



Exploring Peritumoral White Matter Fibers for Neurosurgical Planning

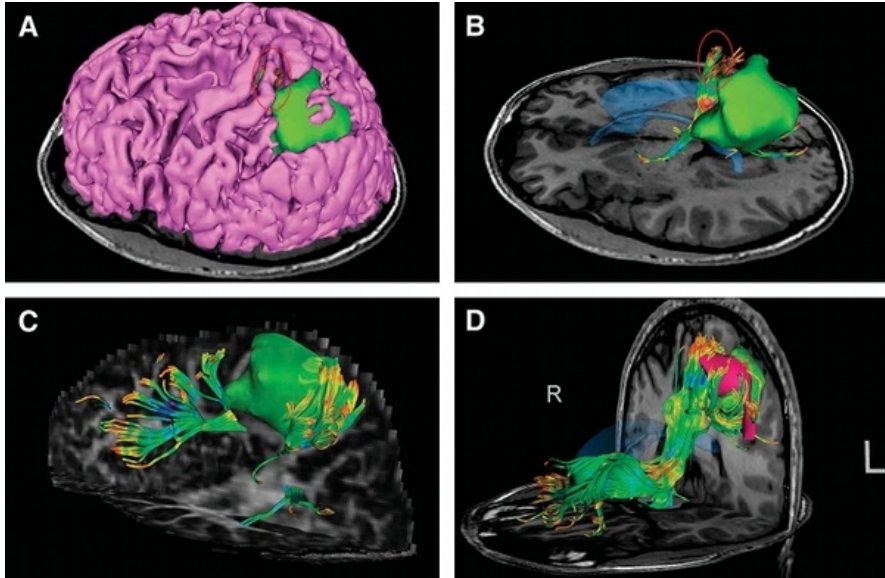
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Surgical Planning Laboratory

Harvard University

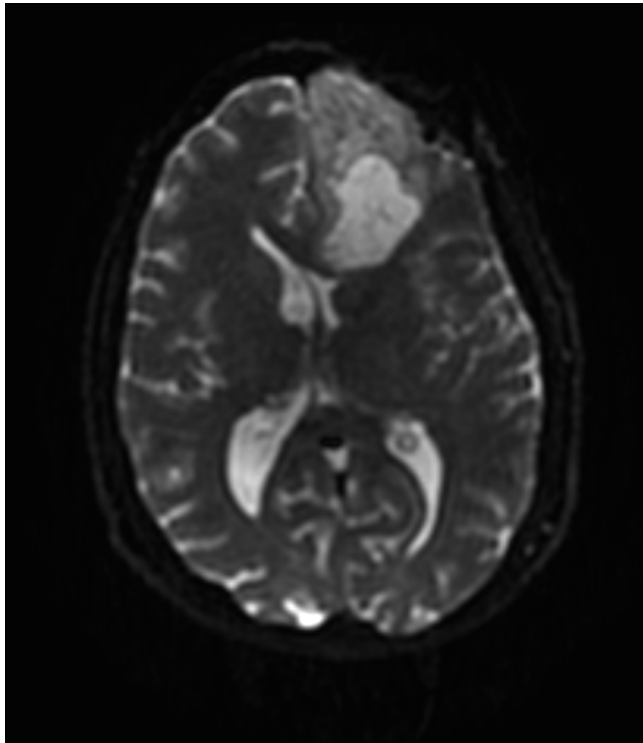
Clinical Goal



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.

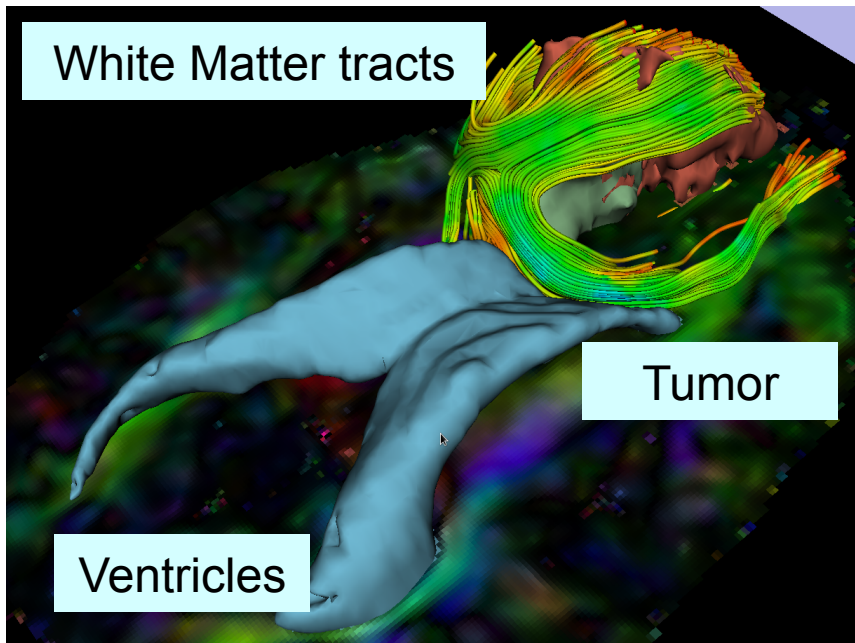
Image Courtesy of Dr. Alexandra Golby, Brigham and Women's Hospital, Boston, MA..

Clinical Case



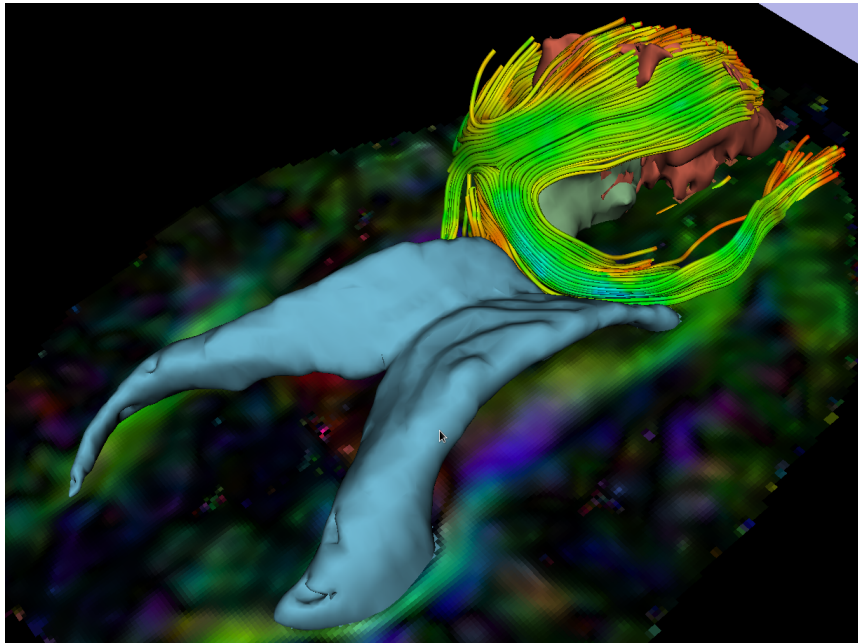
- 35 year-old male diagnosed with Glioblastoma multiforme (GBM)
- Diffusion Weighted Imaging (DWI) acquisition for neurosurgical planning

Clinical Goal



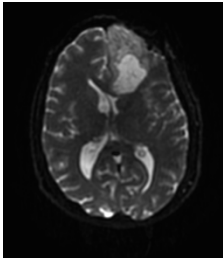
The goal of this tutorial is to explore white matter fibers surrounding a tumor using Diffusion Tensor Imaging (DTI) Tractography.

Image Analysis Pipeline

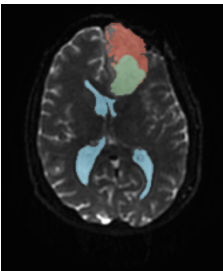


The image analysis pipeline described in this tutorial uses three different algorithms: the “Grow Cut” algorithm for segmentation of the tumor parts, the Marching Cube algorithm for surface modeling, and the single tensor streamline tractography algorithm for tract generation.

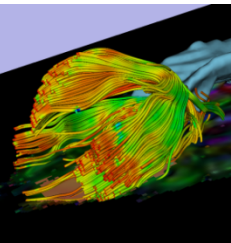
Overview of the analysis pipeline



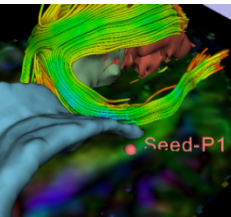
Part 1: Loading & Visualization of Diffusion Data



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

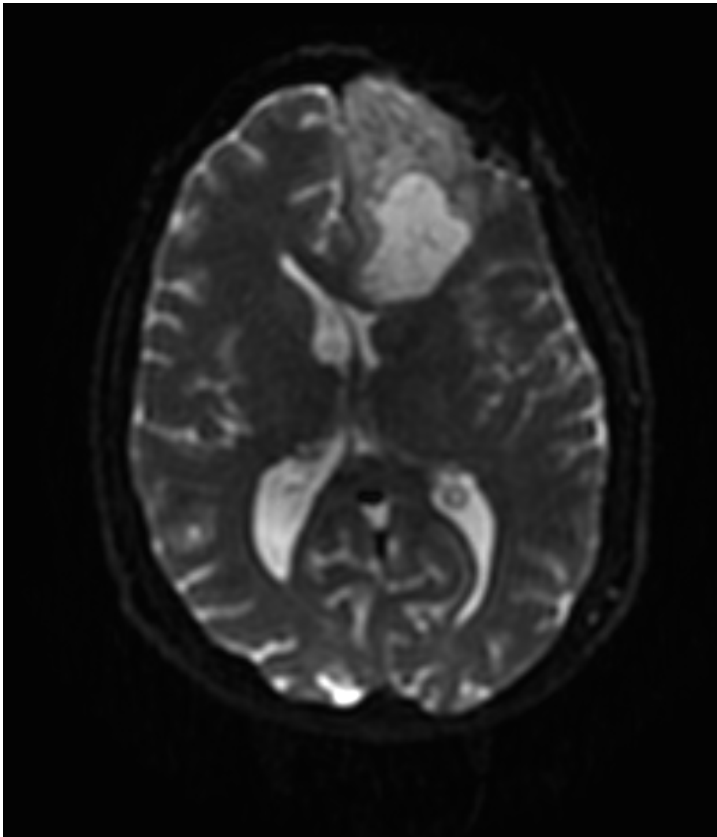


Part 3: Tractography reconstruction of the white matter fibers in the peri-tumoral volume



Part 4: Tractography exploration of the ipsilateral and contralateral side

Part 1: Loading and Visualization of Diffusion Data

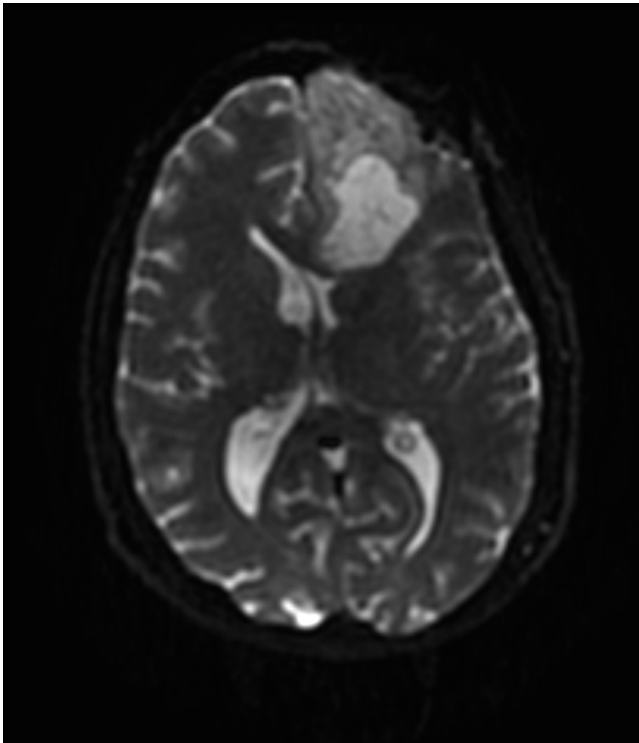
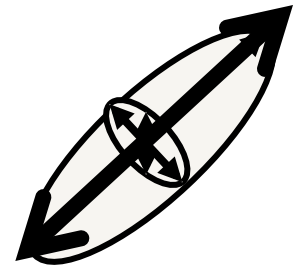


Diffusion Tensor Imaging

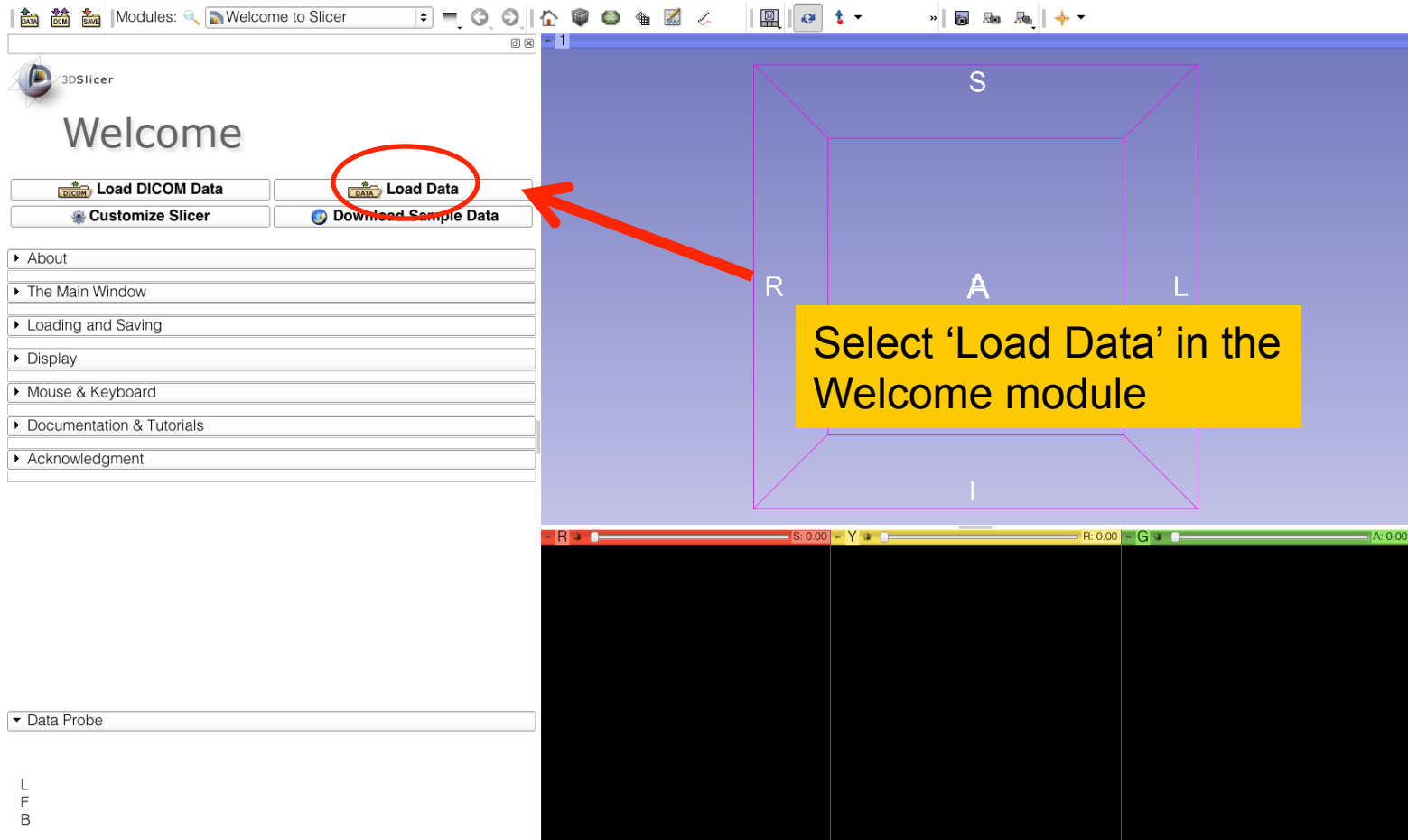
$$S_i = S_0 e^{-b \hat{g}_i^T \underline{D} \hat{g}_i}$$

(Stejskal and Tanner 1965, Basser 1994)

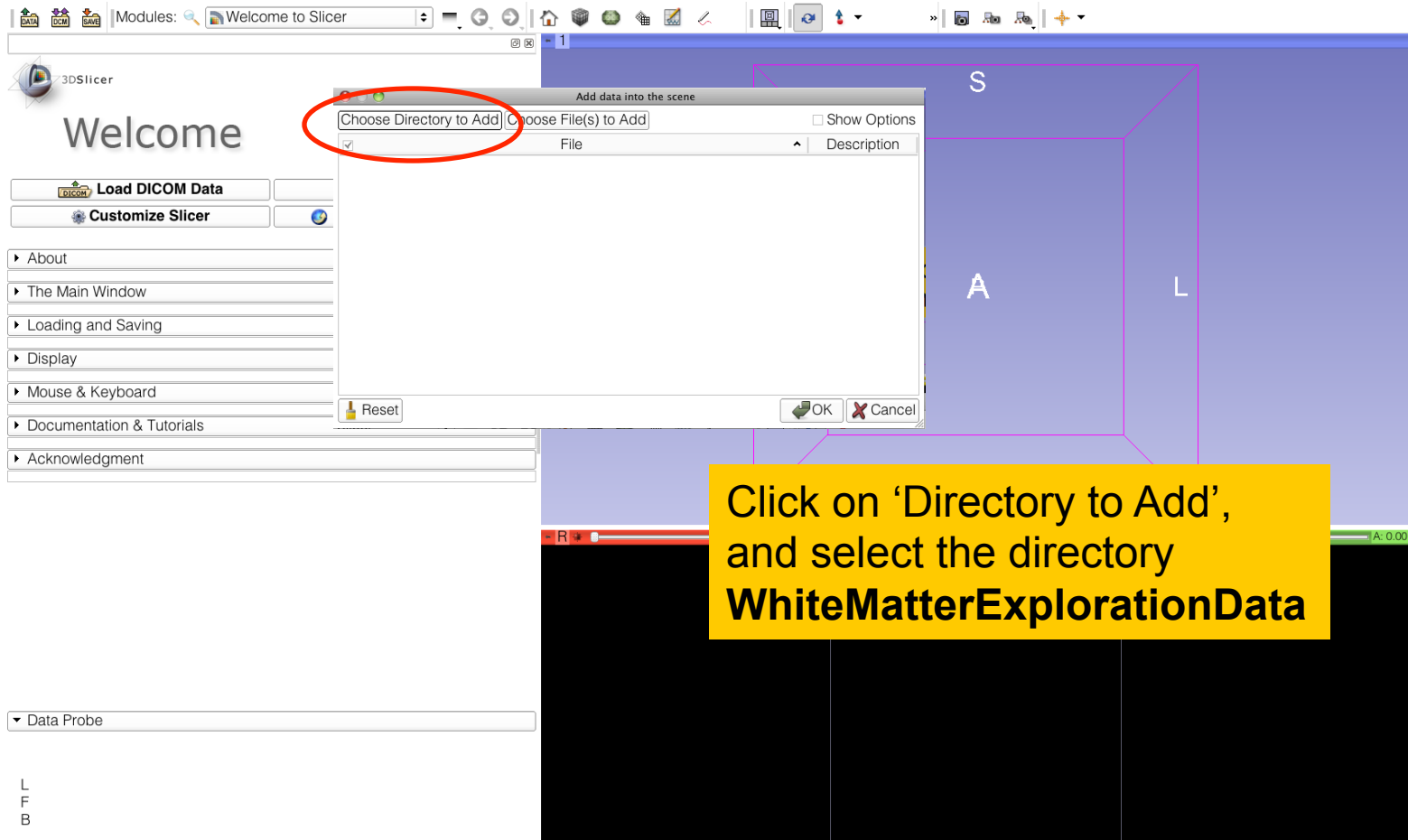
$$\underline{D} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix}$$



Loading DTI and Baseline Data



Loading DTI and Baseline Data



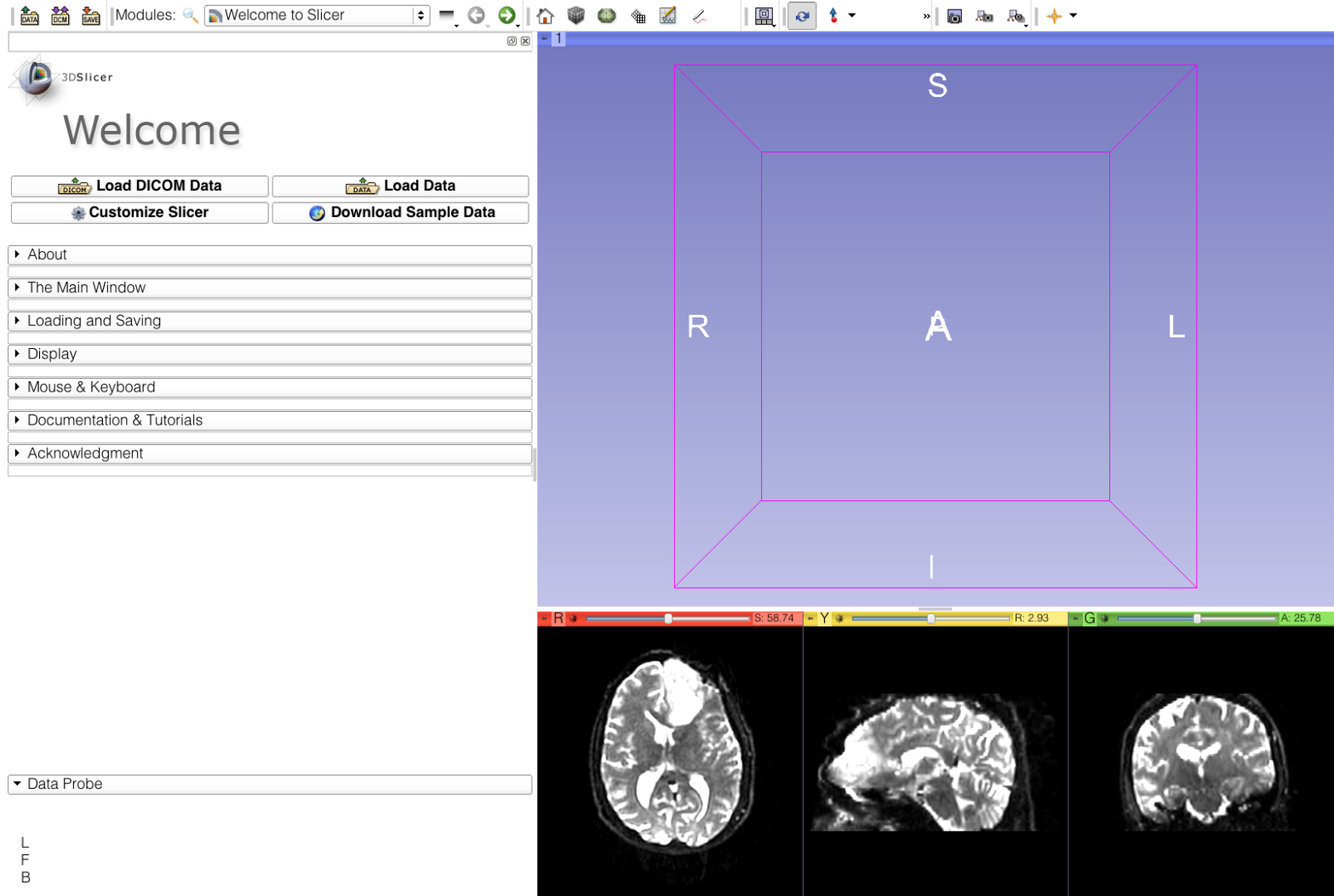
Loading DTI and Baseline Data

The screenshot shows the Slicer software interface with a file selection dialog open. The dialog has two tabs: "Choose Directory to Add" and "Choose File(s) to Add". The "Choose File(s) to Add" tab is active, showing a list of files with checkboxes. Three files are selected: `/Users/spujol/data/WhiteMatterExplorationData/DTIVolume.raw.gz`, `/Users/spujol/data/WhiteMatterExplorationData/DTIVolume.nhdr`, and `/Users/spujol/data/WhiteMatterExplorationData/BaselineVolume.nrrd`. The file names are circled in red. The dialog also has "OK" and "Cancel" buttons. In the background, a 3D brain model is visible with anatomical planes labeled S (Superior), A (Anterior), L (Lateral), and I (Inferior).

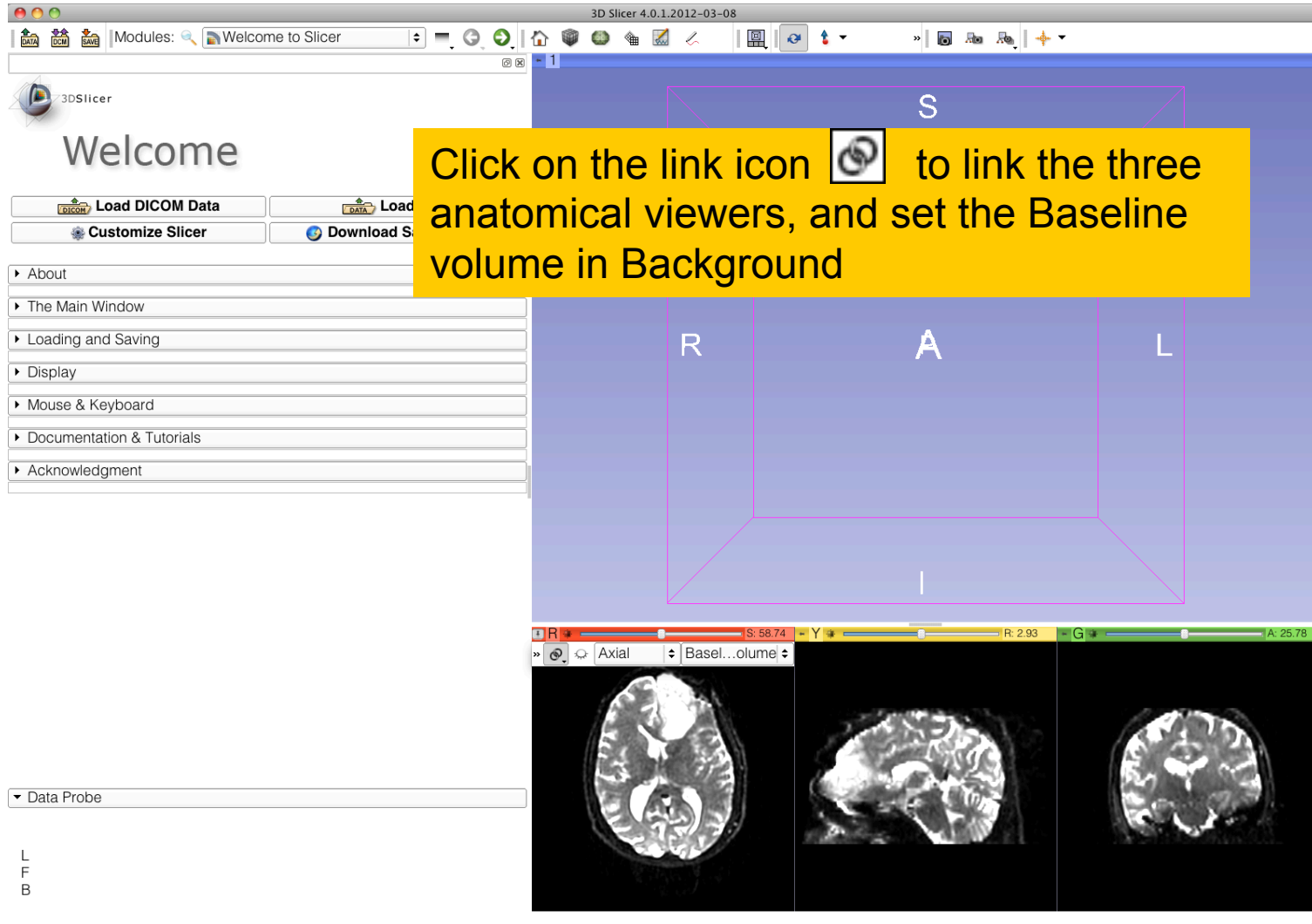
Select the directory
WhiteMatterExplorationData

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

The screenshot displays the 3D Slicer software interface. The top toolbar includes icons for DATA, DICOM, SAVE, and other functions. The 'Modules' dropdown menu is set to 'Volumes'. The left sidebar shows the '3D Slicer' logo and a list of panels: 'Help & Acknowledgement', 'Active Volume: BaselineVolume', 'Volume Information', 'Display', 'Lookup Table: Grey', 'Interpolate: checked', 'Window Level editor presets' (with a red circle around the 'Manual W/L' button), 'W: 3200', 'Threshold: Off', and 'Histogram'. The main 3D view shows a blue brain model with a purple wireframe bounding box. The bounding box is labeled with 'S' (Superior), 'I' (Inferior), 'R' (Right), and 'L' (Left). A yellow callout box with black text reads: 'Select the module **Volumes** and adjust the Window and Level values of the Baseline Volume.' Below the 3D view, there are three 2D slice views: an axial slice (labeled 'R'), a sagittal slice (labeled 'S'), and a coronal slice (labeled 'A'). Each slice view has a corresponding color-coded slider for windowing: red for R (S: 58.74), yellow for Y (R: 2.93), and green for G (A: 25.78). The bottom left corner of the interface shows the 'Data Probe' panel with 'L', 'F', and 'B' labels.

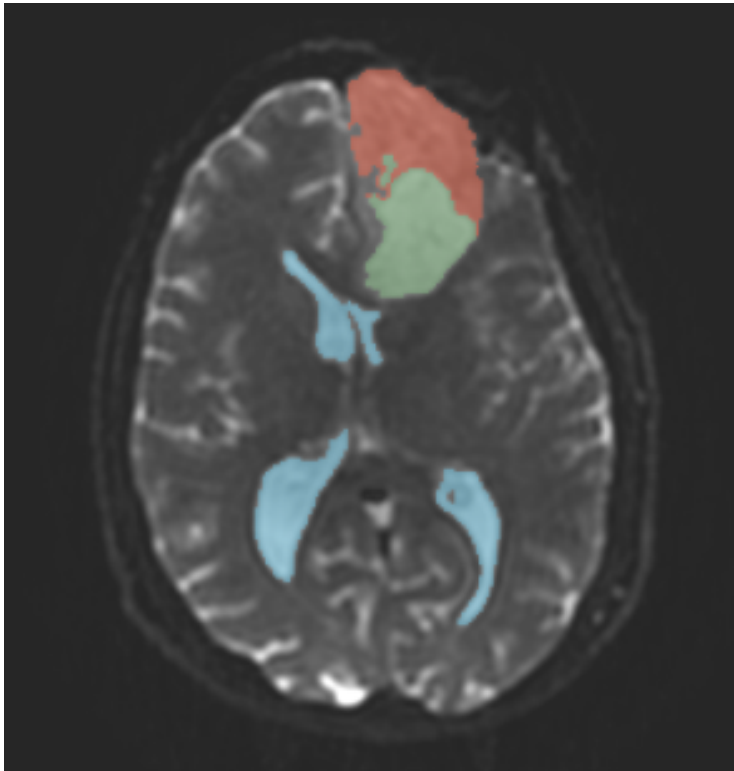
Loading DTI and Baseline Data

The screenshot shows the 3D Slicer software interface. On the left, the 'Display' panel is visible, showing the 'Active Volume' as 'BaselineVolume' and various display settings like 'Lookup Table: Grey', 'Interpolate: checked', and 'Window Level editor presets'. The main window displays an axial MRI slice of a brain. A context menu is open over the slice, listing various layout options. The 'Red slice only' option is circled in red. A yellow callout box at the bottom of the image contains the text 'Select Red Slice Only Layout'. The status bar at the bottom left shows 'L', 'F', and 'B'.

- 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

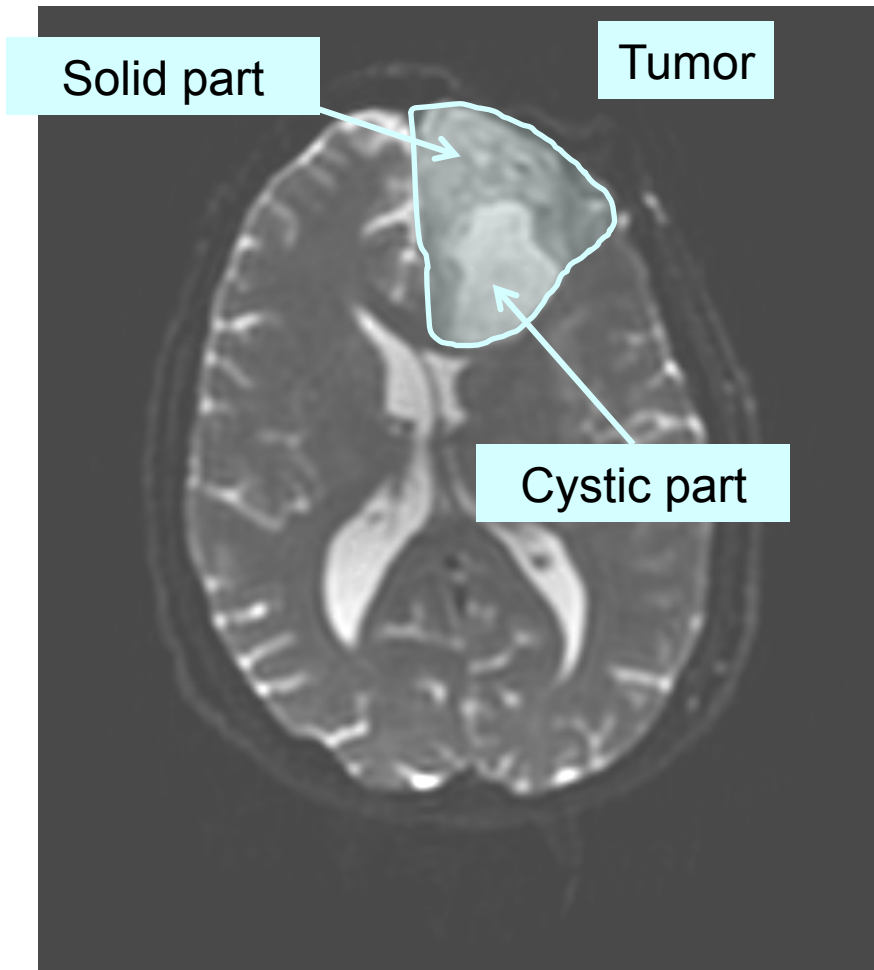
Select Red Slice Only Layout

L
F
B



Part 1: Segmenting the tumor and ventricles

Tumor Segmentation



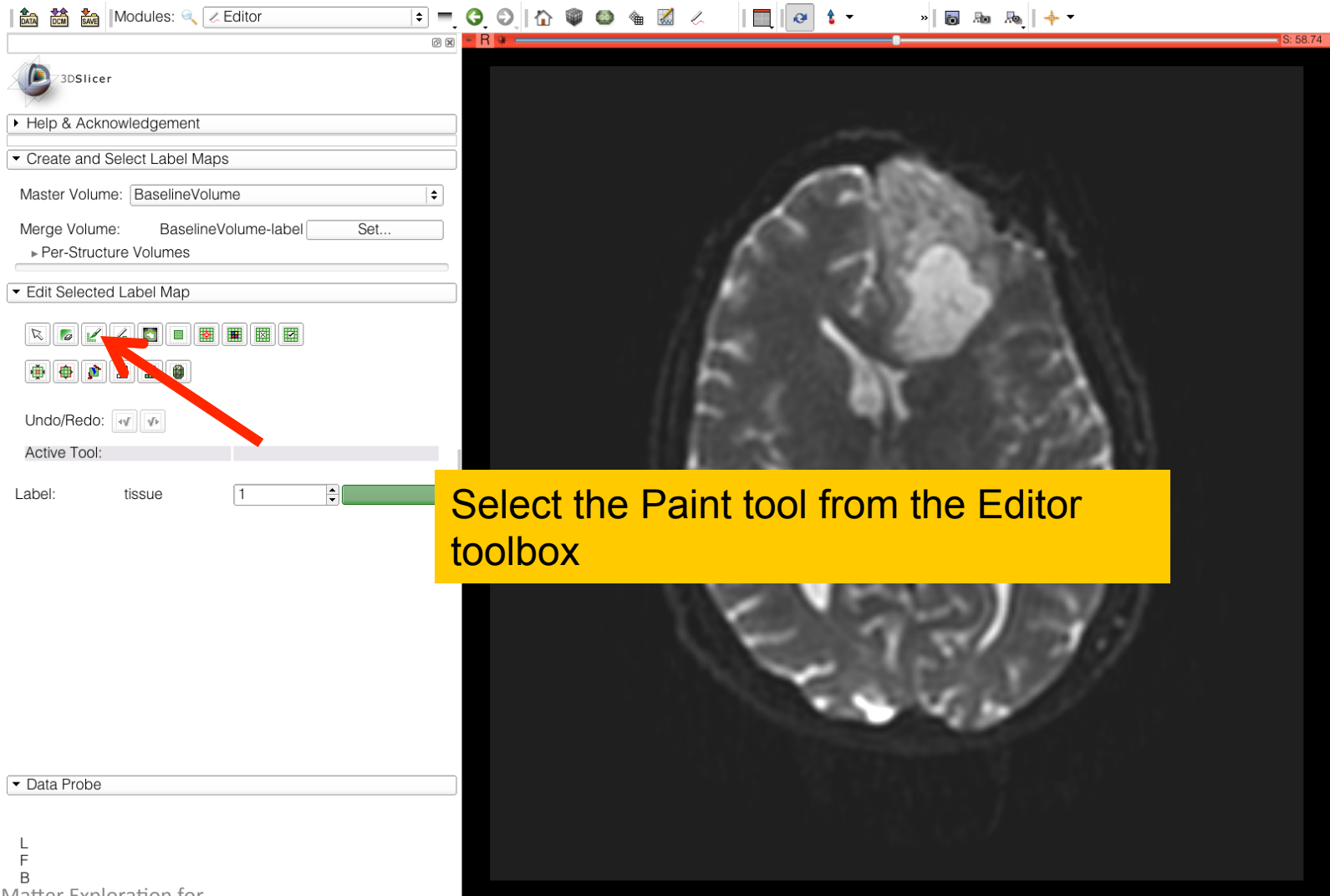
The tumor in this clinical case is composed of two parts: a solid part, and a cystic part.

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 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 area says: "Select the color table 'Generic Anatomy Colors' and click on Apply".

Tumor Segmentation



Tumor Segmentation

Set the label #293 region_1 and draw a short line in the **cystic part of the tumor**

3DSlicer

Modules: Editor

Help & Acknowledgement

Create and Select Label Maps

Master Volume: BaselineVolume

Merge Volume: BaselineVolume-label Set...

Per-Structure Volumes

Edit Selected Label Map

Undo/Redo: [Undo] [Redo]

Active Tool: Undo

Label: region_1 293

Paint Over

Threshold Paint

Radius: 5.00mm

Smudge

[?]

Data Probe

L
F
B

Tumor Segmentation

3DSlicer

Modules: Editor

Help & Acknowledgement

Create and Select Label Maps

Master Volume: BaselineVolume

Merge Volume: BaselineVolume-label Set...

Per-Structure Volumes

Edit Selected Label Map

Undo/Redo: [Undo] [Redo]

Active Tool: Undo

Label: mass 7

Paint Over

Threshold Paint

Radius: 5.00mm

Smudge

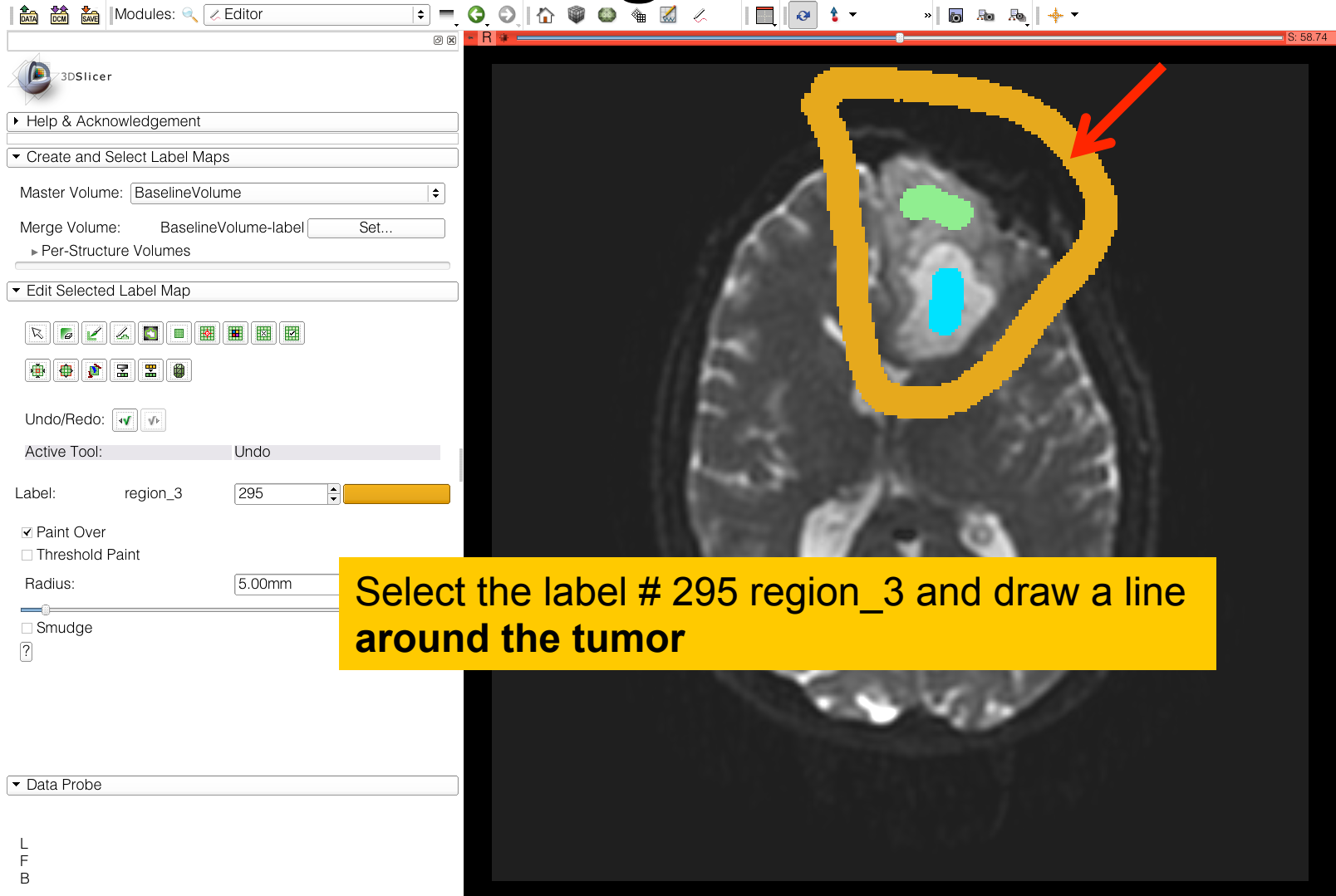
?

Data Probe

L
F
B

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

Tumor Segmentation



The screenshot displays the 3D Slicer software interface. The main window shows an axial MRI slice of a brain with a tumor region highlighted in yellow. A red arrow points to the yellow boundary. The left sidebar contains several panels: 'Help & Acknowledgement', 'Create and Select Label Maps', 'Edit Selected Label Map', and 'Data Probe'. The 'Edit Selected Label Map' panel is active, showing a toolbar with various editing tools, an 'Undo/Redo' section, and a 'Label' dropdown set to 'region_3' with a value of '295'. A yellow text box is overlaid on the image, containing the instruction: 'Select the label # 295 region_3 and draw a line around the tumor'. The 'Data Probe' panel is also visible at the bottom left.

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

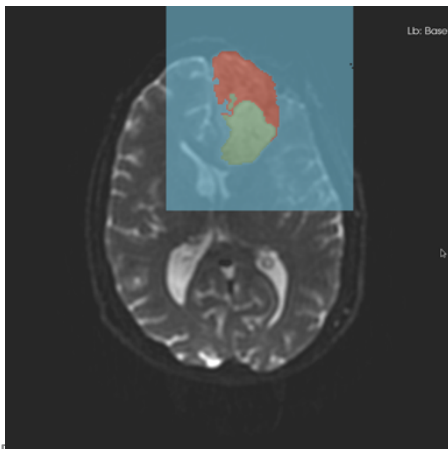
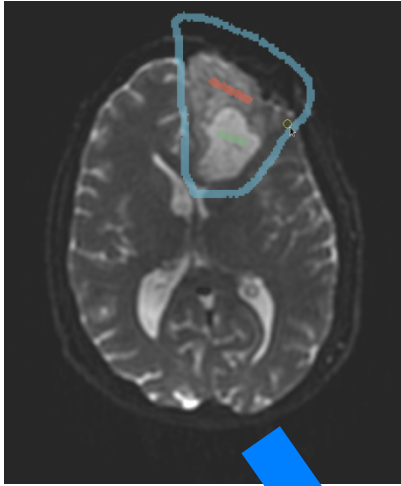
Run the GrowCut segmentation on the current label map. This will use your current segmentation as an example to fill in the rest of the volume.

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

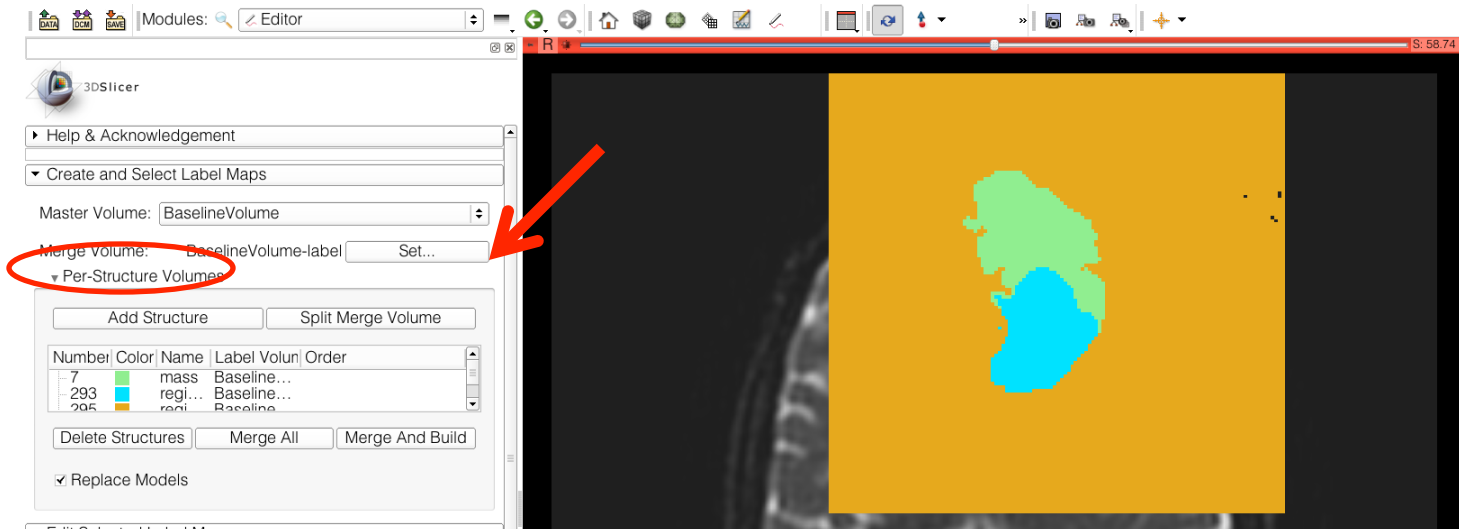
The image shows the 3D Slicer software interface. On the left, the 'Create and Select Label Maps' panel is visible, showing 'Master Volume: BaselineVolume' and 'Merge Volume: BaselineVolume-label'. A yellow box highlights the segmentation results, and a green box contains the text 'Slicer displays the results of the segmentation'. The main window displays an axial MRI slice of a brain with a tumor. The tumor is segmented into two parts: a solid part (green) and a cystic part (blue). A yellow box highlights the segmentation results, and a green box contains the text 'Slicer displays the results of the segmentation'. Two white arrows point from labels 'Solid part' and 'Cystic part' to their respective regions. The 'Data Probe' panel at the bottom left shows 'region_3' with a value of '295' and an orange color swatch. Below it, there is a text box with the instruction '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.' and an 'Apply' button. The 'LFB' orientation indicator is visible at the bottom left.

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 text box at the bottom contains the following instructions:

Expand the Per-Structure Volumes Tab and click on 'Split Merge Volume'

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_2-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:

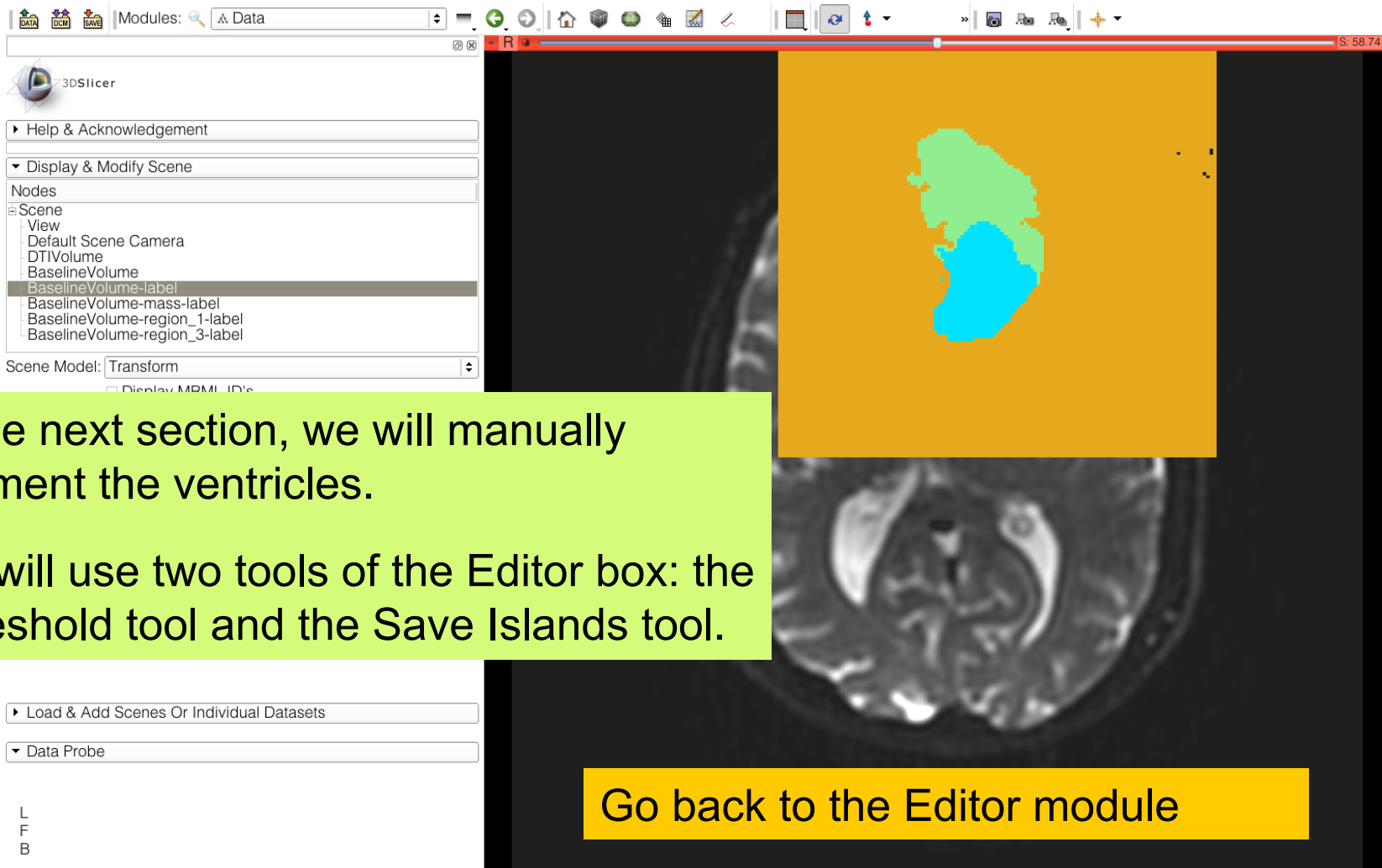
Load & Add Scenes Or Individual Datasets

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 main window displays an axial MRI slice of a brain with segmented ventricles in green and blue. The left sidebar contains a 'Nodes' list with 'BaselineVolume-label' selected. Below the nodes list is a 'Scene Model' dropdown set to 'Transform' and a checkbox for 'Display MRML IDs'. A yellow text box at the bottom of the main window reads 'Go back to the Editor module'. On the left side of the slide, there are two text boxes: a green one with the text 'In the next section, we will manually segment the ventricles.' and a yellow one with the text 'We will use two tools of the Editor box: the Threshold tool and the Save Islands tool.' Below these text boxes 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'

The screenshot shows the software interface with a table of structures and a threshold tool. A red arrow points to the structure 'BaselineVolume-region_3-label' in the table. Another red arrow points to the '1700.00' value in the 'Threshold Range' field. The 'Apply' button is also visible.

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

Buttons: Add Structure, Split Merge Volume, Delete Structures, Merge All, Merge And Build

Checkbox: Replace Models

Section: Edit Selected Label Map

Active Tool: ThresholdEffect

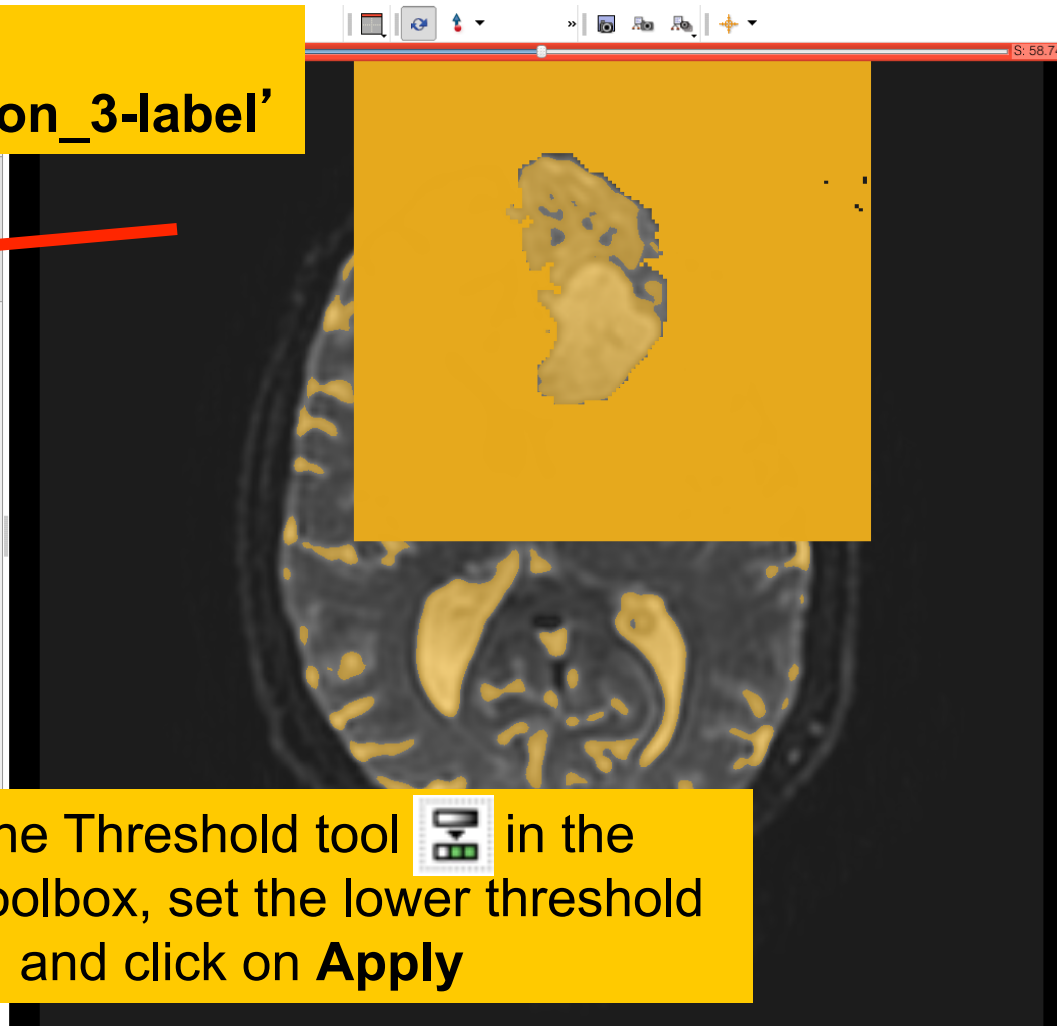
Label: region_3, 295


Threshold Range: 1700.00, 18197.00

Buttons: Use For Paint, Apply

Section: Data Probe

Orientation: 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

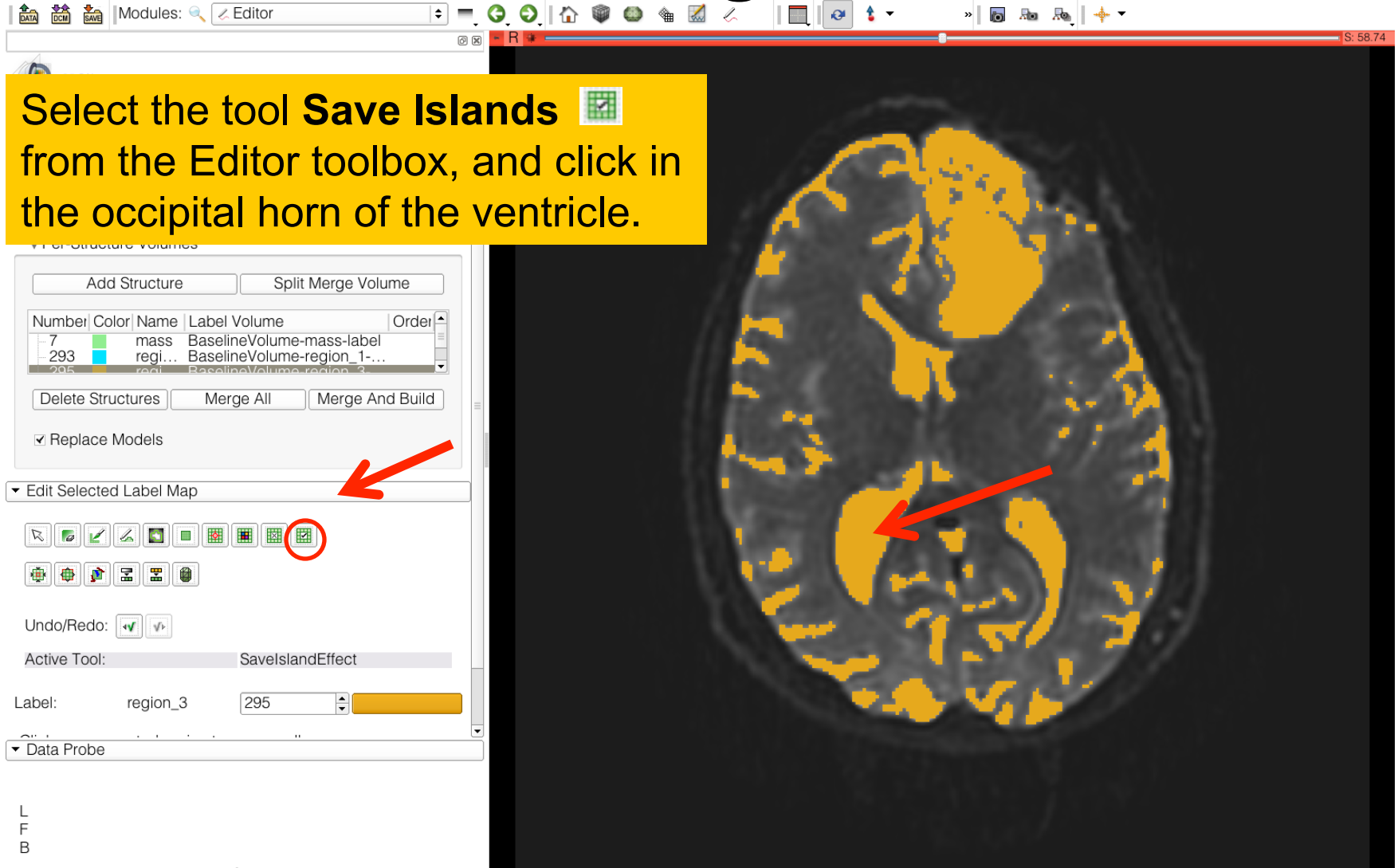
The screenshot shows the Slicer software interface. The main window displays an axial brain MRI slice with segmented ventricles highlighted in yellow. The left sidebar contains several panels:

- 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 with columns 'Number', 'Color', 'Name', 'Label Volume', and 'Order'; 'Delete Structures', 'Merge All', and 'Merge And Build' buttons; 'Replace Models' checkbox checked.
- Edit Selected Label Map:** A grid of icons for editing; 'Undo/Redo' buttons; 'Active Tool' dropdown set to 'DefaultTool'; 'Label' dropdown set to 'region_3' with a value of '295' and a color swatch.
- Data Probe:** Empty panel.

Orientation indicators 'L', 'F', and 'B' are visible at the bottom left.

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

The screenshot shows the 3D Slicer software interface. The main view displays an axial brain MRI slice with segmented ventricles highlighted in yellow. The left sidebar contains several panels:

- Help & Acknowledgement**
- 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 with columns 'Number', 'Color', 'Name', 'Label Volume', and 'Order'; 'Delete Structures', 'Merge All', and 'Merge And Build' buttons; 'Replace Models' checkbox (checked).
- Edit Selected Label Map**: A grid of icons for various editing tools; 'Undo/Redo' buttons; 'Active Tool: Undo'; 'Label: region_3' with a value of 295 and a yellow color swatch.
- Data Probe**

At the bottom left, the letters 'L', 'F', and 'B' are stacked vertically, indicating the patient's orientation (Left, Front, Back).

Slicer displays the result of the segmentation of the ventricles.

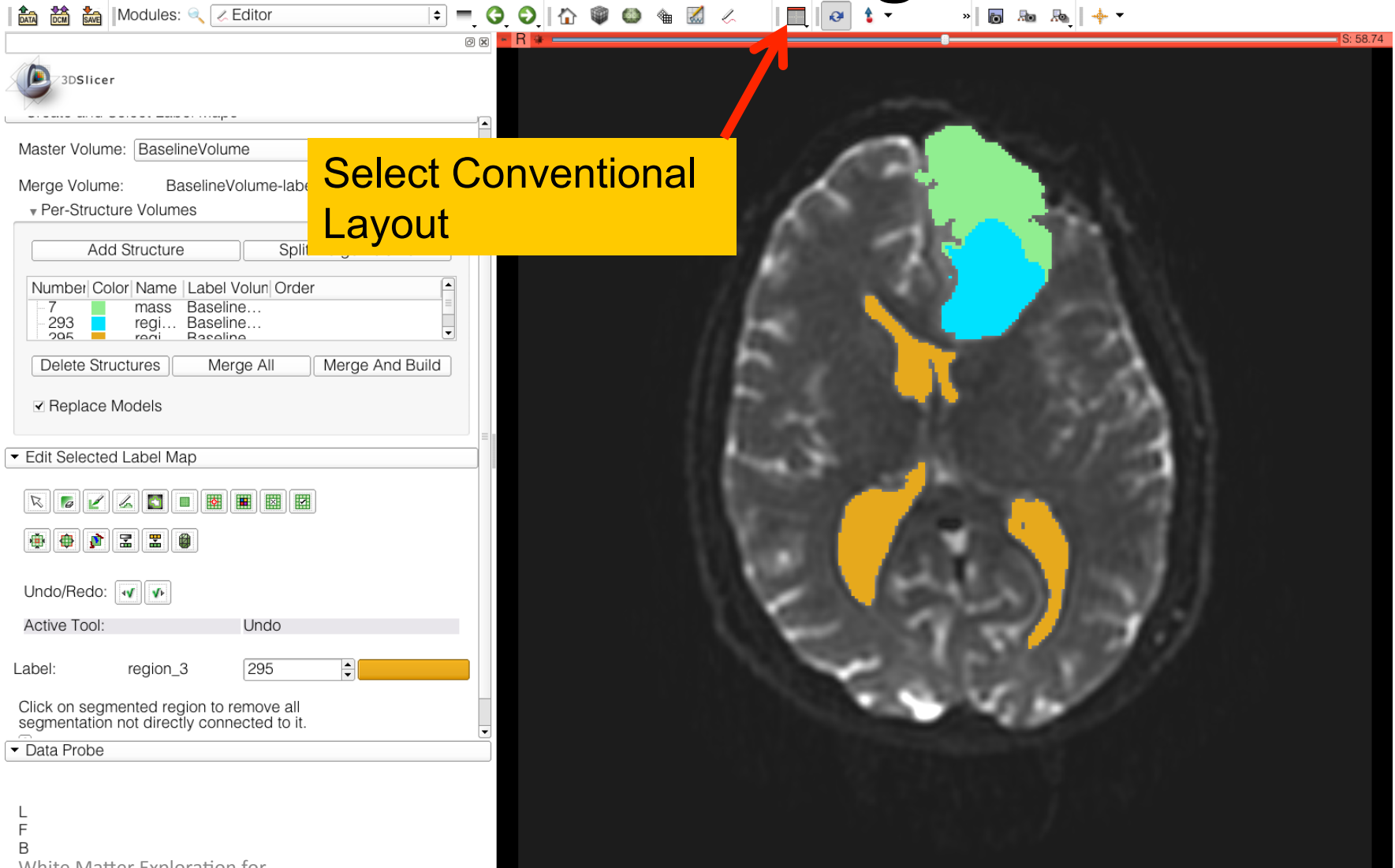
Final Result of the Segmentation

The screenshot shows the 3D Slicer software interface. On the left, the 'Per-Structure Volumes' panel is visible, containing a table of segmented regions and buttons for 'Merge All' and 'Merge And Build'. A red arrow points to the 'Merge And Build' button. Below this panel is the 'Edit Selected Label Map' section with various tool icons and a 'Data Probe' section. On the right, a large window displays a brain MRI slice with two yellow segmented regions. A yellow text box is overlaid on this window, providing instructions on how to use the 'Merge and Build' button.

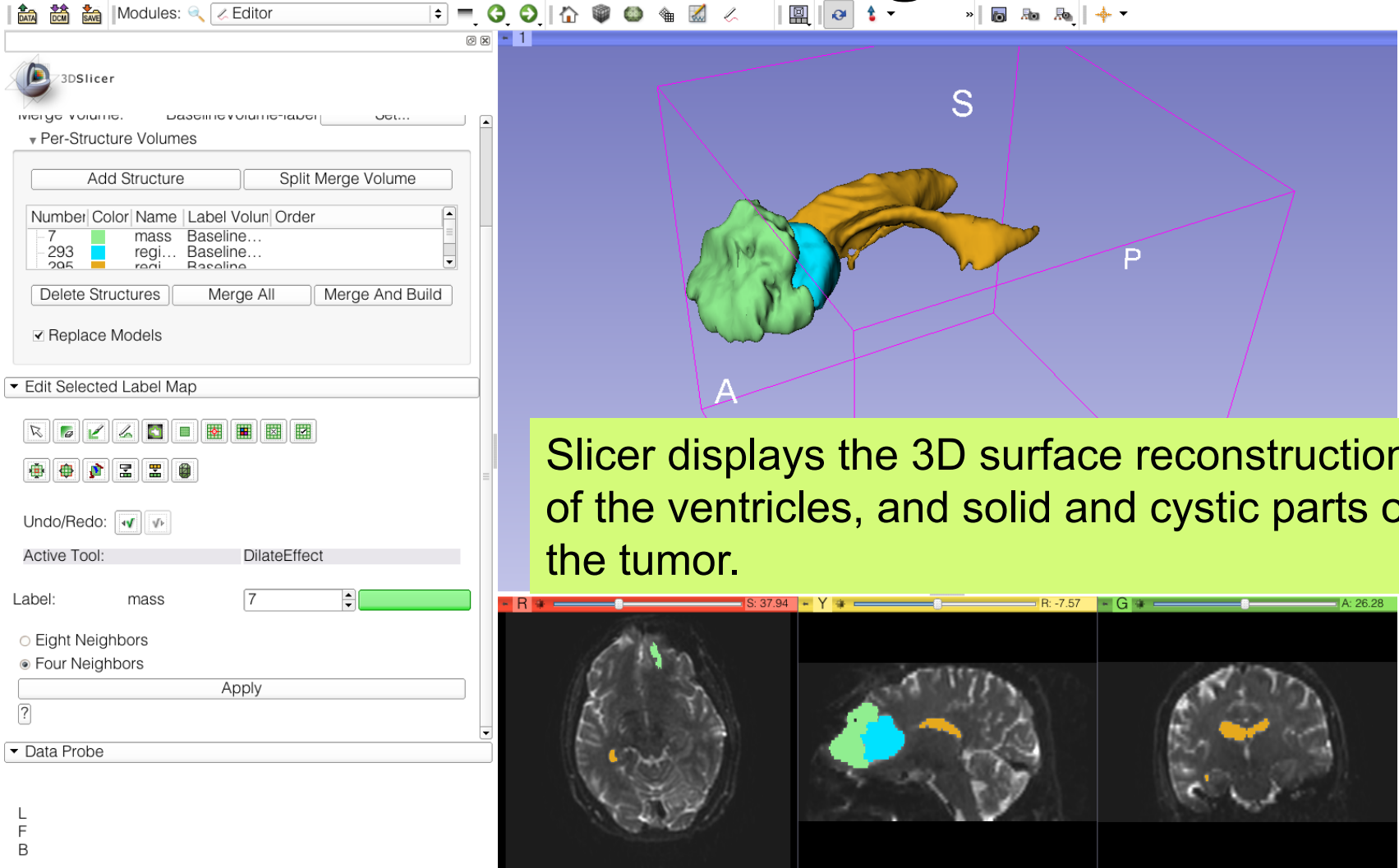
Number	Color	Name	Label Volun	Order
7	Green	mass	Baseline...	
293	Blue	regi...	Baseline...	
295	Yellow	regi...	Baseline...	

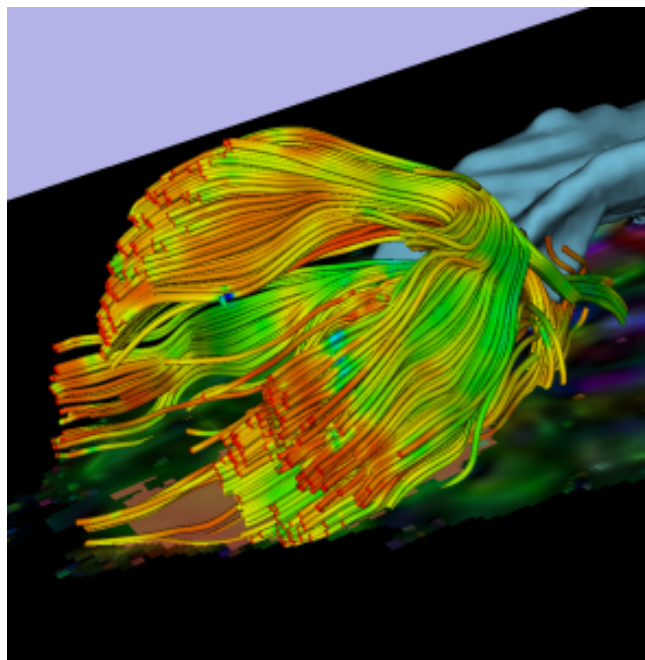
Click on **Merge and Build** to merge the different label maps, and generate the 3D models of the tumor and ventricles using a Marching Cubes algorithm

Final Result of the Segmentation



Final Result of the Segmentation

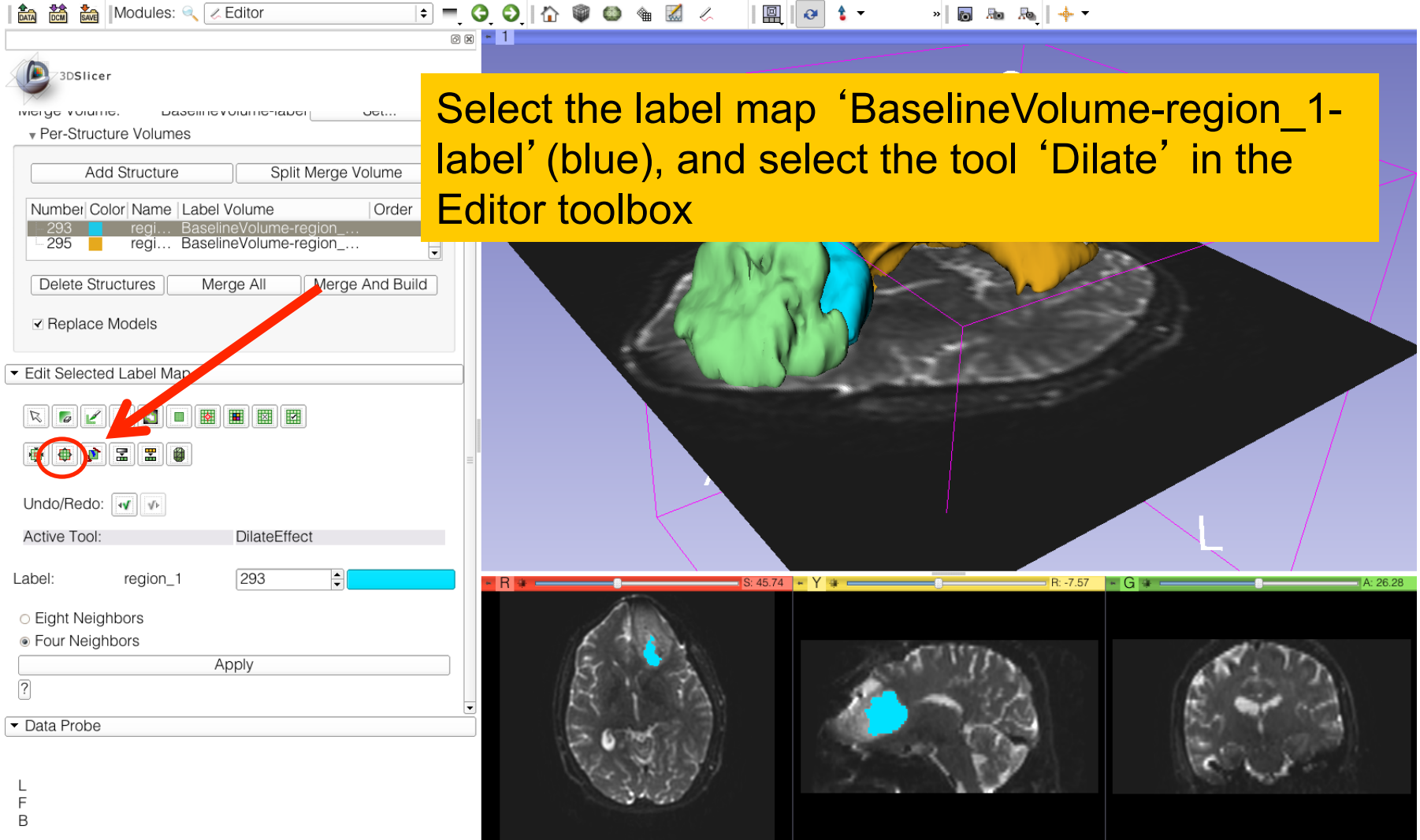




Part 2: Tractography exploration of peri- tumoral white matter fibers

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

The screenshot shows the 3D Slicer software interface. The main window displays a 3D model of a brain tumor with a blue region highlighted. The left sidebar shows the 'Per-Structure Volumes' panel with a table of regions and an 'Apply' button circled in red. The bottom panel shows three axial slices of the brain with the blue region highlighted in the first slice, and a red arrow pointing to it.

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

Active Tool: Undo

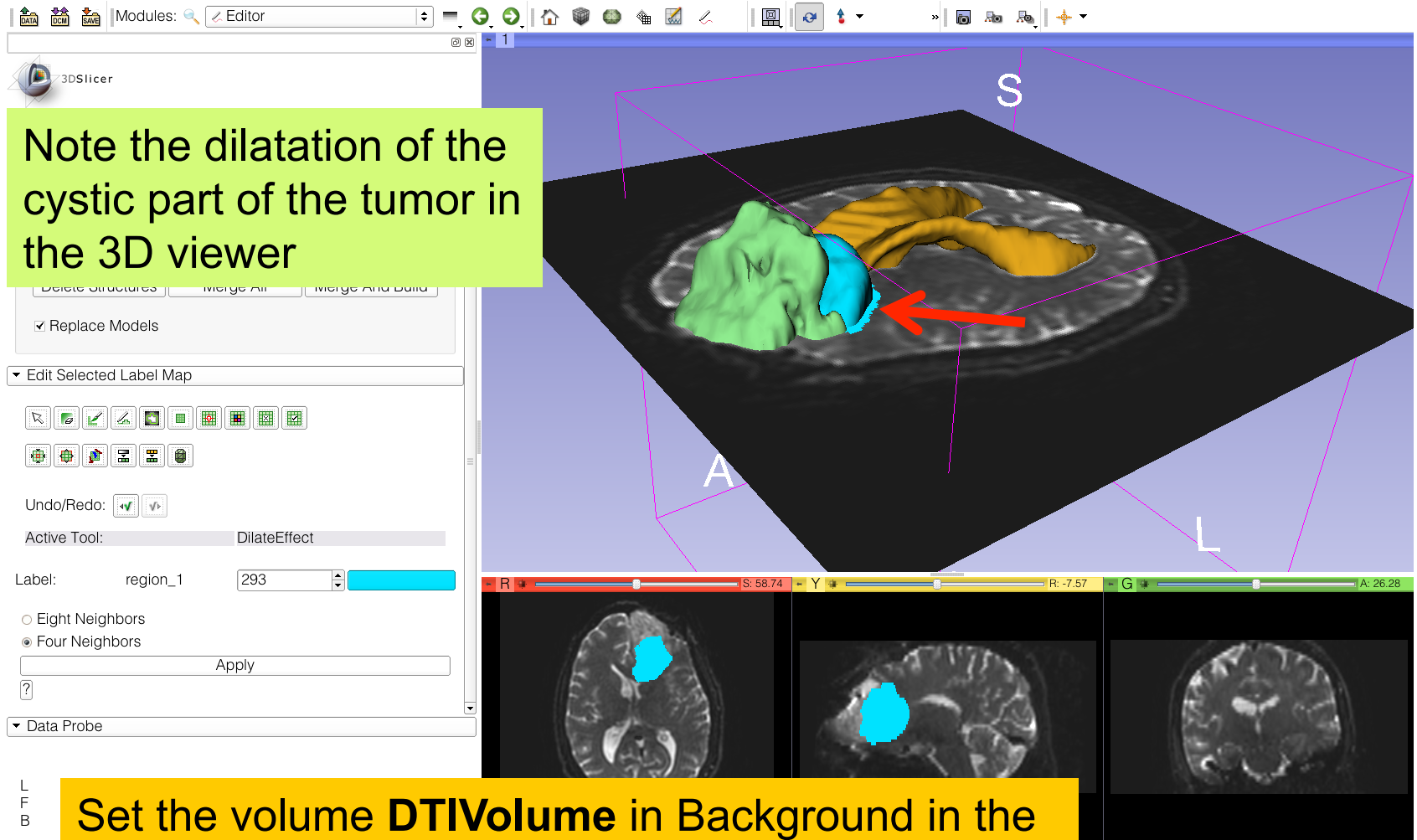
Label: region_1 293

Eight Neighbors
 Four Neighbors

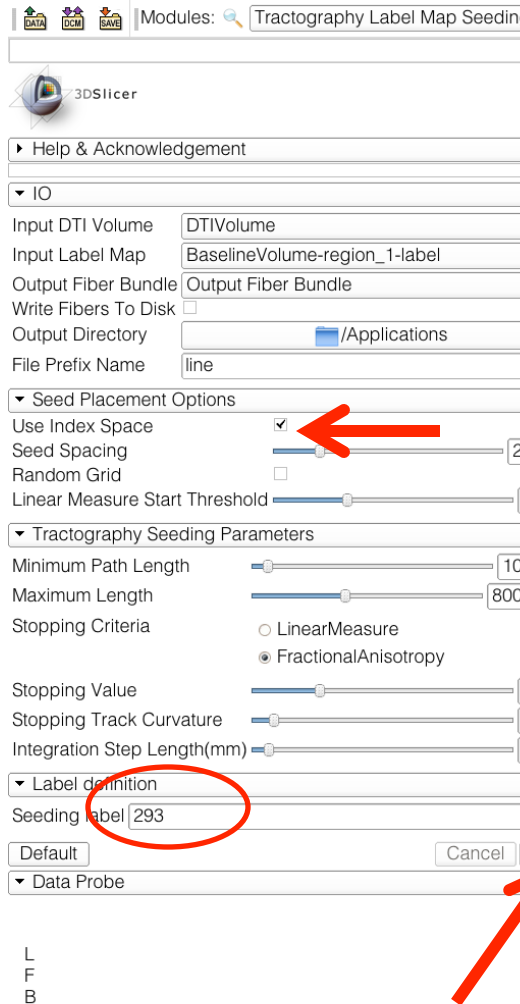
Apply

L
F
B

Visualization of the DTI Volume



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 New

- **Seed Placement Options**:

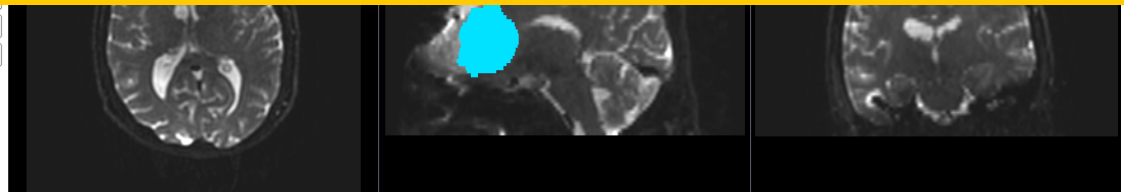
Check **Use Index Space**

- **Stopping Value**

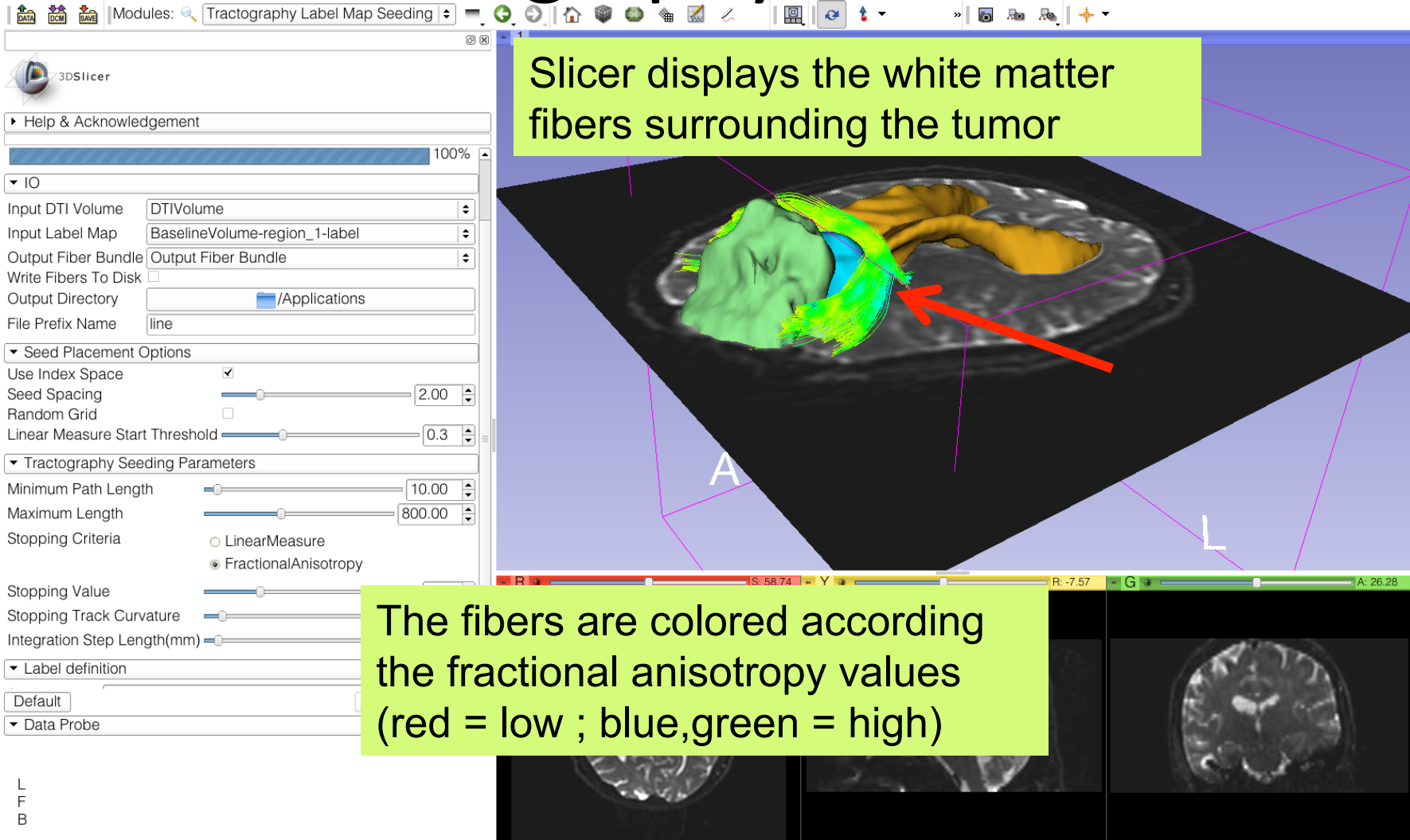
Set the FA threshold to 0.15

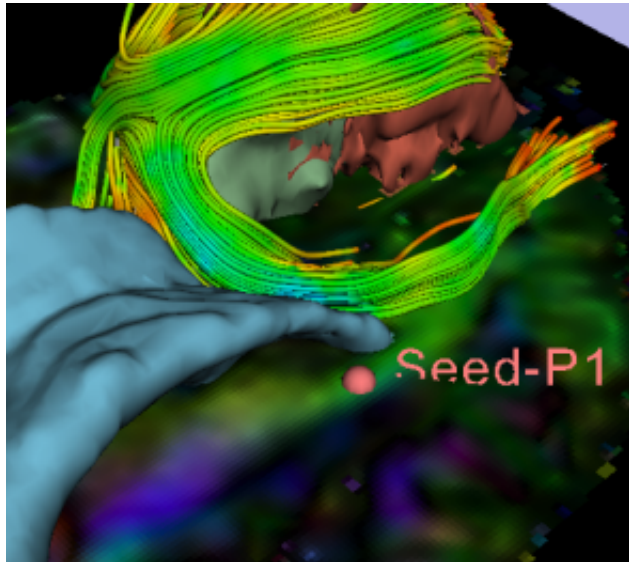
- **Label Definition**:

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

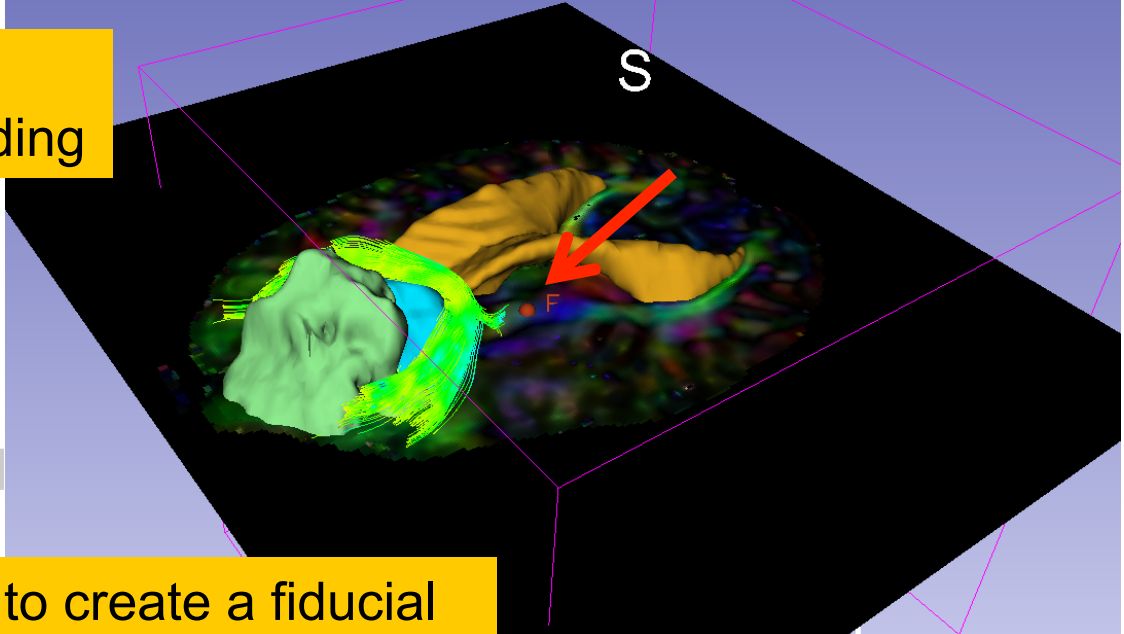
Input DTI Volume: DTIVolume
Input Fiducial List or Model: Select a AnnotationHierarchyNode
Output Fiber Bundle: Select a FiberBundle

Seed Placement Options

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

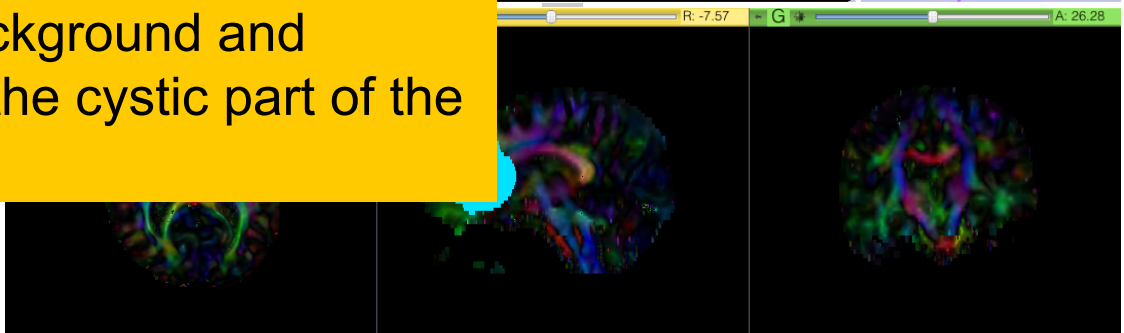
Tractography Seeding Parameters

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

Set Input DTI Volume to DTIVolume
Set Fiducial List or Model to FiducialList

Set the Minimum Path Length to 10 mm
Set the FA Stopping Criteria to 0.15

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

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

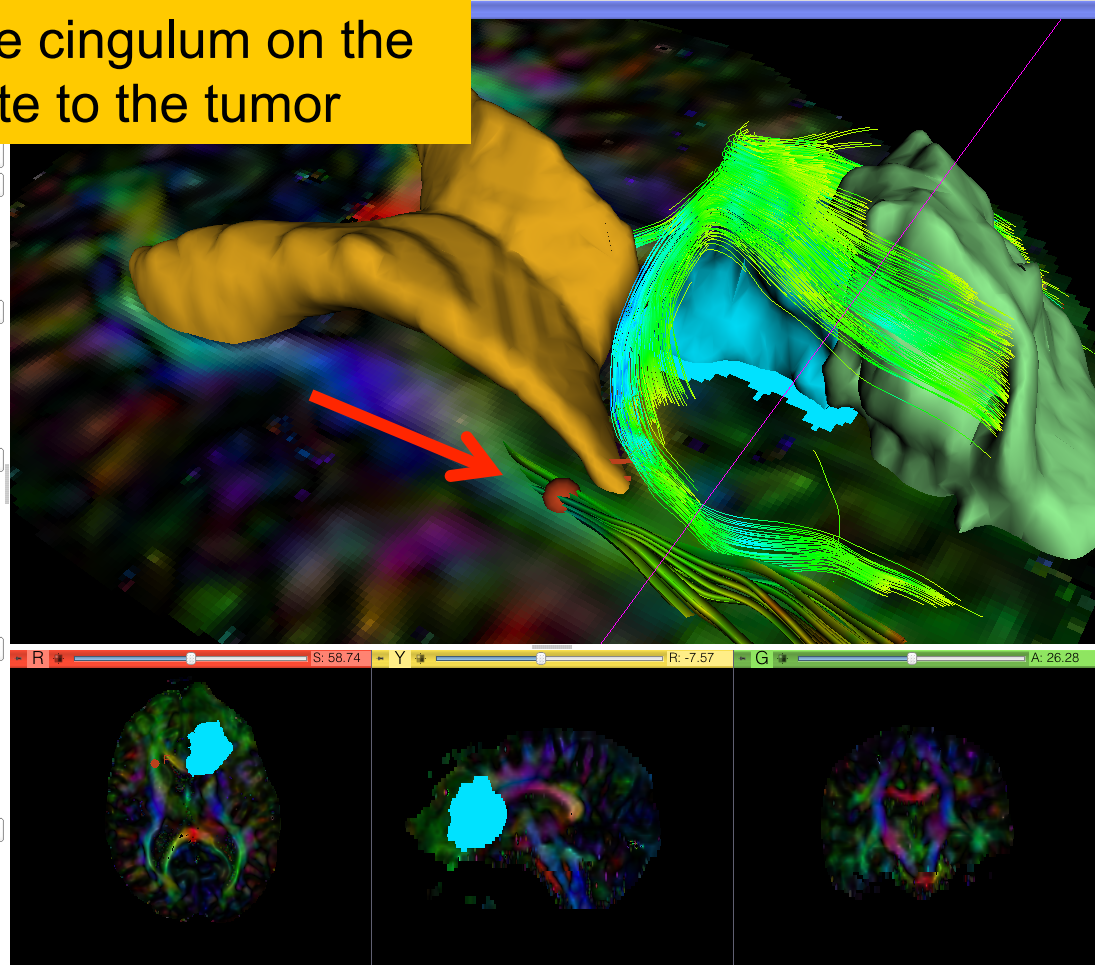
Enabling Options

Create Tracts Initially As: Tubes

Enable Seeding Tracts:

Data Probe

L
F
B



Tractography on-the-fly

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

3DSlicer

Modules: Tractography Fiducial Seeding

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

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).



DTI Tractography for Neurosurgical Planning: A Grand Challenge

MICCAI 2012 Conference
Acropolis Convention Center
Nice, France

www.miccai-org

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