Diffusion Tensor Imaging Tutorial

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DTI tutorial

This tutorial is an introduction to the advanced Diffusion MR capabilities of the Slicer3 software for medical image analysis.
Outline

This tutorial guides you through the process of loading diffusion MR data, estimating diffusion tensors, and performing tractography of white matter bundles.
The processing pipeline uses 9 image analysis modules of Slicer3.6

1. Data
2. Volumes
3. Diffusion Tensor Estimation
4. Diffusion Tensor Scalar Measurements
5. Editor
6. LabelMap Seeding
7. Fiber Bundles
8. Fiducials
9. Fiducial Seeding
The Diffusion MR tutorial dataset is composed of a Diffusion Weighted MR scan of the brain acquired with 12 gradient directions and 2 baseline.
DTI Processing Pipeline

- DWI Acquisition
- Tensor Calculation
- Scalar Maps
- 3D Visualization
Start Slicer3

Linux/Mac users
Launch the Slicer3 executable located in the Slicer3.6 directory

Windows users
Select
Start → All Programs → Slicer3-3.6-RC3-2010-06-04 → Slicer3
Slicer Welcome

The **SlicerWelcome** module is the module displayed by default. This module gives an overview of the GUI of Slicer3, and data loading & saving functionalities.
Part 1:
Diffusion data loading and tensor estimation
Diffusion Tensor

Stejskal-Tanner

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

\[
\mathbf{D} = \begin{bmatrix}
D_{xx} & D_{xy} & D_{xz} \\
D_{yx} & D_{yy} & D_{yz} \\
D_{zx} & D_{zy} & D_{zz}
\end{bmatrix}
\]
The dataset used in this tutorial is in the **Nrrd file format**, which is part of the NA-MIC kit.

To convert your own Dicom data to Nrrd, use the **DicomToNrrdConverter** module in Slicer.
DicomToNrrd converter

The DICOMToNrrdConverter is located in the Converters category in the Modules menu.

Use .nhdr for Output Filename extension.
A list of supported DWI formats can be found on the documentation page of the DicomToNrrdconverter:

http://www.slicer.org/slicerWiki/index.php/Modules:DicomToNRRD-3.6
Loading the DWI Volume

Select **File → Add Volume** from the **File** menu
Loading the DWI Volume

Browse to the location of the Diffusion tutorial dataset directory and select the file dwiDataset.nhdr.

Click on Apply to load the volume.
Loading the DWI Volume

Left click on the menu Modules and select All Modules to display the list of over 100 modules available for image analysis and 3D visualization.

Select the Volumes module
Select the Active Volume `dwiDataset` and adjust the Window/Level Parameters.

Slicer displays the anatomical views of the baseline volume of the diffusion dataset in the 2D Slice Viewer.
Tensor Estimation

Left click on the Modules menu and select Diffusion Tensor Estimation.
Tensor Estimation

Select the Input DWI Volume `dwiDataset`

Left click on **Output DTIVolume** and select **Create New Diffusion Tensor Volume**

Left click on **Output Baseline Volume** and select **Create New Volume**

Left click on **Otsu Threshold Mask** and select **Create New Volume**
Tensor Estimation

Select the Tensor Estimation Parameters LS (Least Squares), and click on Apply to estimate the tensors.
Tensor Estimation

Left click on **Output Baseline Volume** to display the list of volumes that have been computed by Slicer.
Tensor Estimation

Output DTI Volume is the volume of estimated tensors

Output Baseline Volume is the Baseline volume

Otsu Threshold Mask is the tensor mask (blue)
Tensor Estimation

Click on the link icon, left click on **Output Threshold Mask** and select **None**
Tensor Estimation

Select the **Volumes** icon in the Modules toolbar
Set the Active Volume to Output Baseline Volume and click on the Display tab.
Adjust the **Window/Level** parameters of the baseline volume using the slider.
Tensor Estimation

Browse through the baseline images, which correspond to the volumes that have been acquired without gradient.
Part 2:

Scalar Measurements
Scalar Measurements

Select the category **Diffusion → Utilities** from the list of modules, and left click on the **Diffusion Tensor Scalar Measurements** module.
Scalar Measurements

Set the Input DTI Volume to Output DTI Volume

Set the Output Scalar Volume to Create New Volume

Set the Estimation Parameters to Fractional Anisotropy, and click on Apply
Left click on the **Slicer Viewer Menu** icon, and select **Show label volume outlines**.
Fractional Anisotropy Volume

Slicer displays the outline of the tensor mask overlaid on the Fractional Anisotropy volume.
Move the mouse over the Fractional Anisotropy map to explore the FA values which range from 0 to 1, and are displayed in the bottom corner of the active (Bg) window.
Part 3: Region of Interest Based Tractography
LabelMap Generation

Select the Editor module in the Modules menu.

Set the Master Volume to Output Scalar Volume.
LabelMap Generation

Click on **Set** and then on **Create New** to create the seeding label map.
LabelMap Generation

Left click on the **Color Table** dropdown box and select **Discrete → Labels**.

Click **Apply**.
Left click on the Label Map Selection, and select the Output Scalar Volume-label label map.
LabelMap Generation

Left click on the **Slicer Viewer Menu** icon, and select **Don’t show label volume outlines**.
LabelMap Generation

Select the label 2 (pink), click on the Paint icon, set the radius to 2 and draw a region of interest within the corpus callosum in the sagittal view on a set of 2 or 3 slices.
LabelMap Seeding

Select the **Labelmap Seeding** module from the **All Modules** menu.
LabelMap Seeding

- Set the Input DTI volume
- Output DTI Volume
- Select the Input Label Map
- Output Scalar Volume-label
- Select Output Fiber Bundle
- Create New Fiber Bundle
In the **Seed Placement Options** tab, check mark **Use Index Space**.

In the **Tractography Seeding Parameters** tab, set the **Stopping Mode** to **Fractional Anisotropy**, and use the default parameters for the Minimum and Maximum Length, Stopping Value, Stopping Track Curvature and Integration Step Length.

In the **Label Definition** tab, set Seeding label to label 2, and click on **Apply**.
LabelMap Seeding

The tracts generated within the corpus callosum region appear in the 3DViewer.

The color map used represent the FA values along the tracts.
LabelMap Seeding

Select the **FiberBundles** module, and click on the **Tube** tab in the **Display** panel.

Check the visibility box to display the tubes.
LabelMap Seeding

Slicer displays the computed tracts as tubes colored with FA values.
Part 4:

Tractography on-the-fly
Fiducial Seeding

Select the **Fiducials** module in the **All Modules** menu
Fiducial Seeding

Set Fiducial List to Create New Fiducial List
Fiducial Seeding

Left click on **Fiducial List** and select **Rename**
Enter the new name **Seed** and click on **Apply**
Fiducial Seeding

Click on the cross icon to add a fiducial to the Seed list.
Fiducial Seeding

The fiducial Seed-P appears in the 3D Viewer
Fiducial Seeding

Position the fiducial in the cingulum region located above the corpus callosum
Fiducial Seeding

Check the box to select the ‘Seed-P’ fiducial: we will use this fiducial to drive the tractography.

Once selected, the fiducial Seed-P is displayed in pink letters in the 3D viewer.
Fiducial Seeding

Set the **Output FiberBundleNode** to Create New FiberBundle

**Important:** this step **must** be done first

Select the **Fiducial Seeding** module

Set the DTI Volume to **Output DTI Volume**

Select Fiducial List: **Seed**
Fiducial Seeding

Set the **Stopping Mode** to **Fractional Anisotropy** and set the tractography parameters to the values that we used for the corpus callosum:

- **Stopping Value**: 0.1
- **Stopping Track Curvature**: 0.8
- **Integration Step Length**: 0.8 mm
- **Minimum Path Length**: 10 mm
- **Fiducial Seeding Region Size**: 5 mm
- **Fiducial Seeding Step Size**: 1.5 mm
Slicer displays the tracts seeded from the Fiducial Seed-P.

The tracts correspond to the region of the cingulum located above the corpus callosum.

For better visualization, uncheck the visibility box under **Tubes** in the **Fiber Bundles** module (Slide 45).
Move the fiducial **Seed-P** from the left cingulum to the corresponding region in the right cingulum in the coronal slice.
Fiducial Seeding

Slicer displays a portion of the right cingulum tracts which are seeded from the new position of the fiducial Seed-P.
Part 5: Saving a DTI Scene
DTI Scene

Select the **Data** module

Slicer displays the list of volumes and models generated in this tutorial.
Saving a DTI Scene

Select **File**→**Save** from the Main menu
Saving a DTI Scene

Browse to a directory where you would like to save the data. Once you have selected a directory, select all the files that have been created during this tutorial and click on **Save Selected**.
Saving a DTI Scene

Select File ➔ Close Scene to close the current DTI Scene
Loading a DTI Scene

Select **File ➤ Load Scene** and browse to the location where you saved the **SlicerScene1.mrml** scene file.
Loading a DTI Scene

Select the SlicerScene1.mrml scene file and click on Open
Loading a DTI Scene

Select the **Data** module
Loading a DTI Scene

Slicer loads all the elements of the DTI Scene that were previously computed.
Conclusion

This tutorial guided you through some of the Diffusion MR capabilities of the Slicer3 software for studying the brain white matter pathways.

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