



Exploring Peritumoral White Matter Fibers for Neurosurgical Planning

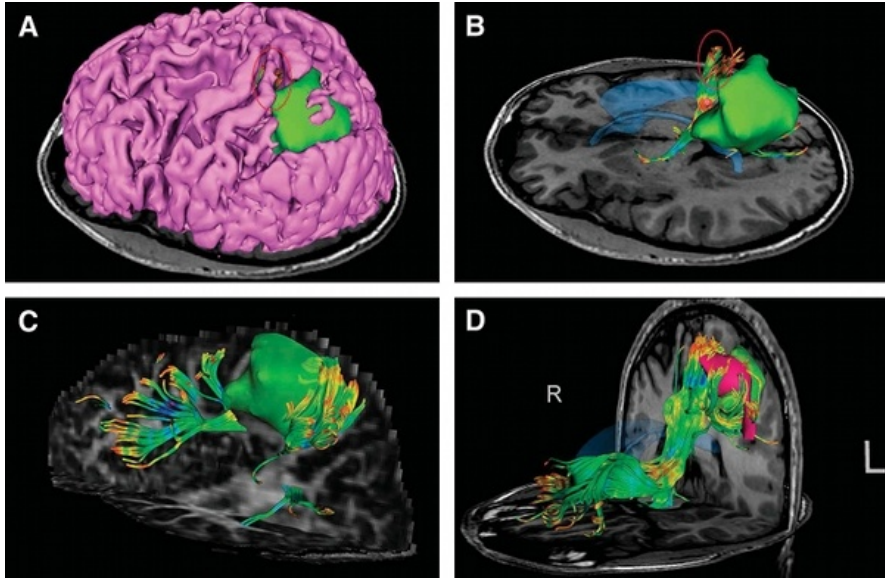
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Surgical Planning Laboratory

Harvard University

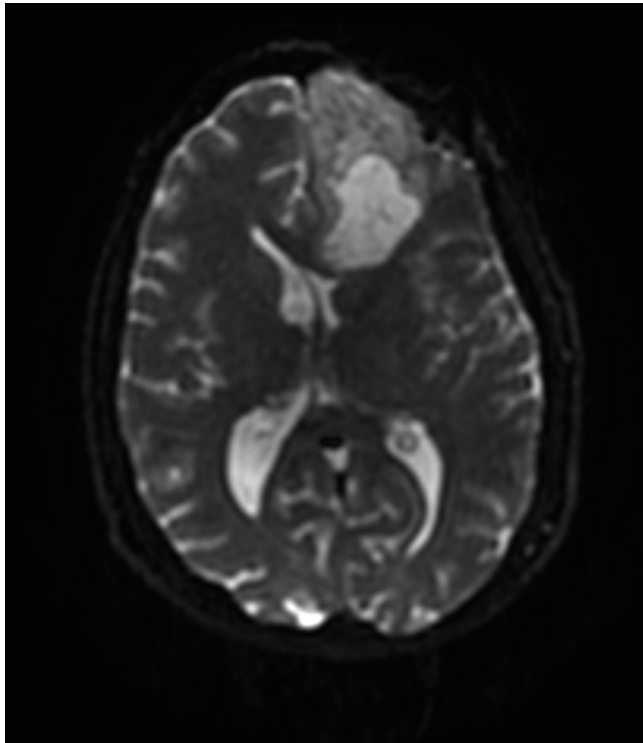
Clinical Goal



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.

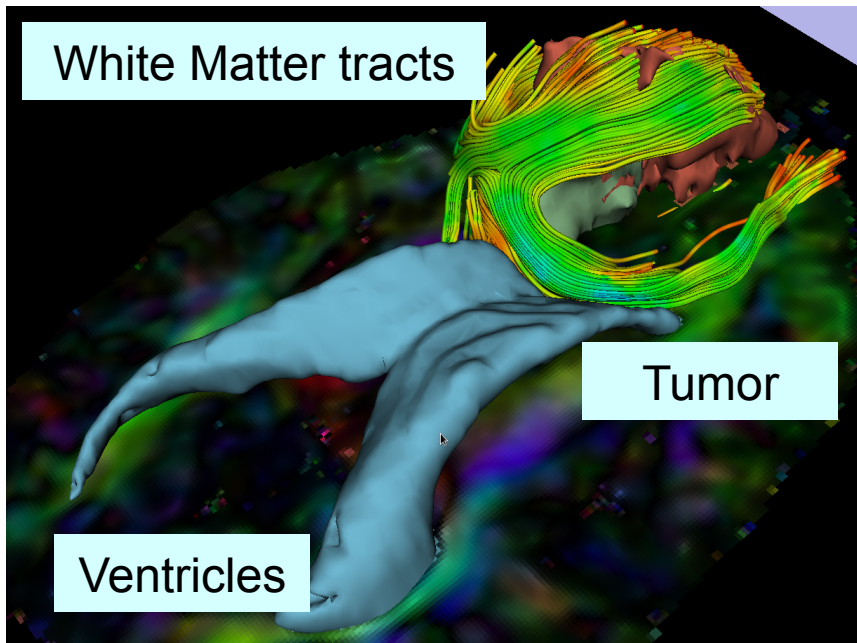
Image Courtesy of Dr. Alexandra Golby, Brigham and Women's Hospital, Boston, MA..

Clinical Case



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

Clinical Goal



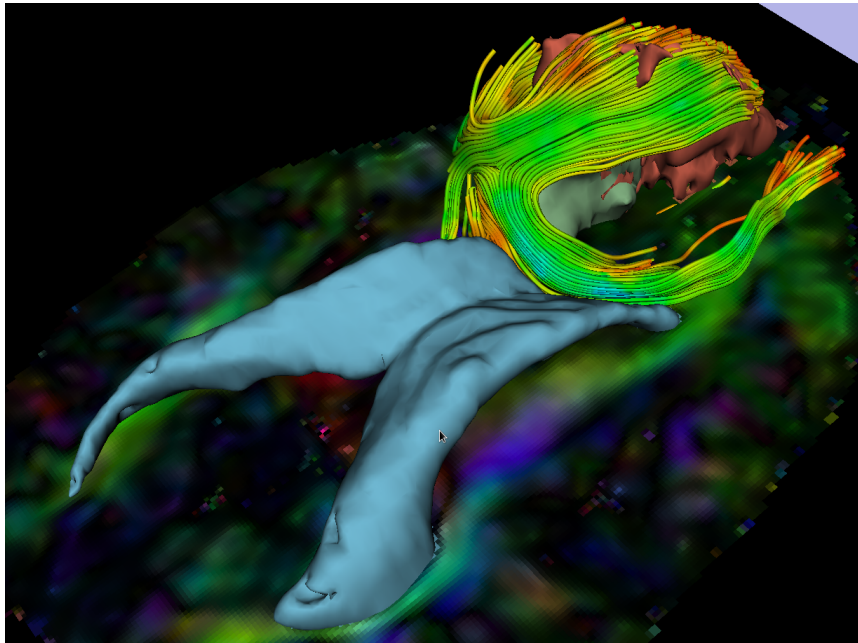
The goal of this tutorial is to explore white matter fibers surrounding a tumor using Diffusion Tensor Imaging (DTI) Tractography.

Tutorial Material

- **Software:** Slicer4.1 release
- **Dataset:** WhiteMatterExplorationDataset

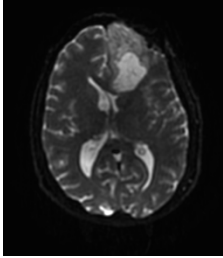
www.slicer.org

Image Analysis Pipeline

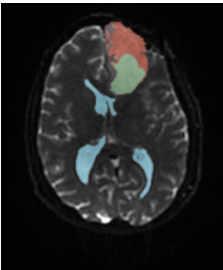


The image analysis pipeline described in this tutorial uses three different algorithms: the “Grow Cut” algorithm for segmentation of the tumor parts, the Marching Cube algorithm for surface modeling, and the single tensor streamline tractography algorithm for tract generation.

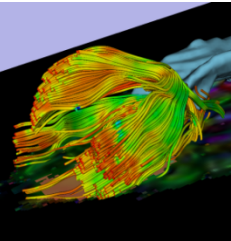
Overview of the analysis pipeline



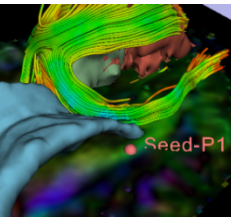
Part 1: Loading & Visualization of Diffusion Data



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

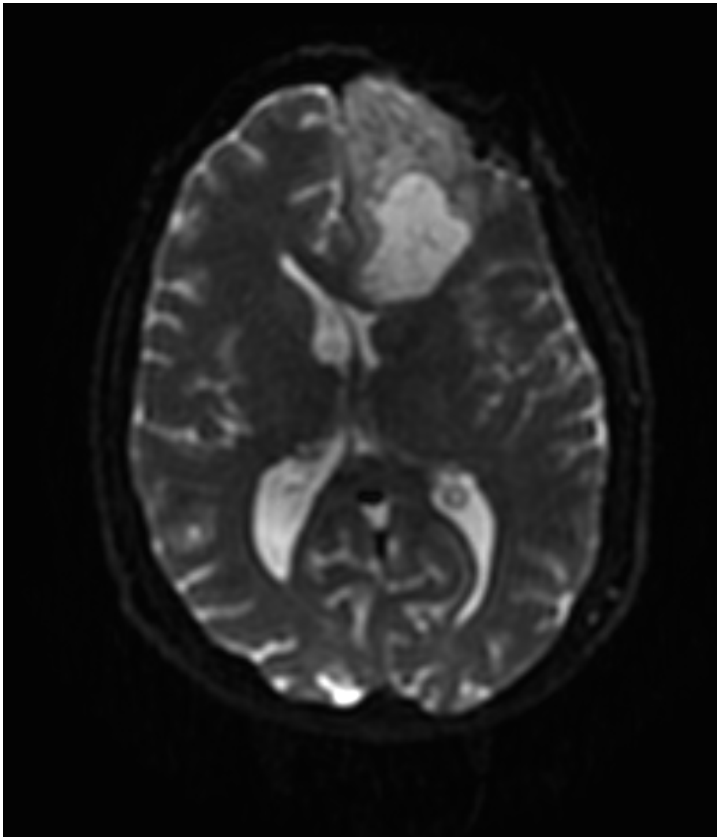


Part 3: Tractography reconstruction of the white matter fibers in the peri-tumoral volume



Part 4: Tractography exploration of the ipsilateral and contralateral side

Part 1: Loading and Visualization of Diffusion Data

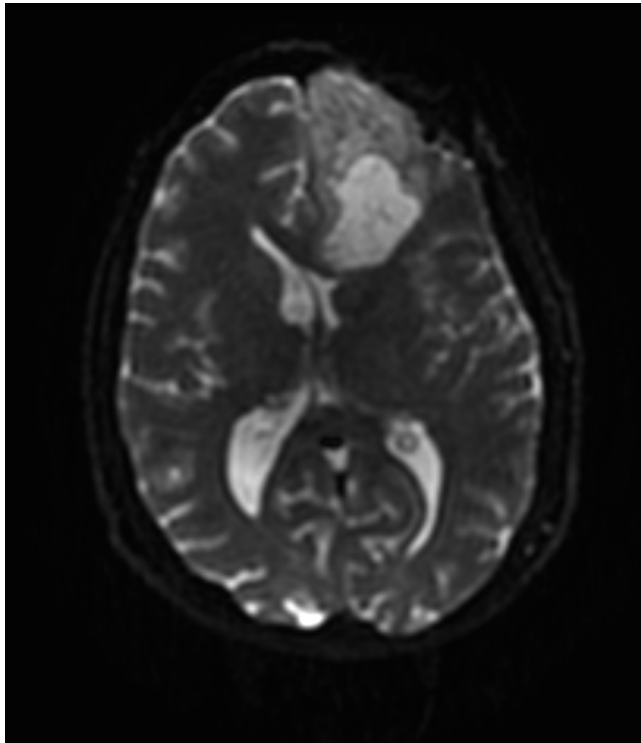
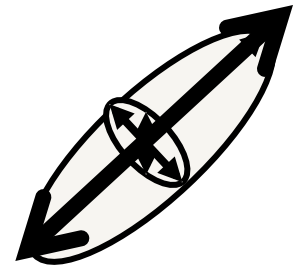


Diffusion Tensor Imaging

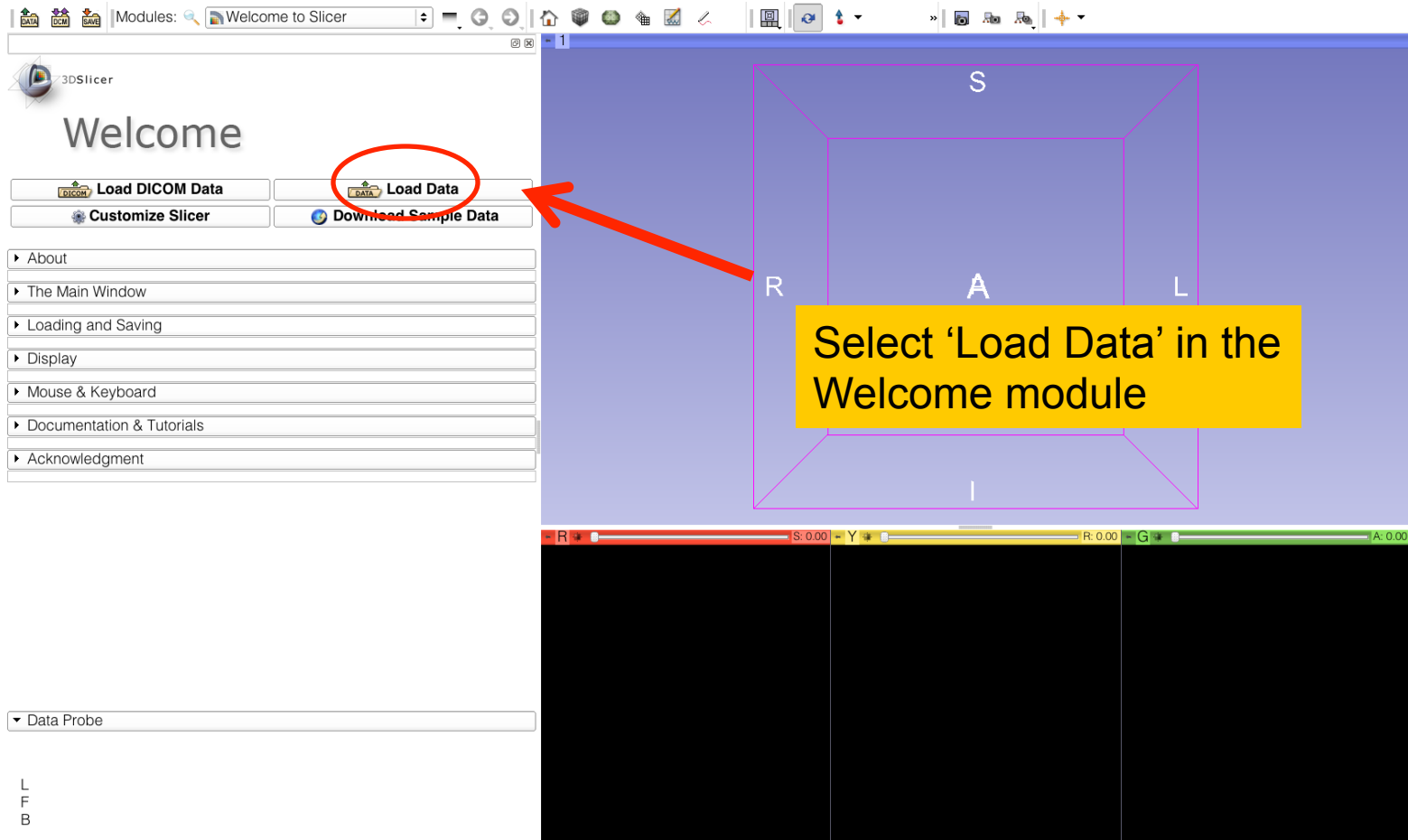
$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$

(Stejskal and Tanner 1965, Basser 1994)

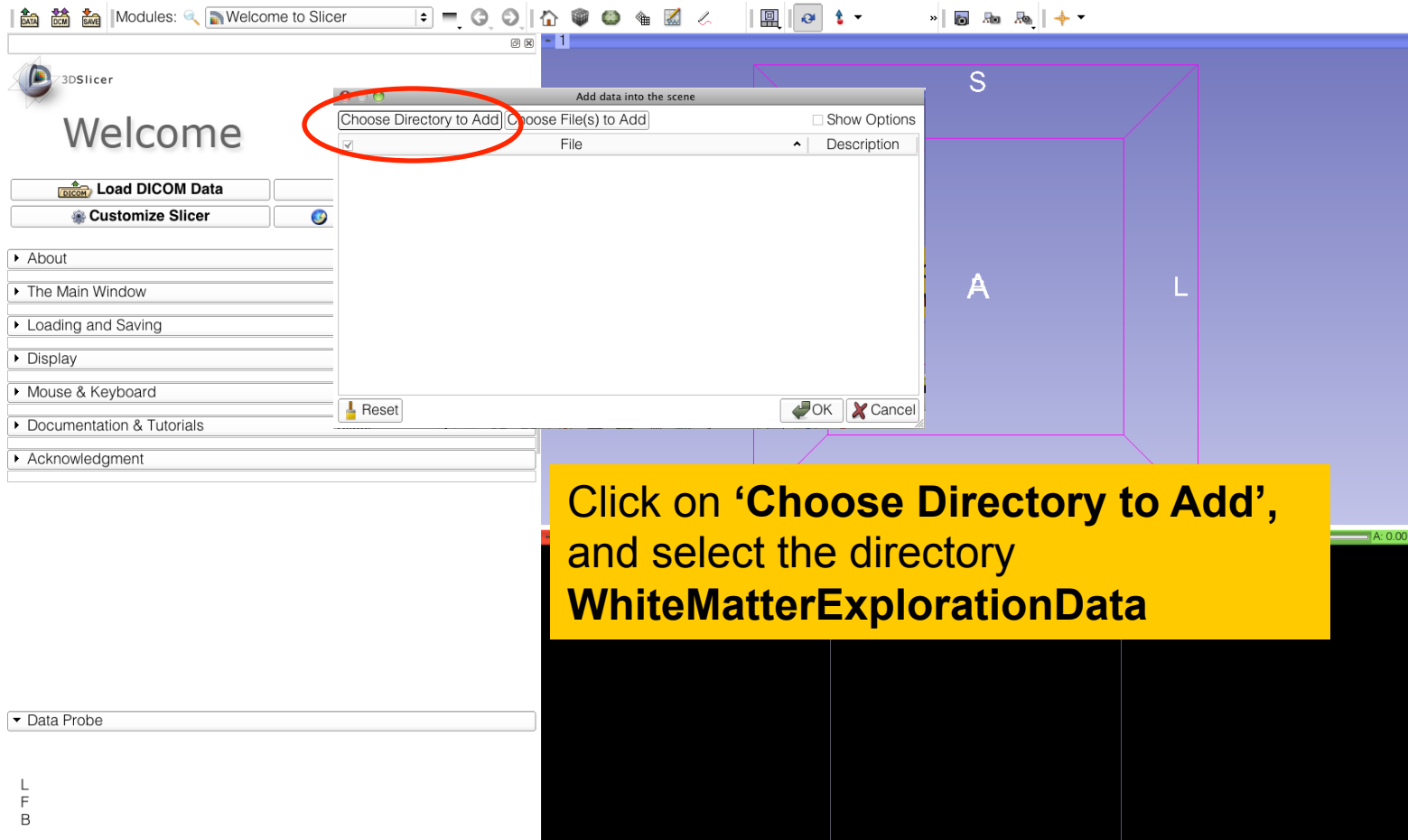
$$\underline{D} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix}$$



Loading DTI and Baseline Data



Loading DTI and Baseline Data



Loading DTI and Baseline Data

3D Add data into the scene

Choose Directory to Add Choose File(s) to Add Show Options

File	Description
<input type="checkbox"/> /Users/spujol/data/WhiteMatterExplorationData/DTIVolume.raw.gz	Volume
<input checked="" type="checkbox"/> /Users/spujol/data/WhiteMatterExplorationData/DTIVolume.nhdr	Volume
<input checked="" type="checkbox"/> /Users/spujol/data/WhiteMatterExplorationData/BaselineVolume.nrrd	Volume

Buttons: About, The Me, Loadin, Display, Mouse, Docum, Reset, Acknowledgment, OK, Cancel

▼ Data Probe

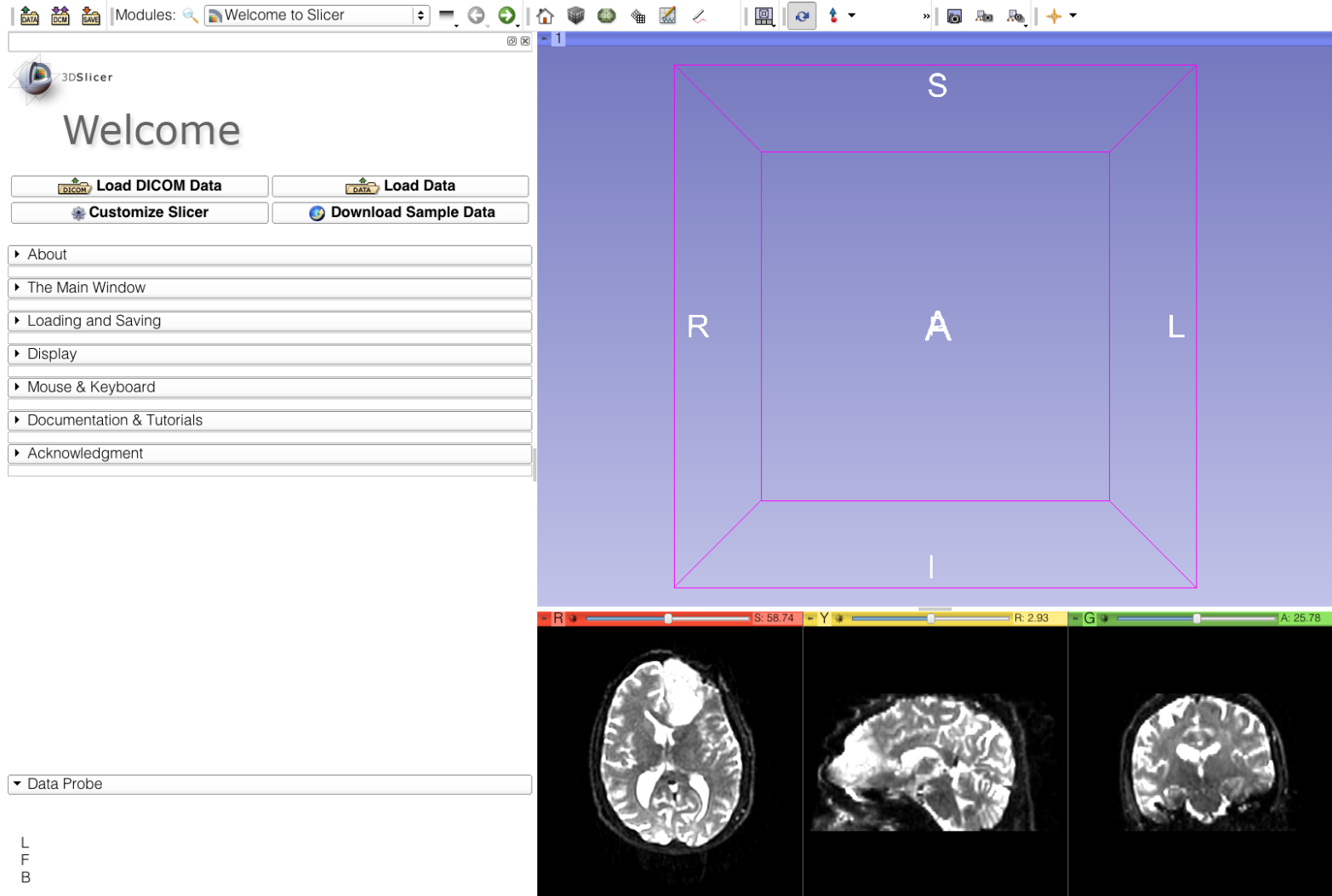
L
F
B

S
A
L
I

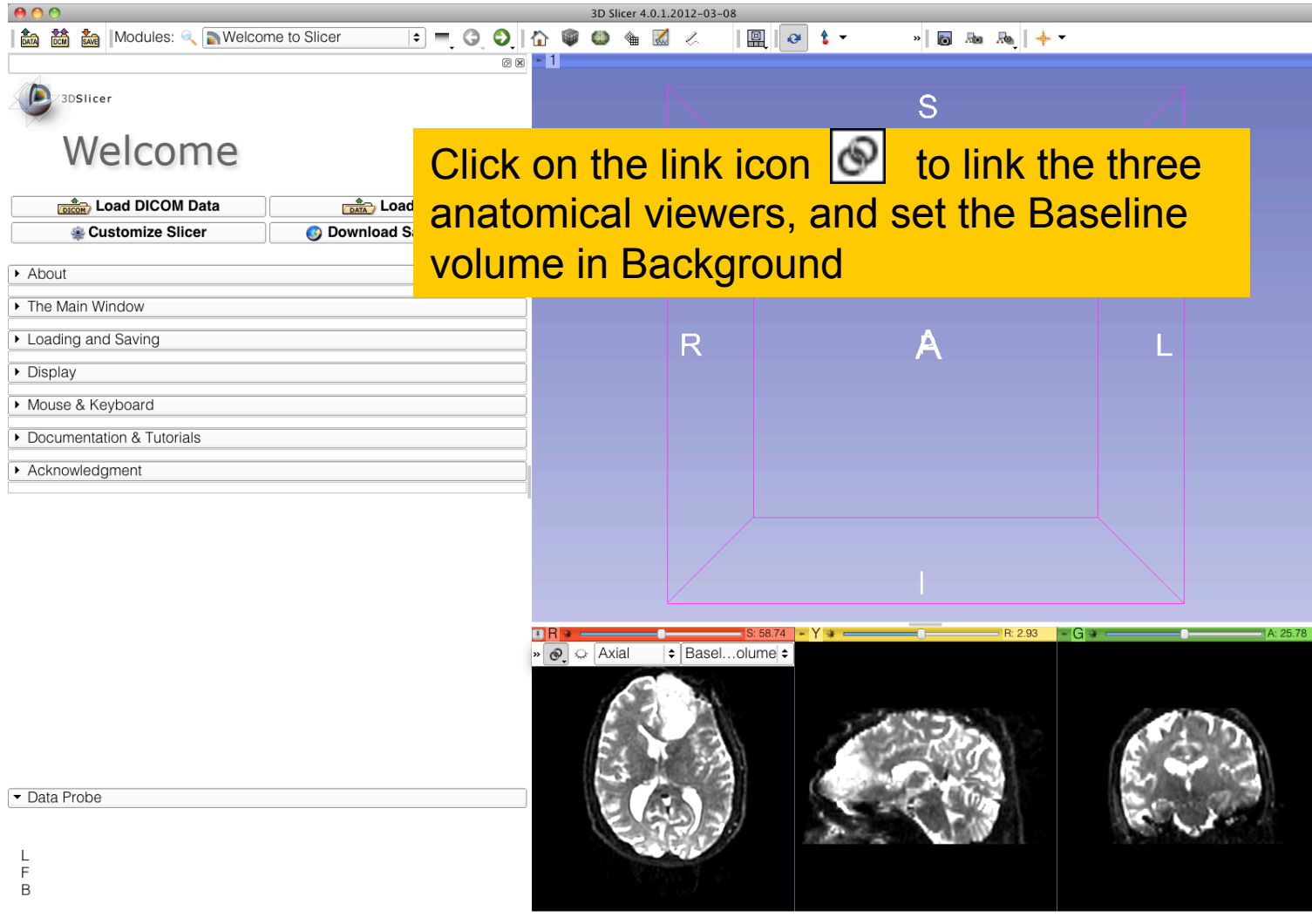
Select the directory
WhiteMatterExplorationData

Select the files
BaselineVolume.nrrd and
DTIVolume.nhdr and click on **OK**

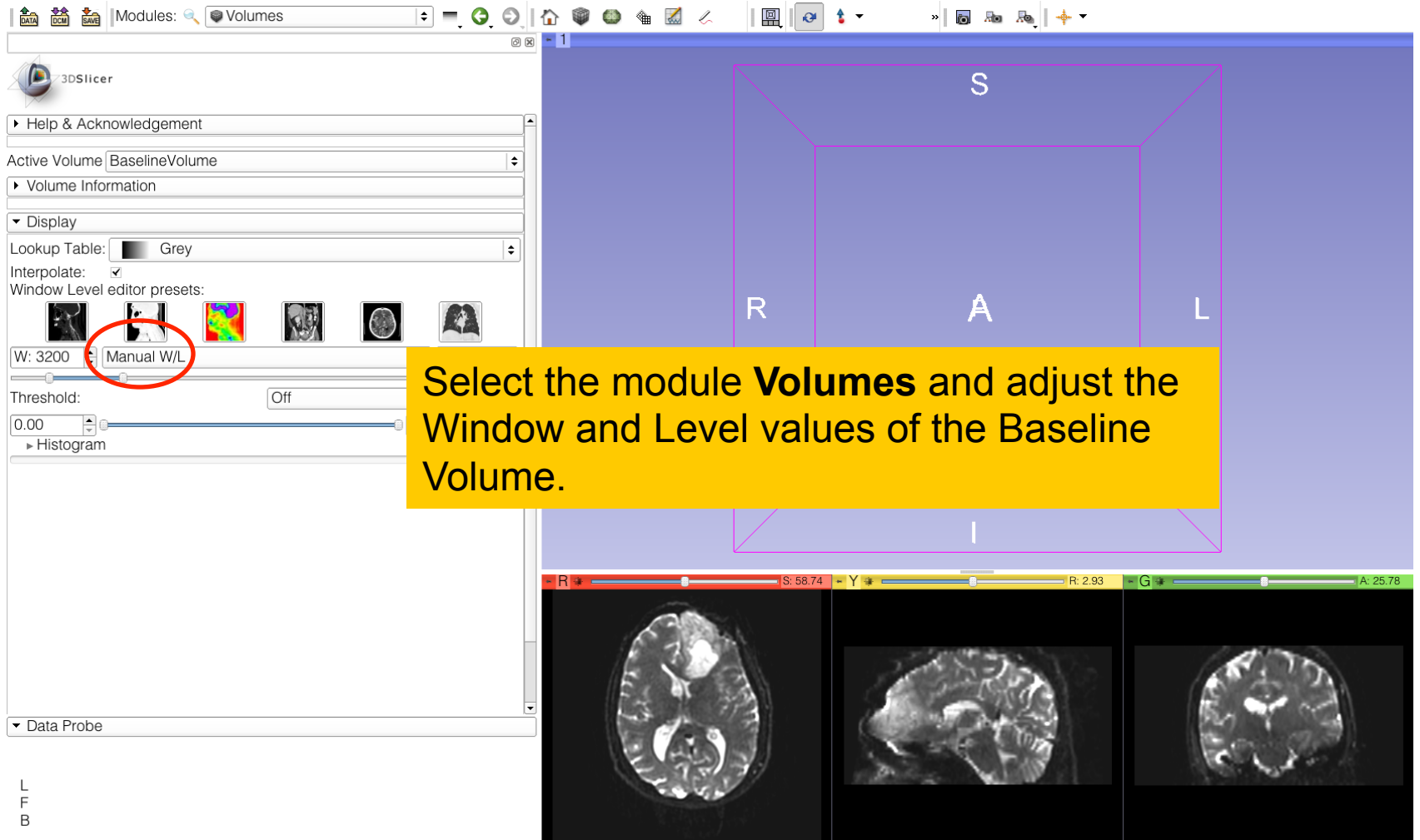
Loading DTI and Baseline Data



Loading DTI and Baseline Data



Loading DTI and Baseline Data



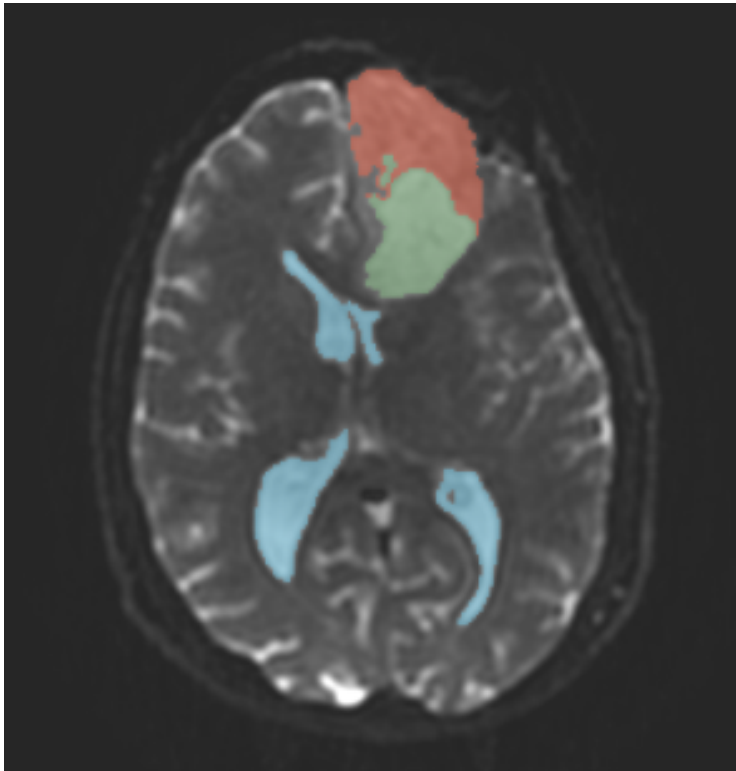
Loading DTI and Baseline Data

The screenshot shows the 3D Slicer software interface. On the left, the 'Display' panel is visible, showing 'Active Volume: BaselineVolume', 'Lookup Table: Grey', and 'Interpolate: checked'. The 'Window Level editor presets' section shows several icons. The 'Threshold' is set to 'Off' with a range from 0.00 to 18197.00. A 'Histogram' button is also present. On the right, a menu is open over the main 3D view, listing various layout options. The 'Red slice only' option is circled in red. A yellow callout box at the bottom of the 3D view contains the text 'Select Red Slice Only Layout'. The main 3D view shows a grayscale axial MRI slice of a brain.

- Conventional
- Conventional Widescreen
- Conventional Quantitative
- Four-Up
- Four-Up Quantitative
- Dual 3D
- Triple 3D
- 3D only
- Red slice only**
- Yellow slice only
- Green slice only
- Tabbed 3D
- Tabbed slice
- Compare
- Compare Widescreen
- Compare Grid
- Three over three
- Four over four
- Two over Two

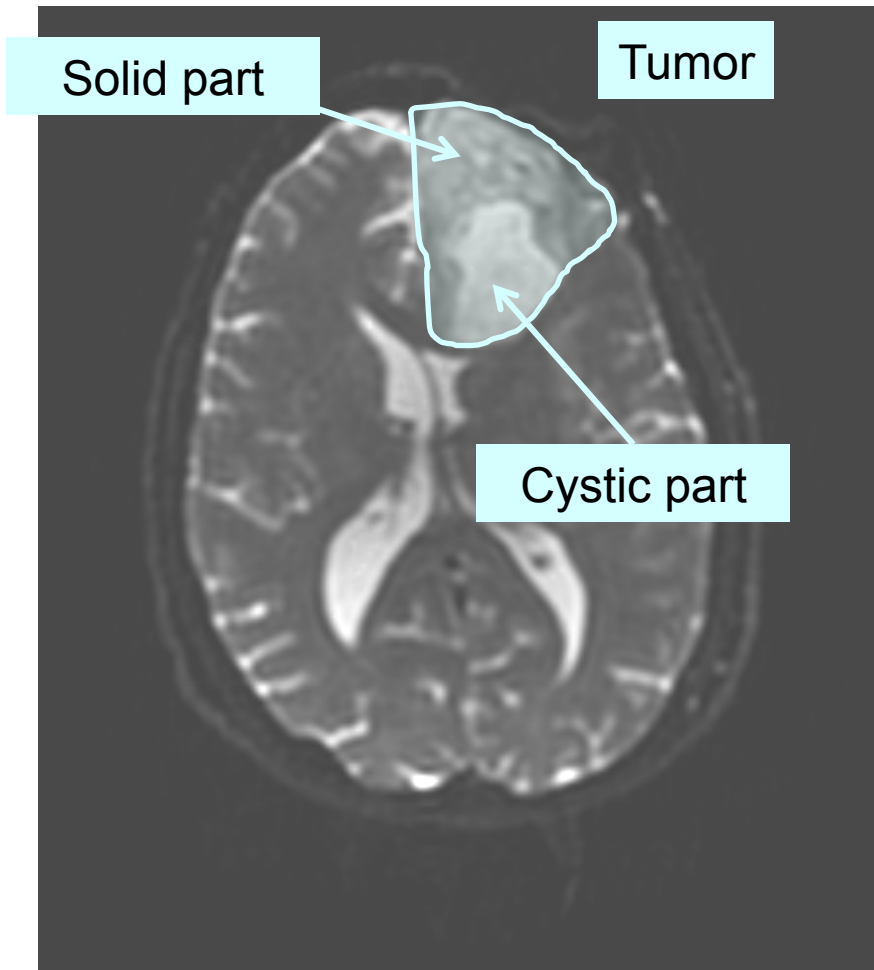
Select Red Slice Only Layout

L
F
B



Part 1: Segmenting the tumor and ventricles

Tumor Segmentation



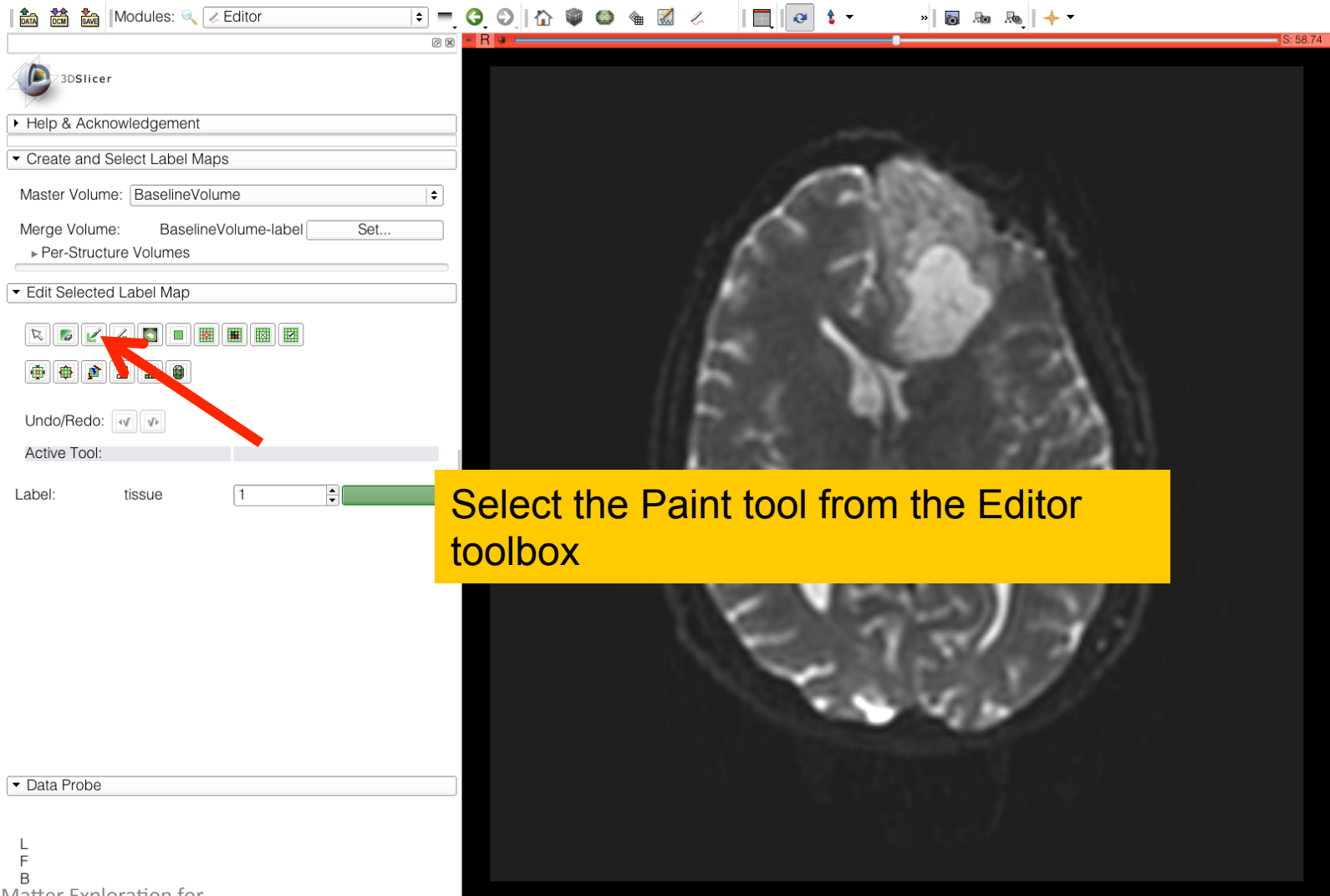
The tumor in this clinical case is composed of two parts: a solid part, and a cystic part.

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

Tumor Segmentation

The screenshot shows the 3D Slicer software interface. The 'Modules' dropdown menu at the top left is open, and the 'Editor' option is circled in red. A yellow callout box points to this menu with the text: "Select the module **Editor** from the main menu". Below the menu, the 'Create and Select Label Maps' panel is visible, showing 'Master Volume: BaselineVolume' and 'Merge Volume: None'. A dialog box is open in the center, titled 'Create a merge label map for selected master volume BaselineVolume. New volume will be BaselineVolume-label. Select the color table node will be used for segmentation labels.' The dialog box has a dropdown menu set to 'GenericAnatomyColors' and two buttons: 'Apply' and 'Cancel'. A red arrow points to the 'Apply' button. A yellow callout box at the bottom of the dialog box area says: "Select the color table 'Generic Anatomy Colors' and click on Apply".

Tumor Segmentation



Tumor Segmentation

The screenshot displays the 3DSlicer software interface. On the left, the 'Edit Selected Label Map' panel is active, showing the following settings:

- Master Volume: BaselineVolume
- Merge Volume: BaselineVolume-label
- Label: region_1, 293
- Active Tool: Undo
- Radius: 5.00mm
- Paint Over:
- Threshold Paint:
- Smudge:

A yellow text box overlaid on the interface reads: "Set the label #293 region_1 and draw a short line in the **cystic part of the tumor**".

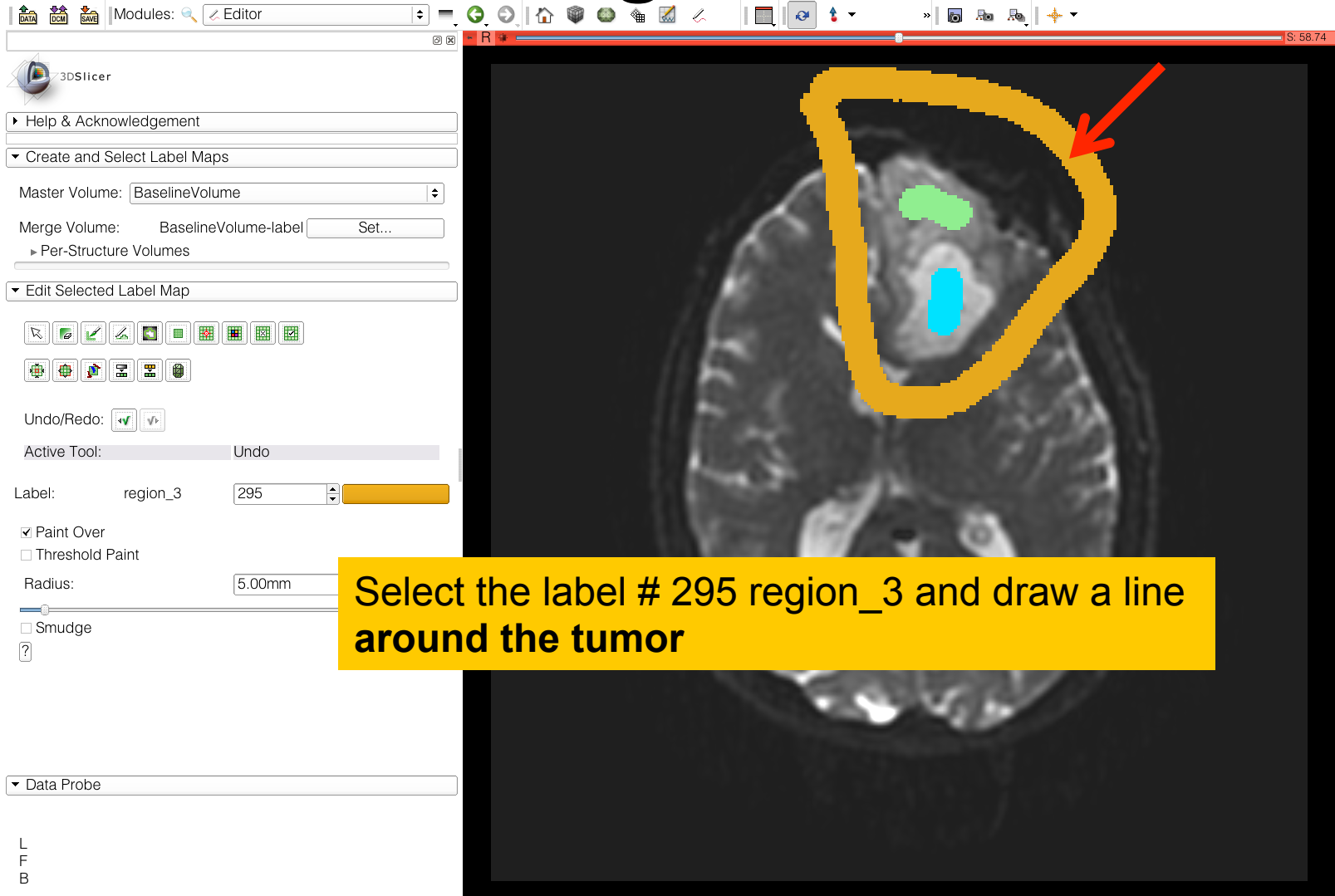
The main window shows an axial MRI slice of a brain with a cyan-colored segmented tumor region. A red arrow points to this region.

Tumor Segmentation

The screenshot shows the 3D Slicer software interface. On the left, the 'Edit Selected Label Map' panel is active, showing 'Label: mass' with a value of '7' and a green color swatch. The 'Active Tool' is set to 'Undo'. The main view displays an axial MRI brain slice with two segmented regions: a green region and a blue region. A red arrow points to the green region. A yellow text box at the bottom of the image contains the following text:

Select the label #7 (mass) and draw a short line in the **solid part of the tumor**

Tumor Segmentation



Tumor Segmentation

Select the Grow Cut segmentation algorithm

Merge Volume: BaselineVolume-label Set...

Per-Structure Volumes

Edit Selected Label Map

Undo/Redo: [undo] [redo]

Active Tool: GrowCutEffect

Label: region_3 295

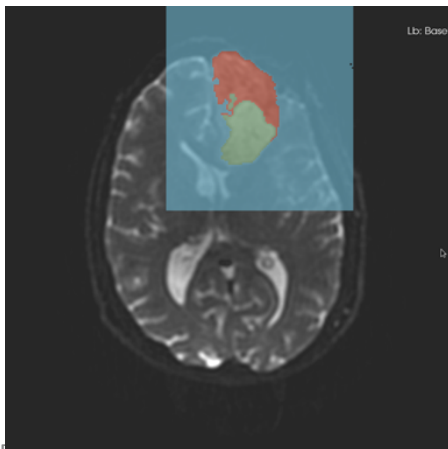
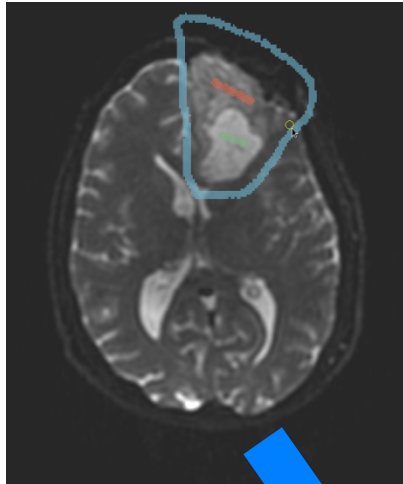
Run the GrowCut segmentation on the current label map. This will use your current segmentation as an example to fill in the rest of the volume.

Apply

Data Probe

L
F
B

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

Click on Apply to start the Grow Cut segmentation algorithm

3DSlicer

Modules: Editor

Merge Volume: BaselineVolume-label Set...

Per-Structure Volumes

Edit Selected Label Map

Undo/Redo: [Undo] [Redo]

Active Tool: GrowCutEffect

Label: region_3 295

Run the GrowCut segmentation on the current label map. This will use your current segmentation as an example to fill in the rest of the volume.

Apply

Data Probe

L
F
B

Tumor Segmentation

The screenshot shows the 3D Slicer interface with an MRI slice of a brain. A tumor is segmented into two parts: a solid part (green) and a cystic part (blue). A yellow box highlights the segmentation results. A green box contains the text "Slicer displays the results of the segmentation".

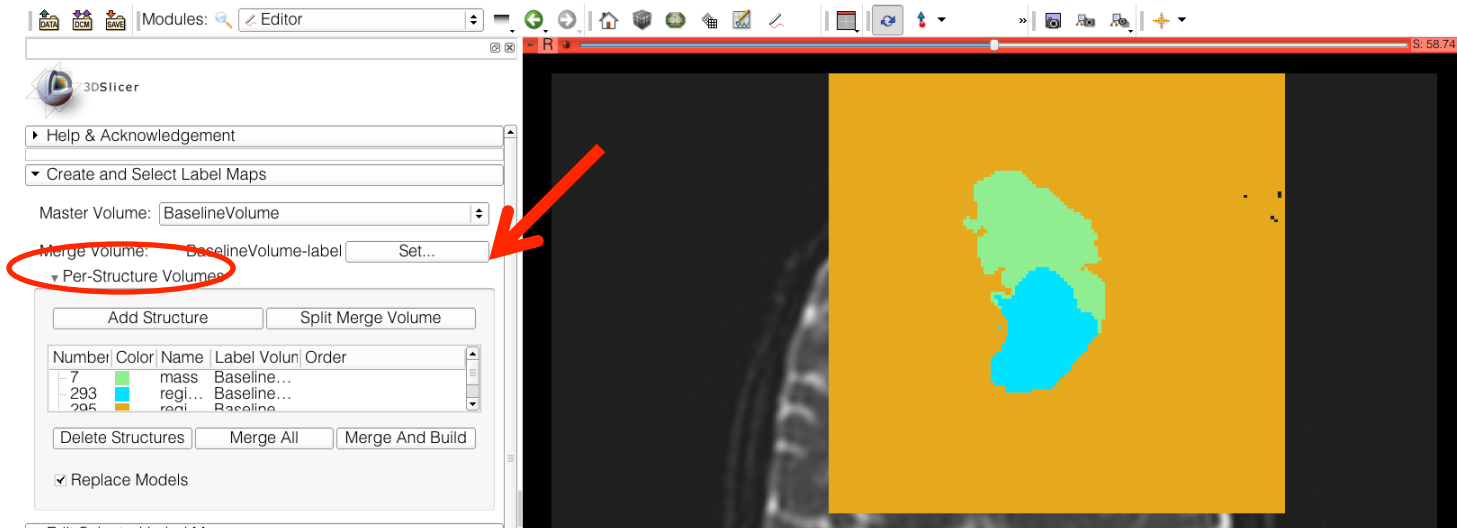
Labels in the image:

- Slicer displays the results of the segmentation
- Solid part
- Cystic part

Tumor Segmentation

The screenshot shows the 3D Slicer software interface. On the left, the 'Per-Structure Volumes' tab is selected and circled in red. A red arrow points to the 'Split Merge Volume' button. The central 3D view displays a brain slice with segmented regions in green, blue, and orange. A yellow box at the bottom contains the instruction: 'Expand the Per-Structure Volumes Tab and click on 'Split Merge Volume''. The interface also shows a 'Merge Volume' dropdown set to 'BaselineVolume-label' and a 'Set...' button. The 'Edit Selected Label Map' section contains various icons for editing the segmentation. The 'Data Probe' section is visible at the bottom left.

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

L
F
B

Tumor Segmentation

3DSlicer

Modules:

Help & Acknowledgement

Display & Modify Scene

Nodes

- Scene
 - View
 - Default Scene Camera
 - DTIVolume
 - BaselineVolume
 - BaselineVolume-label**
 - BaselineVolume-mass-label
 - BaselineVolume-region_1-label
 - BaselineVolume-region_3-label

Scene Model:

- Display MRML ID's
- Show Hidden nodes

Filter:

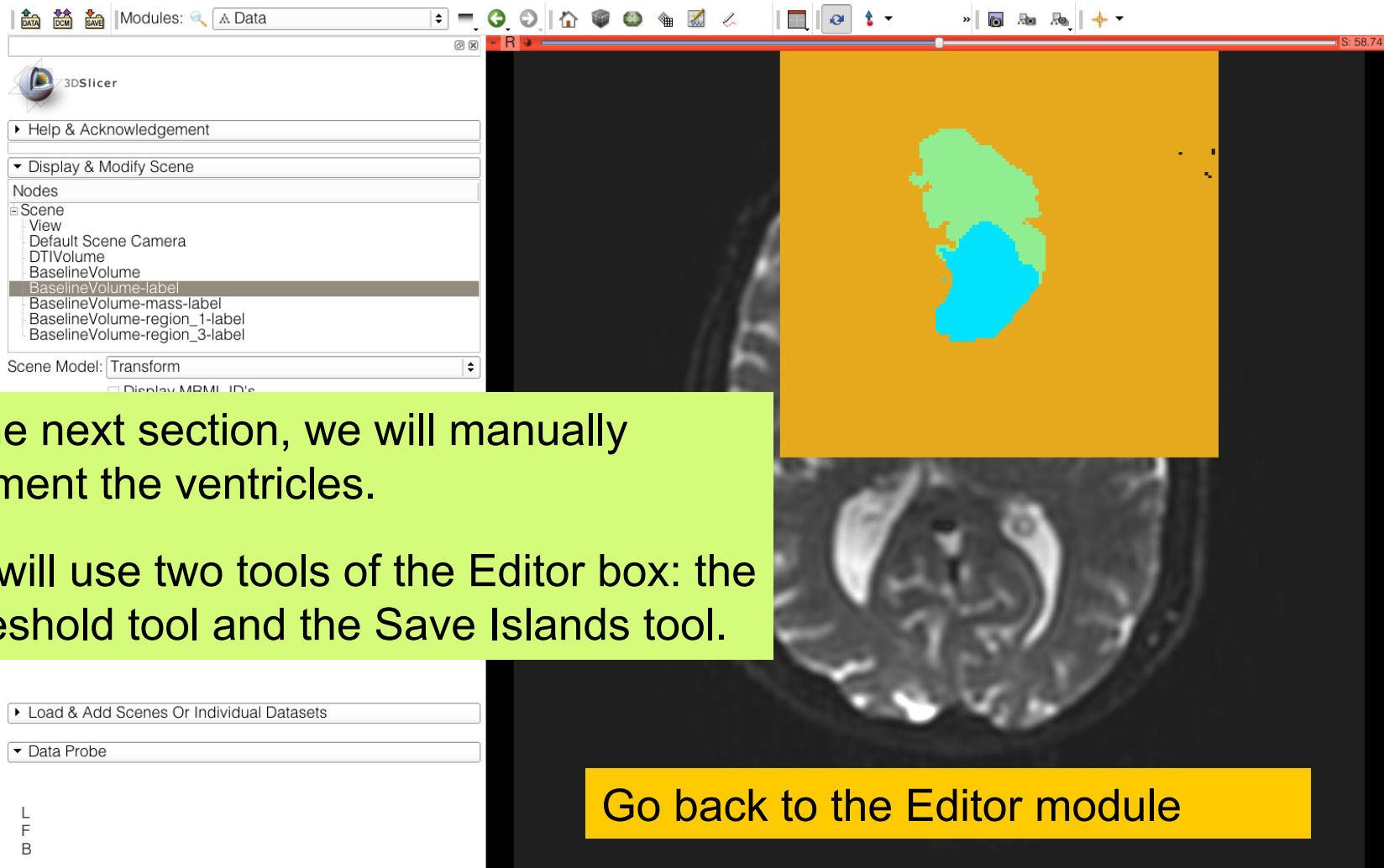
Load & Add Scenes Or Individual Datasets

Data Probe

L
F
B

Select the module Data and note the different label maps that have been generated

Ventricles Segmentation



The screenshot shows the 3D Slicer interface. The top toolbar includes icons for DATA, DICOM, SAVE, and a search bar for modules. The left sidebar contains a tree view with 'Display & Modify Scene' expanded, showing a list of nodes: Scene, View, Default Scene Camera, DTIVolume, BaselineVolume, BaselineVolume-label (selected), BaselineVolume-mass-label, BaselineVolume-region_1-label, and BaselineVolume-region_3-label. The main view displays a coronal MRI slice of a brain with segmented ventricles in green and blue against a yellow background. A yellow text box at the bottom of the main view reads 'Go back to the Editor module'. Below the main view, there are two input fields: 'Load & Add Scenes Or Individual Datasets' and 'Data Probe'. At the bottom left, the letters 'L', 'F', and 'B' are stacked vertically.

In the next section, we will manually segment the ventricles.

We will use two tools of the Editor box: the Threshold tool and the Save Islands tool.

Go back to the Editor module

Ventricles Segmentation

Select the volume
'BaselineVolume-region_3-label'

Add Structure Split Merge Volume

Number	Color	Name	Label Volume	Order
293		regi...	BaselineVolume-region_1-...	
295		regi...	BaselineVolume-region_3-...	

Delete Structures Merge All Merge And Build

Replace Models

▼ Edit Selected Label Map

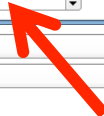


Undo/Redo:

Active Tool: ThresholdEffect

Label: region_3 295

Threshold Range: 1700.00 18197.00

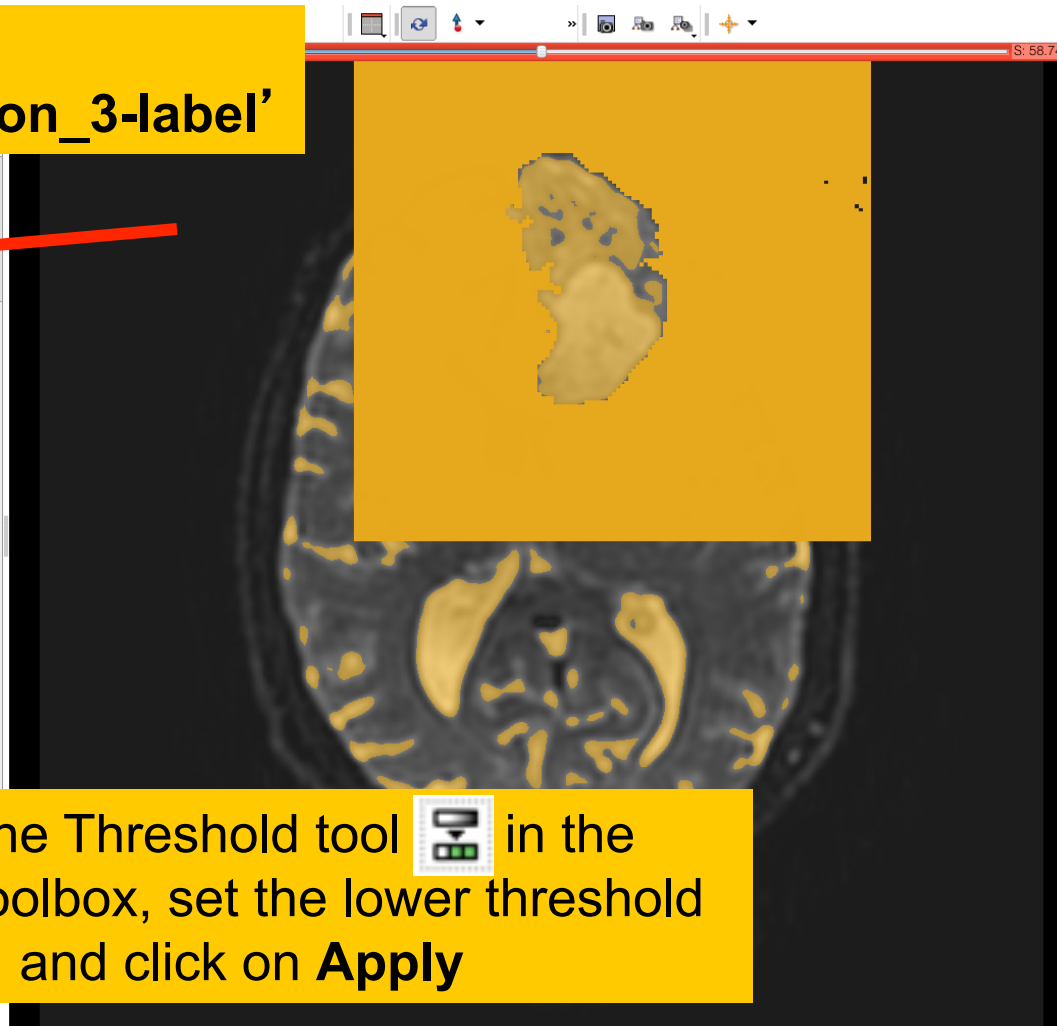


Use For Paint

Apply

▼ Data Probe

L
F
B



Select the Threshold tool in the Editor toolbox, set the lower threshold to 1700, and click on **Apply**

Ventricles Segmentation

Slicer displays the result of the threshold

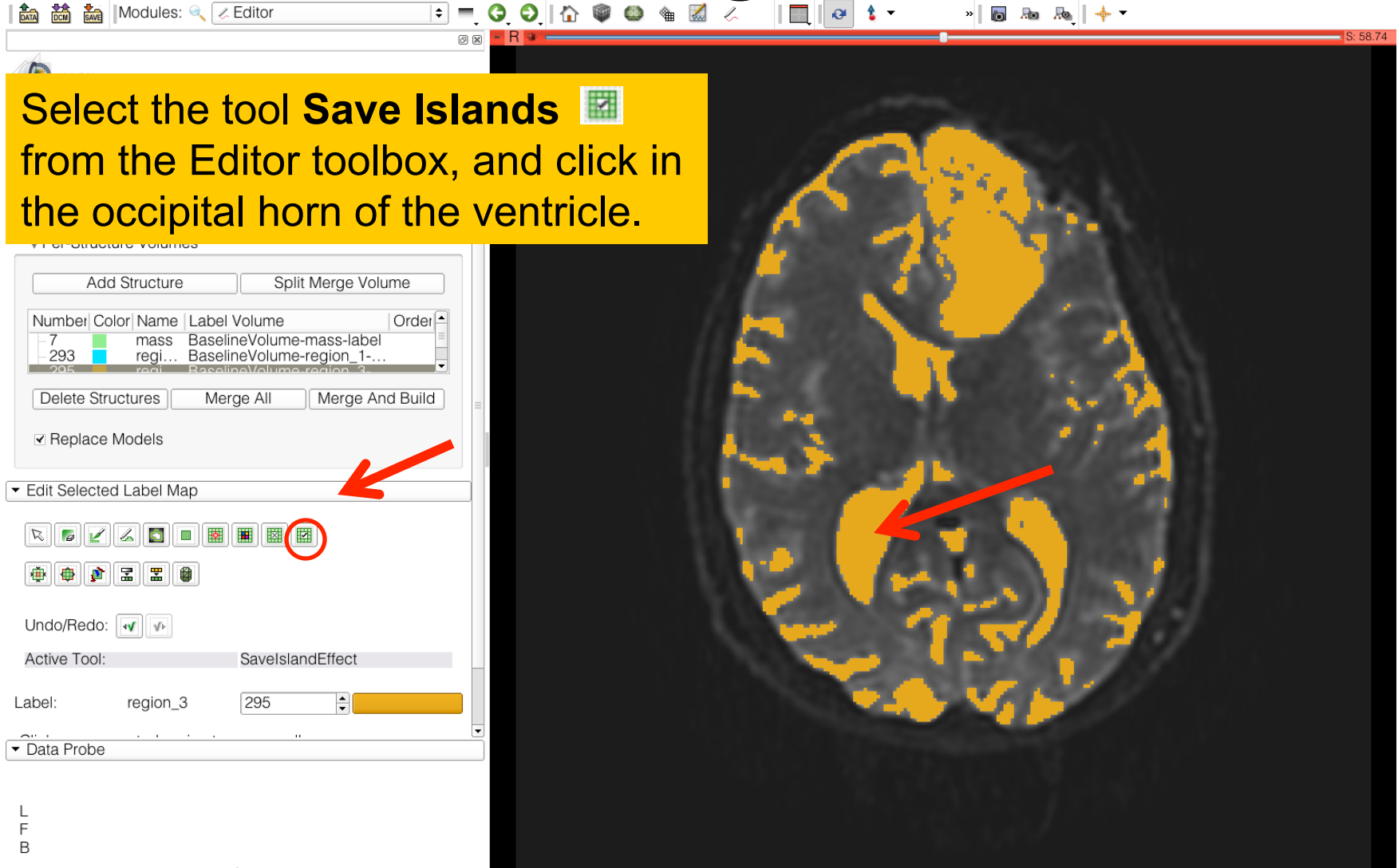
The screenshot shows the Slicer software interface. The main window displays an axial brain MRI slice with segmented ventricles highlighted in yellow. The left sidebar contains several panels:

- Create and Select Label Maps:** Master Volume: BaselineVolume; Merge Volume: BaselineVolume-label; Per-Structure Volumes section with 'Add Structure' and 'Split Merge Volume' buttons; a table of label maps; 'Delete Structures', 'Merge All', and 'Merge And Build' buttons; and a checked 'Replace Models' option.
- Edit Selected Label Map:** A toolbar with various editing tools, 'Undo/Redo' buttons, and an 'Active Tool' dropdown set to 'DefaultTool'.
- Data Probe:** Label: region_3; Value: 295; a color bar for the selected label.

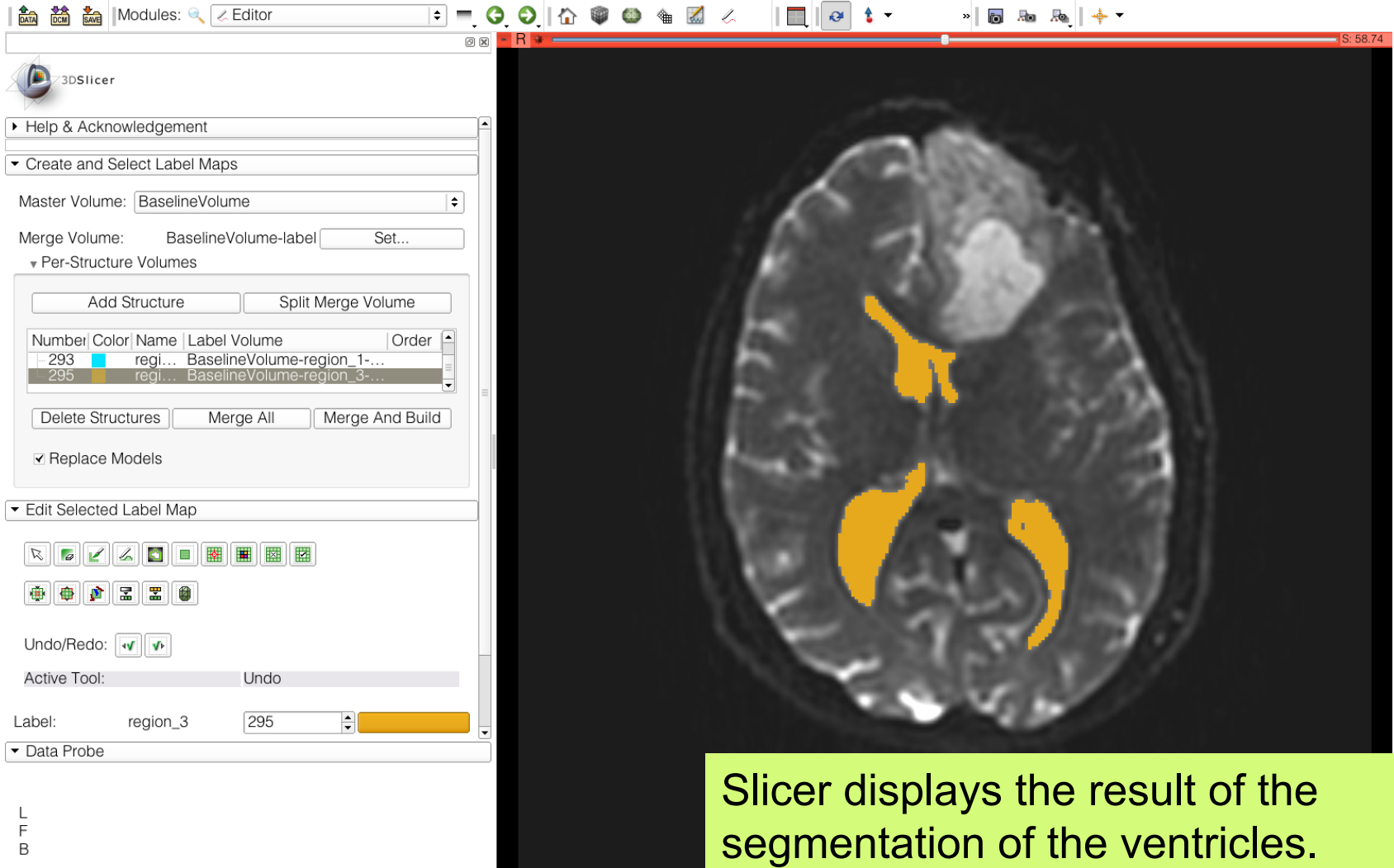
Number	Color	Name	Label Volume	Order
7	Green	mass	BaselineVolume-mass-label	
293	Blue	regi...	BaselineVolume-region_1-...	
295	Yellow	regi...	BaselineVolume-region_3	

Ventricles Segmentation

Select the tool **Save Islands** from the Editor toolbox, and click in the occipital horn of the ventricle.



Final Result of the Segmentation



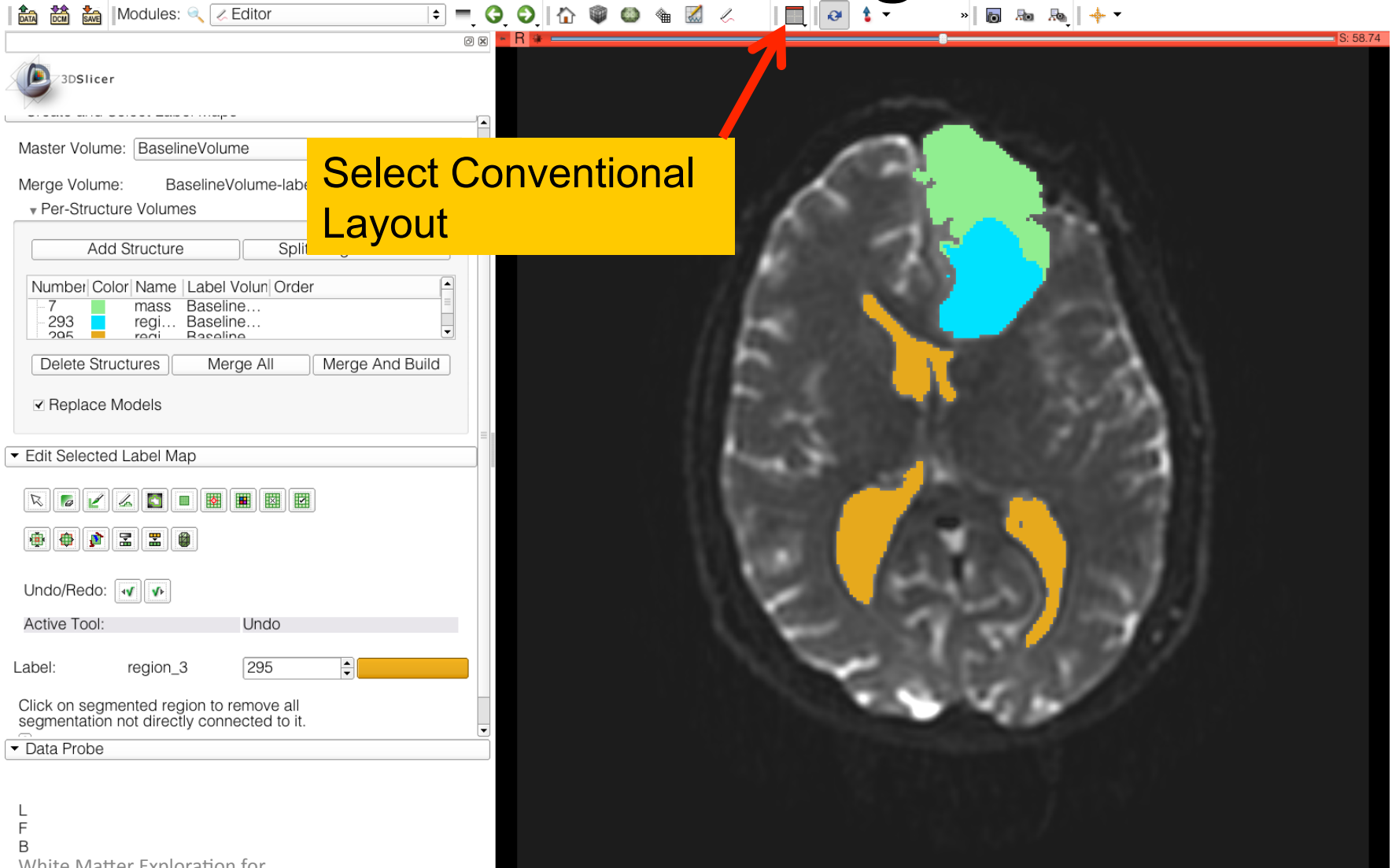
Slicer displays the result of the segmentation of the ventricles.

Final Result of the Segmentation

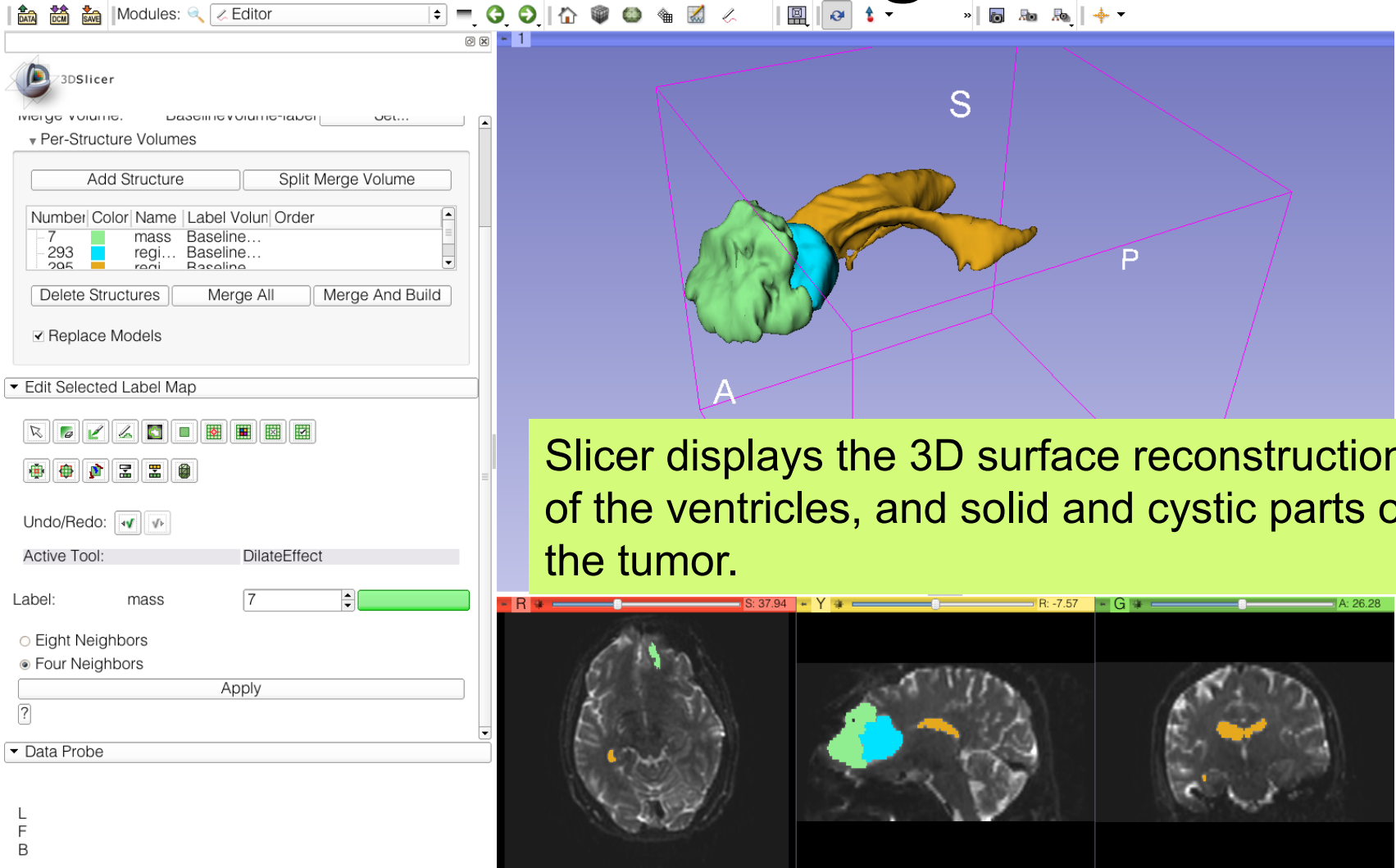
The screenshot shows the 3D Slicer software interface. On the left, the 'Per-Structure Volumes' panel is visible, containing a table of segmented volumes and a 'Merge And Build' button highlighted with a red arrow. The table lists three volumes: 'mass' (green), 'regi...' (blue), and 'radi...' (orange). Below the table are buttons for 'Delete Structures', 'Merge All', and 'Merge And Build'. The 'Merge And Build' button is highlighted with a red arrow. The 'Edit Selected Label Map' panel below shows various tools and a 'Label: region_3' dropdown set to '295'. The main 3D view on the right shows a brain scan with two yellow segmented regions.

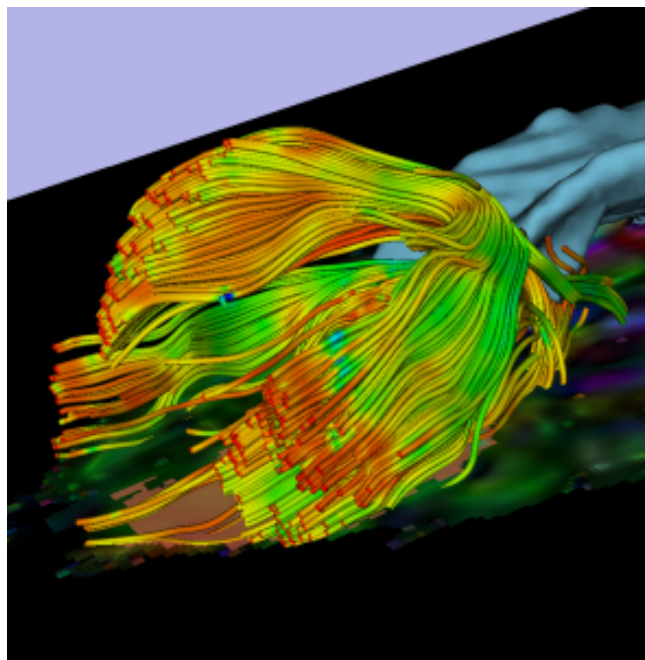
Click on **Merge and Build** to merge the different label maps, and generate the 3D models of the tumor and ventricles using a Marching Cubes algorithm

Final Result of the Segmentation



Final Result of the Segmentation

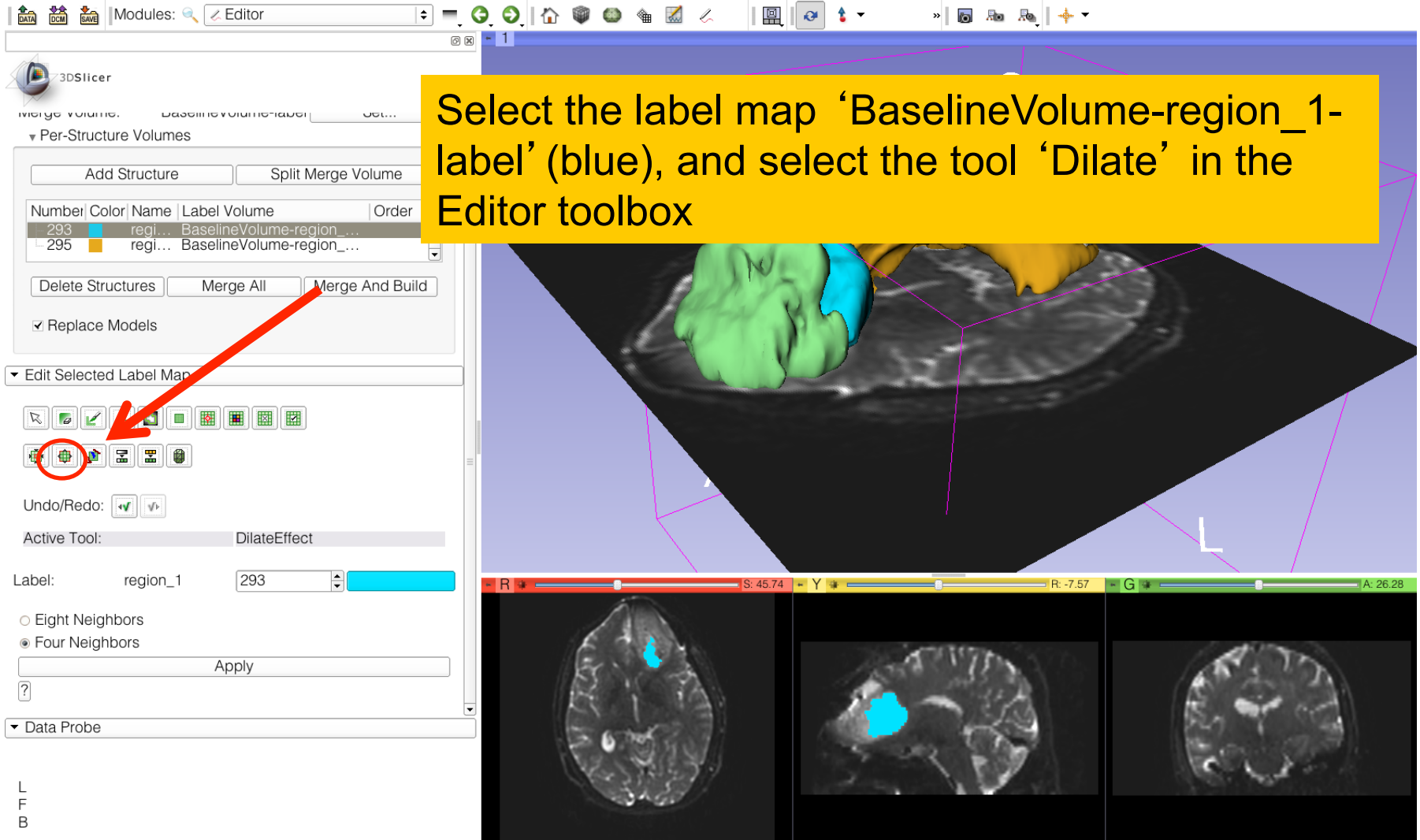




Part 2: Tractography exploration of peri- tumoral white matter fibers

Definition of the peri-tumoral volume

Select the label map 'BaselineVolume-region_1-label' (blue), and select the tool 'Dilate' in the Editor toolbox



Definition of the peri-tumoral volume

Position the mouse the cystic part of the tumor in the axial slice, and click on Apply three times to generate the peritumoral volume

3DSlicer

Per-Structure Volumes

Number	Color	Name	Label Volume
293	Blue	regi... BaselineVolume-region_1-label	
295	Orange	regi... BaselineVolume-region_3-label	

Edit Selected Label Map

Label: region_1 293

Apply

Data Probe

L
F
B

Visualization of the DTI Volume

Note the dilatation of the cystic part of the tumor in the 3D viewer

3DSlicer

Modules: Editor

Delete Structures Merge All Merge And Build

Replace Models

Edit Selected Label Map

Undo/Redo:

Active Tool: DilateEffect

Label: region_1 293

Eight Neighbors
 Four Neighbors

Apply

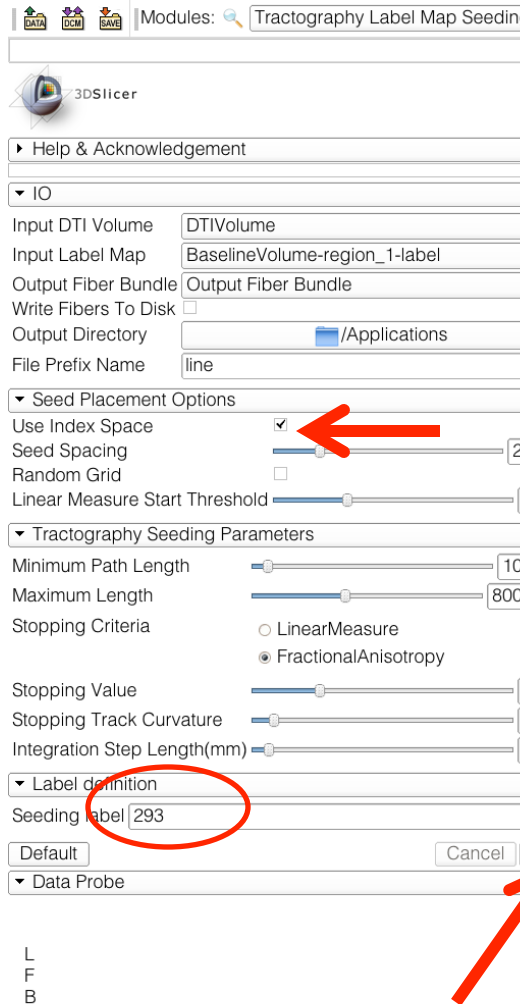
Data Probe

L
F
B

S
A
L

R S: 58.74 Y R: -7.57 G A: 26.28

Tractography Parameters



Select the module **Tractography Label Map Seeding**

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

Input DTI Volume: DTIVolume

Input Label Map: BaselineVolume-region_1-label

Output Fiber Bundle: Create NewFiberBundle

- **Seed Placement Options**:

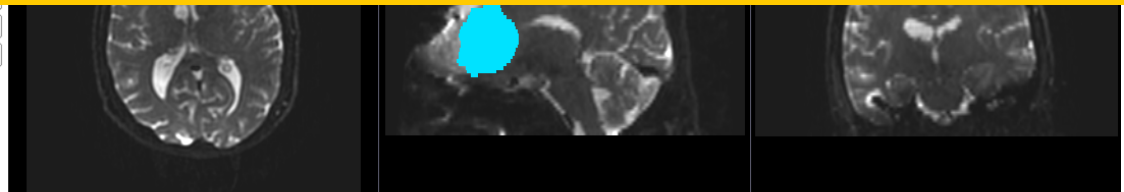
Check **Use Index Space**

- **Stopping Value**

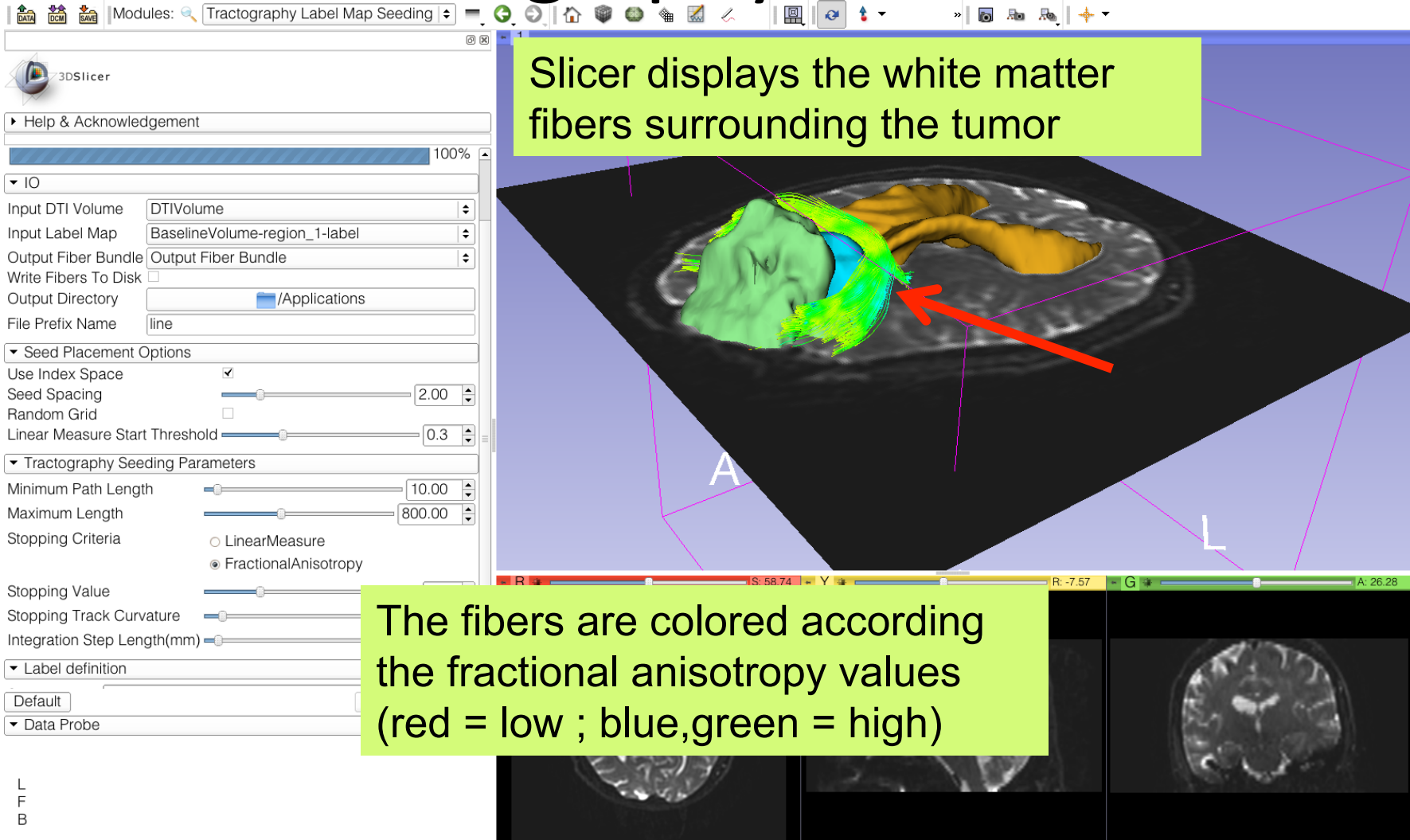
Set the FA threshold to 0.15

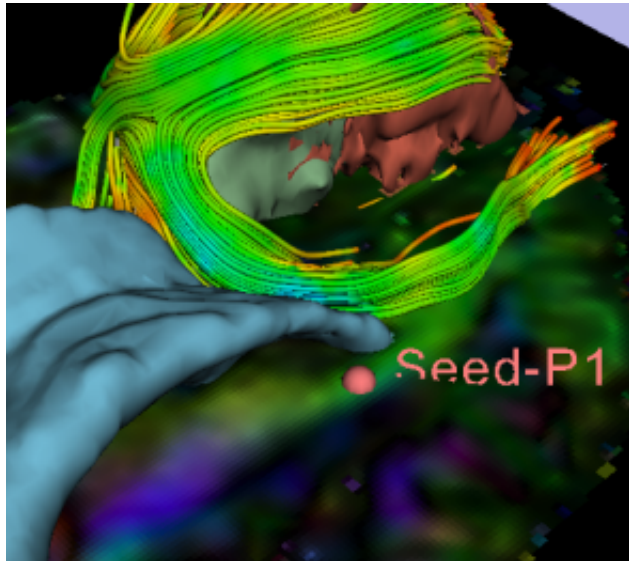
- **Label Definition**:

Enter Seeding Label **293**, and Click on **Apply**



Tractography Results





Part 4: Tractography exploration of the ipsilateral and contralateral side

Tractography on-the-fly



Select the module
Tractography Fiducial Seeding

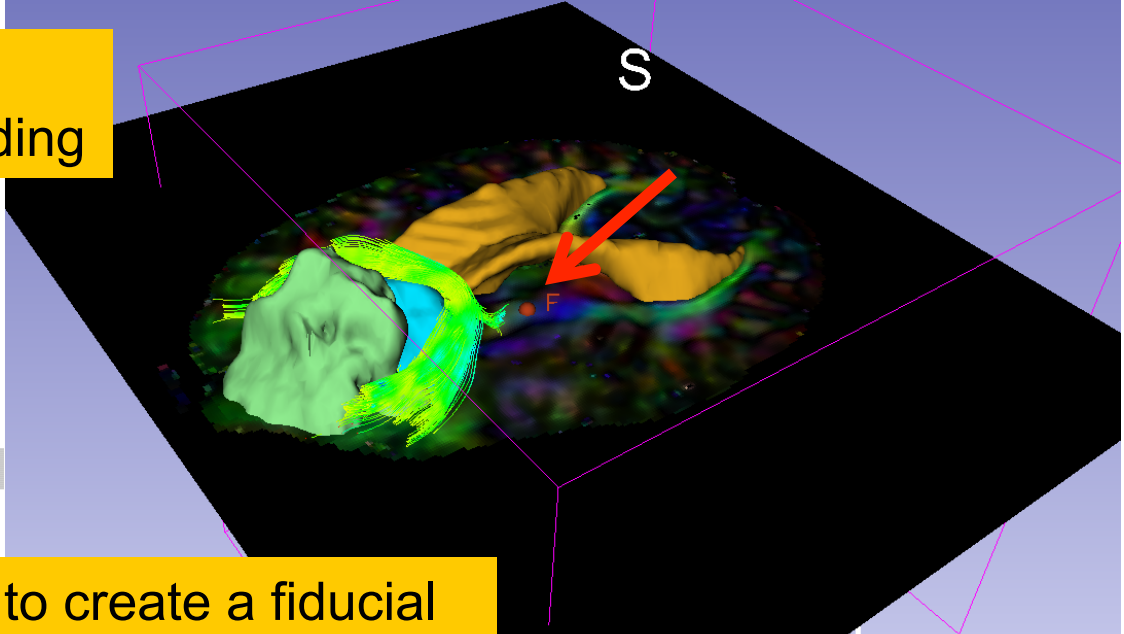
Input DTI Volume: DTIVolume
Input Fiducial List or Model: Select a AnnotationHierarchyNode
Output Fiber Bundle: Select a FiberBundle

Seed Placement Options

Fiducial Region Size: 2.50mm
Fiducial Seeding Step Size: 1.00mm
Seed Selected Fiducials:
Max Number of Seeds: 100

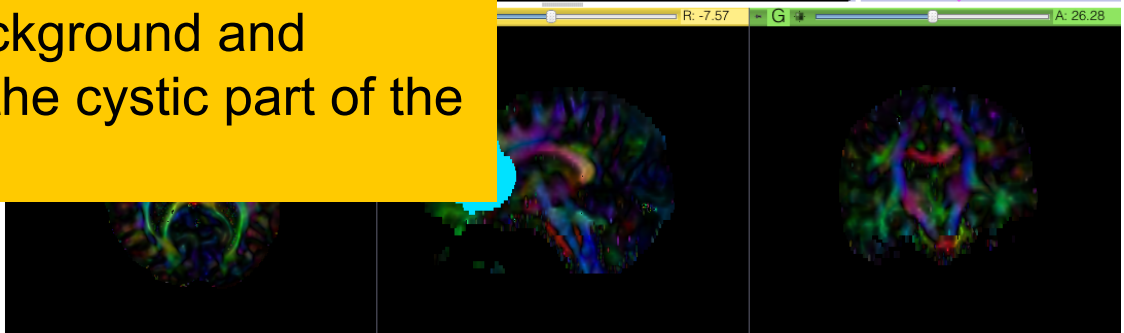
Tractography Seeding Parameters

Minimum Path Length: 20.00mm
Stopping Criteria: Fractional Anisotropy
Stopping Value: 0.25



Click on the Fiducial Icon to create a fiducial
Set the DTI volume in background and
position the fiducial near the cystic part of the
tumor in the 3D viewer

L
F
B



Tractography on-the-fly

3DSlicer

Modules: Tractography Fiducial Seeding

Parameter set: FiducialSeedingParameters

IO

Input DTI Volume: DTIVolume

Input Fiducial List or Model: Fiducials List

Output Fiber Bundle: FiberBundle

Seed Placement Options

Fiducial Region Size: 2.00mm

Fiducial Seeding Step Size: 1.00mm

Seed Selected Fiducials:

Max Number of Seeds: 100

Tractography Seeding Parameters

Minimum Path Length: 10.00mm

Stopping Criteria: Fractional Anisotropy

Stopping Value: 0.15

Stopping Track Curvature: 0.70

Integration Step Length: 0.50mm

Enabling Options

Create Tracts Initially As: Tubes

Enable Seeding Tracts:

Data Probe

L
F
B

S: 48.34 Y R: -7.57 G A: 26.28

Set Input DTI Volume to **DTIVolume**
Set Fiducial List or Model to **FiducialsList**
Set Output Fiber Bundle to **Create new Fiber Bundle**
Set the Minimum Path Length to 10 mm
Set the FA Stopping Criteria to 0.15

Fiducial Seeding

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

Parameter set: FiducialSeedingParameters

IO

Input DTI Volume: DTIVolume

Input Fiducial List or Model: Fiducials List

Output Fiber Bundle: FiberBundle

Seed Placement Options

Fiducial Region Size: 2.00mm

Fiducial Seeding Step Size: 1.00mm

Seed Selected Fiducials:

Max Number of Seeds: 100

Tractography Seeding Parameters

Minimum Path Length: 10.00mm

Stopping Criteria: Fractional Anisotropy

Stopping Value: 0.15

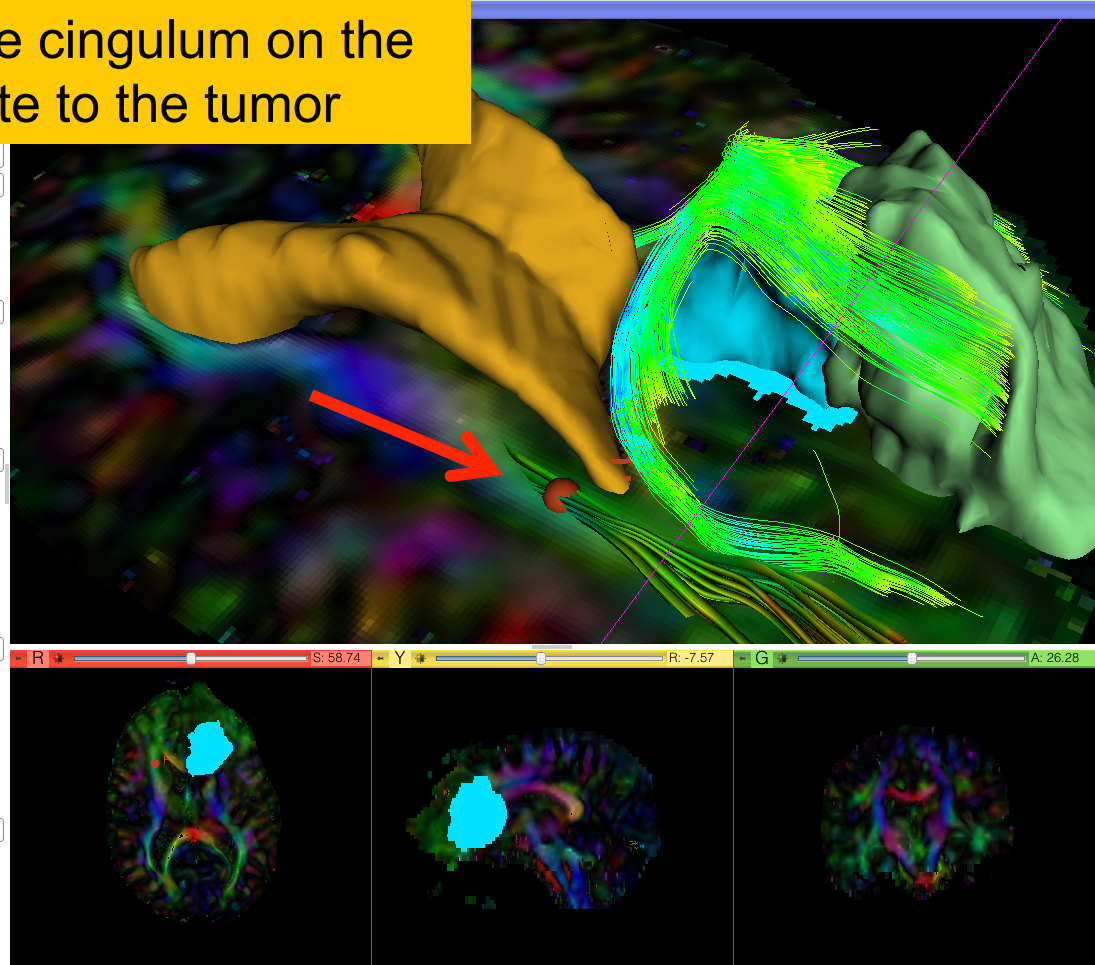
Stopping Track Curvature: 0.70

Integration Step Length: 0.50mm

Enabling Options

Create Tracts Initially As: Tubes

Enable Seeding Tracts:



Tractography on-the-fly

Explore the aspect of the cingulum in the contralateral and ipsilateral sides

3DSlicer

Modules: Tractography Fiducial Seeding

Help & Acknowledgement

Output Fiber Bundle: FiberBundle

Seed Placement Options

- Fiducial Region Size: 2.00mm
- Fiducial Seeding Step Size: 1.00mm
- Seed Selected Fiducials:
- Max Number of Seeds: 100

Tractography Seeding Parameters

- Minimum Path Length: 10.00mm
- Stopping Criteria: Fractional Anisotropy
- Stopping Value: 0.15
- Stopping Track Curvature: 0.70
- Integration Step Length: 0.50mm

Enabling Options

- Create Tracts Initially As: Tubes
- Enable Seeding Tracts:

Data Probe

L
F
B

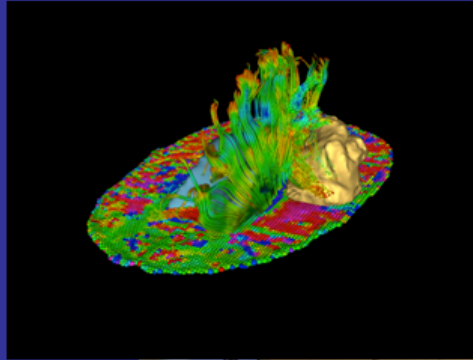
S: 58.74 Y: R: -7.57 G: A: 26.28

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 (peri-tumoral tracts) for neurosurgical planning

MICCAI 2011 DTI Challenge

14th International Conference on Medical Image Computing and Computer Assisted Intervention



DTI Tractography for Neurosurgical Planning: A Grand Challenge



MICCAI 2011 Workshop
Sunday September 18, 9am-6pm
Westin Harbour Castle
Toronto, Canada

Workshop Faculty

Sonia Pujol, PhD, Surgical Planning Laboratory, Harvard Medical School
Ron Kikinis, MD, Surgical Planning Laboratory, Harvard Medical School
Alexandra Golby, MD, Brigham and Women's Hospital, Harvard Medical School
Guido Gerig, PhD, The Scientific Computing and Imaging Institute, University of Utah
Martin Styner, PhD, Neuroimage Research and Analysis Laboratory, University of North Carolina
William Wells, PhD, Surgical Planning Laboratory, Harvard Medical School
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Sylvain Gouttard, MSc, The Scientific Computing and Imaging Institute, University of Utah

National Alliance for Medical Image Computing

http://www.na-mic.org/Wiki/index.php/Events_DTI_Tractography_Challenge_MICCAI_2011

Neurosurgical Planning Workshop, October 1st, 2012 – Nice, France

MICCAI 2012 DTI Tractography Challenge Second Edition

INTRODUCTION THE CHALLENGE FACULTY KEYNOTE SPEAKER DATA LOGISTICS CONTACT

+ add new ⚙

Welcome to the 2nd edition of the MICCAI DTI Tractography Challenge. The workshop will be held on Monday October 1st, 2012 as part of the 15th International Conference on Medical Image Computing and Computer Assisted Intervention (MICCAI 2012).



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