

CLI Application

Tractography selection and measurements

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Pre-requisite

- This tutorial is a follow-up tutorial of:
 - “Diffusion Tensor Imaging Tutorial” by Sonia Pujol, PhD
 - https://www.slicer.org/slicerWiki/index.php/Documentation/4.5/Training#Slicer4_Diffusion_Tensor_Imaging_Tutorial
 - “Fiber Bundle Selection and Scalar Measurements” by Fan Zhang
 - https://www.slicer.org/slicerWiki/index.php/Documentation/4.5/Training#Fiber_Bundle_Selection_and_Scalar_Measurements
- Please go through them ahead.

Learning Objectives

- Following this tutorial, you'll be able to conduct the fiber bundle selection and calculate fiber tract scalar measurement in a command line interface (CLI) mode.

CLI

- CLI is standalone executable with a limited input/output arguments complexity (simple argument types, no user interactions).
- Applying CLI can be efficient when there are a large amount of data to process, for example of conducting patient/control group study.

Tutorial Software

The tutorial uses the 3DSlicer (Version 4.5.0-1 Stable Release) software available at <http://download.slicer.org>

Disclaimer

It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules. Slicer is a tool for research, and is not FDA approved.

Tutorial Data

The tutorial uses 5 datasets (case 1 to 5), in which:

- Case 1 is from the neurosurgery tutorial dataset, downloaded at:
[https://www.slicer.org/slicerWiki/images/b/bb/
WhiteMatterExplorationData.zip](https://www.slicer.org/slicerWiki/images/b/bb/WhiteMatterExplorationData.zip)
- Case 2 is from the diffusion MRI tutorial dataset, downloaded at:
https://www.slicer.org/slicerWiki/images/e/e6/Dti_tutorial_data.zip
- Cases 3 to 5 are from the Human Connectome Project (HCP)*, download at: <http://www.humanconnectome.org>

For each case, the following data are provided:

- Baseline image
- Down sampled whole brain tractography (conducted as in the DWI tutorial and down-sampled to about 10000 fibers using Tractography Display module)
- Corpus callosum label map (drawn as in the DWI tutorial)

Data available at http://www.na-mic.org/Wiki/images/6/66/Cli_data.zip

*Data courtesy of the Human Connectome Project

Data preview

The screenshot shows the 3D Slicer application interface. On the left, there is a file browser window titled "cli_data" showing a list of files. A red arrow points from the text "Drag and drop the file onto the viewer of the Slicer application" to the list of files. In the center, there is a 3D viewer window with three orthogonal planes labeled R (right), P (posterior), and L (left). A red arrow points from the text "Load the tractography as FiberBundle" to the "FiberBundle" dropdown menu in the viewer's control panel. Another red arrow points from the text "Click OK to load the dataset to Slicer" to the "OK" button in the dialog box. A green box at the bottom contains a note about CLI operations.

Locate the data of one case:

Drag and drop the file onto the viewer of the Slicer application

Load the tractography as FiberBundle

Click OK to load the dataset to Slicer

Please notice that the CLI operation is conducted outside 3D Slicer interface. The screenshots with 3D Slicer interface in this tutorial are used only for visualizing the data.

Data preview

Data loaded from case 2, including:

- Whole brain tractography
- Baseline image
- Corpus callosum (CC) mask

Load other cases for preview

The image shows the 3D Slicer software interface. On the left, a sidebar displays various modules and case information. A large green box highlights the text "Data loaded from case 2, including:" followed by a bulleted list. Below this box is the text "Load other cases for preview". To the right of the sidebar is a 3D brain model with a pink wireframe cube around it. The brain is colored with green and yellow tractography fibers. Labels "R", "S", "L", and "I" indicate the Right, Superior, Left, and Inferior directions respectively. At the bottom, there are three 2D grayscale brain slices (axial, coronal, sagittal) showing the baseline image with a green Corpus Callosum (CC) mask overlaid. Each slice has a scale bar of 5 cm.

3D Slicer 4.5.0-1

Welcome to Slicer

3DSlicer

Load DICOM

Customize

Feedback

Share your 3D Slice

We are always looking for feedback. Your submission will be reviewed and considered.

About

The Main Window

Loading and Saving

Display

Mouse & Keyboard

Documentation & Tutorials

Acknowledgment

Data Probe

Show Zoomed Slice

L
F
B

R S: 0.000mm Y R: 1.500mm G A: 1.500mm

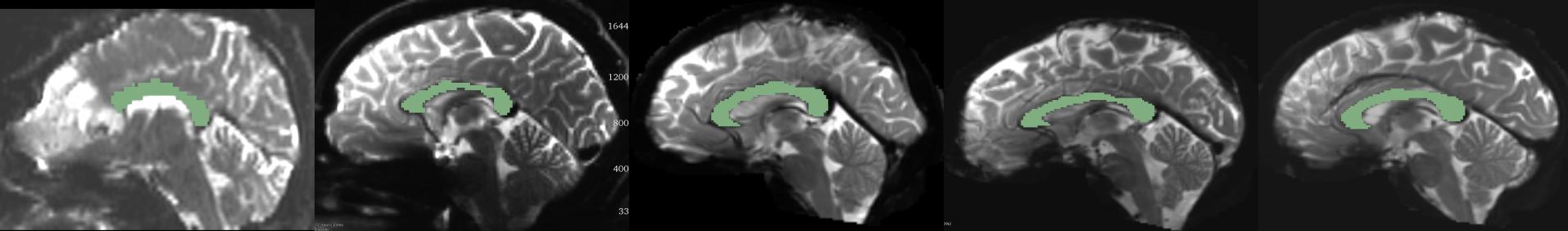
L: case_2_CC_label (100%)
B: case_2_baseline

L: case_2_CC_label (100%)
B: case_2_baseline

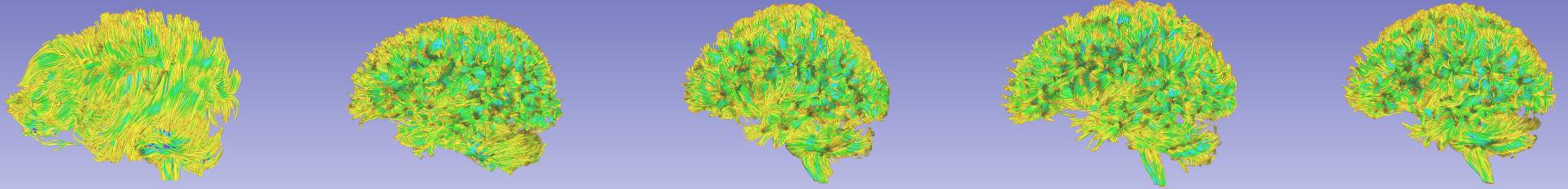
L: case_2_CC_label (100%)
B: case_2_baseline

Data preview

CC label on baseline image (from left view)



Whole brain tractography (from left view)



Case 1

Case 2

Case 3

Case 4

Case 5

Shell script

```
cli_tutorial_script.sh *  
1 # Written by Fan Zhang, fzhang@bwh.harvard.edu, BWH and USYD  
2  
3 datafolder='.' # . is current folder. User may replace it with the data base path.  
4 slicerpath='/Applications/Slicer2.app/Contents' # replace it with your local 3D Slicer.  
5  
6 # Step 1: fiber bundle selection of CC  
7 fiberbundleselectCLI=$slicerpath/lib/Slicer-4.5/cli-modules/FiberBundleLabelSelect  
8 echo "Step 1: Conducting fiber bundle selection"  
9 for vtkfile in `ls $datafolder/case_*_tractography_p.vtk`  
10 do  
11     caseid=${vtkfile: ${#vtkfile}-25:6}  
12  
13     wholebraintractography=$datafolder/$caseid\_tractography_p.vtk  
14     CClabelmap=$datafolder/$caseid\_CC_label.nrrd  
15     extractedCC=$datafolder/$caseid\_CC_extracted.vtk  
16     clicommand="$fiberbundleselectCLI $CClabelmap $wholebraintractography $extractedCC -p 1"  
17  
18     echo "#Fiber bundle selection from CC of $caseid"  
19     echo " - Input tractography: $wholebraintractography"  
20     echo " - Input CC label map: $CClabelmap"  
21     echo " - Output CC bundle: $extractedCC"  
22     echo " - CLI command of this process: $clicommand"  
23     $clicommand  
24  
25 done  
26  
27 # Step 2: fiber tract scalar measurement  
28 fiberbundleselectCLI=$slicerpath/lib/Slicer-4.5/cli-modules/FiberTractMeasurements  
29 echo "Step 2: Conducting fiber tract scalar measurement"  
30  
31 tractfolder=$datafolder # Use datafolder as input to measure the tractography we just obtained  
both whole brain and CC)  
32 measurefile="$datafolder/tractmeasurements.txt"  
33 clicommand="$fiberbundleselectCLI --inputtype Fibers_File_Folder --format Column_Hierarchy --  
separator Tab --inputdirectory $tractfolder --outputfile $measurefile"  
34  
35 echo "#Scalar measurements from both the whole brain tractography and the extracted CC tracts"  
36 echo " - Input folder: $tractfolder"  
37 echo " - Output measurement: $measurefile"  
38 echo " - CLI command of this process: $clicommand"  
39 $clicommand  
40  
41 echo "Finished!"
```

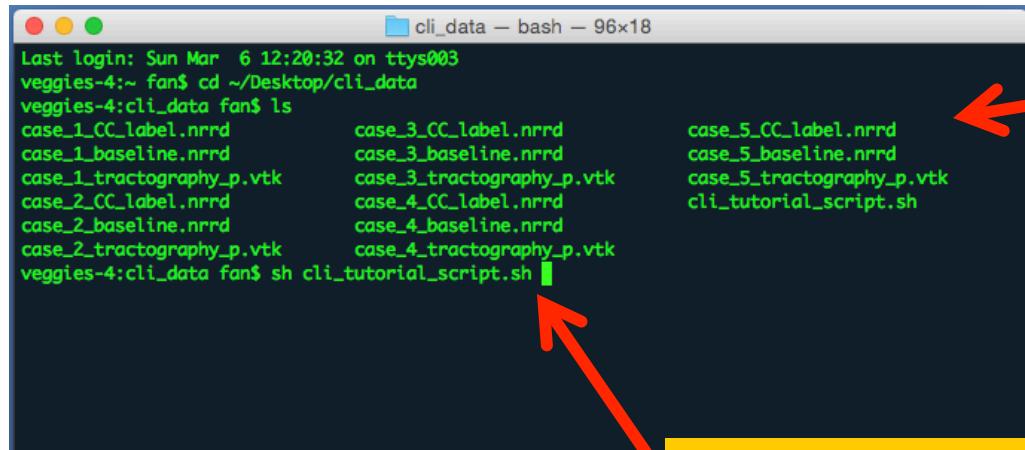
Located in the data folder:
`cli_tutorial_script.sh`

Fiber Bundle Selection

Fiber Tract Measurement

Run script

Open a terminal (The tutorial is based on Mac system:
Go to Application -> Utilities -> Terminal.app)



A screenshot of a Mac OS X terminal window titled "cli_data — bash — 96x18". The window shows a command-line session:

```
Last login: Sun Mar  6 12:20:32 on ttys003
veggies-4:~ fan$ cd ~/Desktop/cli_data
veggies-4:cli_data fan$ ls
case_1_CC_label.nrrd      case_3_CC_label.nrrd
case_1_baseline.nrrd       case_3_baseline.nrrd
case_1_tractography_p.vtk   case_3_tractography_p.vtk
case_2_CC_label.nrrd      case_4_CC_label.nrrd
case_2_baseline.nrrd       case_4_baseline.nrrd
case_2_tractography_p.vtk   case_4_tractography_p.vtk
veggies-4:cli_data fan$ sh cli_tutorial_script.sh
```

Two red arrows point from the text boxes above to the terminal window: one points to the "ls" command output, and another points to the "sh cli_tutorial_script.sh" command.

Go to the data folder
(cd XXX) and view all
files provided (ls).

Execute the script (sh cli_tutorial_script.sh)

Run script

```
Last login: Sun Mar  6 12:20:32 on ttys003
veggies-4:~ fan$ cd ~/Desktop/cli_data
veggies-4:cli_data fan$ ls
case_1_CC_label.nrrd      case_3_CC_label.nrrd      case_5_CC_label.nrrd
case_1_baseline.nrrd       case_3_baseline.nrrd       case_5_baseline.nrrd
case_1_tractography_p.vtk  case_3_tractography_p.vtk  case_5_tractography_p.vtk
case_2_CC_label.nrrd      case_4_CC_label.nrrd      cli_tutorial_script.sh
case_2_baseline.nrrd       case_4_baseline.nrrd
case_2_tractography_p.vtk  case_4_tractography_p.vtk
veggies-4:cli_data fan$ sh cli_tutorial_script.sh
Step 1: Conducting fiber bundle selection
#Fiber bundle selection from CC of case_1
- Input tractography: ./case_1_tractography_p.vtk
- Input CC label map: ./case_1_CC_label.nrrd
- Output CC bundle: ./case_1_CC_extracted.vtk
- CLI command of this process: /Applications/Slicer2.app/Contents/lib/Slicer-4.5/cli-modules/FiberBundleLabelSelect ./case_1_CC_label.nrrd ./case_1_tractography_p.vtk ./case_1_CC_extracted.vtk -p 1
#Fiber bundle selection from CC of case_2
- Input tractography: ./case_2_tractography_p.vtk
- Input CC label map: ./case_2_CC_label.nrrd
- Output CC bundle: ./case_2_CC_extracted.vtk
- CLI command of this process: /Applications/Slicer2.app/Contents/lib/Slicer-4.5/cli-modules/FiberBundleLabelSelect ./case_2_CC_label.nrrd ./case_2_tractography_p.vtk ./case_2_CC_extracted.vtk -p 1
#Fiber bundle selection from CC of case_3
- Input tractography: ./case_3_tractography_p.vtk
- Input CC label map: ./case_3_CC_label.nrrd
- Output CC bundle: ./case_3_CC_extracted.vtk
- CLI command of this process: /Applications/Slicer2.app/Contents/lib/Slicer-4.5/cli-modules/FiberBundleLabelSelect ./case_3_CC_label.nrrd ./case_3_tractography_p.vtk ./case_3_CC_extracted.vtk -p 1
#Fiber bundle selection from CC of case_4
- Input tractography: ./case_4_tractography_p.vtk
- Input CC label map: ./case_4_CC_label.nrrd
- Output CC bundle: ./case_4_CC_extracted.vtk
- CLI command of this process: /Applications/Slicer2.app/Contents/lib/Slicer-4.5/cli-modules/FiberBundleLabelSelect ./case_4_CC_label.nrrd ./case_4_tractography_p.vtk ./case_4_CC_extracted.vtk -p 1
#Fiber bundle selection from CC of case_5
- Input tractography: ./case_5_tractography_p.vtk
- Input CC label map: ./case_5_CC_label.nrrd
- Output CC bundle: ./case_5_CC_extracted.vtk
- CLI command of this process: /Applications/Slicer2.app/Contents/lib/Slicer-4.5/cli-modules/FiberBundleLabelSelect ./case_5_CC_label.nrrd ./case_5_tractography_p.vtk ./case_5_CC_extracted.vtk -p 1
Step 2: Conducting fiber tract scalar measurement
#Scalar measurements from both the whole brain tractography and the extracted CC tracts
- Input folder: .
- Output measurement: ./tractmeasurements.txt
- CLI command of this process: /Applications/Slicer2.app/Contents/lib/Slicer-4.5/cli-modules/FiberTractMeasurements --inputtype Fibers_File_Folder --format Column_Hierarchy --separator Tab --inputdirectory . --outputfile ./tractmeasurements.txt
Name  Num_Points  Num_Fibers  Tensors_.FractionalAnisotropy  Tensors_.LinearMeasurement  Tensors_.MaxEigenvalue  Tensors_.MidEigenvalue  Tensors_.MinEigenvalue  Tensors_.PlanarMeasurement  Tensors_.RelativeAnisotropy
Tensors_.SphericalMeasurement  Tensors_.Trace
/Users/fan/Desktop/cli_data./case_1_CC_extracted.vtk  124160.000000  1039.000000  0.465108  0.453333  0.001389  0.000726  0.000552  NAN  398113524.178083  NAN  NAN
/Users/fan/Desktop/cli_data./case_1_tractography_p.vtk  888495.000000  9536.000000  0.385252  0.369968  0.001214  0.000748  0.000570  NAN  721587263.691522  NAN  NAN
/Users/fan/Desktop/cli_data./case_2_CC_extracted.vtk  295452.000000  1969.000000  0.532239  0.512313  0.001210  0.000557  0.000394  NAN  21330778.985313  NAN  NAN
/Users/fan/Desktop/cli_data./case_2_tractography_p.vtk  1816977.000000  9623.000000  0.453991  0.430557  0.001087  0.000593  0.000424  NAN  11573215.938993  NAN  NAN
/Users/fan/Desktop/cli_data./case_3_CC_extracted.vtk  367134.000000  1959.000000  0.493054  0.485522  0.000807  0.000398  0.000295  0.134541  0.324711  0.379934  NAN
/Users/fan/Desktop/cli_data./case_3_tractography_p.vtk  1160275.000000  8991.000000  0.432076  0.424927  0.000768  0.000427  0.000321  0.143339  0.275661  0.431493  NAN
/Users/fan/Desktop/cli_data./case_4_CC_extracted.vtk  354499.000000  1835.000000  0.482864  0.477798  0.000796  0.000395  0.000300  0.129559  0.318099  0.392733  0.001491
/Users/fan/Desktop/cli_data./case_4_tractography_p.vtk  1268505.000000  9979.000000  0.426978  0.418942  0.000749  0.000419  0.000316  0.145545  0.272013  0.436303  NAN
/Users/fan/Desktop/cli_data./case_5_CC_extracted.vtk  343945.000000  1831.000000  0.514175  0.506502  0.000876  0.000409  0.000304  0.129274  0.344049  0.364222  NAN
/Users/fan/Desktop/cli_data./case_5_tractography_p.vtk  1214516.000000  9385.000000  0.449667  0.438463  0.000828  0.000441  0.000328  0.145413  0.289454  0.415943  NAN
Final output
veggies-4:cli_data fan$ ls
case_1_CC_extracted.vtk  case_2_CC_extracted.vtk  case_3_CC_extracted.vtk  case_4_CC_extracted.vtk  case_5_CC_extracted.vtk  cli_tutorial_script.sh
case_1_CC_label.nrrd    case_2_CC_label.nrrd    case_3_CC_label.nrrd    case_4_CC_label.nrrd    case_5_CC_label.nrrd  tractmeasurements.txt
case_1_baseline.nrrd   case_2_baseline.nrrd   case_3_baseline.nrrd   case_4_baseline.nrrd   case_5_baseline.nrrd
case_1_tractography_p.vtk  case_2_tractography_p.vtk  case_3_tractography_p.vtk  case_4_tractography_p.vtk  case_5_tractography_p.vtk
```

Script output

View all files after the processing (ls)

Command

Command for fiber bundle selection:

```
Step 1: Conducting fiber bundle selection
#Fiber bundle selection from CC of case_1
- Input tractography: ./case_1_tractography_p.vtk
- Input CC label map: ./case_1_CC_label.nrrd
- Output CC bundle: ./case_1_CC_extracted.vtk
- CLI command of this process: /Applications/Slicer2.app/Contents/lib/Slicer-4.5/cli-modules/FiberBundleLabelSelect ./case_1_CC_label.nrrd ./case_1_tractography_p.vtk ./case_1_CC_extracted.vtk -p 1
#Fiber bundle selection from CC of case_2
- Input tractography: ./case_2_tractography_p.vtk
```

Command for fiber tract measurement:

```
Step 2: Conducting fiber tract scalar measurement
#Scalar measurements from both the whole brain tractography and the extracted CC tracts
- Input folder: .
- Output measurement: ./tractmeasurements.txt
- CLI command of this process: /Applications/Slicer2.app/Contents/lib/Slicer-4.5/cli-modules/FiberTractMeasurements --inputtype Fibers_File_Folder --format Column_Hierarchy --separator Tab --inputdirectory . --outputfile ./tractmeasurements.txt
Name      Num_Points      Num_Fibers      Tensors_.FractionalAnisotropy      Tensors_.LinearMeasurement      Tensors
```

Output

```
veggies-4:cli_data fan$ ls
case_1_CC_extracted.vtk
case_1_CC_label.nrrd
case_1_baseline.nrrd
case_1_tractography_p.vtk
case_2_CC_extracted.vtk
case_2_CC_label.nrrd
case_2_baseline.nrrd
case_2_tractography_p.vtk
case_3_CC_extracted.vtk
case_3_CC_label.nrrd
case_3_baseline.nrrd
case_3_tractography_p.vtk
case_4_CC_extracted.vtk
case_4_CC_label.nrrd
case_4_baseline.nrrd
case_4_tractography_p.vtk
case_5_CC_extracted.vtk
case_5_CC_label.nrrd
case_5_baseline.nrrd
case_5_tractography_p.vtk
cli_tutorial_script.sh
tractmeasurements.txt
```

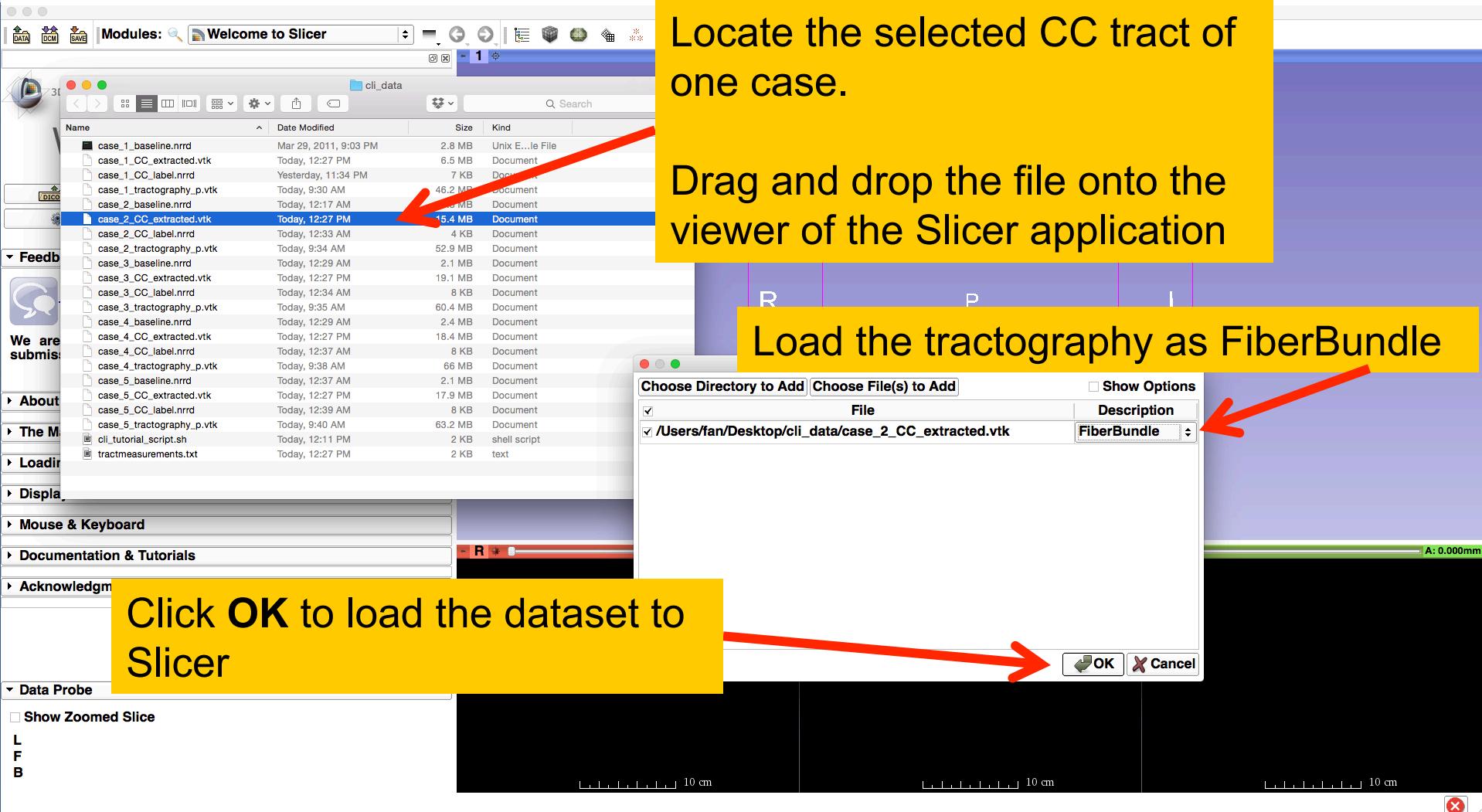
Selected fiber bundles from CC

- case_1_CC_extracted.vtk
- case_2_CC_extracted.vtk
- case_3_CC_extracted.vtk
- case_4_CC_extracted.vtk
- case_5_CC_extracted.vtk

Fiber measurement:

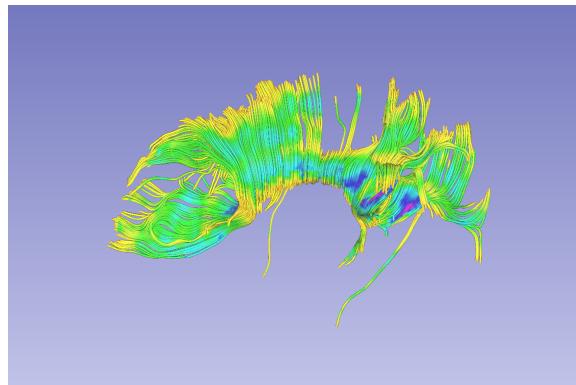
- tractmeasurements.txt

Selection result

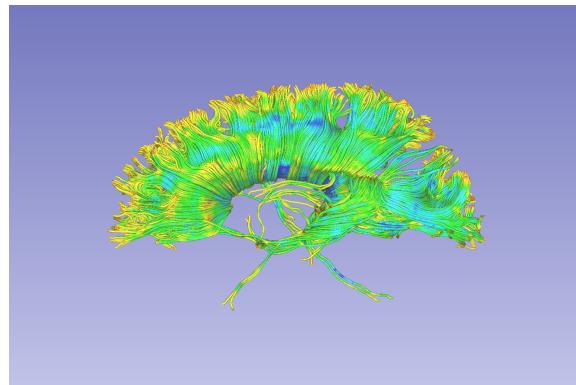


Selection result

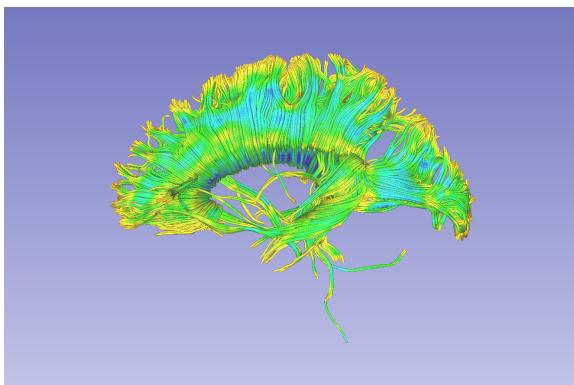
Selected fiber bundles from CC of the 5 cases.



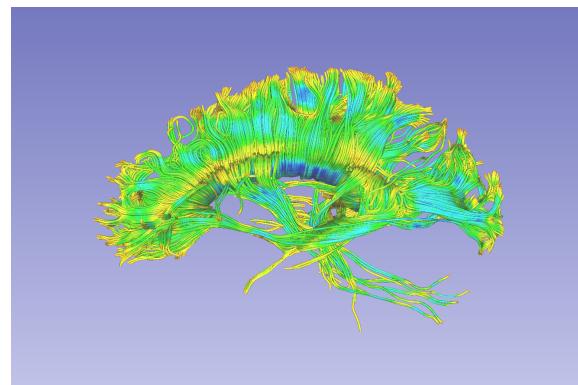
Case 1



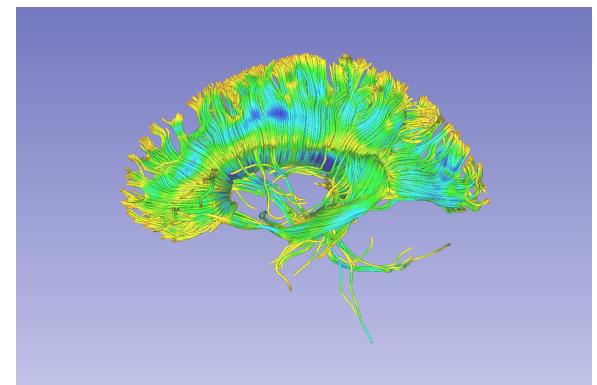
Case 2



Case 3



Case 4



Case 5

Measurement result

The txt file (tractmeasurements.txt) lists the mean scalar value (such as FA and Trace) of all fiber tracts, including the whole brain tractography and CC fiber bundles.

A	B	C	D	E	F	G	H
Name	Num_Points	Num_Fibers	Tensors_.FractionalAnisotropy	Tensors_.LinearMeasurement	Tensors_.MaxEigenvalue	Tensors_.MidEigenvalue	Tensors_.MinEigenvalue
./case_1_CC_extracted.vtk	124160	1039	0.465108	0.453333	0.001389	0.000726	0.000552
./case_1_tractography_p.vtk	888495	9536	0.385252	0.369968	0.001214	0.000748	0.00057
./case_2_CC_extracted.vtk	295452	1969	0.532239	0.512313	0.00121	0.000557	0.000394
./case_2_tractography_p.vtk	1016977	9623	0.453991	0.430557	0.001087	0.000593	0.000424
./case_3_CC_extracted.vtk	367134	1959	0.493054	0.485522	0.000807	0.000398	0.000295
./case_3_tractography_p.vtk	1160275	8991	0.432076	0.424927	0.000768	0.000427	0.000321
./case_4_CC_extracted.vtk	354499	1835	0.482864	0.477708	0.000796	0.000395	0.0003
./case_4_tractography_p.vtk	1268505	9979	0.42697	0.418042	0.000749	0.000419	0.000316
./case_5_CC_extracted.vtk	343945	1831	0.514175	0.506502	0.000876	0.000409	0.000304
./case_5_tractography_p.vtk	1214516	9385	0.449067	0.438463	0.00082	0.000441	0.000328

Conclusion

This tutorial guided you through the fiber bundle label selection and fiber tract scalar measurements in the CLI mode.



The terminal window displays the following content:

```
1 # Written by Fan Zhang, fzhang@bwh.harvard.edu, BWH and USYD
2
3 #datafolder='./' # .. is current folder, User may replace it with the data base path.
4 #slicerpath='/Applications/Slicer2.app/Contents' # replace it with your local 3D Slicer.
5
6 # Step 1: fiber bundle selection of CC
7 fiberbundleselectCLI=$slicerpath/lib/Slicer-4.5/cli-modules/FiberBundleLabelSelect
8 echo "Step 1: Conducting fiber bundle selection"
9 echo $vtkfile in '$datafolder/base_tractography_p.vtk'
10 do
11     caseid=$(vtkfile|grep -oP '(?=>)[^>]+')
12     wholebraintractography $datafolder/$caseid_CC_label.nrrd
13     extractedCC=$datafolder/$caseid_CC_extracted.vtk
14     clicommand="#fiberbundleselectCLI $CClabelmap $extractedCC -p 1"
15
16     echo "#Fiber bundle selection from CC of $caseid"
17     echo "# Input tractography: $wholebraintractography"
18     echo "# Input CC label map: $CClabelmap"
19     echo "# Output CC bundle: $extractedCC"
20     echo "# CLI command of this process: $clicommand"
21     $clicommand
22
23 done
24
25 # Step 2: fiber tract scalar measurement
26 fiberbundleselectCLI=$slicerpath/lib/Slicer-4.5/cli-modules/FiberTractMeasurements
27 echo "Step 2: Conducting fiber tract scalar measurement"
28
29 tractfolder=$datafolder # use datafolder as input to measure the tractography we just obtained (both whole brain and CC)
30 measurefile=$datafolder/tractmeasurements.txt
31 clicommand="#fiberbundleselectCLI $tractfolder $measurefile -p 1"
32 separatorTab="--inputdirectory $"
33
34 echo "#Scalar measurements from both"
35 echo "# Input folder: $tractfolder"
36 echo "# Output measurement: $measurefile"
37 echo "# CLI command of this process: $clicommand"
38 $clicommand
39
40 echo "Finished!"
```

Below the terminal window, there are five brain tractography visualizations labeled Case 1 through Case 5. Each visualization shows a brain with colored tracts (green, yellow, blue) representing different fiber bundles.

A	B	C	D	E	F	G	H
Name	Num_Points	Num_Fibers	Tensors_FractionalAnisotropy	Tensors_LinearMeasurement	Tensors_MaxEigenvalue	Tensors_MidEigenvalue	Tensors_MinEigenvalue
./case_1_CC_extracted.vtk	124160	1039	0.465108	0.453333	0.001389	0.000726	0.000552
./case_1_tractography_p.vtk	888495	9536	0.385252	0.369968	0.001214	0.000748	0.00057
./case_2_CC_extracted.vtk	295452	1969	0.532239	0.512313	0.00121	0.000557	0.000394
./case_2_tractography_p.vtk	1016977	9623	0.453991	0.430557	0.001087	0.000593	0.000424
./case_3_CC_extracted.vtk	367134	1959	0.493054	0.485522	0.000807	0.000398	0.000295
./case_3_tractography_p.vtk	1160275	8991	0.432076	0.424927	0.000768	0.000427	0.000321
./case_4_CC_extracted.vtk	354499	1835	0.482864	0.477708	0.000796	0.000395	0.0003
./case_4_tractography_p.vtk	1268505	9979	0.42697	0.418042	0.000749	0.000419	0.000316
./case_5_CC_extracted.vtk	343945	1831	0.514175	0.506502	0.000876	0.000409	0.000304
./case_5_tractography_p.vtk	1214516	9385	0.449067	0.438463	0.00082	0.000441	0.000328

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