Exploring Peritumoral White Matter Fibers for Neurosurgical Planning

Sonia Pujol, Ph.D.

Ron Kikinis, M.D.

Surgical Planning Laboratory

Harvard University

Clinical Goal

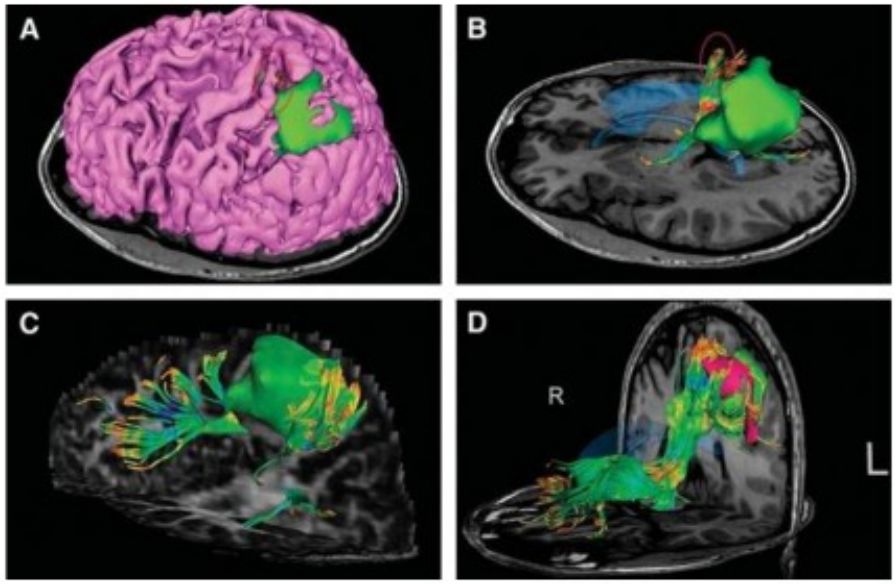
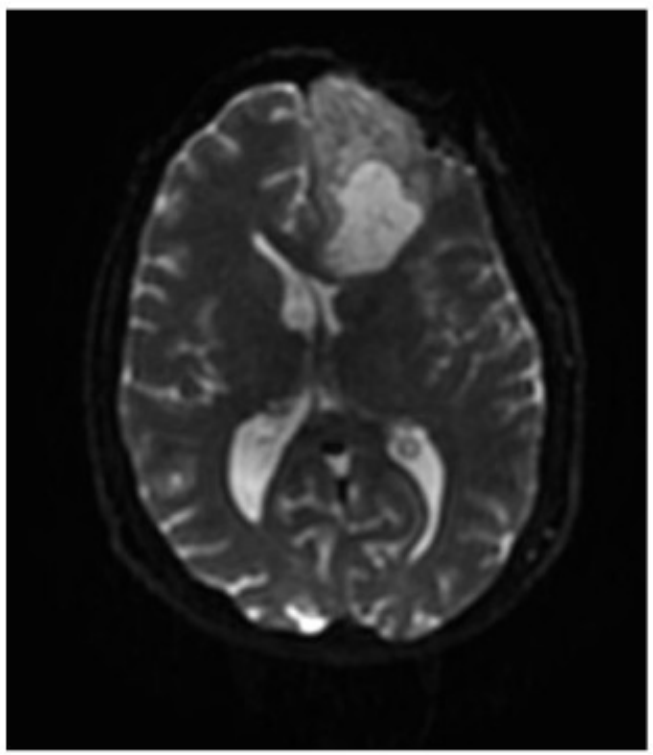


Image Courtesy of Dr. Alexandra Golby, Brigham and Women's Hospital, Boston, MA..

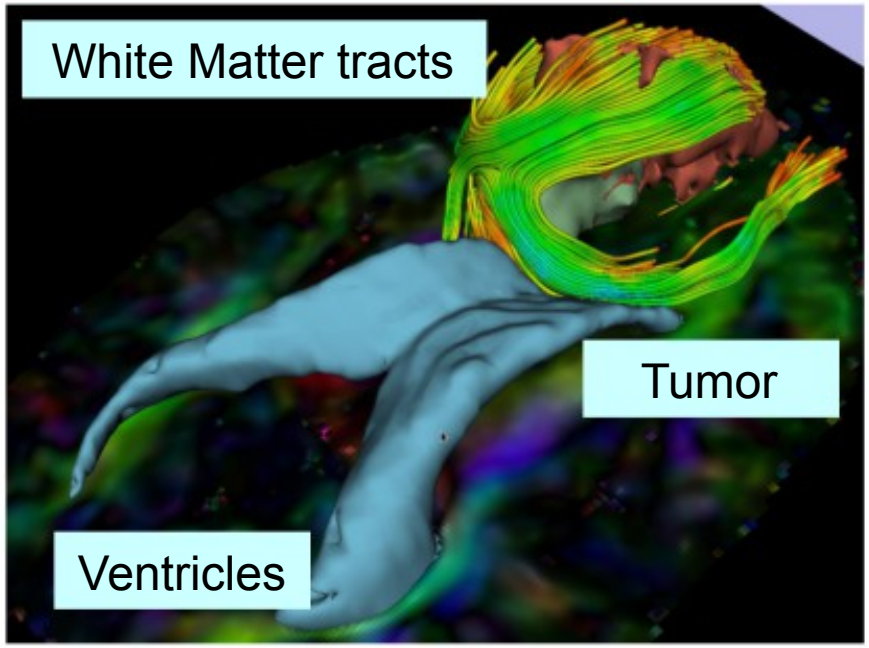
Diffusion Tensor Imaging (DTI) Tractography has the potential to bring valuable spatial information on tumor infiltration and tract displacement for neurosurgical planning of tumor resection.

Clinical Case



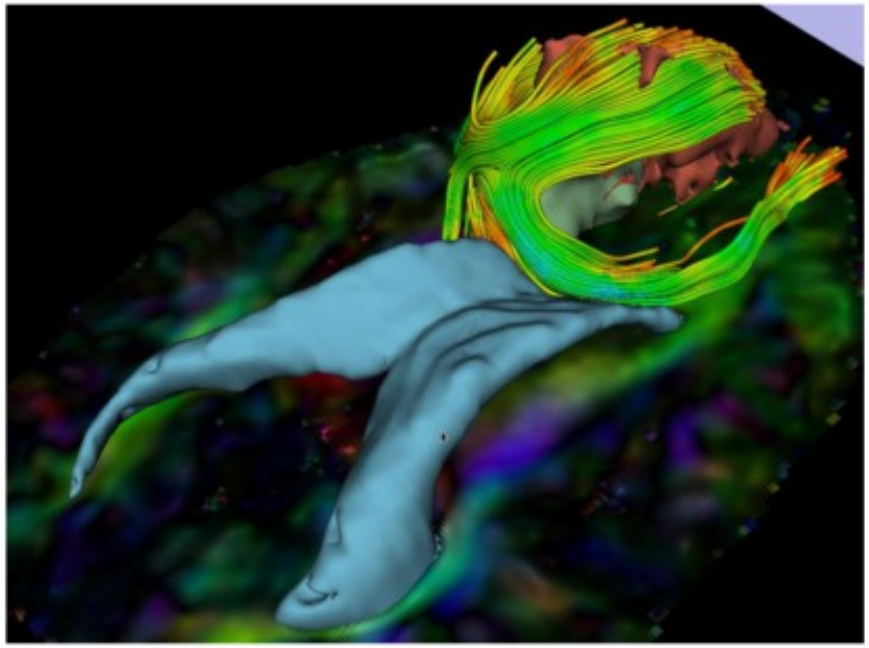
- 35 year-old male diagnosed with Glioblastoma multiform (GBM)
- Diffusion Weighted Imaging (DWI) acquisition for neurosurgical planning

Clinical Goal



The goal of this tutorial is to explore white matter fibers surrounding a tumor using Diffusion Tensor Imaging (DTI) Tractography.

Image Analysis Pipeline



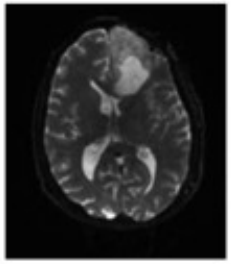
The image analysis pipeline described in this tutorial uses three different algorithms:

1) Grow Cut algorithm for segmentation of the tumor parts

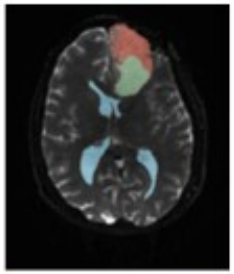
2) Marching Cube algorithm for surface modeling

3) Single tensor streamline tractography algorithm for tract generation.

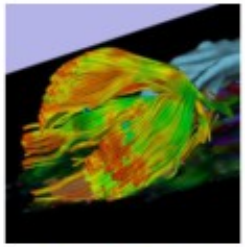
Overview of the analysis pipeline



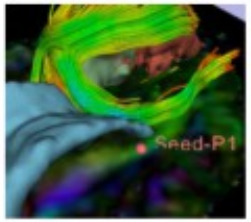
Part 1: Loading &Visualization of Diffusion Data



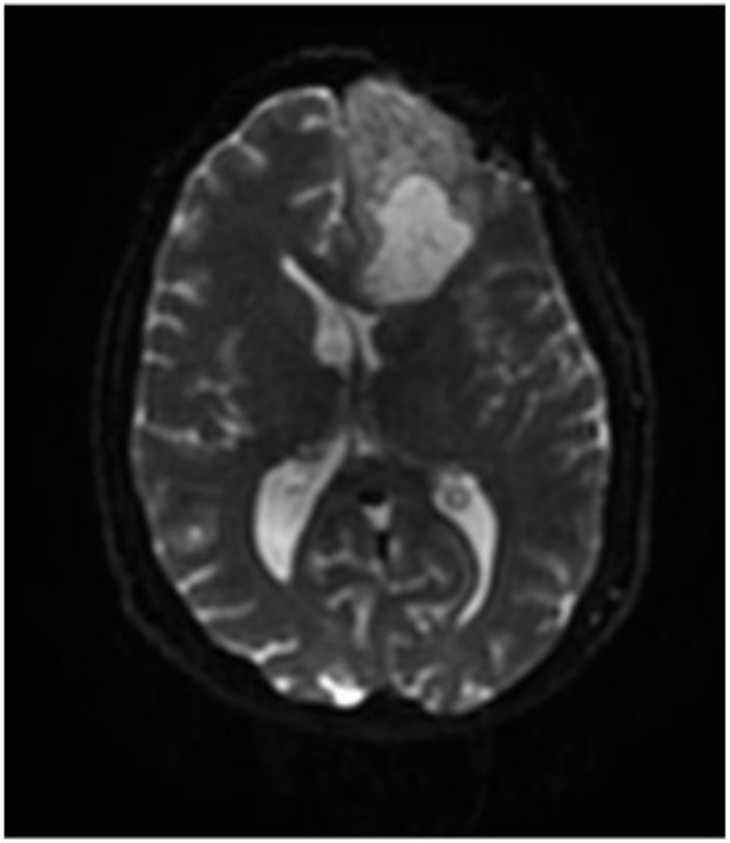
Part 2: Segmentation of lat. ventricles, and solid and cystic parts of the tumor



Part 3: Tractography reconstruction of white matter fibers in the peri-tumoral volume

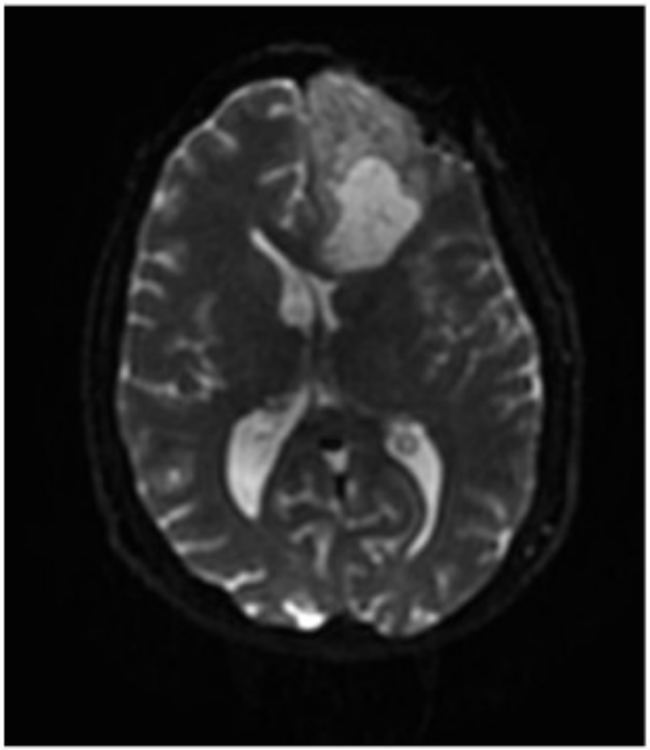


Part 4: Tractography exploration of the ipsilateral and contralateral side



Part 1: Loading and Visualization of Diffusion Data

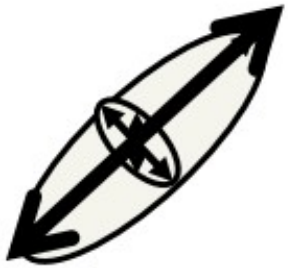
Diffusion Tensor Imaging



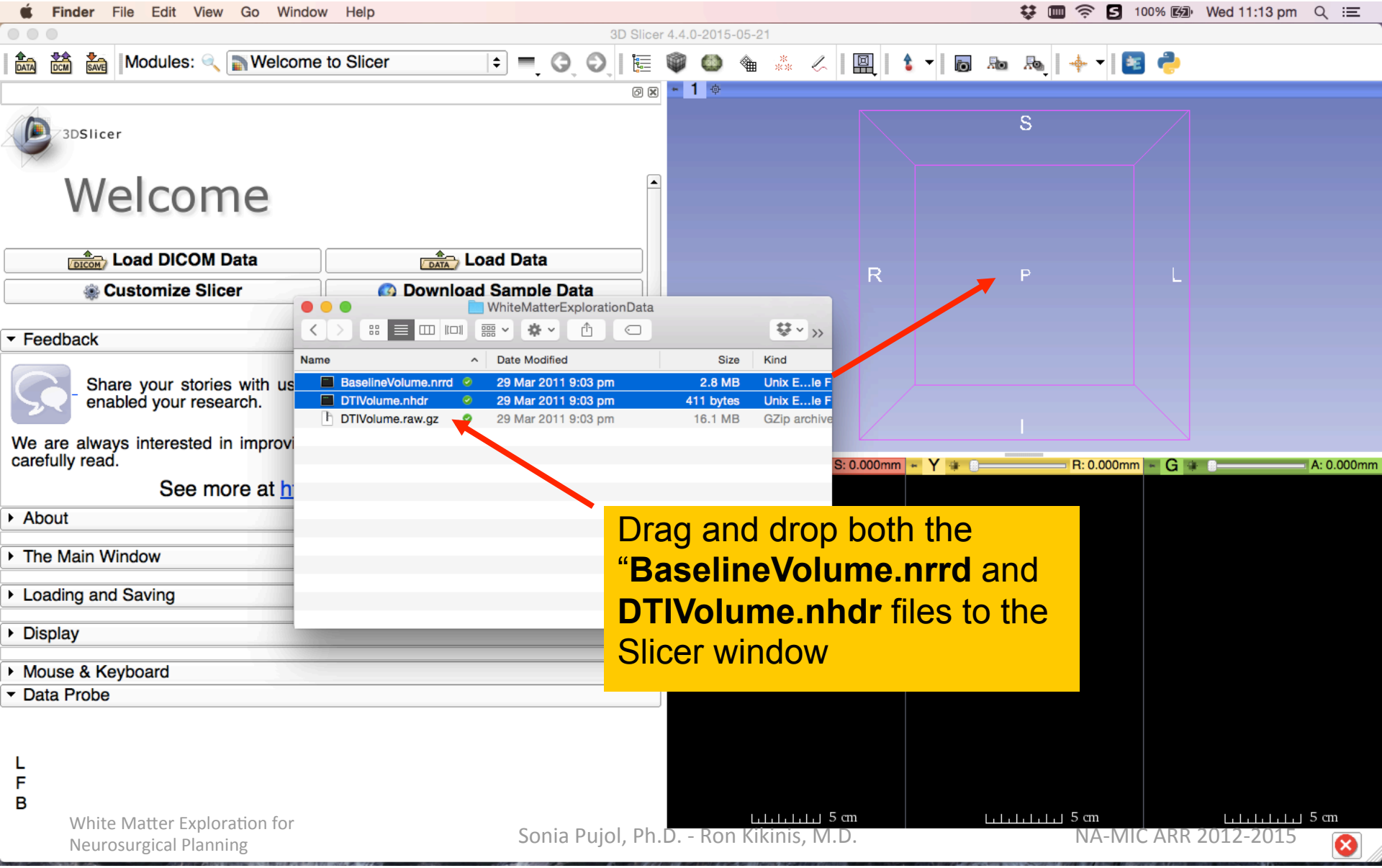
$$S_i = S_0 e^{-b\hat{g}i^T D \hat{g}_i}$$

(Stejskal and Tanner 1965, Basser 1994)

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

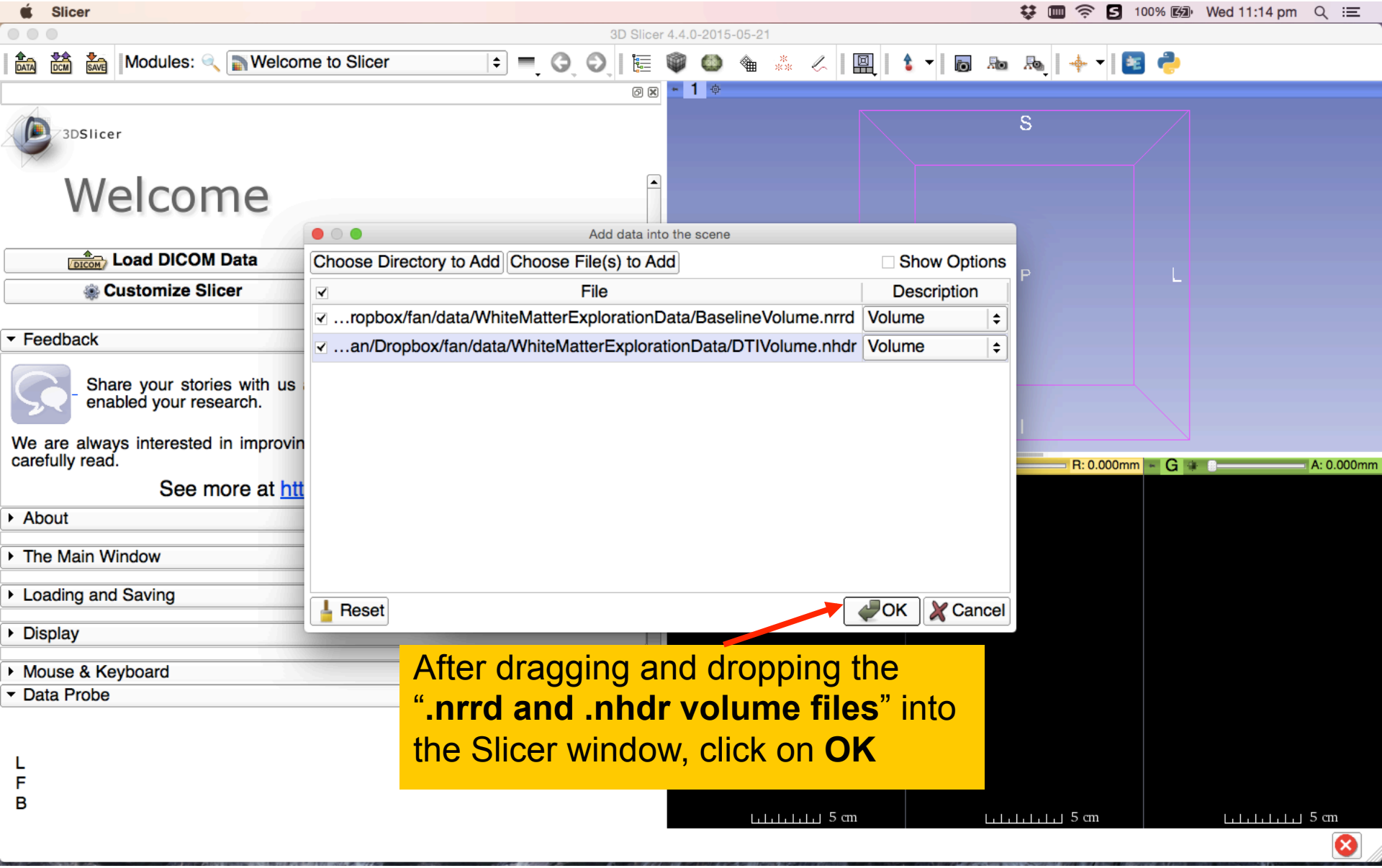


Loading DTI and Baseline Data



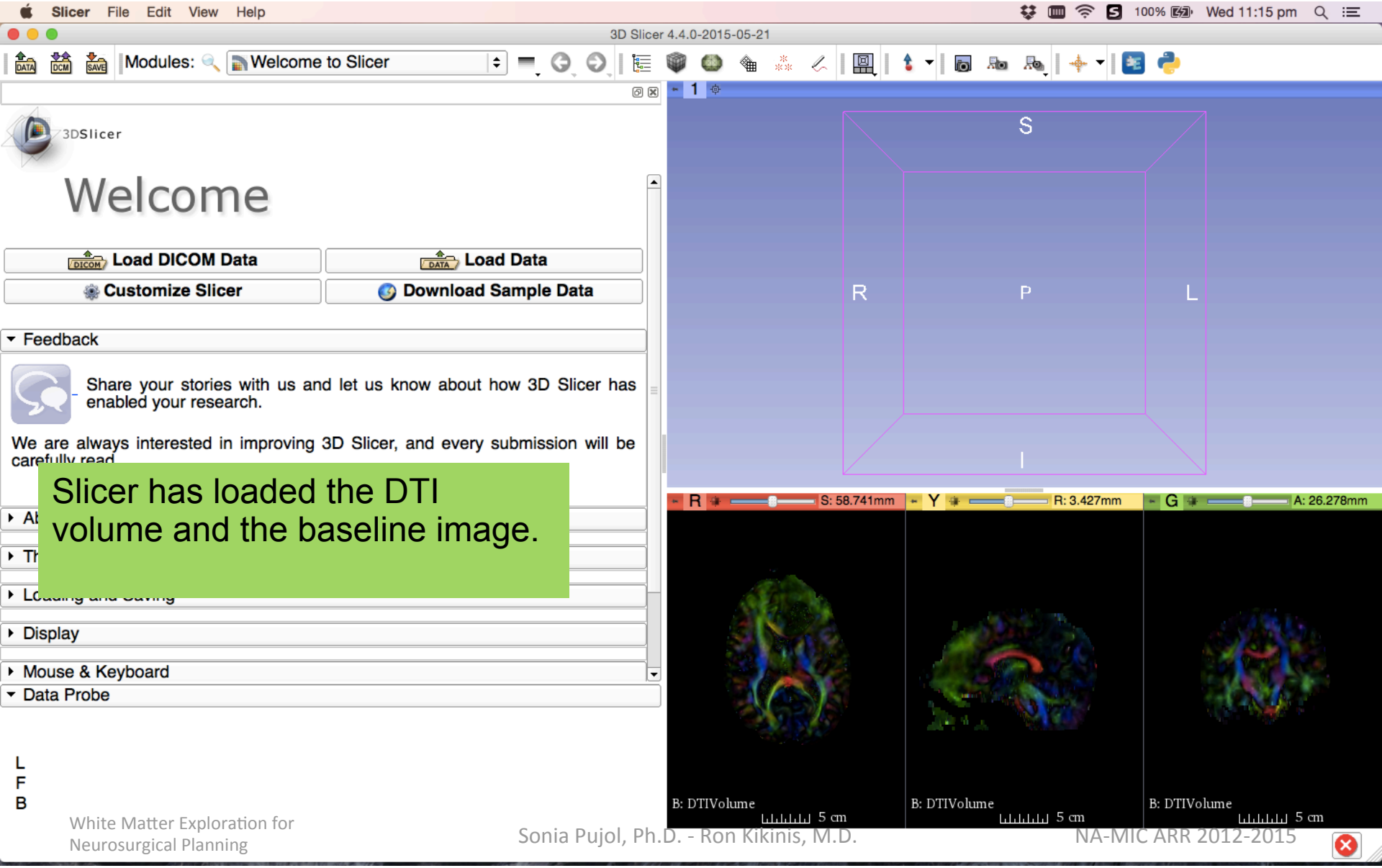
Drag and drop both the "**BaselineVolume.nrrd** and **DTIVolume.nhdr** files to the Slicer window

Loading DTI and Baseline Data



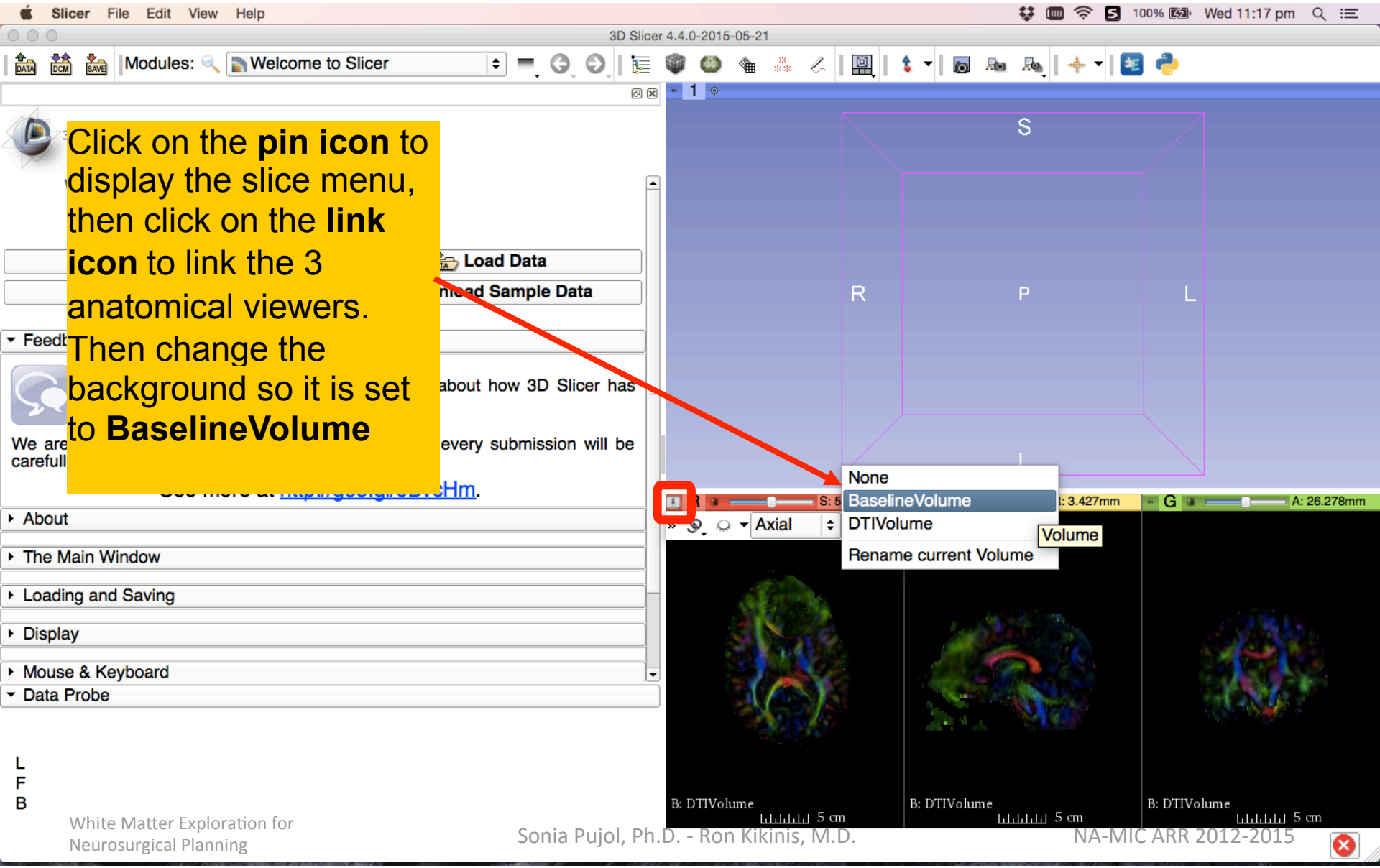
After dragging and dropping the "**.nrrd and .nhdr volume files**" into the Slicer window, click on **OK**

Loading DTI and Baseline Data



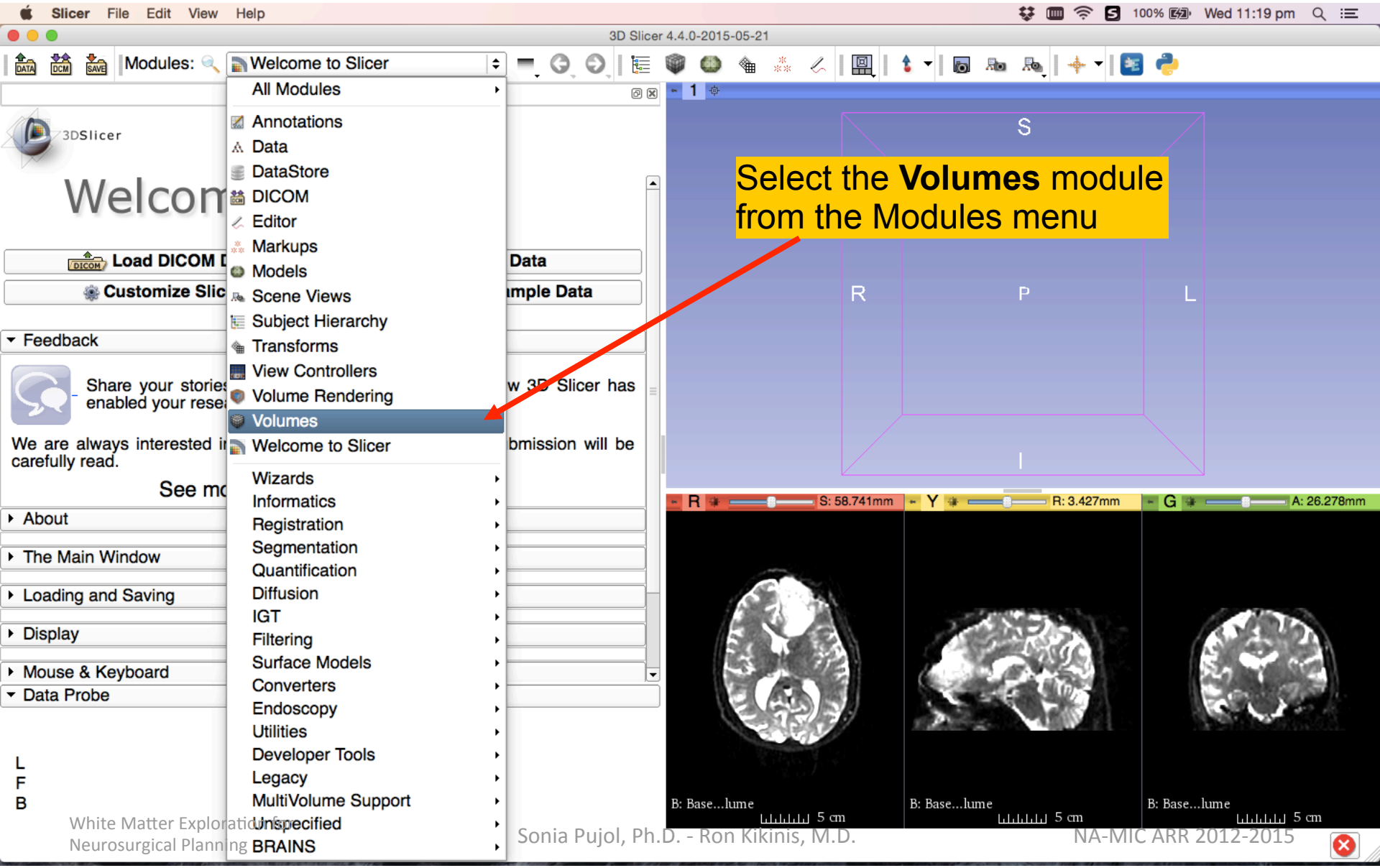
Slicer has loaded the DTI volume and the baseline image.

Loading DTI and Baseline Data

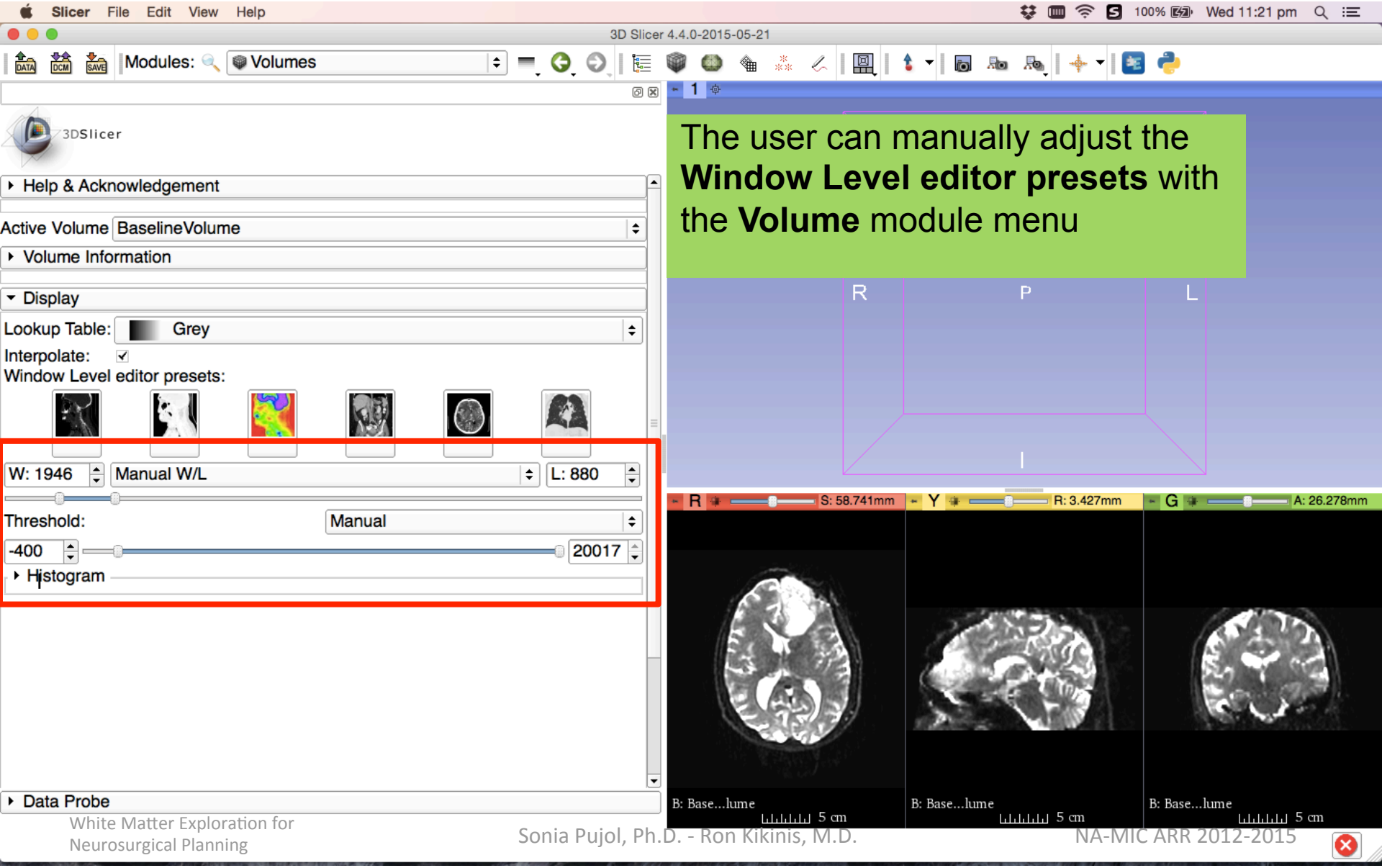


Click on the **pin icon** to display the slice menu, then click on the **link icon** to link the 3 anatomical viewers. Then change the background so it is set to **BaselineVolume**

Loading DTI and Baseline Data

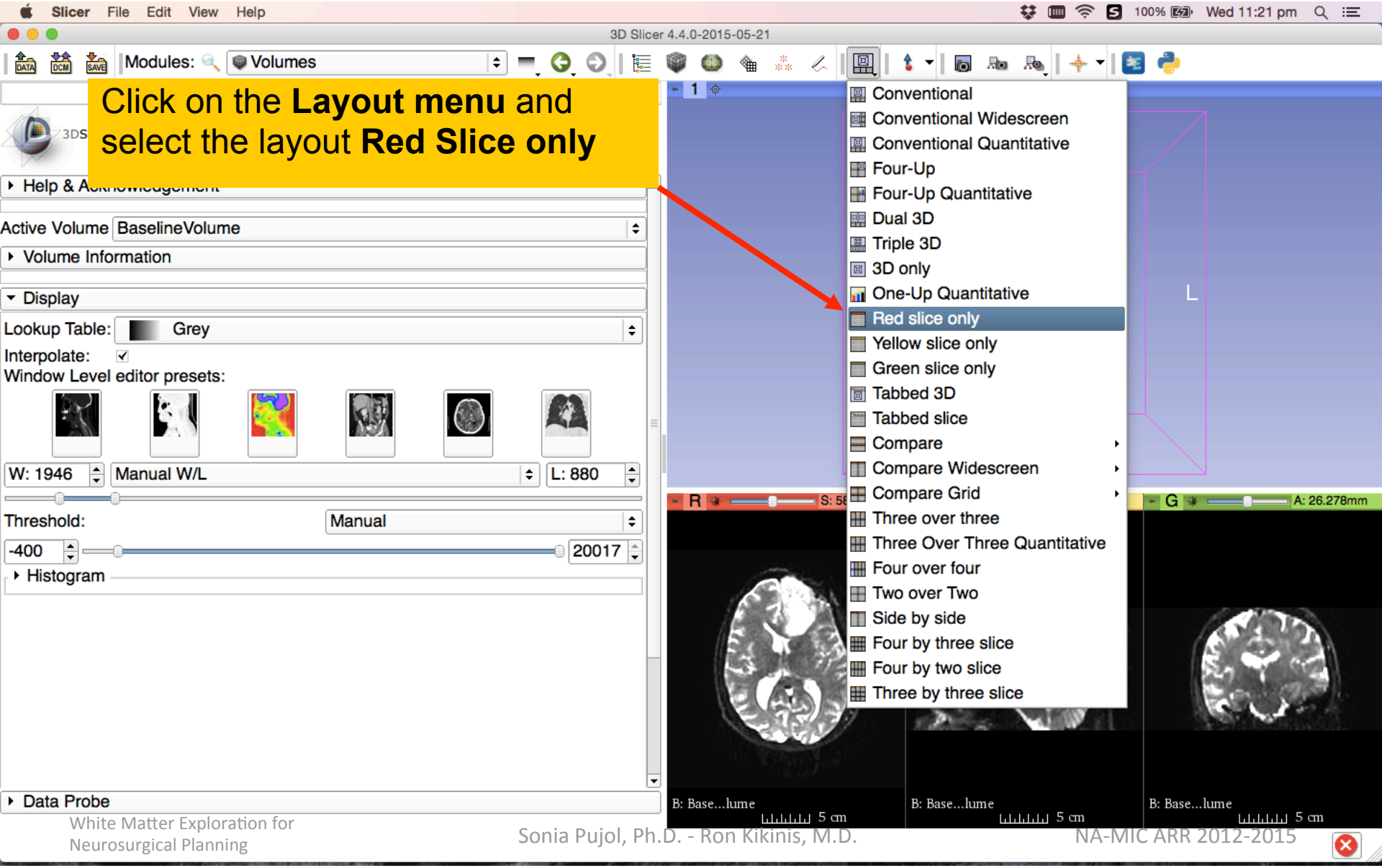


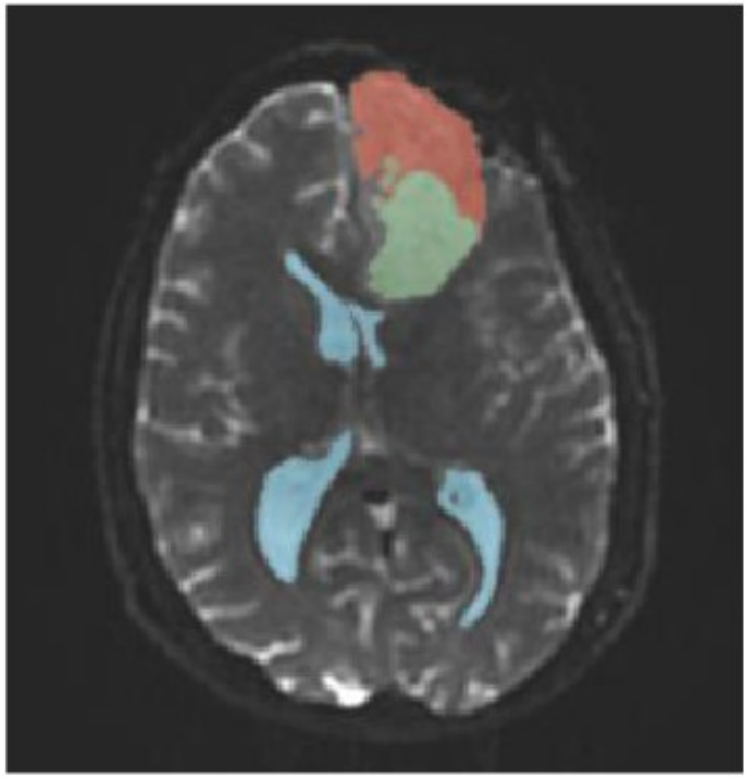
Loading DTI and Baseline Data



The user can manually adjust the **Window Level editor presets** with the **Volume** module menu

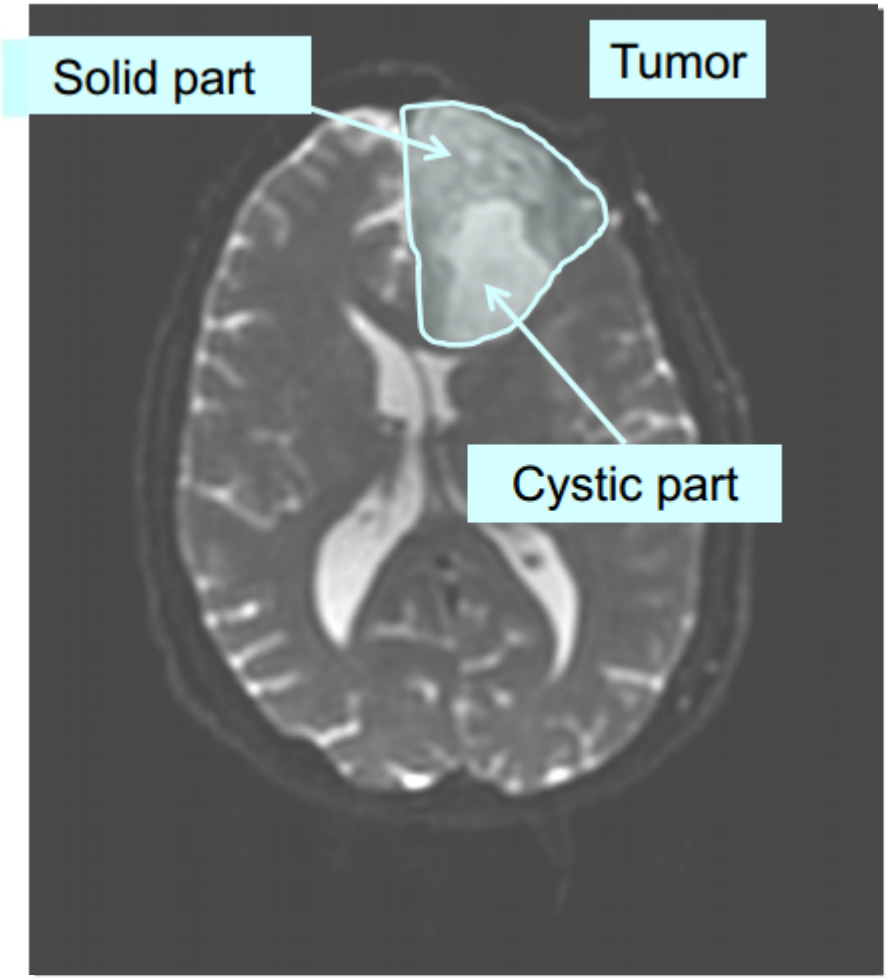
Loading DTI and Baseline Data





Part 1: Segmenting the tumor and ventricles

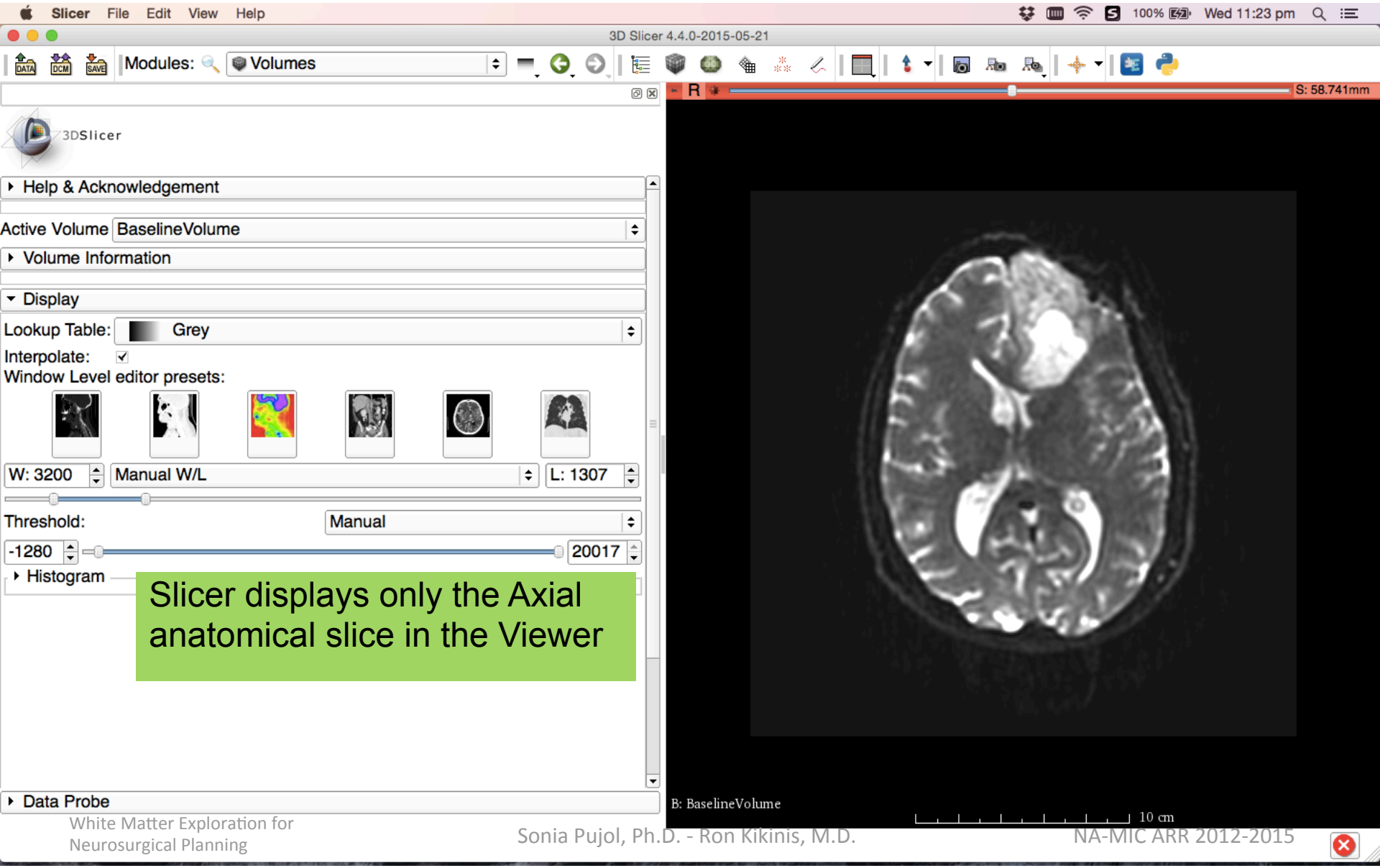
Tumor Segmentation



The tumor in this clinical case is composed of two parts: a solid part, and a cystic part.

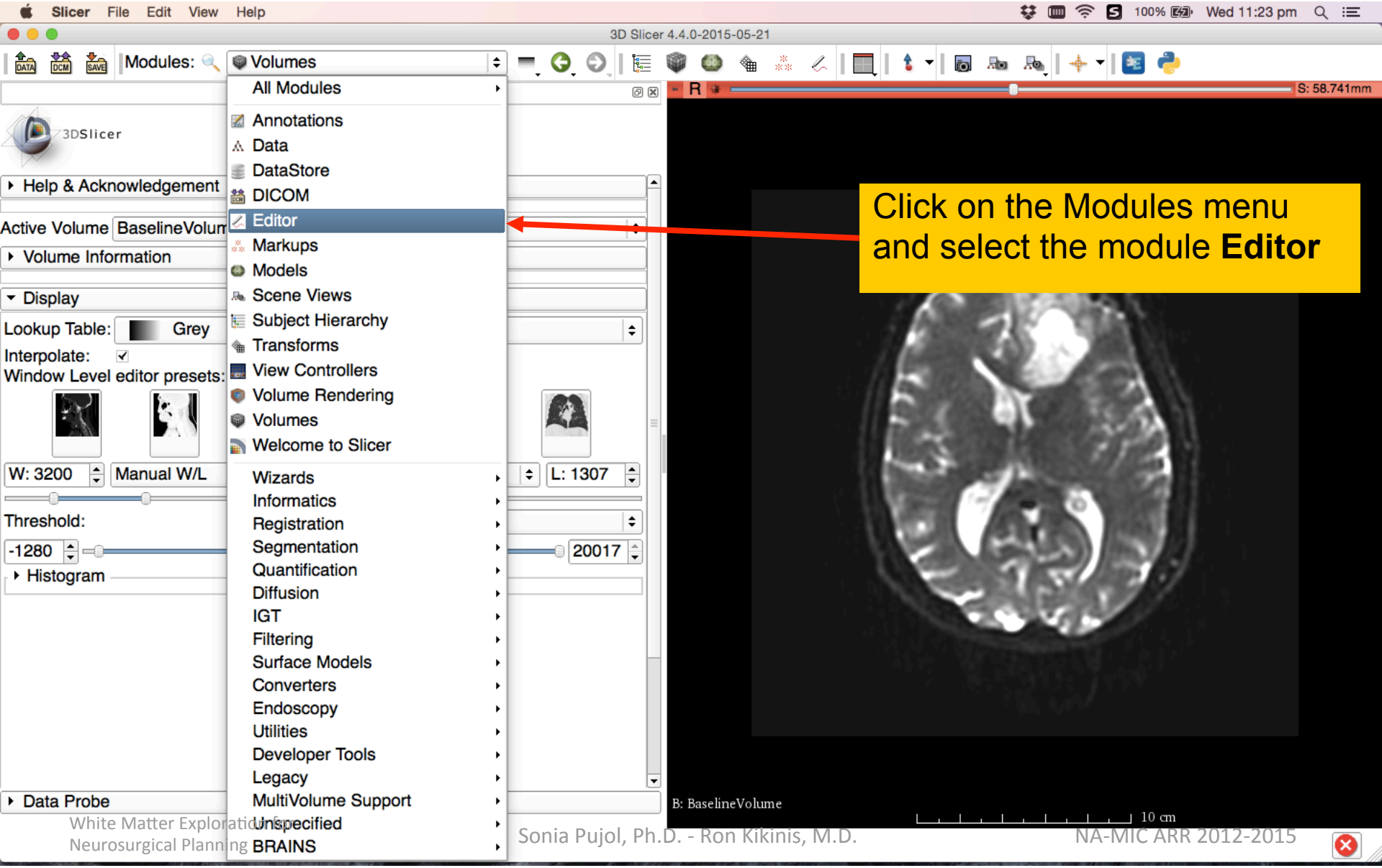
In this section, we will segment the different parts of the tumor using a Grow Cut Segmentation algorithm.

Tumor Segmentation

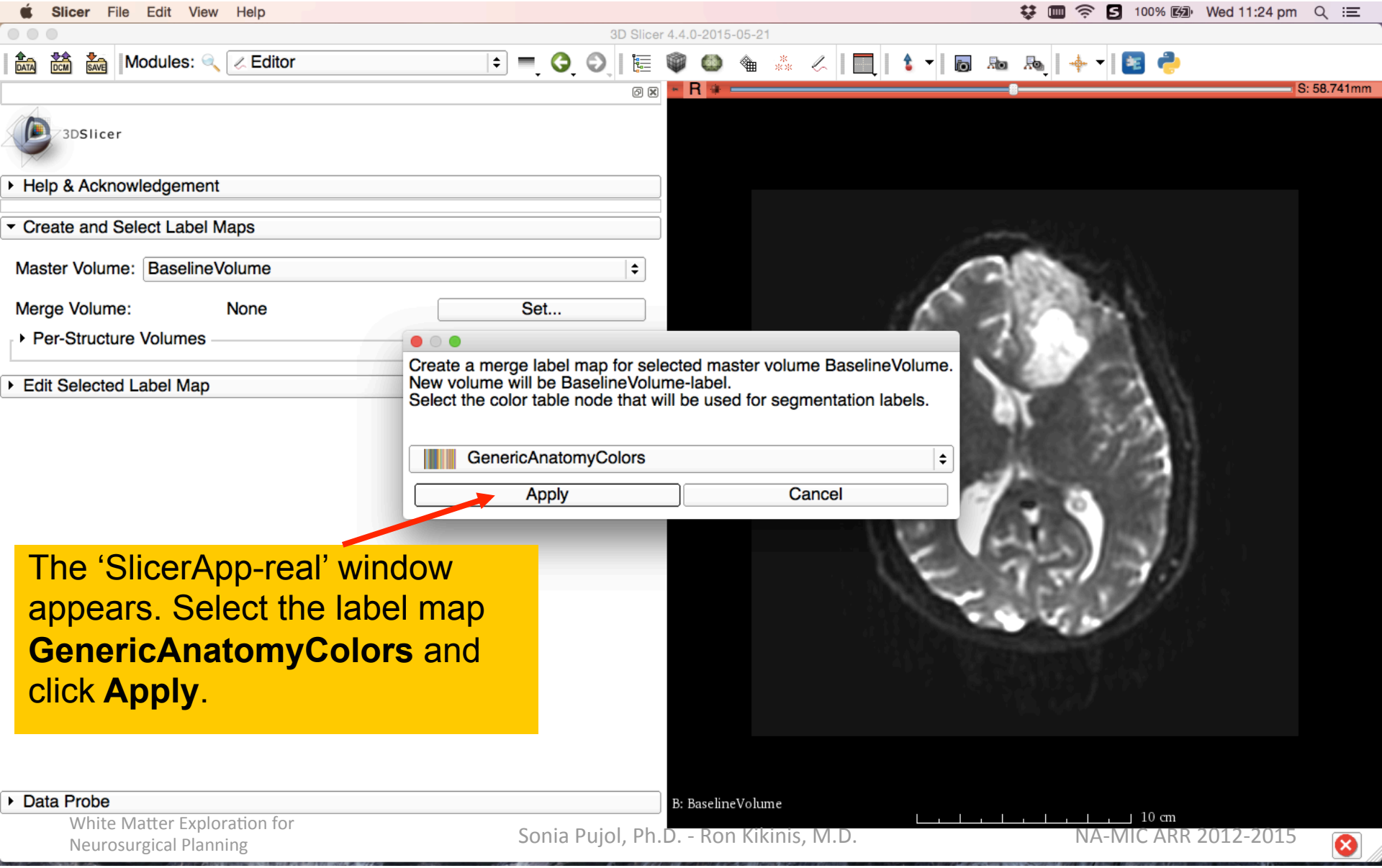


Slicer displays only the Axial anatomical slice in the Viewer

Tumor Segmentation

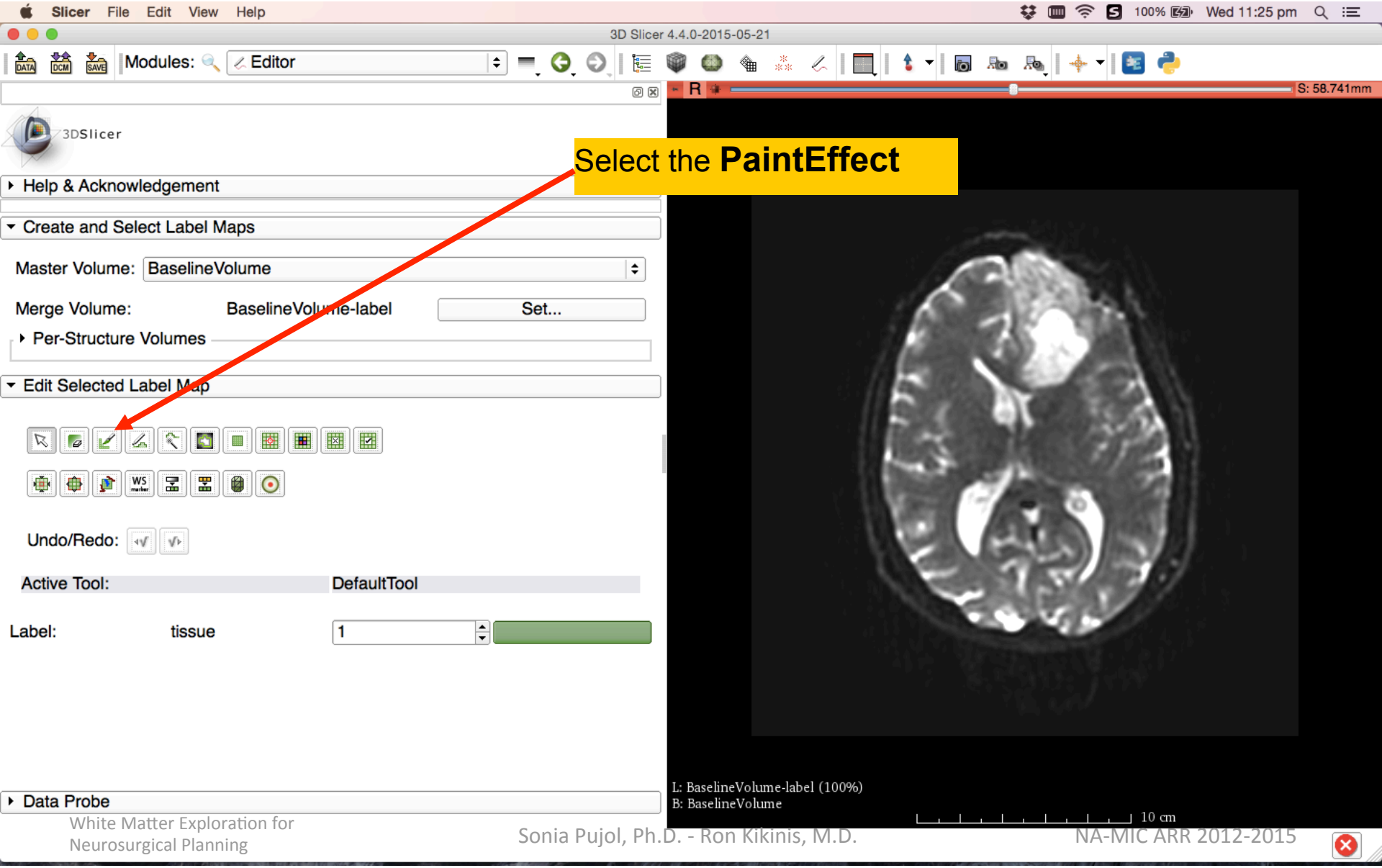


Tumor Segmentation

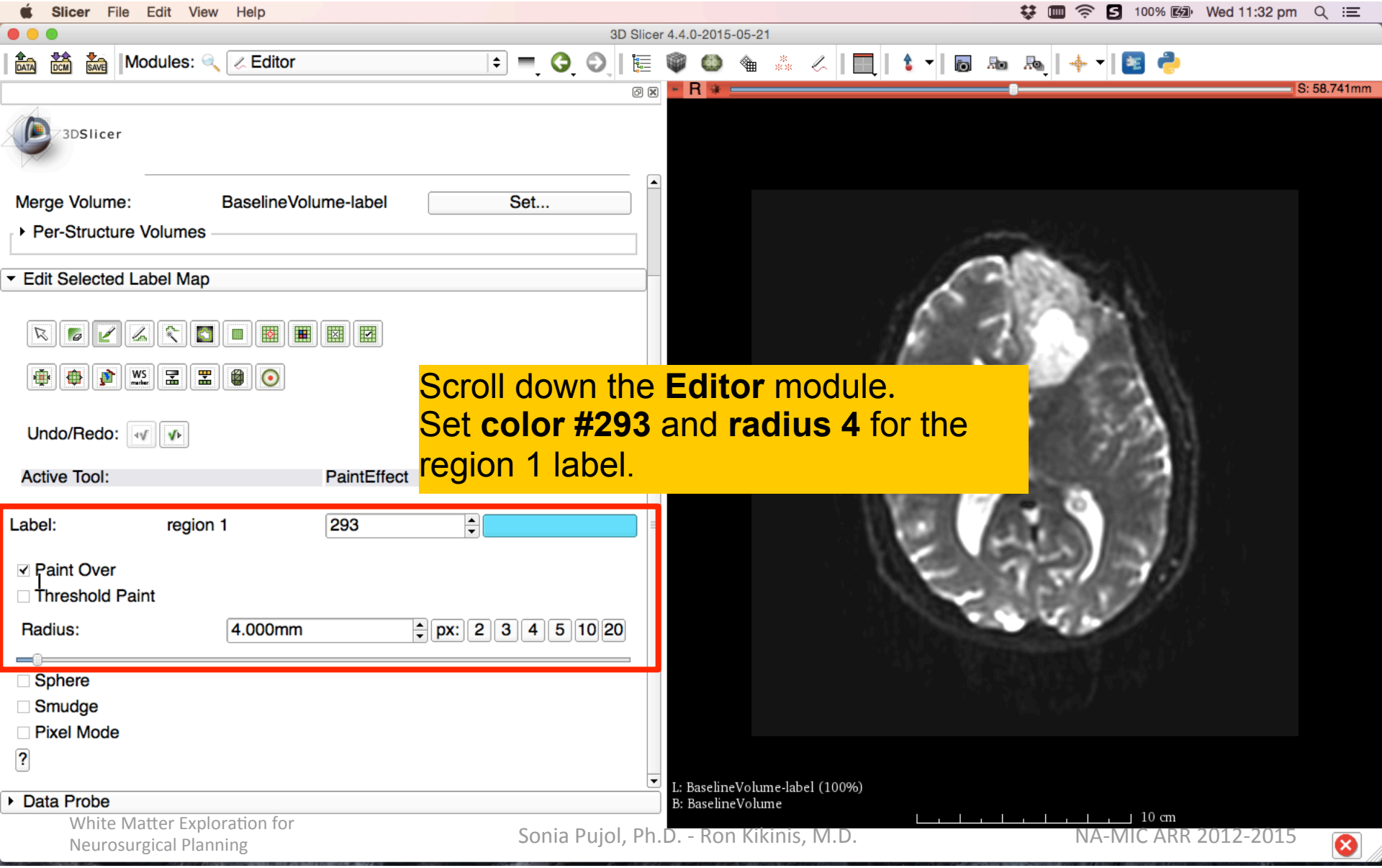


The 'SlicerApp-real' window appears. Select the label map **GenericAnatomyColors** and click **Apply**.

Tumor Segmentation

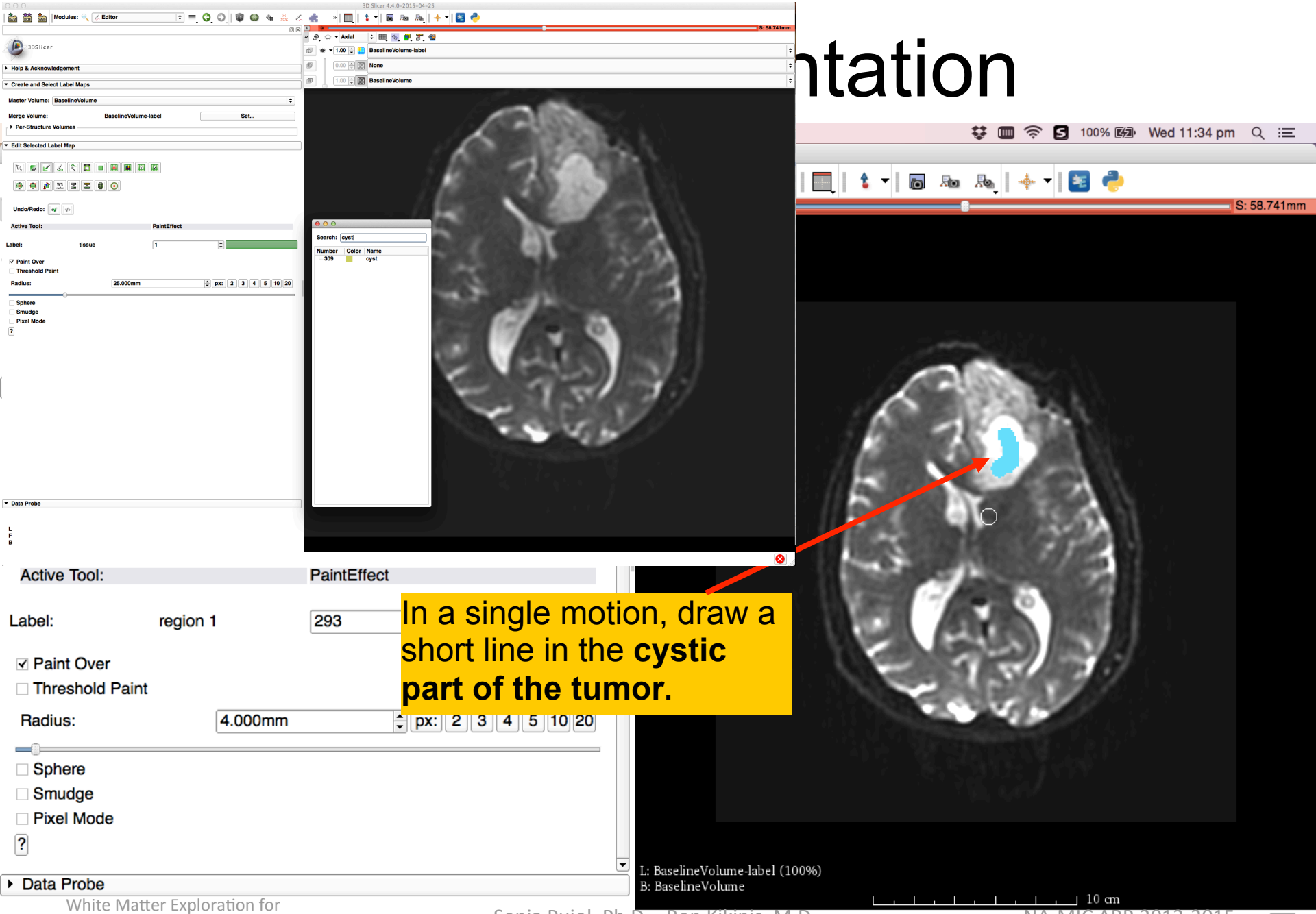


Tumor Segmentation



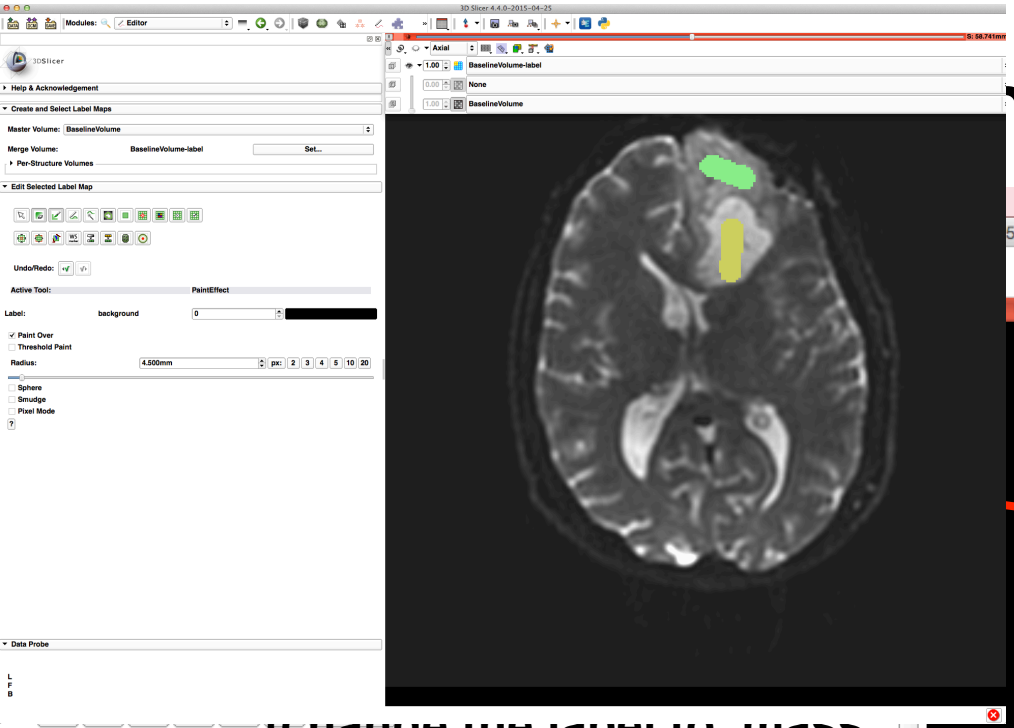
Scroll down the **Editor** module.
Set **color #293** and **radius 4** for the region 1 label.

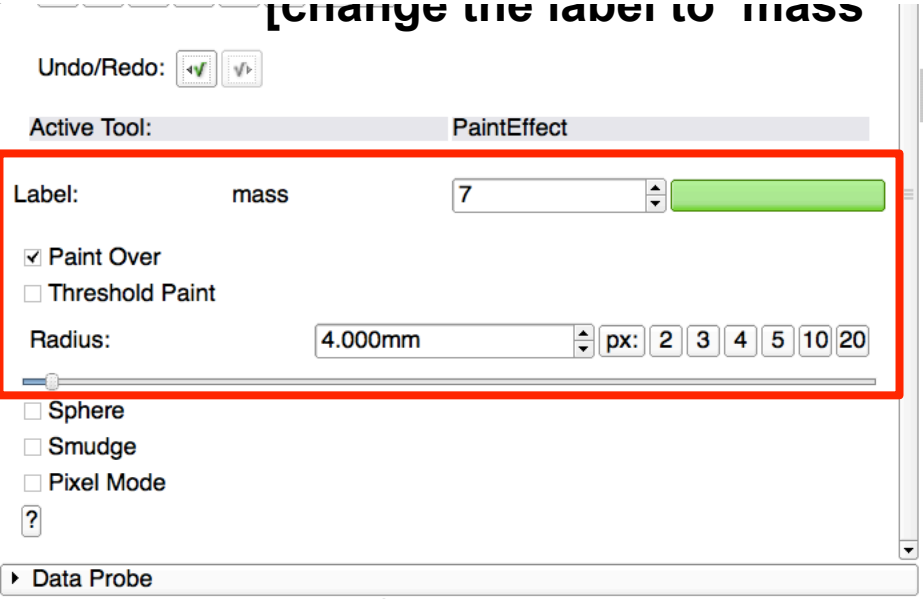
ntation



In a single motion, draw a short line in the **cystic part of the tumor.**

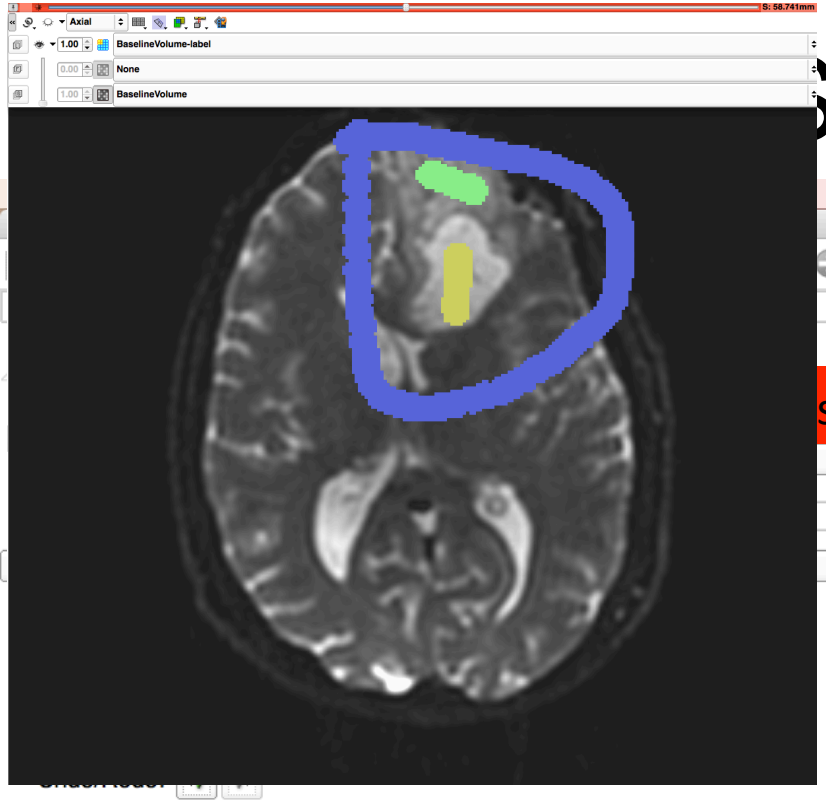
mentation



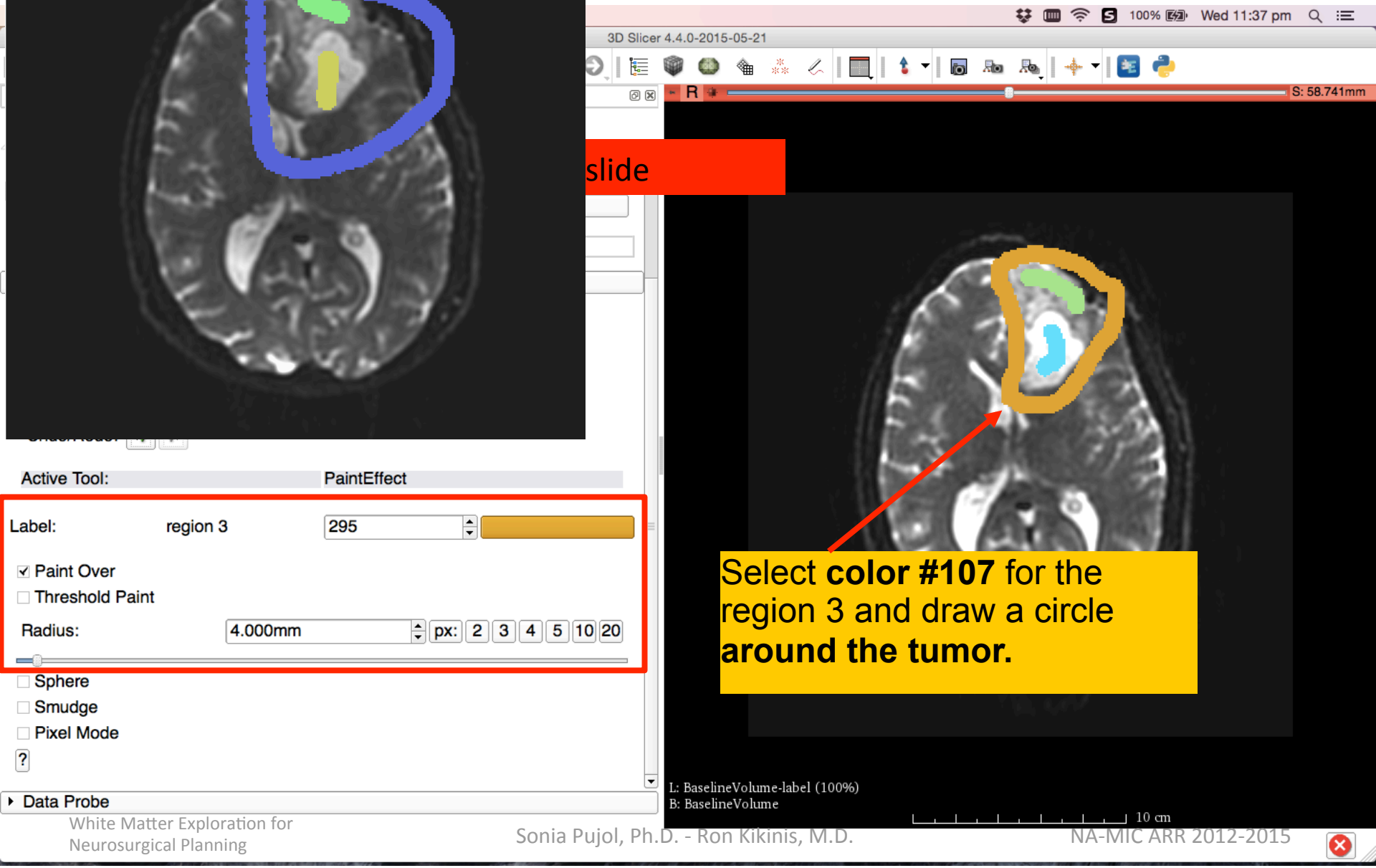

[change the label to "mass
Undo/Redo:
Active Tool:
PaintEffect
Label:
mass
7
Paint Over
Threshold Paint
Radius:
4.000mm
px:
2
3
4
5
10
20
Sphere
Smudge
Pixel Mode
?
Data Probe


100%
Wed 11:36 pm
5-05-21
S: 58.741mm
L: BaselineVolume-label (100%)
B: BaselineVolume
10 cm

Segmentation

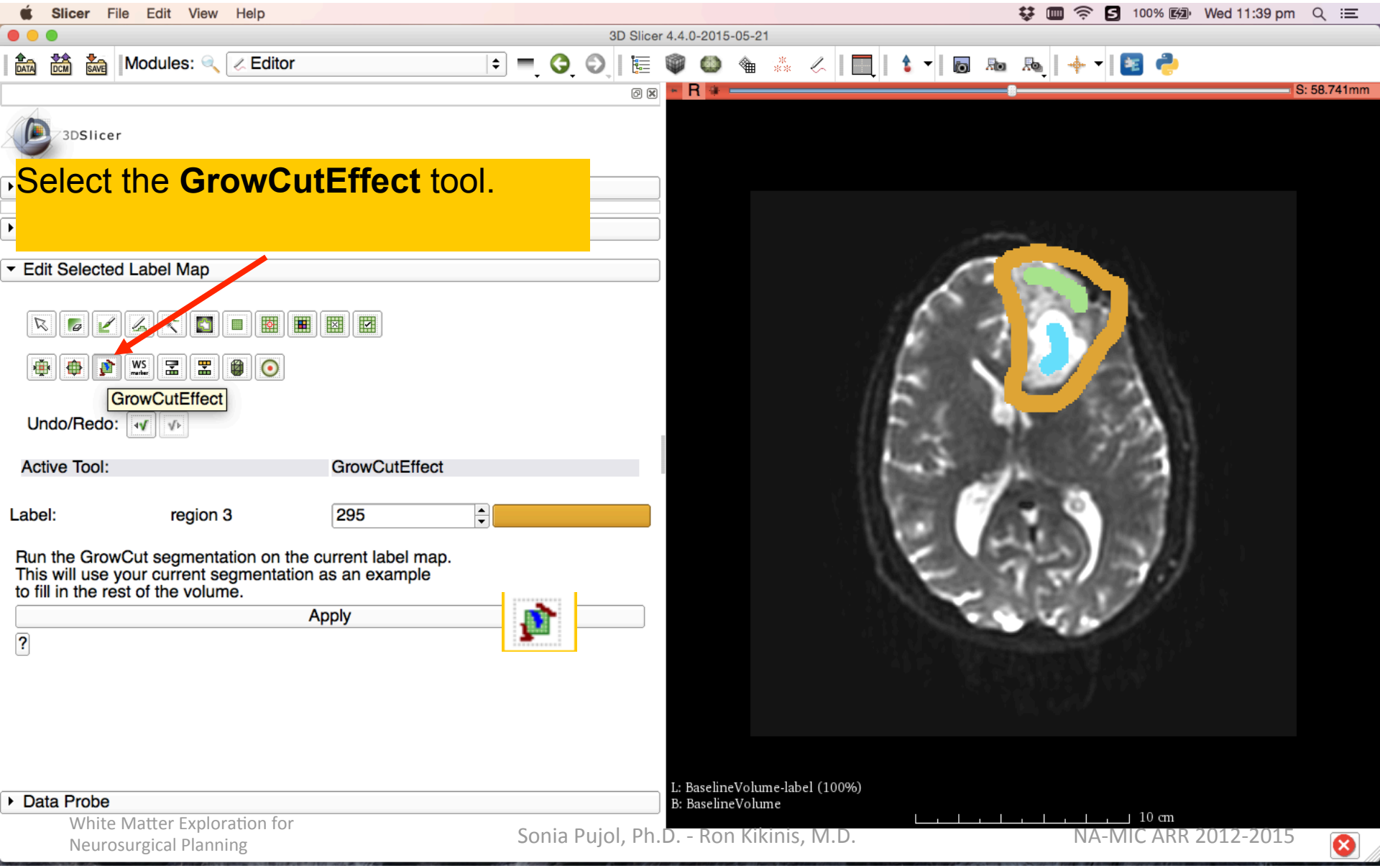


slide

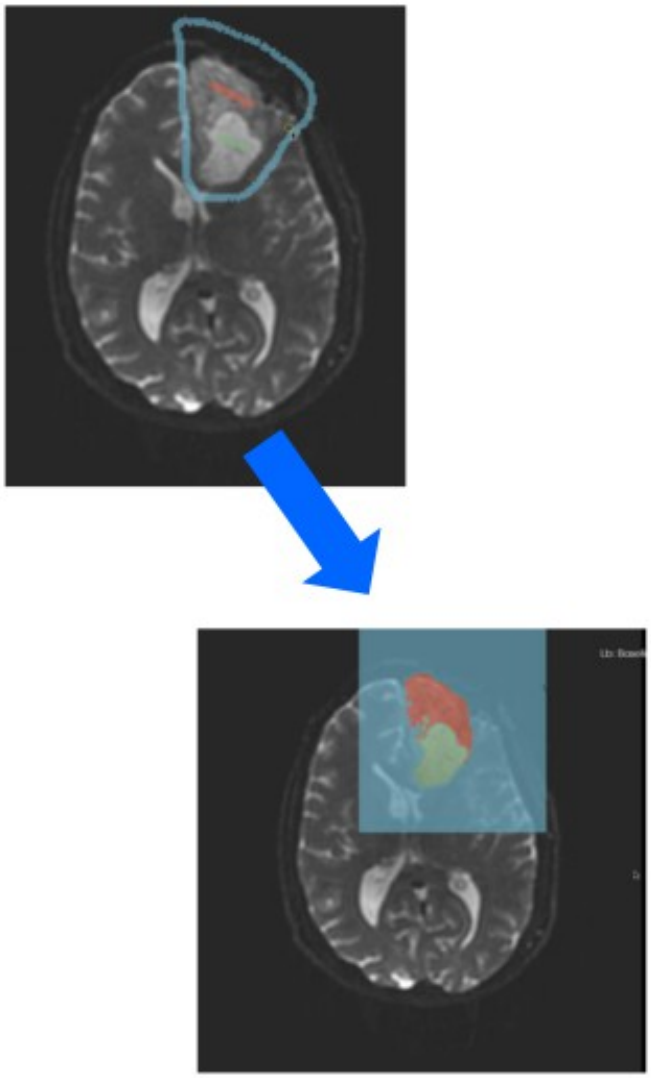


Select **color #107** for the region 3 and draw a circle **around the tumor.**

Tumor Segmentation

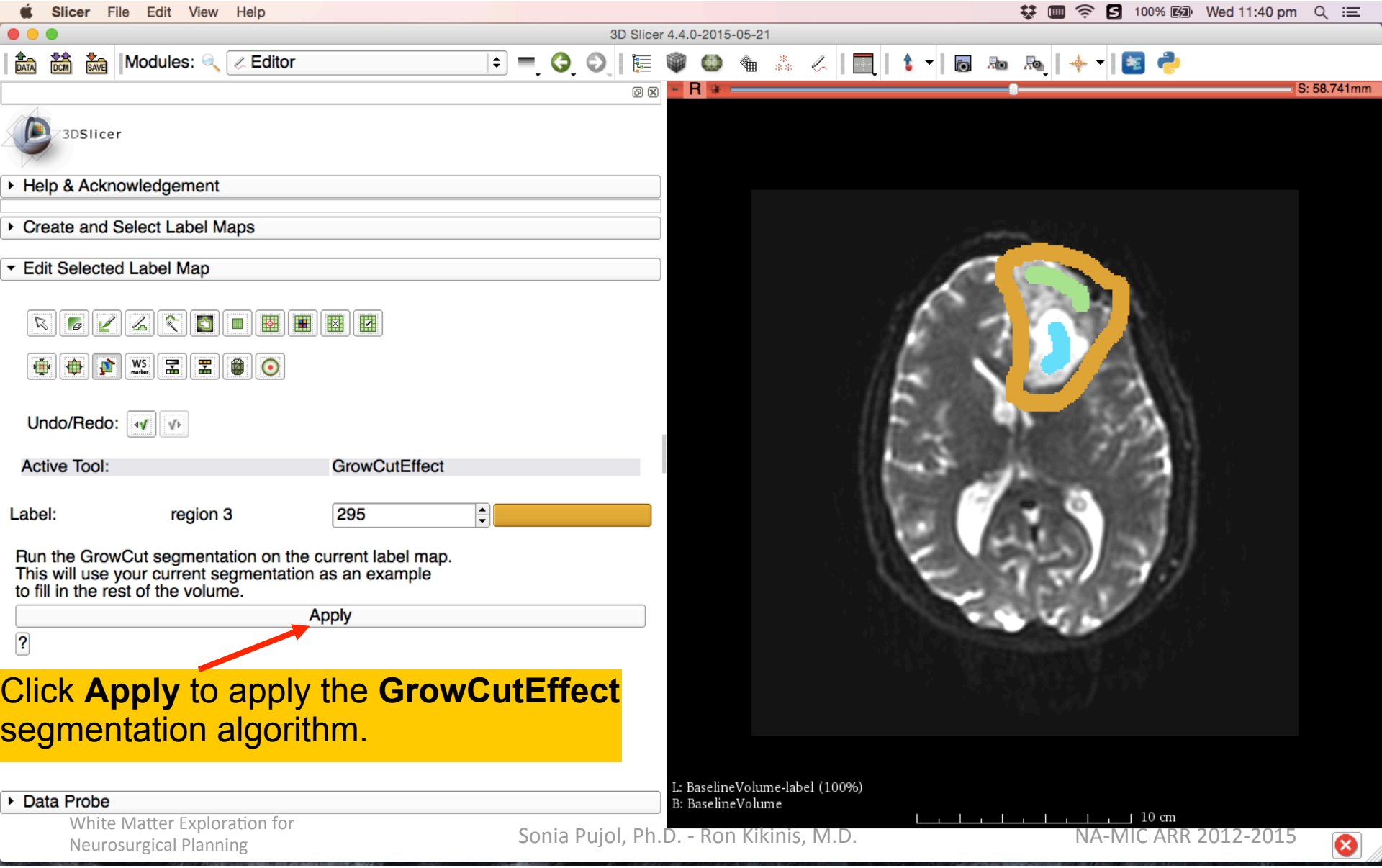


Grow Cut Segmentation

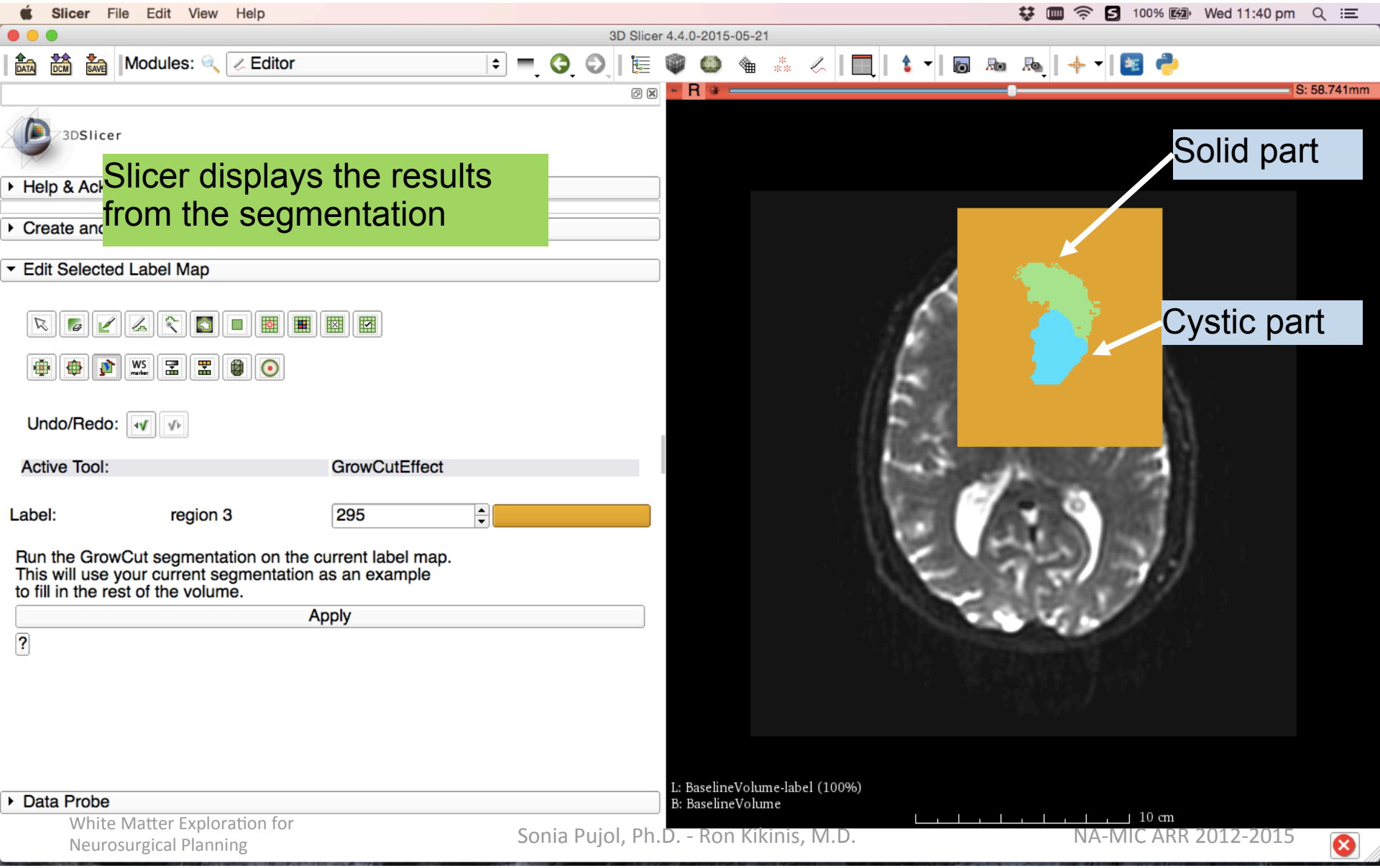


- The Grow Cut Segmentation method is a competitive region growing algorithm using Cellular Automata.
- The algorithm performs multi-label image segmentation using a set of user input scribbles.
- V. Vezhnevets, V. Konouchine. "Grow-Cut" - Interactive Multi-Label N-D Image Segmentation". Proc. Graphicon. 2005 . pp. 150-156.

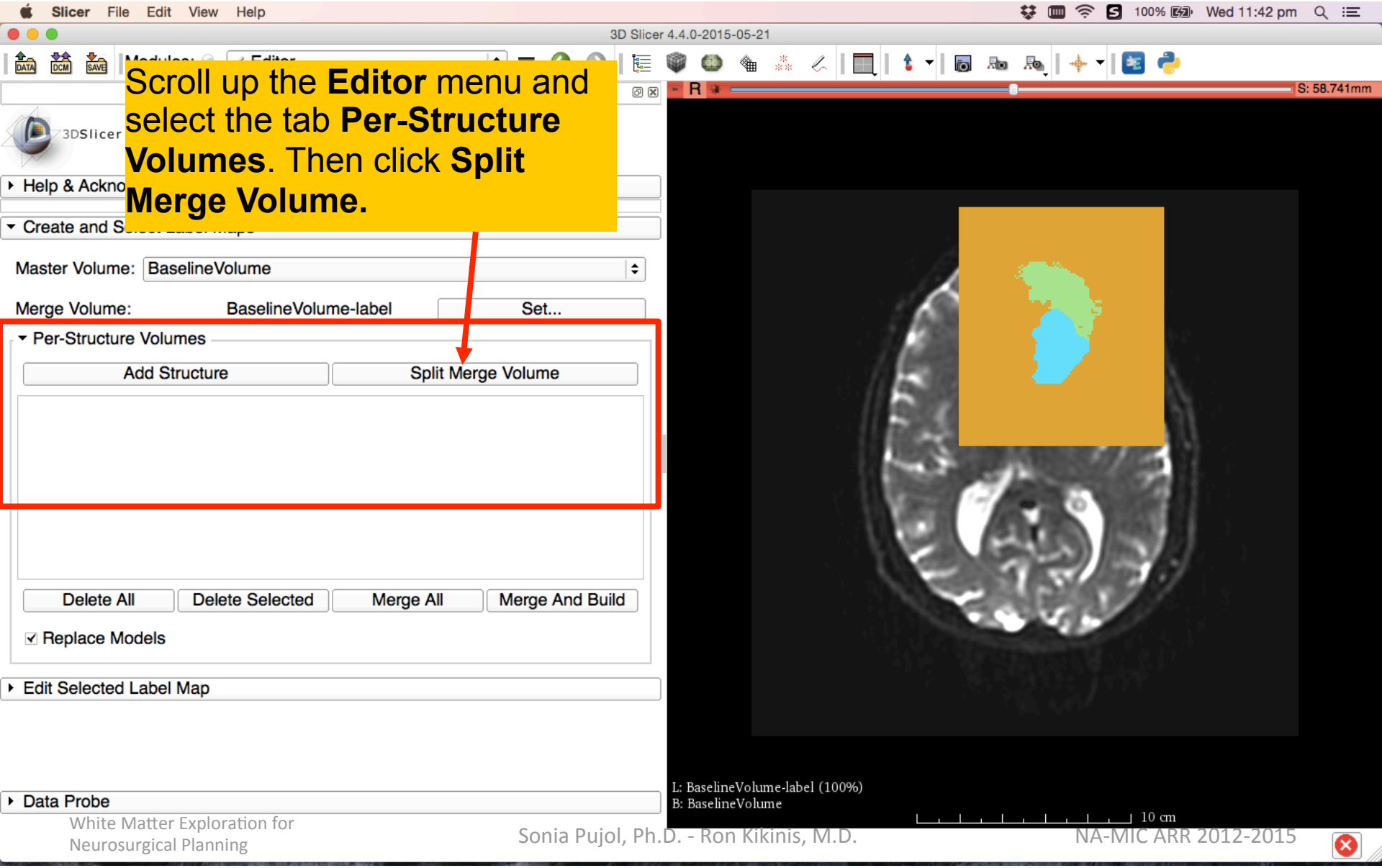
Tumor Segmentation



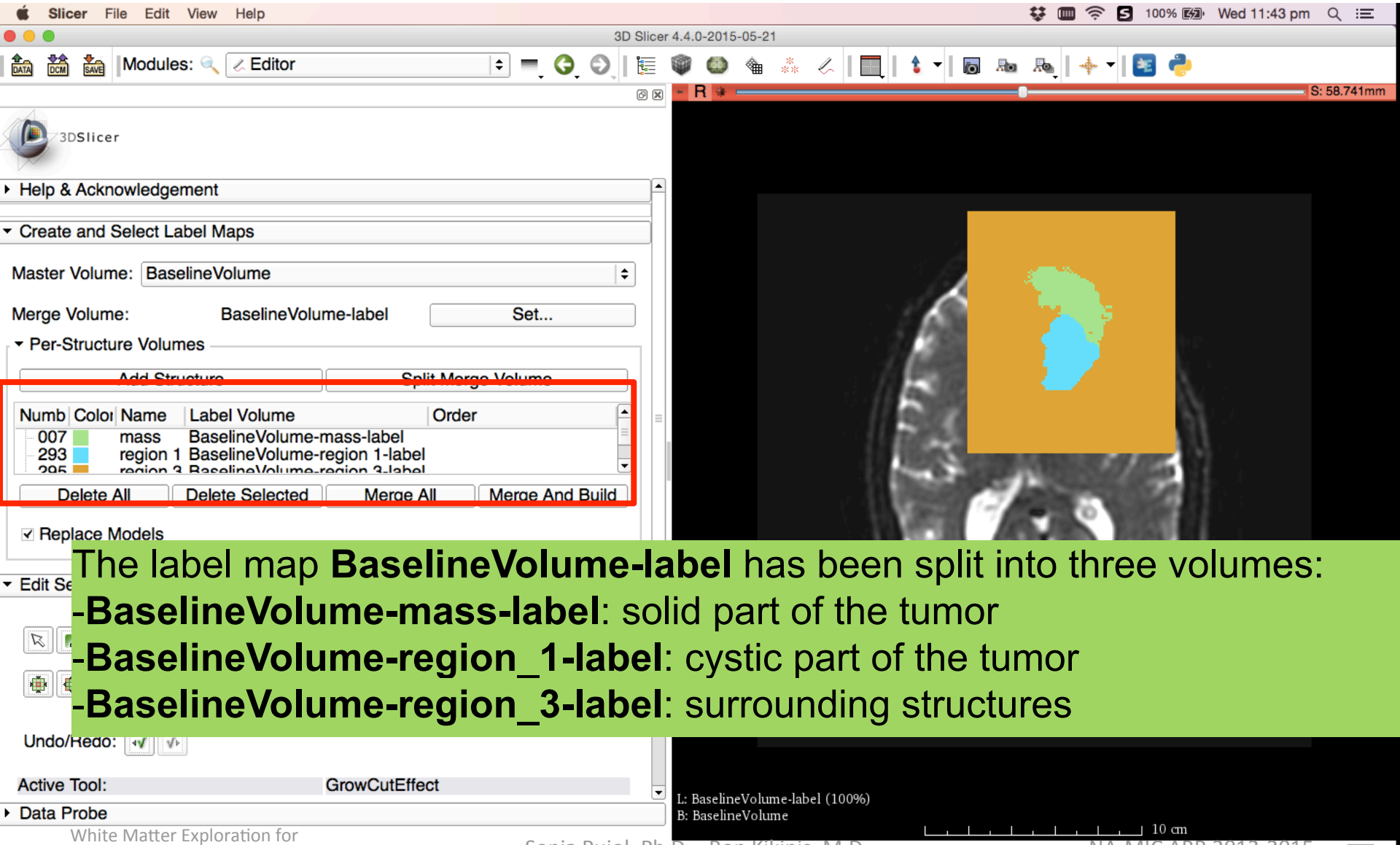
Tumor Segmentation



Tumor Segmentation



Tumor Segmentation



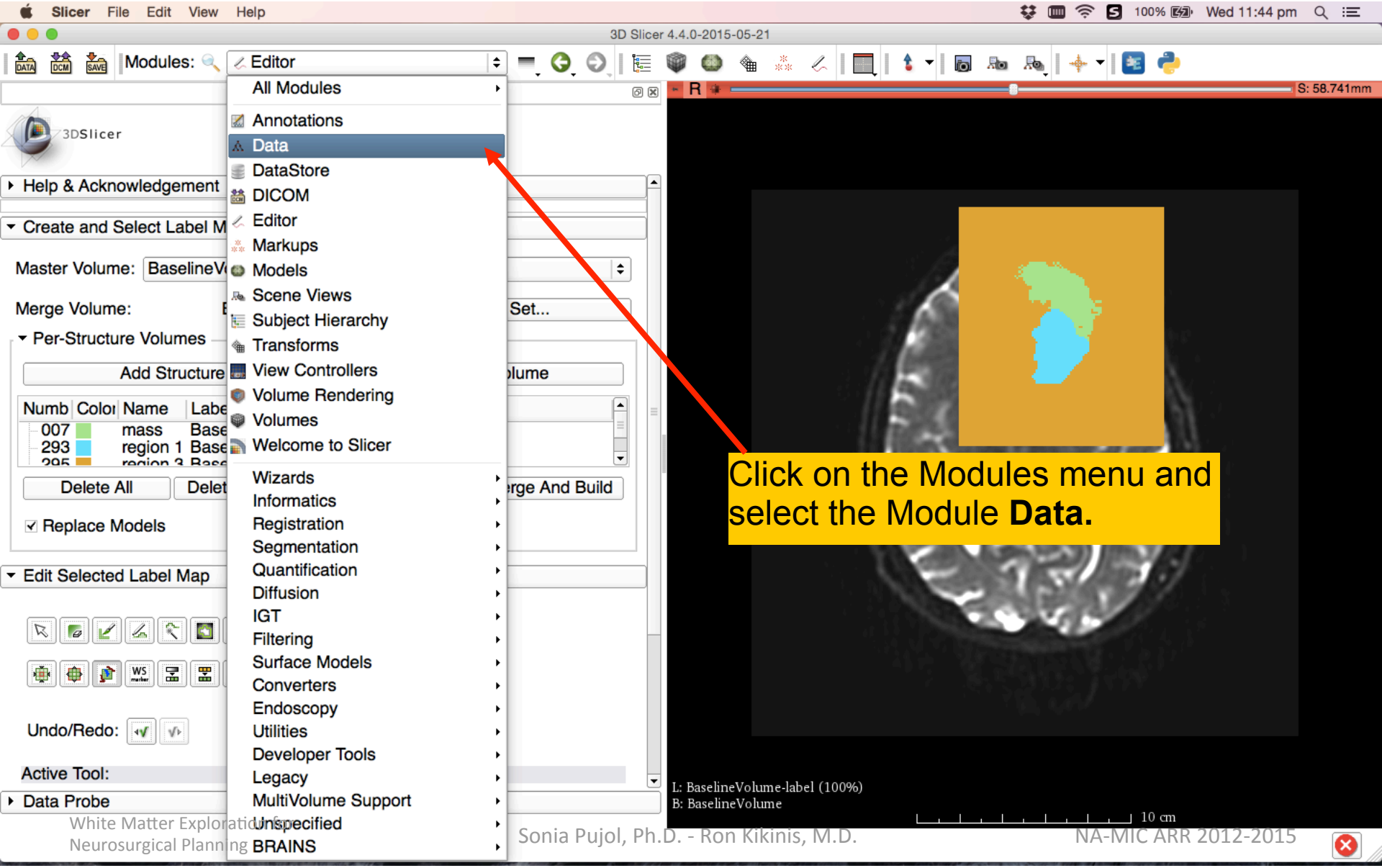
The label map **BaselineVolume-label** has been split into three volumes:

-**BaselineVolume-mass-label**: solid part of the tumor

-**BaselineVolume-region_1-label**: cystic part of the tumor

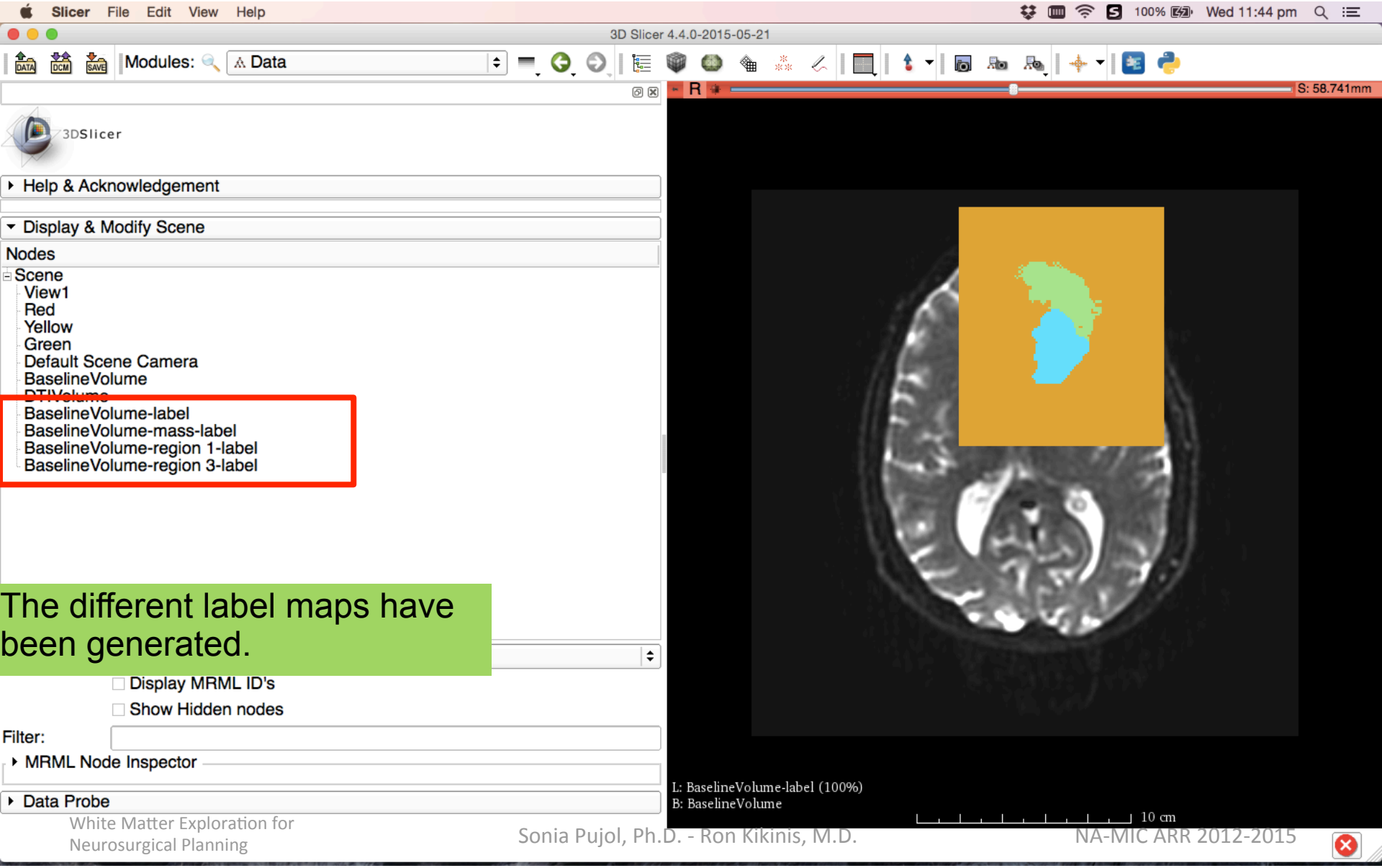
-**BaselineVolume-region_3-label**: surrounding structures

Tumor Segmentation



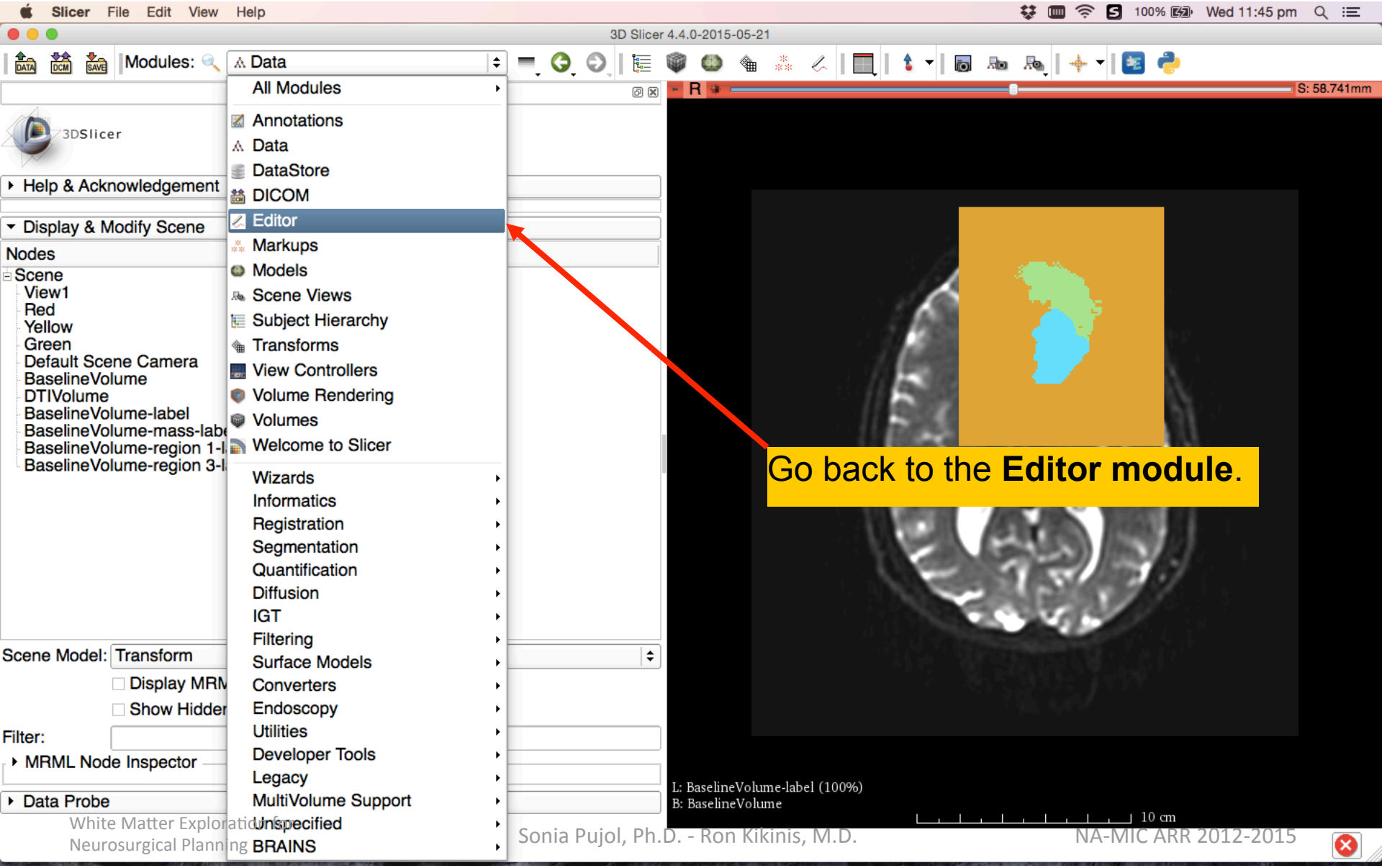
Click on the Modules menu and select the Module **Data.**

Tumor Segmentation

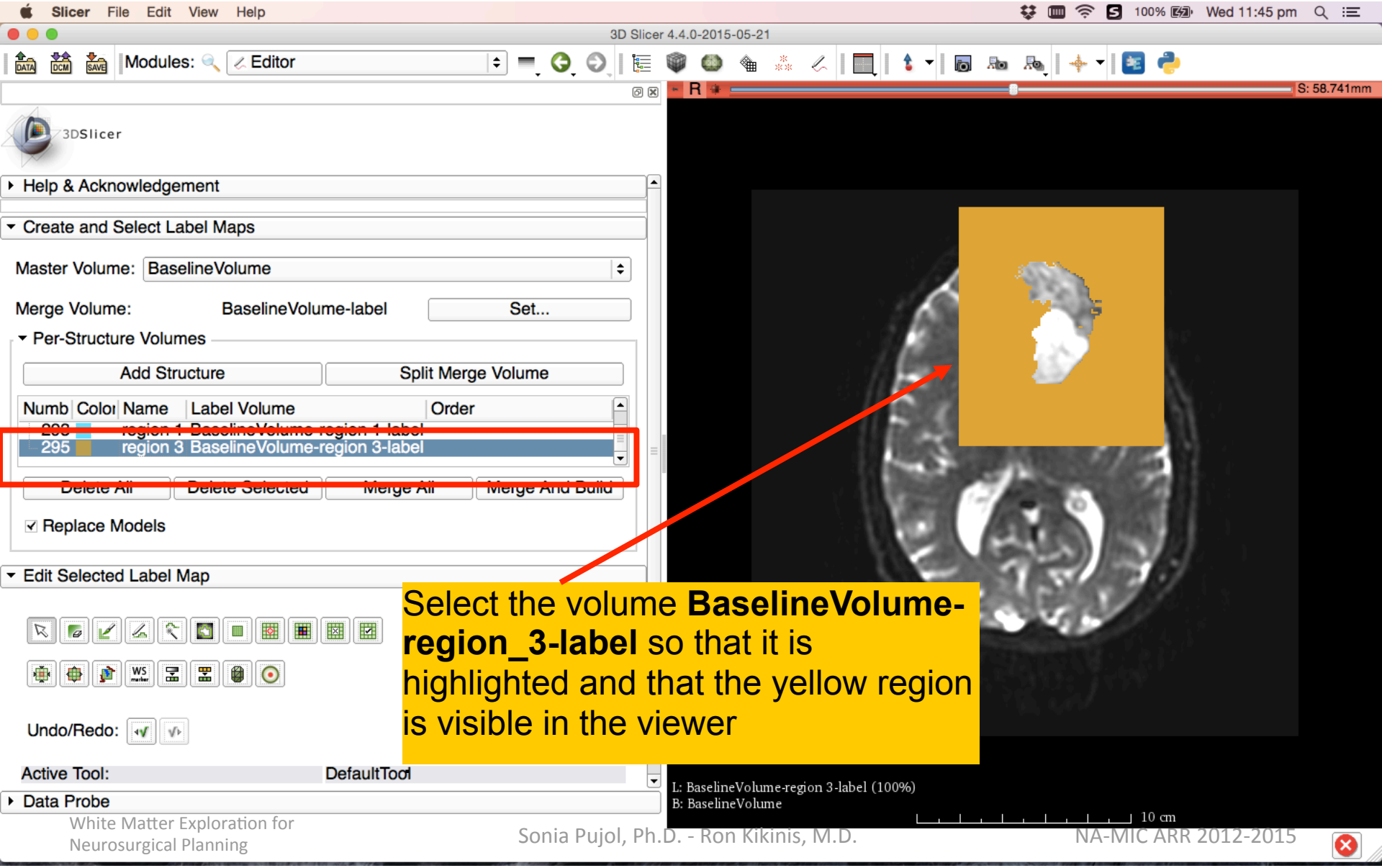


The different label maps have been generated.

Ventricles Segmentation

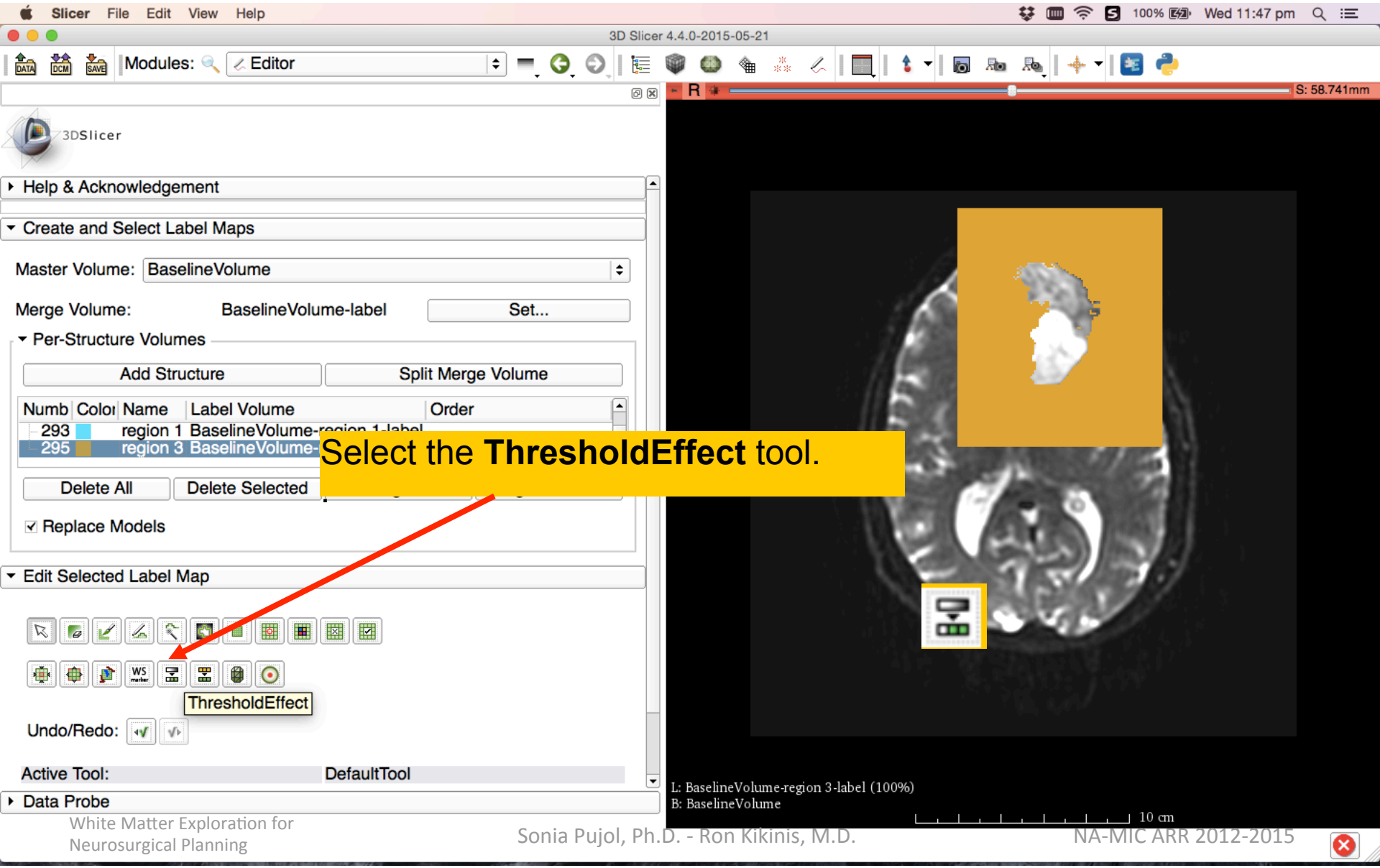


Ventricles Segmentation



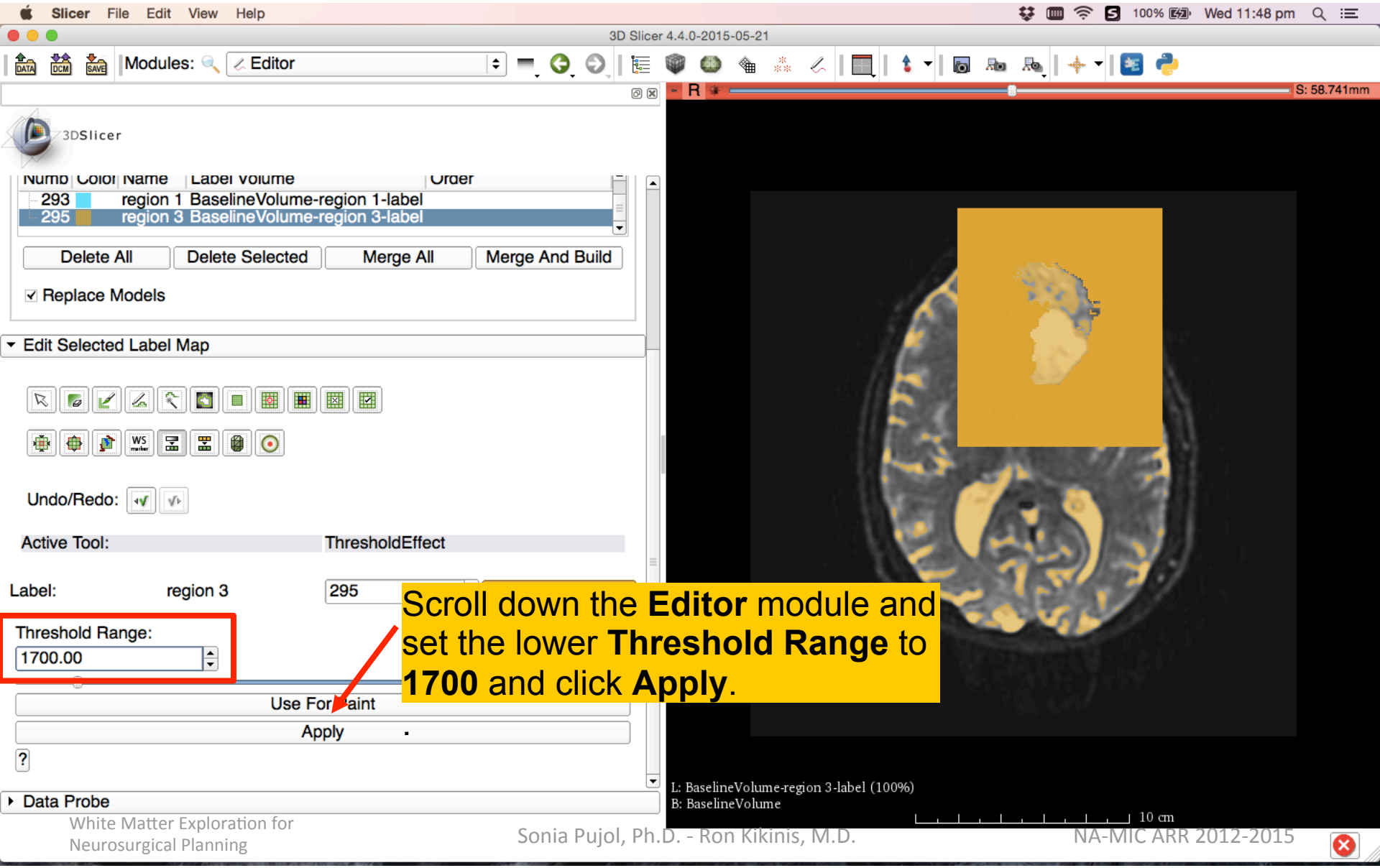
Select the volume **BaselineVolume-region_3-label** so that it is highlighted and that the yellow region is visible in the viewer

Ventricles Segmentation



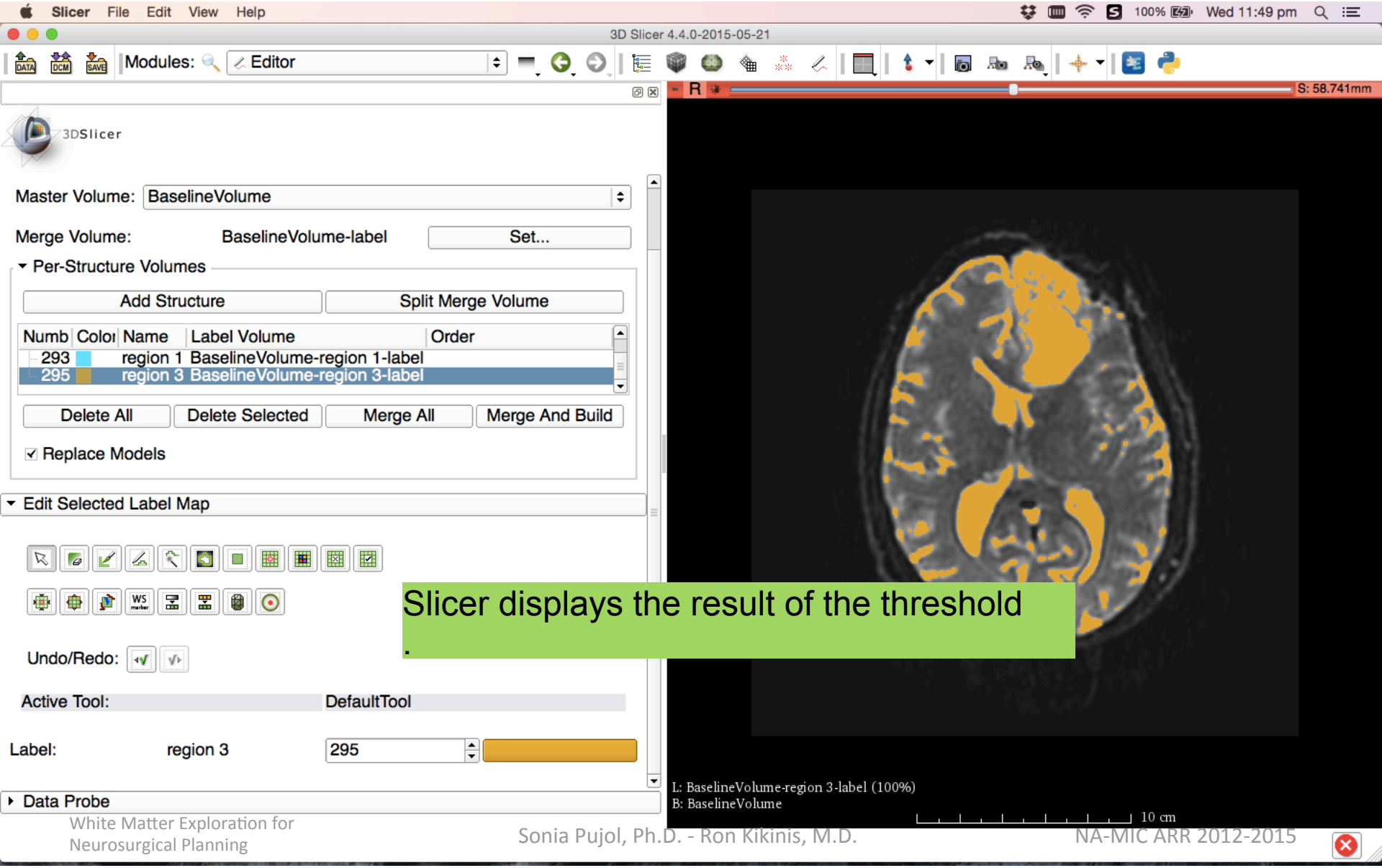
Select the **ThresholdEffect** tool.

Ventricles Segmentation



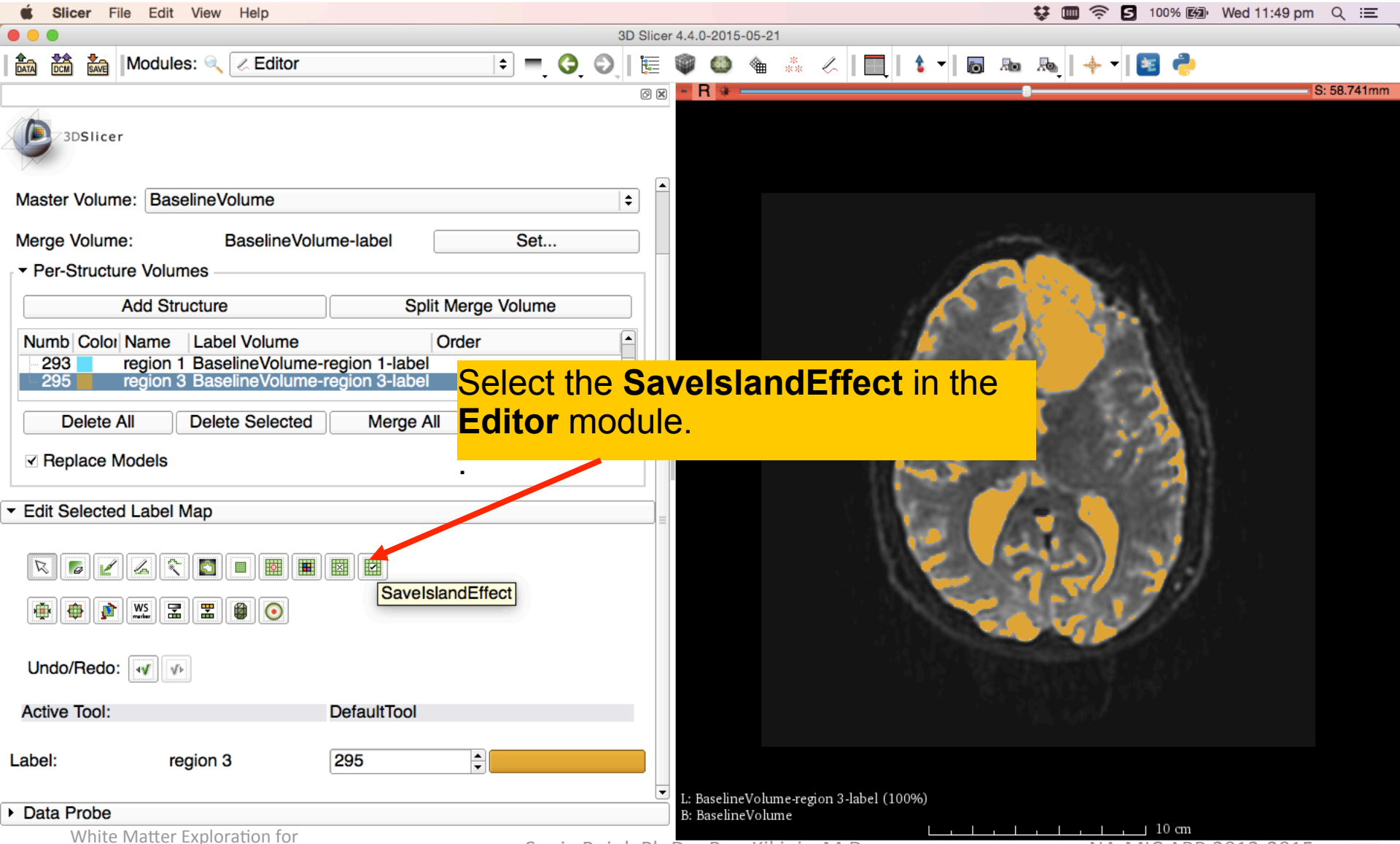
Scroll down the **Editor** module and set the lower **Threshold Range** to **1700** and click **Apply**.

Ventricles Segmentation



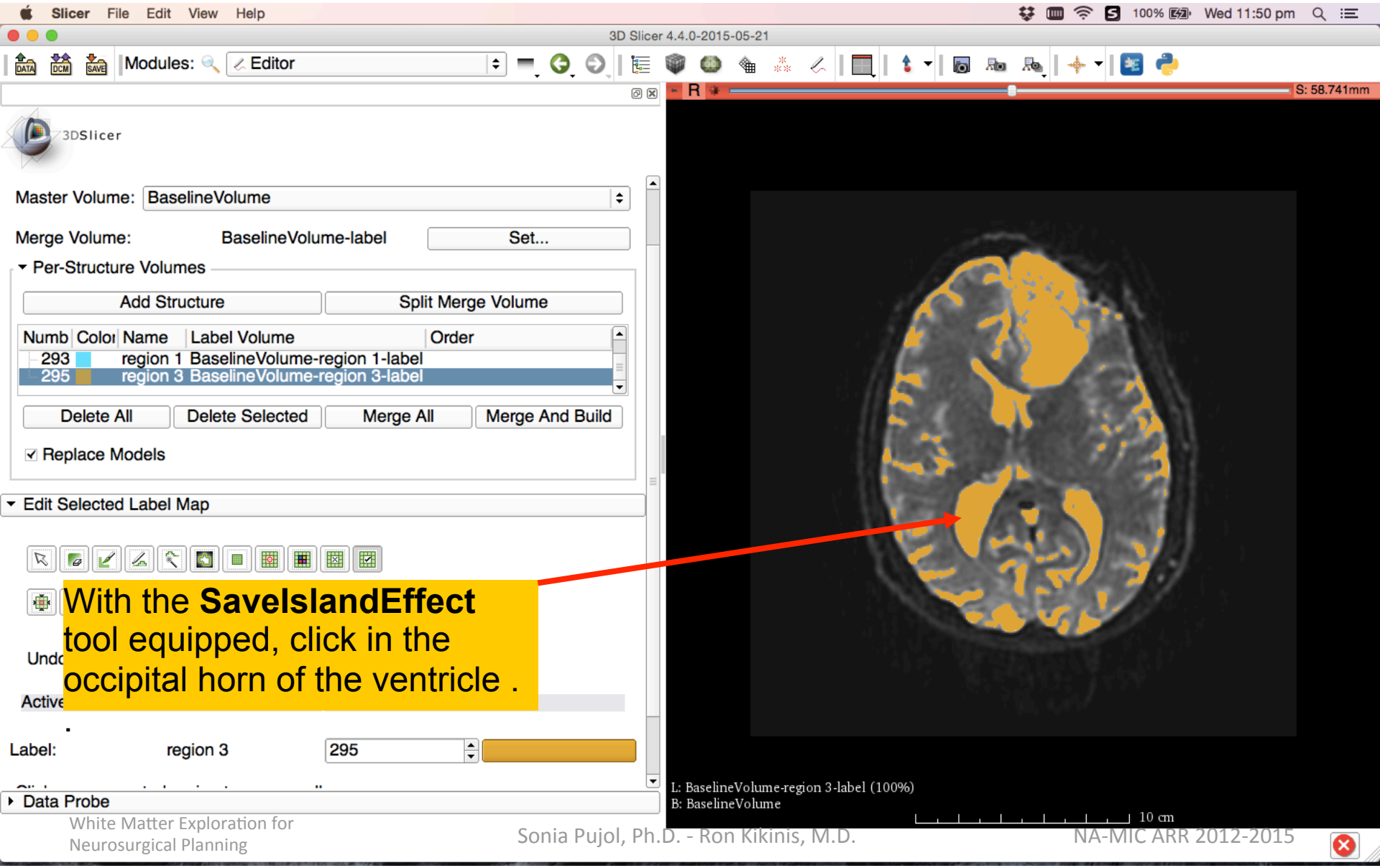
Slicer displays the result of the threshold
.

Ventricles Segmentation



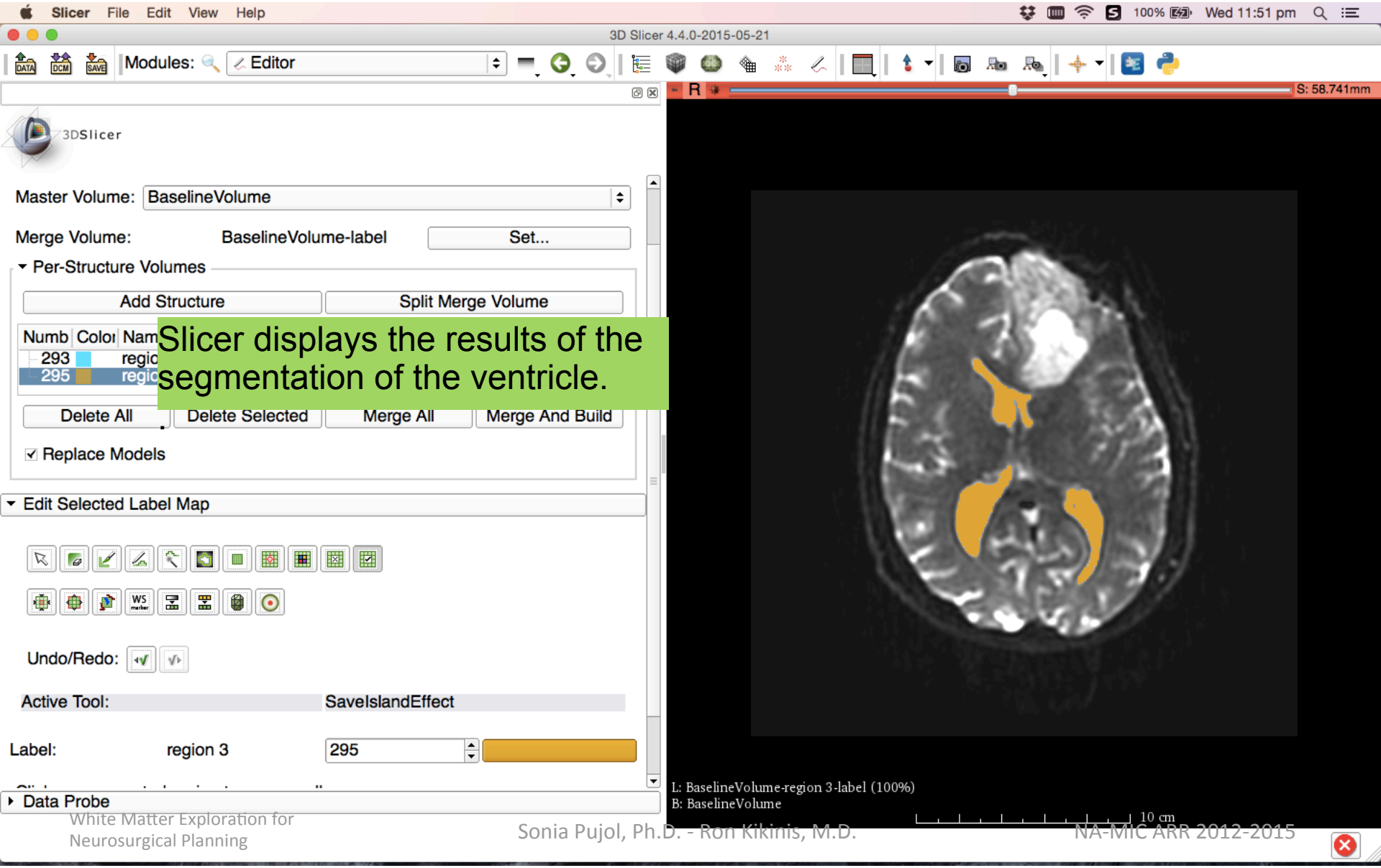
Select the **SaveIslandEffect** in the **Editor** module.

Ventricles Segmentation



With the **SaveIslandEffect** tool equipped, click in the occipital horn of the ventricle .

Final Result of Segmentation



Slicer displays the results of the segmentation of the ventricle.

Final Result of Segmentation

Scroll back up and cllick on Merge and Build to merge the diferent label maps, and generate the 3D models of the tumor and ventricles using a Marching Cubes algorithm.

.

Slicer File Edit View Help

Modules: Editor

3DSlicer

Master Volume: BaselineVolume

Merge Volume: BaselineVolume-lab

Per-Structure Volumes

Add Structure | Split Merge Volume

Numb	Color	Name	Label Volume	Order
293		region 1	BaselineVolume-region 1-label	
295		region 3	BaselineVolume-region 3-label	

Delete All | Delete Selected | Merge All | Merge And Build

Replace Models

Edit Selected Label Map

Undo/Redo:

Active Tool: SaveIslandEffect

Label: region 3 295

Data Probe

S: 58.741mm

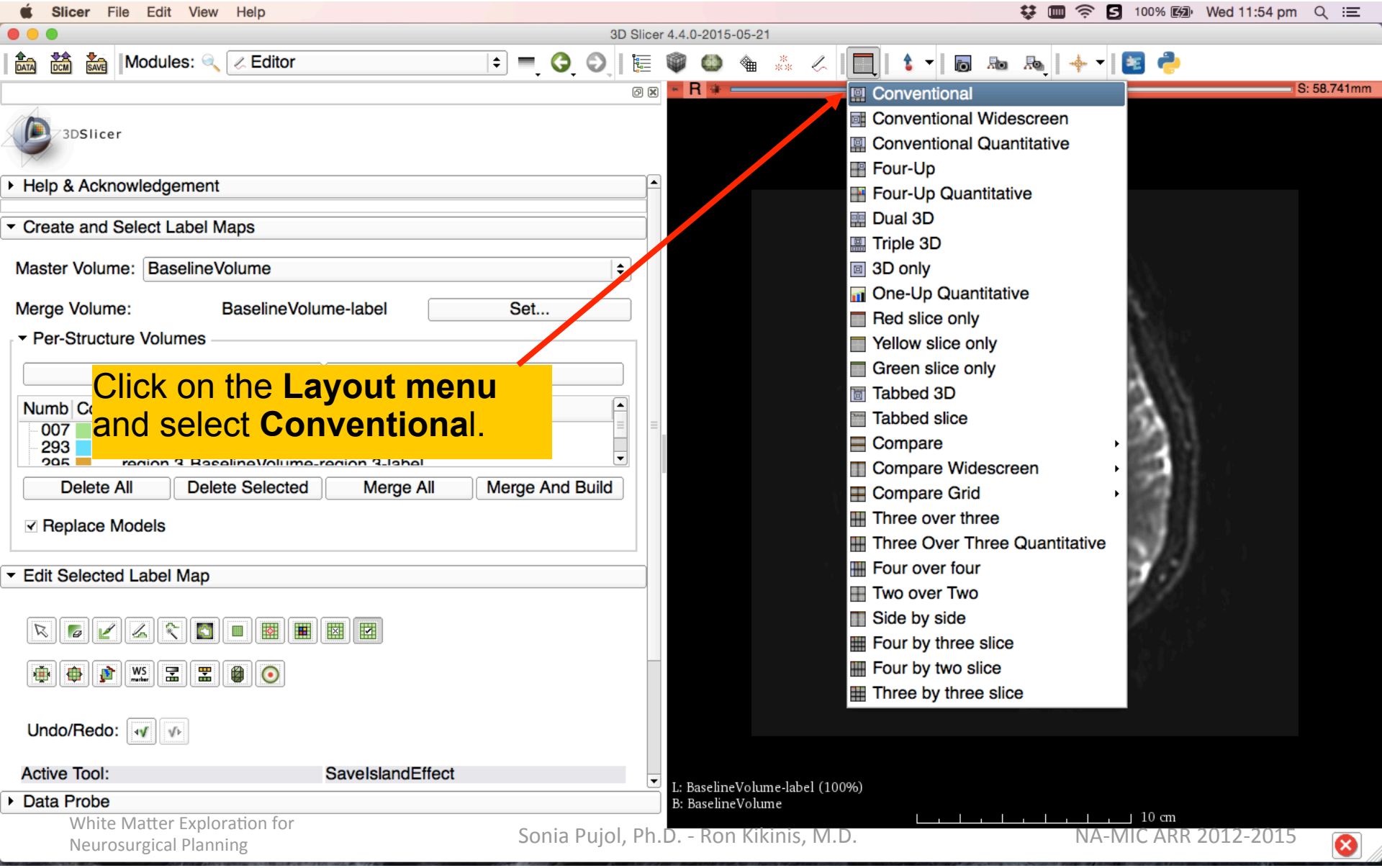
L: BaselineVolume-region 3-label (100%)
B: BaselineVolume

10 cm

Final Result of Segmentation

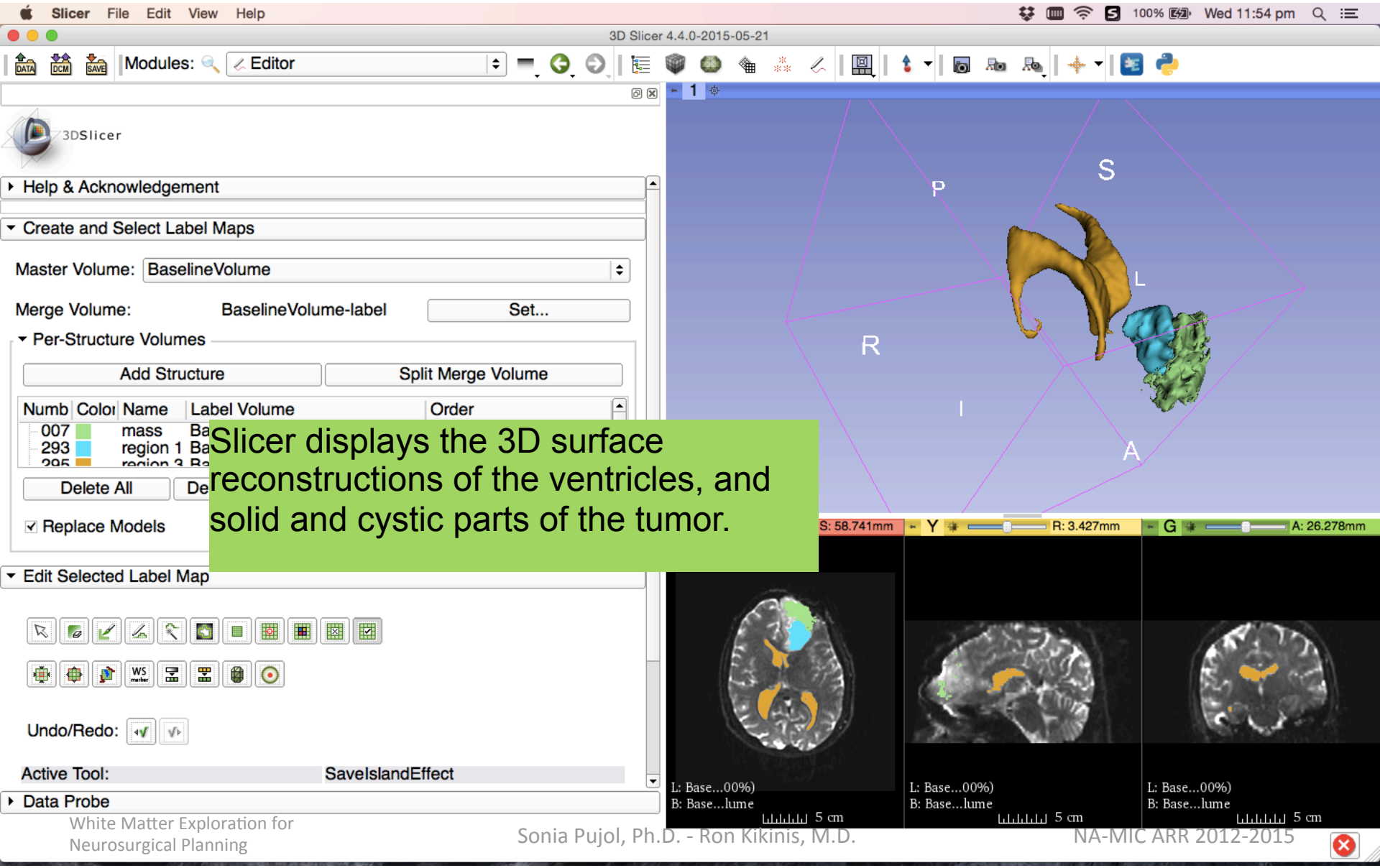
Slicer displays the results of the merging of the segmentations of the ventricles and the tumor in the Viewer.

Final Result of Segmentation



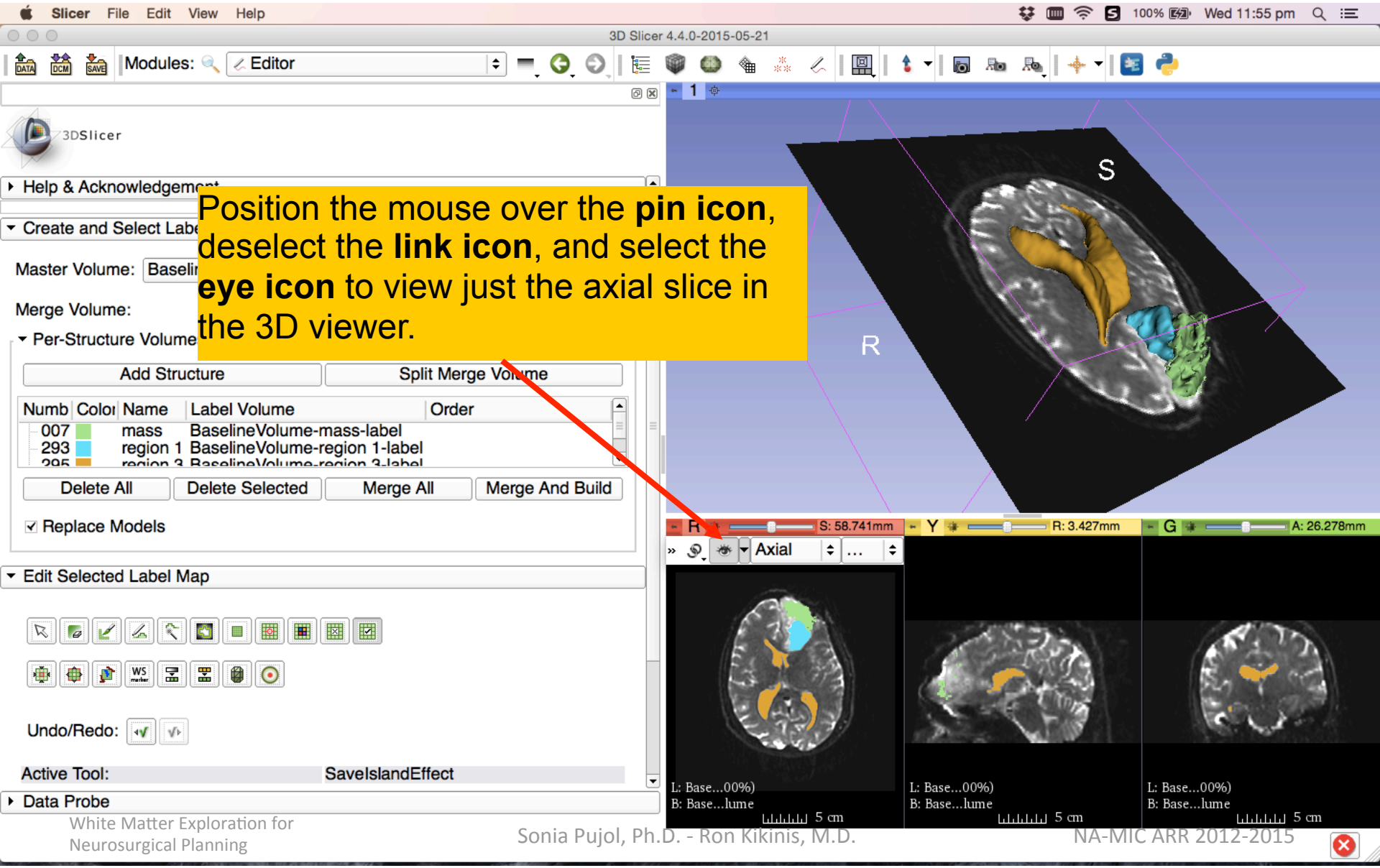
Click on the **Layout menu** and select **Conventional**.

Final Result of Segmentation



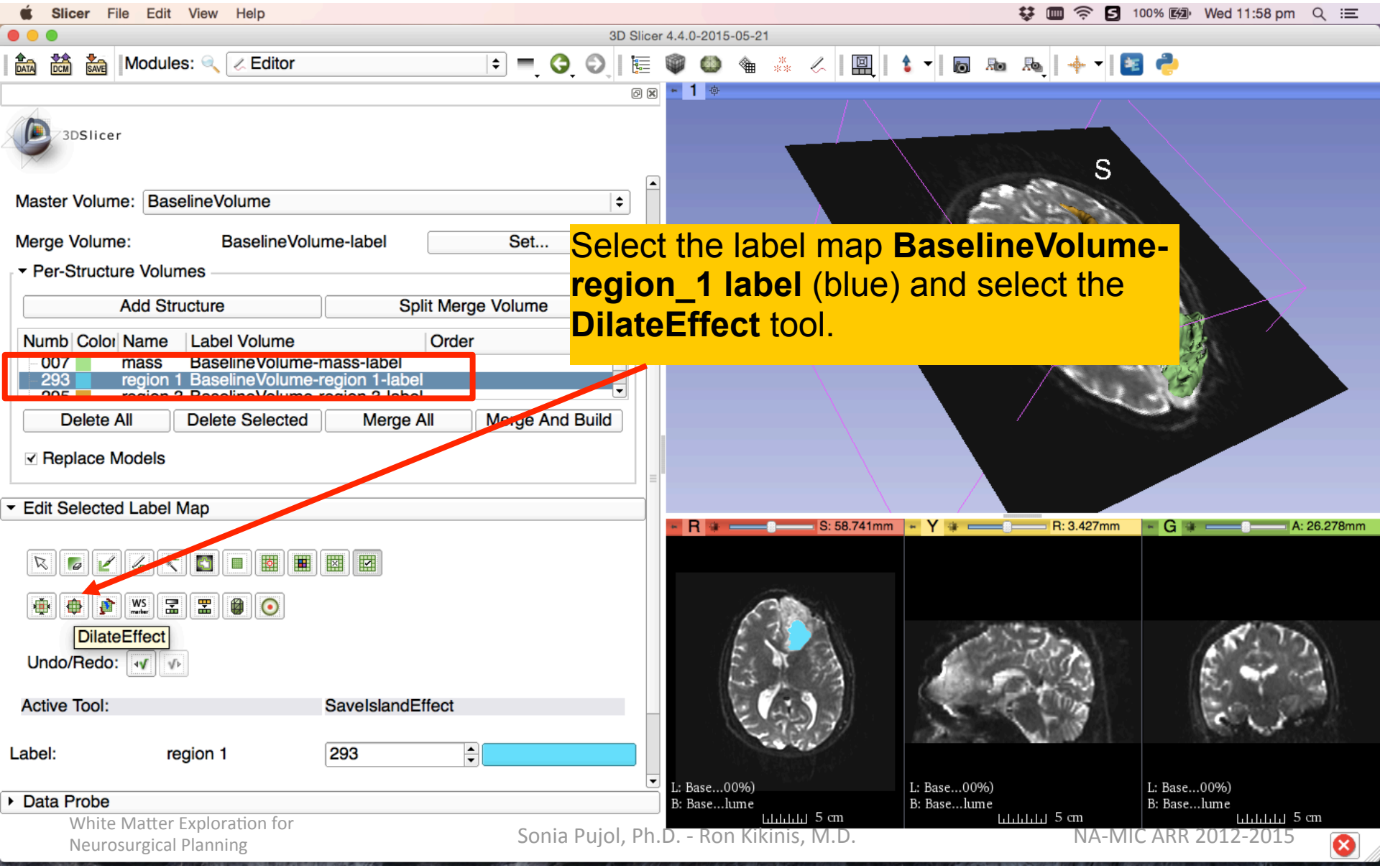
Slicer displays the 3D surface reconstructions of the ventricles, and solid and cystic parts of the tumor.

Definition of peri-tumoral volume

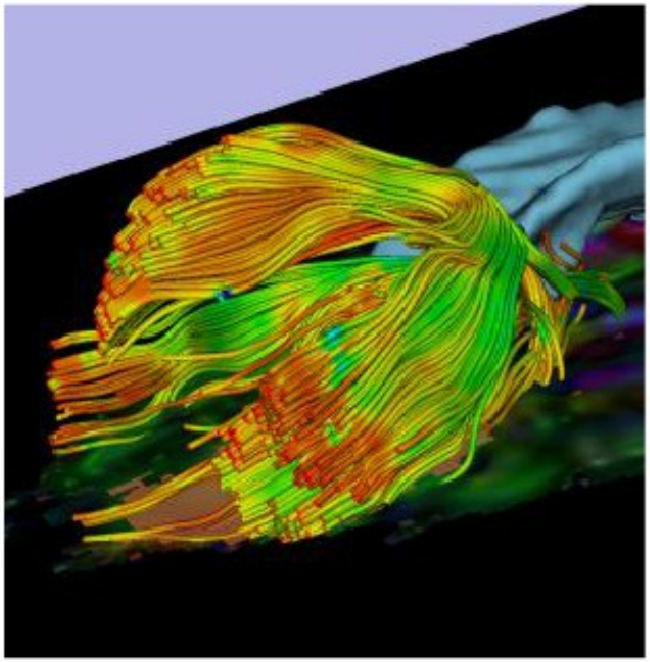


Position the mouse over the **pin icon**, deselect the **link icon**, and select the **eye icon** to view just the axial slice in the 3D viewer.

Definition of peri-tumoral volume

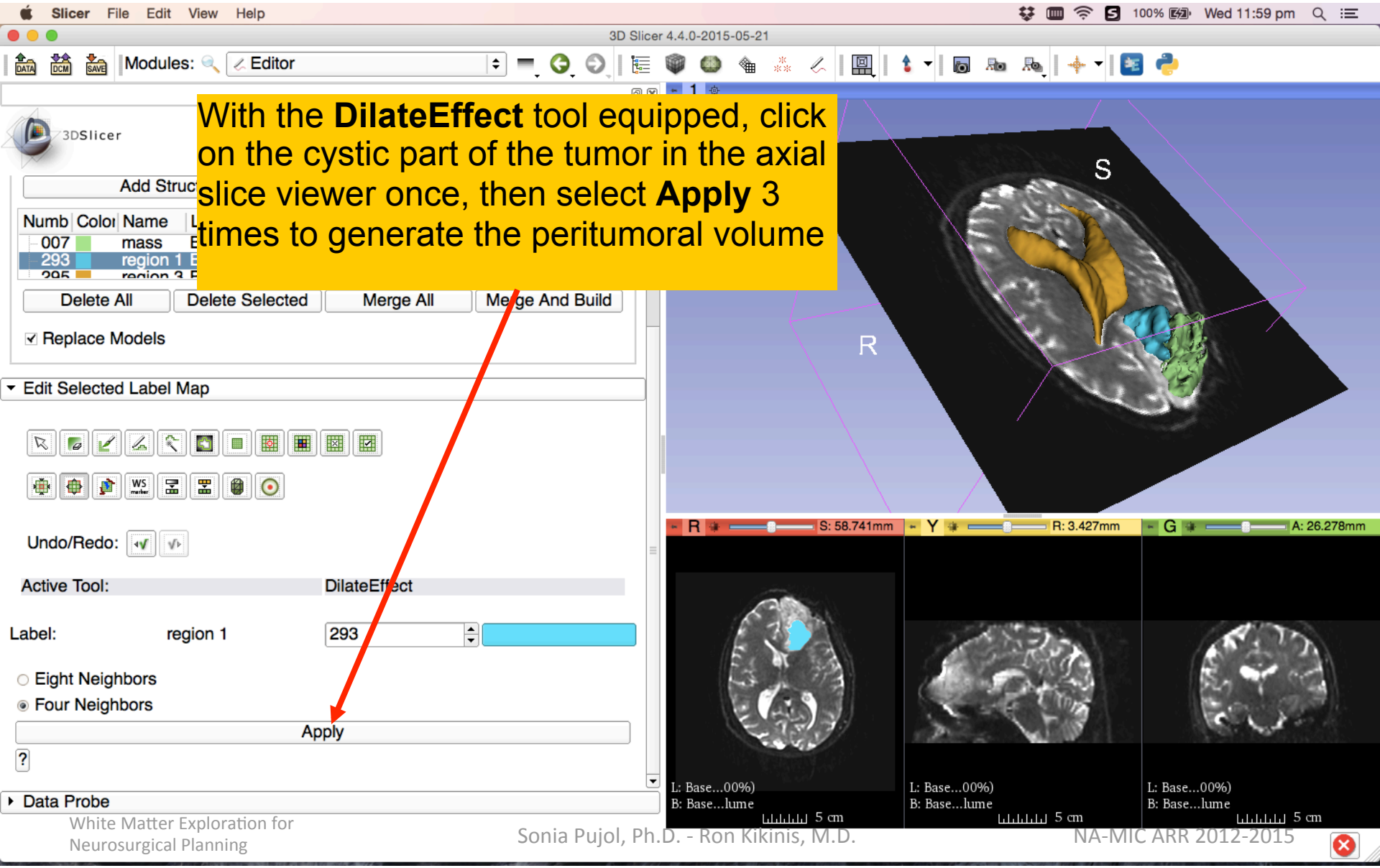


Select the label map **BaselineVolume-region_1 label** (blue) and select the **DilateEffect** tool.



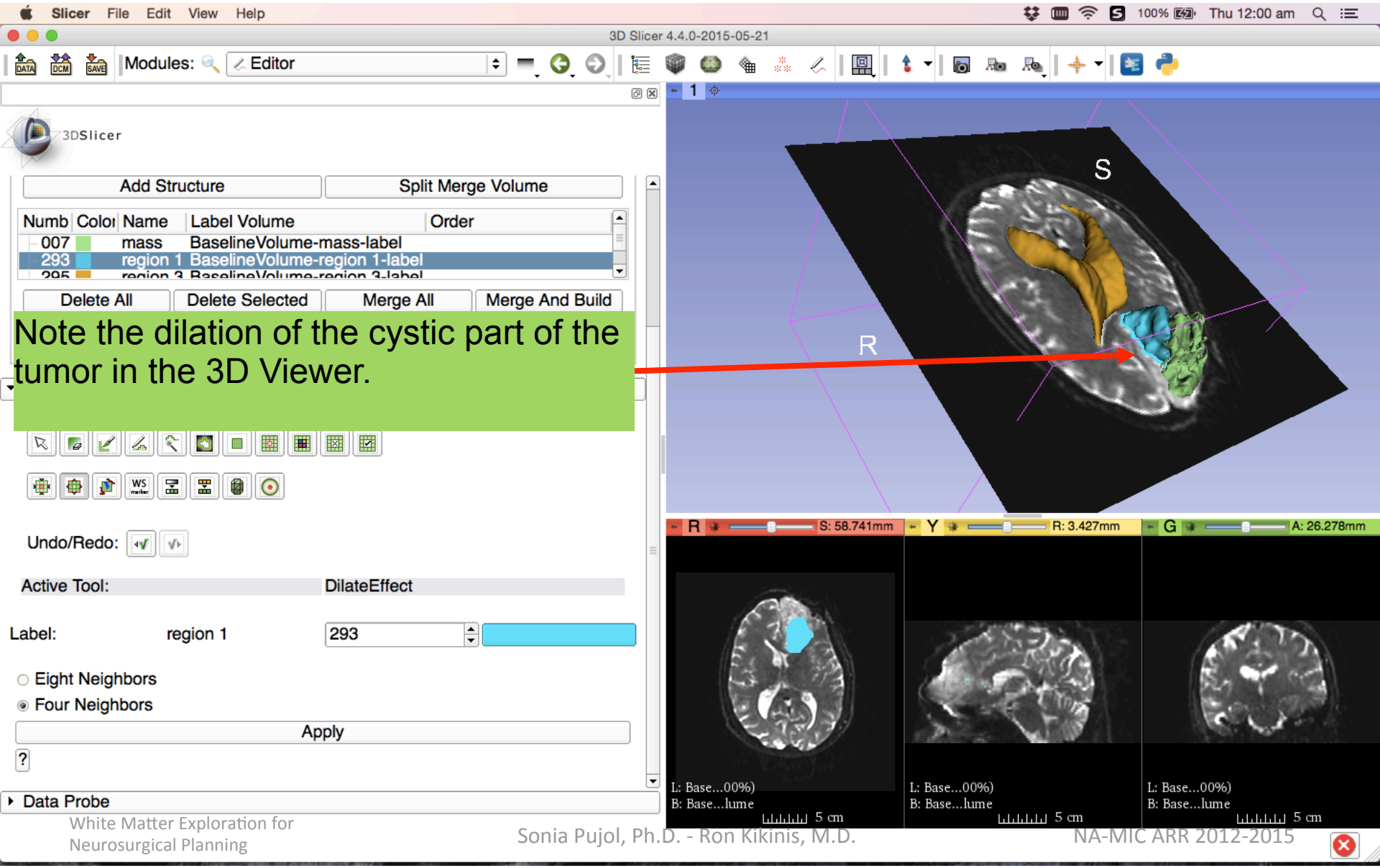
Part 2: Tractography exploration of peri-tumoral white matter fibers

Definition of peri-tumoral volume



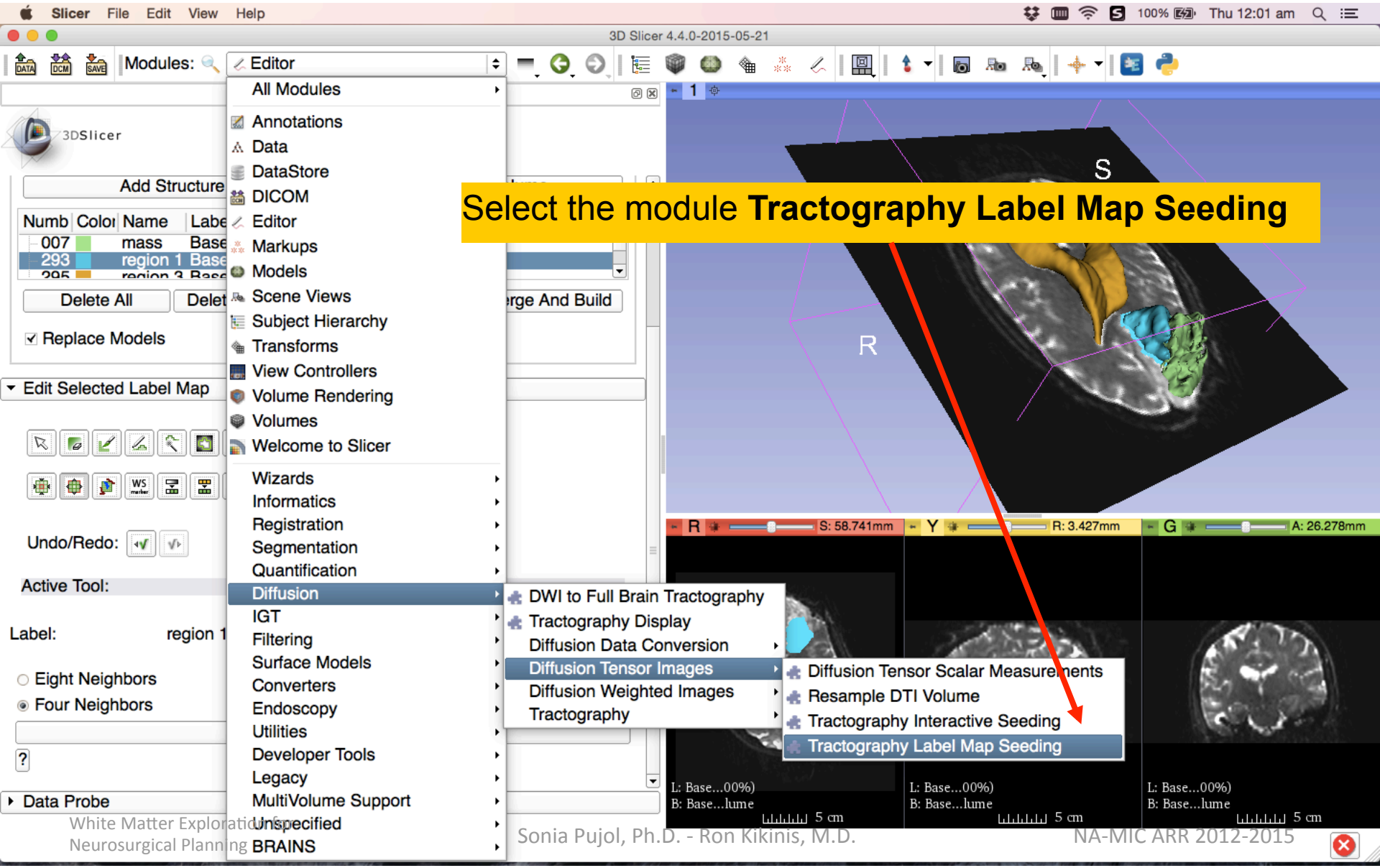
With the **DilateEffect** tool equipped, click on the cystic part of the tumor in the axial slice viewer once, then select **Apply** 3 times to generate the peritumoral volume

Definition of peritumoral volume

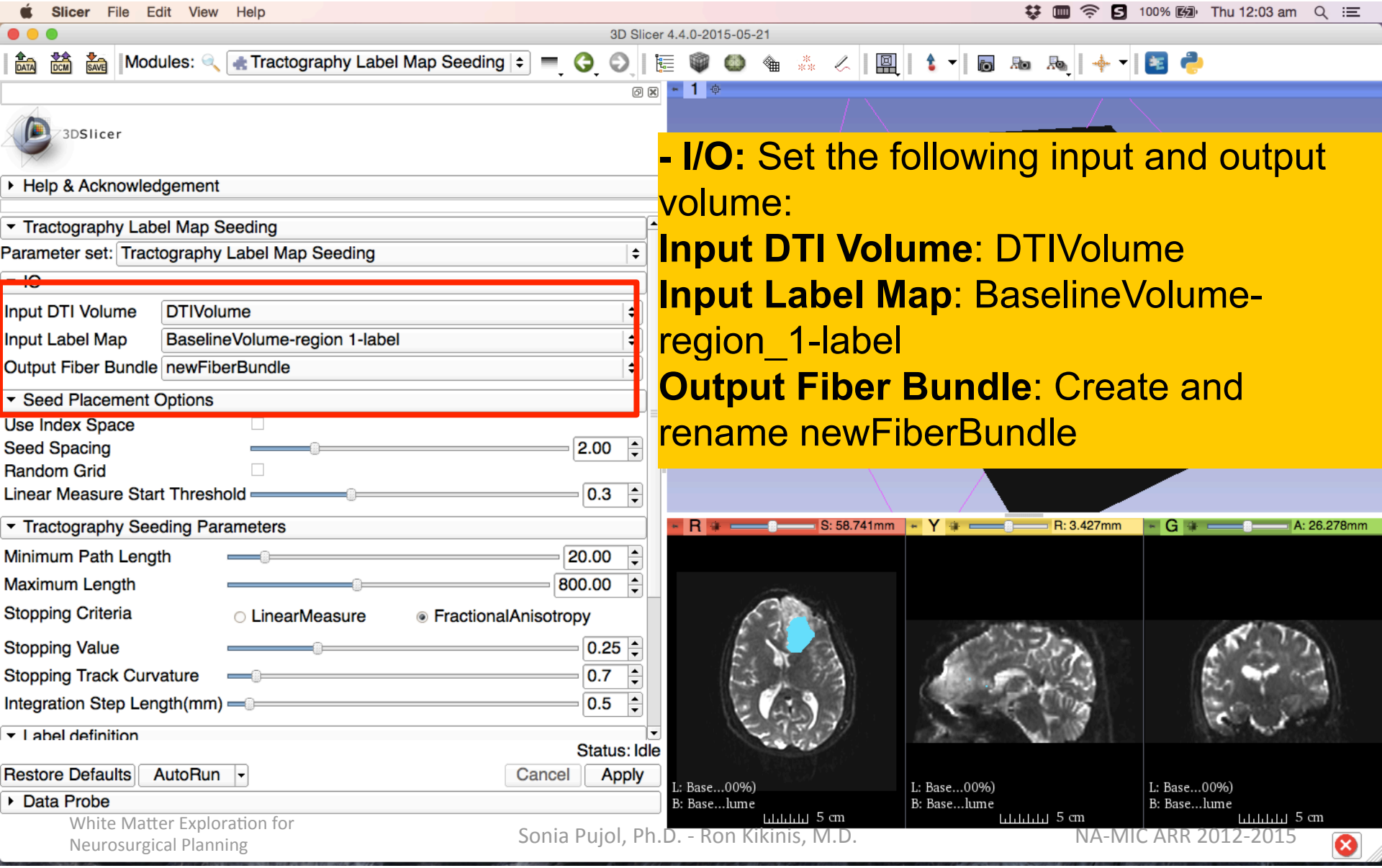


Note the dilation of the cystic part of the tumor in the 3D Viewer.

Final Result of Segmentation



Final Result of Segmentation



- I/O: Set the following input and output volume:

Input DTI Volume: DTIVolume

Input Label Map: BaselineVolume-region_1-label

Output Fiber Bundle: Create and rename newFiberBundle

Final Result of Segmentation

Scroll down and set the following values:

- Seed Placement Options:

Check **Use Index Space**

Slicer File Edit View Help

3D Slicer 4.4.0-2015-05-21

Modules: Tractography Label Map Seeding

3DSlicer

Help & Acknowledgement

Tractography Label Map Seeding

Parameter set: Tractography Label Map Seeding

IO

Input DTI Volume: DTIVolume

Input Label Map: BaselineVolume-region 1-label

Output Fiber Bundle: newFiberBundle

Seed Placement Options

Use Index Space ☑

Seed Spacing: 2.00

Random Grid ☐

Linear Measure Start Threshold: 0.3

Tractography Seeding Parameters

Minimum Path Length: 20.00

Maximum Length: 800.00

Stopping Criteria: LinearMeasure / FractionalAnisotropy

Stopping Value: 0.25

Stopping Track Curvature: 0.7

Integration Step Length(mm): 0.5

Label definition

Status: Idle

Restore Defaults | AutoRun | Cancel | Apply

Data Probe

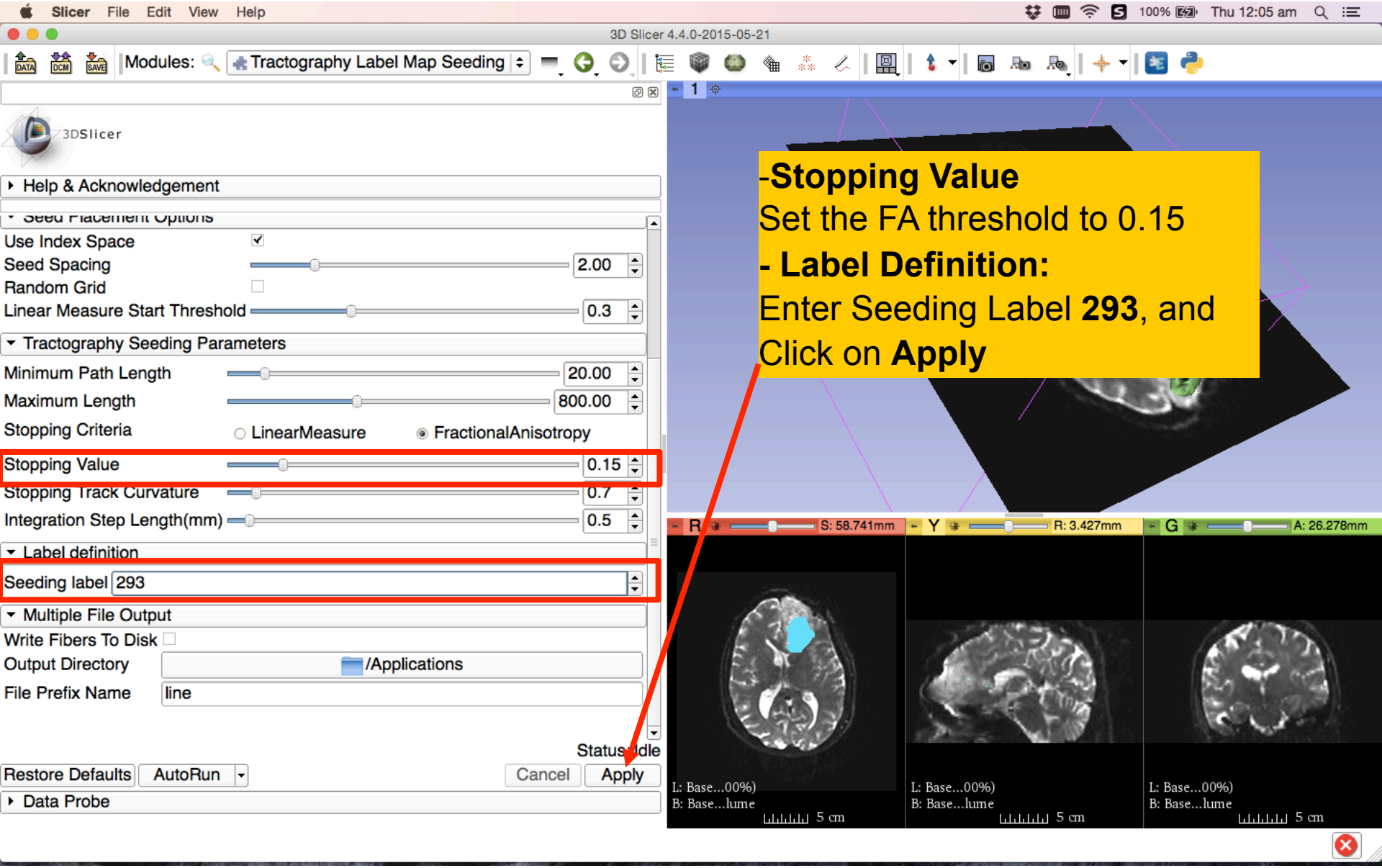
R: S: 58.741mm

Y: R: 3.427mm

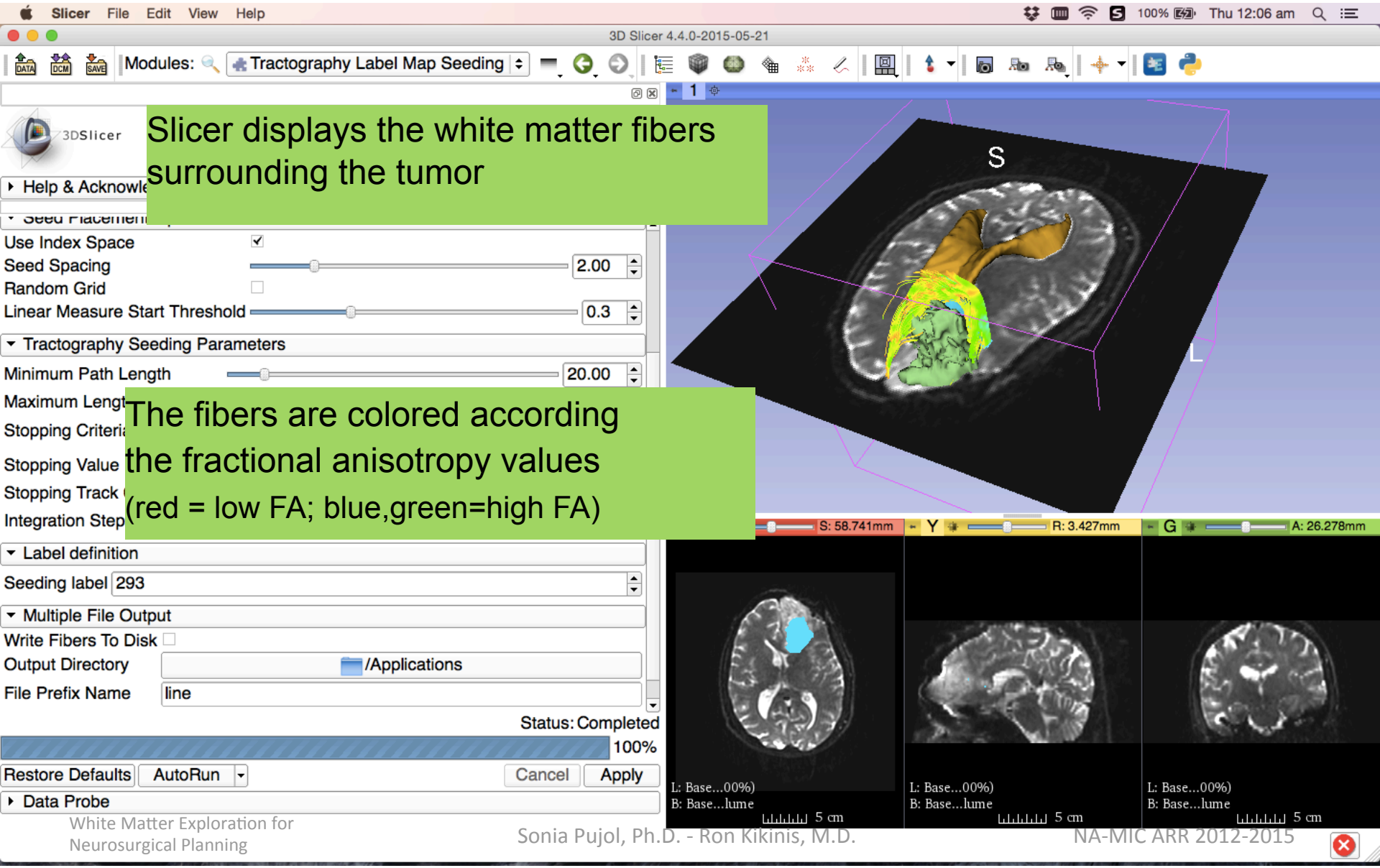
G: A: 26.278mm

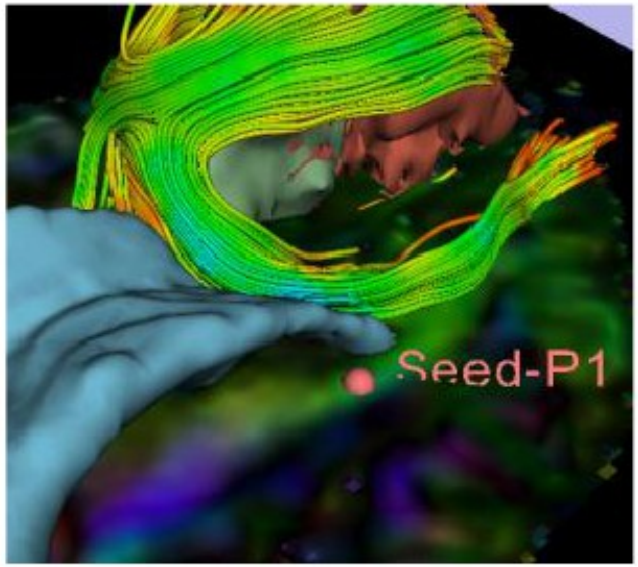
L: Base...00%)
B: Base...lume
5 cm

Final Result of Segmentation



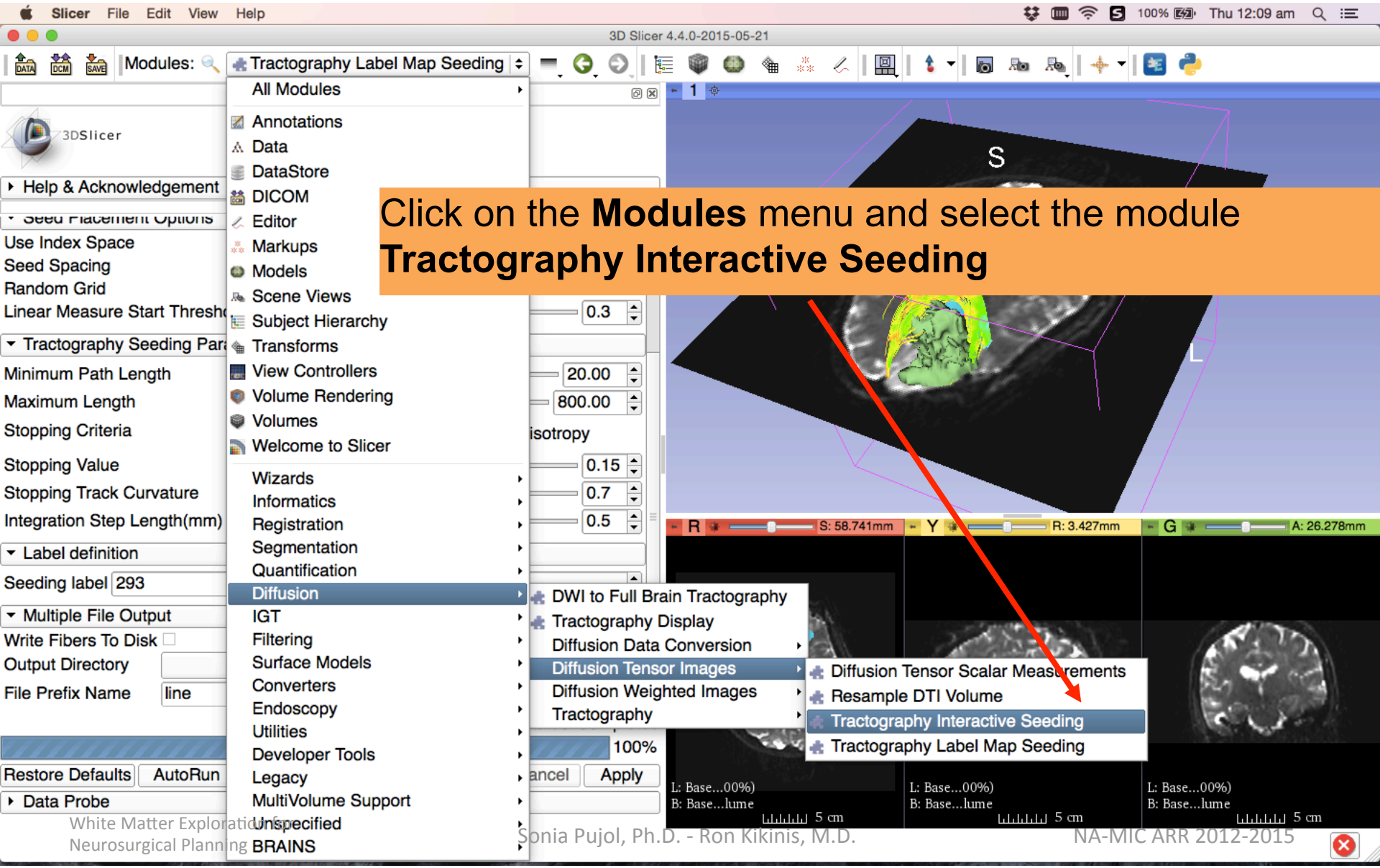
Final Result of Segmentation



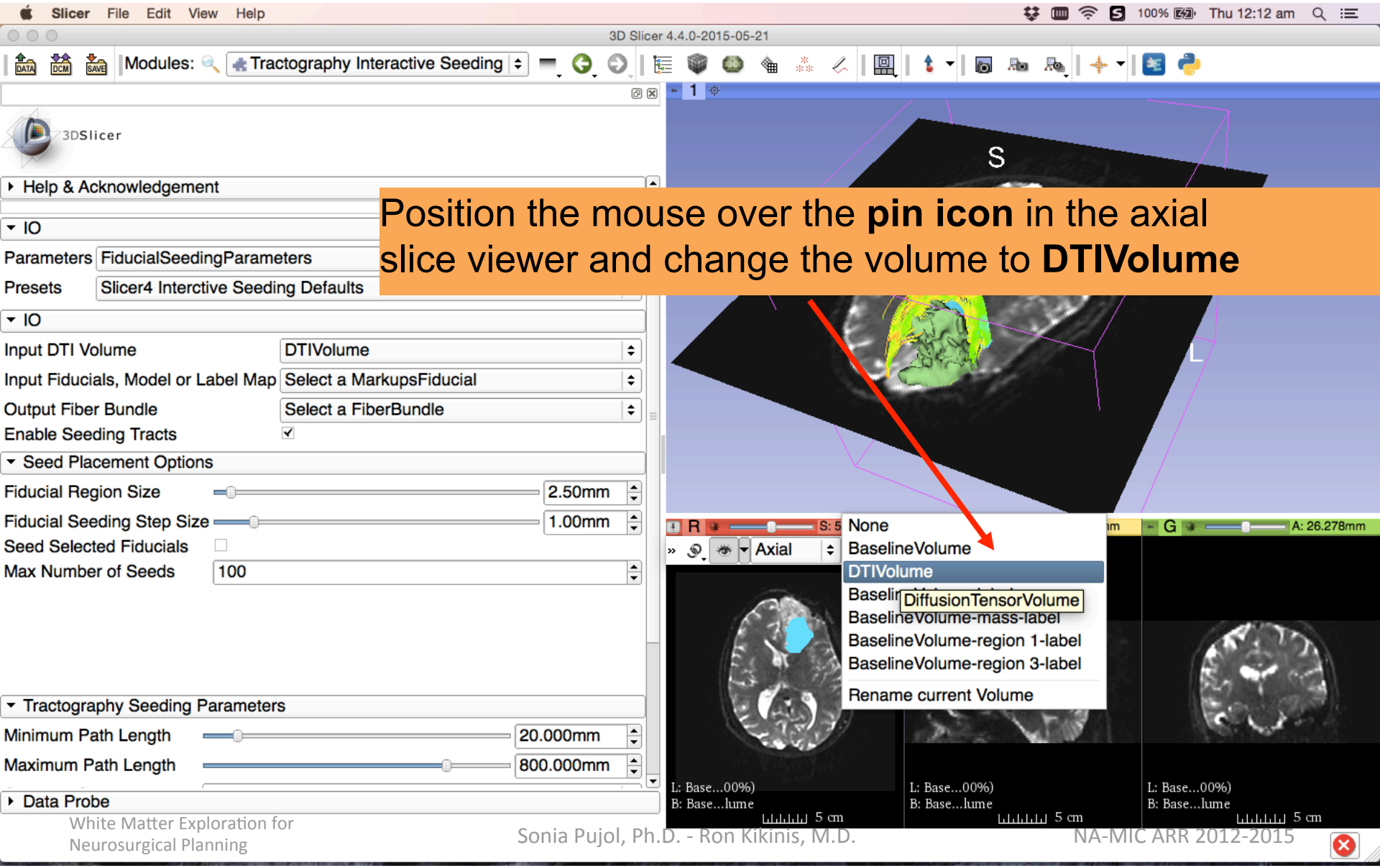


Part 4: Tractography exploration of the ipsilateral and contralateral side

Tractography on-the-fly

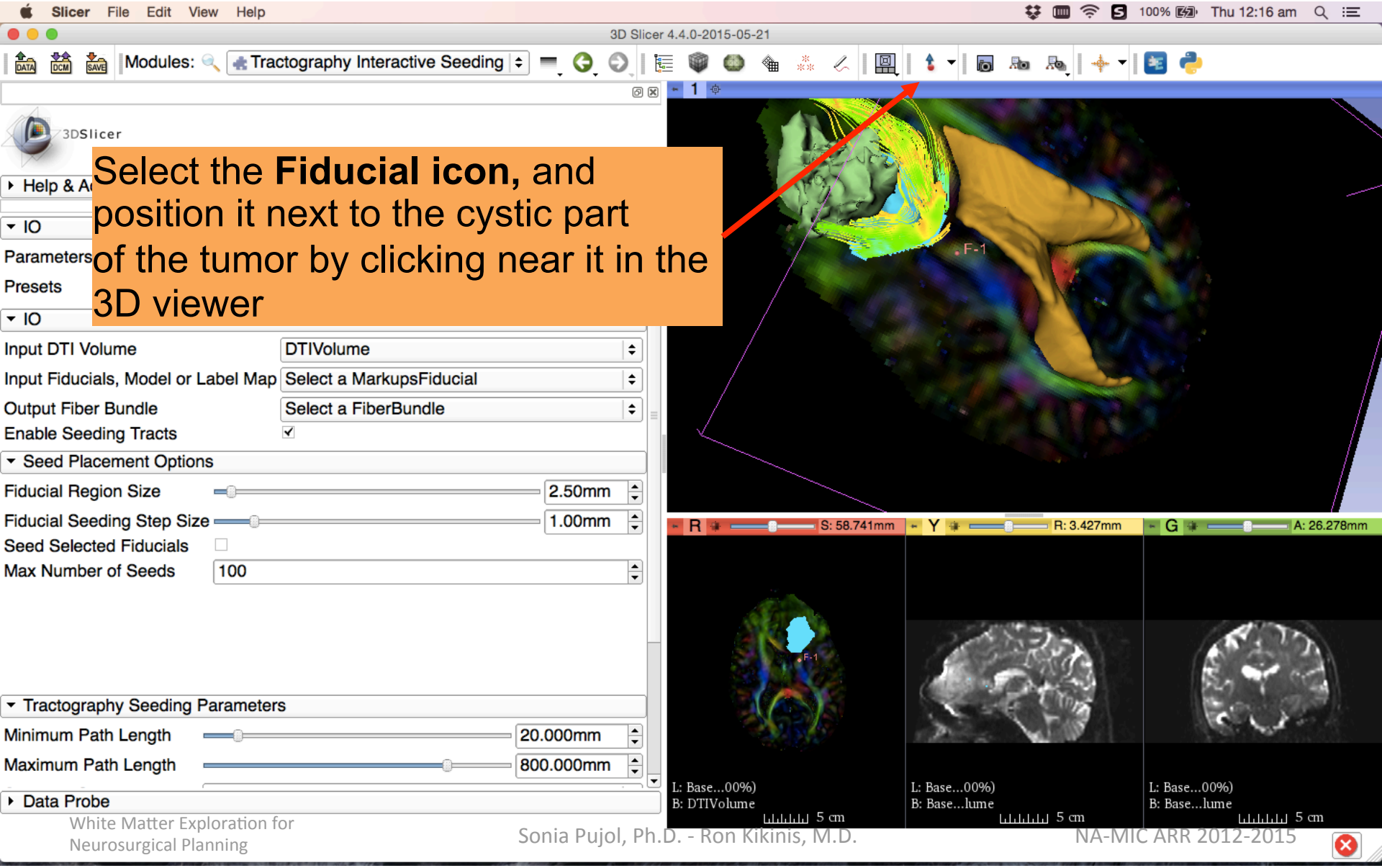


Tractography on-the-fly



Position the mouse over the **pin icon** in the axial slice viewer and change the volume to **DTIVolume**

Tractography on-the-fly



Select the **Fiducial icon,** and position it next to the cystic part of the tumor by clicking near it in the 3D viewer

Tractography on-the-fly

Slicer File Edit View Help

3D Slicer 4.4.0-2015-05-21

Modules: Tractography Interactive Seeding

3DSlicer

Help & Acknowledgement

IO

Parameters: FiducialSeedingParameters

Presets: Slicer4 Interctive Seeding Defaults

IO

Input DTI Volume: DTIVolume

Input Fiducials, Model or Label Map: F

Output Fiber Bundle: FiberBundle_F

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

Tractography Seeding Parameters

Minimum Path Length: 20.000mm

Maximum Path Length: 800.000mm

Data Probe

F-1

R: S: 58.741mm | Y: R: 3.427mm | G: A: 26.278mm

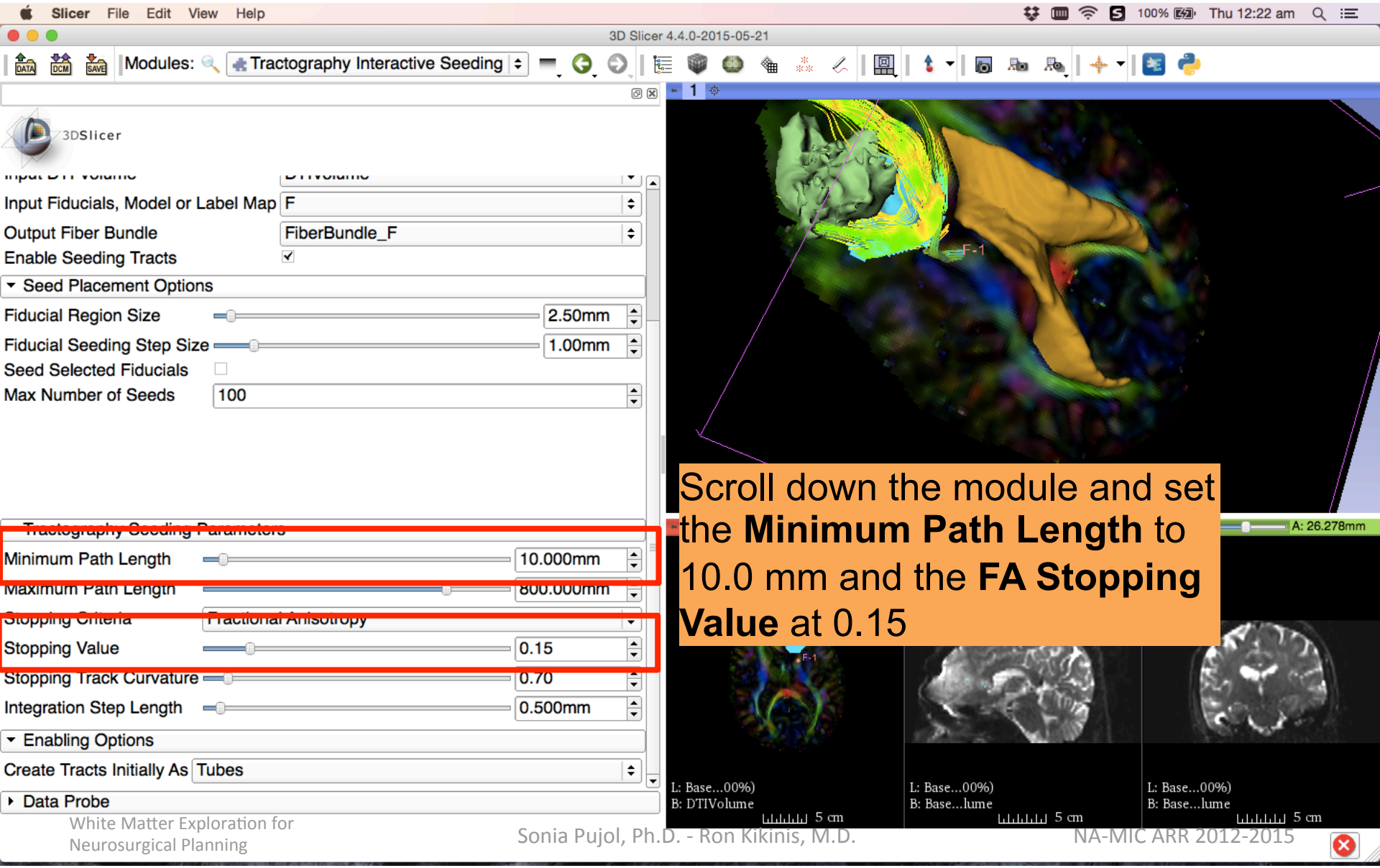
L: Base...00%) B: DTIVolume 5 cm

L: Base...00%) B: Base...lume 5 cm

L: Base...00%) B: Base...lume 5 cm

Set Input DTI Volume to **DTIVolume**
Set Fiducial List or Model to **F**
Set Output Fiber Bundle to **Create new Fiber Bundle**

Tractography on-the-fly



Scroll down the module and set the **Minimum Path Length** to 10.0 mm and the **FA Stopping Value** at 0.15

Acknowledgments

- National Alliance for Medical Image Computing (NA-MIC)

  NIH U54EB005149

- Neuroimage Analysis Center (NAC)

  NIH P41RR013218

- Parth Amin, WIT , Farukh Kohistani, BC, Fan Zhang, University of Sydney