



# Exploring Peritumoral White Matter Fibers for Neurosurgical Planning

Sonia Pujol, Ph.D.

Ron Kikinis, M.D.

Surgical Planning Laboratory

Harvard University

# Clinical Goal

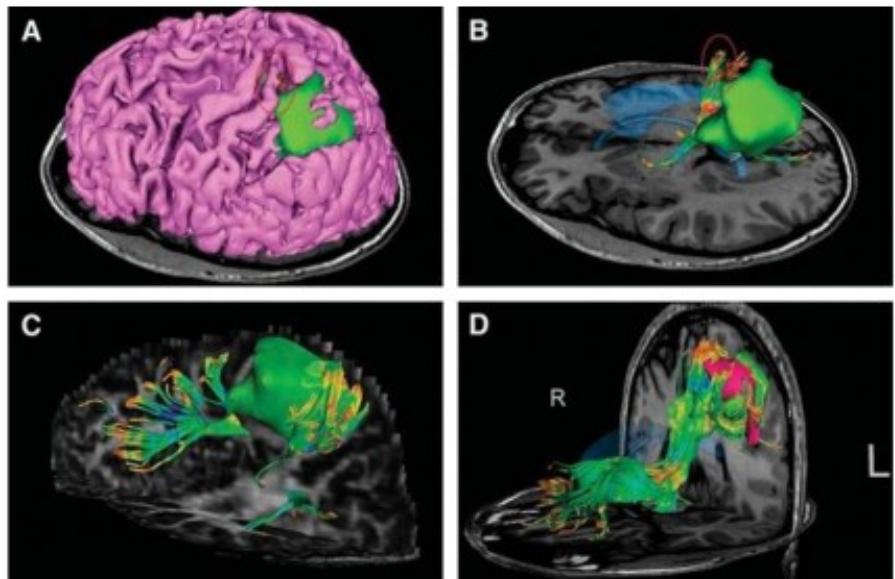
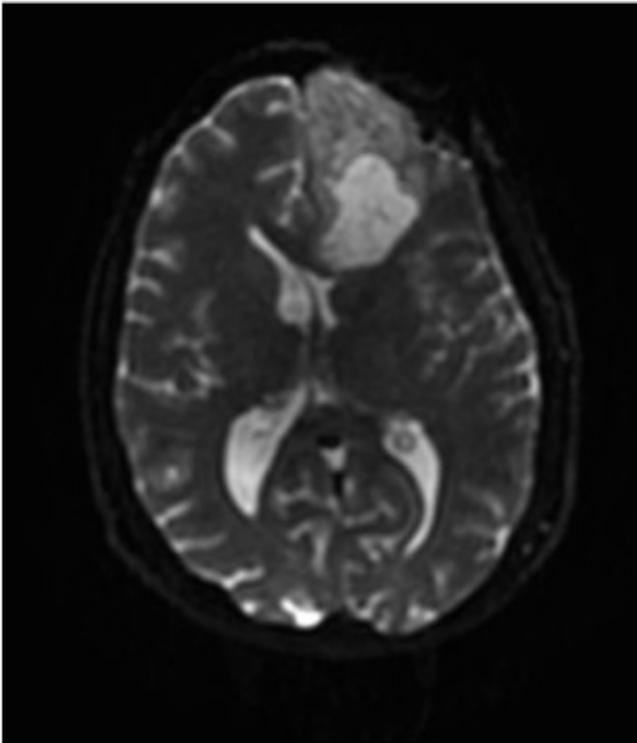


Image Courtesy of Dr. Alexandra Golby, Brigham and Women's Hospital, Boston, MA..

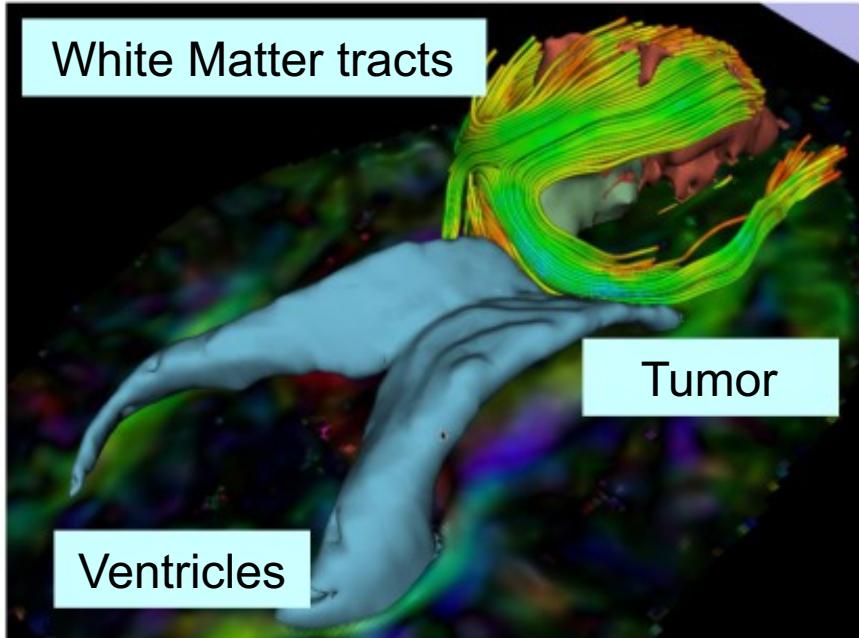
Diffusion Tensor Imaging (DTI) Tractography has the potential to bring valuable spatial information on tumor infiltration and tract displacement for neurosurgical planning of tumor resection.

# Clinical Case

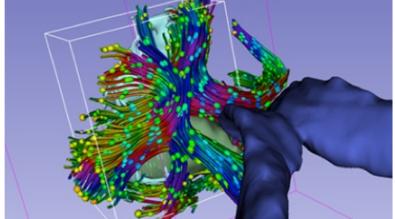


- 35 year-old male diagnosed with Glioblastoma multiform (GBM)
- Diffusion Weighted Imaging (DWI) acquisition for neurosurgical planning

# Clinical Goal



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



# Slicer DMRI

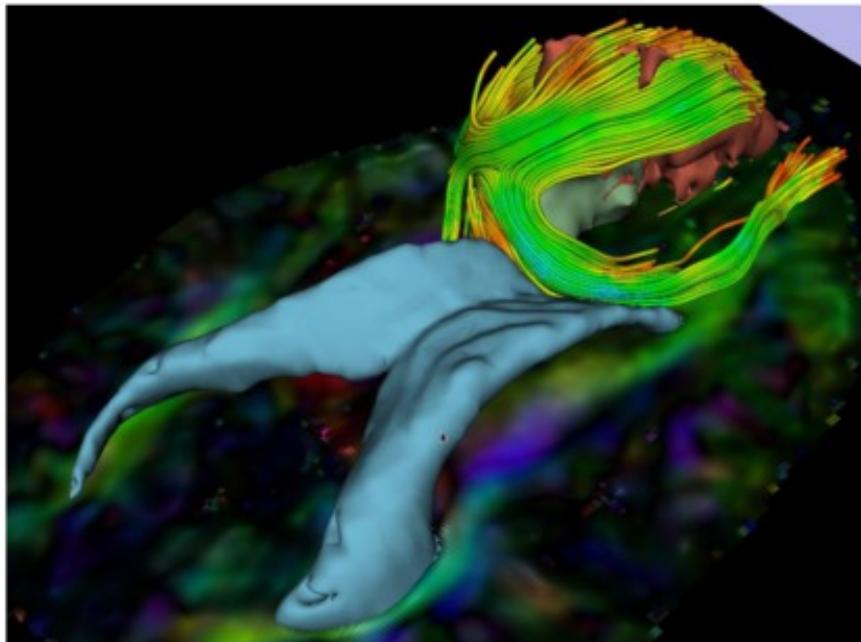
An open-source project to improve and extend diffusion magnetic resonance imaging software in 3D Slicer:

<http://dmri.slicer.org>

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

[http://dmri.slicer.org/docs/diffusion\\_mri\\_analysis](http://dmri.slicer.org/docs/diffusion_mri_analysis)

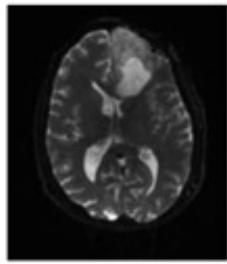
# Image Analysis Pipeline



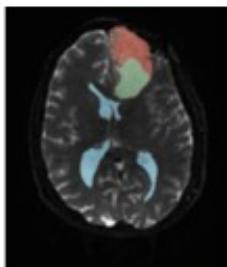
The image analysis pipeline described in this tutorial uses three different algorithms:

- 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.

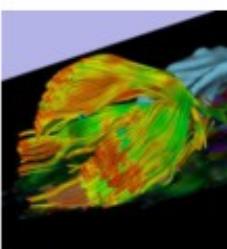
# Overview of the analysis pipeline



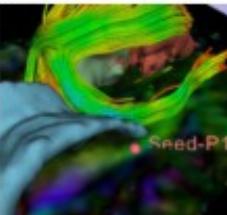
Part 1: Loading & Visualization of Diffusion Data



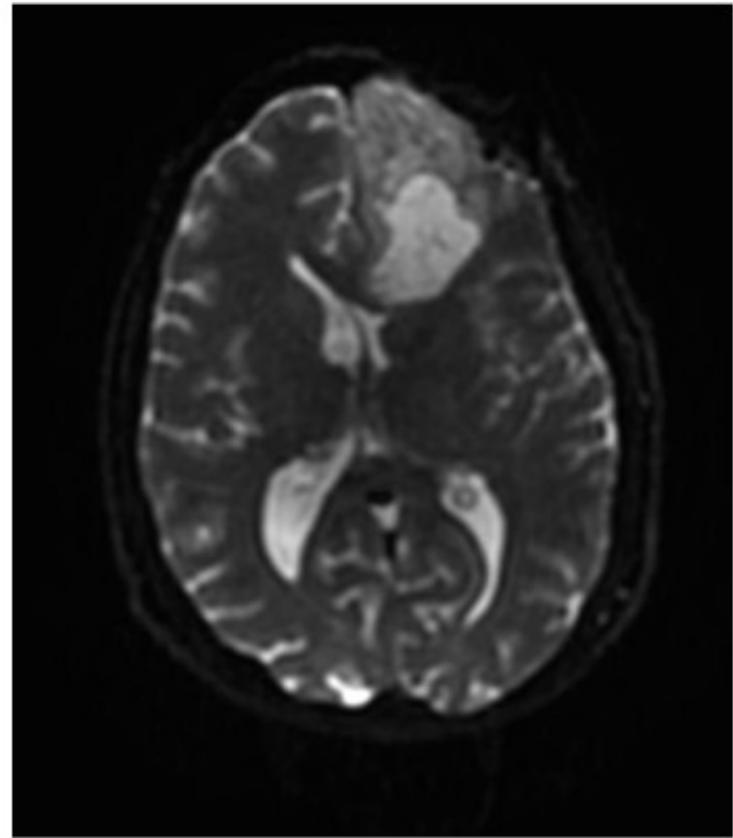
Part 2: Segmentation of lat. ventricles, and solid and cystic parts of the tumor



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

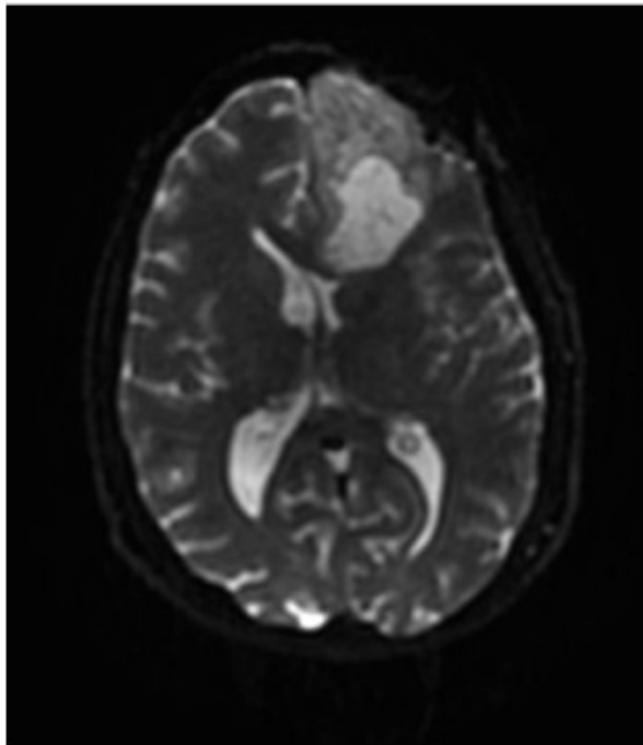


Part 4: Tractography exploration of the ipsilateral and contralateral side



# Part 1: Loading and Visualization of Diffusion Data

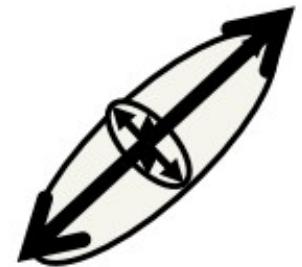
# Diffusion Tensor Imaging



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

(Stejskal and Tanner 1965, Basser 1994 )

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

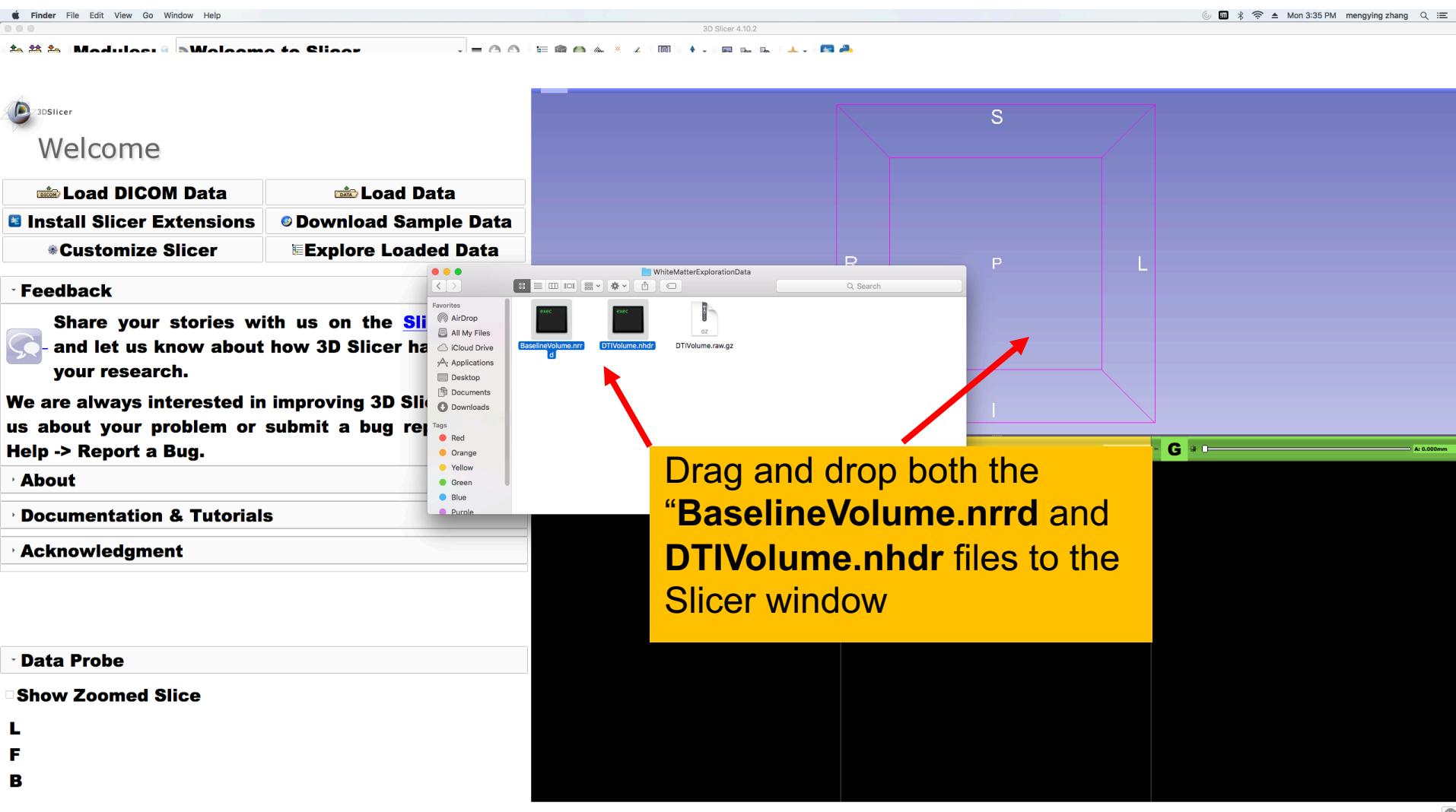


# Tutorial Data

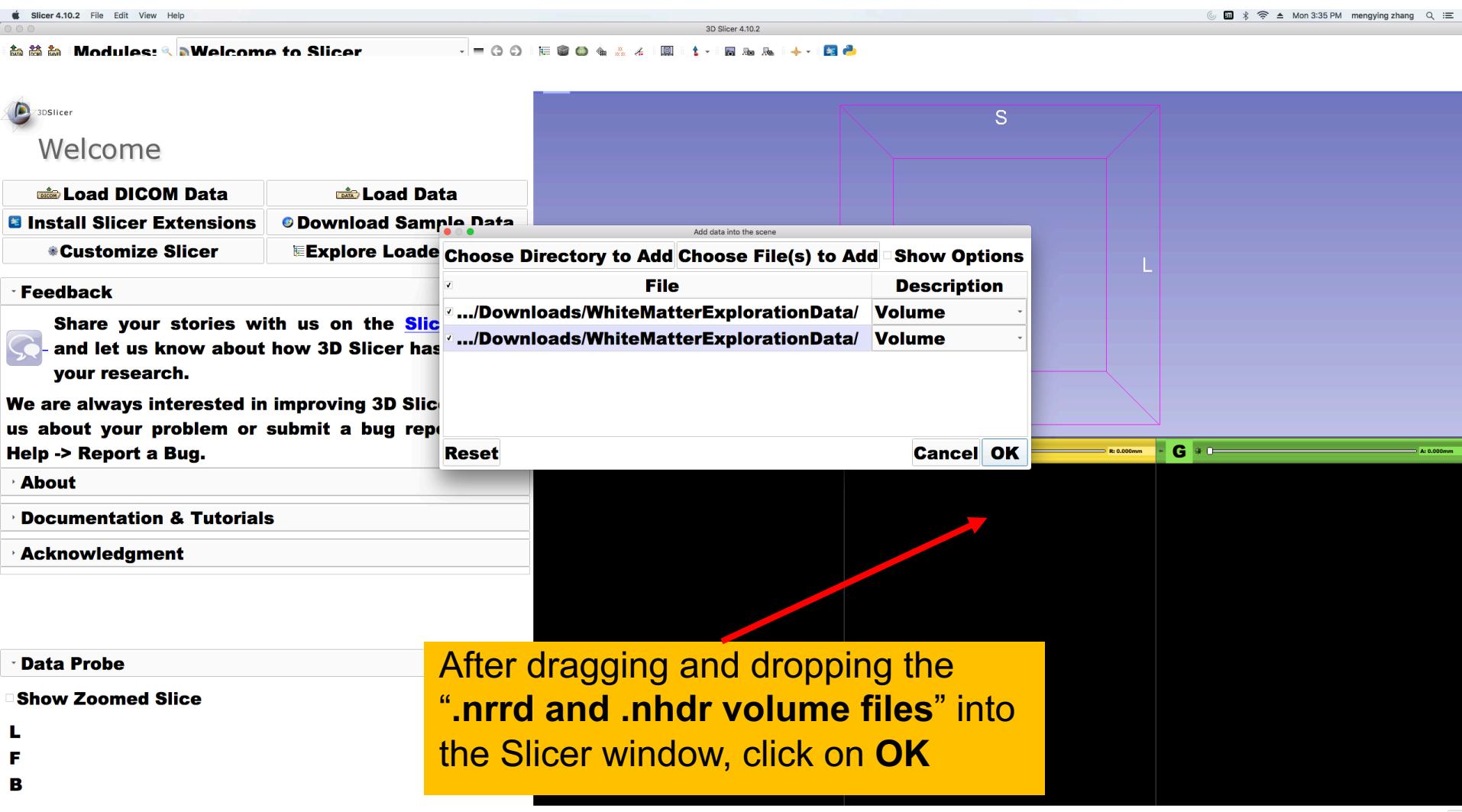
Please download sample data at

[https://www.slicer.org/slicerWiki/images/b  
/bb/WhiteMatterExplorationData.zip](https://www.slicer.org/slicerWiki/images/b/bb/WhiteMatterExplorationData.zip)

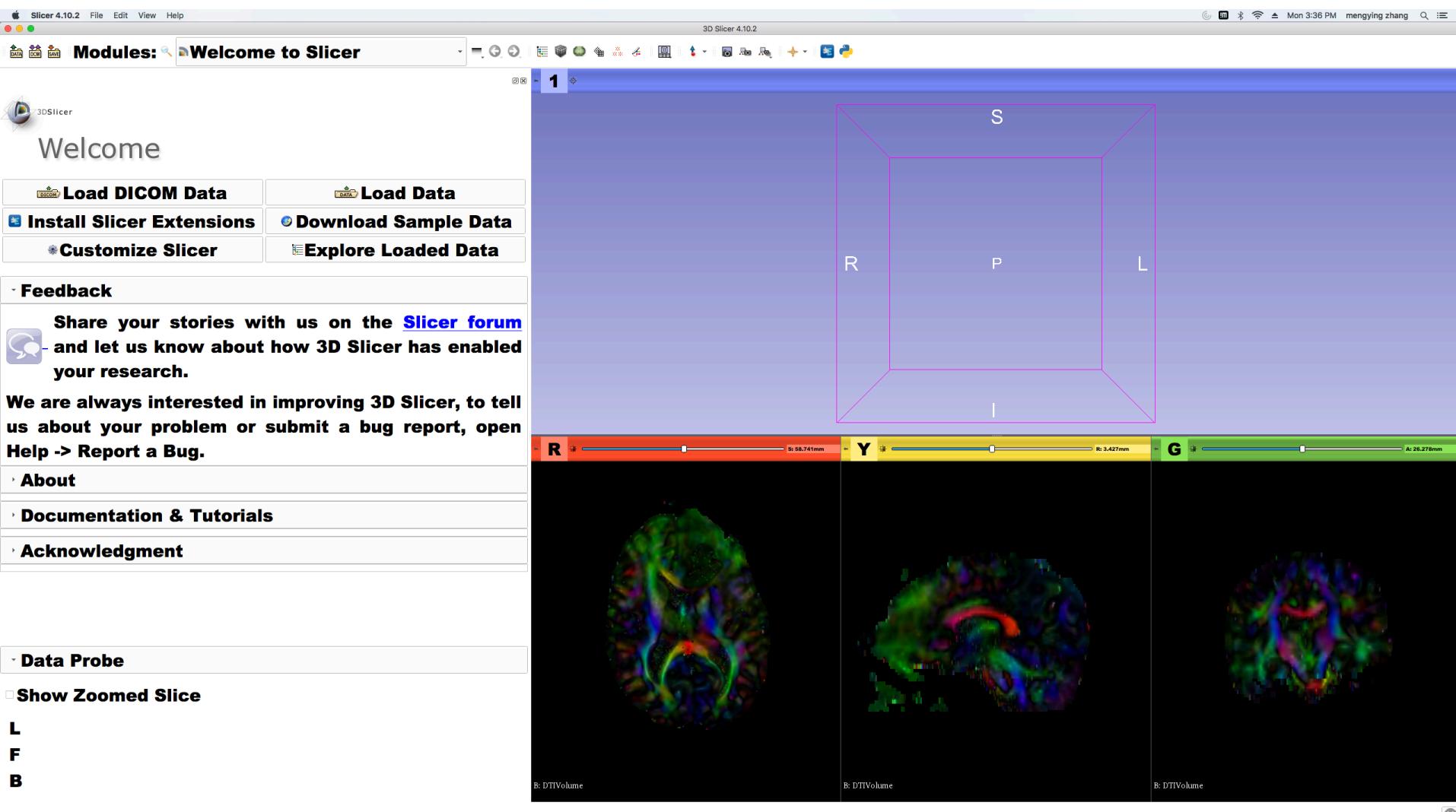
# Loading DTI and Baseline Data



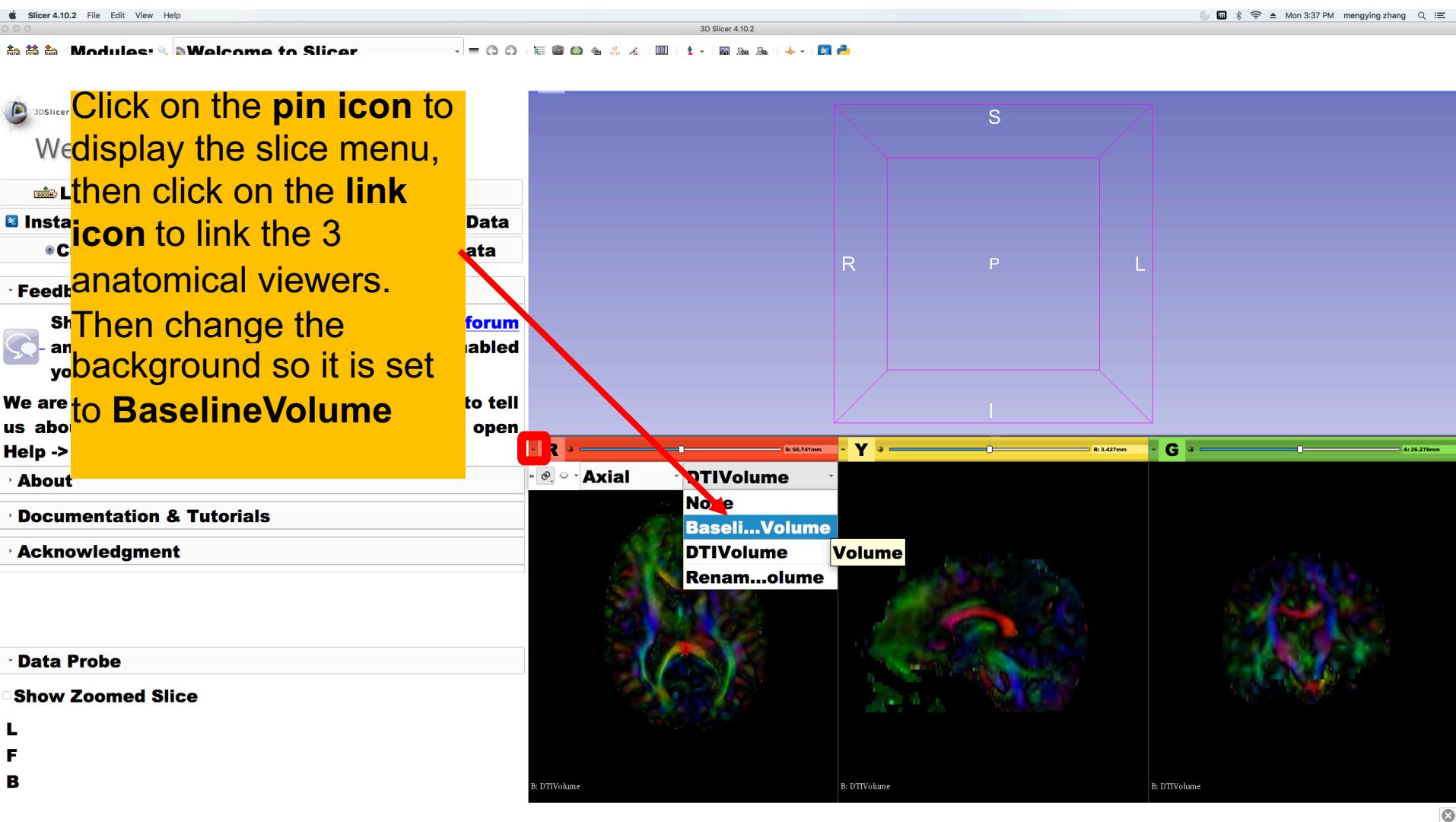
# Loading DTI and Baseline Data



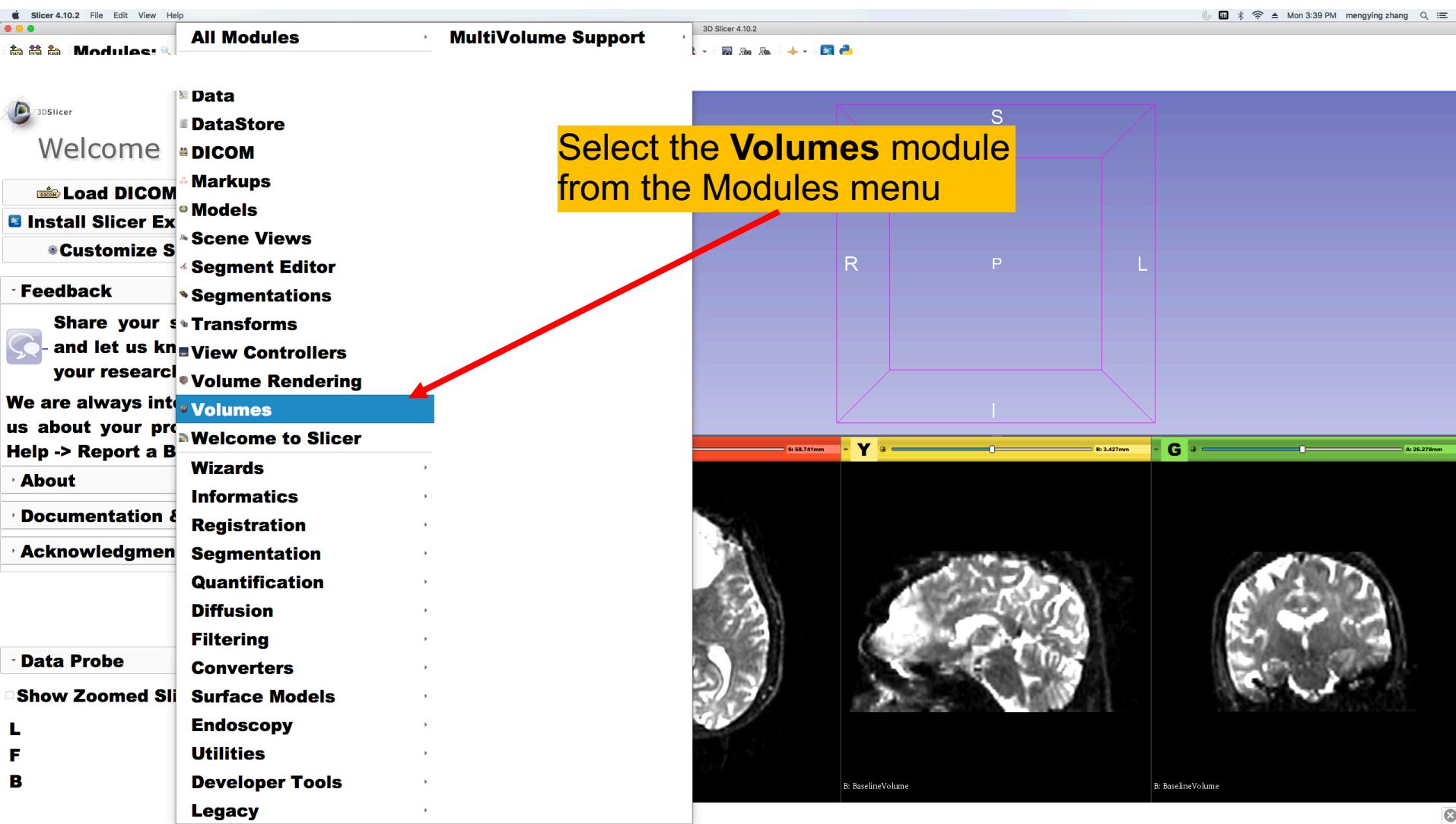
# Loading DTI and Baseline Data



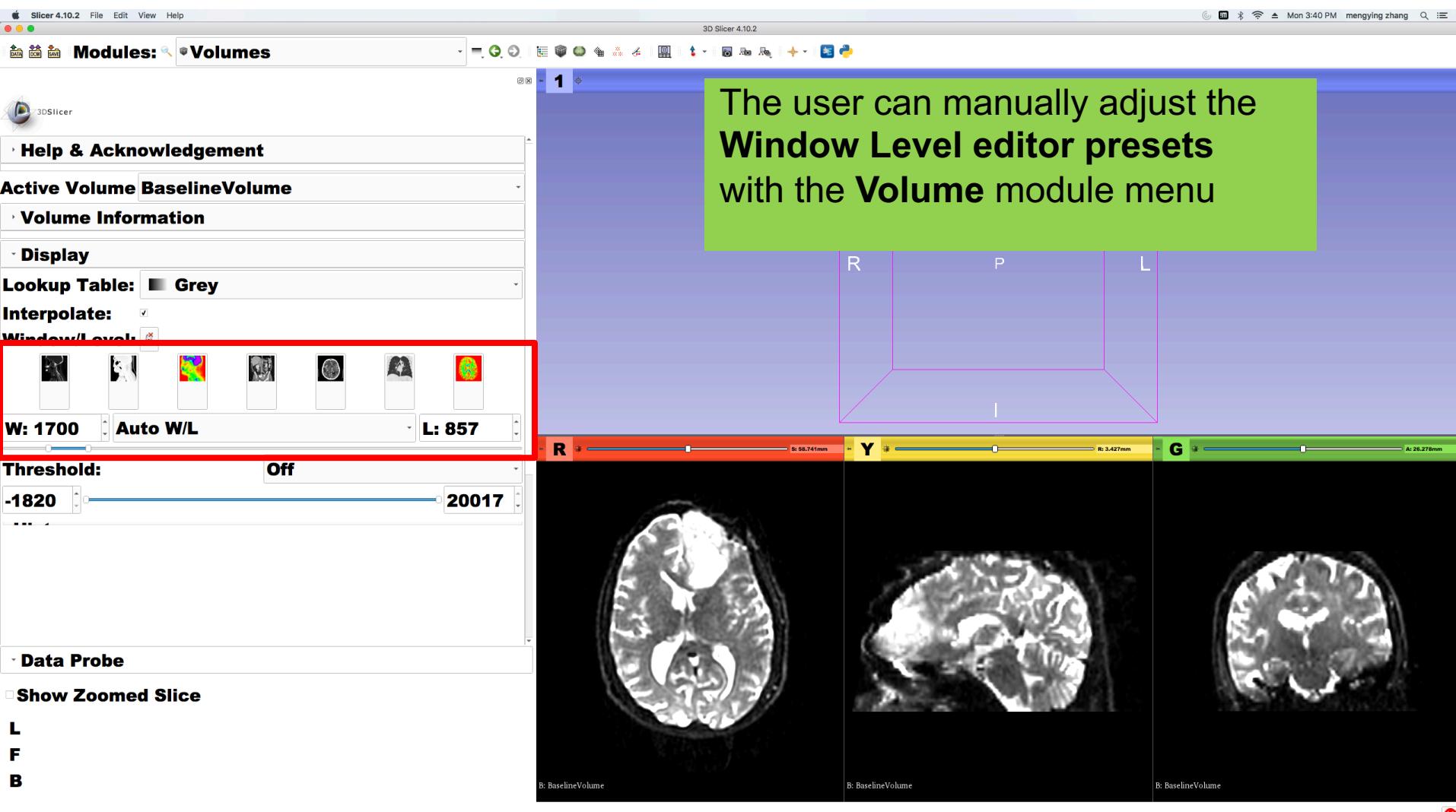
# Loading DTI and Baseline Data



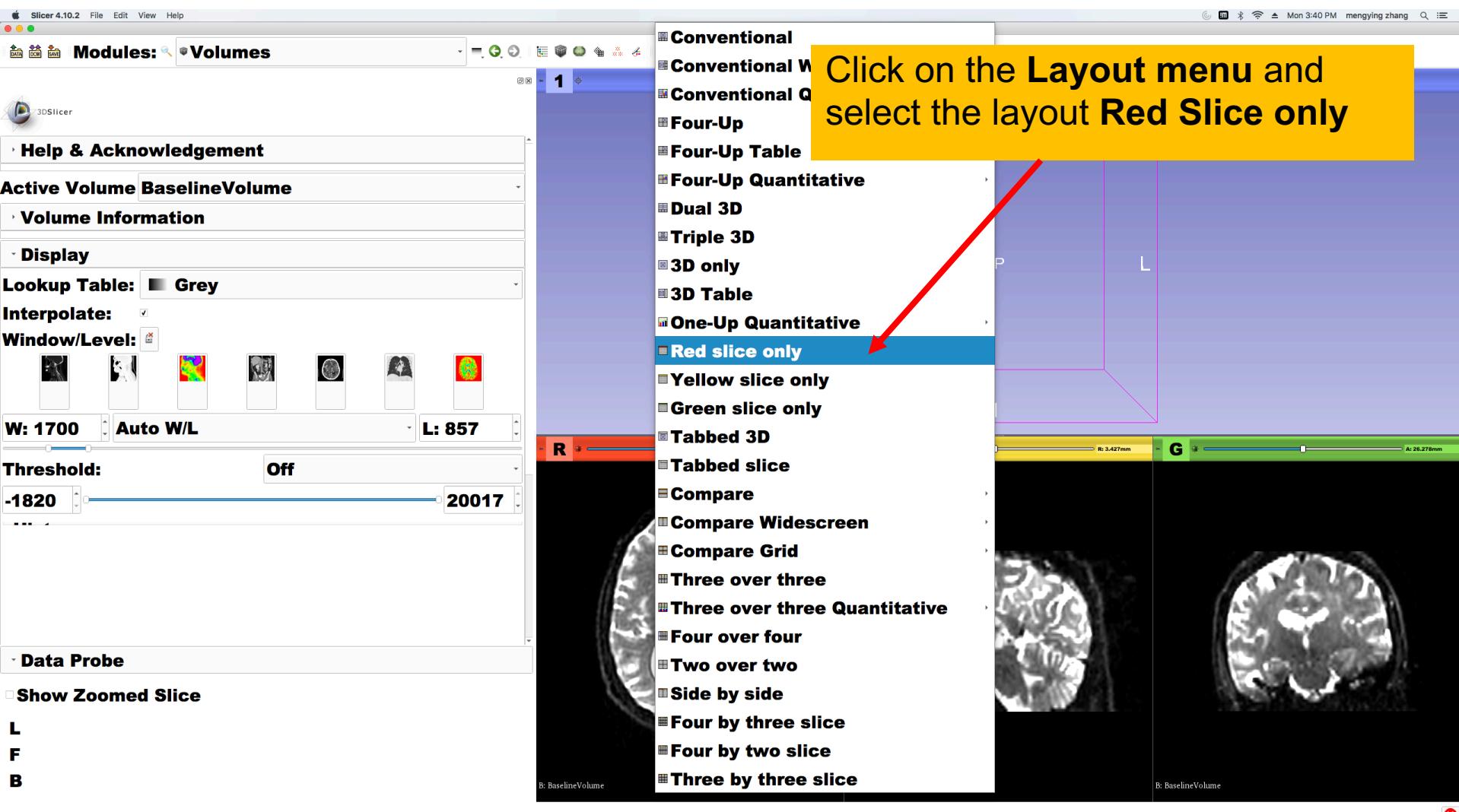
# Loading DTI and Baseline Data

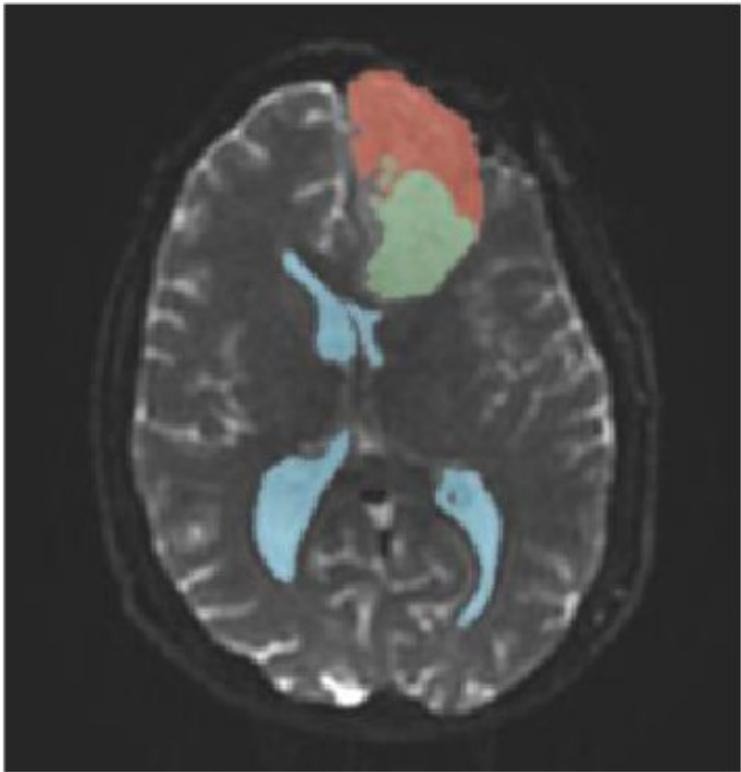


# Loading DTI and Baseline Data



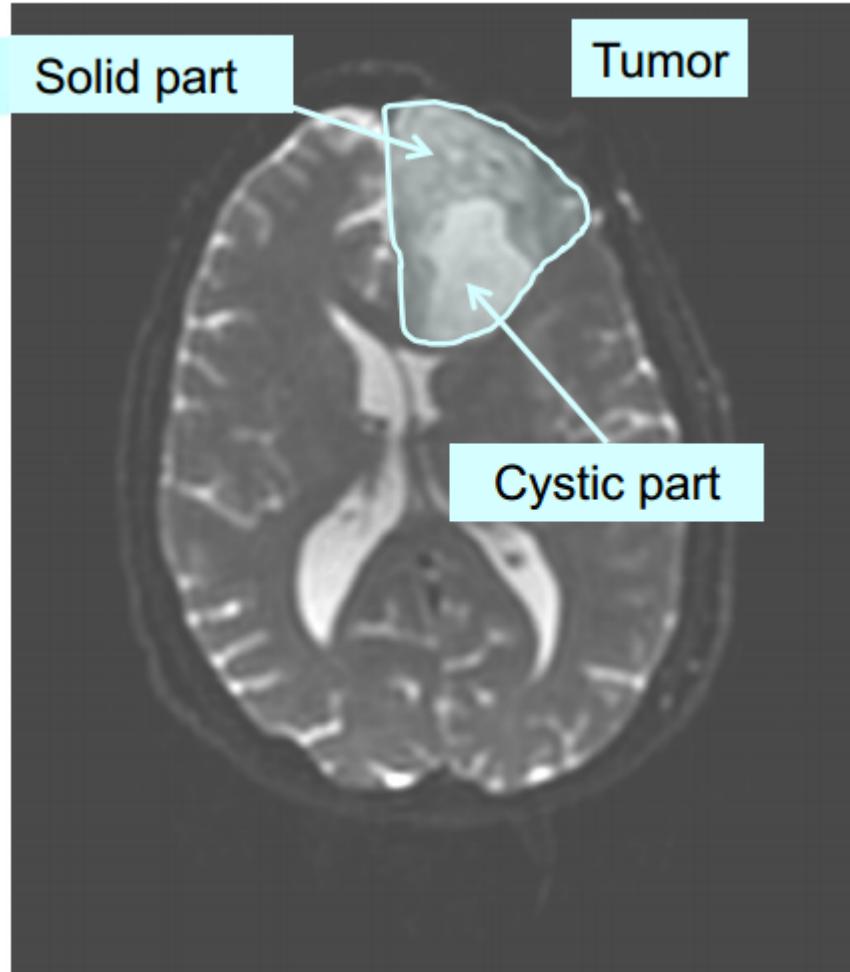
# Loading DTI and Baseline Data





# Part 1: Segmenting the tumor and ventricles

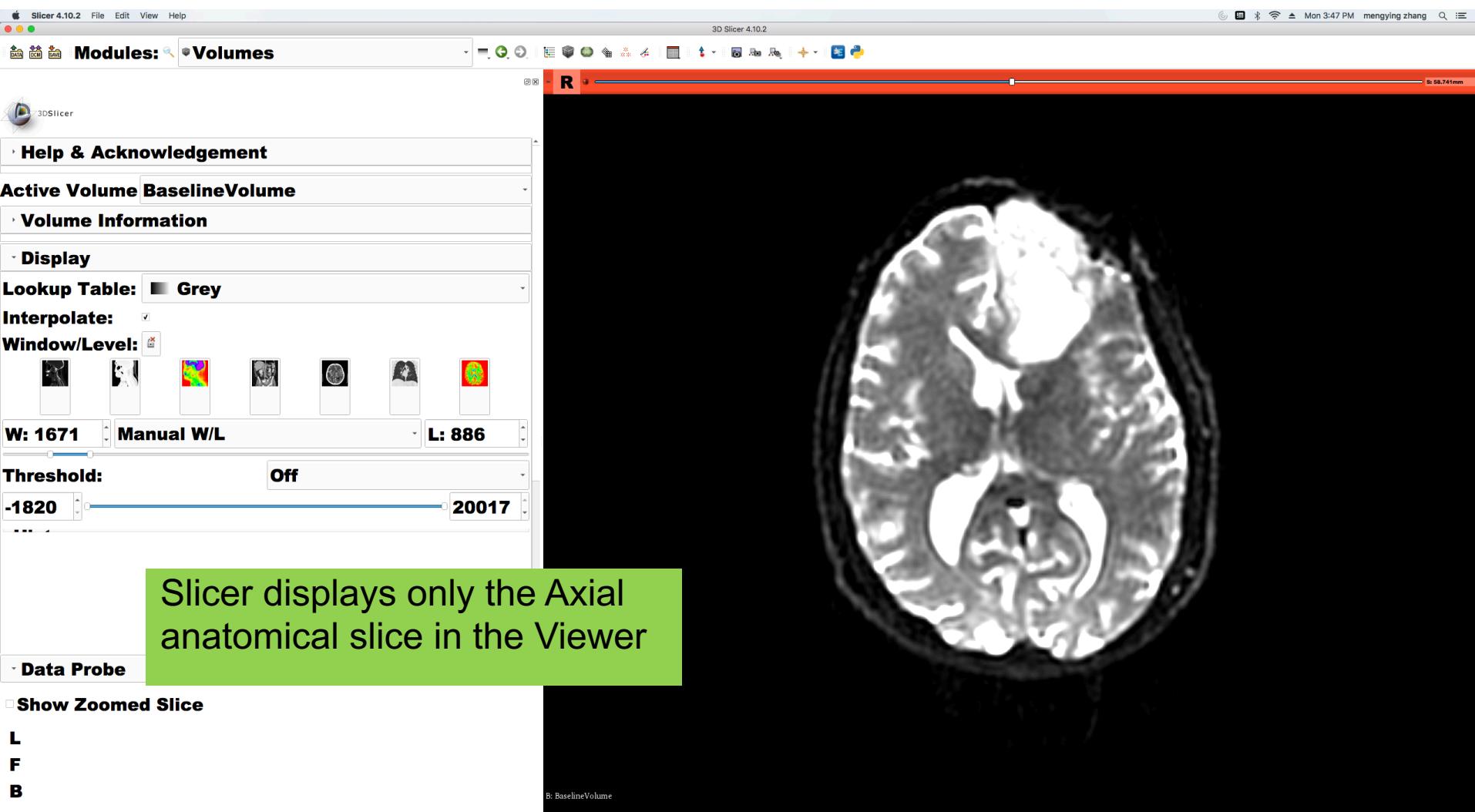
# Tumor Segmentation



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



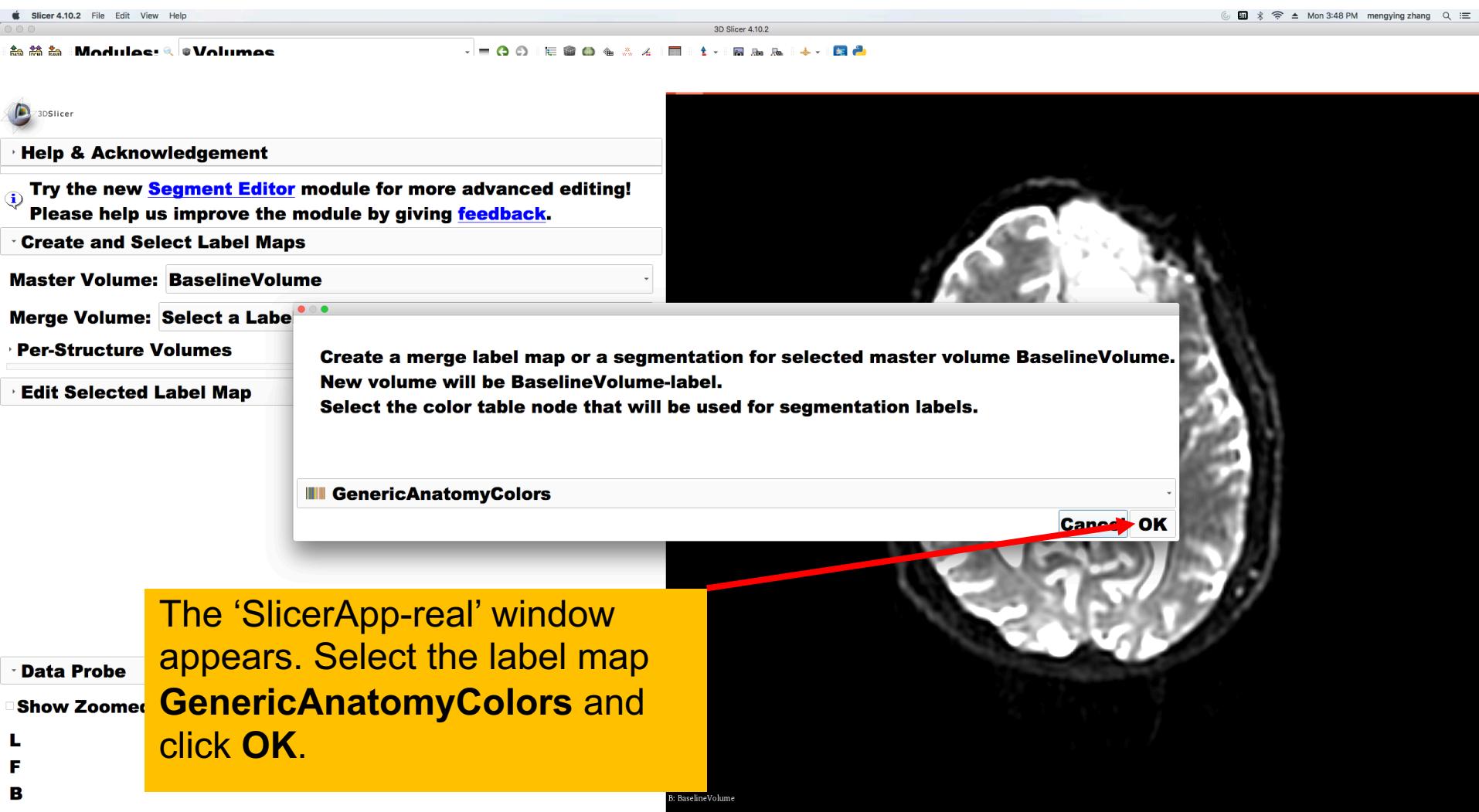
# Tumor Segmentation

The screenshot shows the Slicer 4.10.2 application window. At the top is a menu bar with File, Edit, View, Help. Below it is a toolbar with various icons. The main area is a list of modules under the heading "All modules". A red arrow points from the text in the yellow box to the "Editor" module in the list.

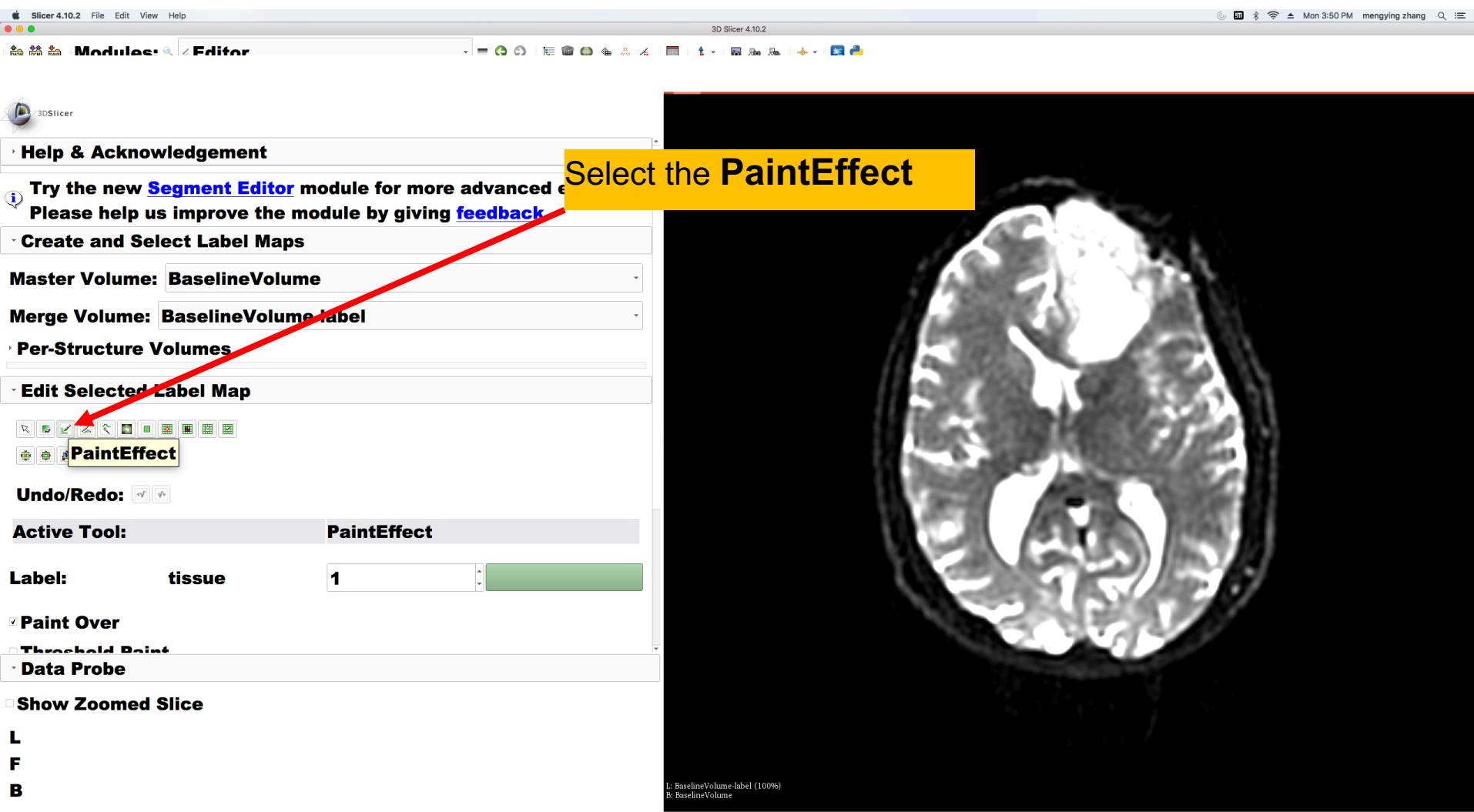
Go to All modules and click on the Modules menu and select the module Editor

- ACPC Transform
- Add Scalar Volumes
- Annotations
- BRAINS Strip Rotation
- BRAINS Transform Convert
- BRAINSDWIcleanup
- Cameras
- Cast Scalar Volume
- CheckerBoard Filter
- Colors
- Compare Volumes
- ConvertVTK
- Create a DICOM Series
- Crop Volume
- Curvature Anisotropic Diffusion
- Data
- DataProbe
- DataStore
- Demon Registration (BRAINS)
- DICOM
- DICOM Diffusion Volume Plugin
- DICOM Patcher
- DICOM Scalar Volume Plugin
- Diffusion Brain Masking
- Diffusion Tensor Estimation
- Diffusion Tensor Scalar Maps
- Diffusion-weighted DICOM Import (DWIConvert)
- DWI to Full Brain Tractography
- Editor **(highlighted)**
- Endoscopy
- Event Broker
- Execution Model Tour
- Expert Automated Registration
- Export tractogram
- Extension Wizard
- Extract DWI Shell
- Extract Skeleton
- Fiducial Registration
- Foreground masking (BRAINS)
- Gaussian Blur Image Filter
- General Registration (BRAINS)
- Gradient Anisotropic Diffusion
- Grayscale Fill Hole Image Filter
- Grayscale Grind Peak Image Filter
- Grayscale Model Maker
- Histogram Matching
- Image Label Combine
- Interactive UKF
- Label Map Smoothing
- Label Statistics
- Label Statistics (BRAINS)
- Landmark Registration
- Markups
- Mask Scalar Volume
- Median Image Filter
- Merge Models
- Metric Test
- Model Maker
- Model To Label Map
- Models
- Multiply Scalar Volumes
- Plots
- Probe Volume With Model
- Reformat
- Resample DTI Volume
- Resample Image (BRAINS)
- Resample Scalar Volume
- Resample Scalar/Vector/DWI Volume
- Resize Image (BRAINS)
- Robust Statistics Segmente
- Sample Data
- Scene Views
- Screen Capture
- Segment Editor
- Segment Statistics
- Segmentations
- Simple Filters
- Simple Region Growing Segmentation
- Subtract Scalar Volumes

# Tumor Segmentation



# Tumor Segmentation



# Tumor Segmentation

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

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

Master Volume: BaselineVolume

Merge Volume: BaselineVolume-label

Per-Structure Volumes

Edit Selected Label Map

Active Tool: PaintEffect

Label: tissue 1

Paint Over

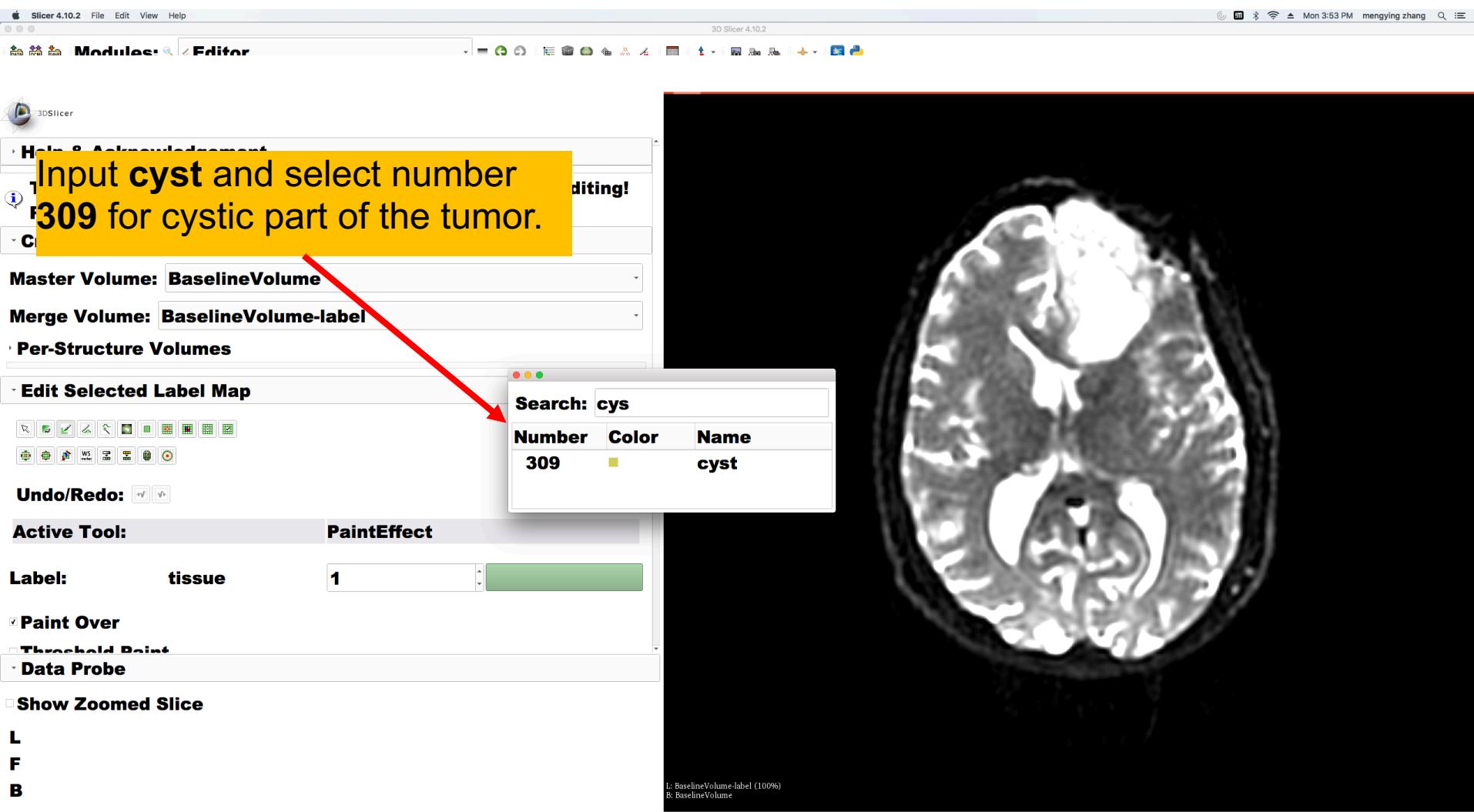
Show Zoomed Slice

L F B

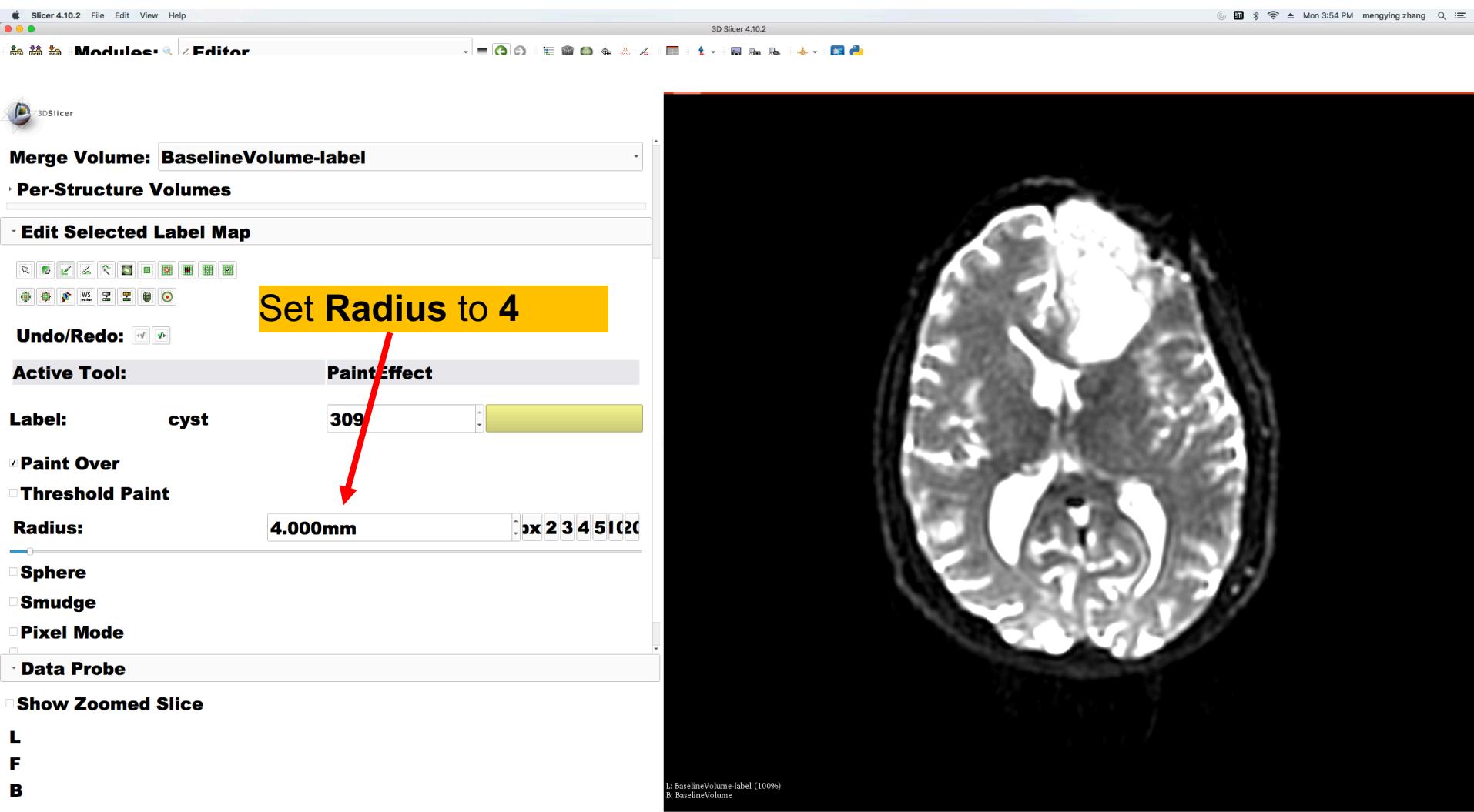
Num Co Name

0	■	background
1	■	tissue
2	■	bone
3	■	skin
4	■	connective tissue
5	■	blood
6	■	organ
7	■	mass
8	■	muscle
9	■	foreign object
10	■	waste
11	■	teeth
12	■	fat
13	■	gray matter
14	■	white matter
15	■	nerve
16	■	vein
17	■	artery
18	■	capillary
19	■	ligament
20	■	tendon
21	■	cartilage
22	■	meniscus
23	■	lymph node
24	■	lymphatic vessel
25	■	cerebro-spinal fluid
26	■	bile
27	■	urine

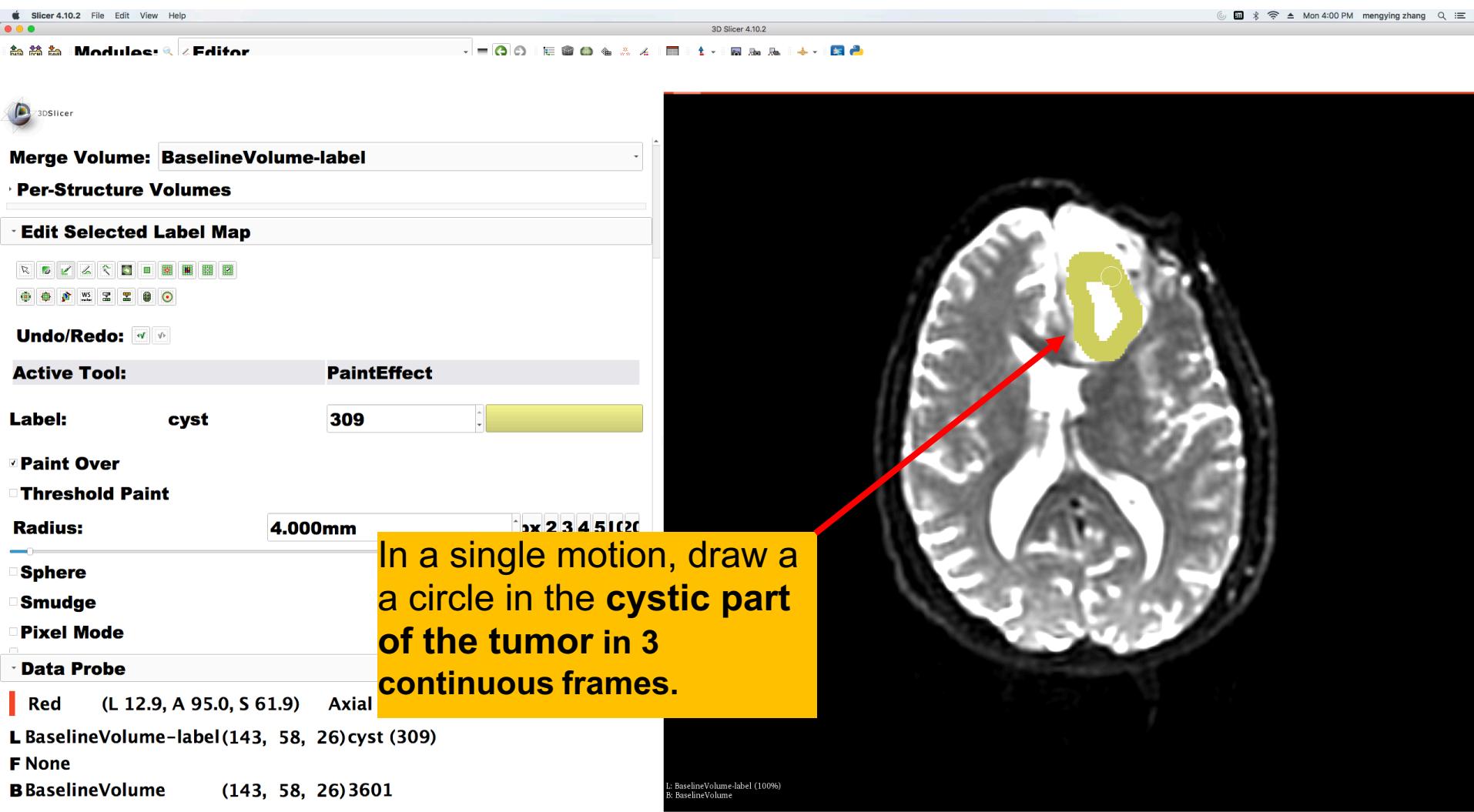
# Tumor Segmentation



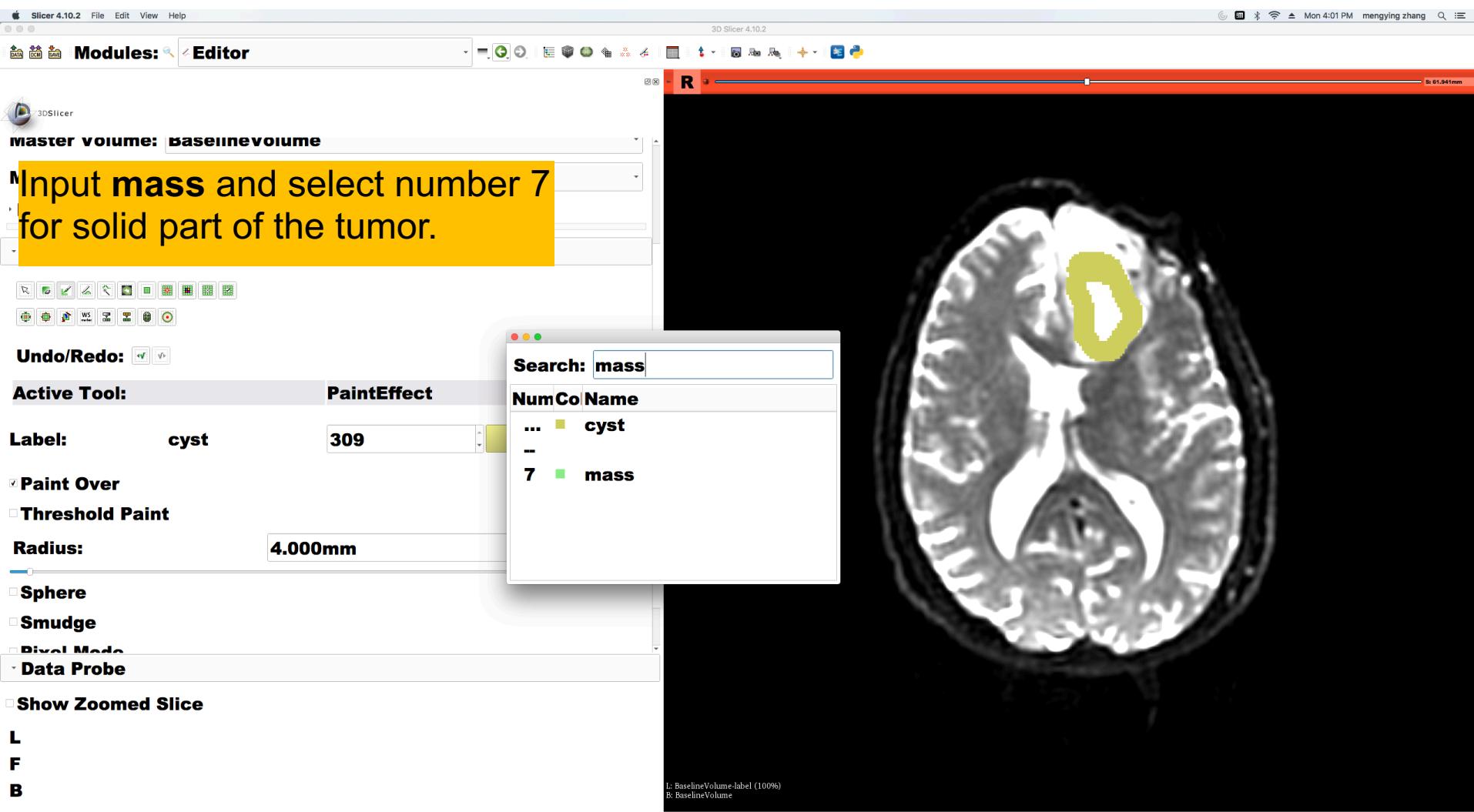
# Tumor Segmentation



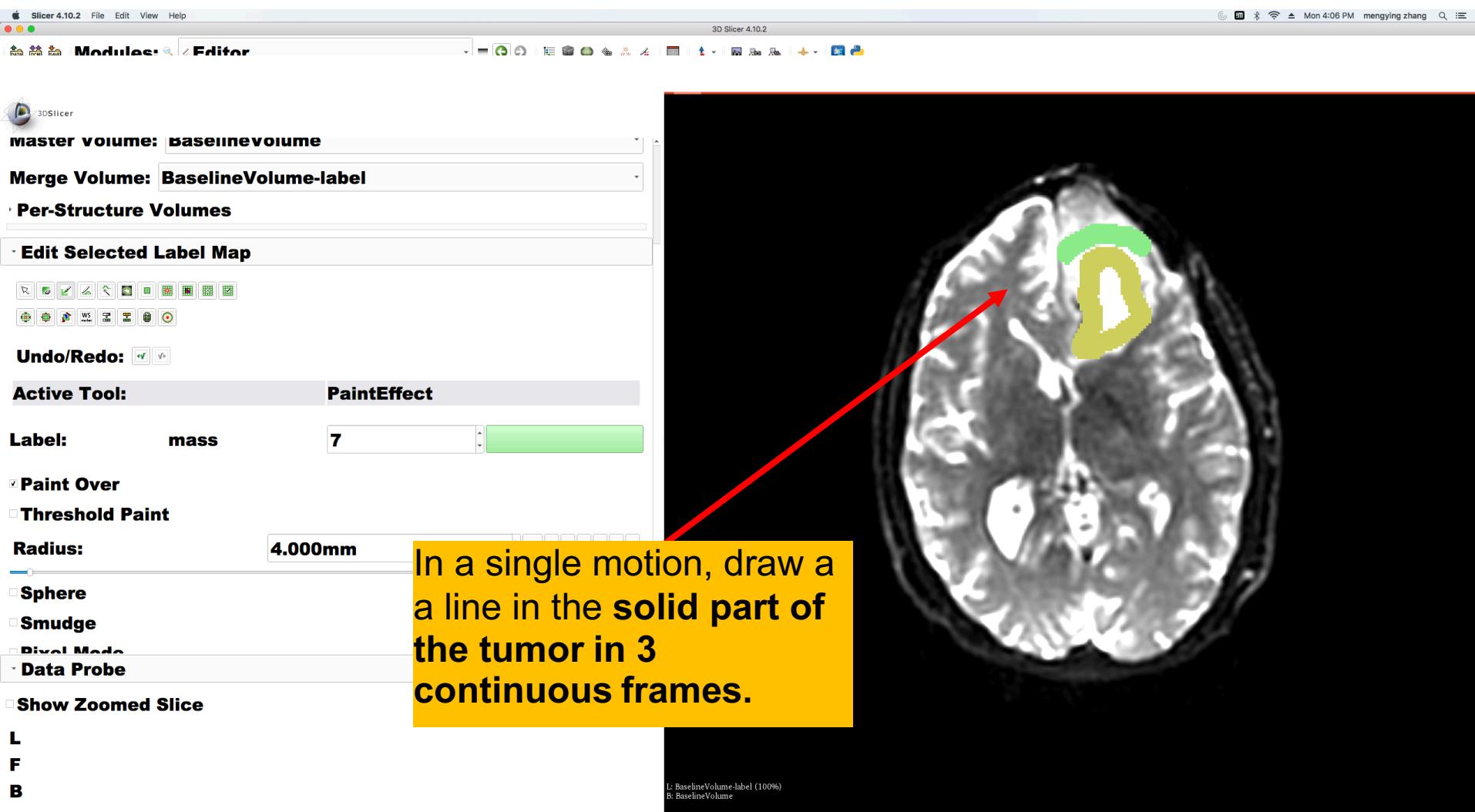
# Tumor Segmentation



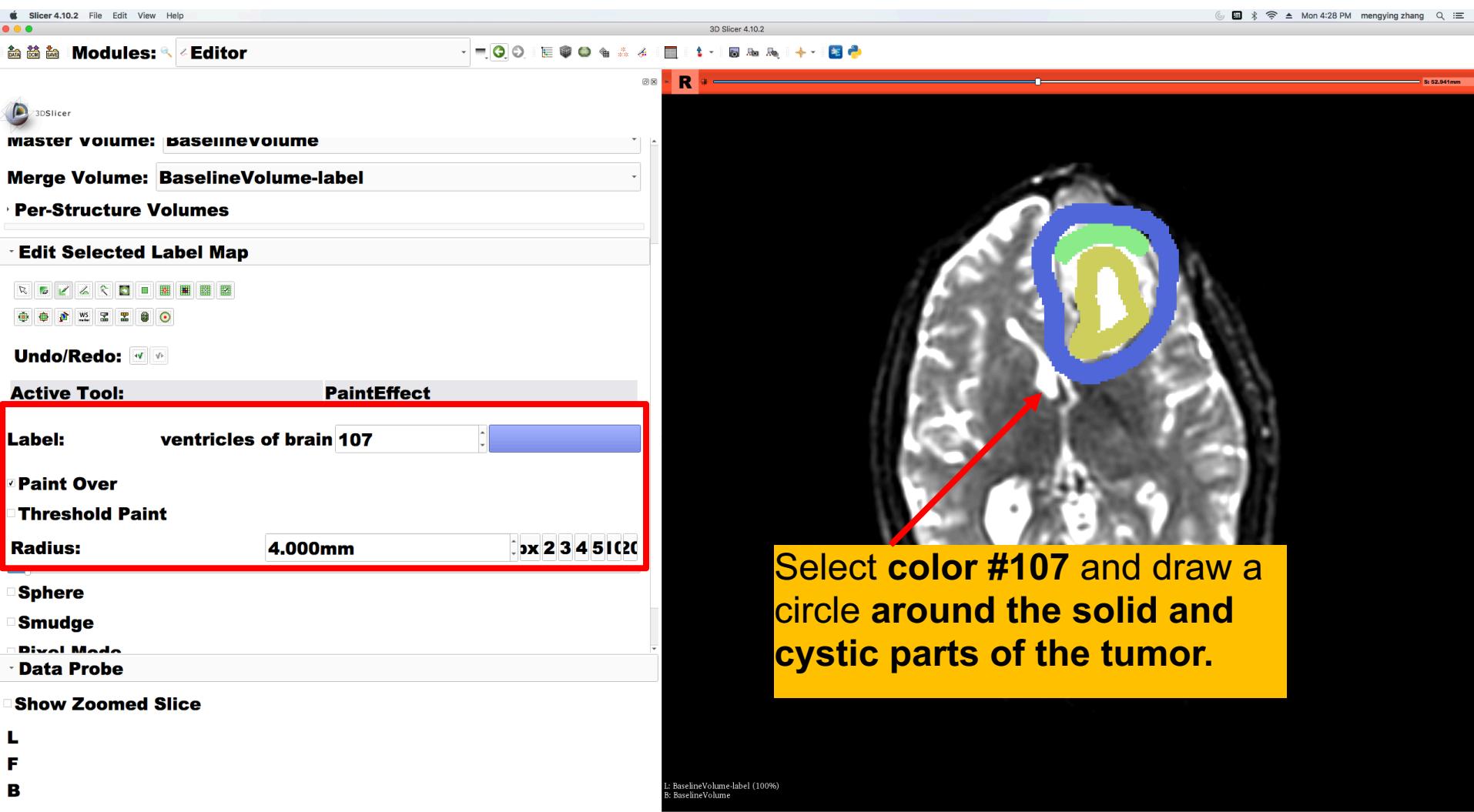
# Tumor Segmentation



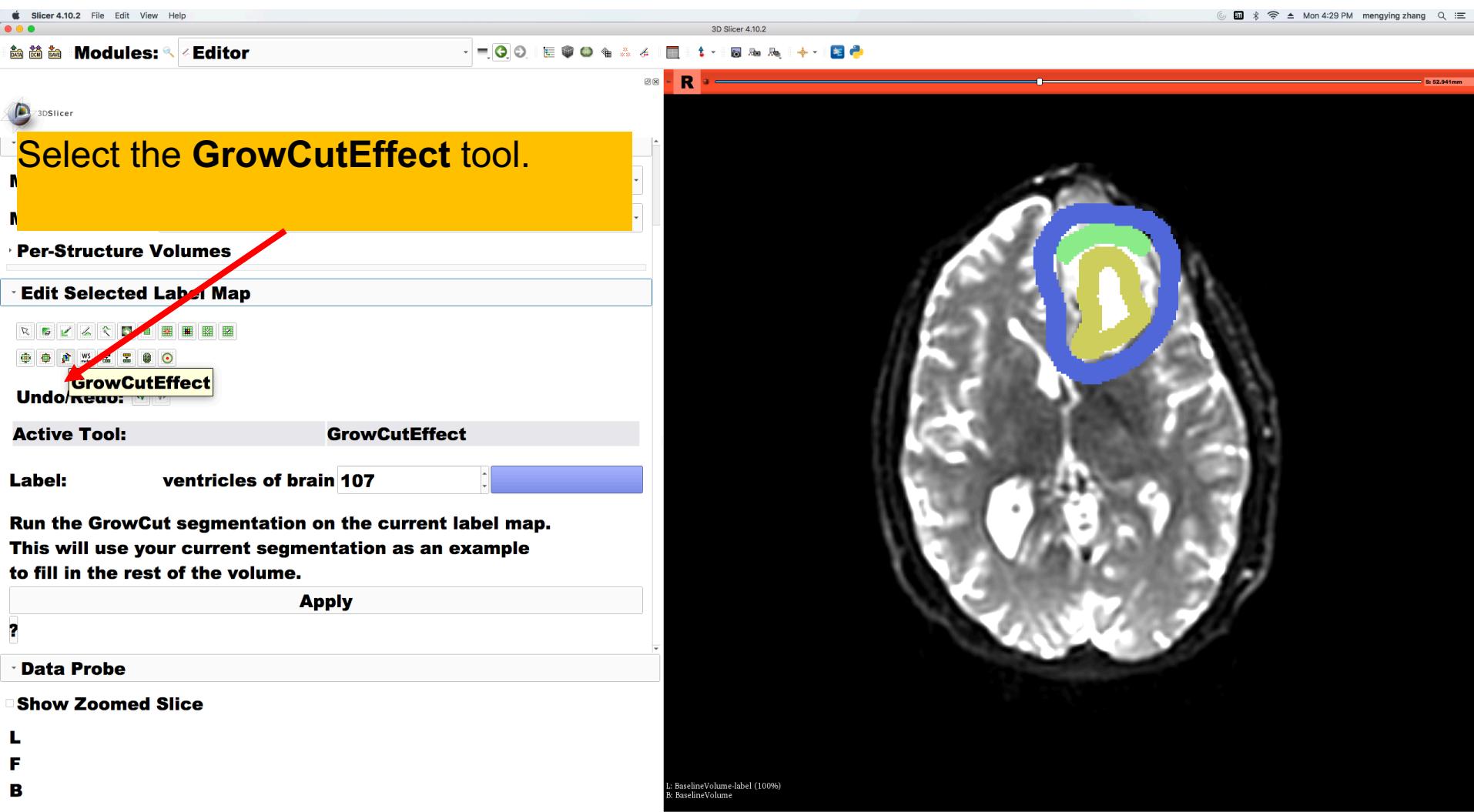
# Tumor Segmentation



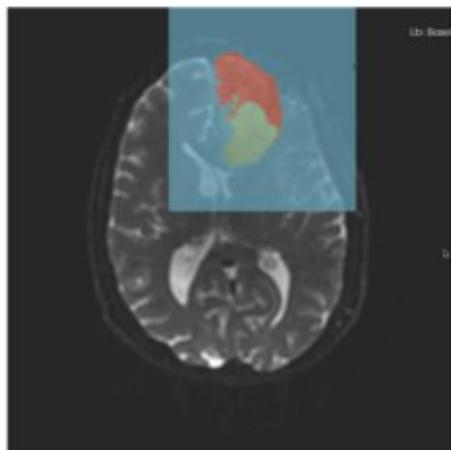
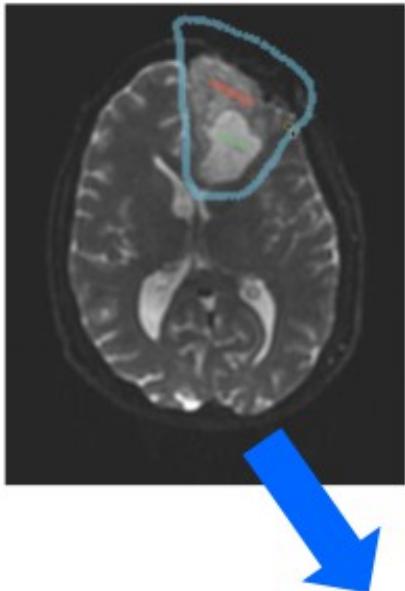
# Tumor Segmentation



# Tumor Segmentation

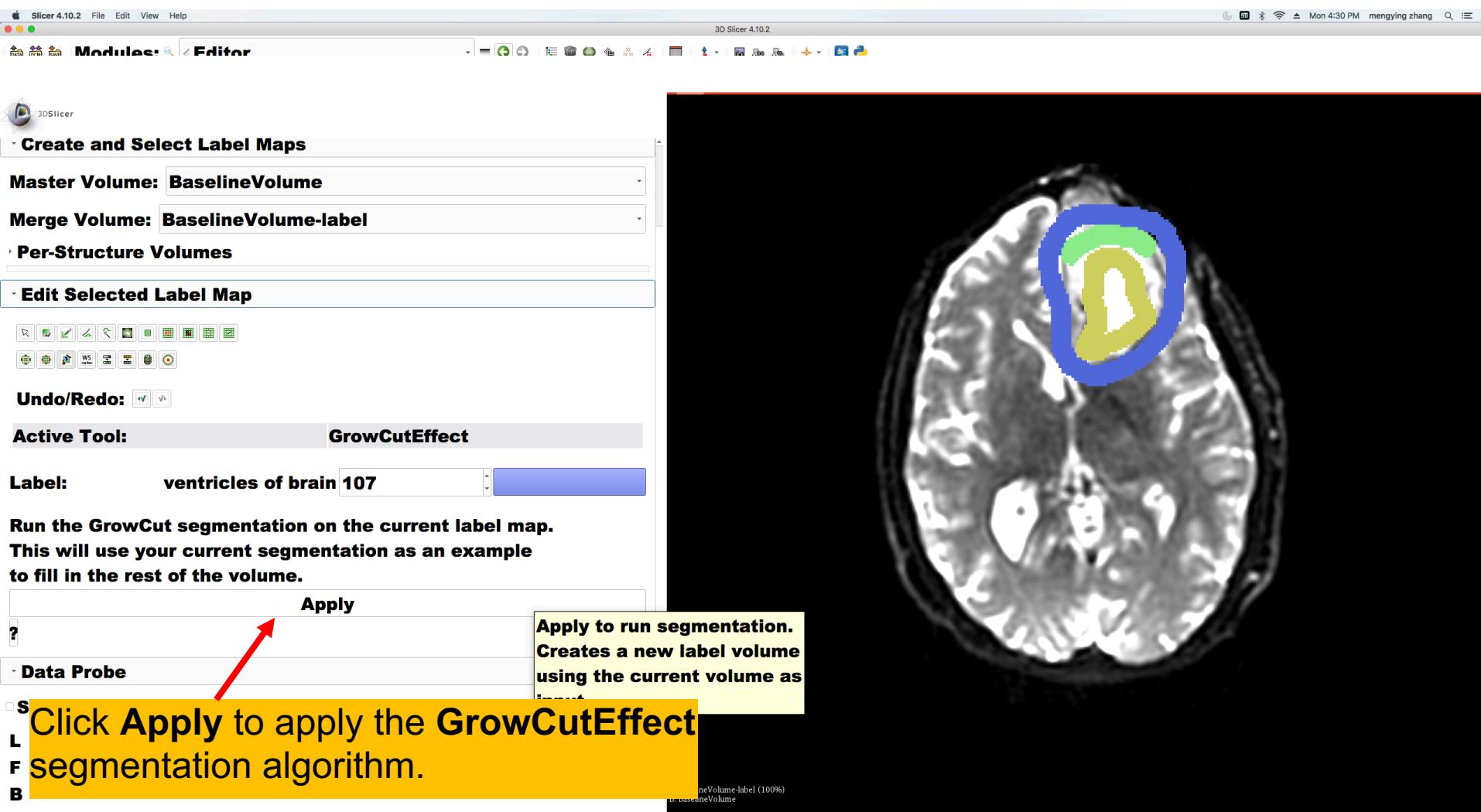


# Grow Cut Segmentation

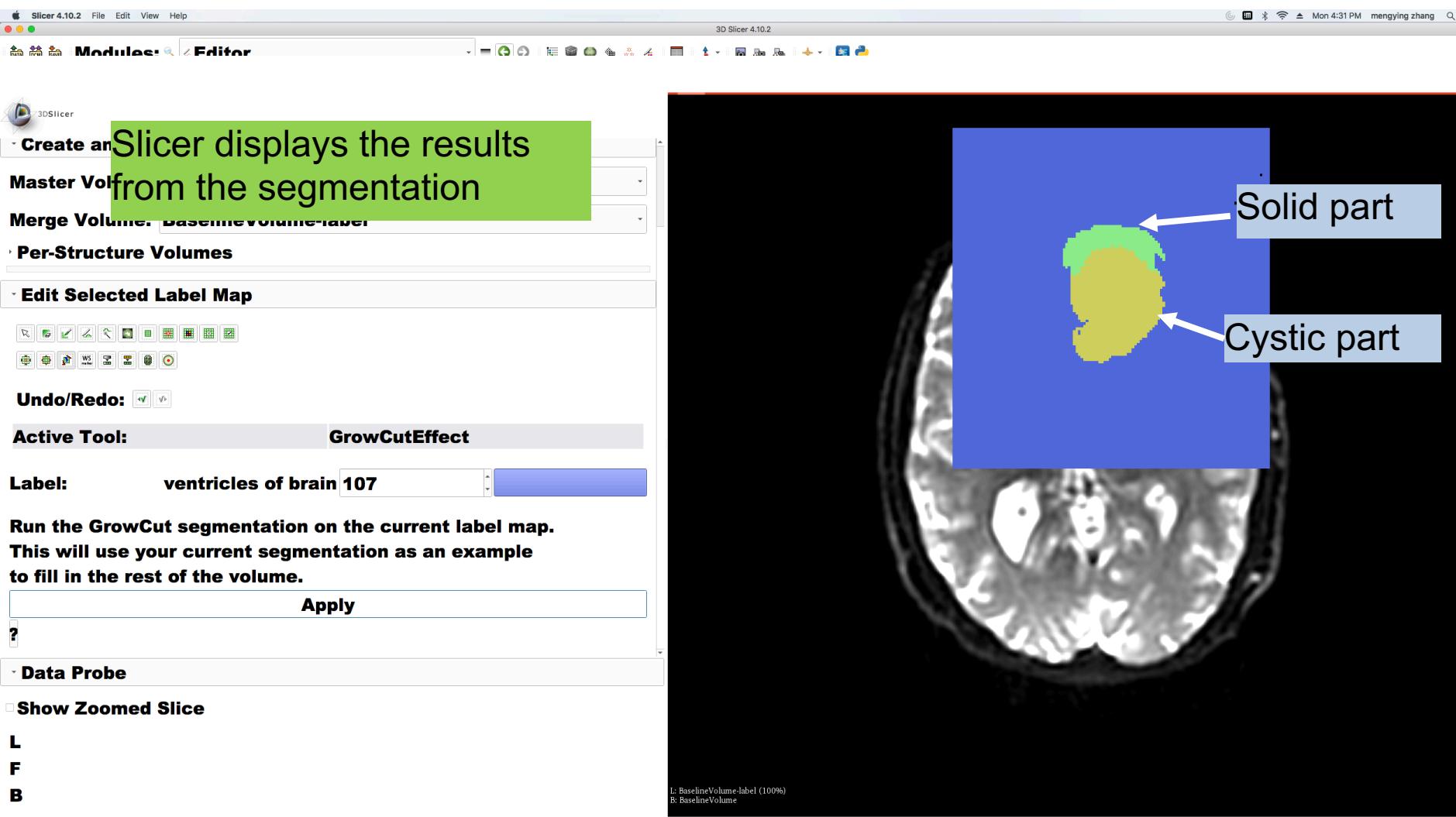


- The Grow Cut Segmentation method is a competitive region growing algorithm using Cellular Automata.
- The algorithm performs multi-label image segmentation using a set of user input scribbles.
- V. Vezhnevets, V. Konouchine. "Grow-Cut" - Interactive Multi-Label N-D Image Segmentation". Proc. Graphicon.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

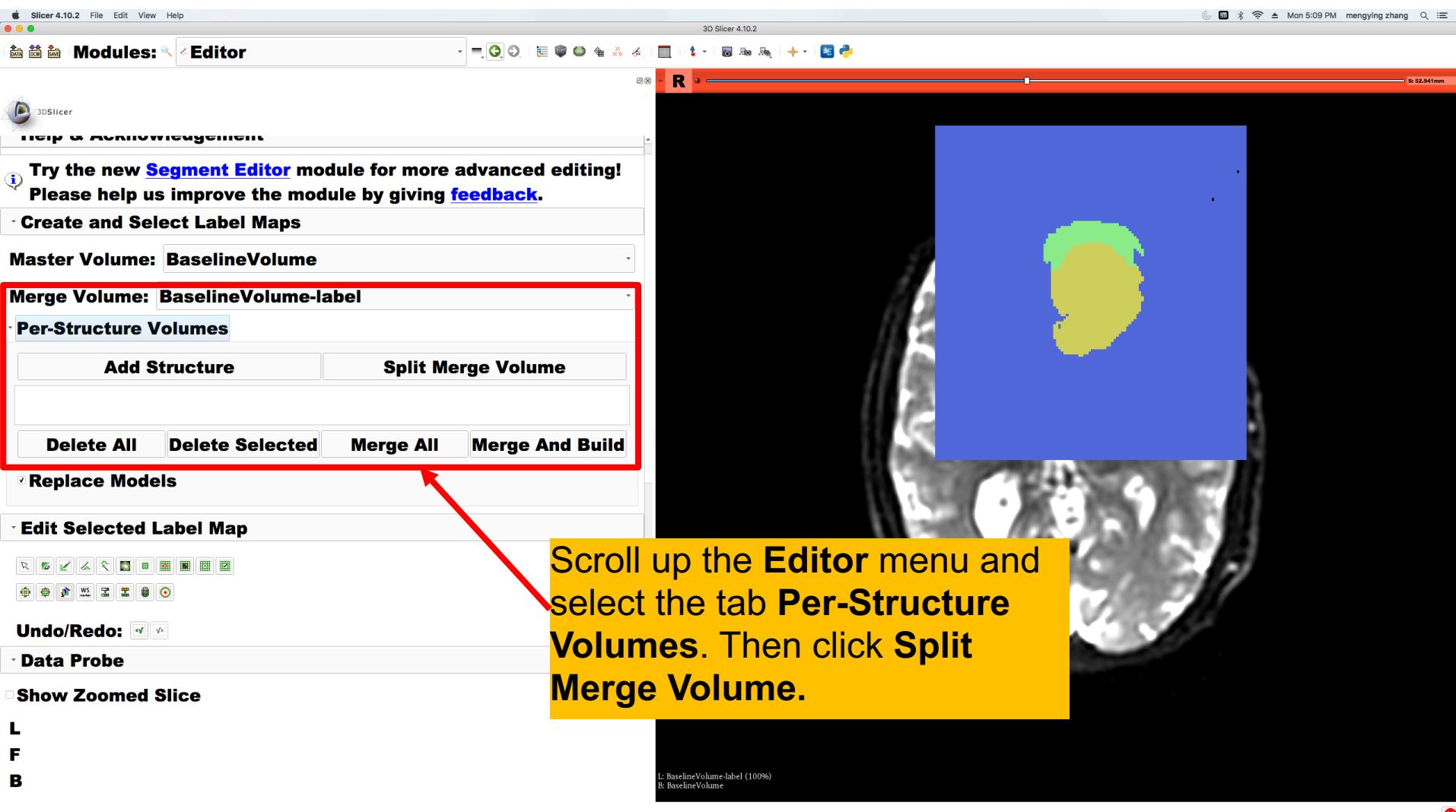
# Tumor Segmentation



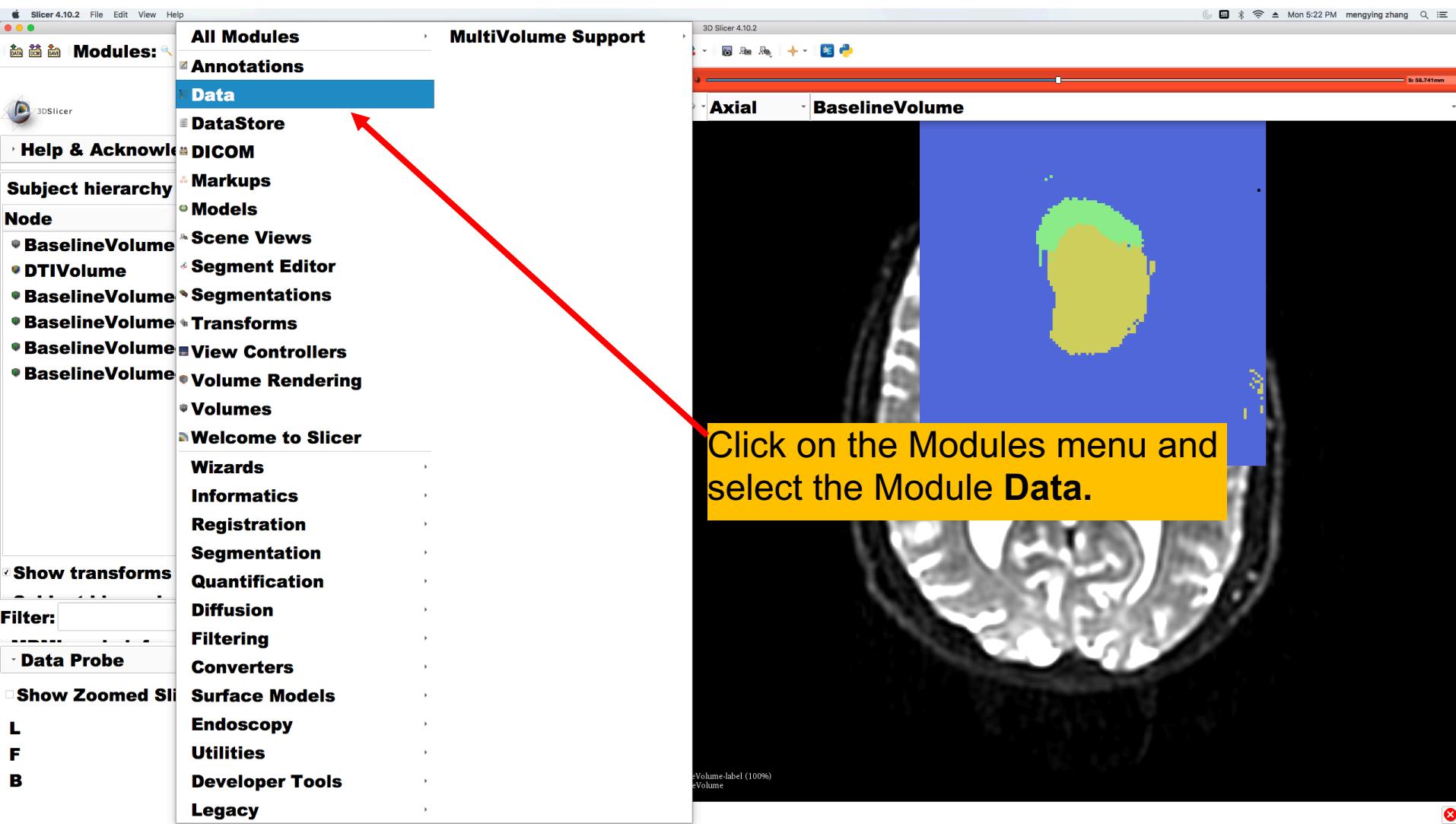
# Tumor Segmentation



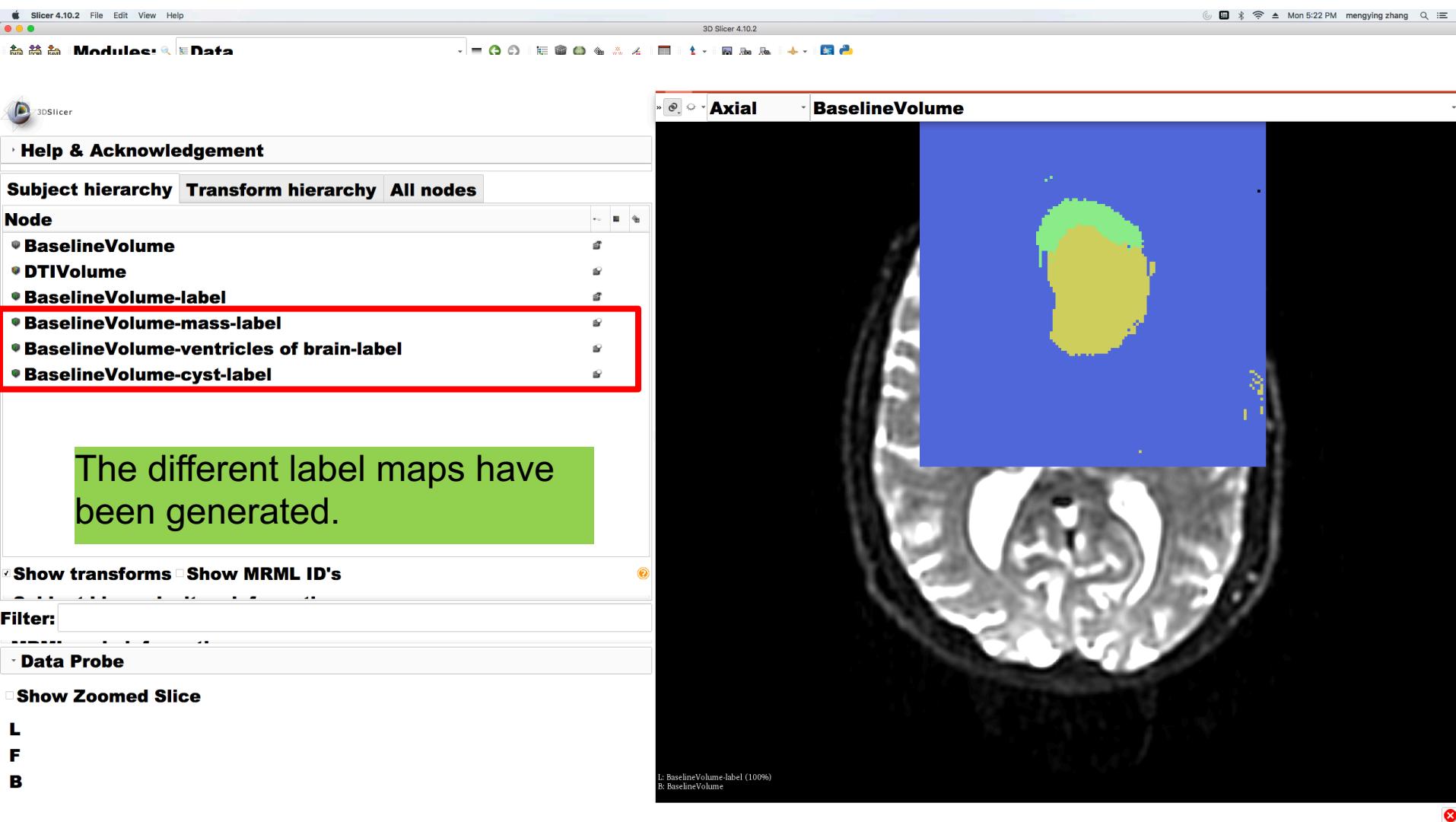
# Tumor Segmentation



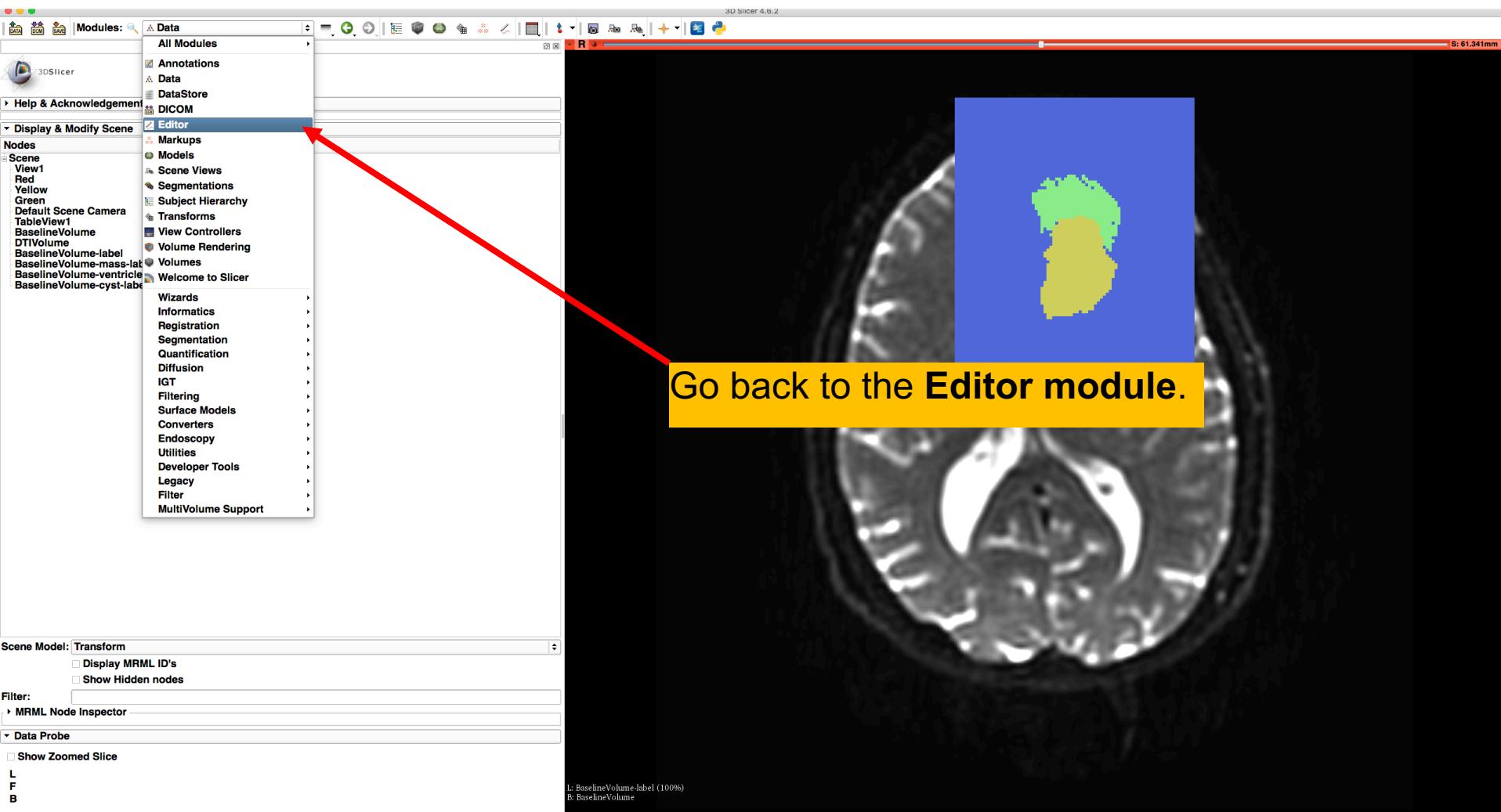
# Tumor Segmentation



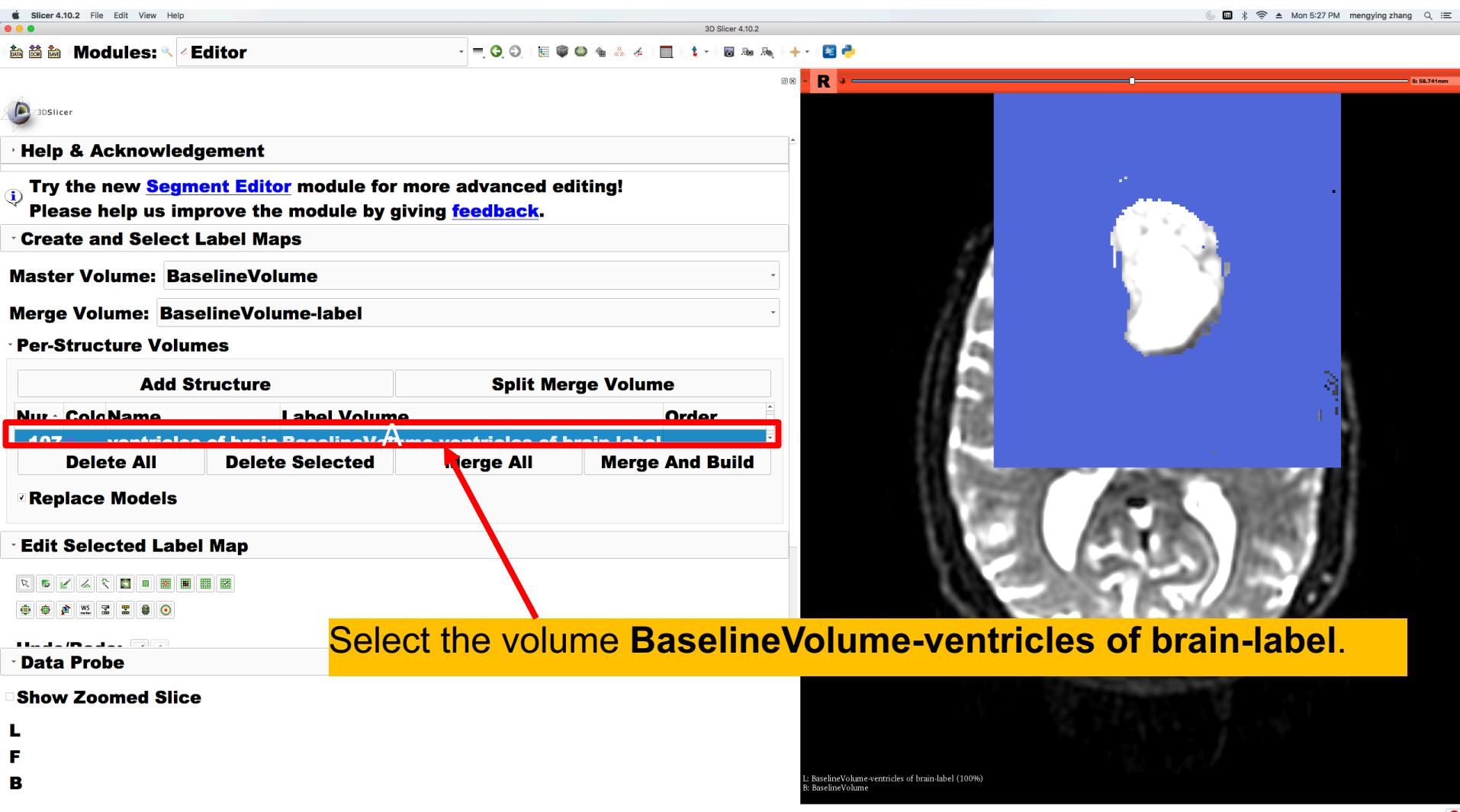
# Tumor Segmentation



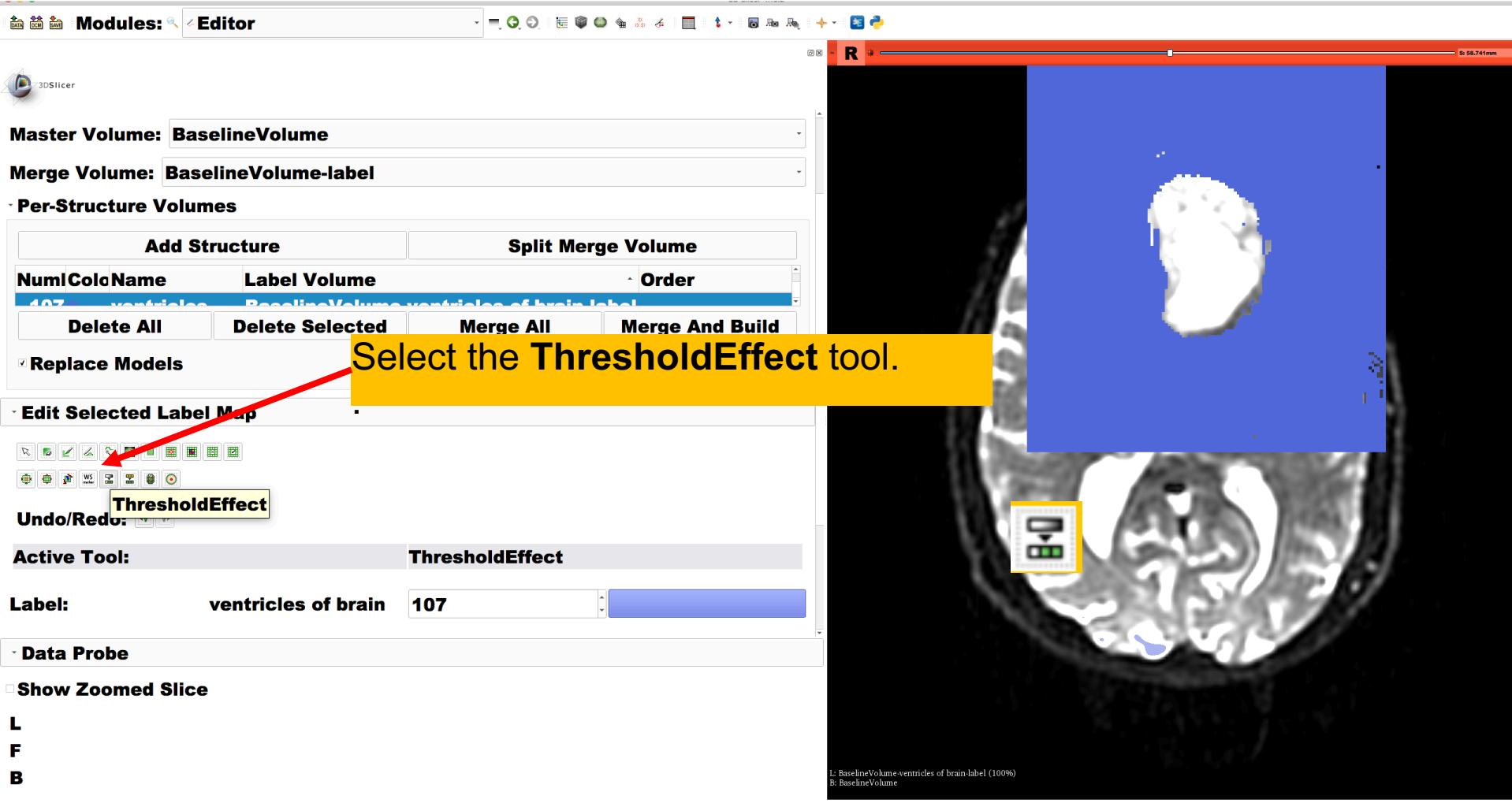
# Ventricles Segmentation



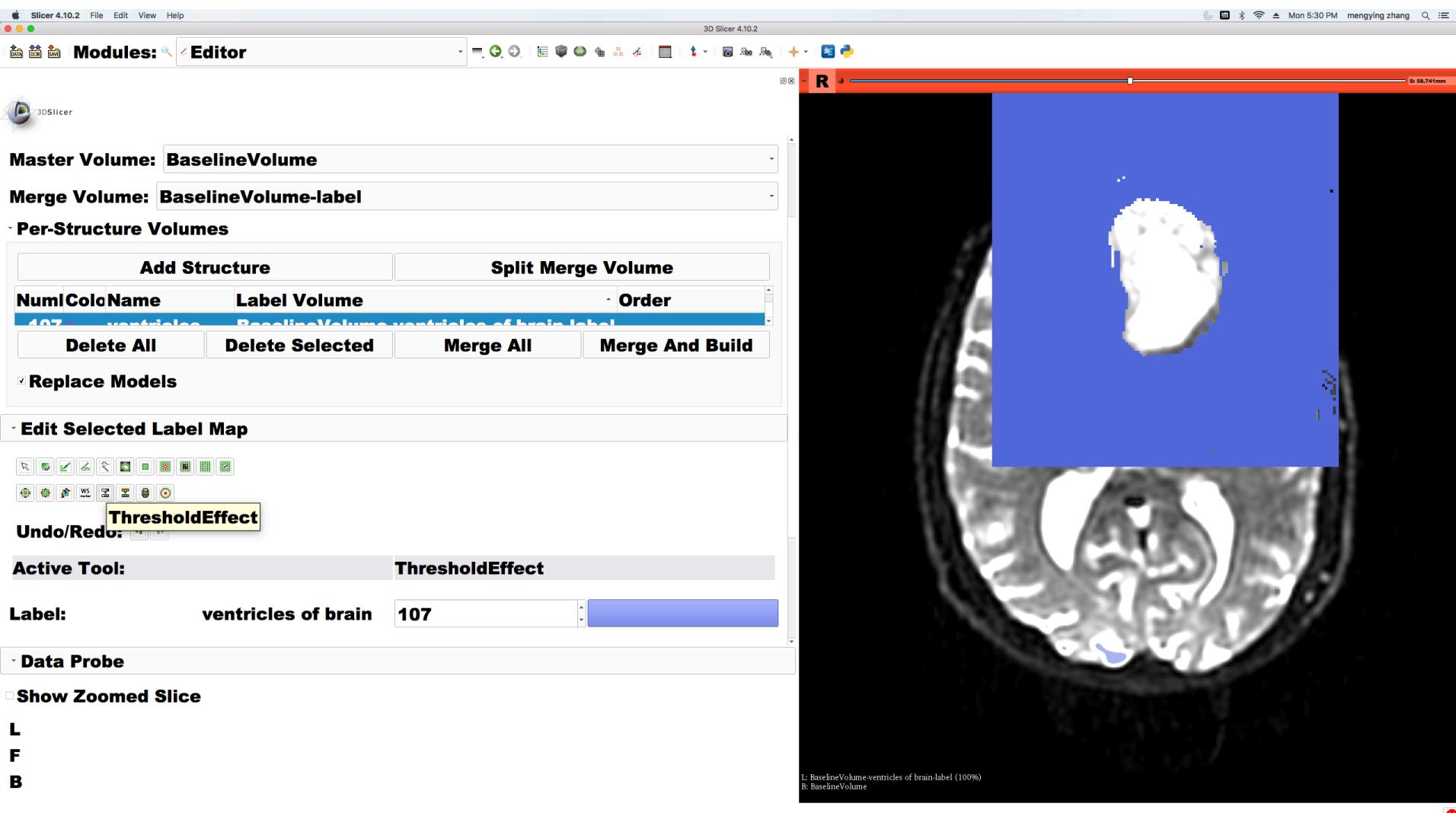
# Ventricles Segmentation



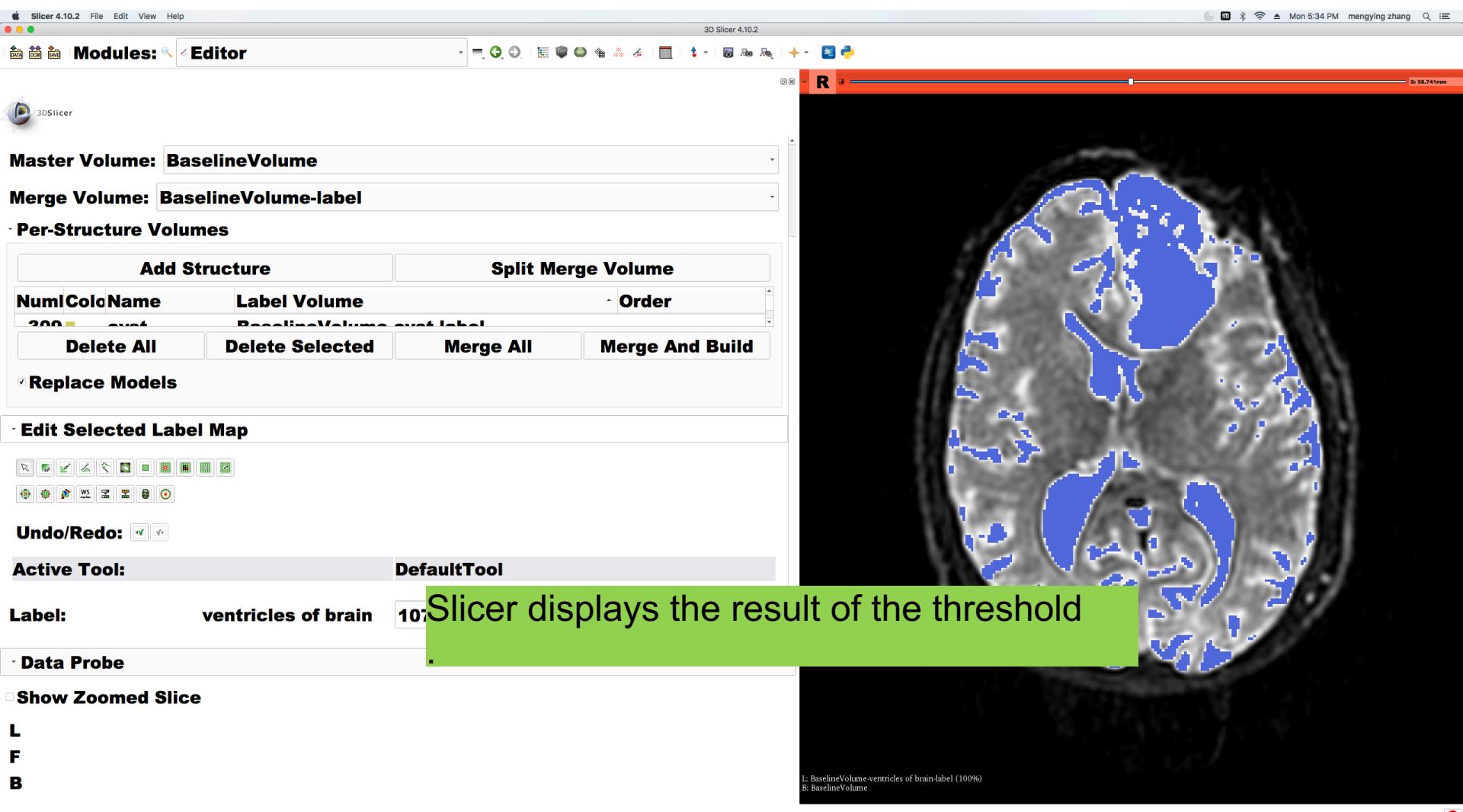
# Ventricles Segmentation



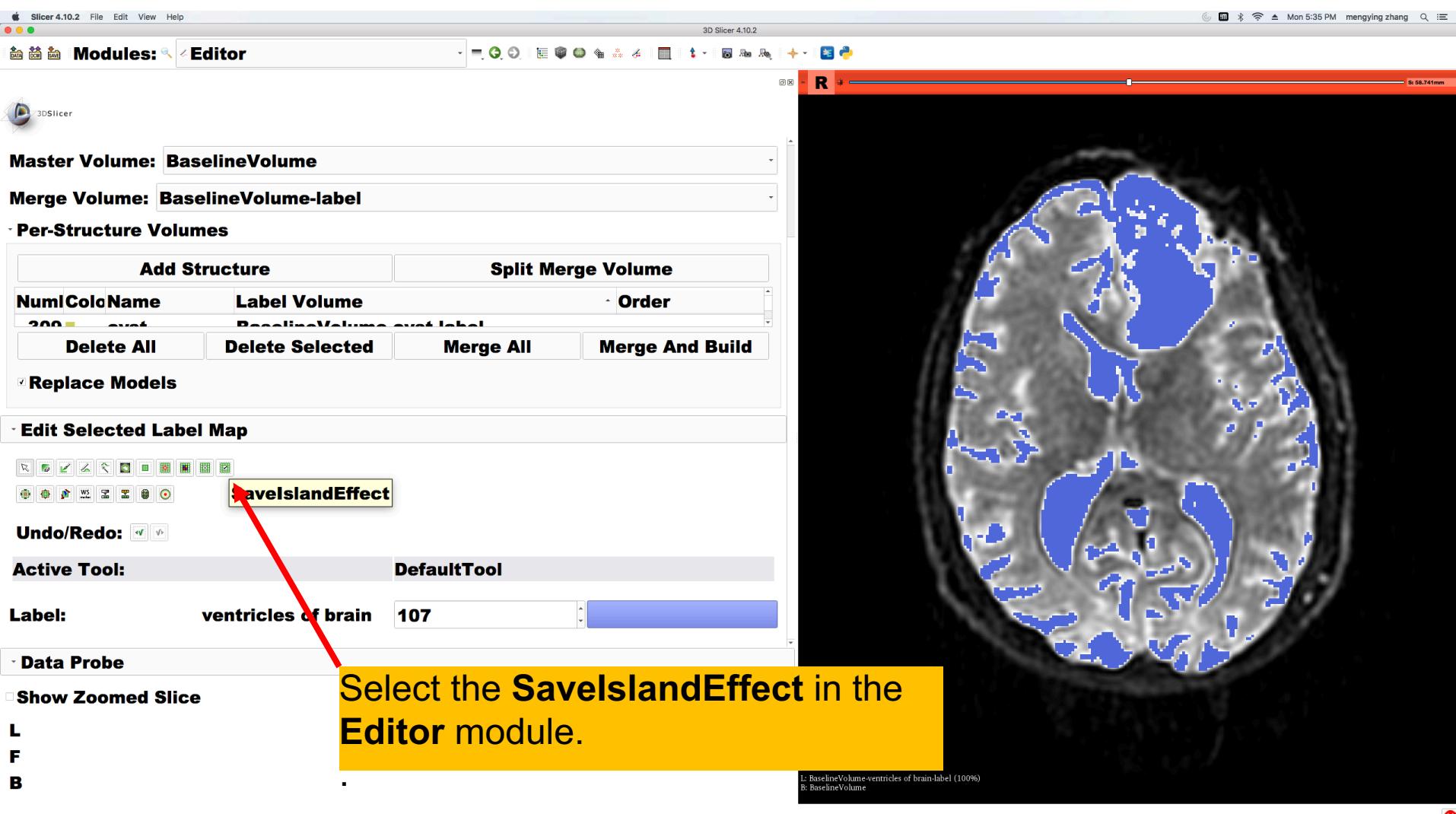
# Ventricles Segmentation



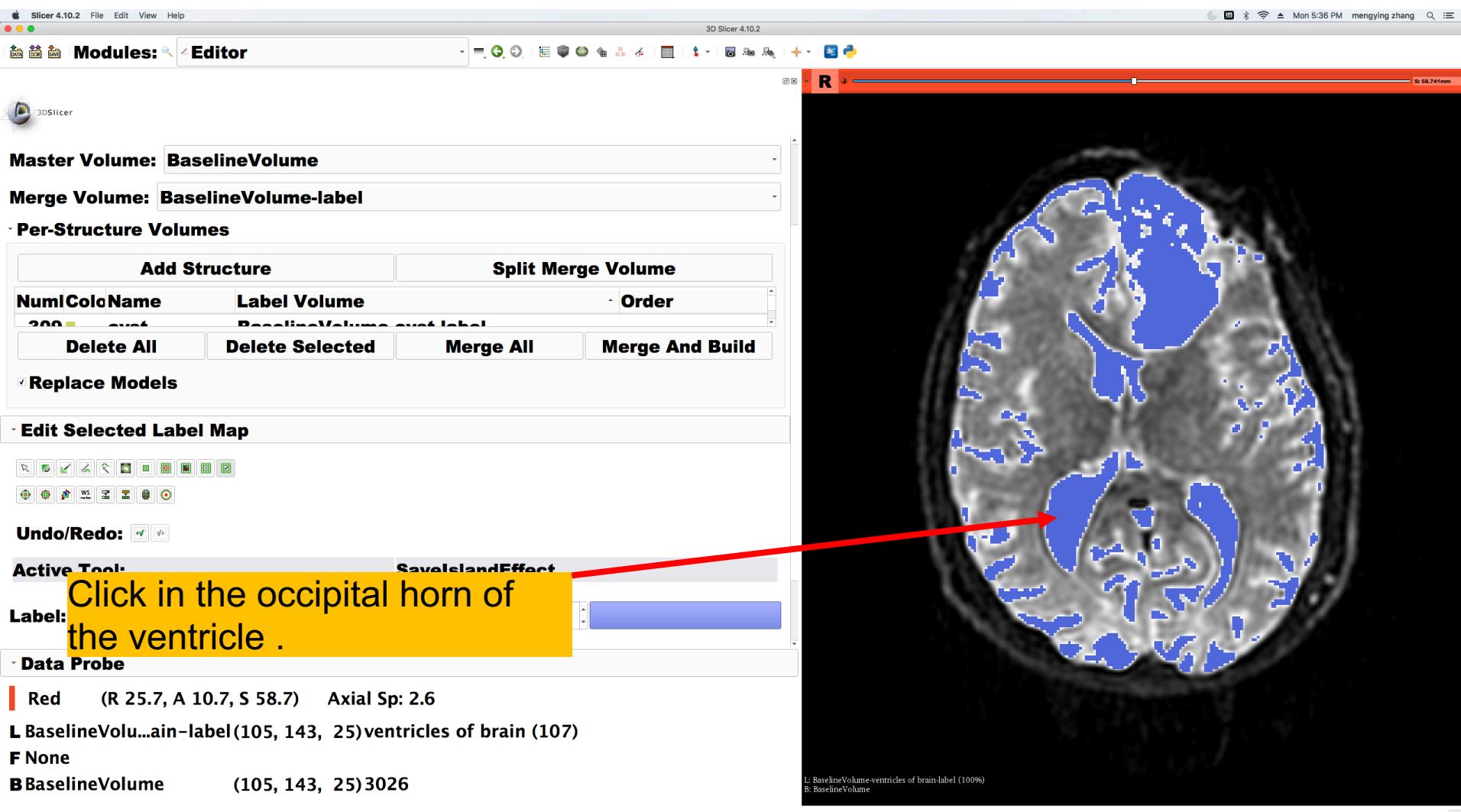
# Ventricles Segmentation



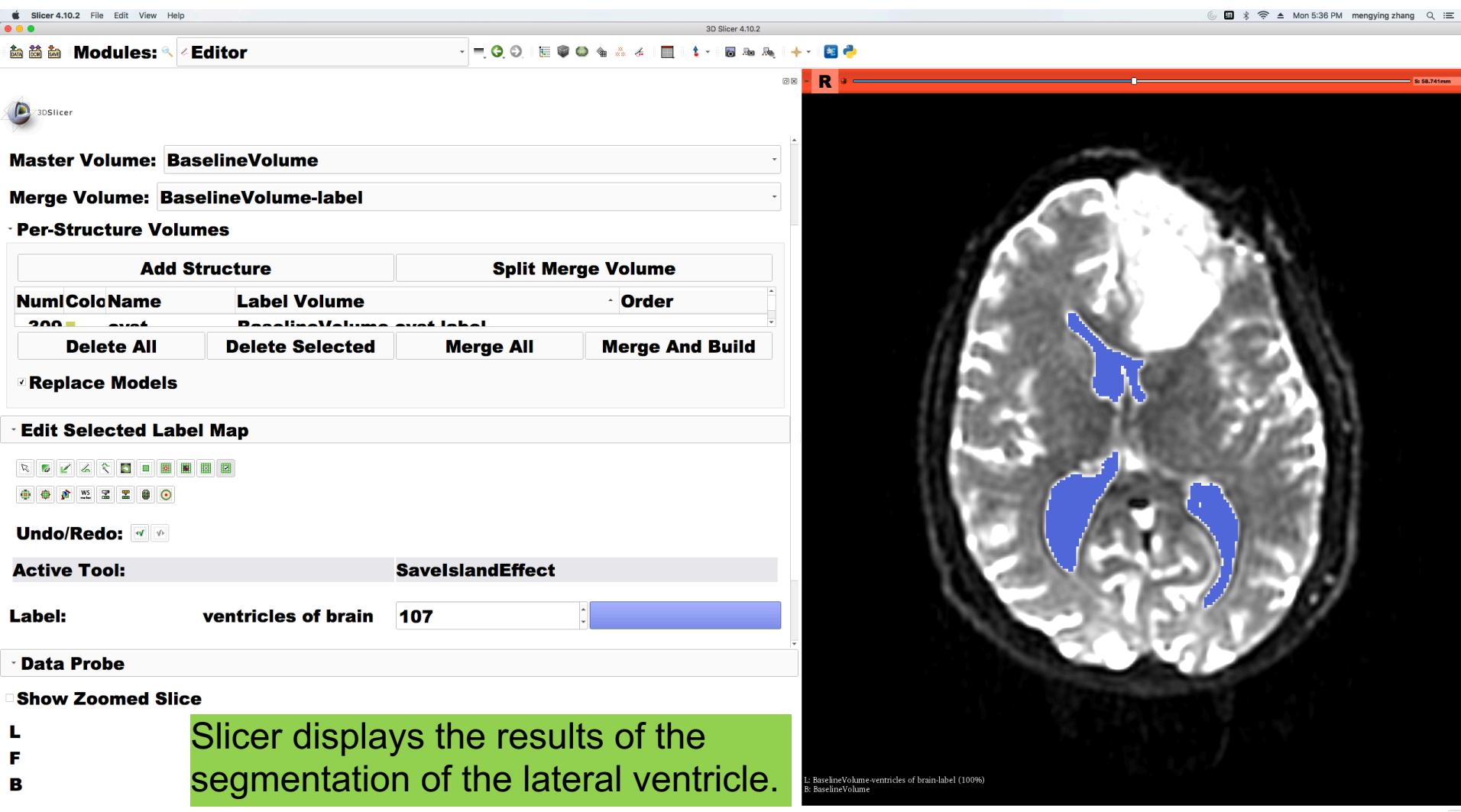
# Ventricles Segmentation



# Ventricles Segmentation



# Ventricles Segmentation



# Ventricles Segmentation

Slicer 4.10.2 File Edit View Help 3D Slicer 4.10.2 Mon 5:37 PM mengying zhang

**Modules:** Editor

Master Volume: BaselineVolume

Merge Volume: BaselineVolume-label

- Per-Structure Volumes

Add Structure	Split Merge Volume
Num Col Name	Label Volume
200	BaselineVolume-label

Delete All Delete Selected Merge All Merge And Build

Replace Models

Edit Selected Label Map

Undo/Redo:

Active Tool: SavelslandEffect

Label:

- Data Proc

Show ZO

L F B

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

R S 58.741mm

L: BaselineVolume-ventricles of brain-label (100%)  
R: BaselineVolume

Merge all structures into Merge Volume and build models from all structures

# Final Result of Segmentation

Screenshot of the Slicer 4.10.2 software interface showing the segmentation results.

**Master Volume:** BaselineVolume

**Merge Volume:** BaselineVolume-label

**Per-Structure Volumes**

Add Structure	Split Merge Volume			
Num	Col	Name	Label Volume	Order
007			BaselineVolume-label	

**Actions:** Delete All, Delete Selected, Merge All, Merge And Build

**Replace Models**

**Edit Selected Label Map**

Tools: Selection, Segmentation, Label, Measure, Region, 3D Slicer, WS, 3D View, 2D View, 3D Slicer

**Undo/Redo:**

**Active Tool:**

**Label:** ventricles

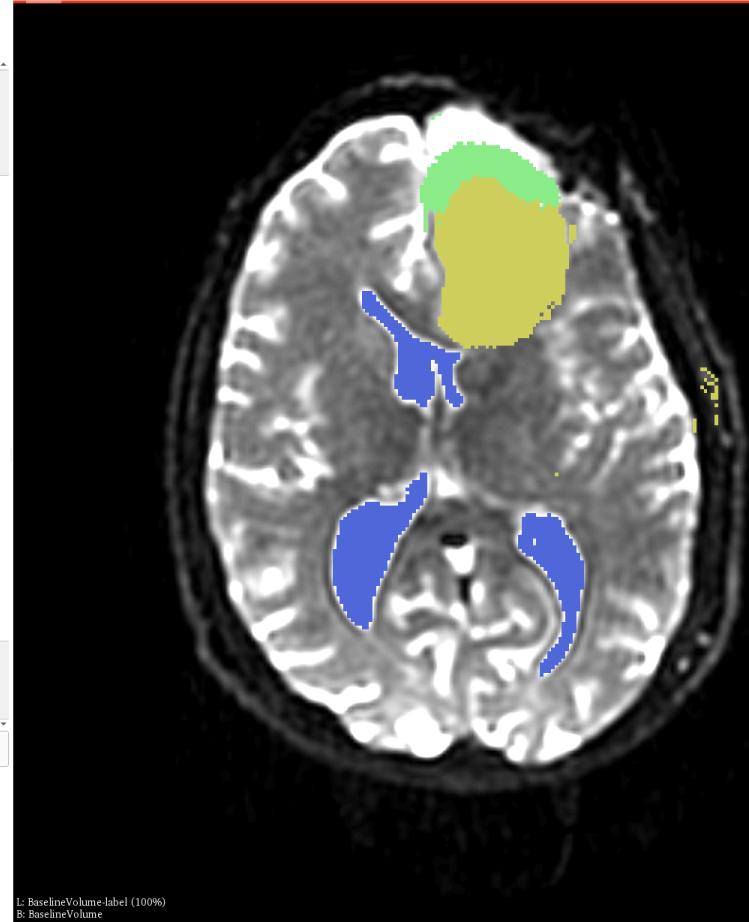
**Data Probe**

**Show Zoomed Slice**

**L**  
**F**  
**B**

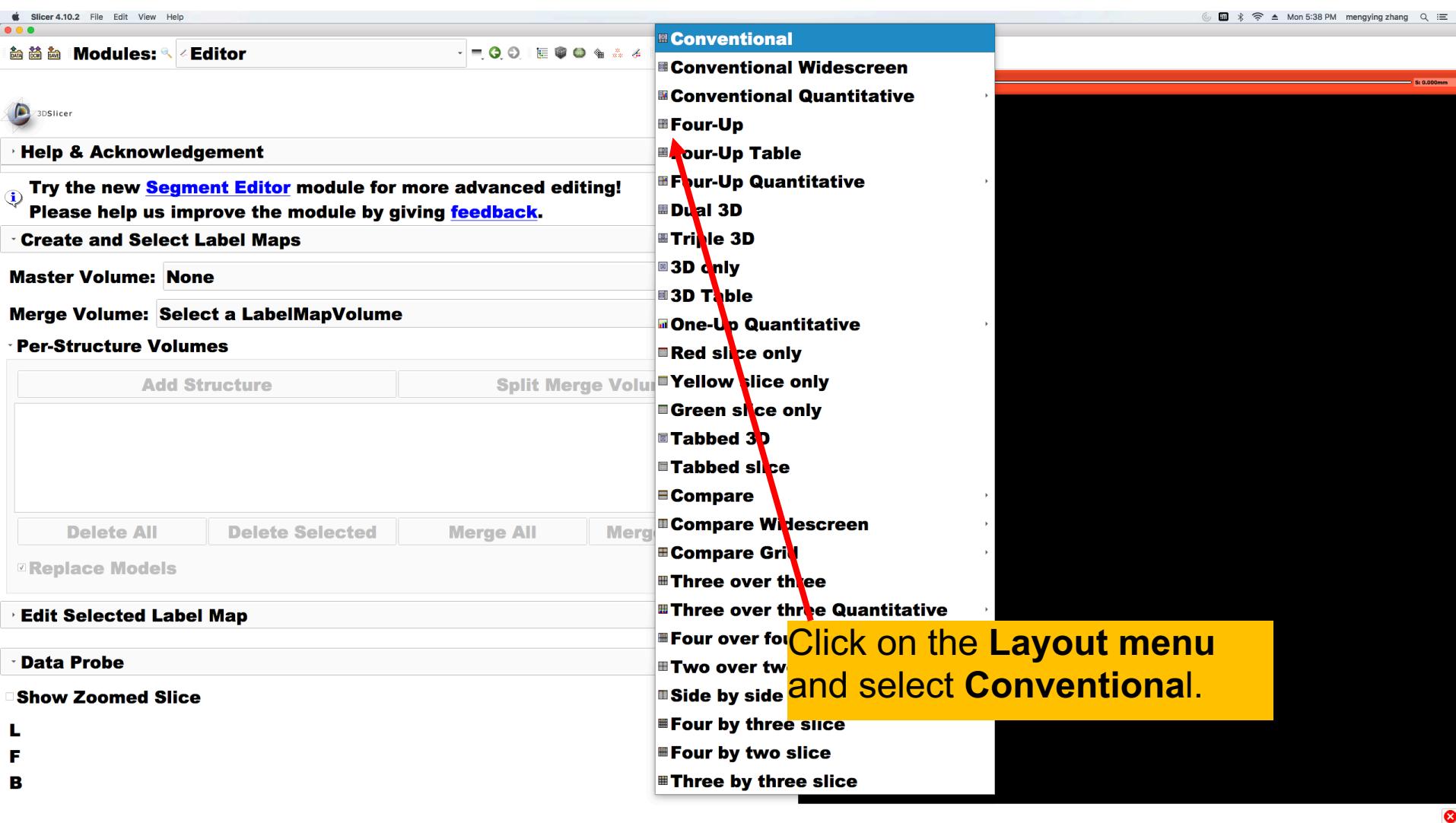
**Annotation:** Slicer displays the results of the merging of the three labelmaps in the 2D viewer.

**2D Viewer:**

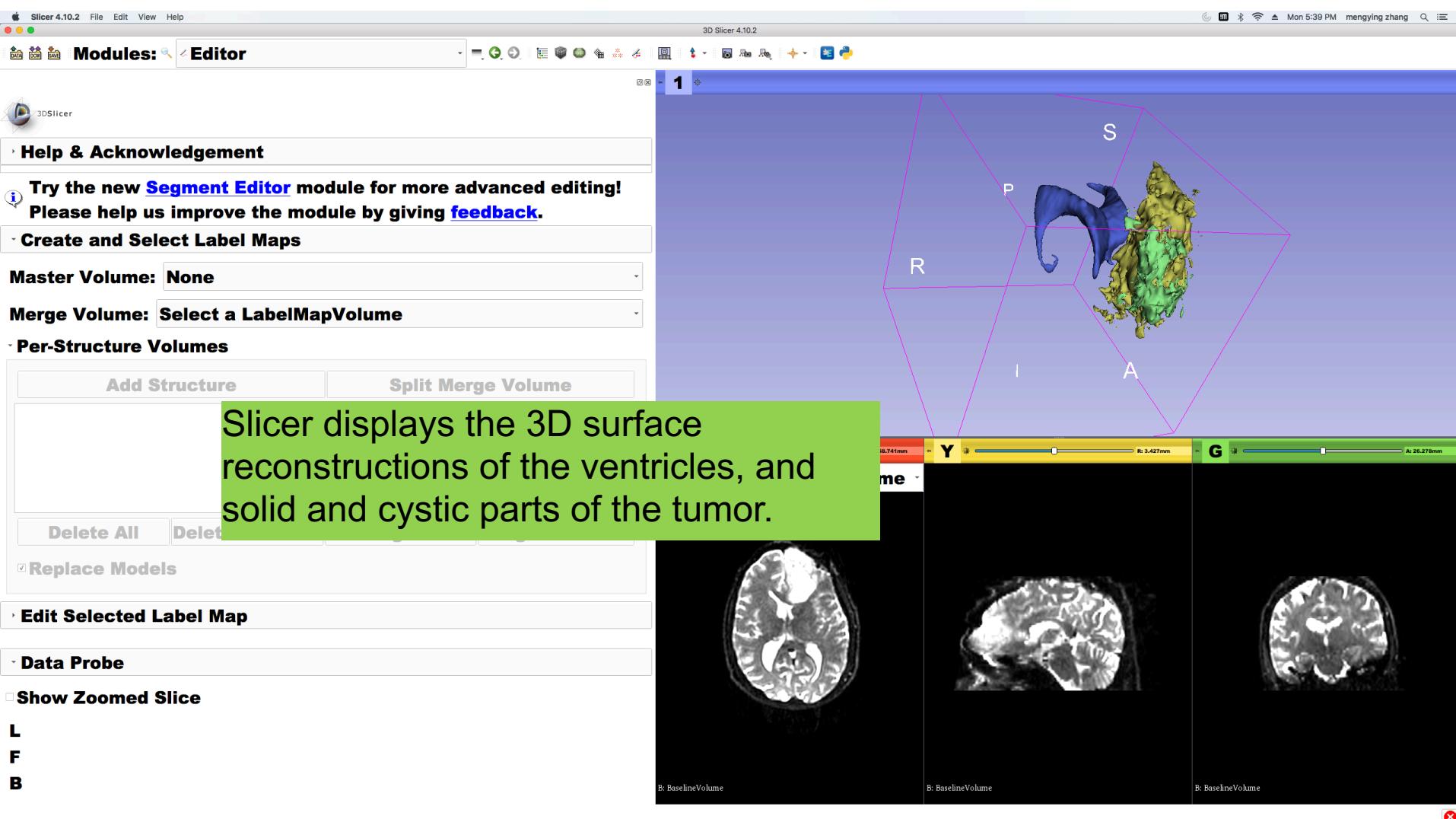


L: BaselineVolume-label (100%)  
R: BaselineVolume

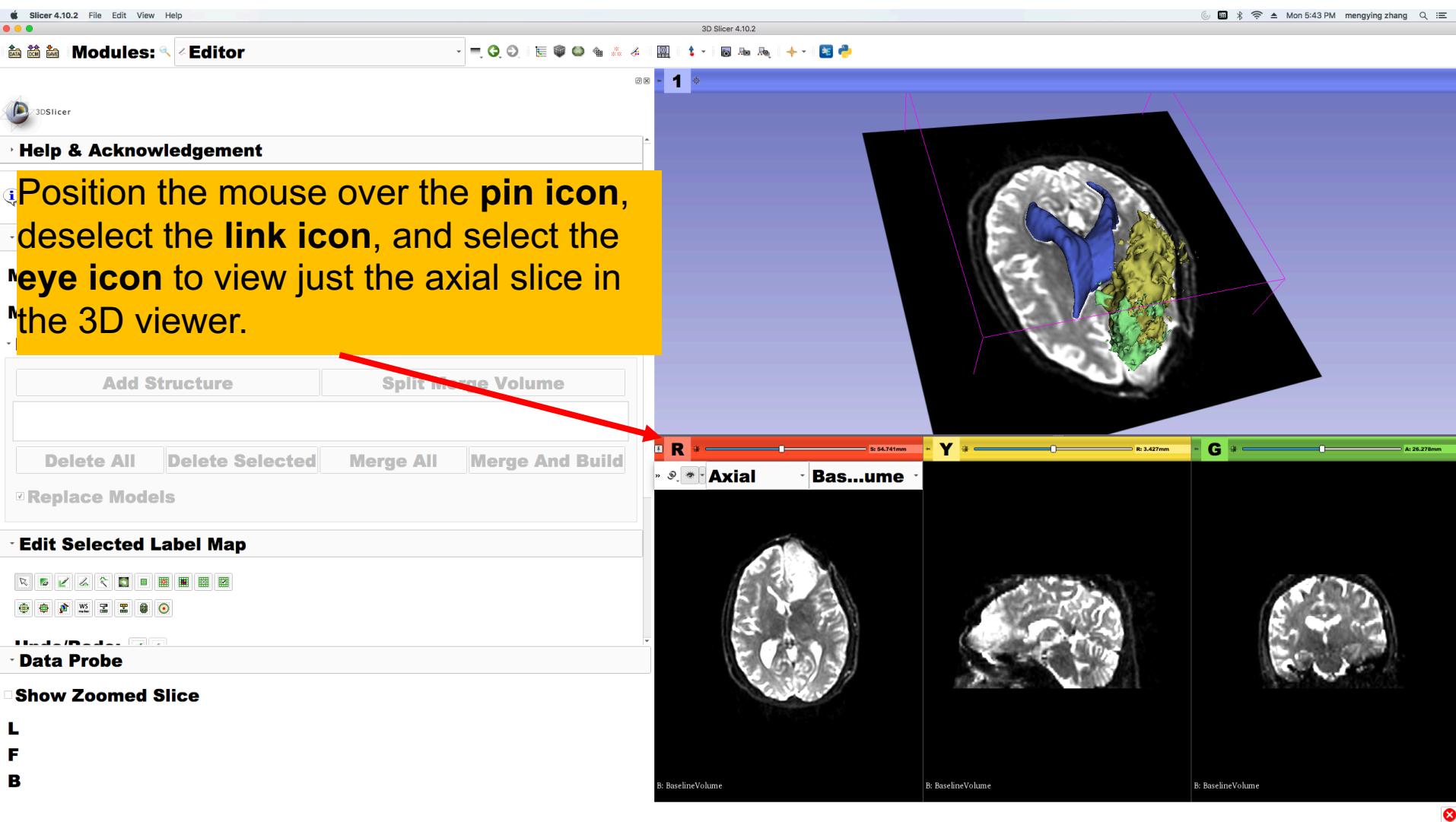
# Final Result of Segmentation



# Final Result of Segmentation



# Definition of peri-tumoral volume



# Definition of peri-tumoral volume

Slicer 4.10.2 File Edit View Help 3D Slicer 4.10.2 Mon 5:46 PM mengying zhang

**Modules:** Editor

**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**

Add Structure	Split Merge Volume
Num Col Name	Label Volume
200 - cyst	BaselineVolume-cyst-label

Delete All Delete Selected Merge All Merge And Build

Replace Models

**Edit Selected Label Map**

DilateEffect

Show Zoomed Slice L F B

Select the label map **BaselineVolume-cyst-label** (yellow) and select the **DilateEffect** tool.

R: 54.741mm Y: 3.427mm G: 26.278mm

Axial

L: Baseline...l (100%) B: BaselineVolume

L: Baseline...l (100%) B: BaselineVolume

L: Baseline...l (100%) B: BaselineVolume

# Definition of peri-tumoral volume

Slicer 4.10.2 File Edit View Help 3D Slicer 4.10.2 Mon 5:50 PM mengying zhang

**Modules:** Editor

Add Structure Split Merge Volume

Num Col Name Label Volume Order

309 cyst BaselineVolume cyst\_label

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

Active Tool: DilateEffect

Label: cyst

309

Eight Neighbors

Four Neighbors

?

Apply

Dilate current label

Data Probe

Show Zoomed Slice

L F B

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

1

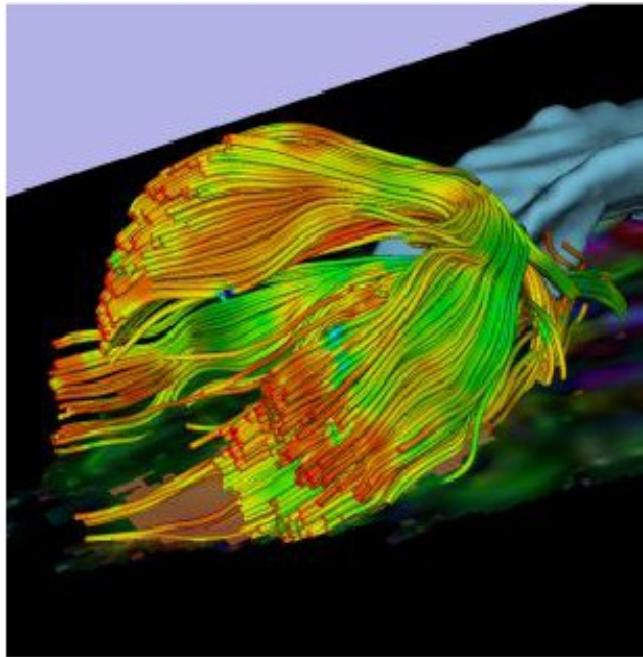
R: 54.741mm Y: 3.427mm G: 26.278mm

Axial

L: Baseline...l (100%) B: BaselineVolume

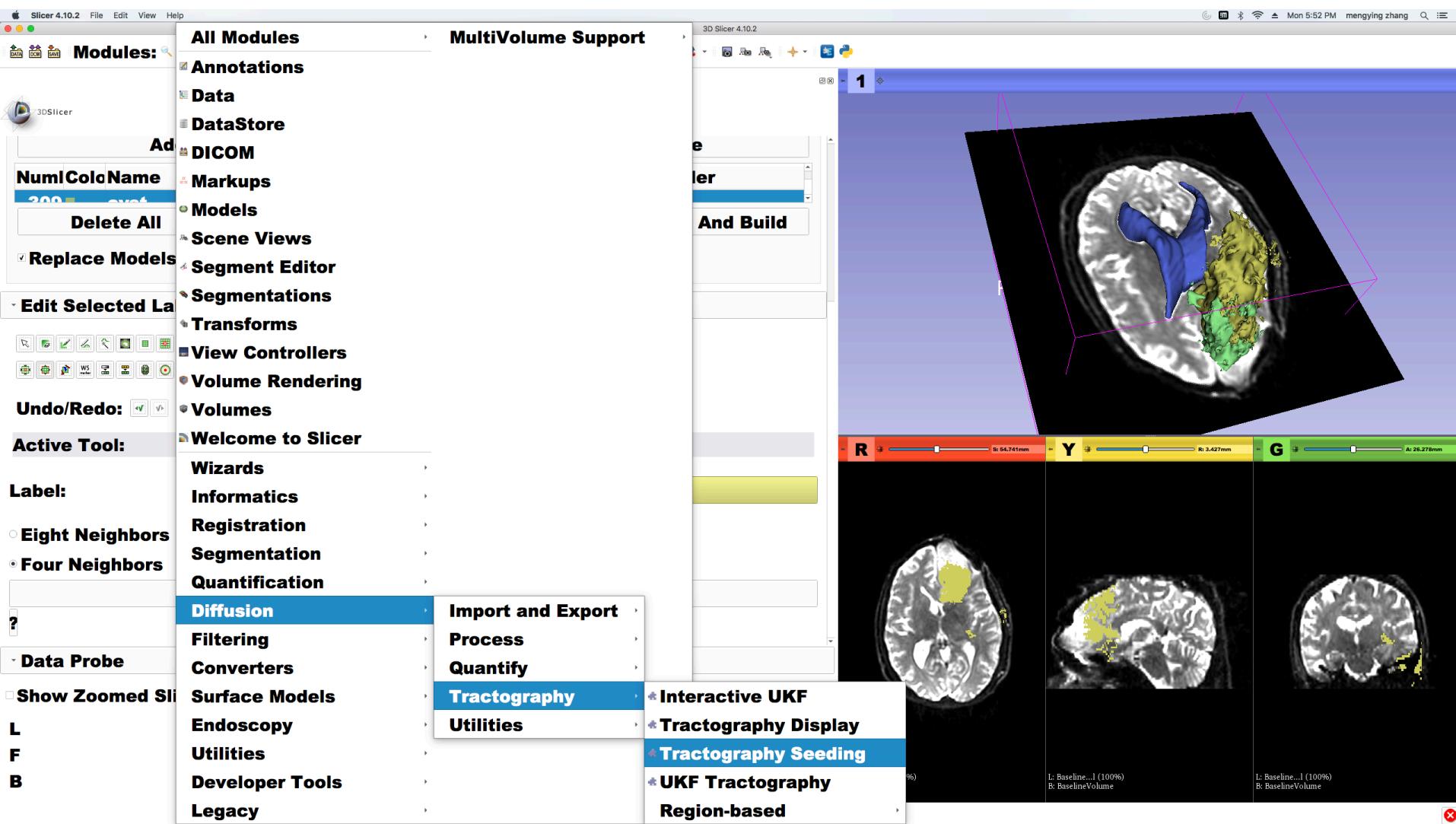
L: Baseline...l (100%) B: BaselineVolume

L: Baseline...l (100%) B: BaselineVolume



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

# Tractography LabelMap Seeding



# Tractography LabelMap Seeding

Slicer 4.10.2 File Edit View Help 3D Slicer 4.10.2 Mon 5:55 PM mengying zhang

Modules: Tractography Seeding

Parameters Node

- IO

Input DTI Volume DTIVolume

Output Fiber Bundle newFiberBundle

- Seeding

Input Fiducials, Model or Label Map BaselineVolume-cyst-label

Seeding Label Value 1

Seed Spacing (mm) 2.00

Use Index Space Random Grid

- Tractography Parameters

Threshold Type Fraction

Seeding Threshold

Stopping Threshold

Integration Step Length (mm)

- Advanced Options

- Data Probe

Show Zoomed Slice L F B

Go to I/O and set the following values:

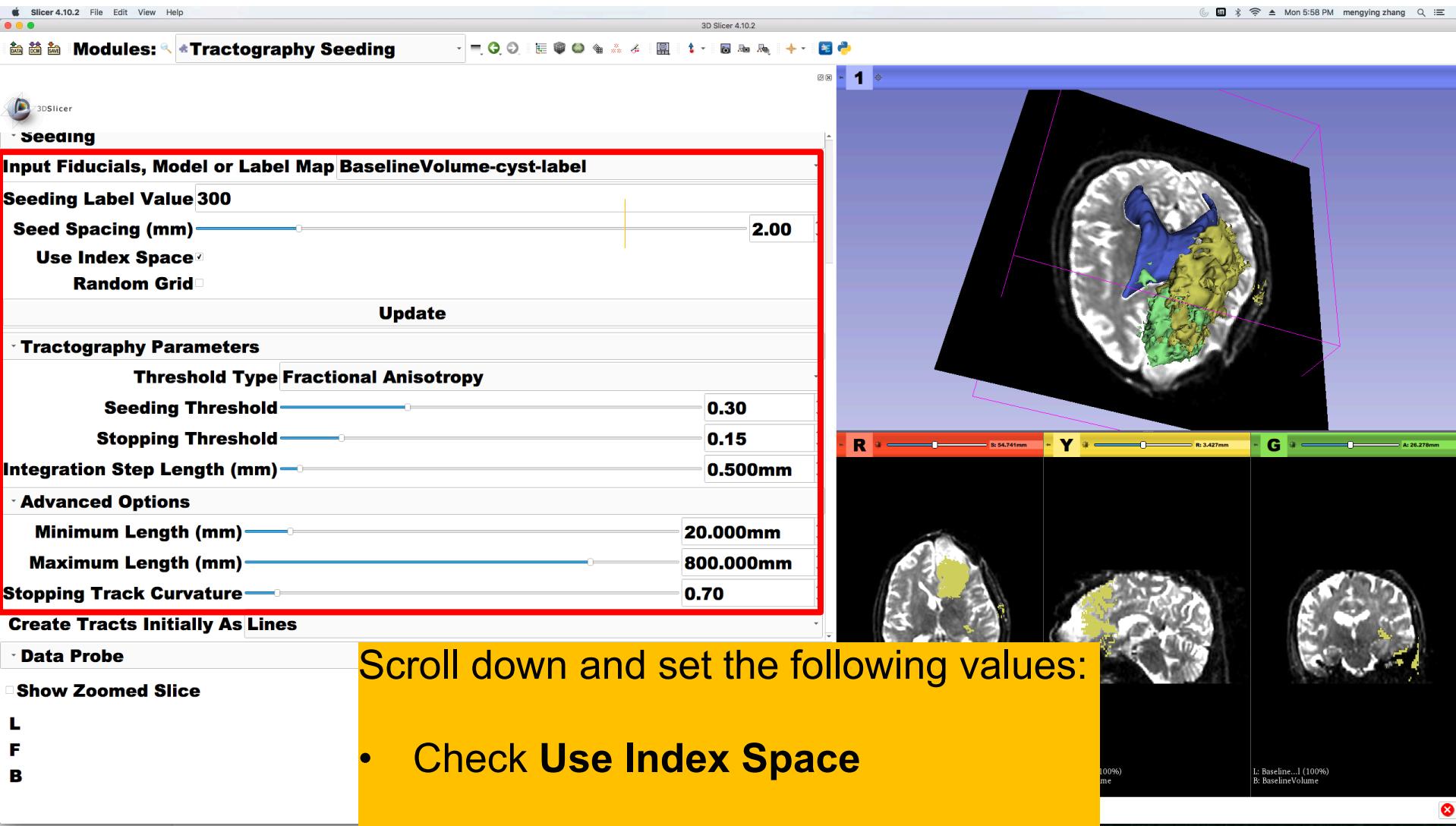
- Input DTI Volume:** DTIVolume
- Input Label Map:** BaselineVolume-cyst-label
- Output Fiber Bundle:** Create and rename newFiberBundle

L: Baseline...l (100%)  
B: BaselineVolume

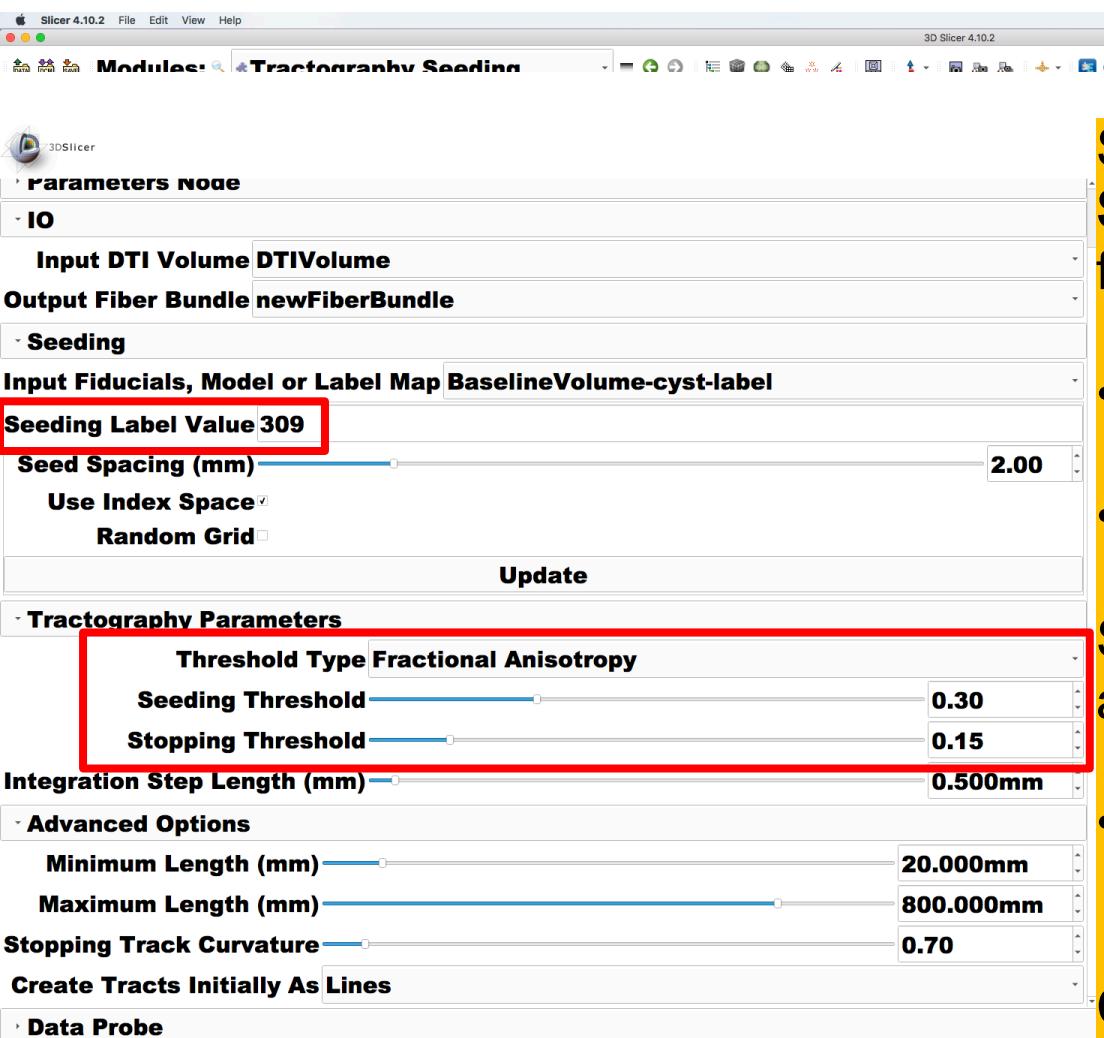
L: Baseline...l (100%)  
B: BaselineVolume

L: Baseline...l (100%)  
B: BaselineVolume

# Tractography LabelMap Seeding



# 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

Slicer displays the white matter fibers surrounding the tumor

Seeding Label Value 309

Seed Spacing (mm) 2.00

Use Index Space  Random Grid

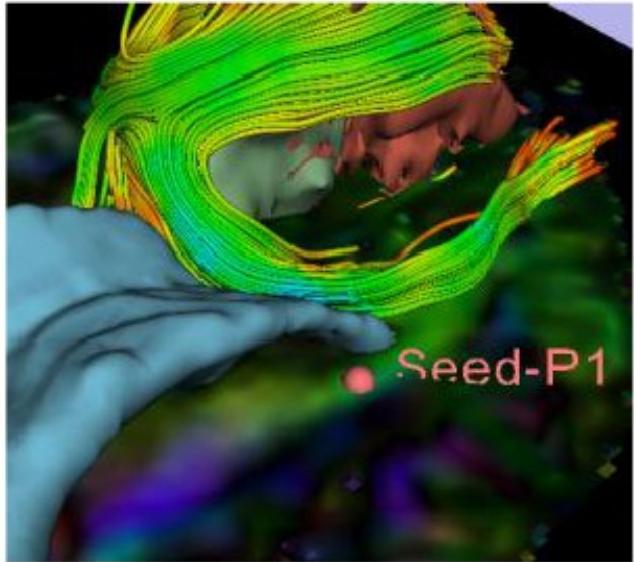
Update

The fibers are colored according to fractional anisotropy values (red = low FA; blue,green=high FA)

L: Baseline...l (100%)  
B: BaselineVolume

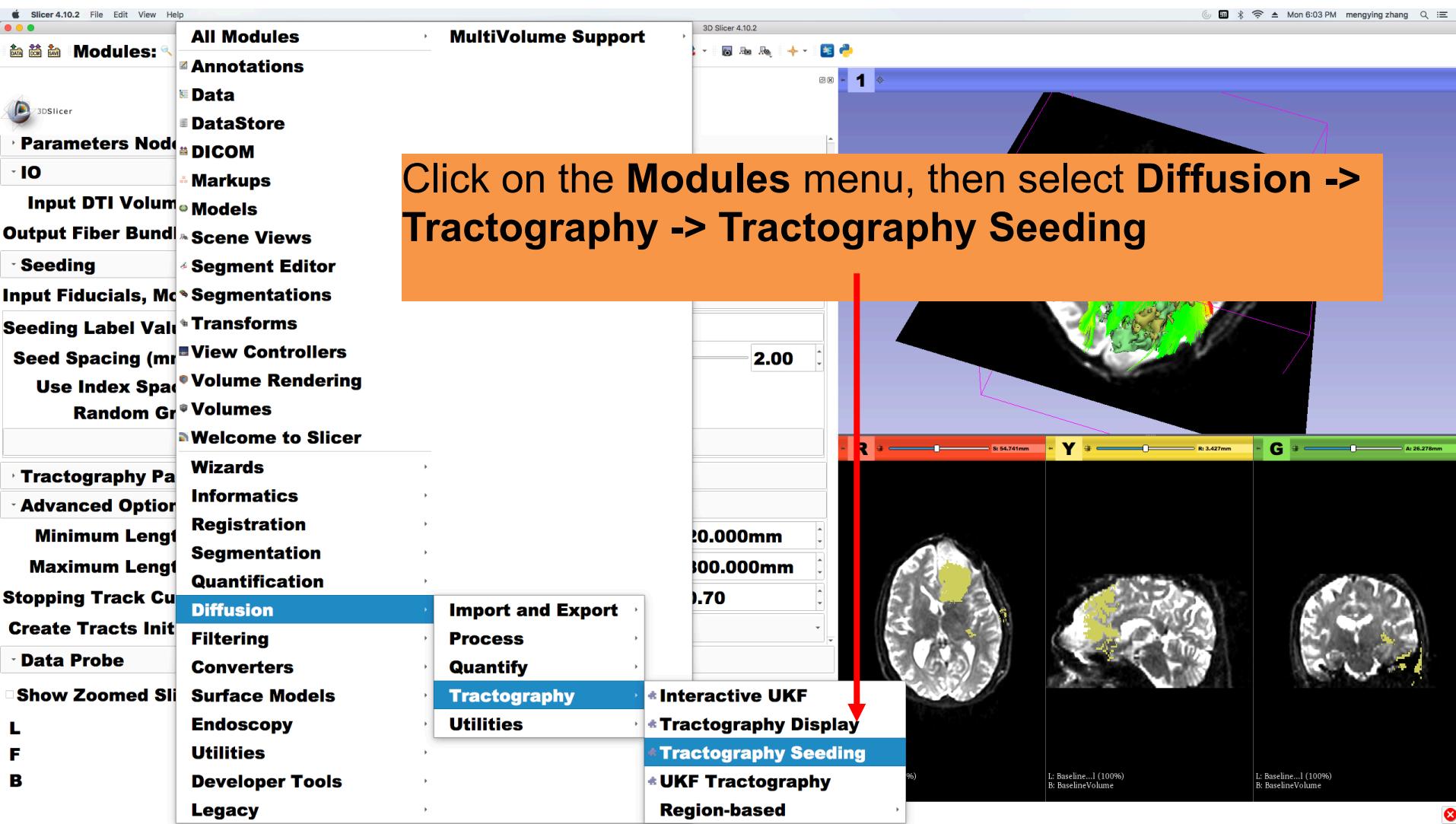
L: Baseline...l (100%)  
B: BaselineVolume

L: Baseline...l (100%)  
B: BaselineVolume

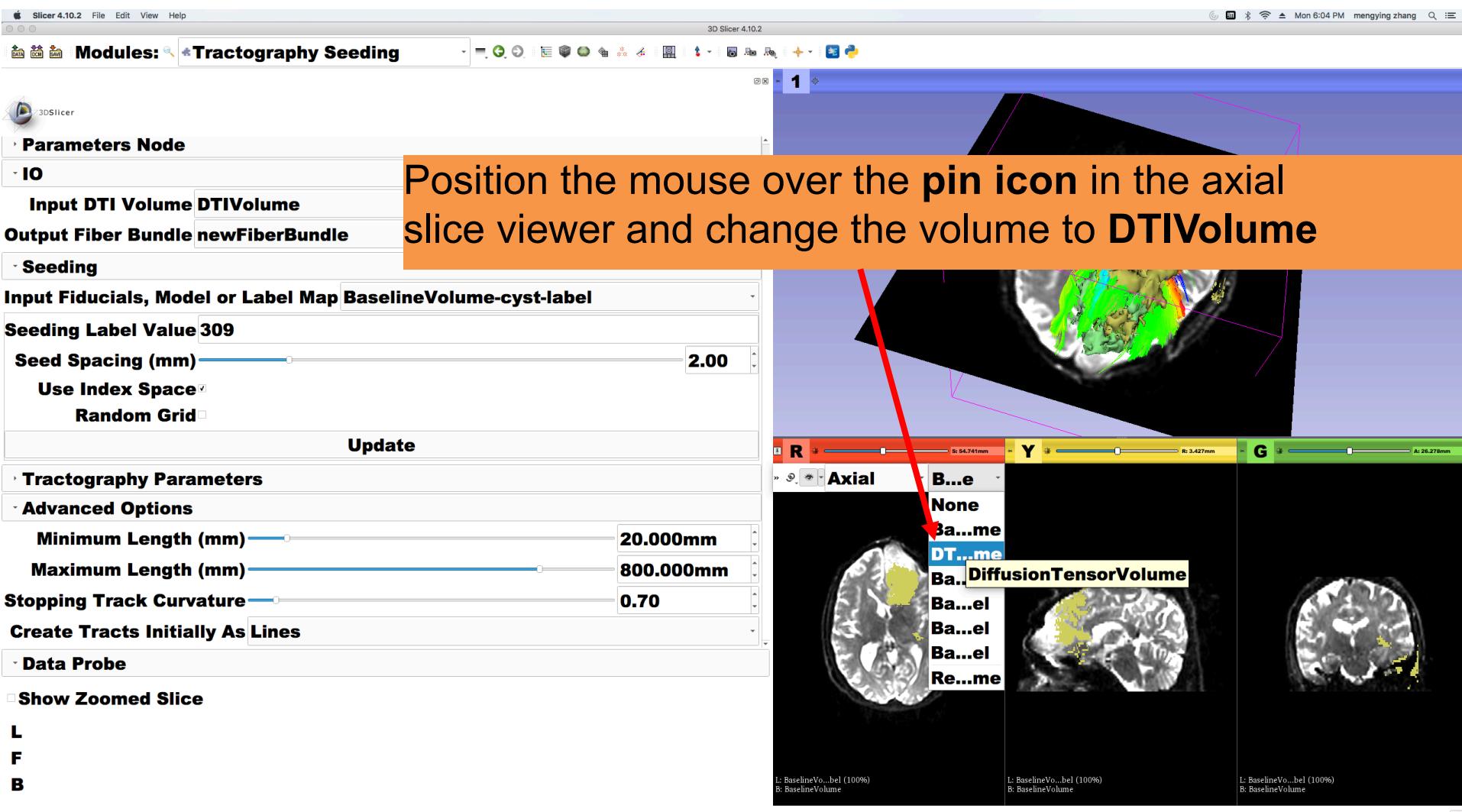


## Part 4: Tractography exploration of the ipsilateral and contralateral side

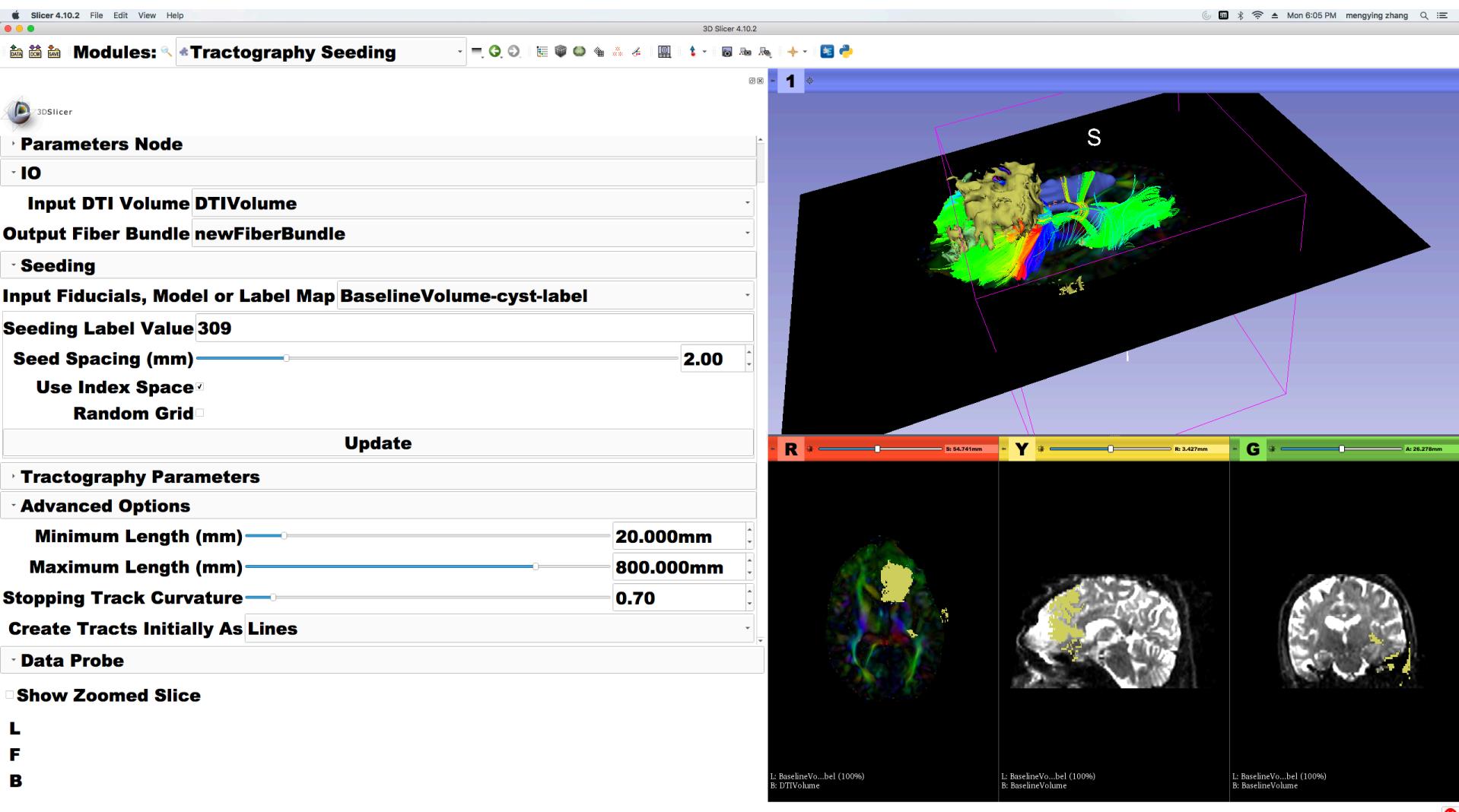
# Tractography on-the-fly



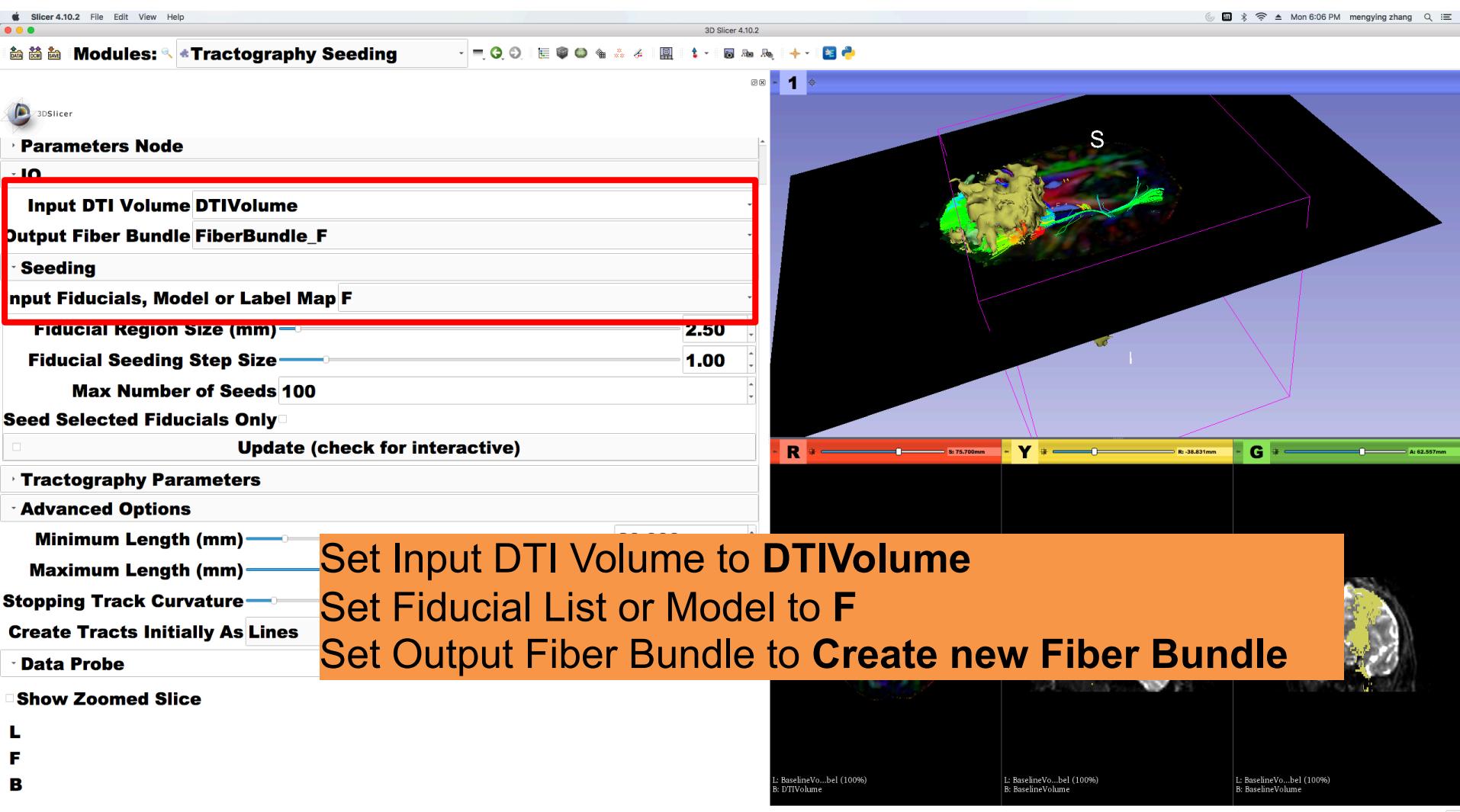
# Tractography on-the-fly



# Tractography on-the-fly



# Tractography on-the-fly



# Tractography on-the-fly

Slicer 4.10.2 File Edit View Help 3D Slicer 4.10.2 Mon 6:09 PM mengying zhang

**Modules:** Tractography Seeding

**Seeding**

**Input Fiducials, Model or Label Map F**

- Fiducial Region Size (mm) 2.50
- Fiducial Seeding Step Size 1.00
- Max Number of Seeds 100

**Seed Selected Fiducials Only**  **Update (check for interactive)**

**Tractography Parameters**

Threshold Type Fractional Anisotropy

- Seeding Threshold 0.30
- Stopping Threshold 0.15

Integration Step Length (mm) 0.500mm

**Advanced Options**

- Minimum Length (mm) 10.000mm
- Maximum Length (mm) 800.000mm
- Stopping Track Curvature 0.70

Create Tracts Initially As Lines

Data Probe

Show Zoomed Slice L F B

1

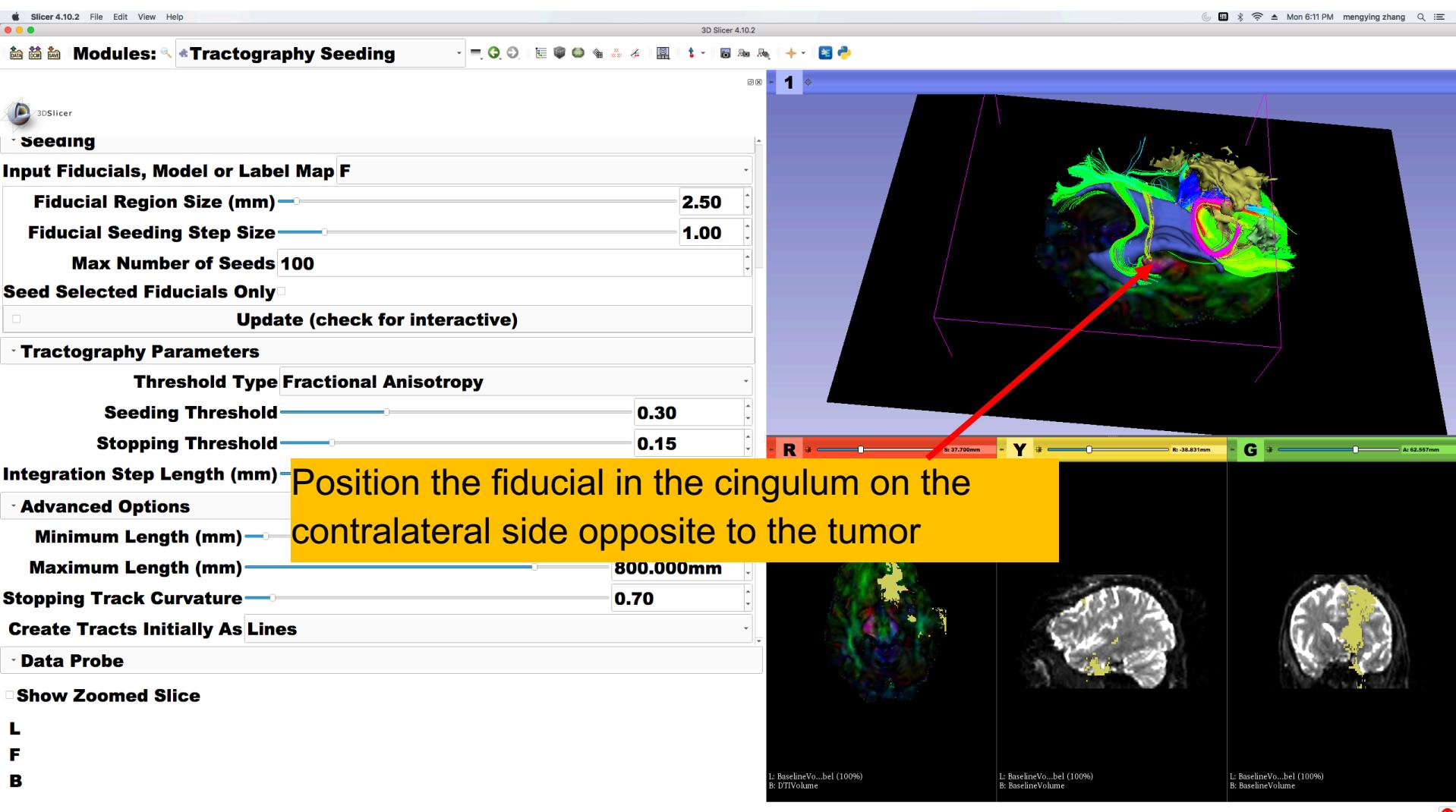
S

L: BaselineVolume (100%)  
B: BaselineVolume

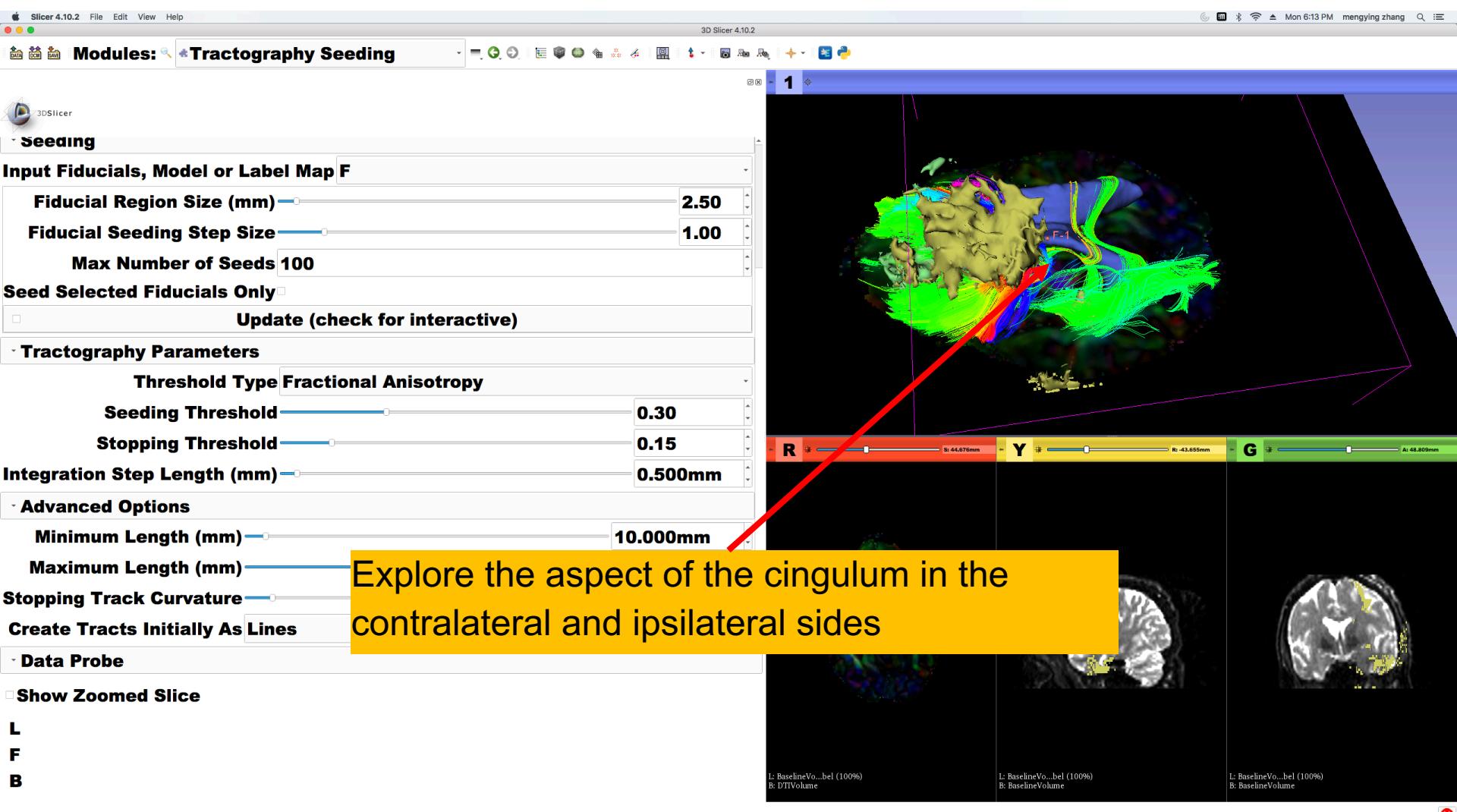
L: BaselineVolume (100%)  
B: BaselineVolume

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

# Tractography on-the-fly



# 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

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