



# Exploring Peritumoral White Matter Fibers for Neurosurgical Planning

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# Clinical Goal

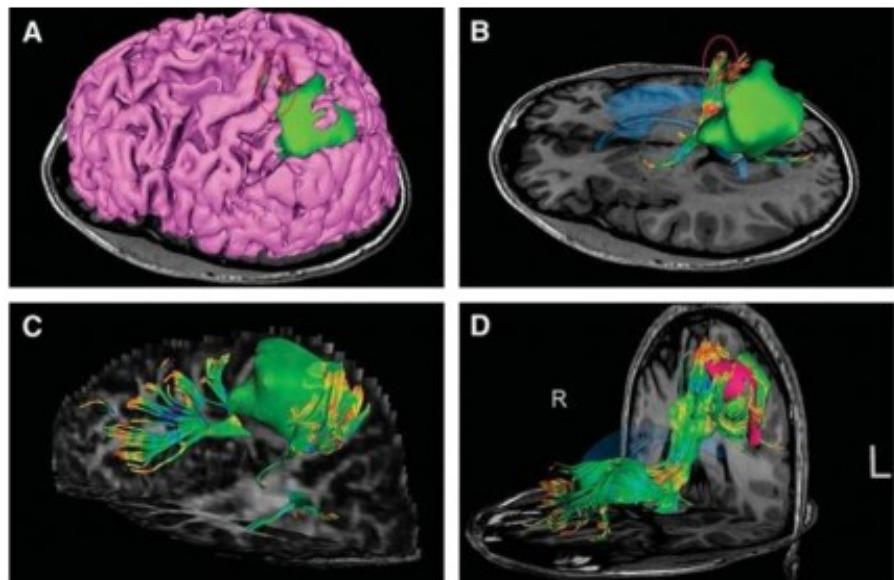
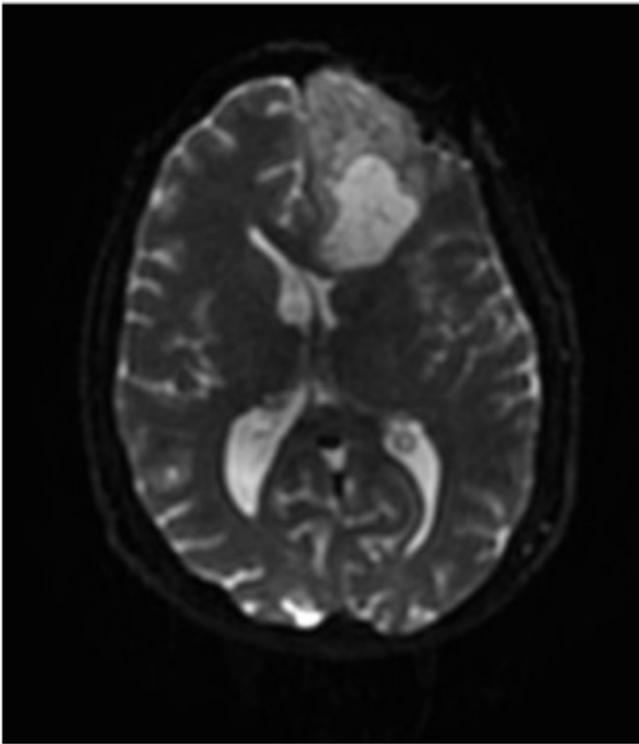


Image Courtesy of Dr. Alexandra Golby, Brigham and Women's Hospital, Boston, MA..

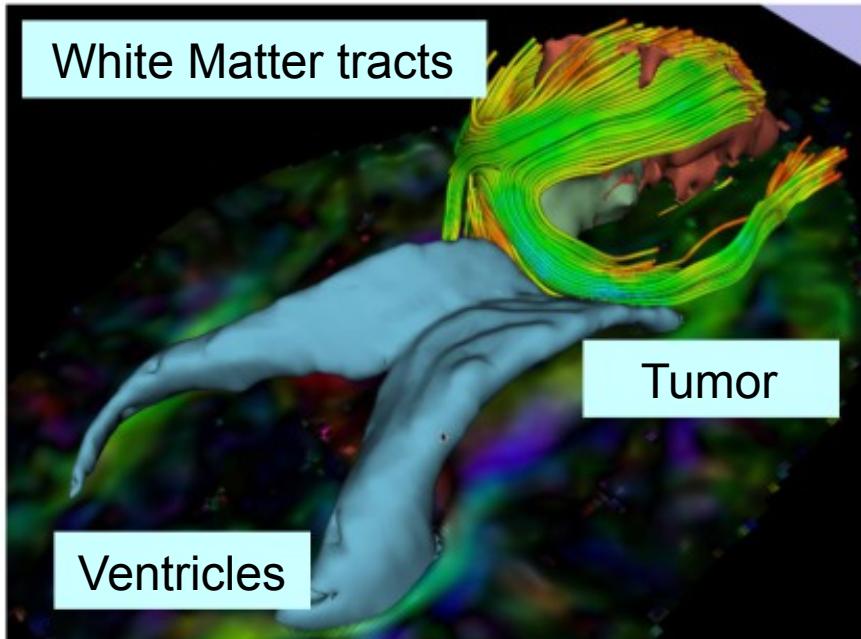
Diffusion Tensor Imaging (DTI) Tractography has the potential to bring valuable spatial information on tumor infiltration and tract displacement for neurosurgical planning of tumor resection.

# Clinical Case

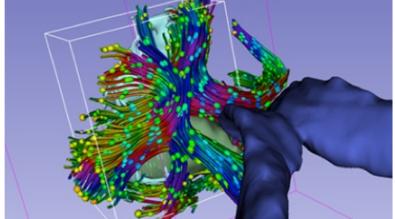


- 35 year-old male diagnosed with **Glioblastoma multiform (GBM)**
- Diffusion Weighted Imaging (DWI) acquisition for neurosurgical planning

# Clinical Goal



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



# Slicer DMRI

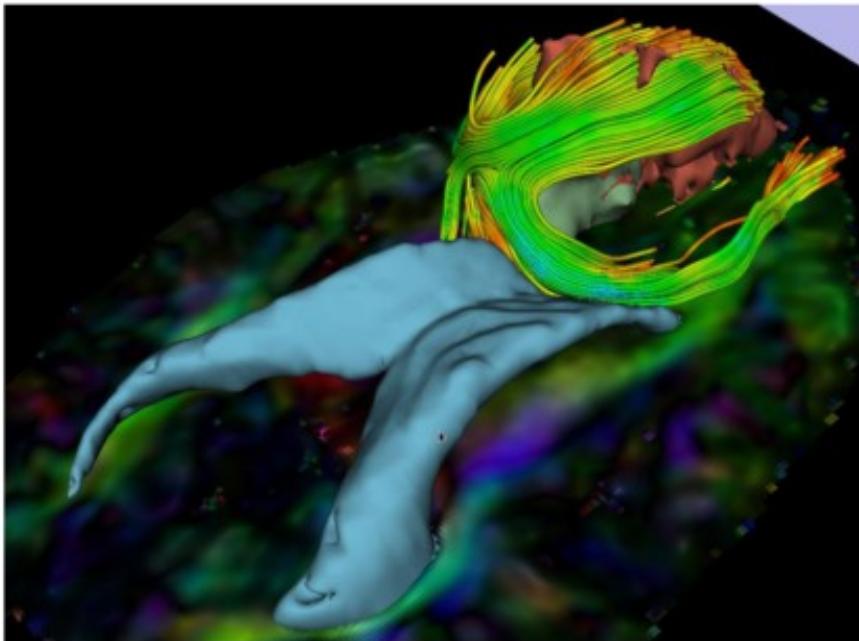
An open-source project to improve and extend diffusion magnetic resonance imaging software in 3D Slicer:

<http://slicerdmri.github.io>

Please read the **Diffusion MRI Analysis** tutorial to install SlicerDMRI:

<https://github.com/SlicerDMRI/slicerdmri.github.io/blob/master/docs/tutorials/DiffusionMRIanalysis.pdf>

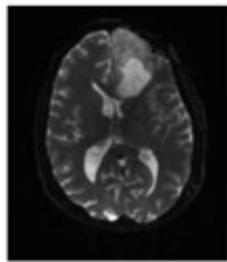
# Image Analysis Pipeline



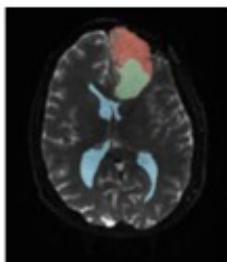
The image analysis pipeline described in this tutorial uses three different algorithms:

- 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.

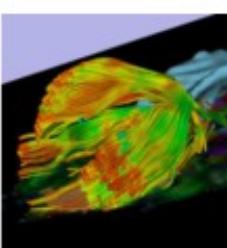
# Overview of the analysis pipeline



Part 1: Loading & Visualization of Diffusion Data



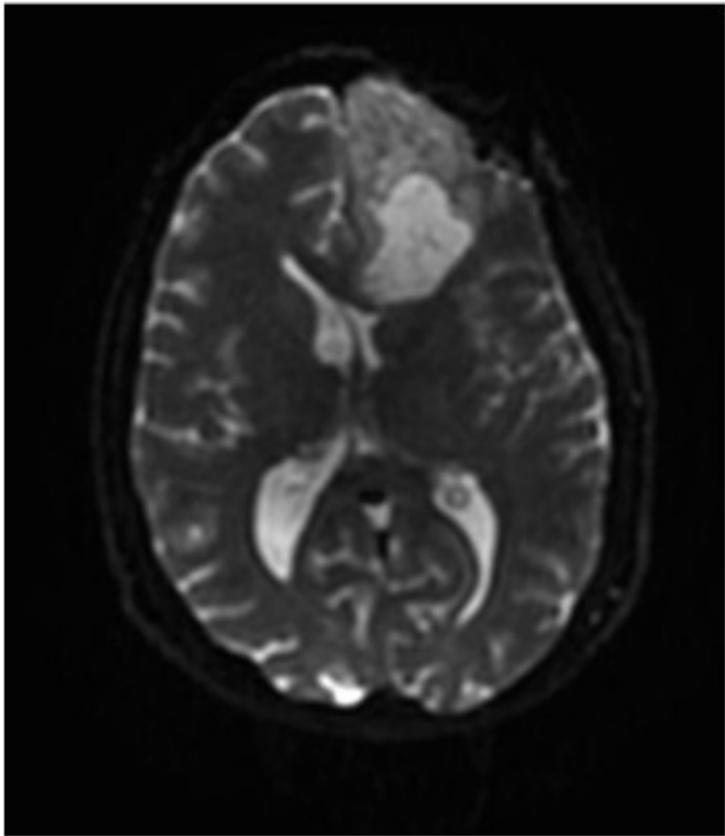
Part 2: Segmentation of lat. ventricles, and solid and cystic parts of the tumor



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

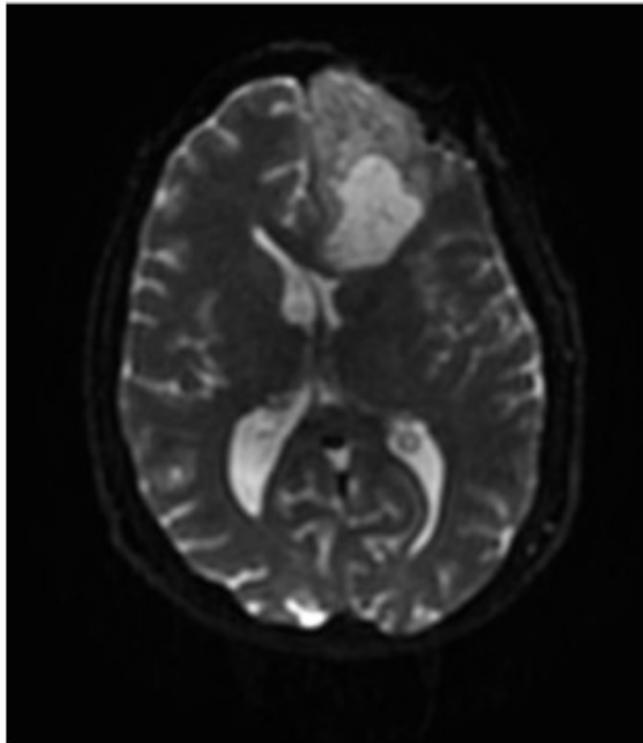


Part 4: Tractography exploration of the ipsilateral and contralateral side



# Part 1: Loading and Visualization of Diffusion Data

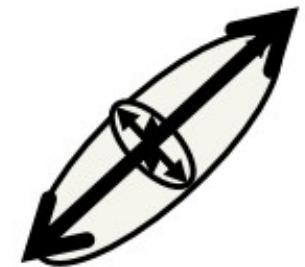
# Diffusion Tensor Imaging



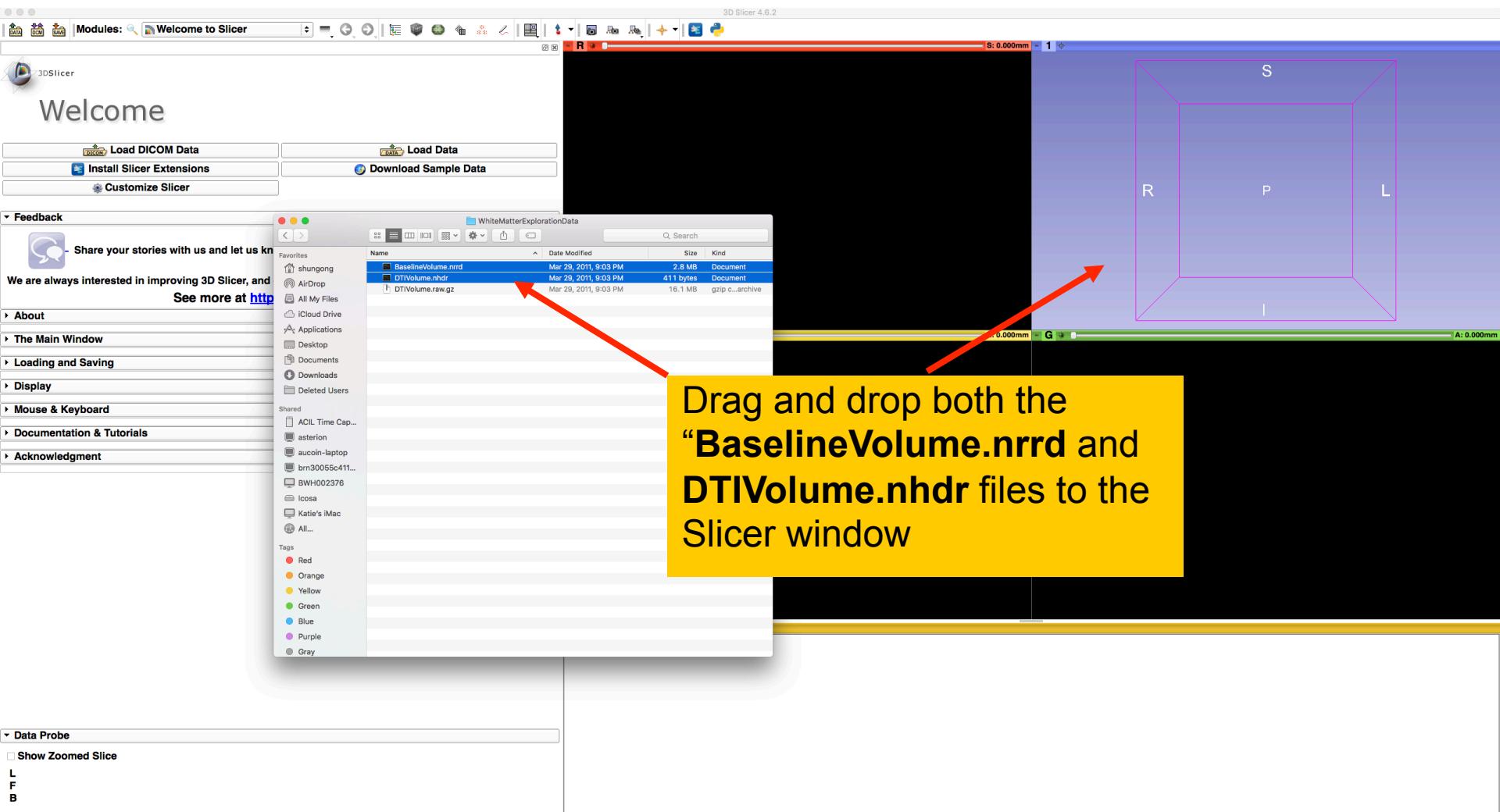
$$S_i = S_0 e^{-b \hat{g}_i^T D \hat{g}_i}$$

(Stejskal and Tanner 1965, Basser 1994 )

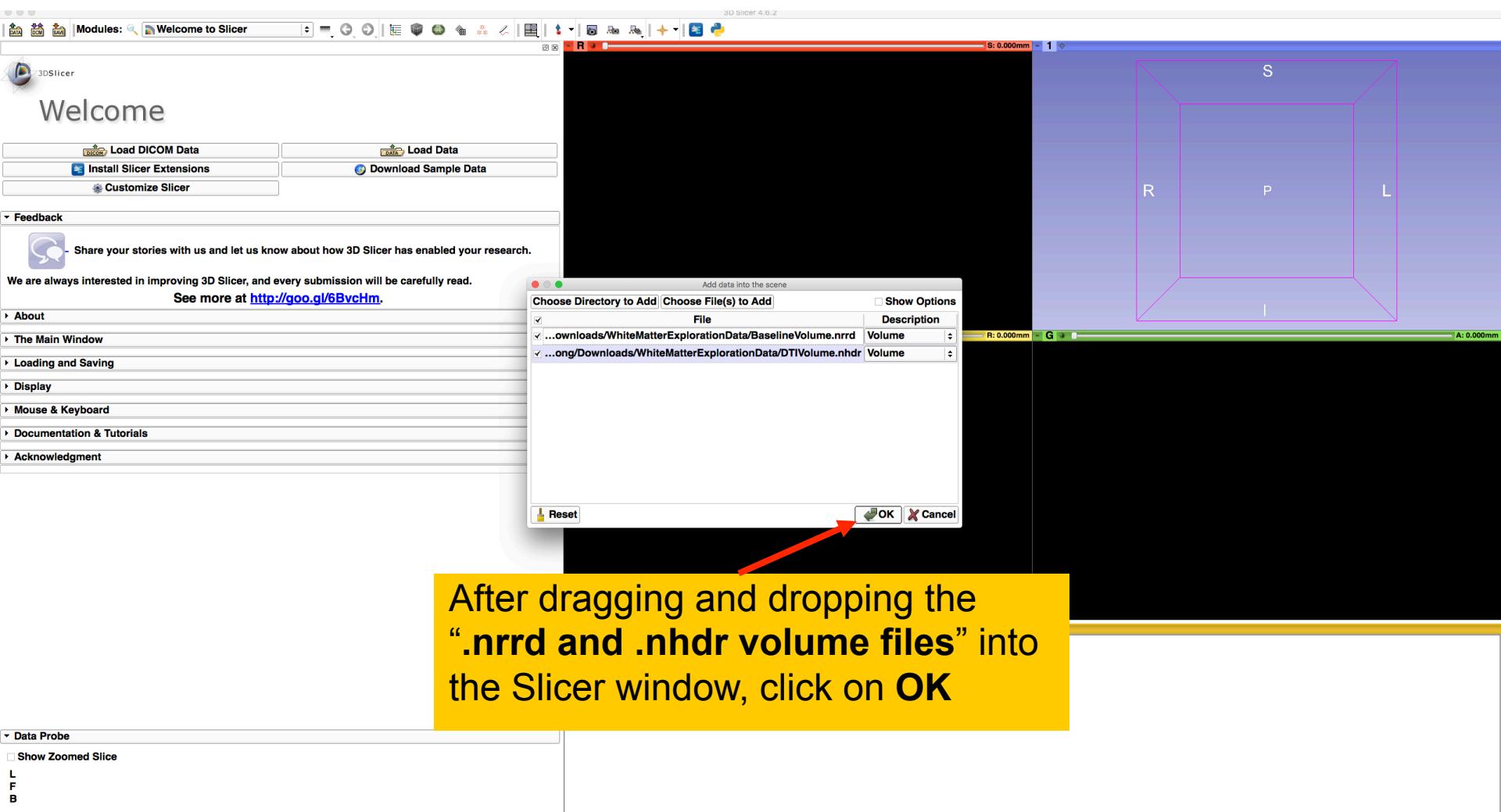
$$\underline{\mathbf{D}} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix}$$



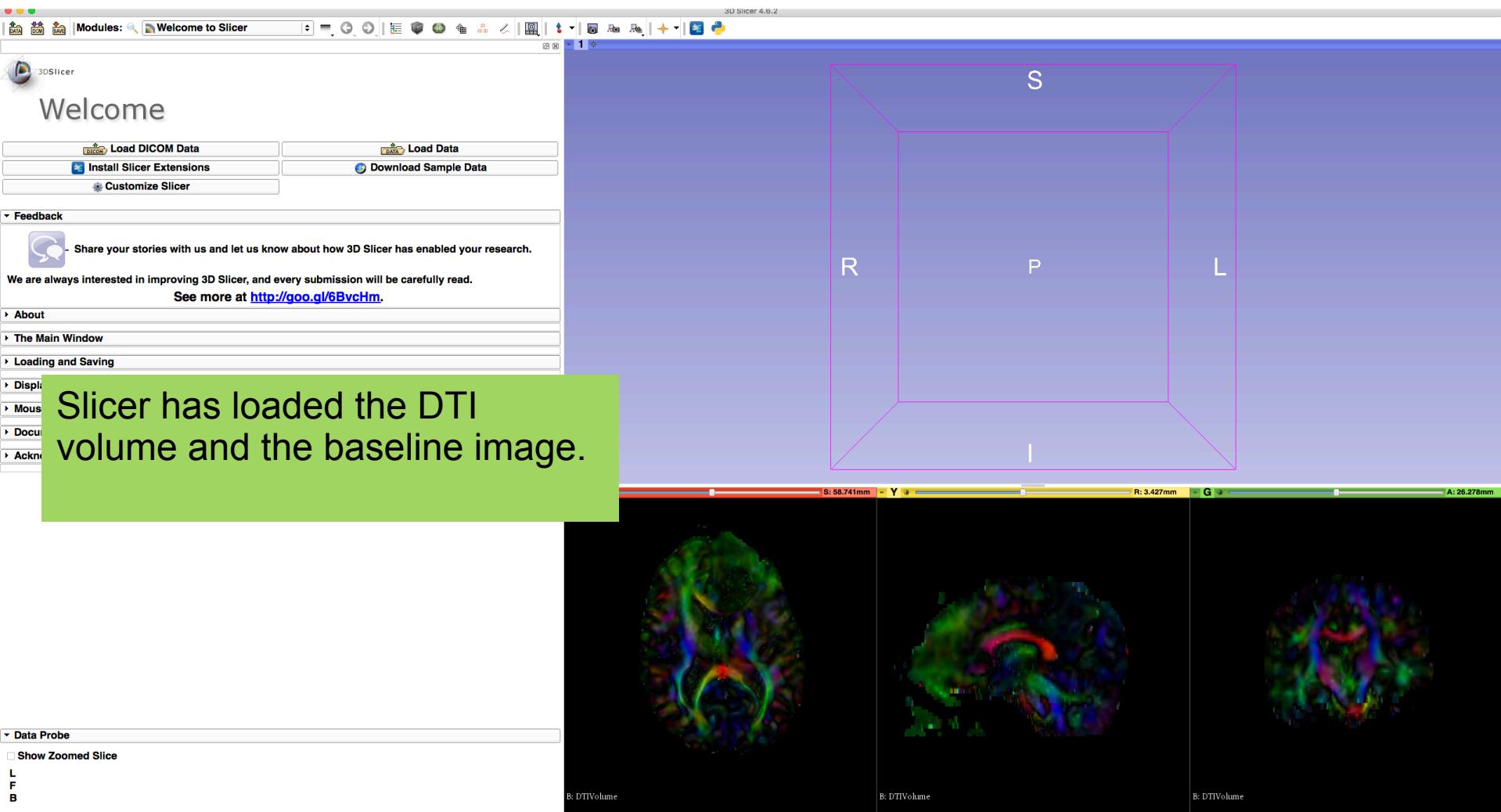
# Loading DTI and Baseline Data



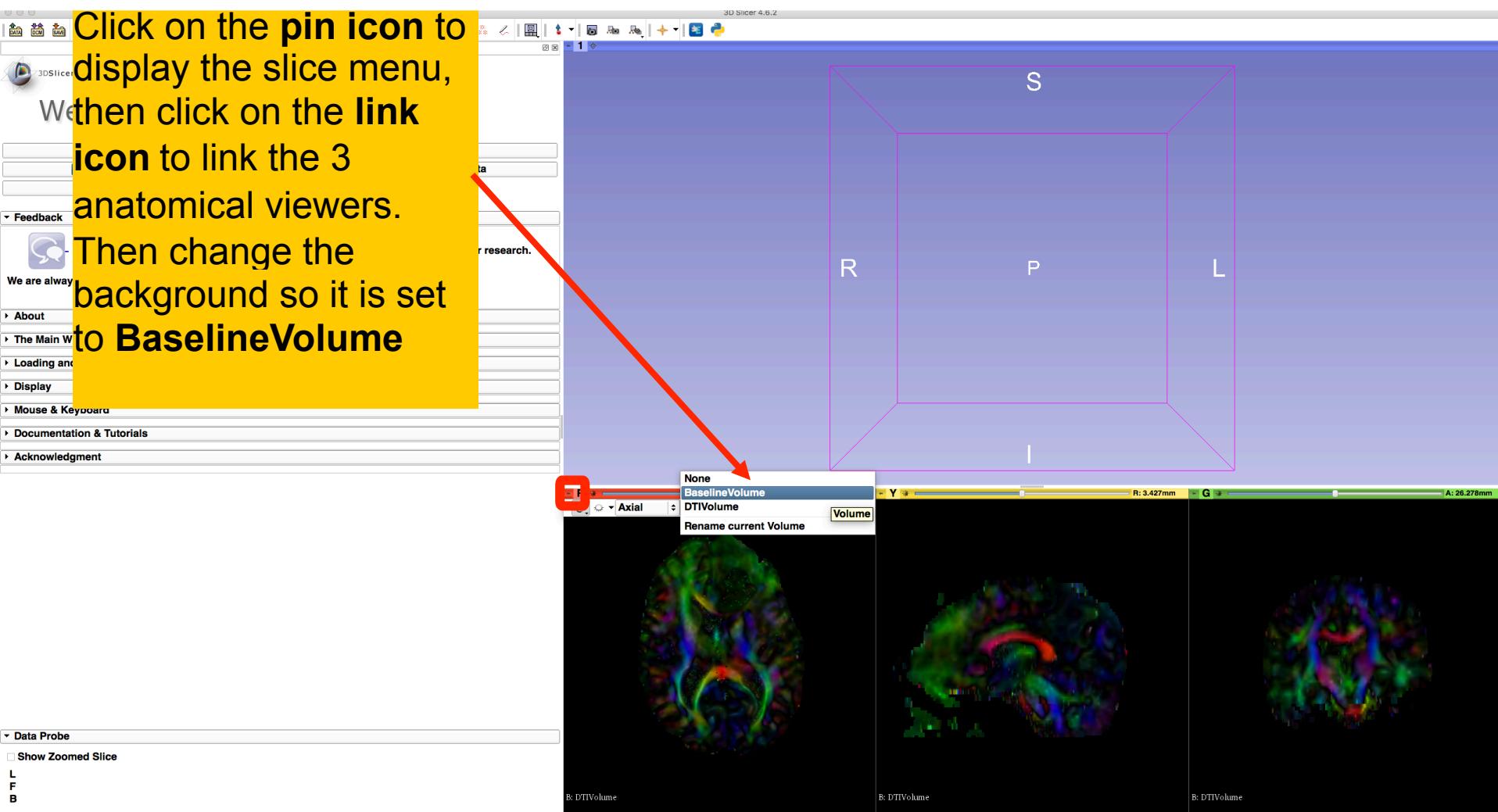
# Loading DTI and Baseline Data



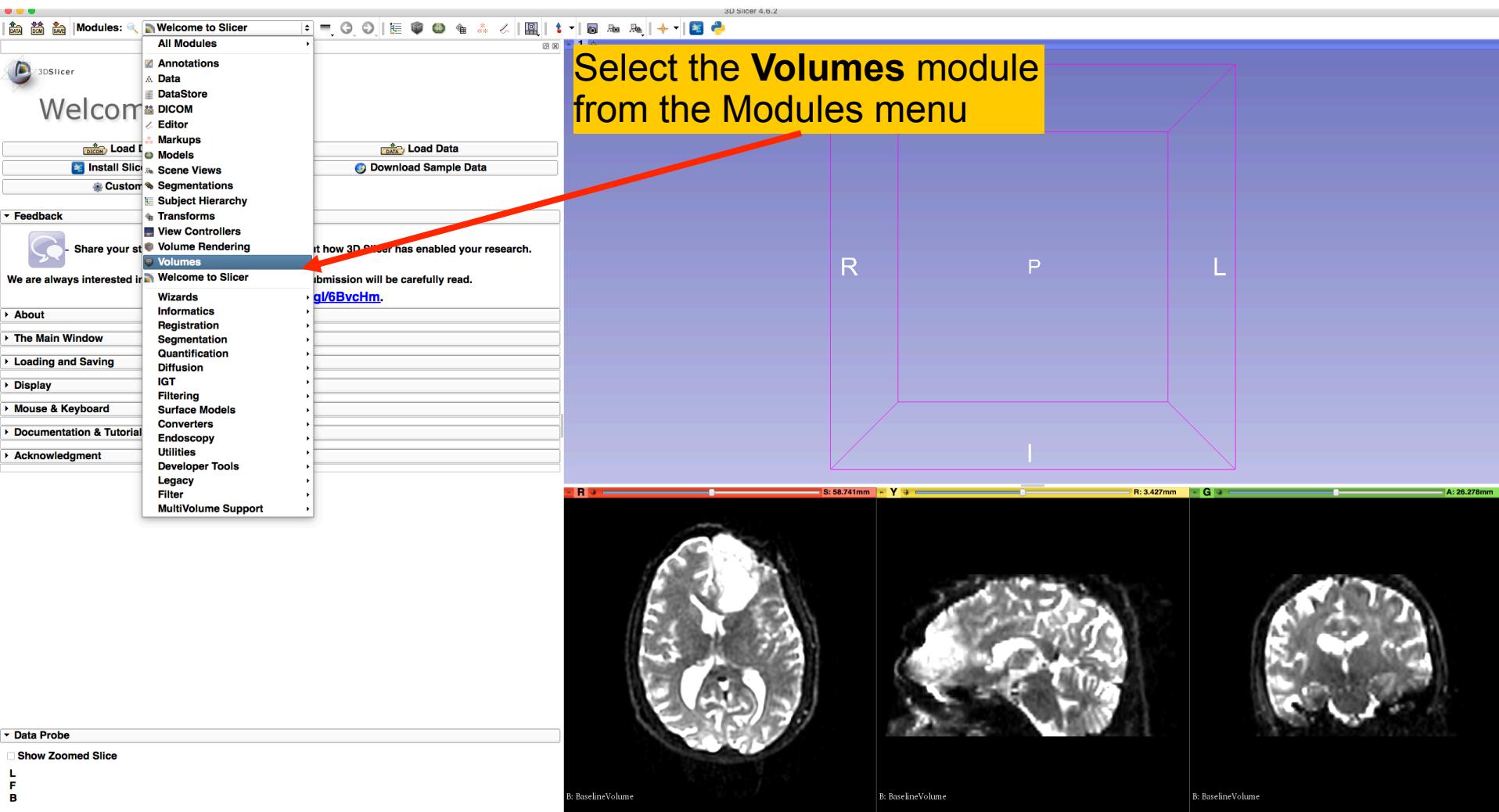
# Loading DTI and Baseline Data



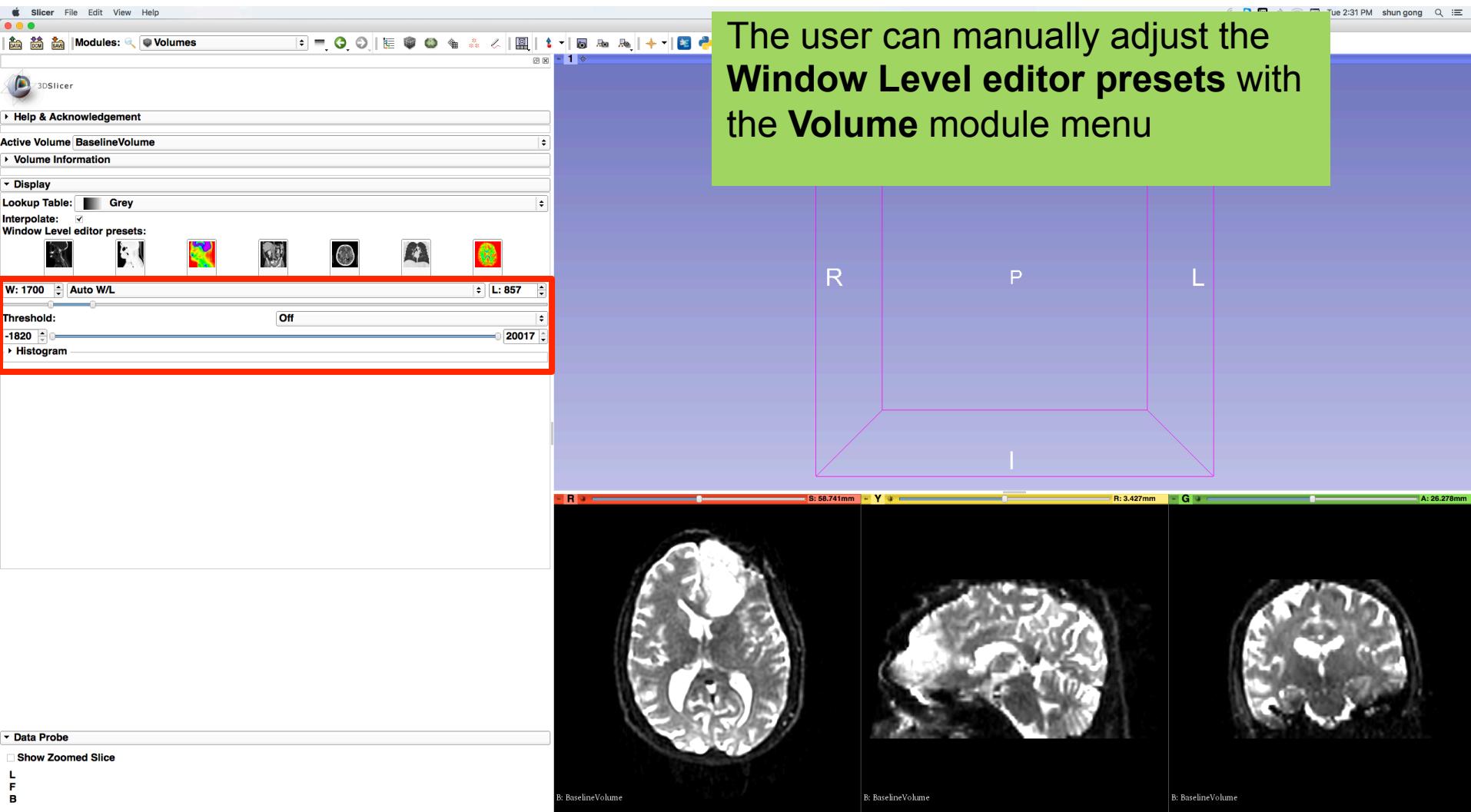
# Loading DTI and Baseline Data



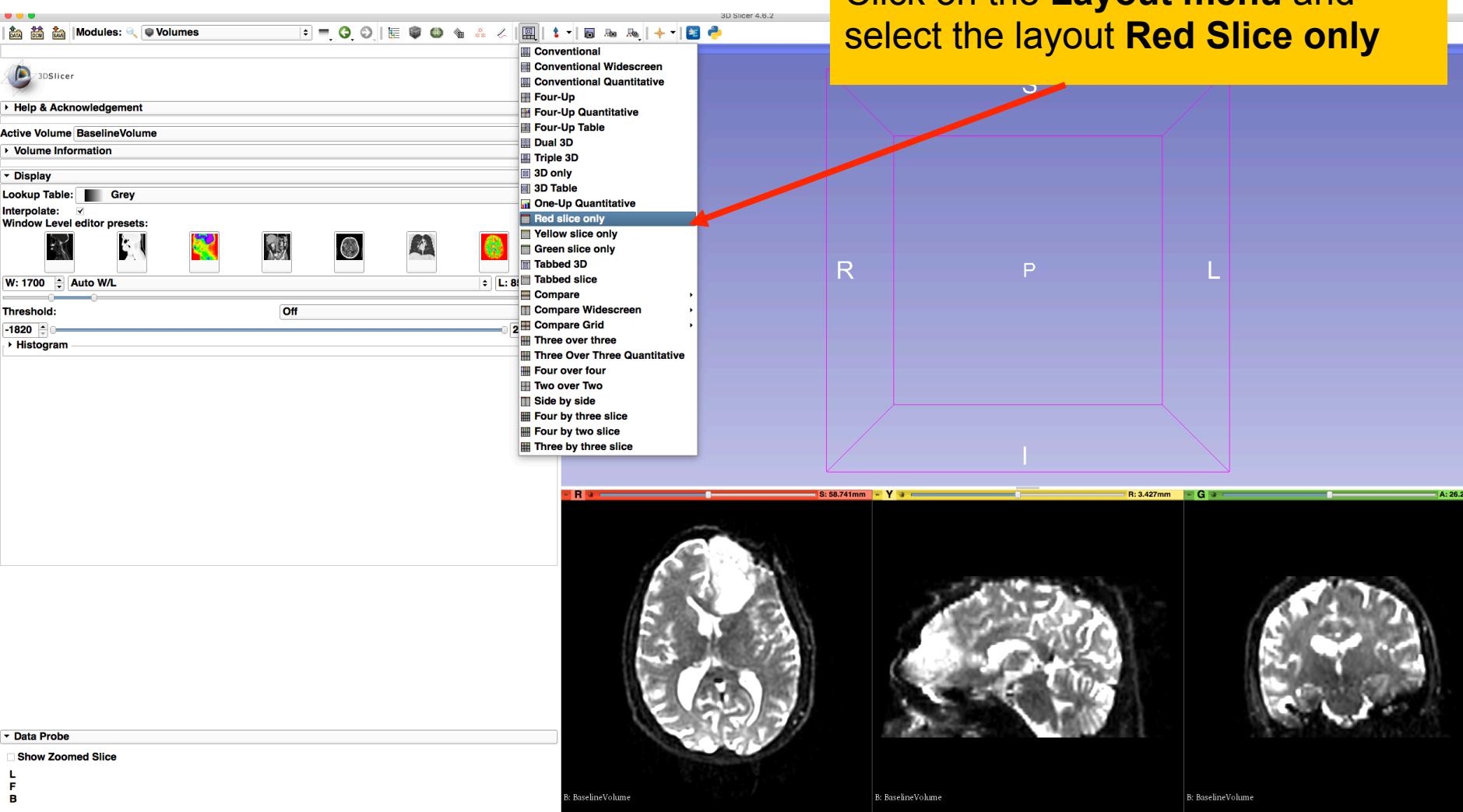
# Loading DTI and Baseline Data

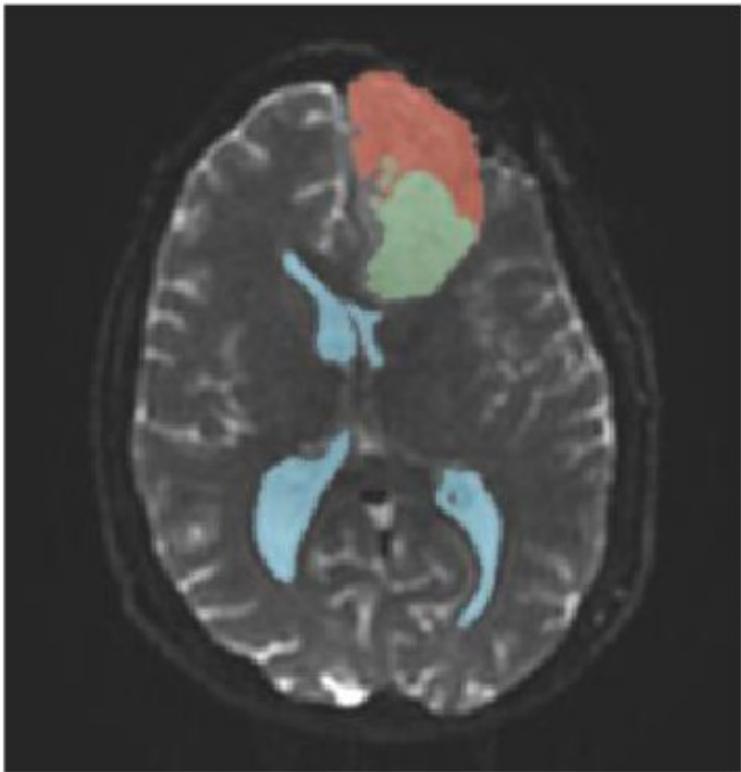


# Loading DTI and Baseline Data



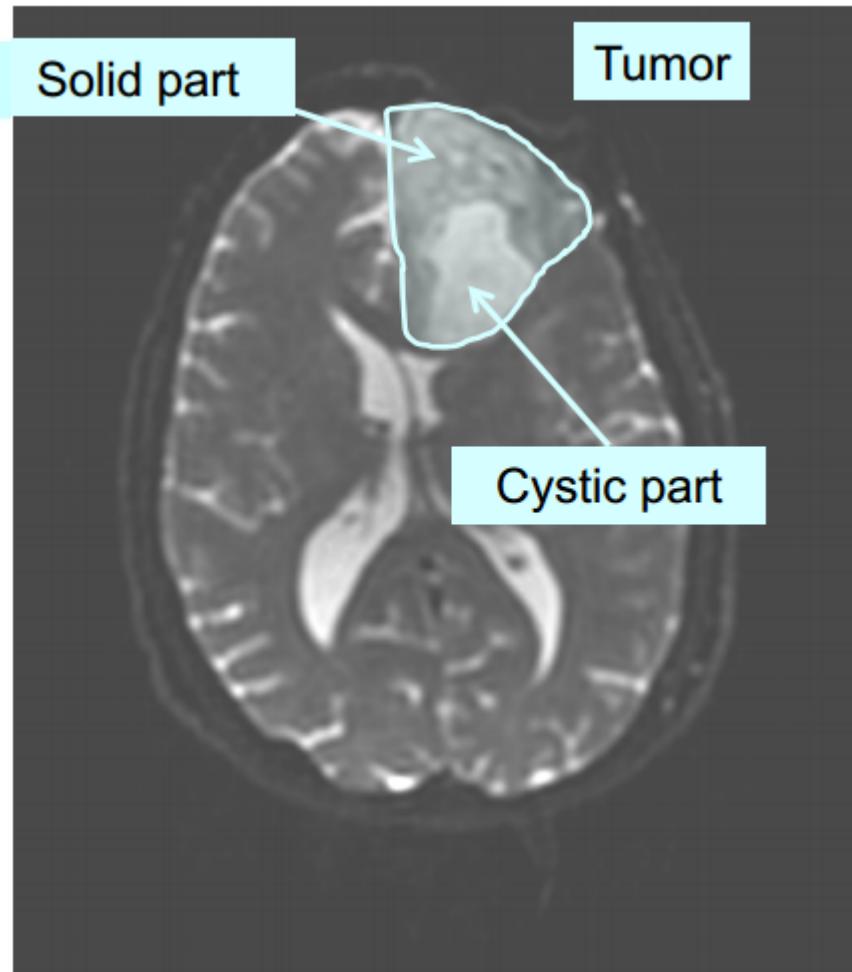
# Loading DTI and Baseline Data





# Part 1: Segmenting the tumor and ventricles

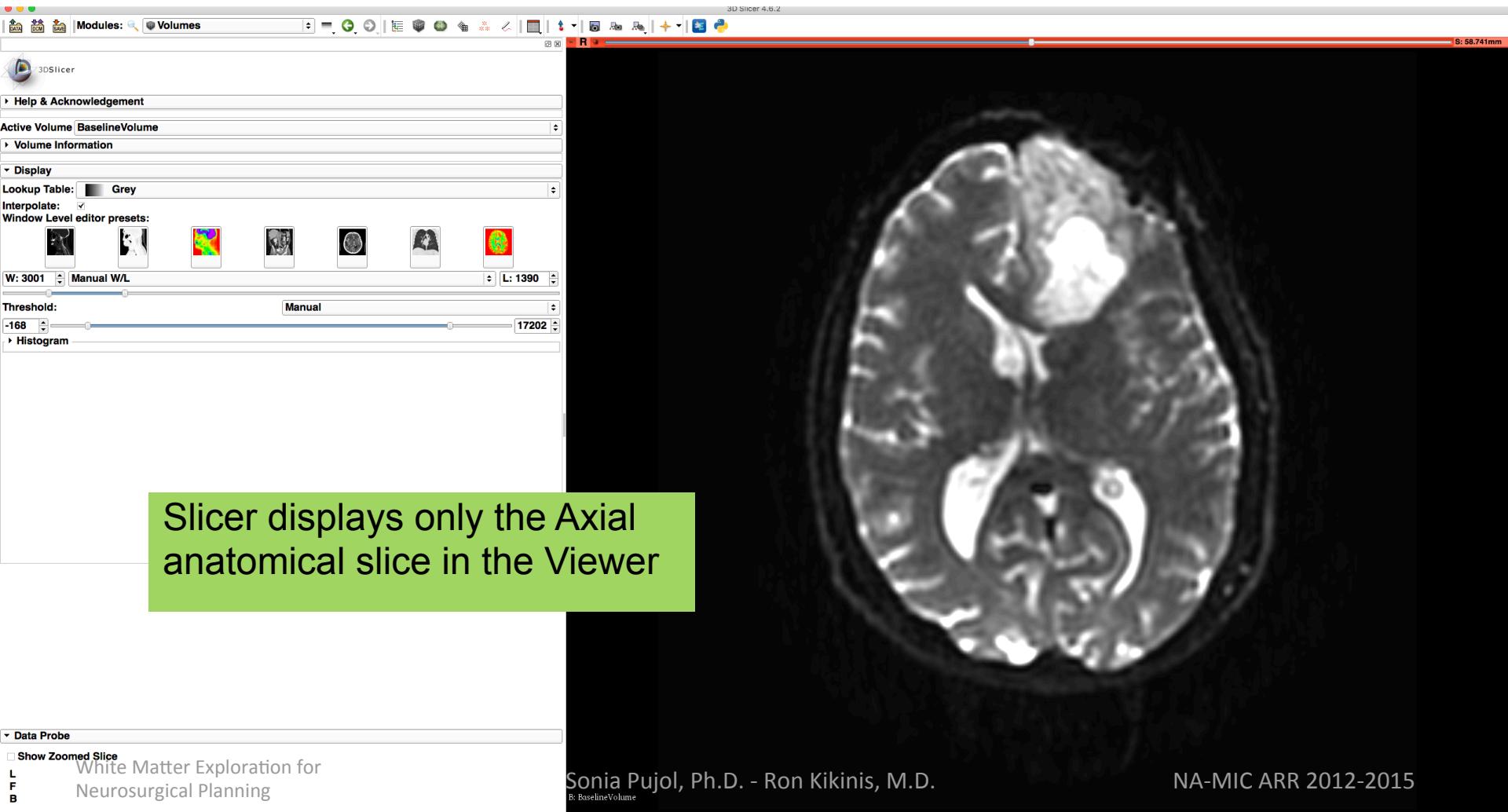
# Tumor Segmentation



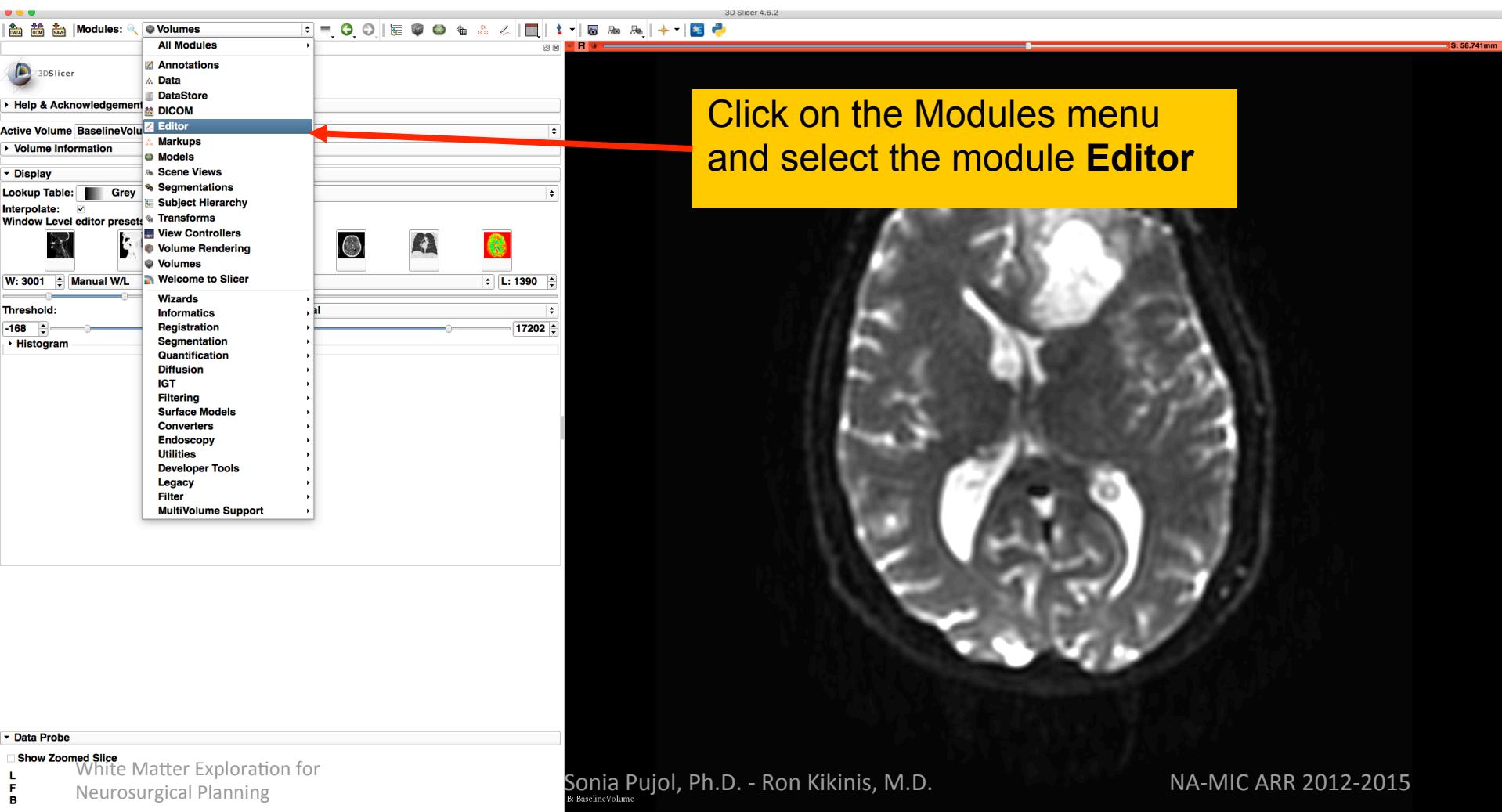
The tumor in this clinical case is composed of two parts: a solid part, and a cystic part.

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

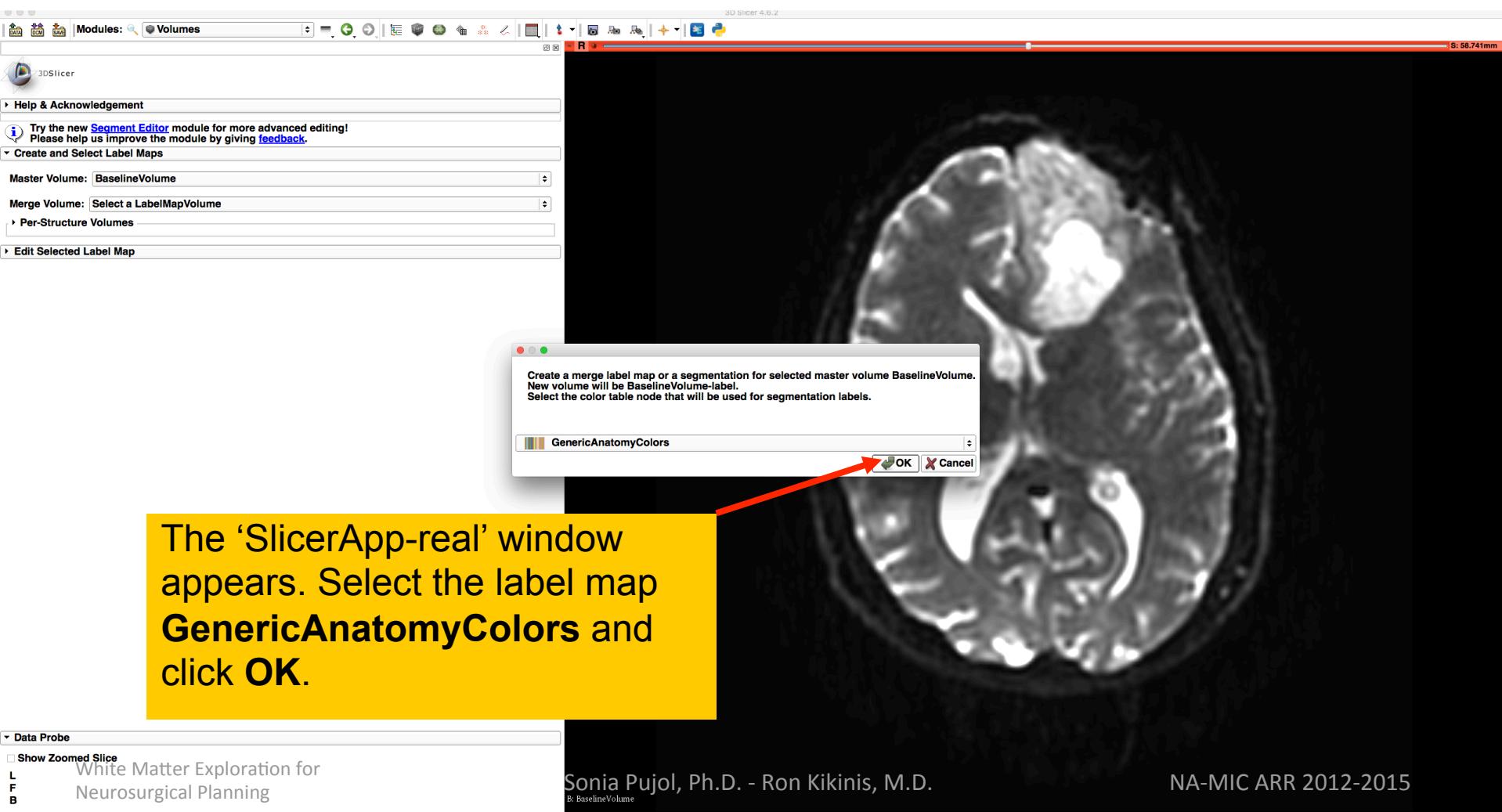
# Tumor Segmentation



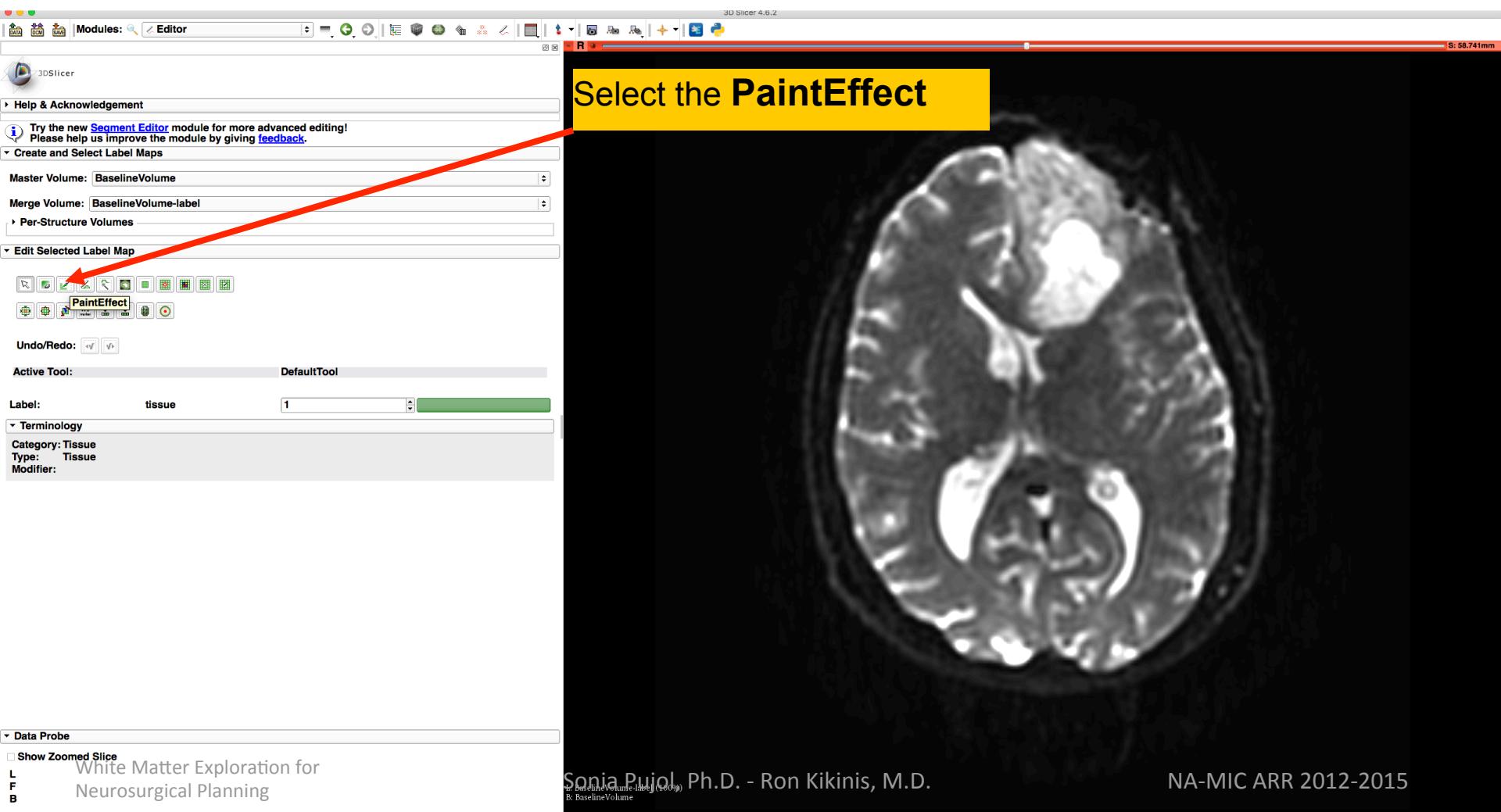
# Tumor Segmentation



# Tumor Segmentation



# Tumor Segmentation



# Tumor Segmentation

Scroll down the **Editor** module.  
Click the **color bar** to search  
the pre-defined label.

Help & Acknowledgement

Try the new Segment Editor module for more advanced editing. Please help us improve the module by giving [feedback](#).

Create and Select Label Maps

Master Volume: BaselineVolume

Merge Volume: BaselineVolume-label

Per-Structure Volumes

Edit Selected Label Map

Tools:

Undo/Redo:

Active Tool: DefaultTool

Label: tissue 1

Terminology

Category: Tissue

Type: Tissue

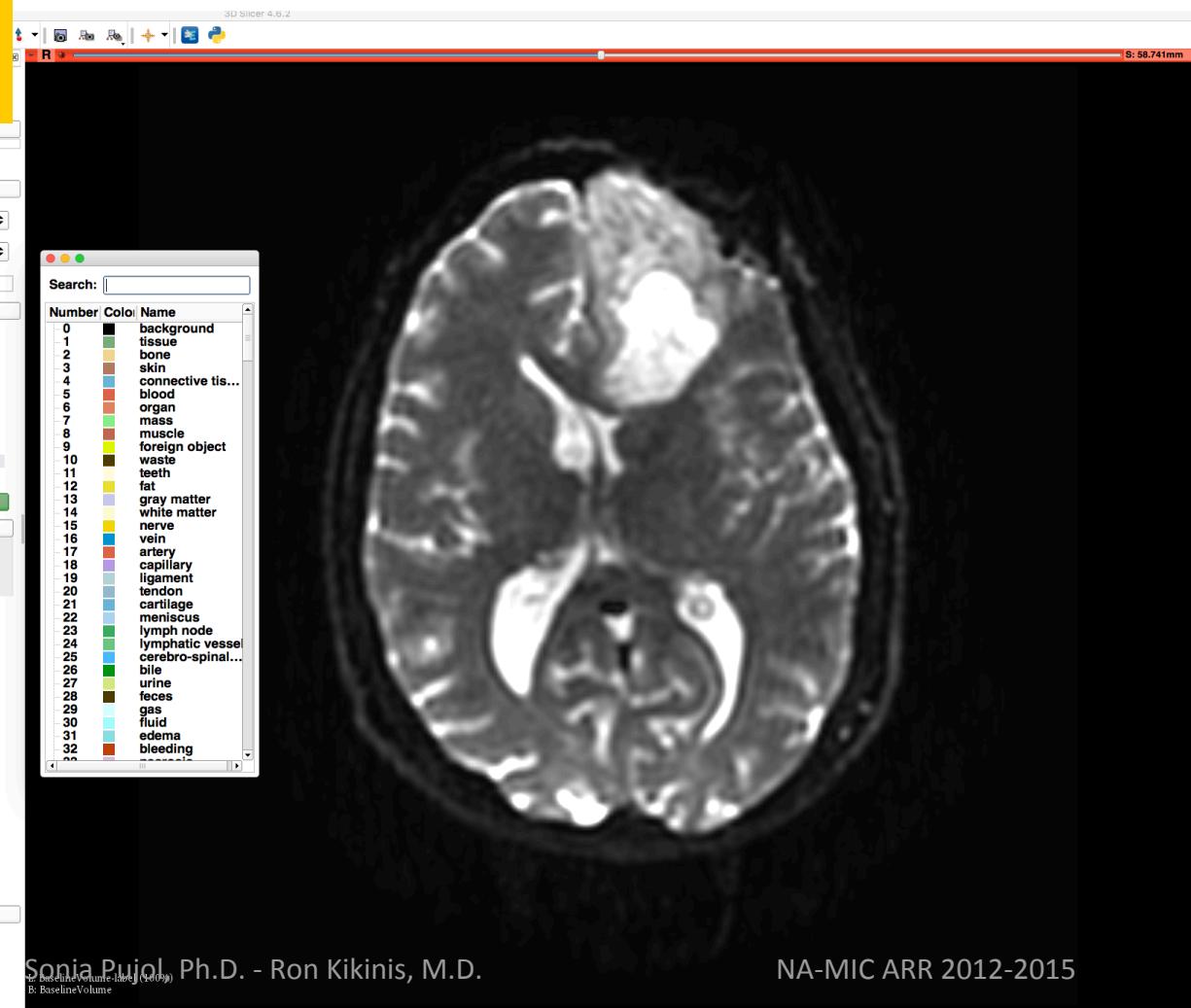
Modifier:

Data Probe

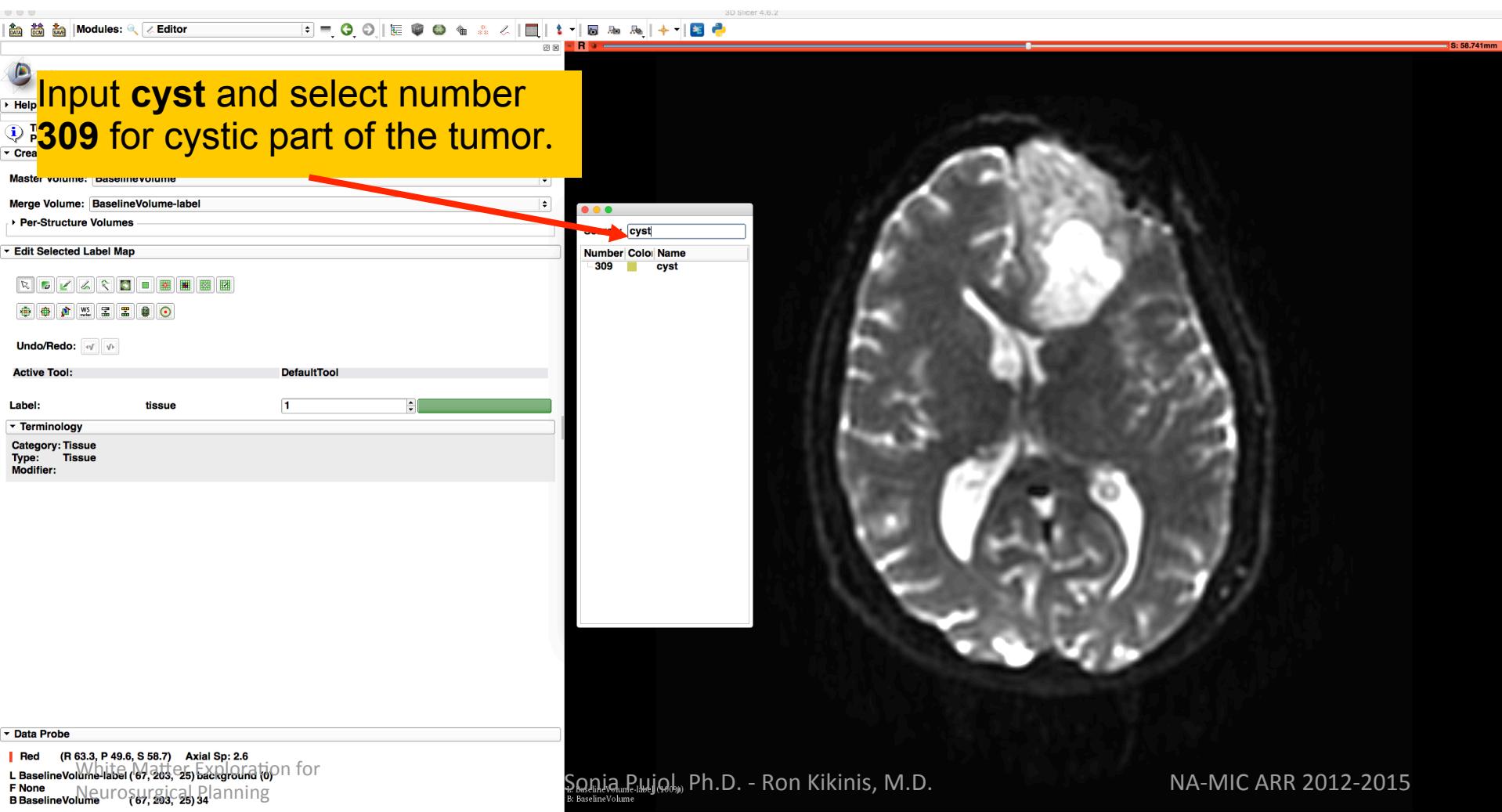
Show Zoomed Slice

White Matter Exploration for Neurosurgical Planning

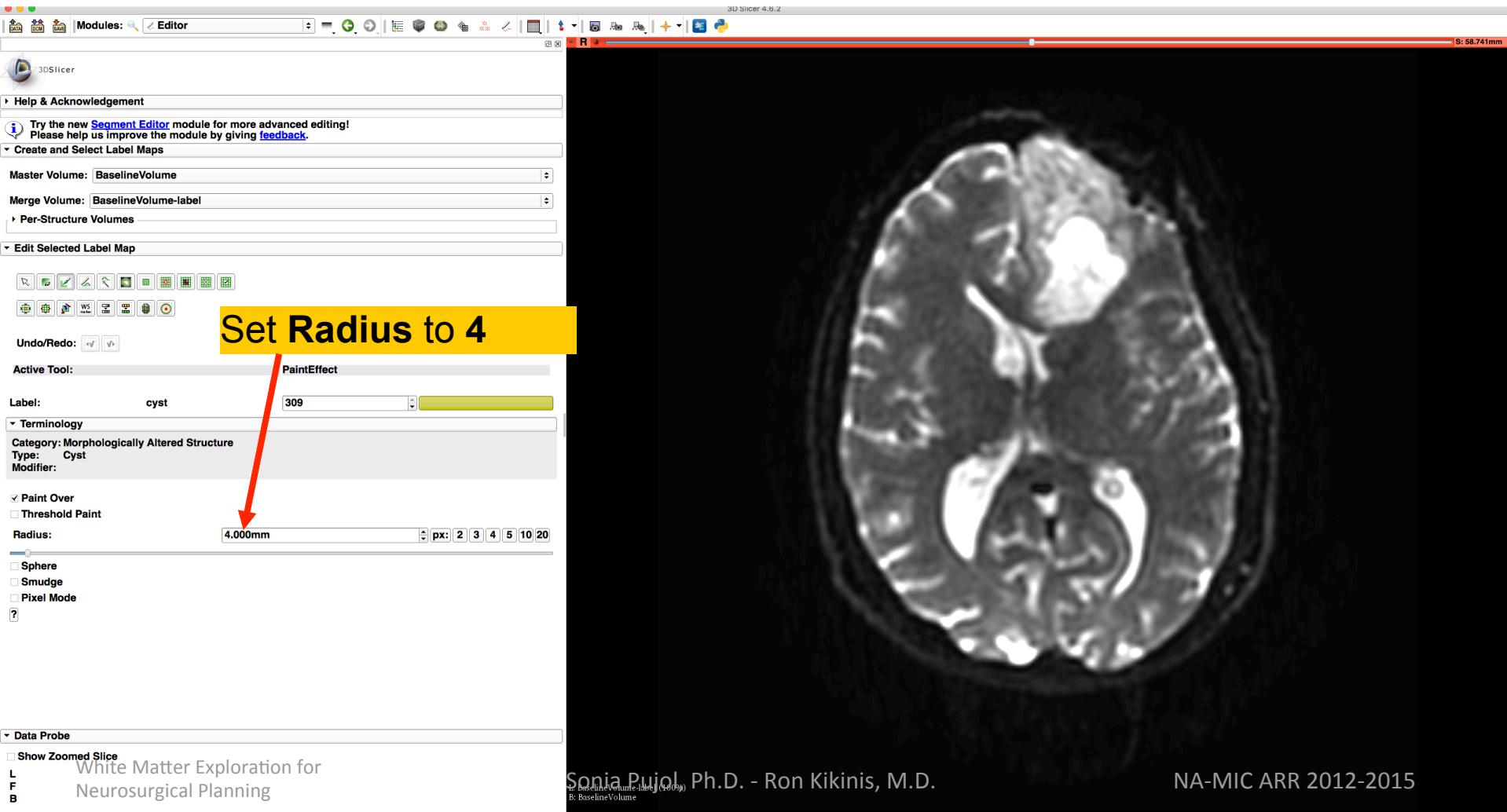
L F B



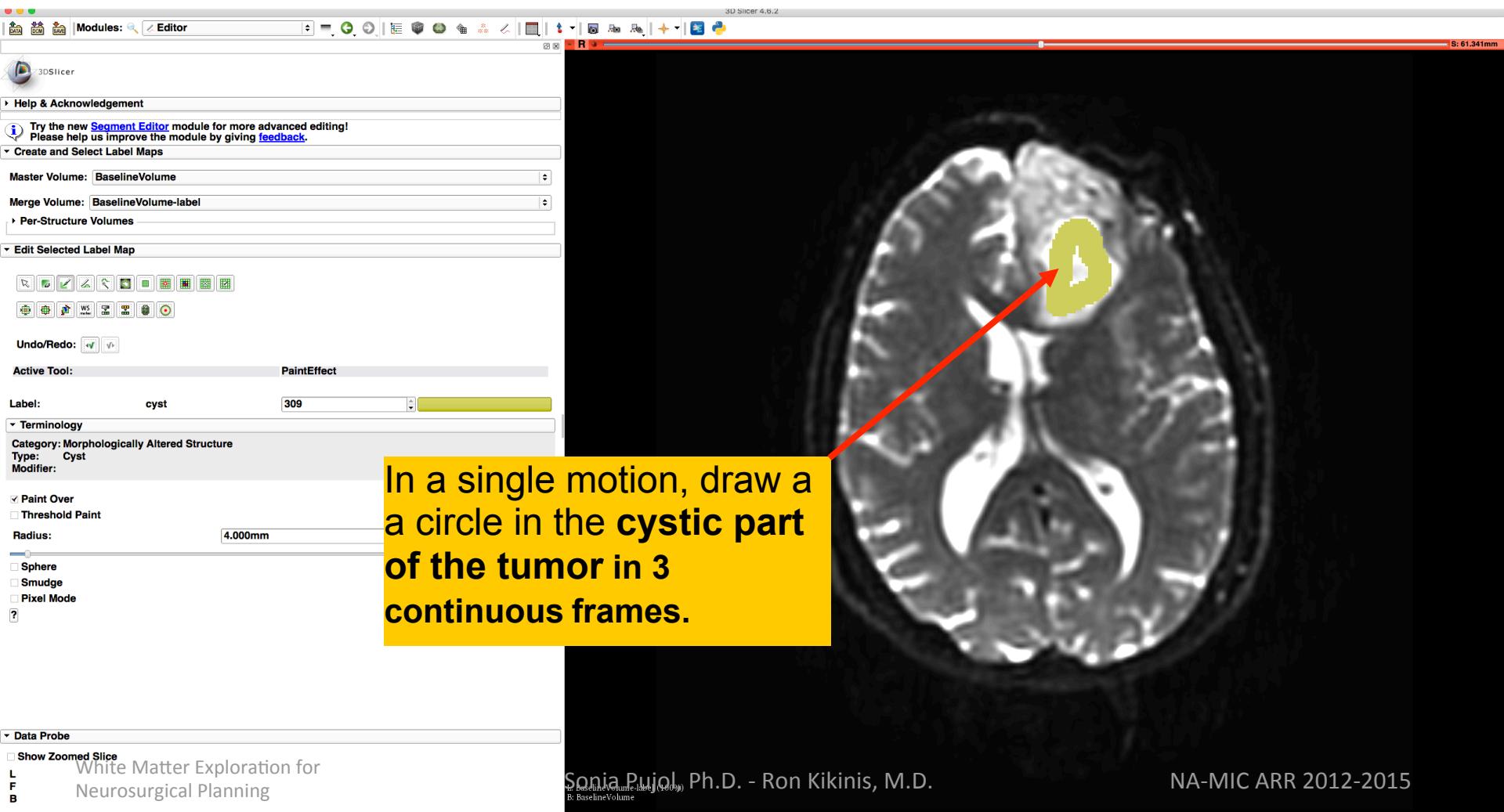
# Tumor Segmentation



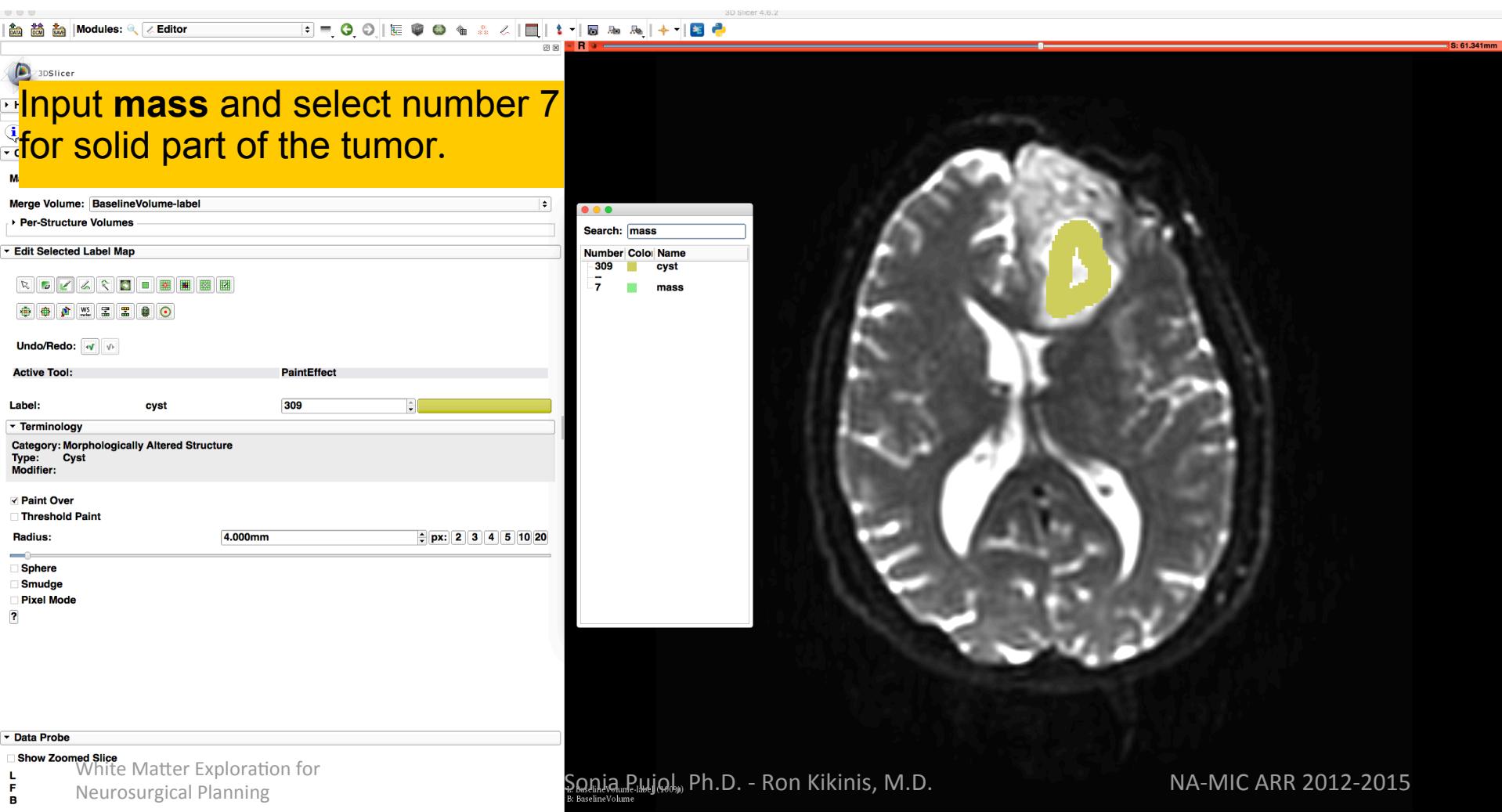
# Tumor Segmentation



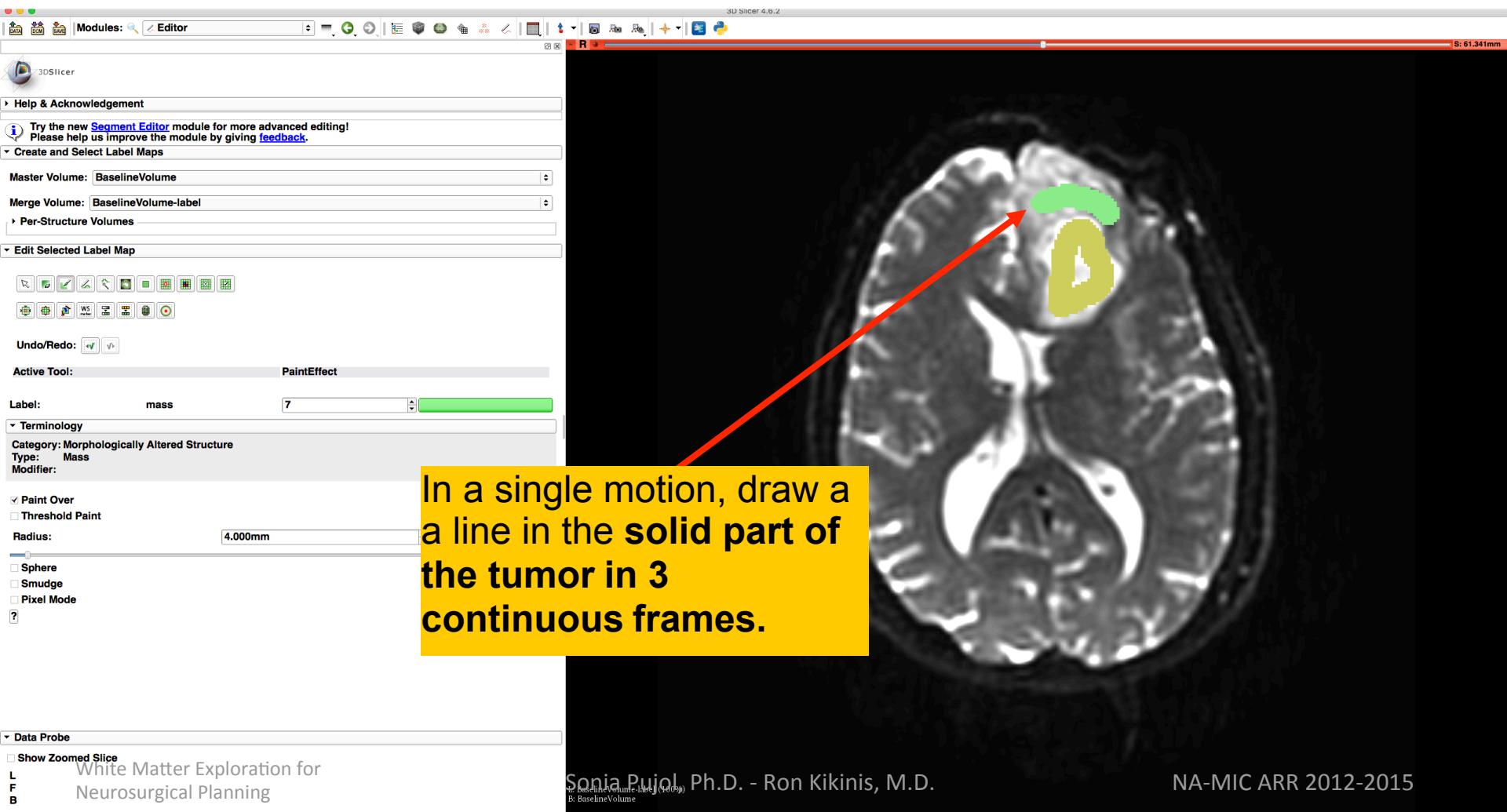
# Tumor Segmentation



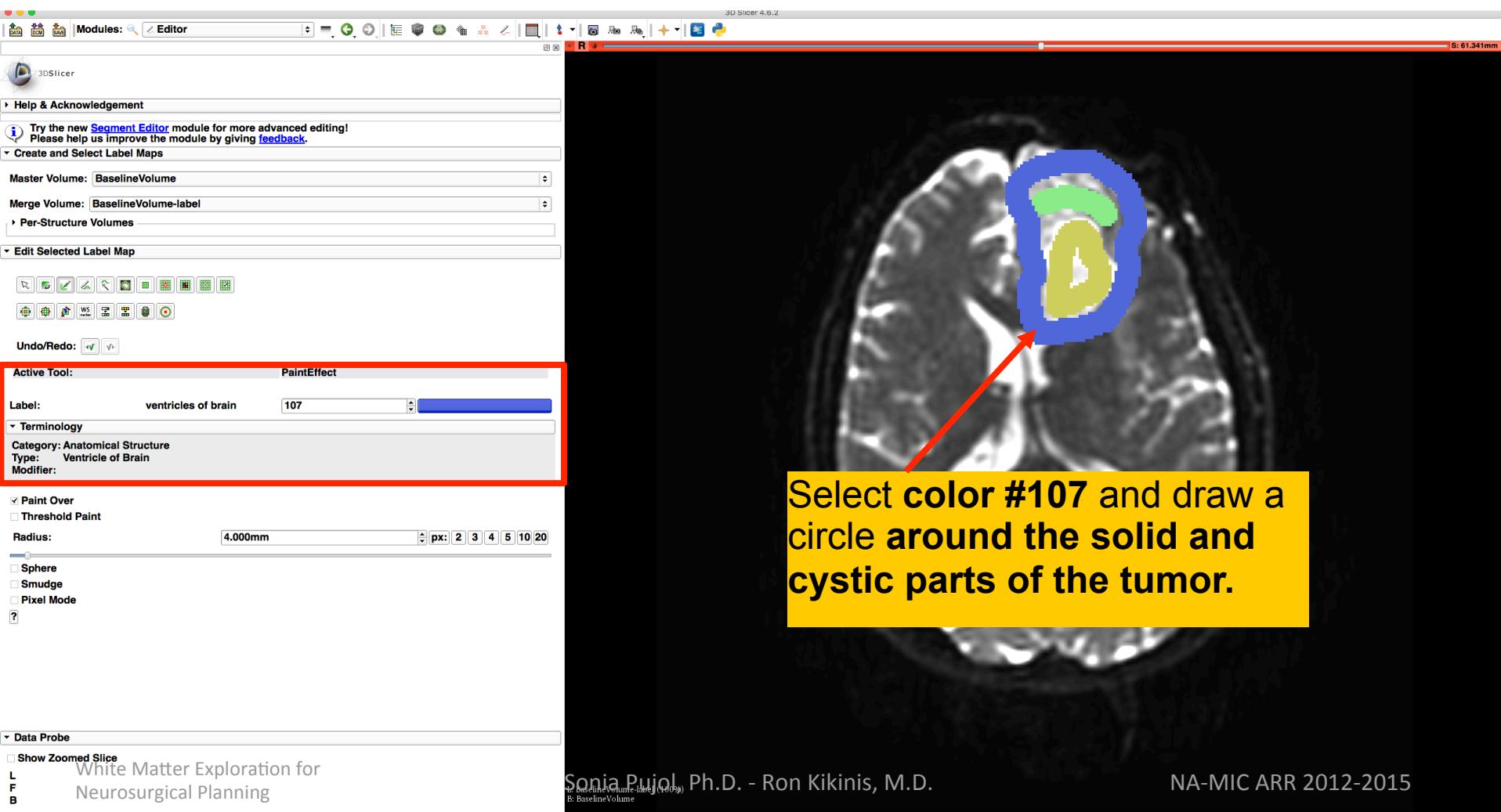
# Tumor Segmentation



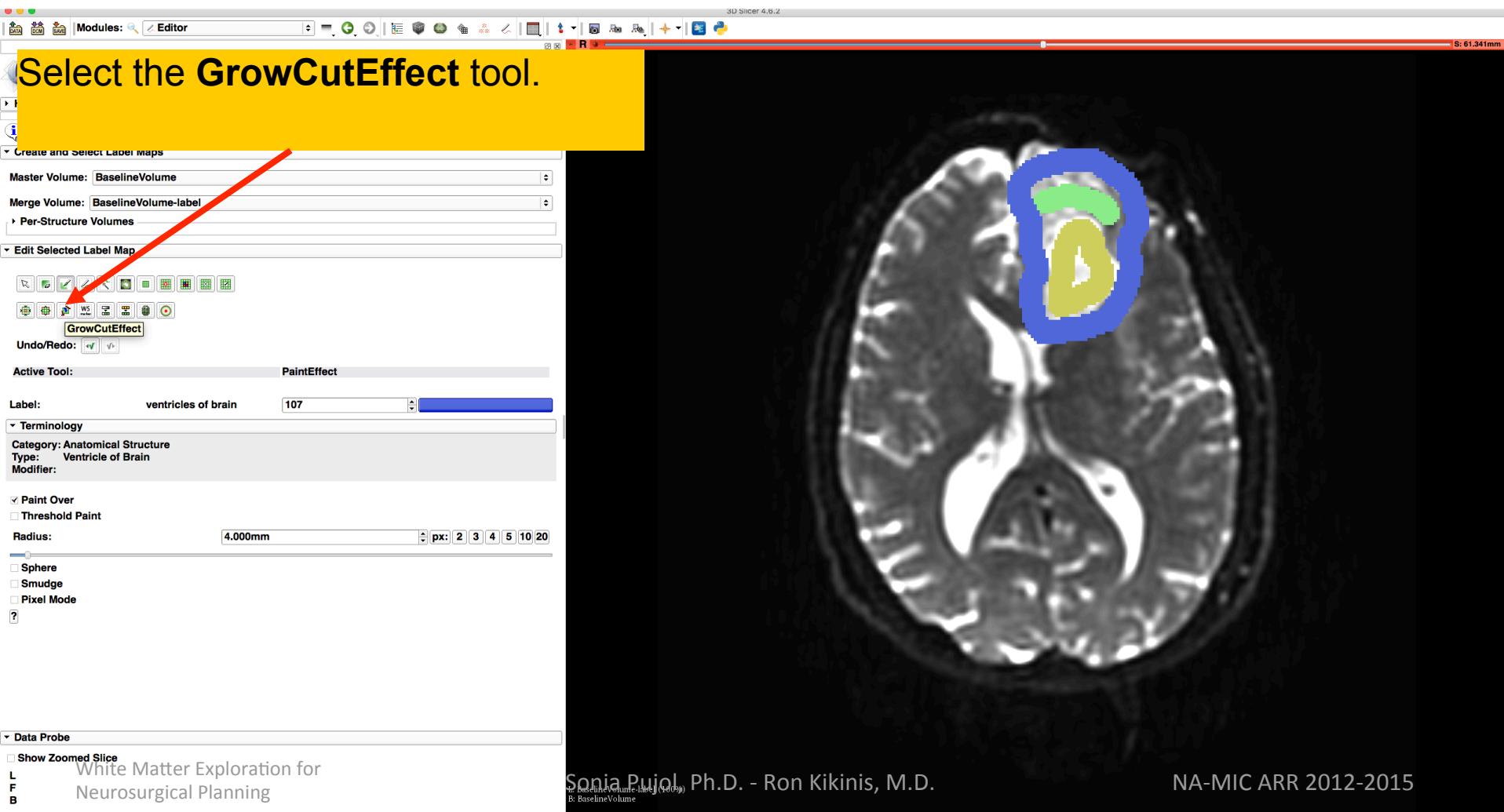
# Tumor Segmentation



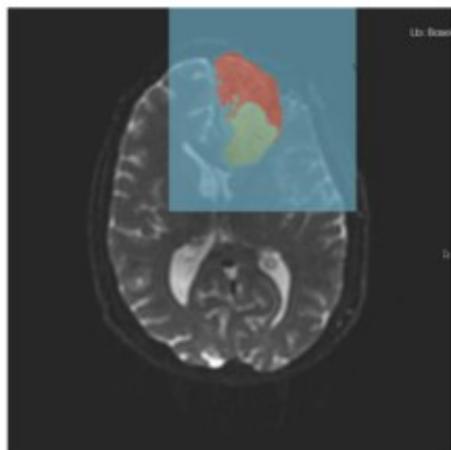
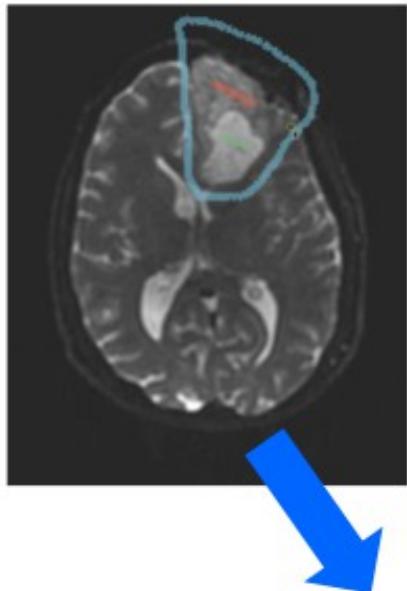
# Tumor Segmentation



# Tumor Segmentation

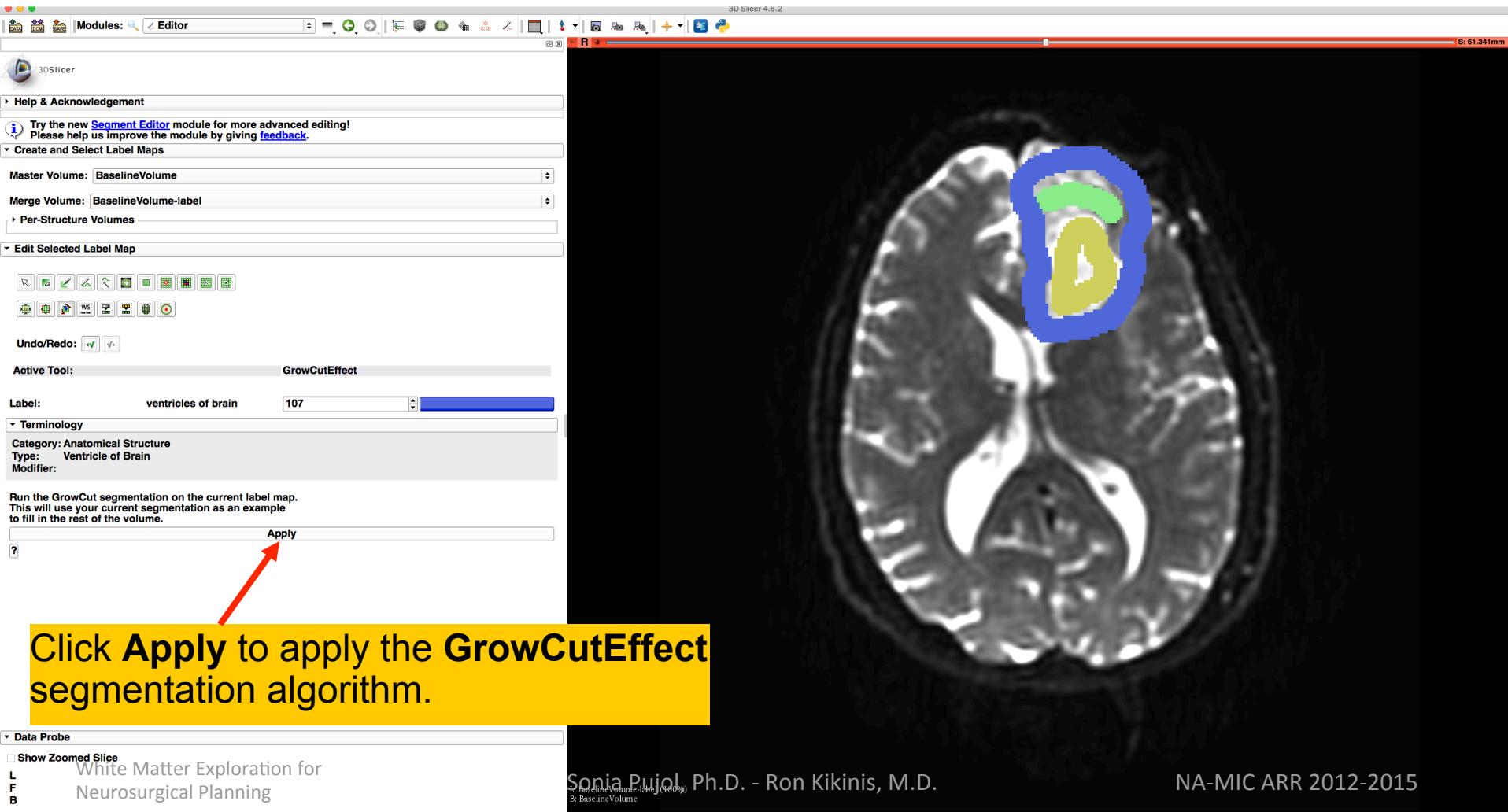


# Grow Cut Segmentation

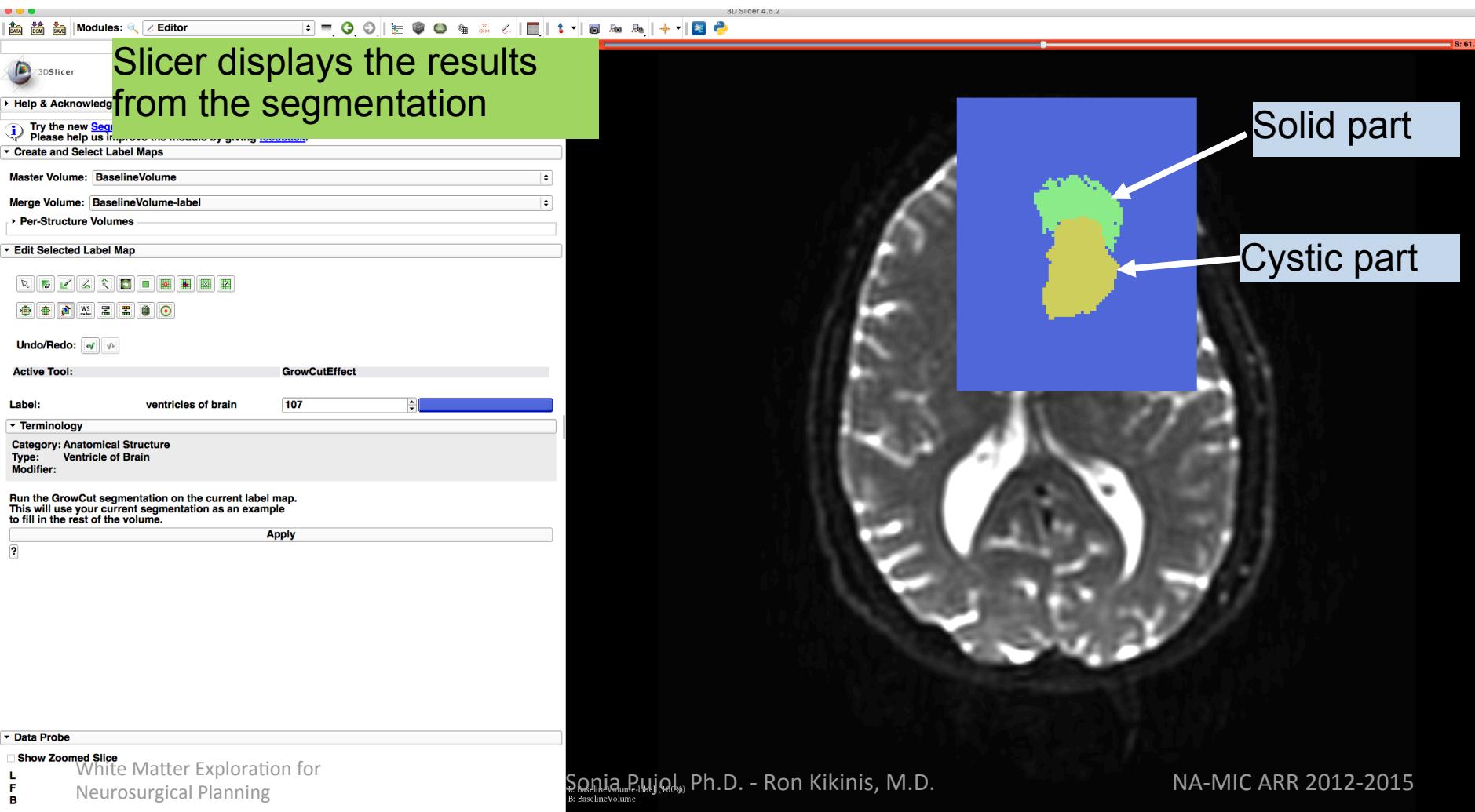


- The Grow Cut Segmentation method is a competitive region growing algorithm using Cellular Automata.
- The algorithm performs multi-label image segmentation using a set of user input scribbles.
- V. Vezhnevets, V. Konouchine. "Grow-Cut" - Interactive Multi-Label N-D Image Segmentation". Proc. Graphicon.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

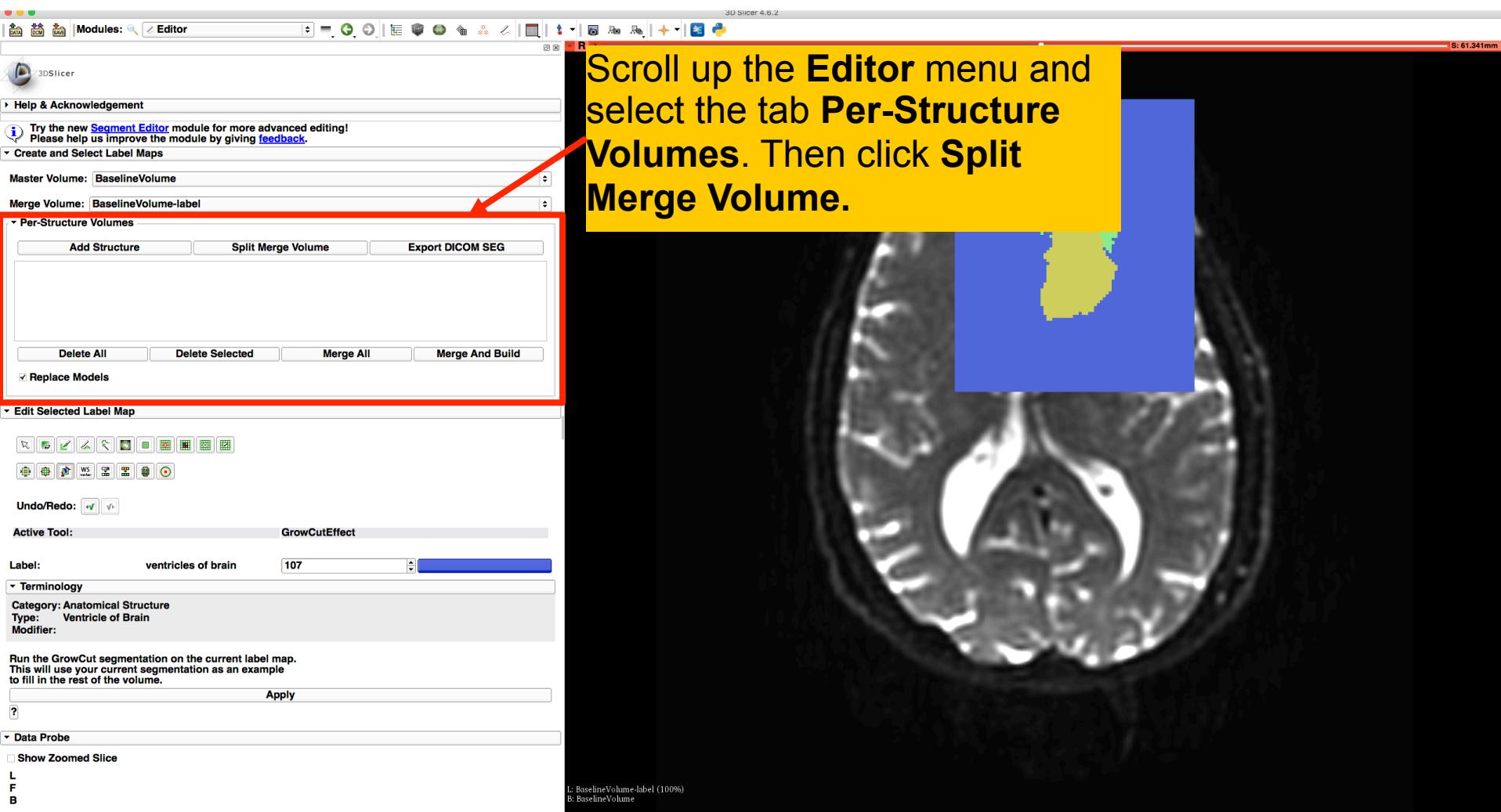
# Tumor Segmentation



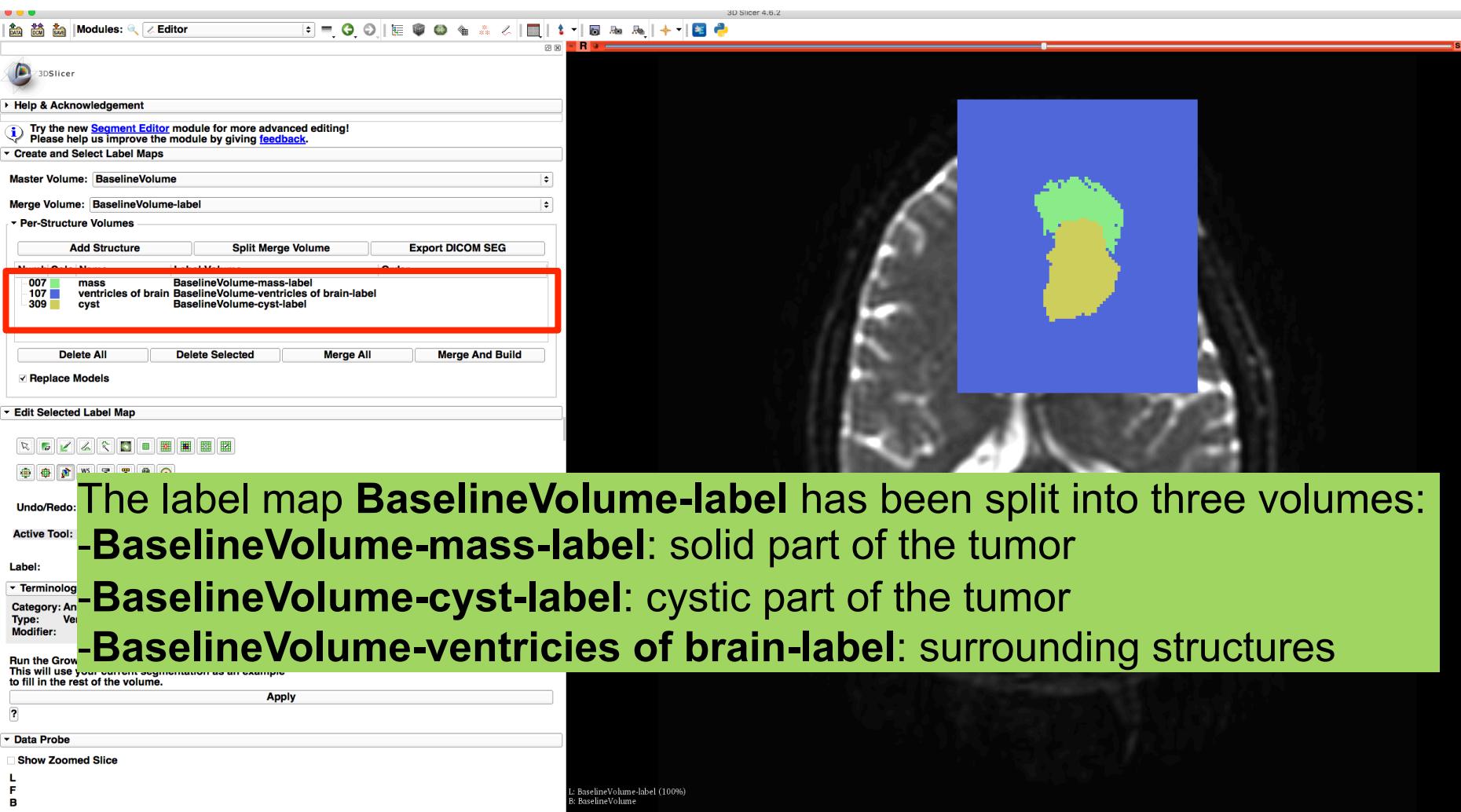
# Tumor Segmentation



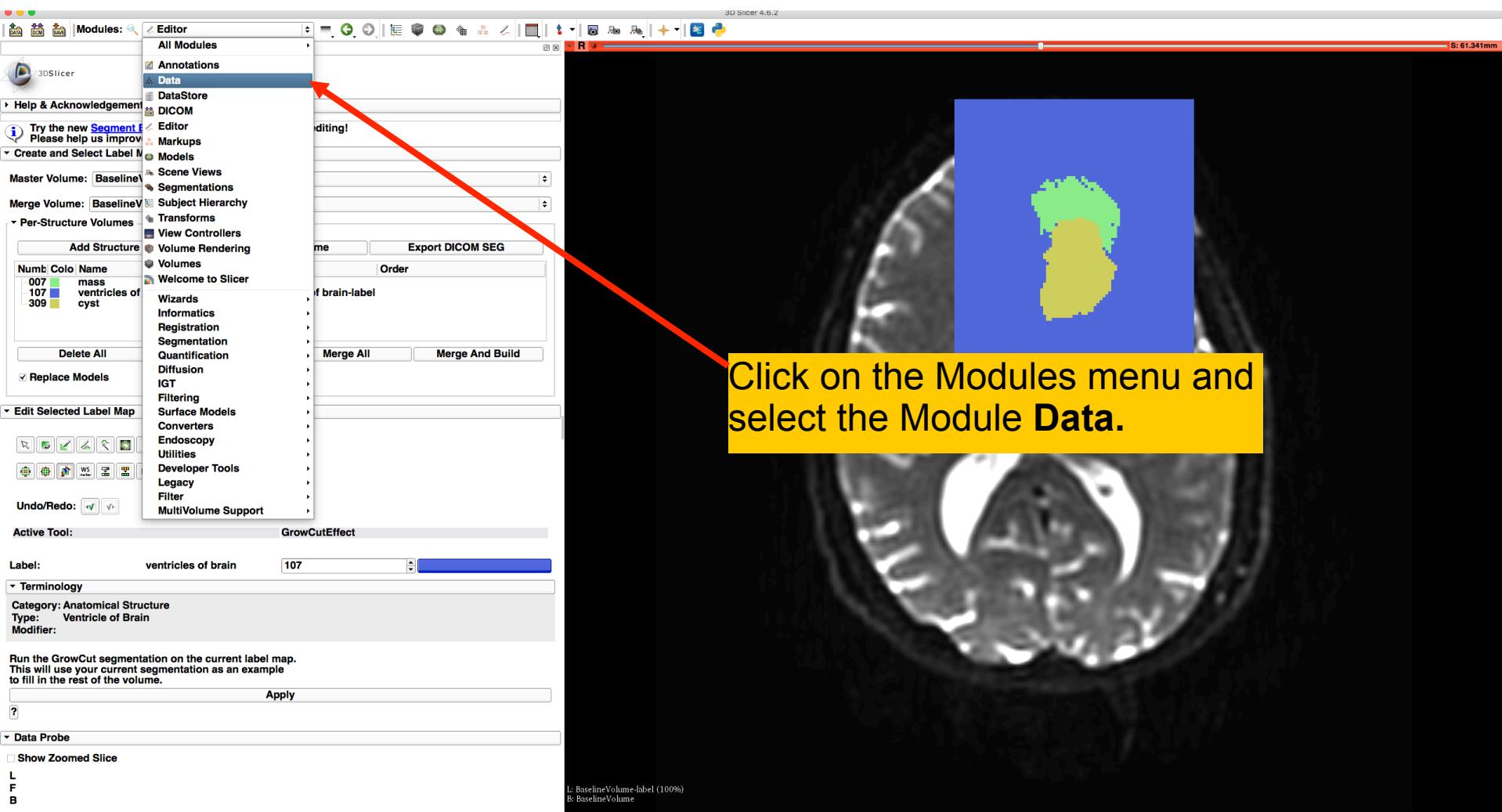
# Tumor Segmentation



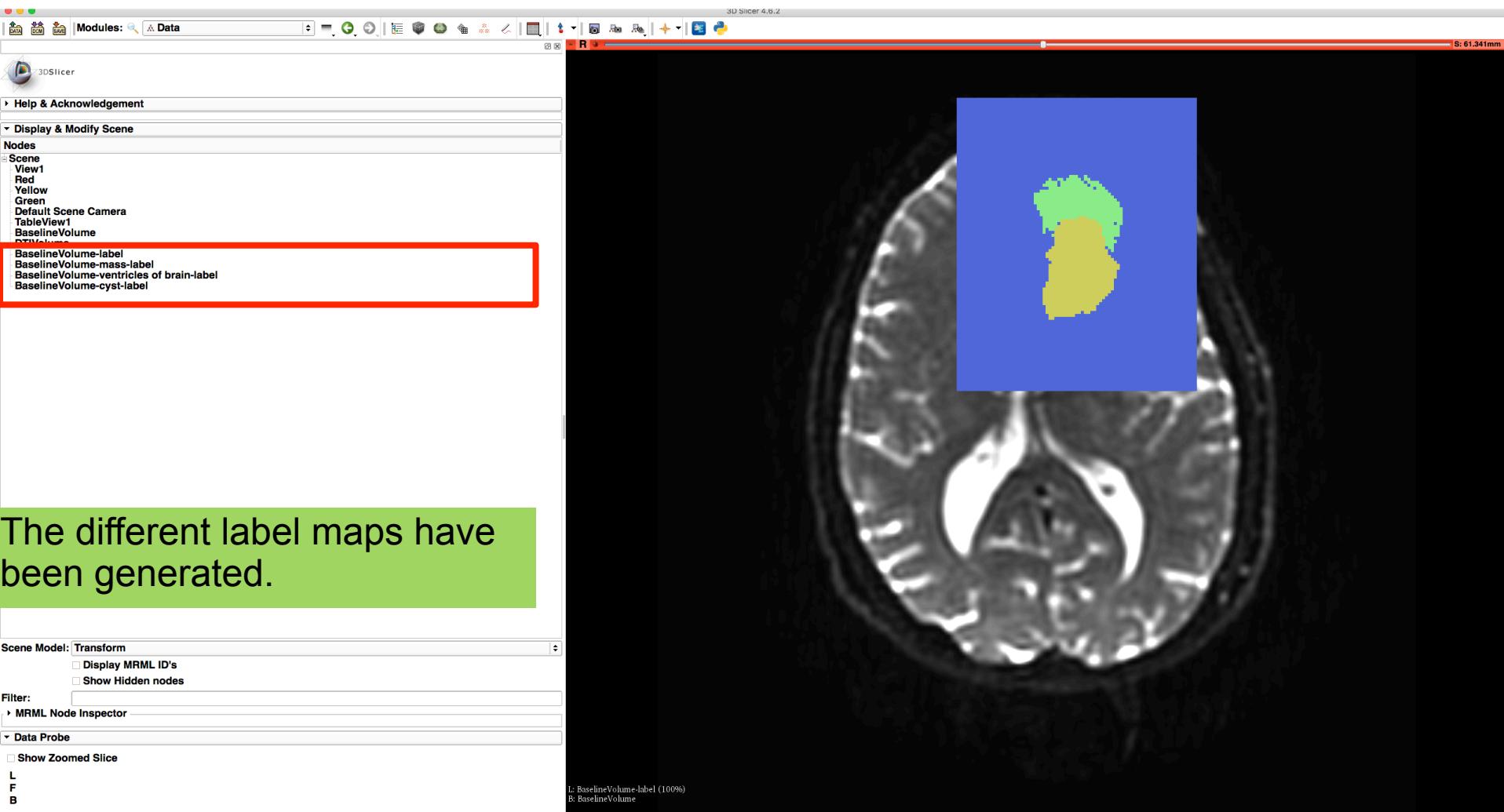
# Tumor Segmentation



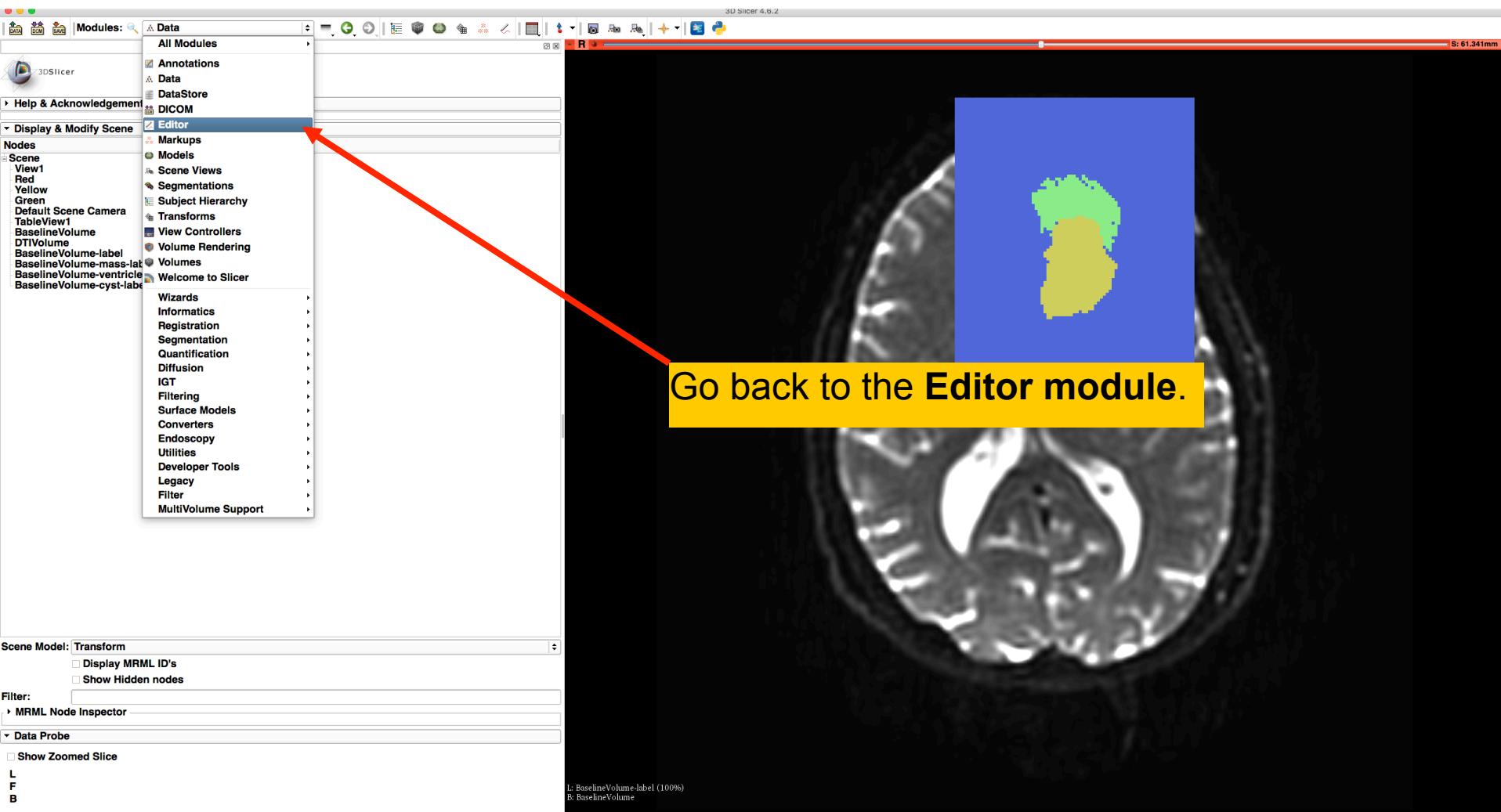
# Tumor Segmentation



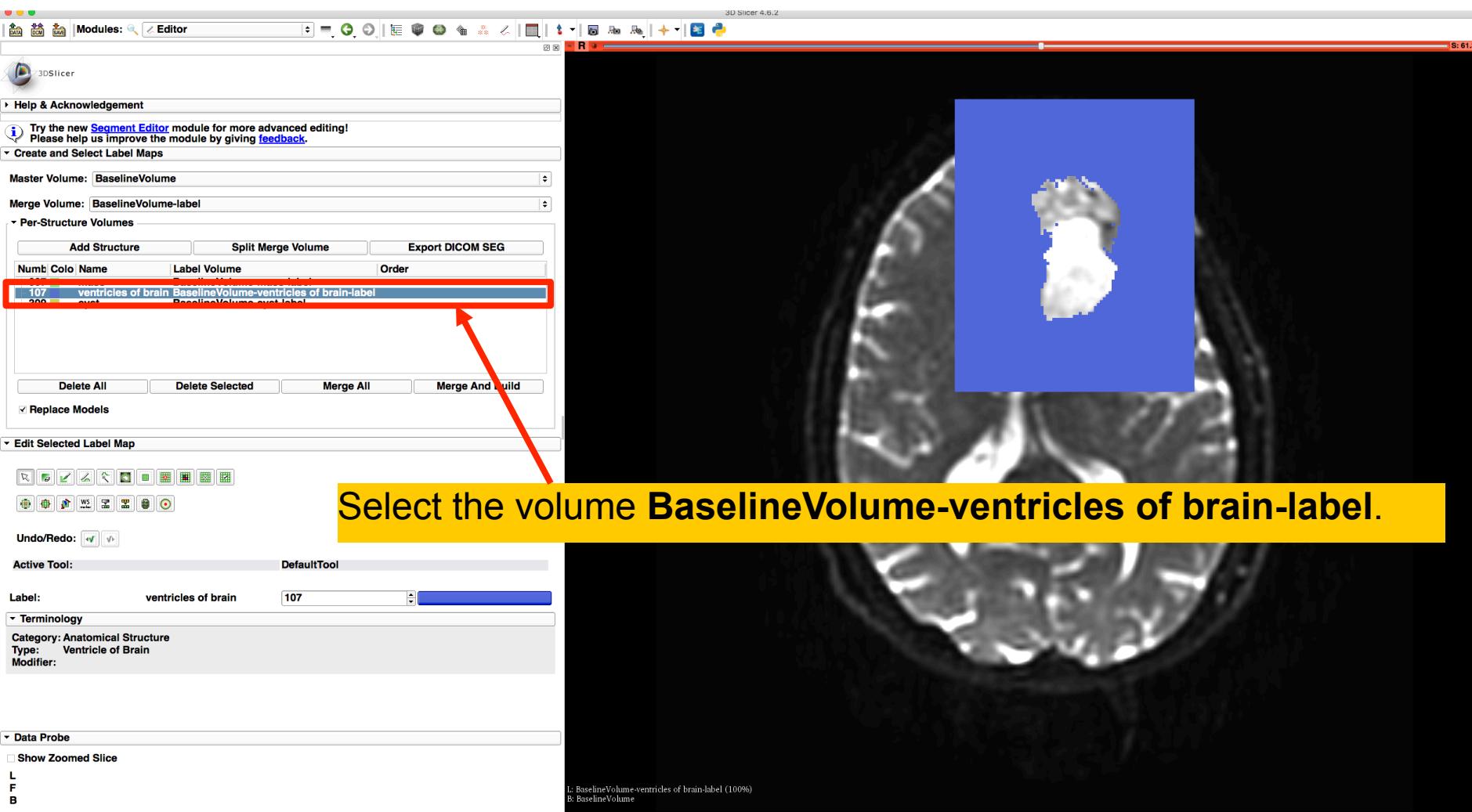
# Tumor Segmentation



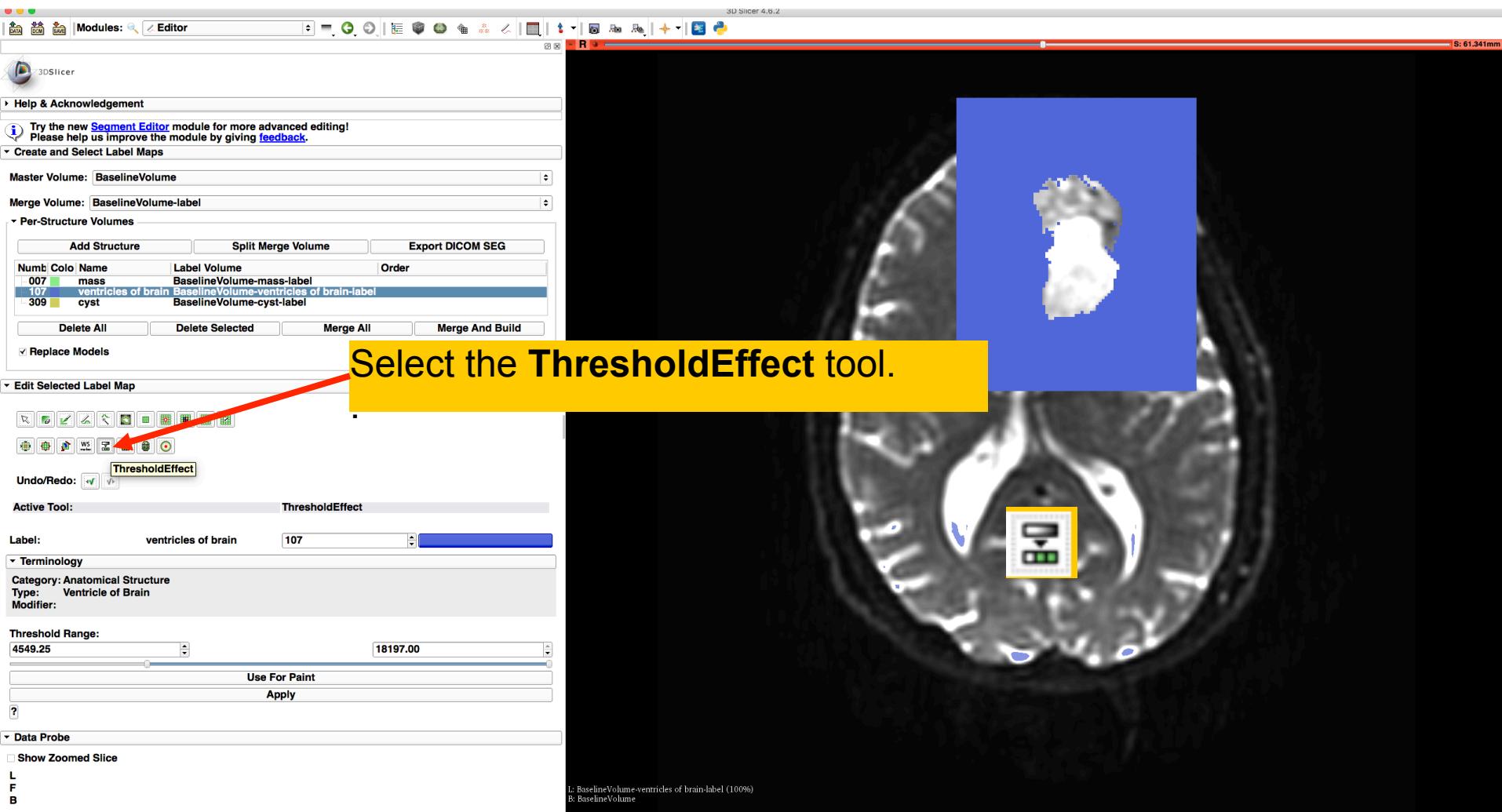
# Ventricles Segmentation



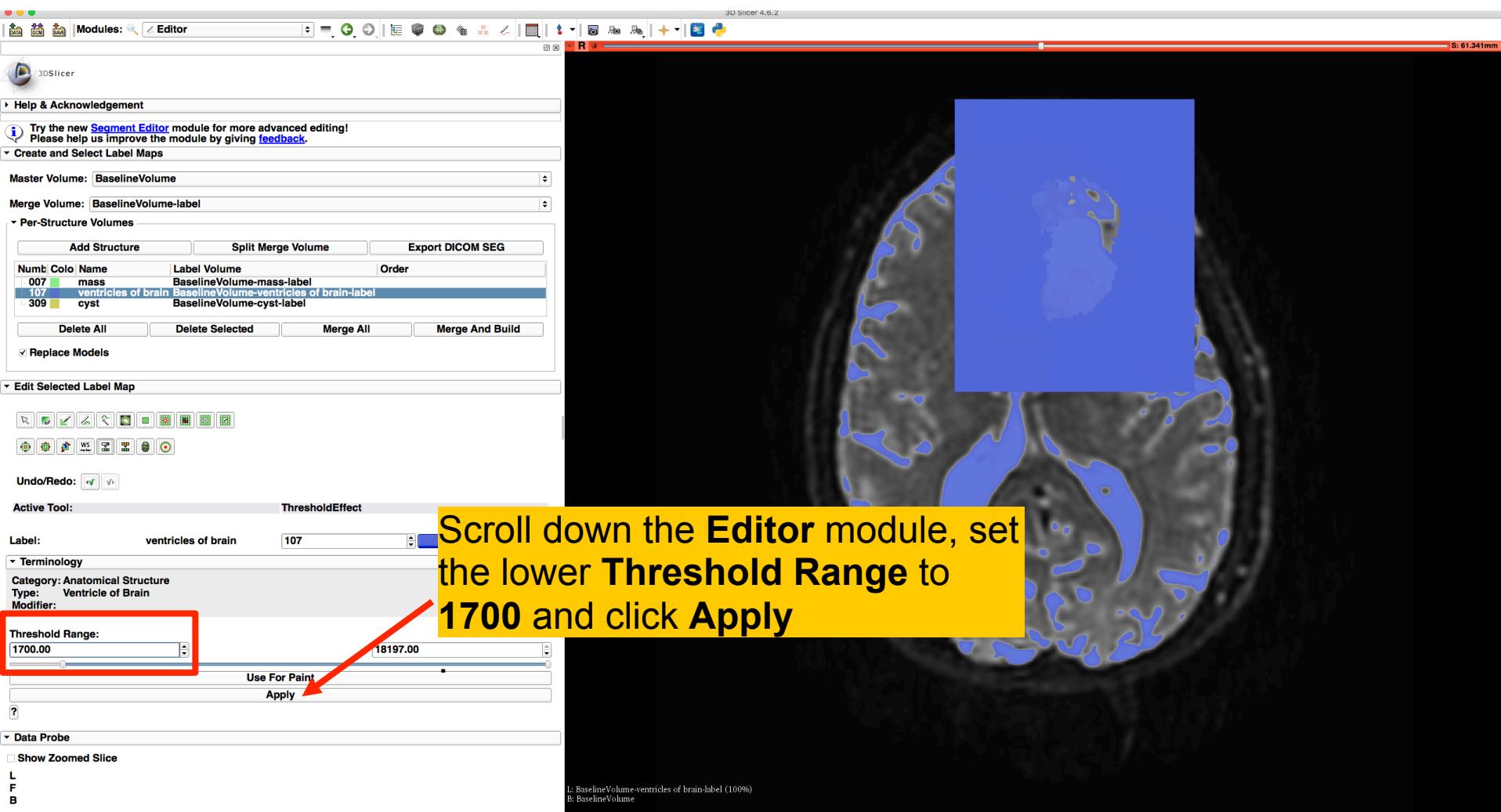
# Ventricles Segmentation



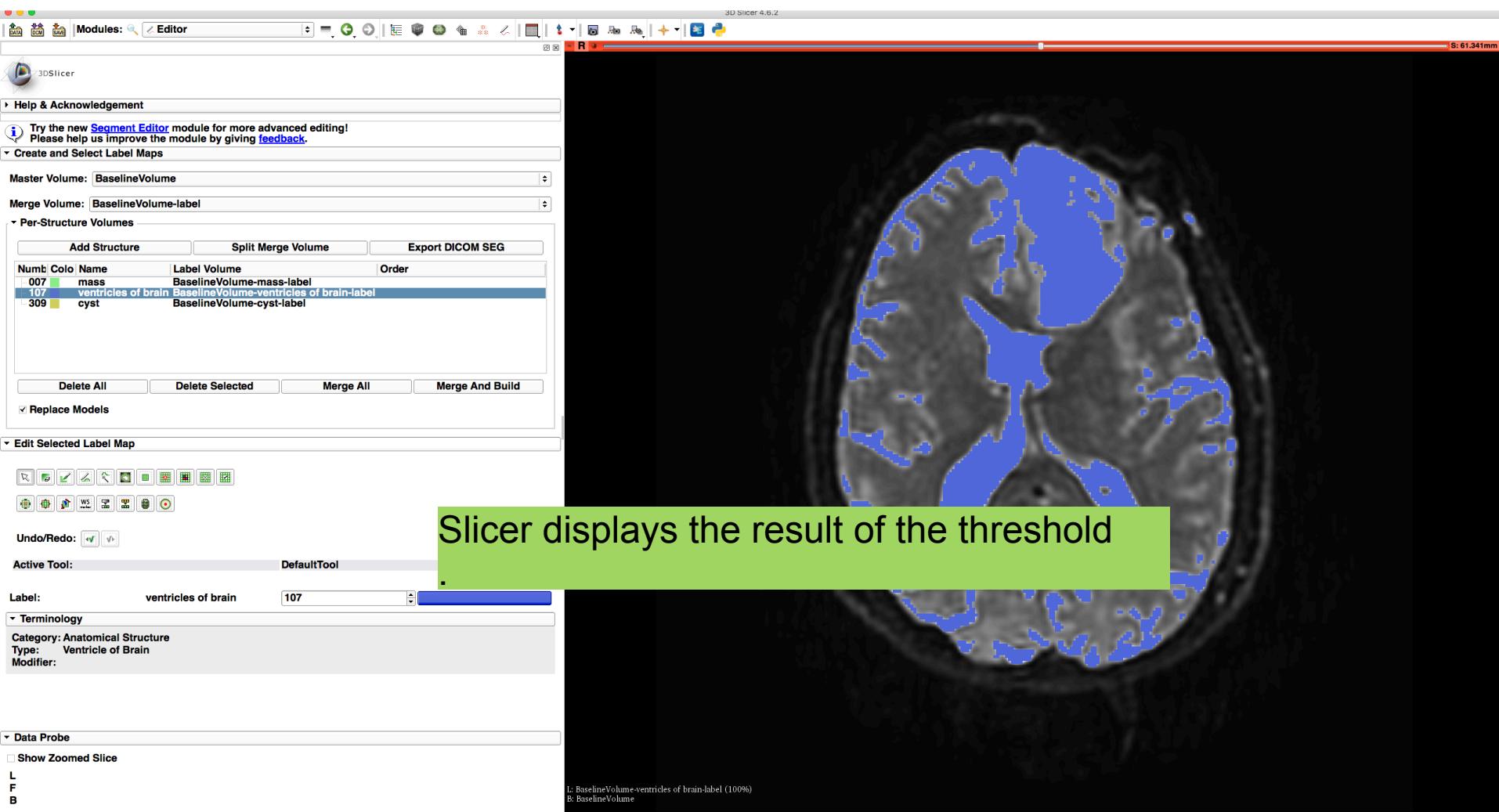
# Ventricles Segmentation



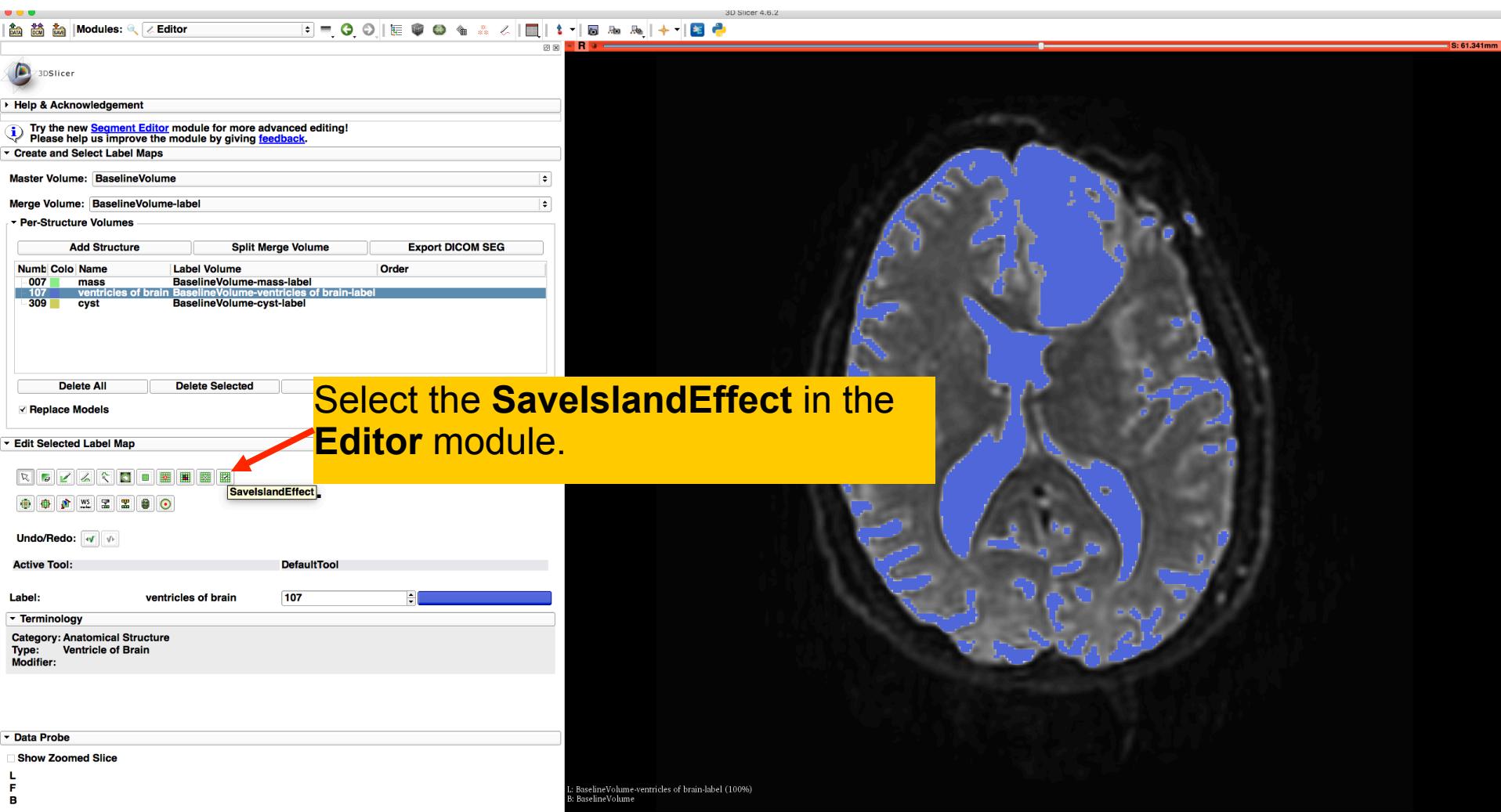
# Ventricles Segmentation



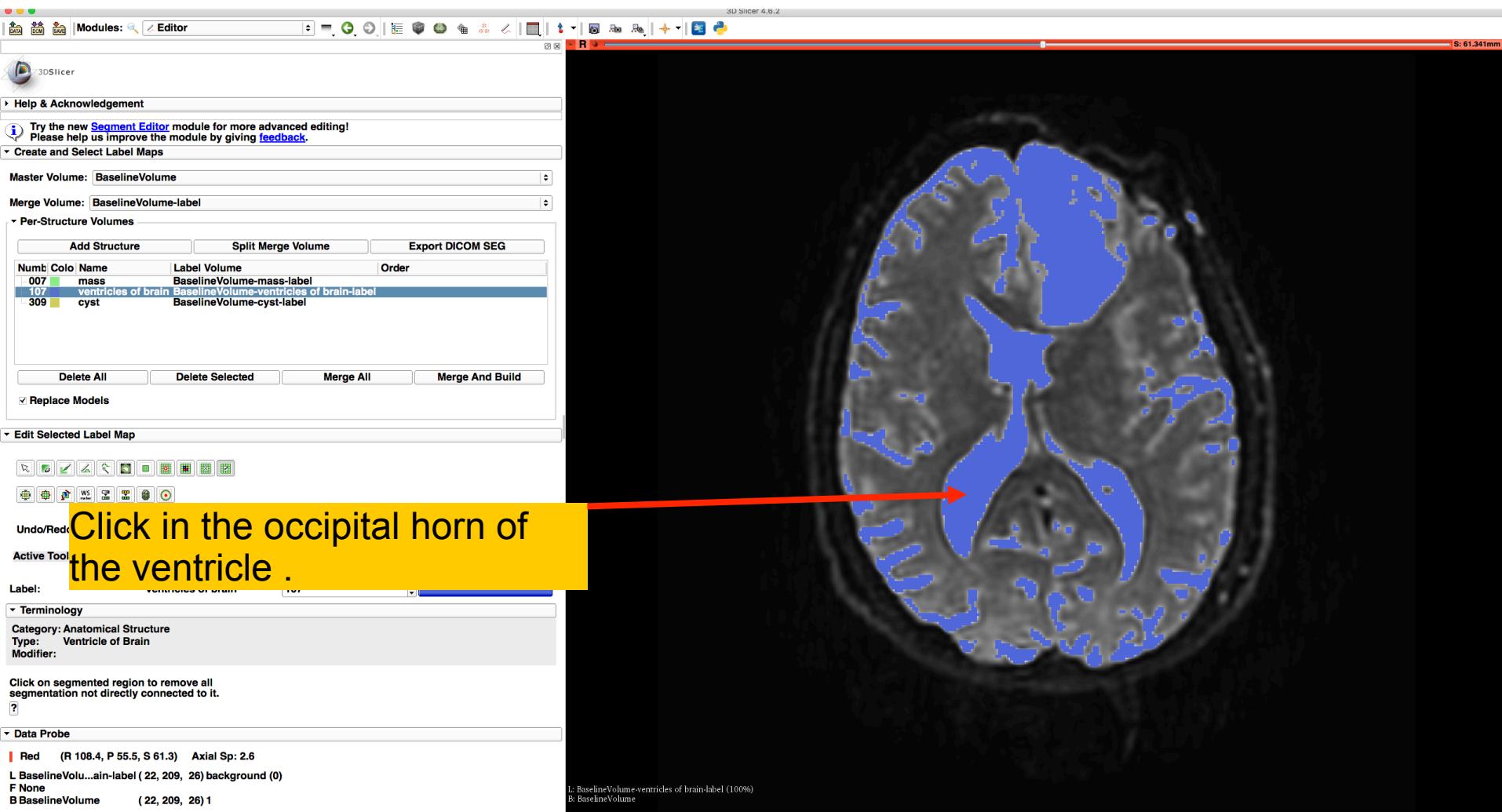
# Ventricles Segmentation



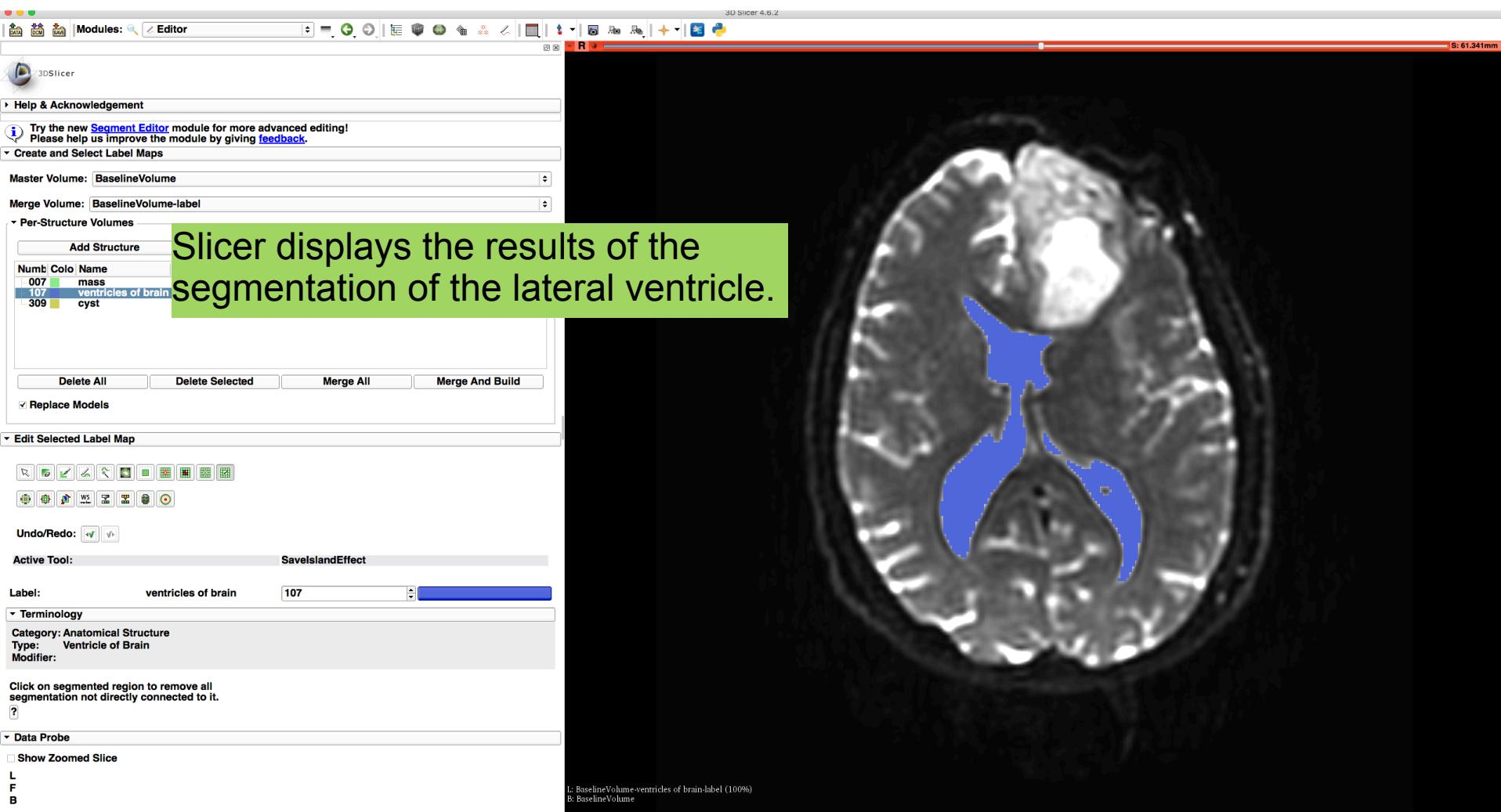
# Ventricles Segmentation



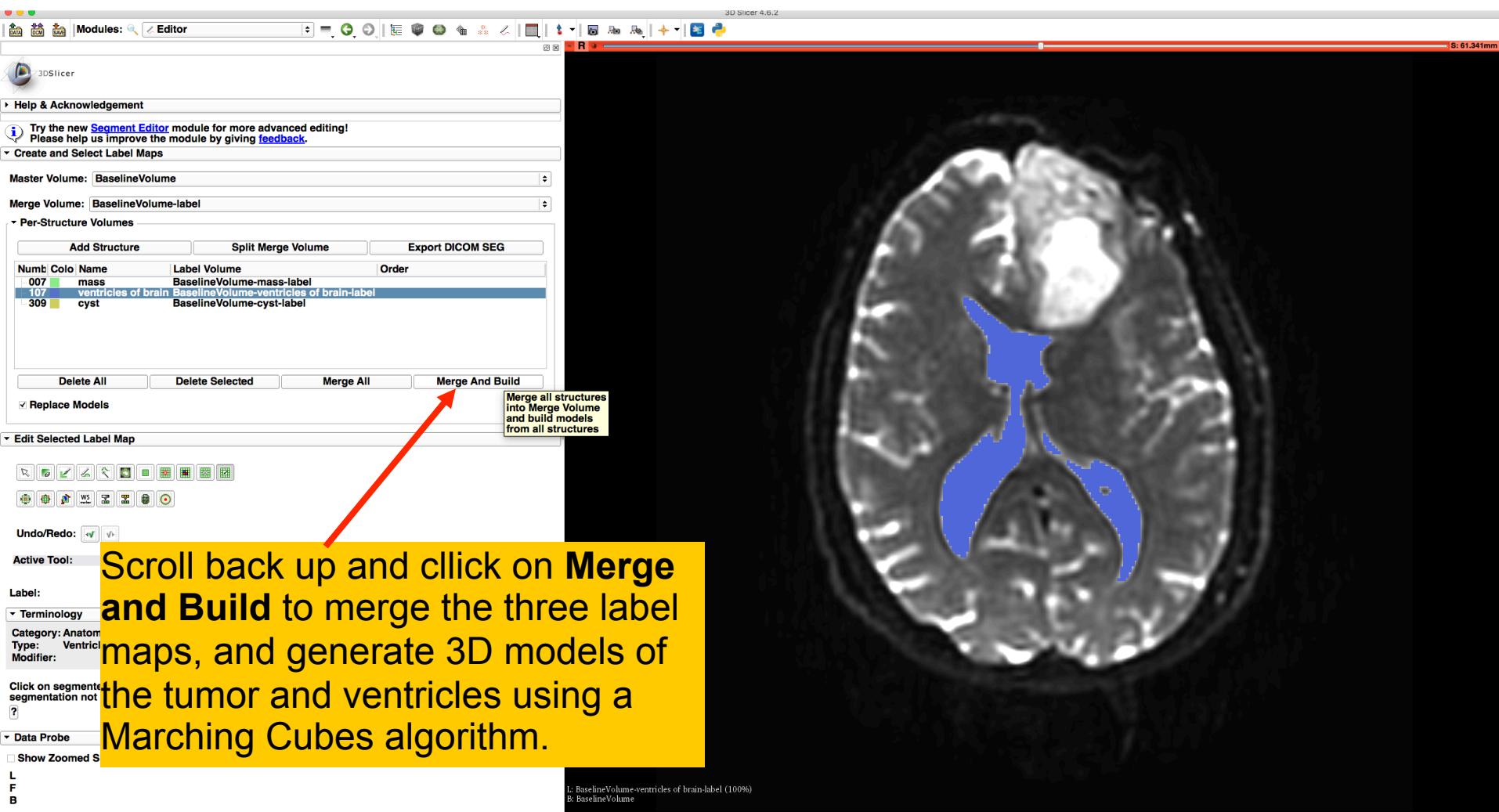
# Ventricles Segmentation



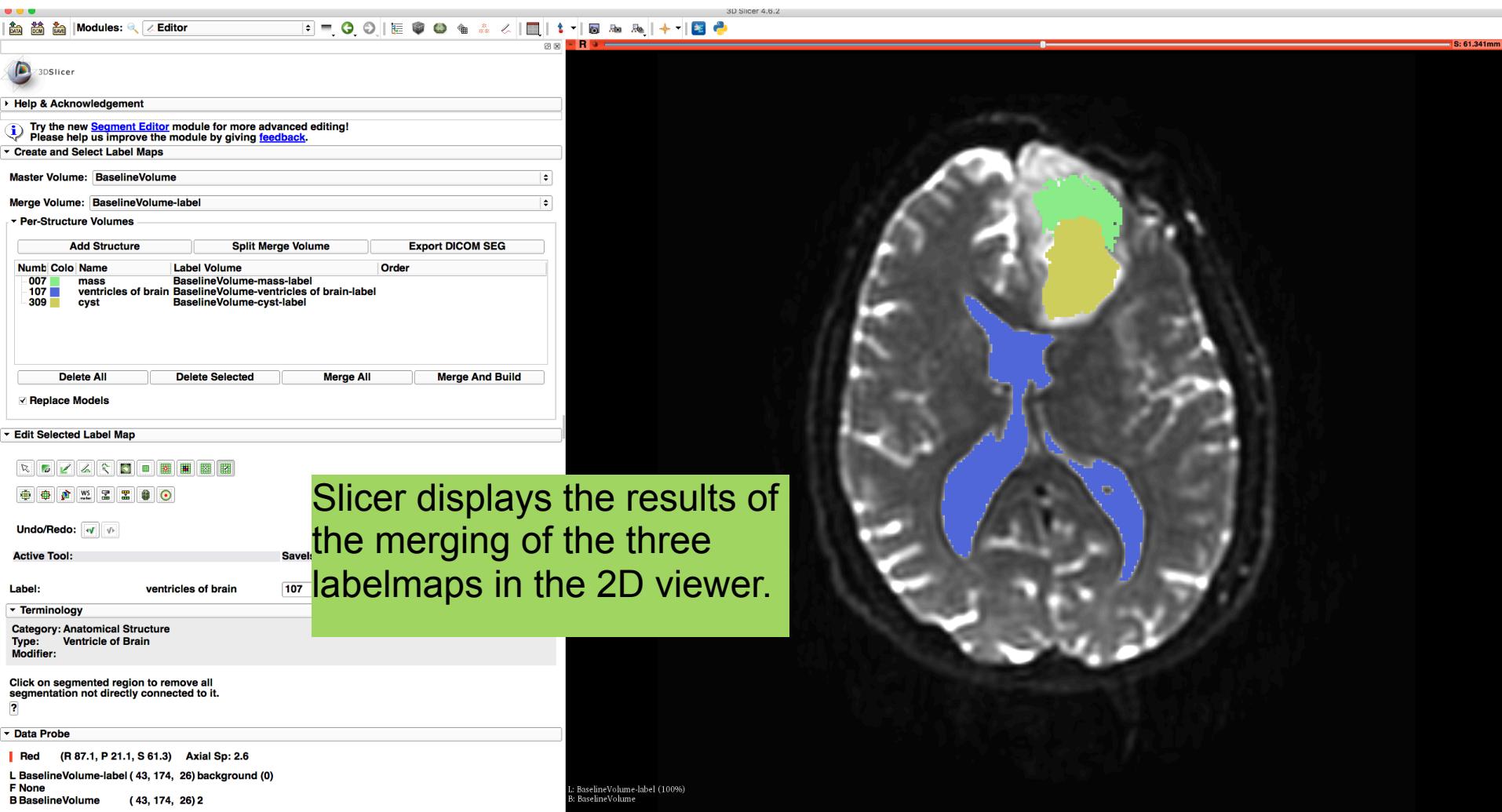
# Ventricles Segmentation



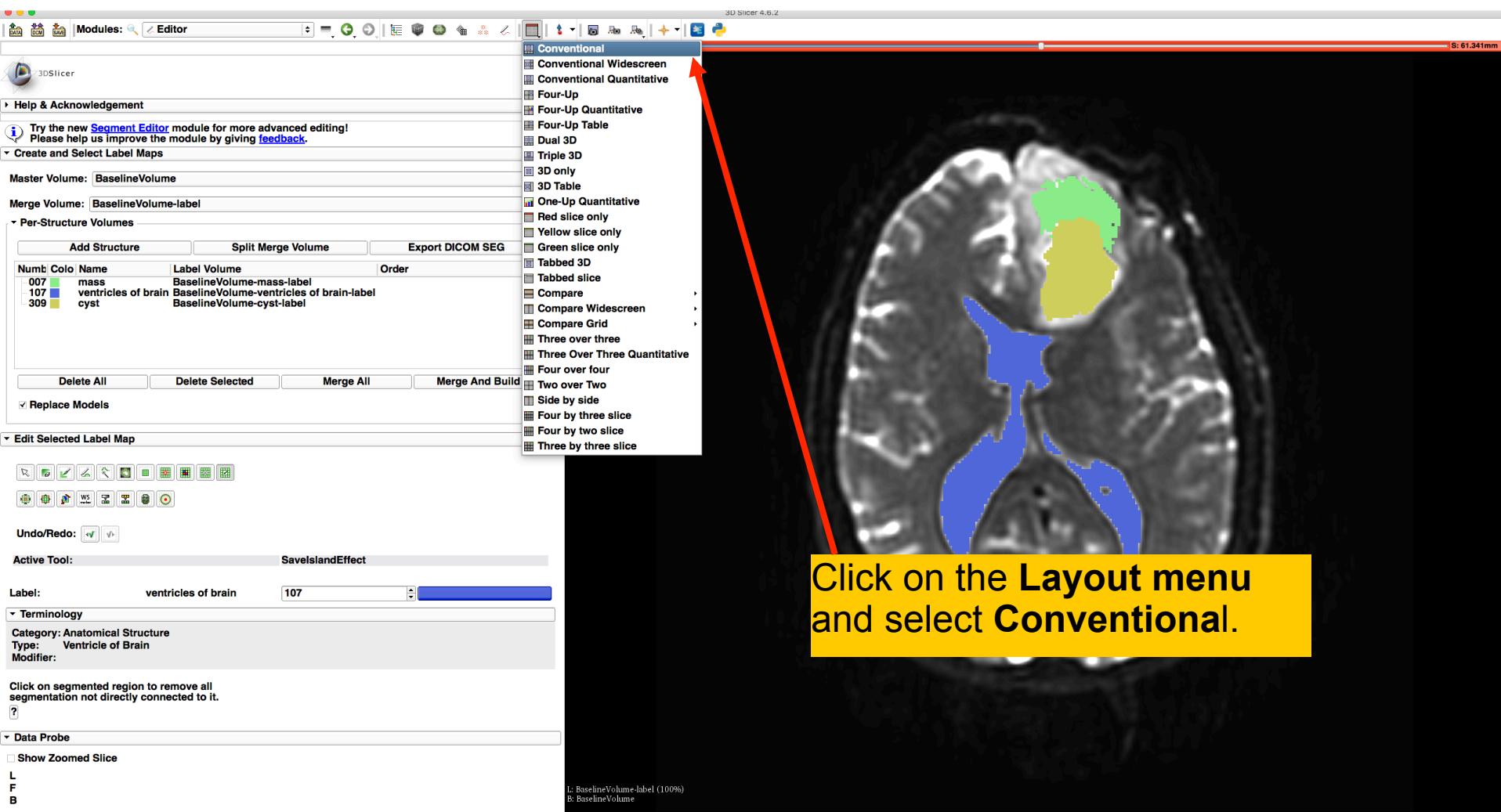
# Ventricles Segmentation



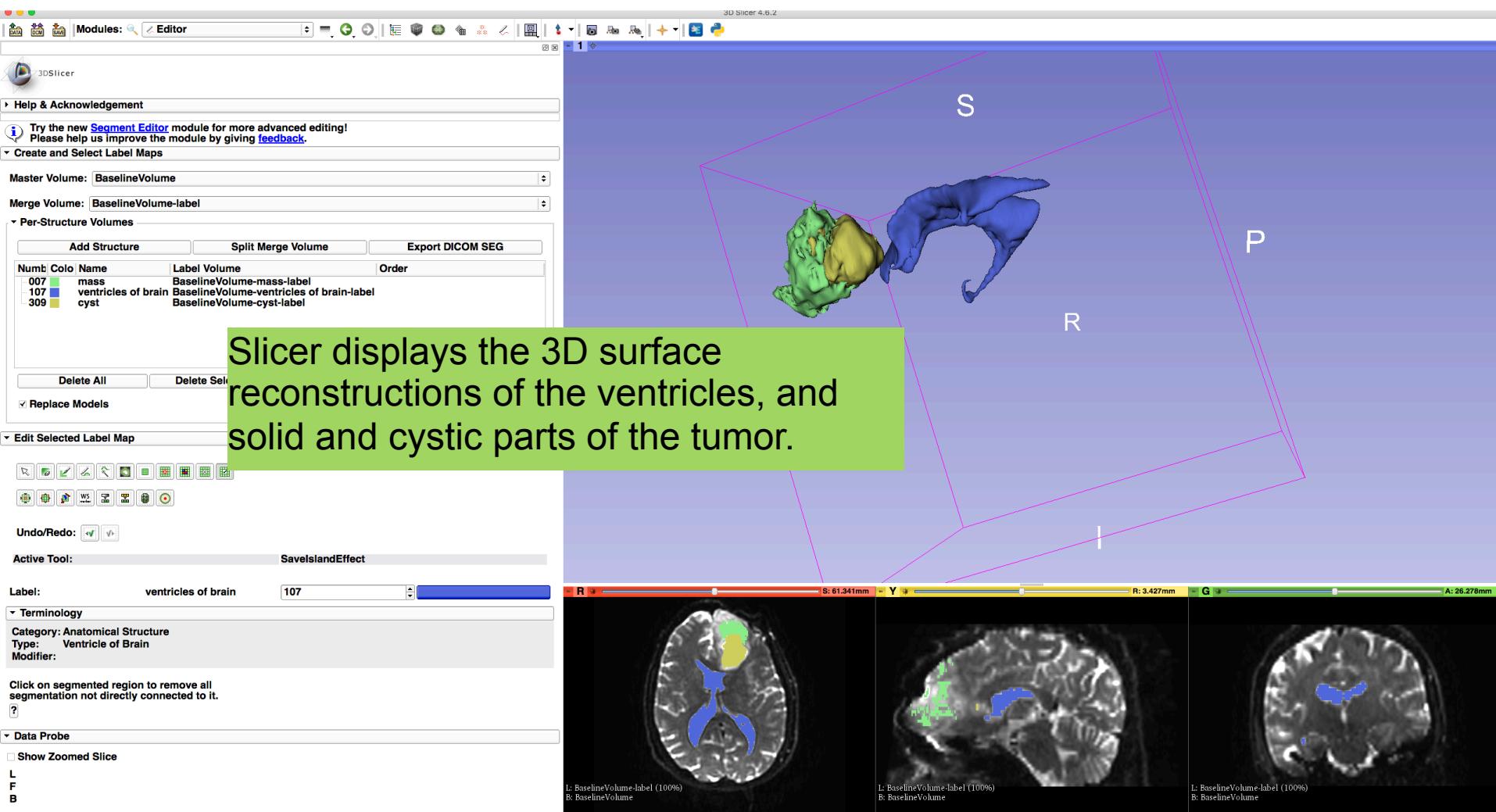
# Final Result of Segmentation



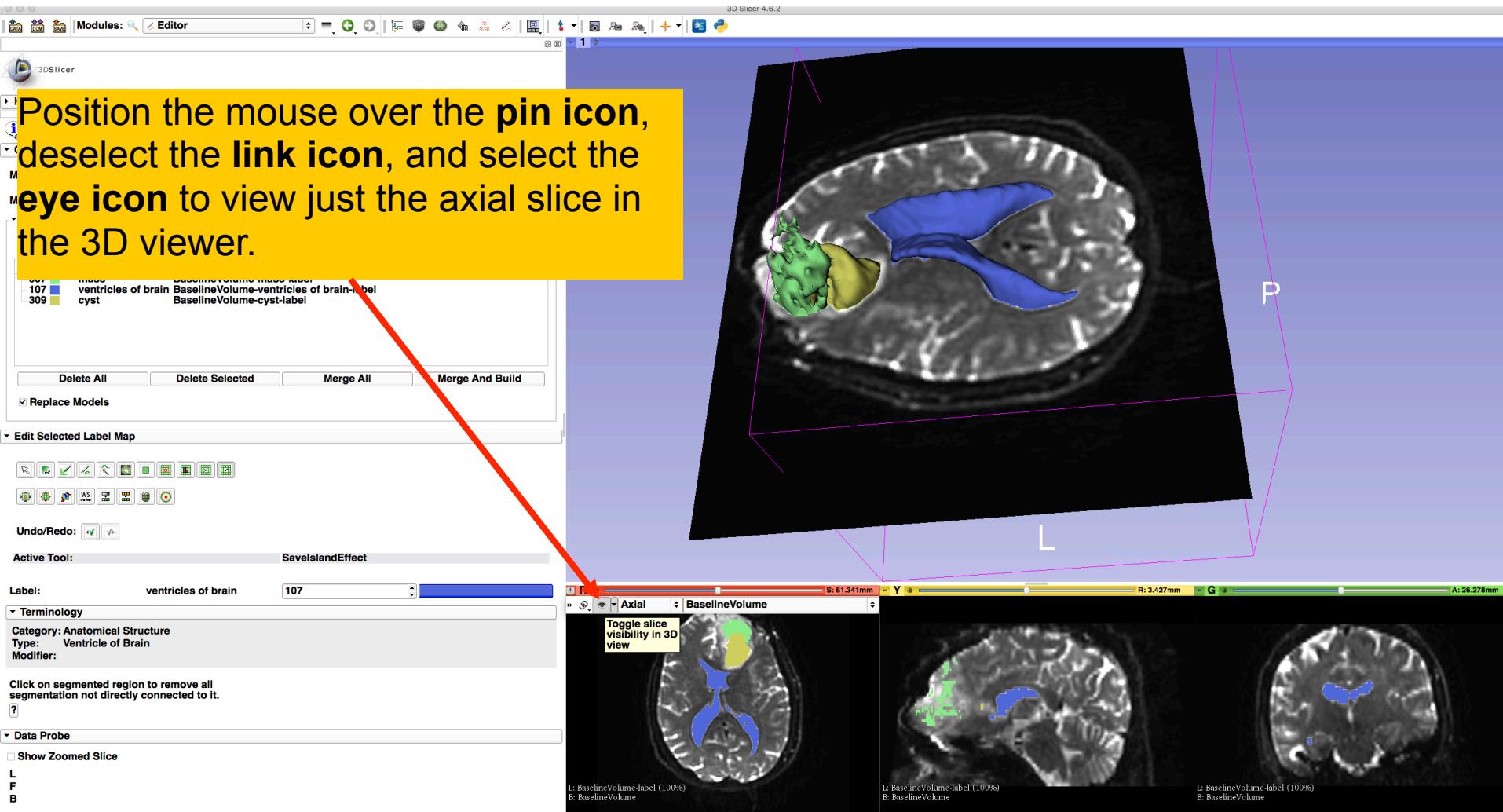
# Final Result of Segmentation



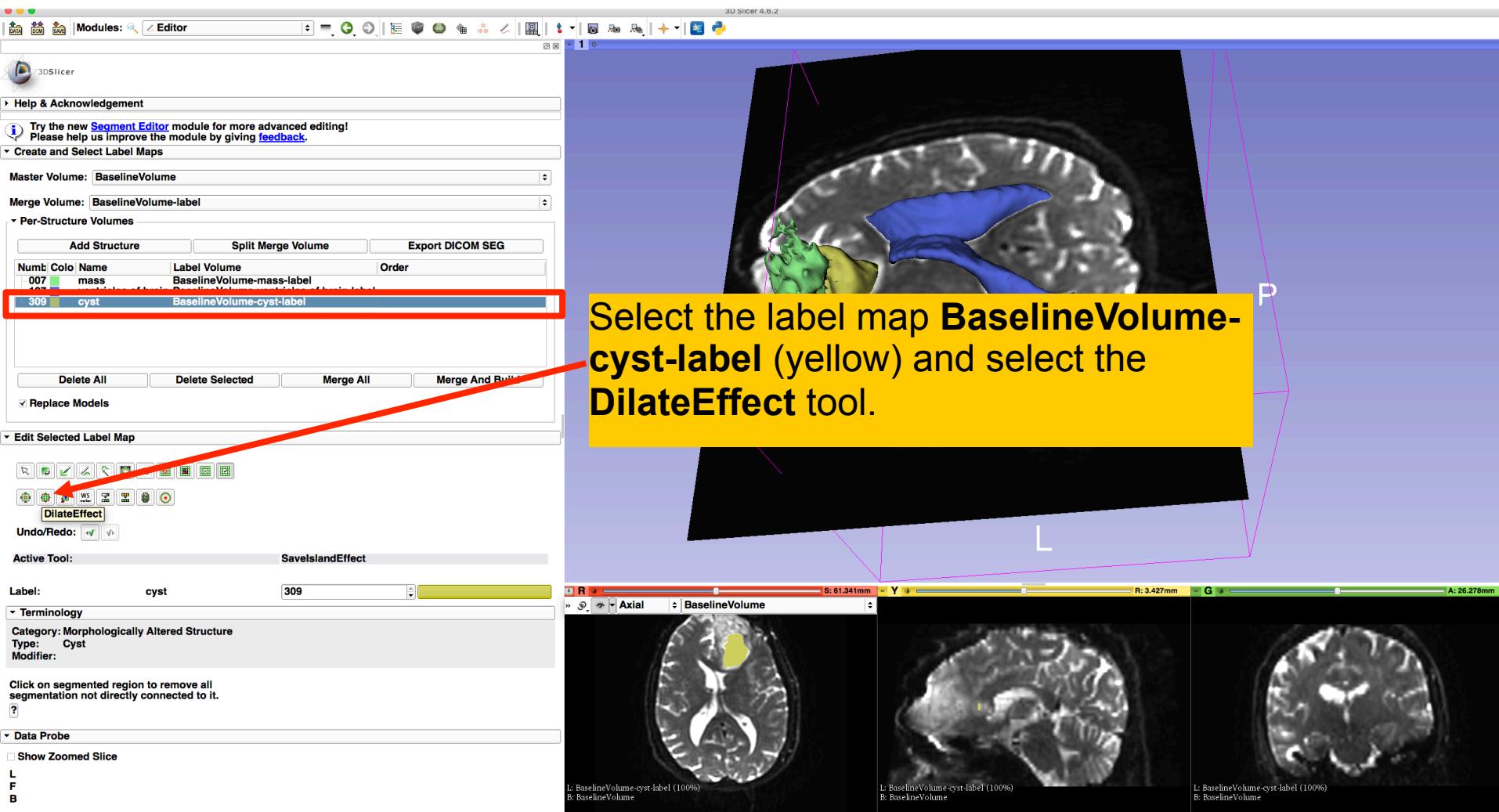
# Final Result of Segmentation



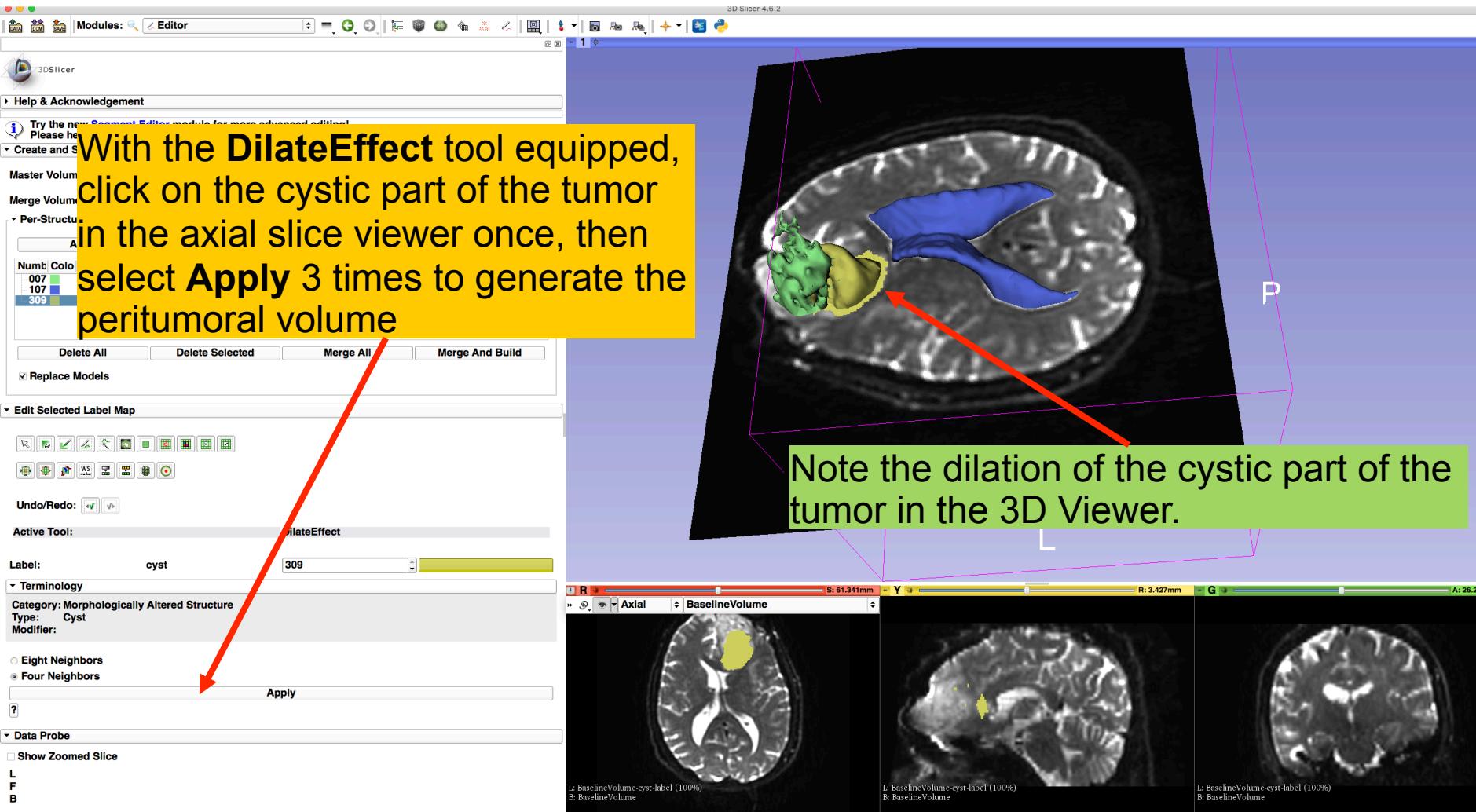
# Definition of peri-tumoral volume

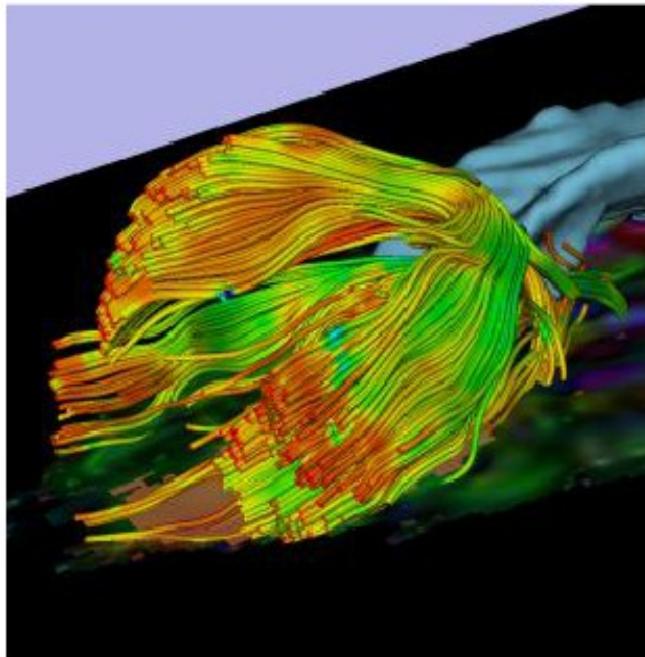


# Definition of peri-tumoral volume



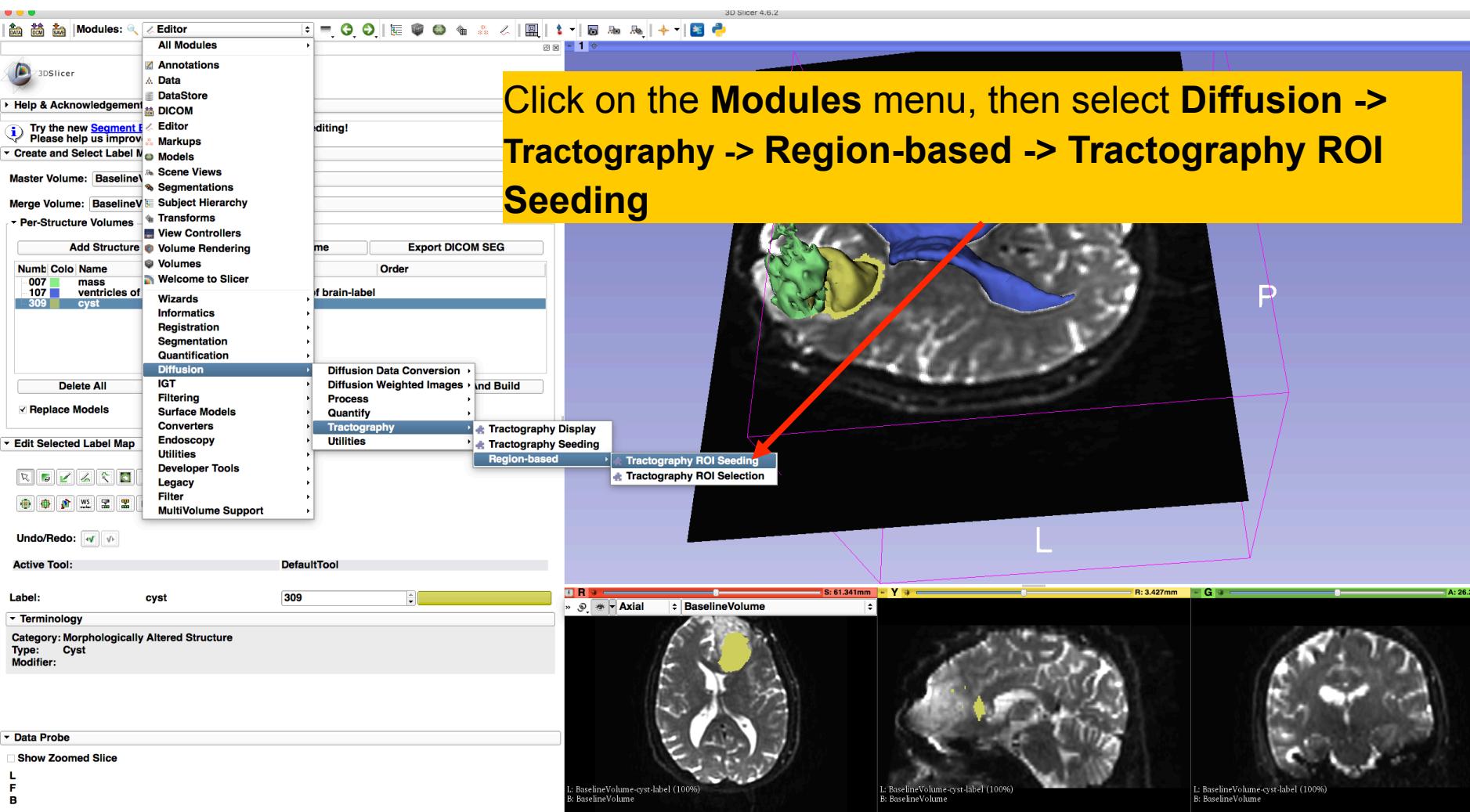
# Definition of peri-tumoral volume



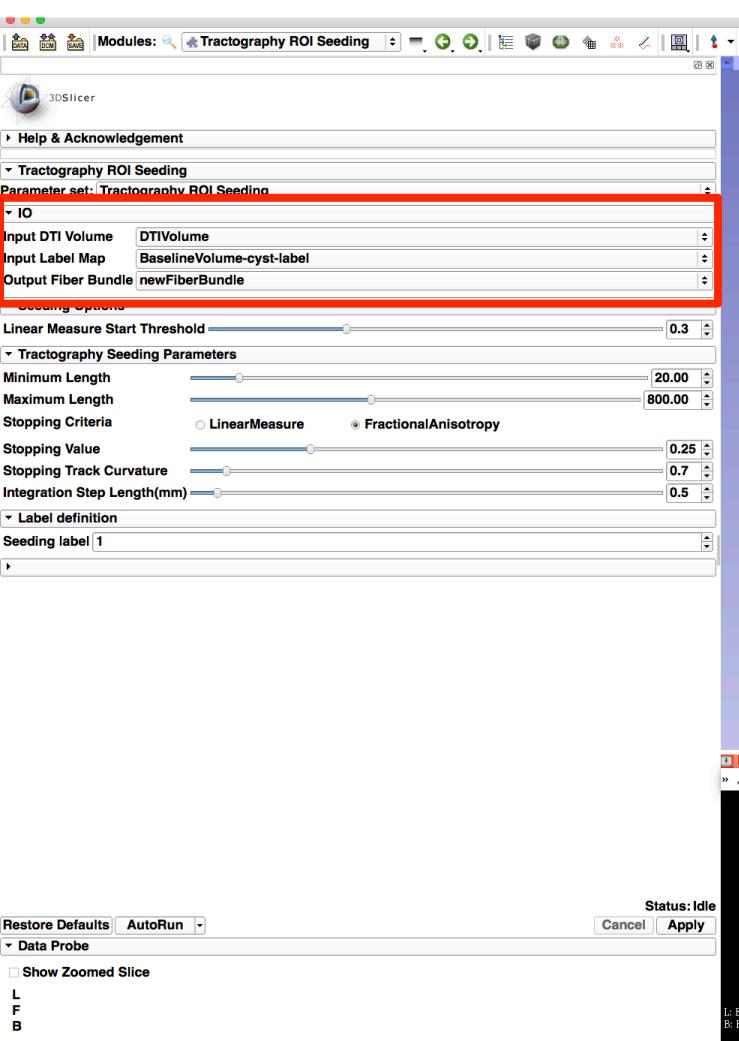


## Part 2: Tractography exploration of peri- tumoral white matter fibers

# Tractography LabelMap Seeding

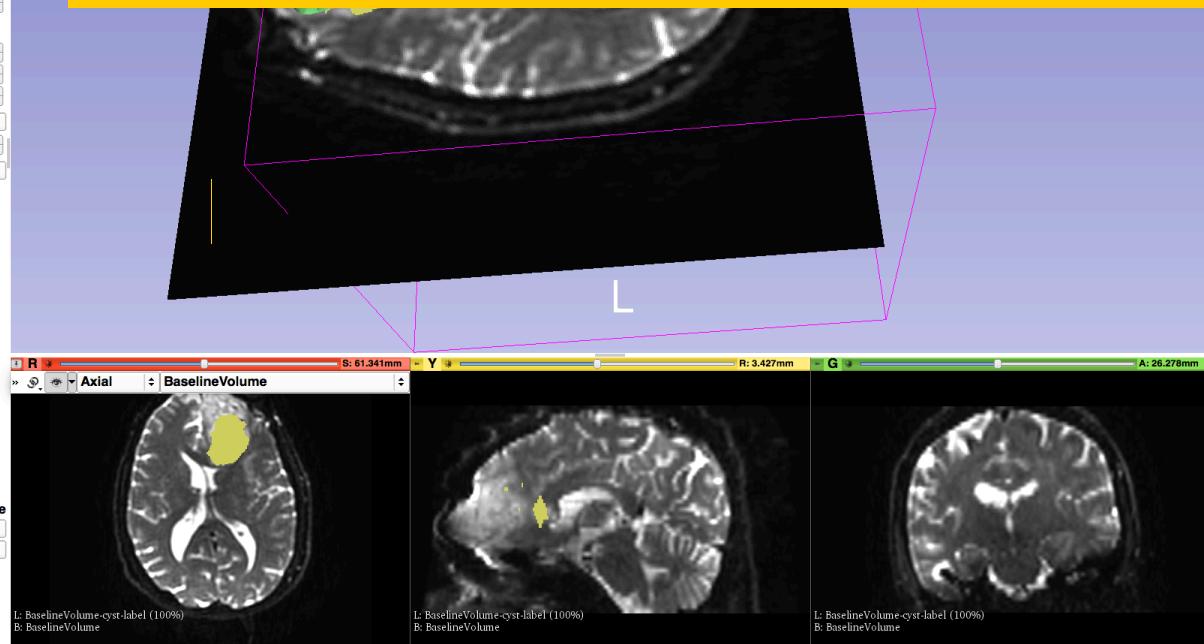


# Tractography LabelMap Seeding



Go to I/O and set the following values:

- Input DTI Volume:** DTIVolume
- Input Label Map:** BaselineVolume-cyst-label
- Output Fiber Bundle:** Create and rename newFiberBundle



# Tractography LabelMap Seeding

3D Slicer 4.6.2

Modules: Tractography ROI Seeding

Help & Acknowledgement

Tractography ROI Seeding

Parameter set: Tractography ROI Seeding

IO

Input DTI Volume: DTIVolume

Input Label Map: BaselineVolume-cyst-label

Output Fiber Bundle: newFiberBundle

Seeding Options

Linear Measure Start Threshold: 0.3

Tractography Seeding Parameters

Minimum Length: 20.00

Maximum Length: 800.00

Stopping Criteria: FractionalAnisotropy

Stopping Value: 0.15

Stopping Track Curvature: 0.7

Integration Step Length(mm): 0.5

Label definition

Seeding label: 309

Use Index Space

Random Grid

Restore Defaults AutoRun

Data Probe

Show Zoomed Slice L F B

Cancel Apply

Status: Idle

3D Slicer 4.6.2

Scroll down and set the following values:

- Check **Use Index Space**

P

L

R

G

Y

S

A

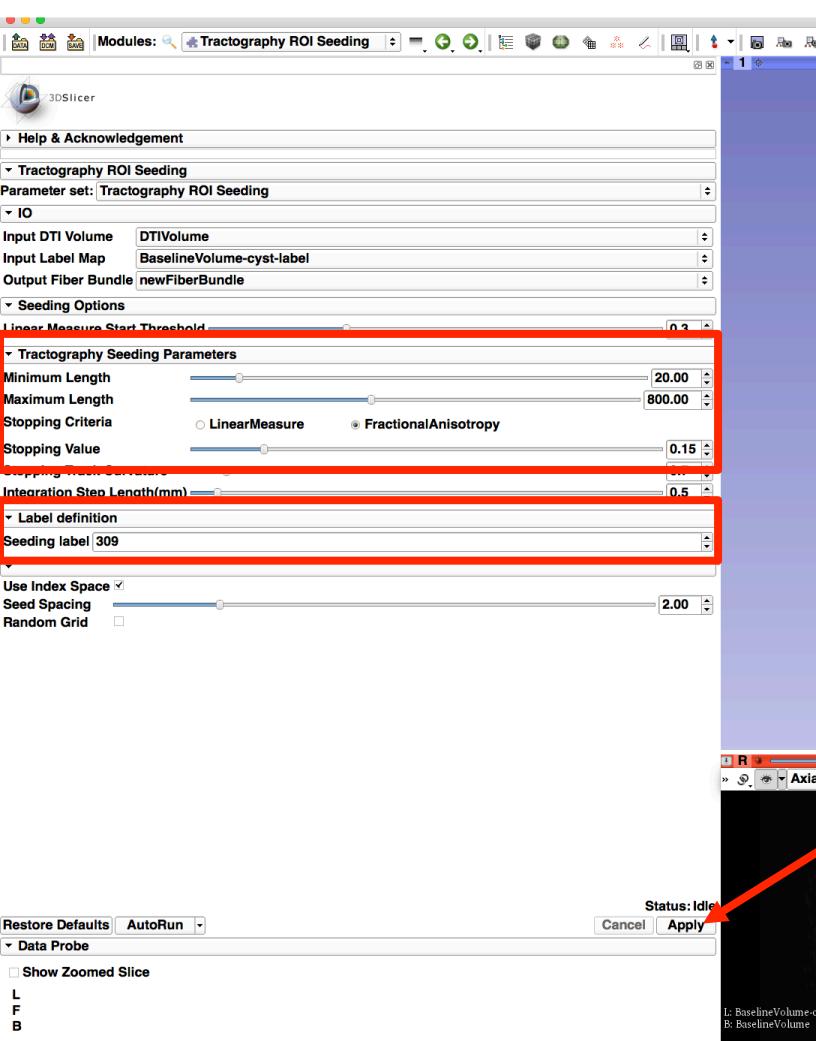
BaselineVolume

L: BaselineVolume-cyst-label (100%)  
R: BaselineVolume

L: BaselineVolume-cyst-label (100%)  
R: BaselineVolume

L: BaselineVolume-cyst-label (100%)  
R: BaselineVolume

# Tractography LabelMap Seeding



Scroll down to **Tractography Seeding Parameters** and set the following values:

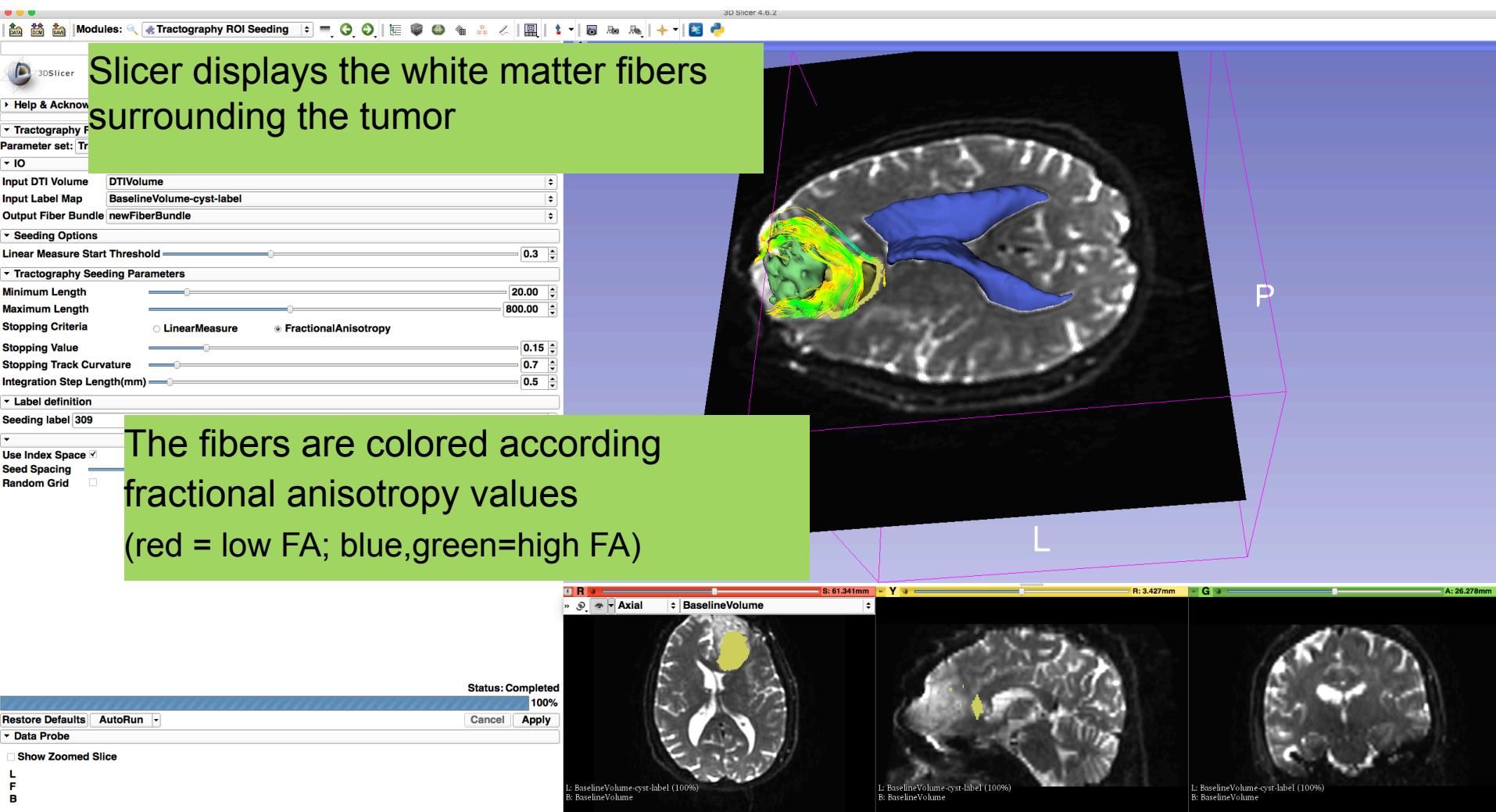
- Set **Stopping Criteria** to **FractionalAnisotropy**
- Set **Stopping Value** to **0.15**

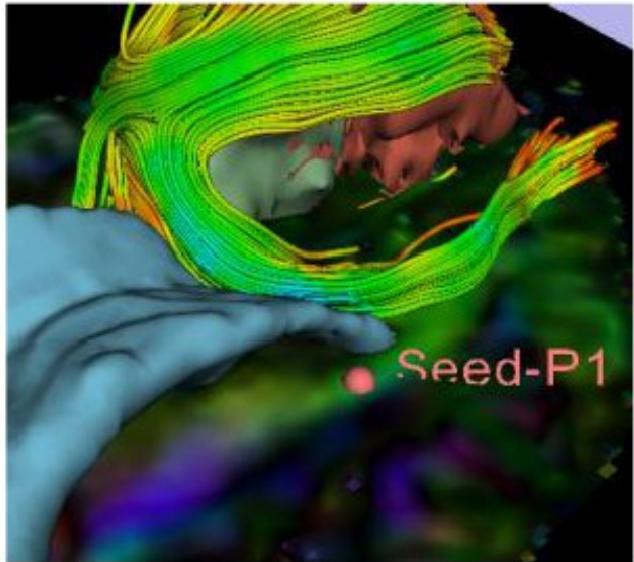
Scroll down to **Label Definition** and set the following values:

- Set **Seeding Label** to **309 (cyst)**

Click on **Apply**

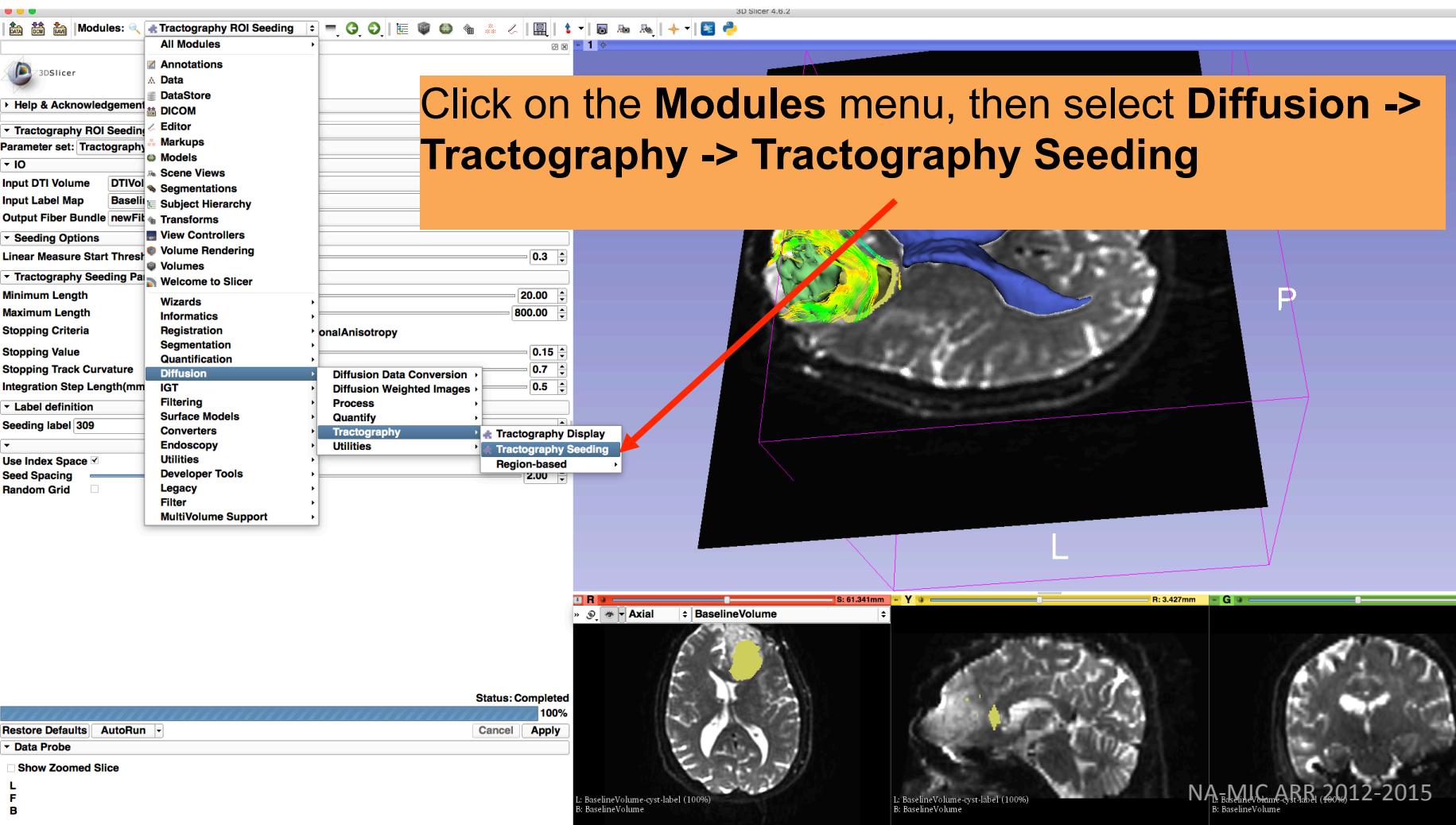
# Tractography LabelMap Seeding



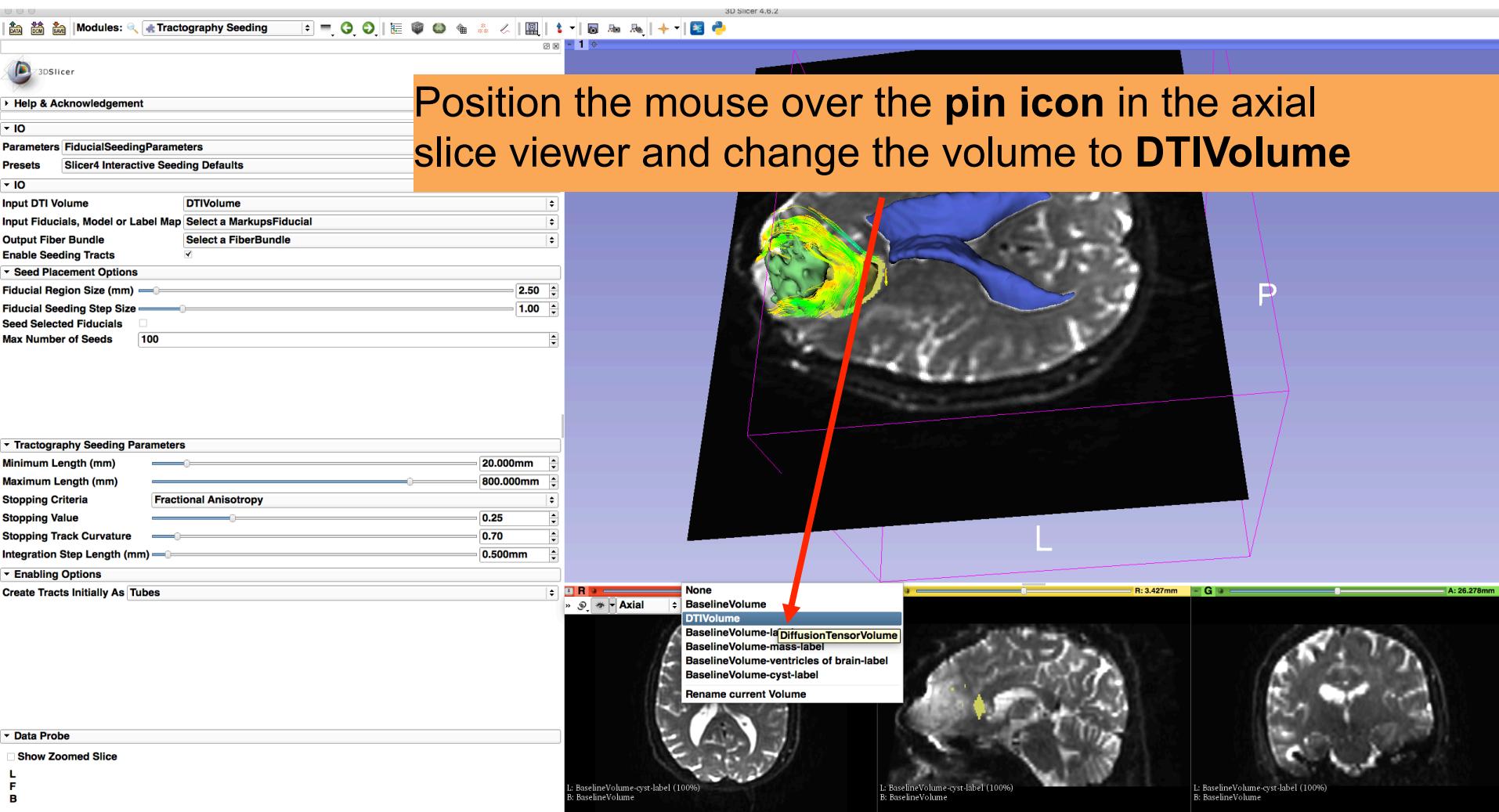


## Part 4: Tractography exploration of the ipsilateral and contralateral side

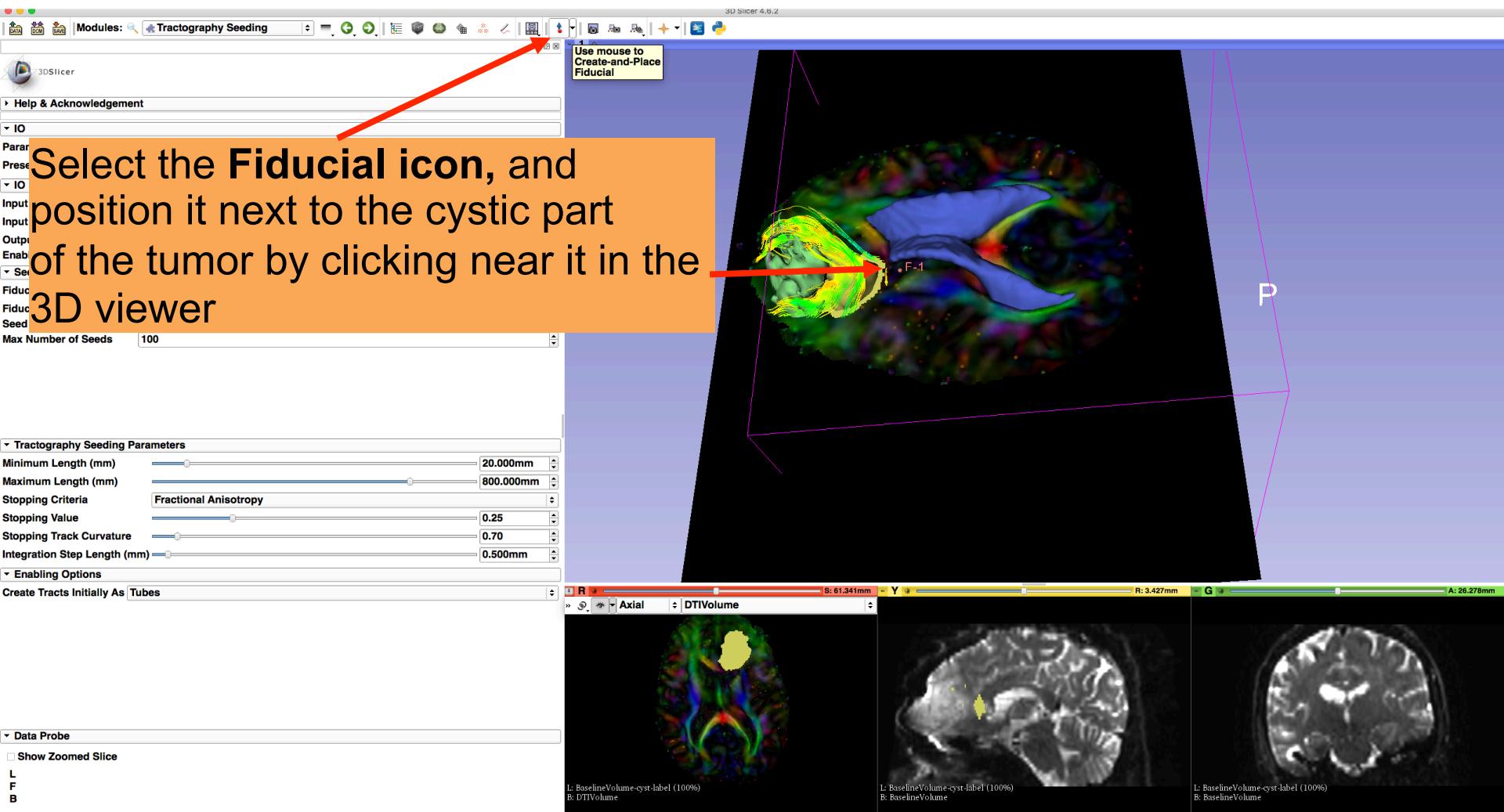
# Tractography on-the-fly



# Tractography on-the-fly



# Tractography on-the-fly



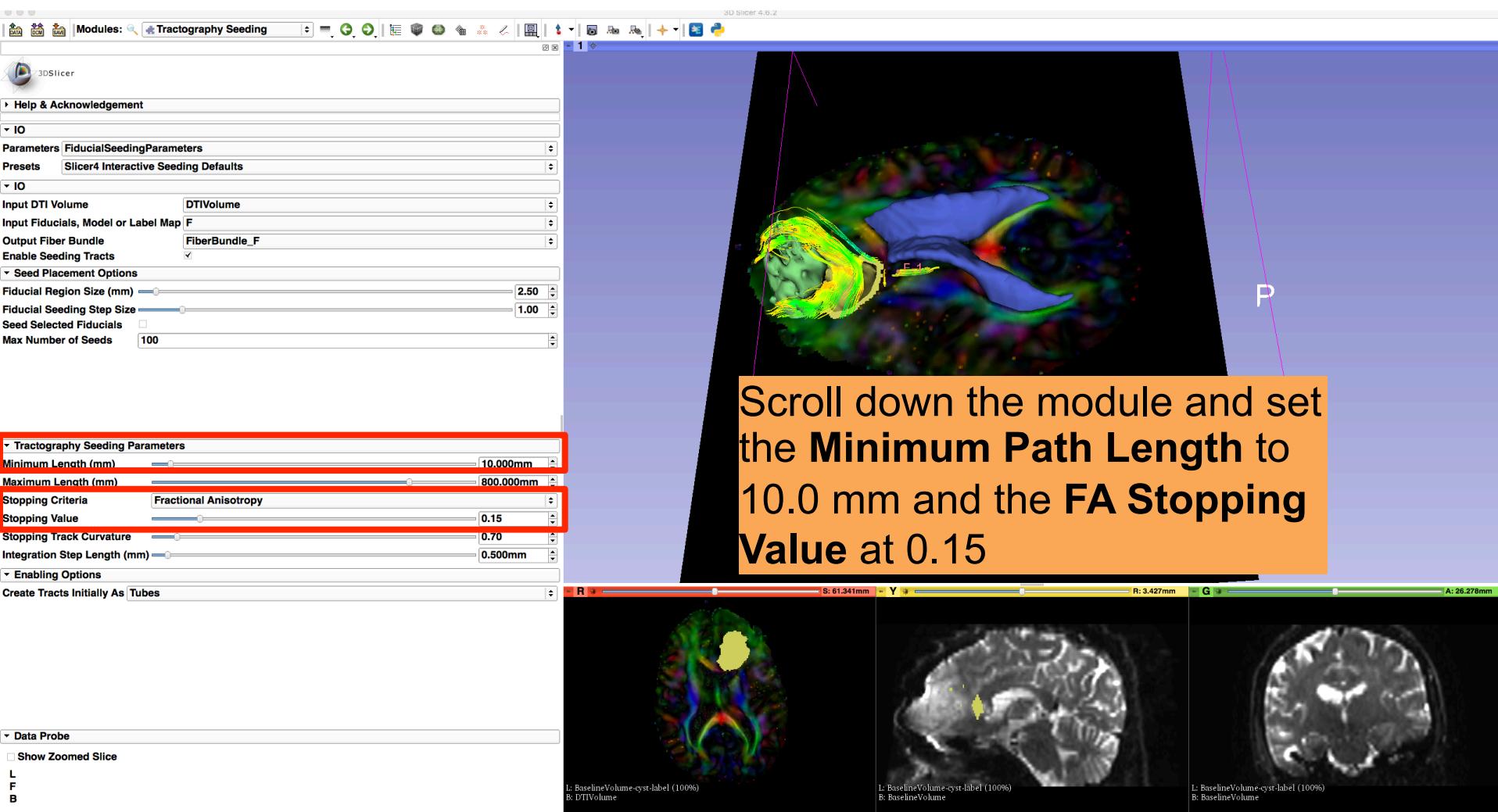
# Tractography on-the-fly

The screenshot shows the 3D Slicer interface version 4.6.2. On the left, the 'Tractography Seeding' module panel is open, displaying various parameters and settings. A red box highlights the 'IO' section where three fields are set: 'Input DTI Volume' to 'DTIVolume', 'Input Fiducials, Model or Label Map' to 'F', and 'Output Fiber Bundle' to 'FiberBundle\_F'. Below this, under 'Tractography Seeding Parameters', there are sliders for 'Minimum Length (mm)', 'Maximum Length (mm)', 'Stopping Criteria' (set to 'Fractional Anisotropy'), 'Stopping Value', 'Stopping Track Curvature', and 'Integration Step Length (mm)'. Under 'Enabling Options', 'Create Tracts Initially As' is set to 'Tubes'. At the bottom of the panel, there's a 'Data Probe' section with checkboxes for 'Show Zoomed Slice' and buttons for 'L', 'F', and 'B'. The main window displays a 3D brain volume with a multi-colored fiber bundle tractography overlay. A pink coordinate system is shown with the 'P' axis pointing upwards. In the bottom right corner of the main window, there's a progress bar with the value 'A: 26.278mm'. Overlaid on the bottom left of the main window is an orange box containing the following text:

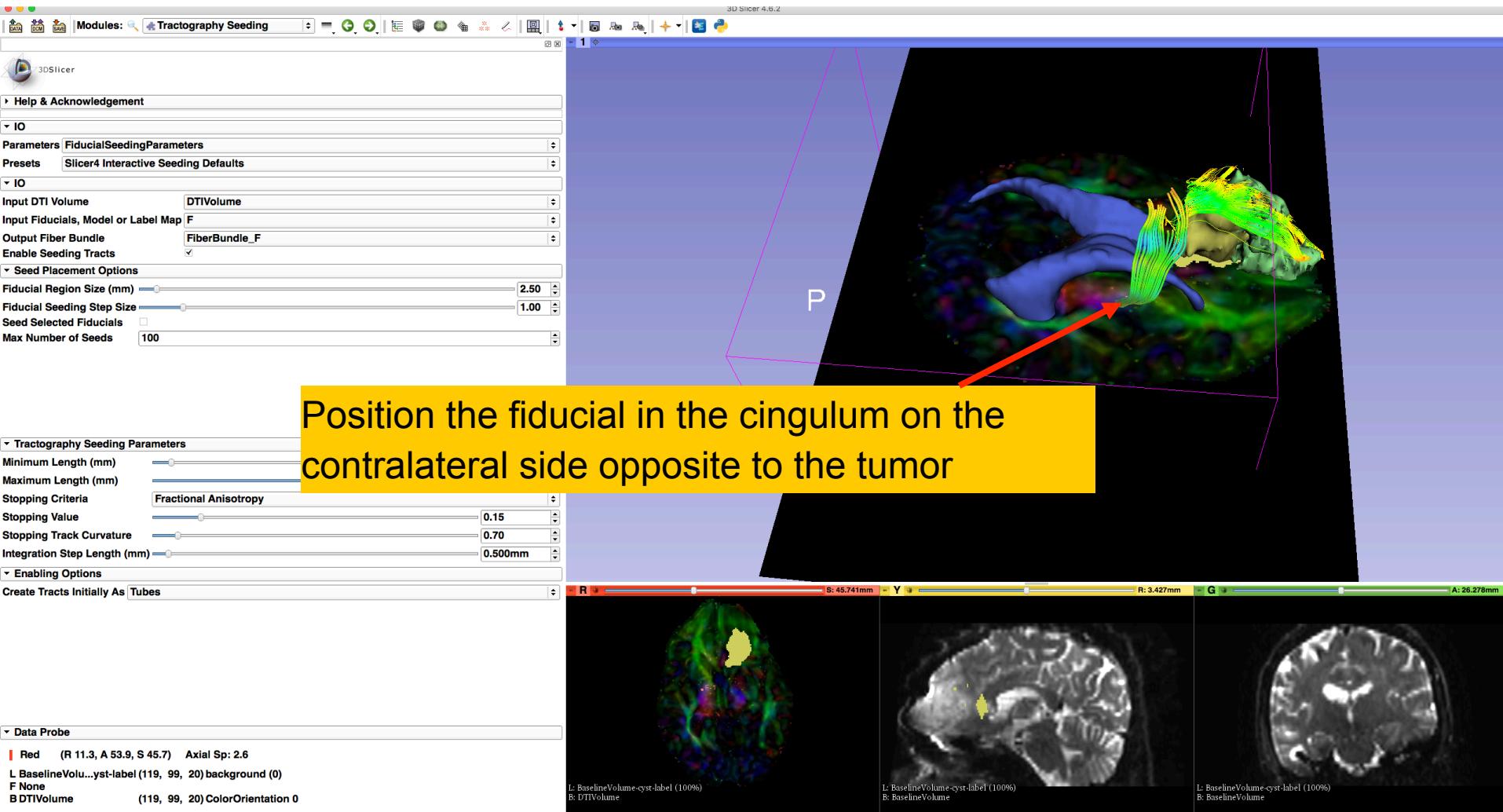
Set Input DTI Volume to **DTIVolume**  
Set Fiducial List or Model to **F**  
Set Output Fiber Bundle to **Create new Fiber Bundle**

Below the main window, there are three smaller grayscale brain slices: a coronal slice showing a yellow lesion, a sagittal slice showing a yellow lesion, and a transverse slice showing a yellow lesion. Each slice has text at the bottom indicating it is a 'BaselineVolume-cyst-label' image.

# Tractography on-the-fly

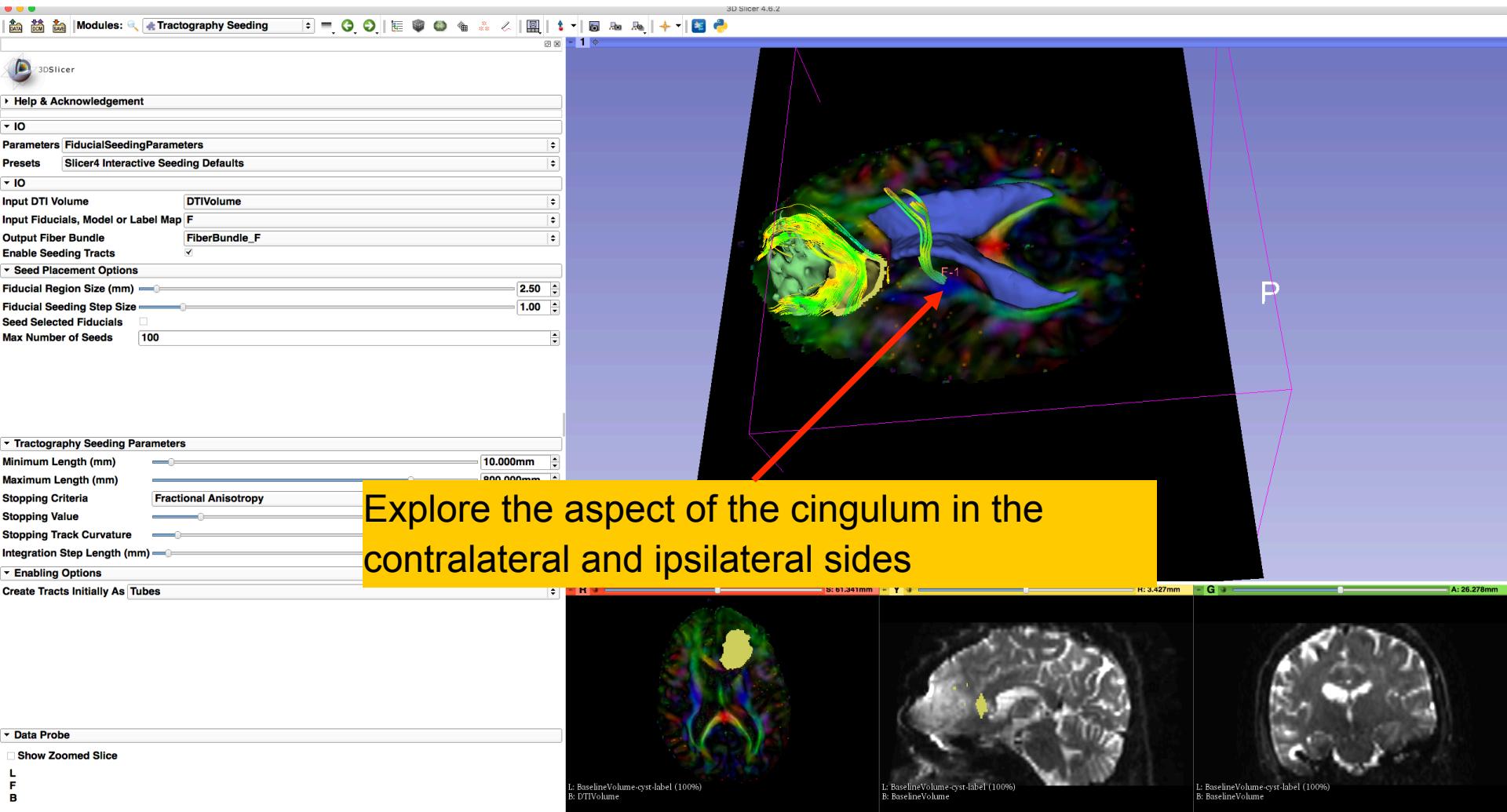


# Tractography on-the-fly



Position the fiducial in the cingulum on the contralateral side opposite to the tumor

# Tractography on-the-fly



# Conclusion

- Fully integrated pipeline for semi-automated tumor segmentation and white matter tract reconstruction
- 3D interactive exploration of the white matter tracts surrounding a tumor (peritumoral tracts) for neurosurgical planning

# 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  
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