Exploring Peritumoral White Matter Fibers for Neurosurgical Planning

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

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

(Stejskal and Tanner 1965, Basser 1994)

\[ D = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix} \]
Loading DTI and Baseline Data

First, click on Load Data
The "Add data into the scene" window appears. Click **Choose Directory to Add**
Locate and select the file WhiteMatterExplorationData and click Choose.
Loading DTI and Baseline Data

Check off the Volumes BaselineVolume.nrrd and DTIVolume.nhdr click OK
Loading DTI and Baseline Data

Slicer displays the elements of the scene, which contains the MR volume of the brain and a series of 3D surface models.
Loading DTI and Baseline Data

Click on the **pin icon** to display the slice menu, then click on the **link icon** to link the 3 anatomical viewers. Make sure that the background is set to **BaselineVolume**.
Loading DTI and Baseline Data

Select the **Volumes** module from the Modules menu.
The user can manually adjust the **Window Level editor presets** with the **Volume module menu**.
Click on the Layout menu and select the layout **Red slice only**
Part 1:
Segmenting the tumor and ventricles
The tumor in this clinical case is composed of two parts: a solid part, and a cystic part.

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

Slicer displays only the Axial anatomical slice in the Viewer
Tumor Segmentation

Click on the Modules menu and select the module Editor
The ‘SlicerApp-real’ window appears. Select the label map `GenericAnatomyColors` and click **Apply**.
Tumor Segmentation

Select the **PaintEffect** tool
Choose color #293 for the region 1 label.
In a single motion, draw a short line in the **cystic part of the tumor**
Tumor Segmentation

Select **color #7** for the mass label and, again in a single motion, draw a short line in the **solid part of the tumor**.
Tumor Segmentation

Select **color #295** for region 3 and draw a circle **around the tumor**.
Select the GrowCutEffect tool
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.

Tumor Segmentation

Click **Apply** to apply the GrowCutEffect segmentation algorithm.
Tumor Segmentation

Slicer displays the results from the segmentation

Solid part

Cystic part

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Scroll up the Editor menu and select the tab **Per-Structure Volumes**. Then click **Split Merge Volume**.
The label map \texttt{BaselineVolume-label} has been split into three volumes:

- \texttt{BaselineVolume-mass-label}: solid part of the tumor
- \texttt{BaselineVolume-region_1-label}: cystic part of the tumor
- \texttt{BaselineVolume-region_3-label}: surrounding structures
Tumor Segmentation

Click on the Modules menu and select the Module Data
Tumor Segmentation

The different label maps have been generated
Ventricles Segmentation

Go back to the Editor module
Select the volume **BaselineVolume-region_3-label** so that it is highlighted and that the yellow region is visible in the viewer.
Ventricles Segmentation

Select the **ThresholdEffect** tool.
Ventricles Segmentation

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

Slicer displays the result of the threshold
Ventricles Segmentation

Select the **SavesIslandEffect** in the **Editor** module.
With the **SaveIslandEffect** tool equipped, click in the occipital horn of the ventricle
Slicer displays the result of the segmentation of the ventricles.
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.
Slicer displays the results of the merging of the segmentations of the ventricles and the tumor in the Viewer.
Click on the **Layout menu** and select **Conventional**
Slicer displays the 3D surface reconstructions of the ventricles, and solid and cystic parts of the tumor.
Definition of peri-tumoral volume

Click on the pin icon, deselect the link icon, and select the eye icon to view just the axial slice in the 3D Viewer.
Definition of peri-tumoral volume

Select the label map BaselineVolume-region_1-label (blue) and select the DilateEffect tool.
Part 2: Tractography exploration of peritumoral white matter fibers
Definition of peri-tumoral volume

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

Note the dilatation of the cystic part of the tumor in the 3D viewer.
Final Result of Segmentation

Click on the **Module search icon**, delete **Editor** and type in **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 Fiber Bundle
Scroll down and set the following values:

- **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**
Final Result of Segmentation

Slicer displays the white matter fibers surrounding the tumor

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

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Part 4: Tractography exploration of the ipsilateral and contralateral side
Tractography on-the-fly

Click on the **Modules** menu and select the module **Tractography Interactive Seeding**, then switch the background of the 3 anatomical slice viewers to **DTIVolume**.
Select the **Fiducial icon**, and position it next to the cystic part of the tumor by clicking near it in the 3D viewer.
Tractography on-the-fly

Set Input DTI Volume to **DTIVolume**
Set Fiducial List or Model to **FiducialsList**
Set Output Fiber Bundle to **Create new Fiber Bundle**
Tractography on-the-fly

Set the **Minimum Path Length** to 10.0 mm and the **FA Stopping Value** at 0.15
Fiducial Seeding

Position the fiducial in the cingulum on the contralateral side opposite to the tumor.
Tractography on-the-fly

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

• National Alliance for Medical Image Computing (NA-MIC)
  NIH U54EB005149

• Neuroimage Analysis Center (NAC)
  NIH P41RR013218

• Parth Amin, WIT ’16
• Matthew Flynn, WIT ‘16