.D.
- Bottom Right:** NA-MIC ARR 2012-2015

Fiducial Seeding

3D Slicer 4.4.0-2015-05-21

Select the module **Markups**

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

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

BRAINS

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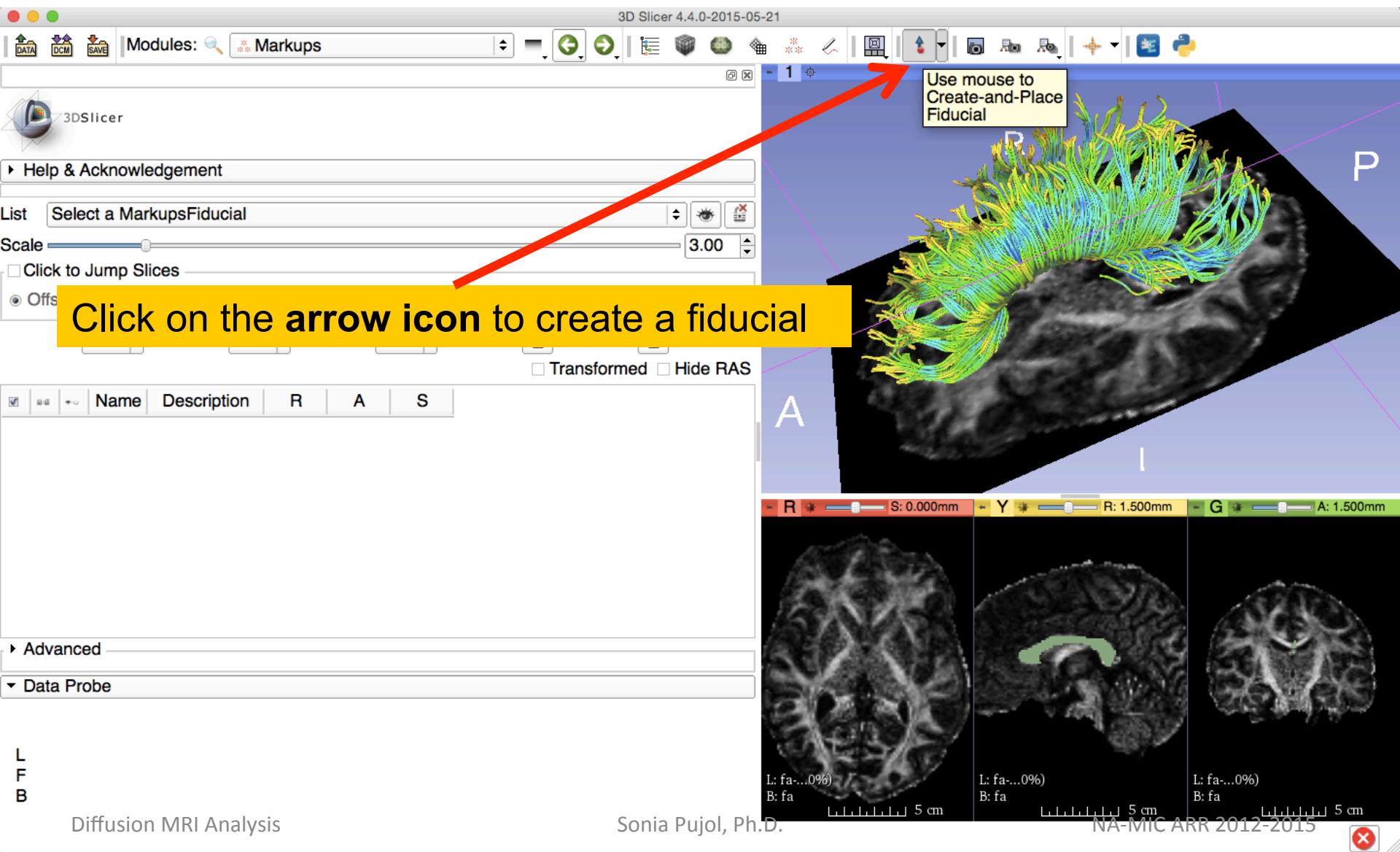
R S: 0.000mm Y R: 1.500mm G A: 1.500mm

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

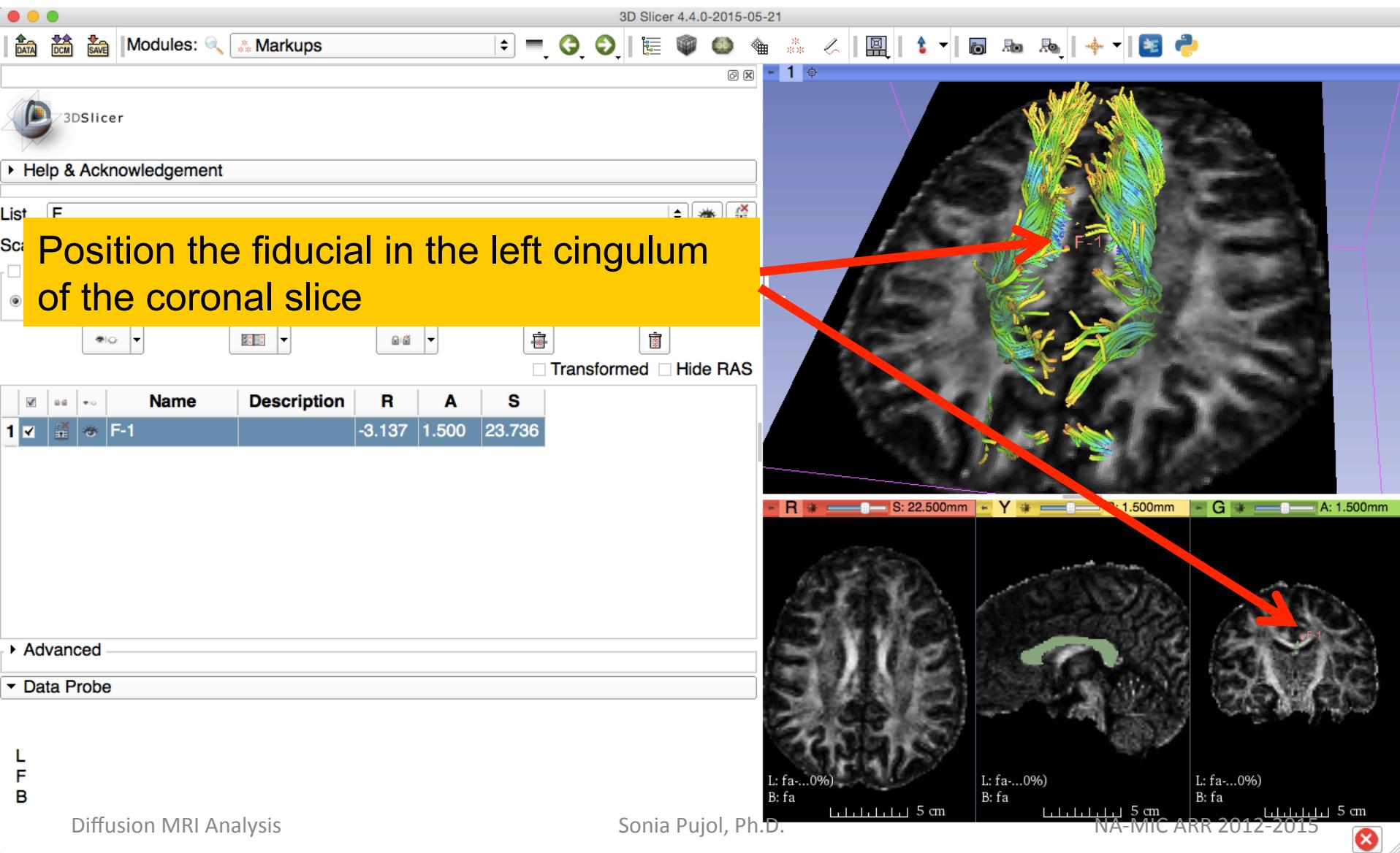
L: fa...% B: fa 5 cm

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

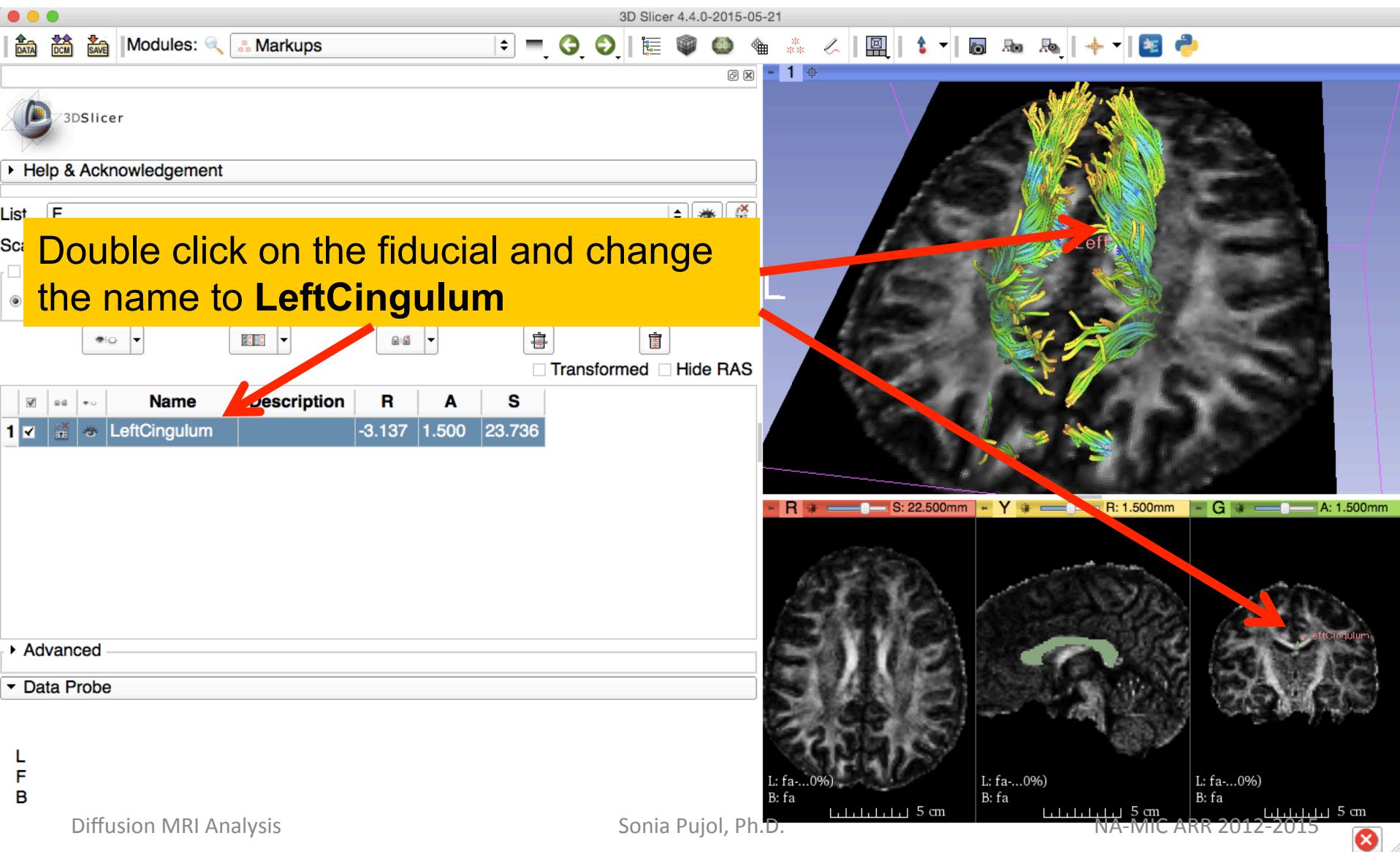
Fiducial Seeding



Fiducial Seeding



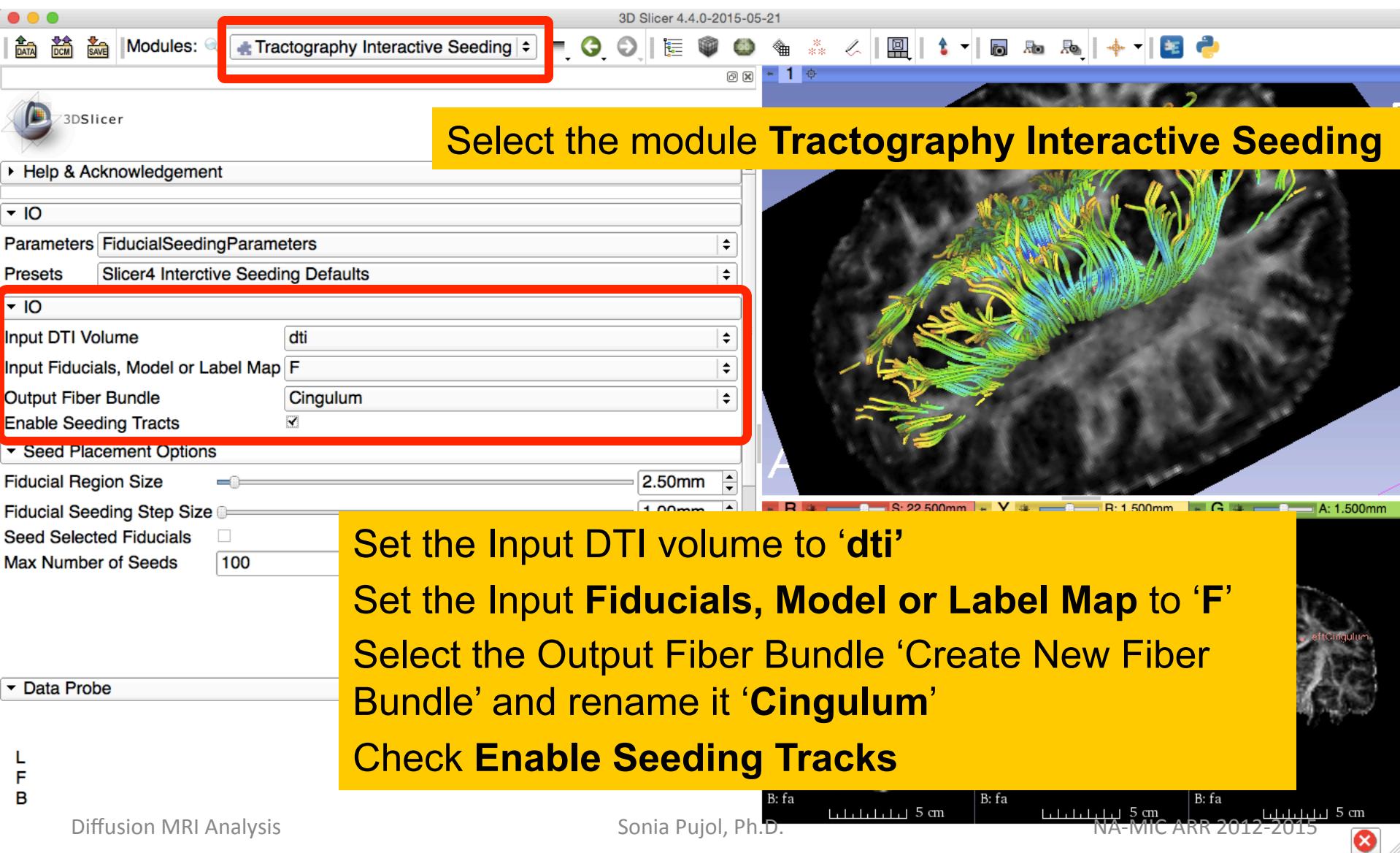
Fiducial Seeding



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 Seeding Tracks**



3D Slicer 4.4.0-2015-05-21

Modules: Tractography Interactive Seeding

3DSlicer

Help & Acknowledgement

IO

Parameters FiducialSeedingParameters

Presets Slicer4 Interactive Seeding Defaults

Input DTI Volume dti

Input Fiducials, Model or Label Map F

Output Fiber Bundle Cingulum

Enable Seeding Tracts

Fiducial Region Size 2.50mm

Fiducial Seeding Step Size 1.00mm

Seed Selected Fiducials

Max Number of Seeds 100

Data Probe

L F B

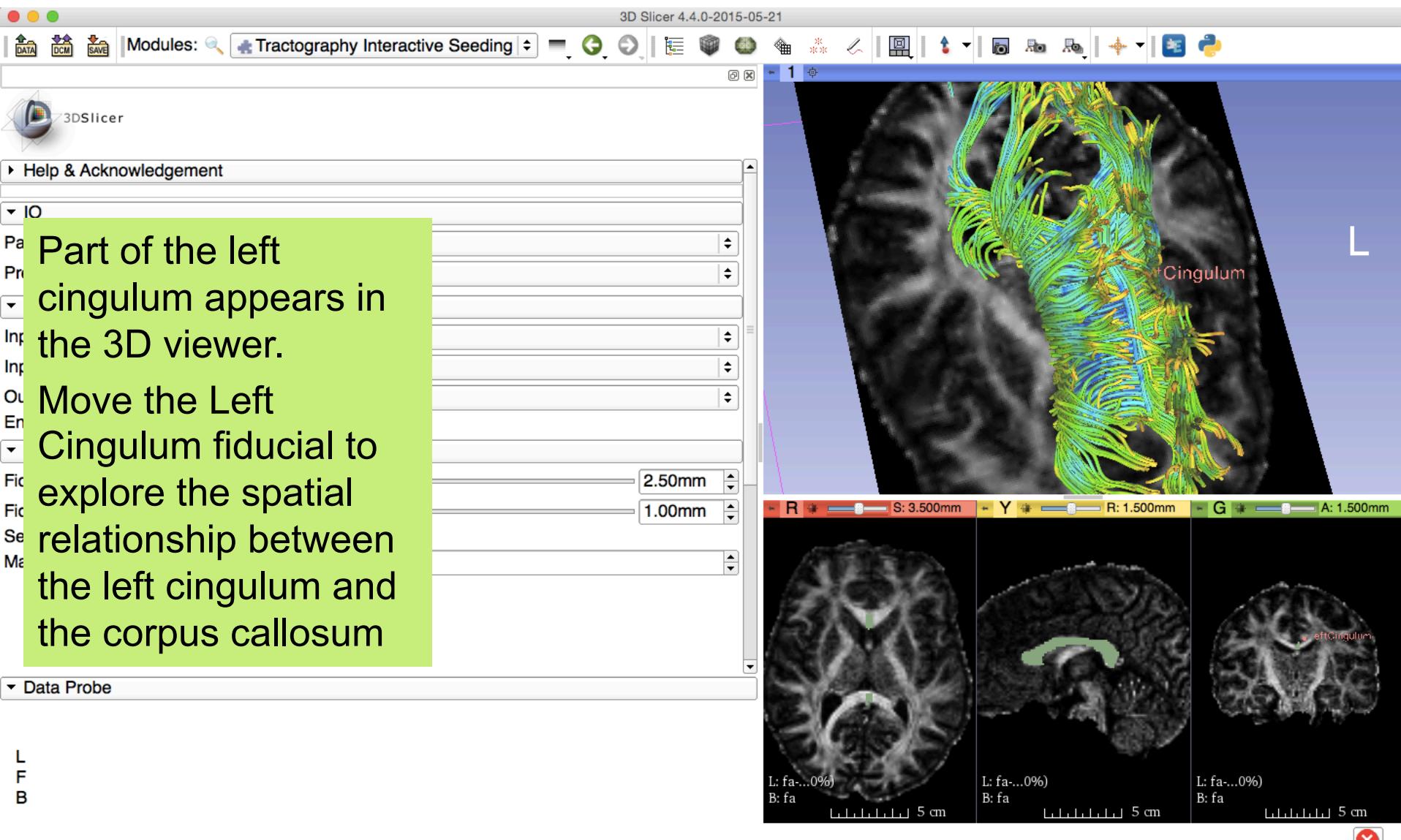
Diffusion MRI Analysis

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

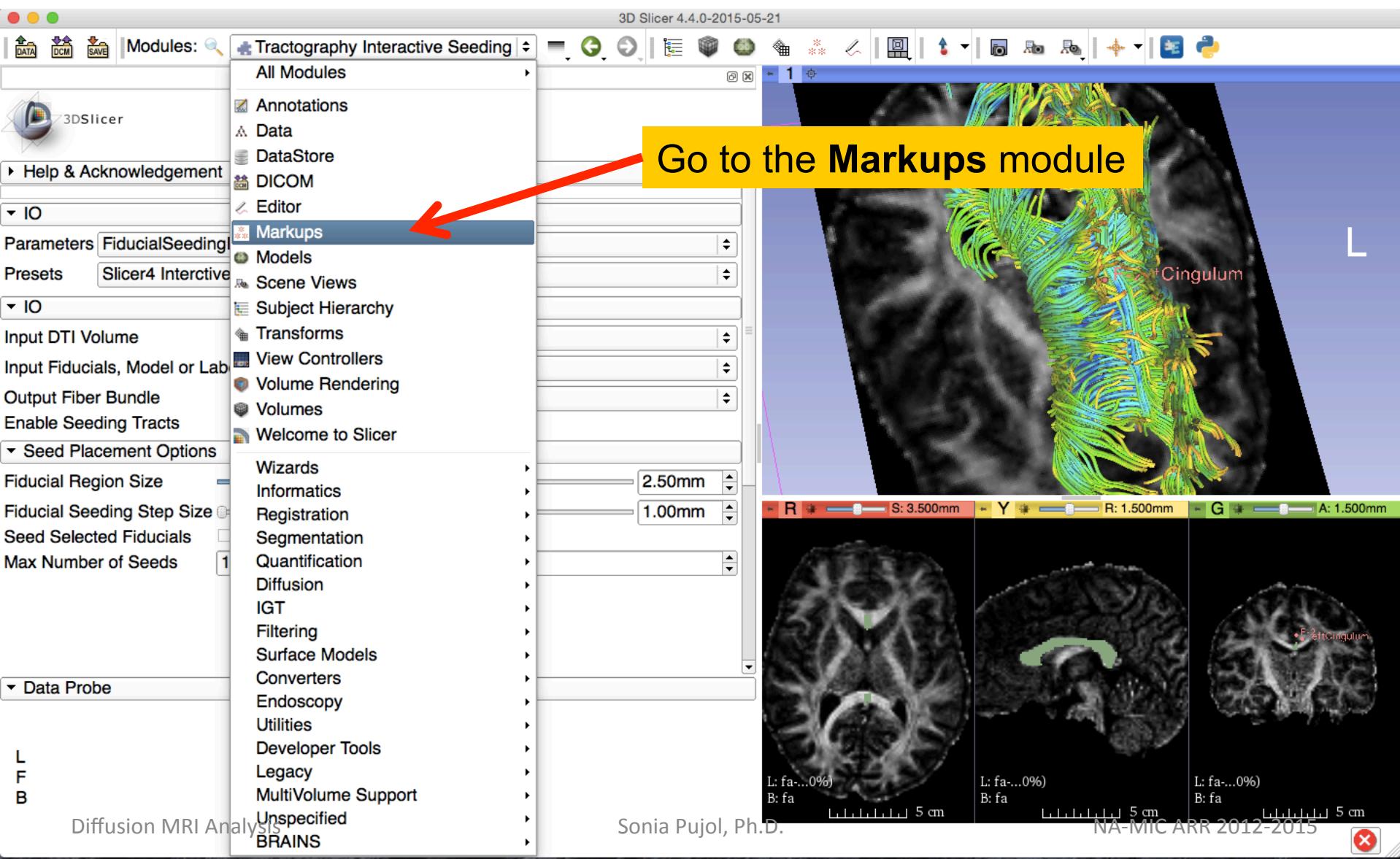
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Fiducial Seeding



Fiducial Seeding



Fiducial Seeding

3D Slicer 4.4.0-2015-05-21

Modules: Markups

DATA DCM SAVE

3DSlicer

Help & Acknowledgement

List F

Scale 3.00

Click to Jump Slices

Offset Centered Show Slice I Transform

Name Description R A S

1	LeftCingulum	-4.691	1.500	24.513
2	RightCingulum	10.855	1.500	26.068

Advanced

Data Probe

L F B

Diffusion MRI Analysis

Position a second fiducial in the right cingulum of the coronal slice

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

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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

3D Slicer 4.4.0-2015-05-21

DATA DCM SAVE Modules: Markups

3DSlicer

Help & Acknowledgement

List F

Scale

Click to Jump Slices

Offset Centered

Name Description

1 LeftCingulum

2 RightCingulum

Advanced

Data Probe

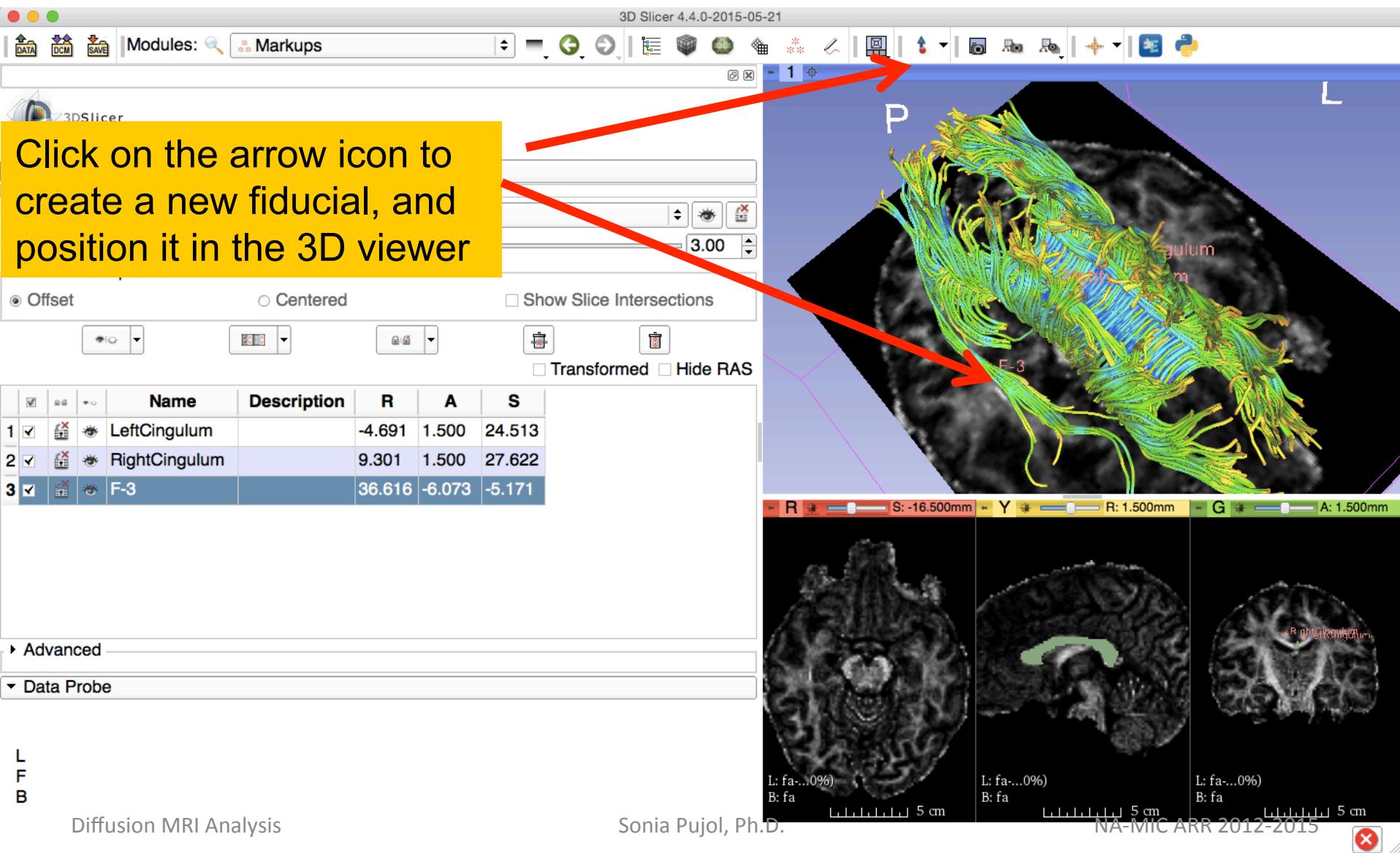
L F B

Diffusion MRI Analysis

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Fiducial Seeding



Fiducial Seeding

3D Slicer 4.4.0-2015-05-21

DATA DCM SAVE Modules: Markups

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

P L

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

5 cm

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

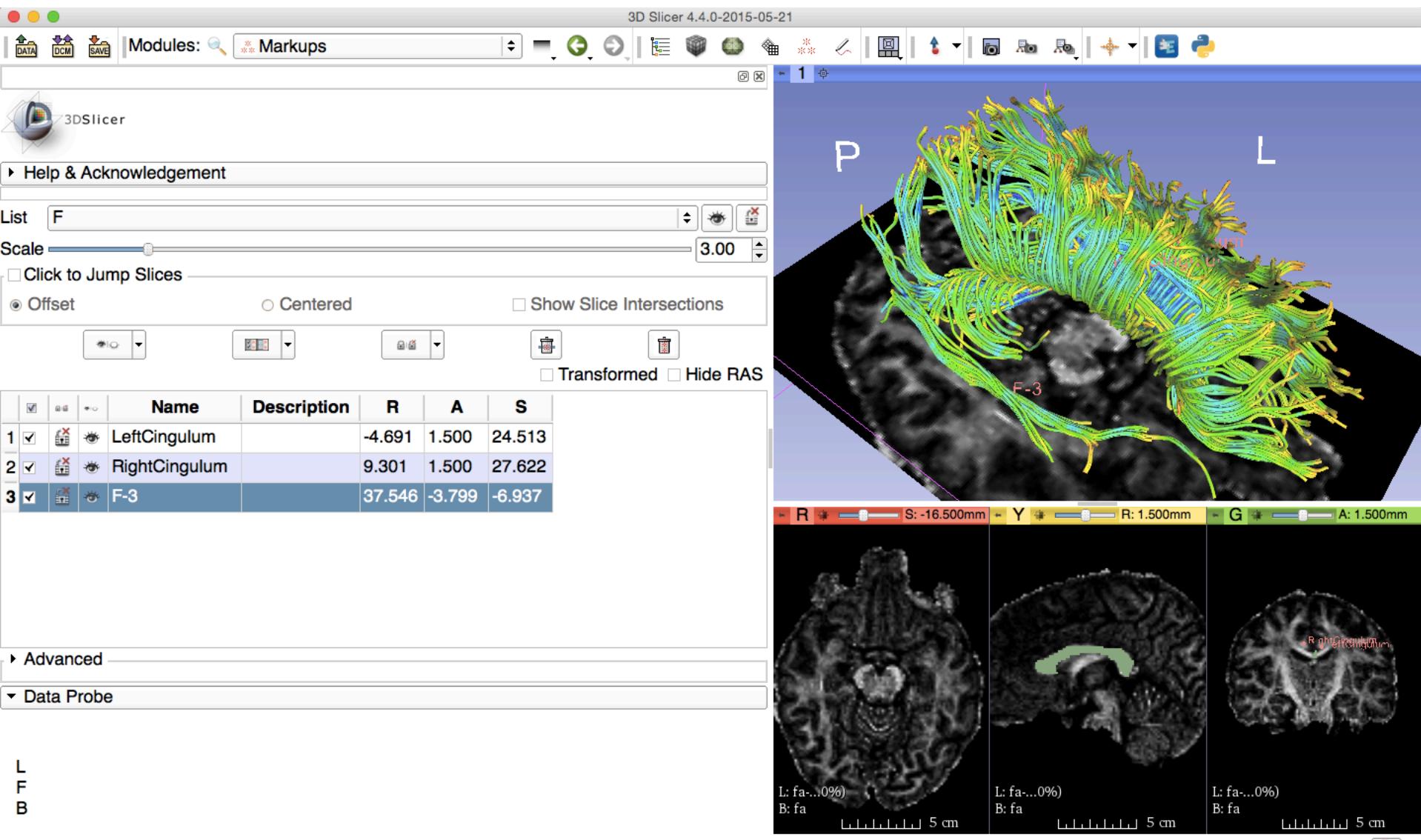
L: fa...0% B: fa 5 cm

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

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Tractography 'on-the-fly'



DTI Analysis

3D Slicer 4.4.0-2015-05-21

DATA DCM SAVE Modules: Data

3DSlicer

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

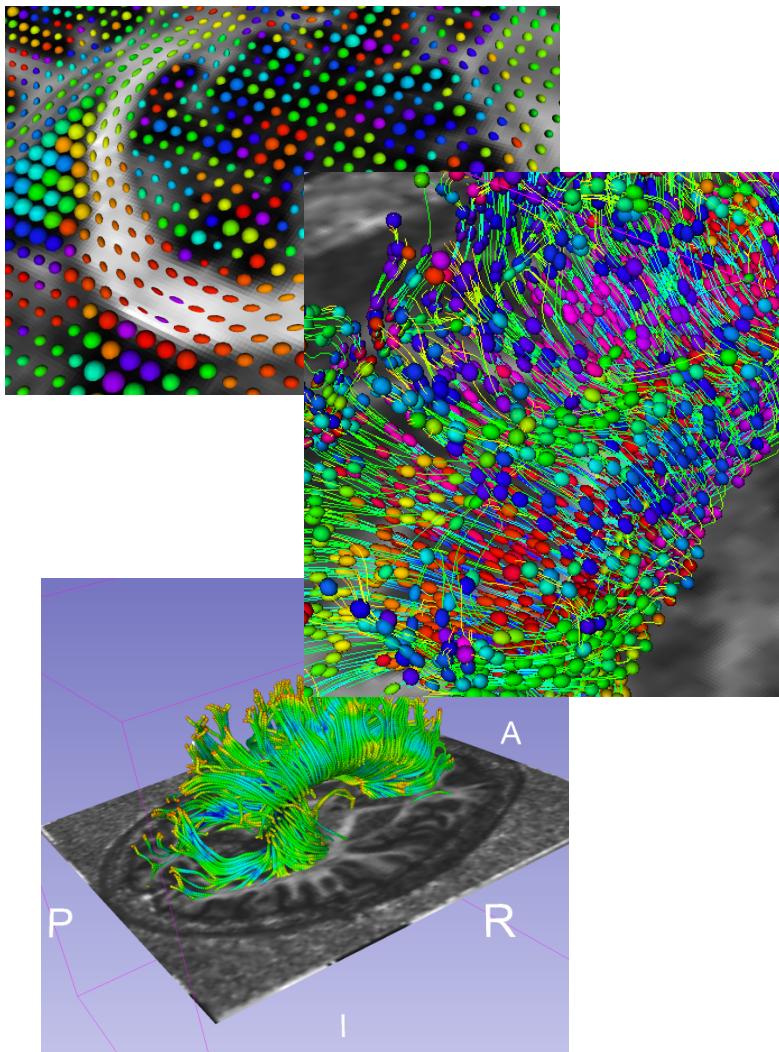
P L

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Diffusion MRI Analysis

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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.

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