

CLI Application

Tractography selection and measurements

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Learning Objectives

- Following this tutorial, you'll be able to conduct the fiber bundle selection and calculate fiber tract scalar measurement in 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.

Pre-requisite

- This tutorial is a follow-up tutorial of:
 - Diffusion MRI analysis
<http://dmri.slicer.org/docs/tutorials/DiffusionMRInalysis.pdf>
 - Fiber Bundle Selection and Scalar Measurements
<http://dmri.slicer.org/docs/tutorials/FiberBundleSelectionAndScalarMeasurement.pdf>
- Please go through them ahead.

3D Slicer

The tutorial uses the 3D Slicer (Version 4.8.1, revision 26813, 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.

SlicerDMRI

An open-source project to improve and extend diffusion magnetic resonance imaging software in 3D Slicer:

<http://dmri.slicer.org>

- Follow the “Diffusion MRI Analysis” to install SlicerDMRI :

<http://dmri.slicer.org/docs/tutorials/DiffusionMRInalysis.pdf>

Tutorial Data

Download sample data, at

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

The tutorial uses 5 datasets (cases 1 to 5, included in the Cli_data.zip), in which:

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

Data preview

Load all three files from case 2 in the folder where all datasets reside.

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

Load the tractography as FiberBundle

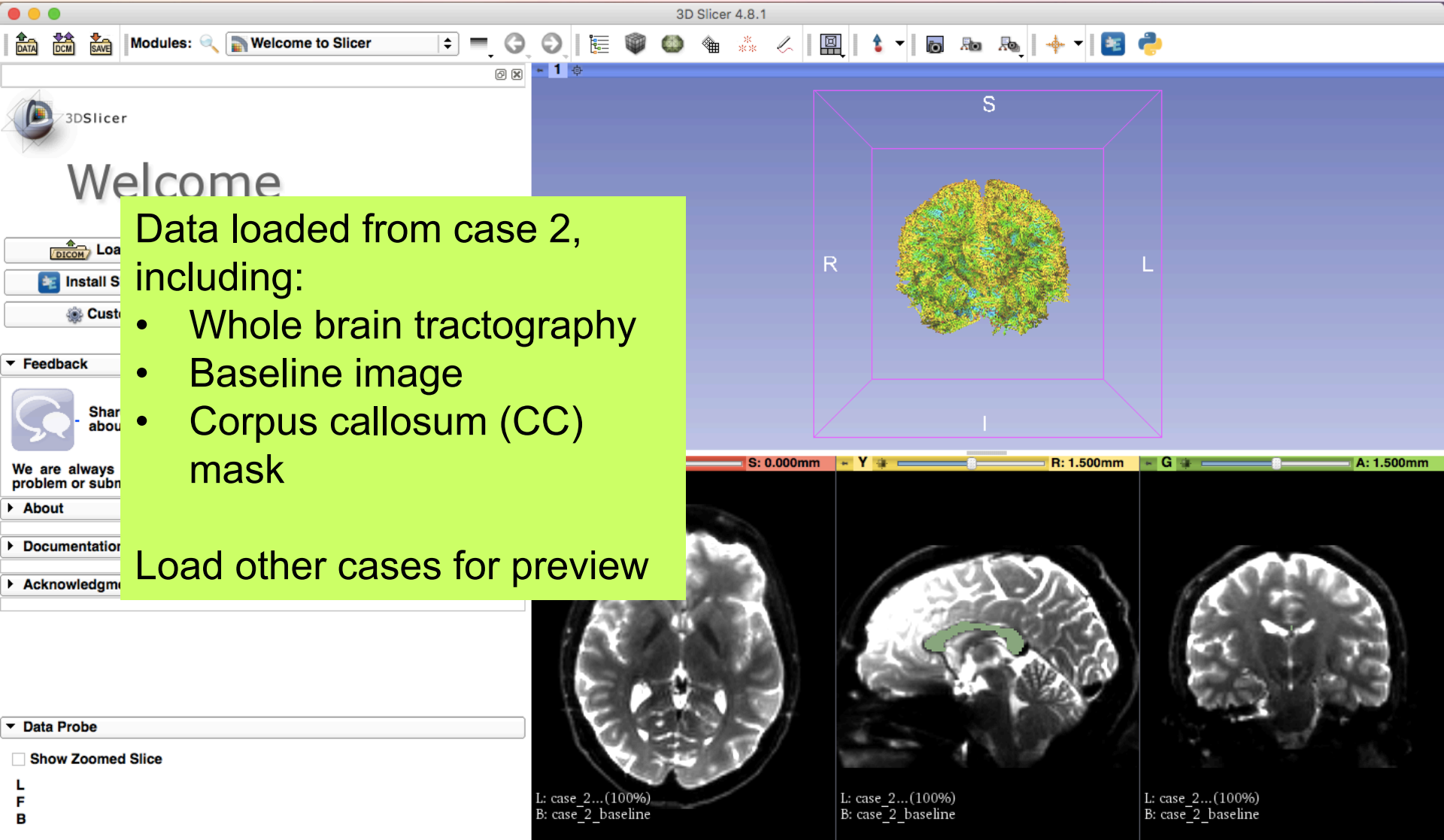
Click **OK to load the dataset to Slicer**

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.

Name	Date Modified	Size
case_1_baseline.nrrd	Mar 29, 2011, 9:03 PM	2.8 MB
case_1_CC_label.nrrd	Mar 5, 2016, 11:34 PM	7 KB
case_1_tra...raphy.p.vtk	Mar 6, 2016, 9:30 AM	46.2 MB
case_2_baseline.nrrd	Mar 6, 2016, 12:17 AM	1.8 MB
case_2_CC_label.nrrd	Mar 6, 2016, 12:33 AM	4 KB
case_2_tra...raphy.p.vtk	Mar 6, 2016, 9:34 AM	52.9 MB
case_3_baseline.nrrd	Mar 6, 2016, 12:29 AM	2.1 MB
case_3_CC_label.nrrd	Mar 6, 2016, 12:34 AM	8 KB
case_3_tra...raphy.p.vtk	Mar 6, 2016, 9:35 AM	60.4 MB
case_4_baseline.nrrd	Mar 6, 2016, 12:29 AM	2.4 MB
case_4_CC_label.nrrd	Mar 6, 2016, 12:37 AM	8 KB
case_4_tra...raphy.p.vtk	Mar 6, 2016, 9:38 AM	66 MB
case_5_baseline.nrrd	Mar 6, 2016, 12:37 AM	2.1 MB
case_5_CC_label.nrrd	Mar 6, 2016, 12:39 AM	8 KB
case_5_tra...raphy.p.vtk	Mar 6, 2016, 9:40 AM	63.2 MB
cli_tutorial_script.sh	Mar 6, 2016, 12:11 PM	2 KB

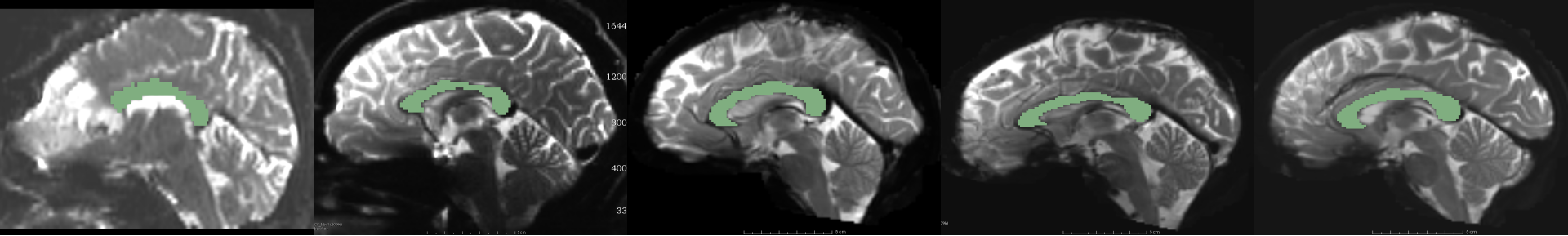
File	Description	LabelMap
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/case_2_baseline.nrrd	Volume case_2_baseline	<input type="checkbox"/>
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/case_2_CC_label.nrrd	Volume case_2_CC_label	<input checked="" type="checkbox"/>
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/case_2_tra...raphy.p.vtk	FiberBundle	<input checked="" type="checkbox"/>

Data preview

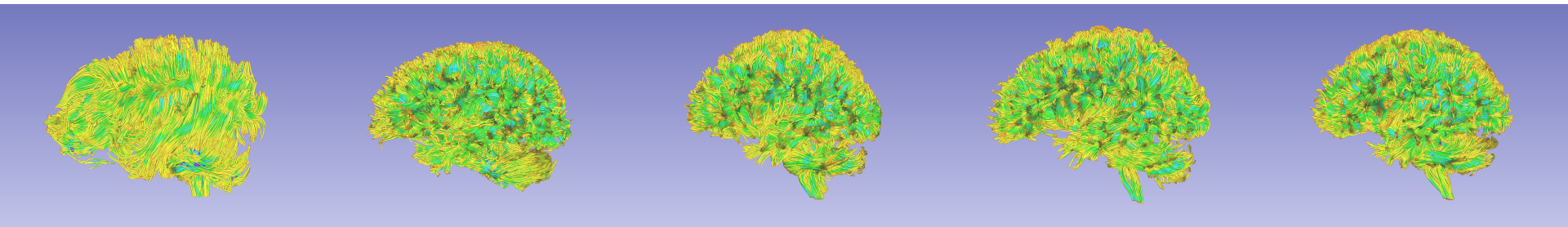


Data preview

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

Copy the code here into a file, name it to **cli_tutorial_script.sh** and put the sh file in the data folder.

```
# Written by Fan Zhang, fzhang@bwh.harvard.edu, BWH, HMS and USYD
```

```
datafolder='.' # . is current folder. User may replace it with the data base path.
```

```
slicerpath=/Applications/Slicer.app/Contents # replace it with your local 3D Slicer.
```

```
slicerdmripath=$slicerpath/Extensions-26813/SlicerDMRI # Please note the Extensions ID could be different
```

```
# Step 1: fiber bundle selection of CC
```

```
fiberbundleselectCLI=$slicerdmripath/lib/Slicer-4.8/cli-modules/FiberBundleLabelSelect
```

```
echo "Step 1: Conducting fiber bundle selection"
```

```
for vtkfile in `ls $datafolder/case_*_tractography_p.vtk`  
do
```

```
    caseid=${vtkfile:${#vtkfile}-25:6}
```

```
    wholebraintractography=$datafolder/$caseid\_tractography_p.vtk
```

```
    CClabelmap=$datafolder/$caseid\_CC_label.nrrd
```

```
    extractedCC=$datafolder/$caseid\_CC_extracted.vtk
```

```
    clicommand="$fiberbundleselectCLI $CClabelmap $wholebraintractography $extractedCC -p 1"
```

```
    echo "#Fiber bundle selection from CC of $caseid"
```

```
    echo " - Input tractography: $wholebraintractography"
```

```
    echo " - Input CC label map: $CClabelmap"
```

```
    echo " - Output CC bundle: $extractedCC"
```

```
    echo " - CLI command of this process: $clicommand"
```

```
    $clicommand
```

```
done
```

Fiber Bundle Selection

```
# Step 2: fiber tract scalar measurement
```

```
fiberbundleselectCLI=$slicerdmripath/lib/Slicer-4.8/cli-modules/FiberTractMeasurements
```

```
echo "Step 2: Conducting fiber tract scalar measurement"
```

```
tractfolder=$datafolder # Use datafolder as input to measure the tractography we just obtained (both whole brain and CC)
```

```
measurefile="$datafolder/tractmeasurements.txt"
```

```
clicommand="$fiberbundleselectCLI --inputtype Fibers_File_Folder --format Column_Hierarchy --separator Tab --inputdirectory $tractfolder --  
outputfile $measurefile"
```

```
echo "#Scalar measurements from both the whole brain tractography and the extracted CC tracts"
```

```
echo " - Input folder: $tractfolder"
```

```
echo " - Output measurement: $measurefile"
```

```
echo " - CLI command of this process: $clicommand"
```

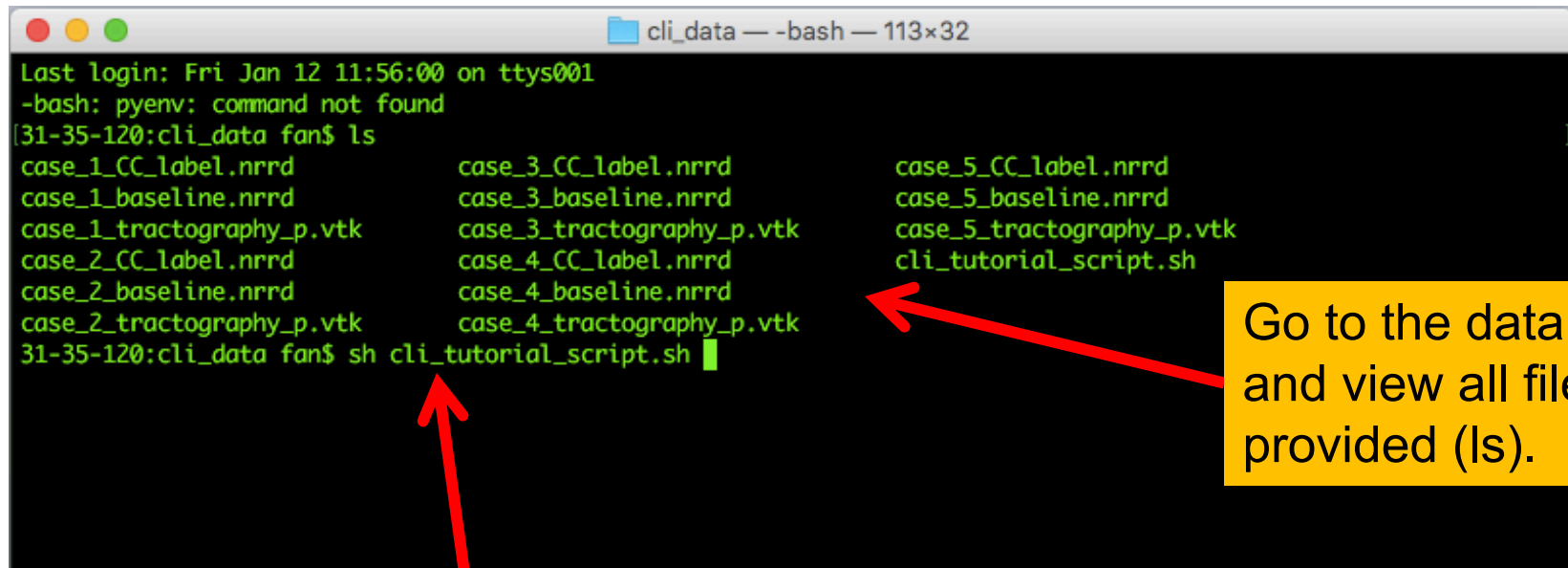
```
$clicommand
```

```
echo "Finished!"
```

Fiber Tract Measurement

Run script

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



```
cli_data — -bash — 113x32
Last login: Fri Jan 12 11:56:00 on ttys001
-bash: pyenv: command not found
[31-35-120: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
31-35-120:cli_data fan$ sh cli_tutorial_script.sh
```

The terminal window displays the output of the 'ls' command, listing files in three columns. A red arrow points from the 'cli_tutorial_script.sh' file in the third column to a yellow callout box. Another red arrow points from the same file to a yellow callout box at the bottom.

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

Execute the script (sh cli_tutorial_script.sh)

Run script

```
Terminal Shell Edit View Window Help
cli_data — -bash — 204x52

Last login: Fri Jan 12 11:56:00 on ttys001
bash: pyenv: command not found
[31-35-120: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
[31-35-120: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/Slicer.app/Contents/Extensions-26813/SlicerDMRI/lib/Slicer-4.8/cli-modules/FiberBundleLabelSelect ./case_1_CC_label.nrrd ./case_1_tractography_p.vtk ./case_1_CC_extracted.vtk -p 1
Sampling Distance: 0.3
Total number of fibers before selection: 9536
Total number of fibers after selection: 1083
#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/Slicer.app/Contents/Extensions-26813/SlicerDMRI/lib/Slicer-4.8/cli-modules/FiberBundleLabelSelect ./case_2_CC_label.nrrd ./case_2_tractography_p.vtk ./case_2_CC_extracted.vtk -p 1
Sampling Distance: 0.3
Total number of fibers before selection: 9623
Total number of fibers after selection: 2094
#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/Slicer.app/Contents/Extensions-26813/SlicerDMRI/lib/Slicer-4.8/cli-modules/FiberBundleLabelSelect ./case_3_CC_label.nrrd ./case_3_tractography_p.vtk ./case_3_CC_extracted.vtk -p 1
Sampling Distance: 0.3
Total number of fibers before selection: 8991
Total number of fibers after selection: 1976
#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/Slicer.app/Contents/Extensions-26813/SlicerDMRI/lib/Slicer-4.8/cli-modules/FiberBundleLabelSelect ./case_4_CC_label.nrrd ./case_4_tractography_p.vtk ./case_4_CC_extracted.vtk -p 1
Sampling Distance: 0.3
Total number of fibers before selection: 9979
Total number of fibers after selection: 1957
#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/Slicer.app/Contents/Extensions-26813/SlicerDMRI/lib/Slicer-4.8/cli-modules/FiberBundleLabelSelect ./case_5_CC_label.nrrd ./case_5_tractography_p.vtk ./case_5_CC_extracted.vtk -p 1
```

Script output

Run script

```
Terminal Shell Edit View Window Help
cli_data --bash-- 204x52

- 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/Slicer.app/Contents/Extensions-26813/SlicerDMRI/lib/Slicer-4.8/cli-modules/FiberBundleLabelSelect ./case_4_CC_label.nrrd ./case_4_tractography_p.vtk ./case_4_CC_extracted.vtk -p 1
Sampling Distance: 0.3
Total number of fibers before selection: 9979
Total number of fibers after selection: 1957
#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/Slicer.app/Contents/Extensions-26813/SlicerDMRI/lib/Slicer-4.8/cli-modules/FiberBundleLabelSelect ./case_5_CC_label.nrrd ./case_5_tractography_p.vtk ./case_5_CC_extracted.vtk -p 1
Sampling Distance: 0.3
Total number of fibers before selection: 9385
Total number of fibers after selection: 1932
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/Slicer.app/Contents/Extensions-26813/SlicerDMRI/lib/Slicer-4.8/cli-modules/FiberTractMeasurements --inputtype Fibers_File_Folder --format Column_Hierarchy --separator Tab --printAllStatistics --inputdirectory . --outputfile ./tractmeasurements.txt
```

Name	Num.Points	Num.Fibers	Mean.Length	Tensors_.FractionalAnisotropy.Mean	Tensors_.LinearMeasure.Mean	Tensors_.MaxEigenvalue.Mean	Tensors_.MeanDiffusivity.Mean	Tensors_.Mi
dEigenvalue.Mean								
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/./case_1_CC_extracted.vtk								
0.000740	0.000566	0.138588	0.308867	0.410402	0.002762			
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/./case_1_tractography_p.vtk								
0.000748	0.000570	0.156563	0.242185	0.473954	0.002540			
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/./case_2_CC_extracted.vtk								
0.000561	0.000398	0.144940	0.360300	0.344502	0.002175			
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/./case_2_tractography_p.vtk								
00701	0.000593	0.000424	0.164333	0.294700	0.404446	0.002106		
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/./case_3_CC_extracted.vtk								
0.000398	0.000295	0.134339	0.324726	0.379850	0.001500			
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/./case_3_tractography_p.vtk								
00505	0.000427	0.000321	0.143339	0.275661	0.431493	0.001517		
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/./case_4_CC_extracted.vtk								
0.000396	0.000301	0.129342	0.316401	0.394448	0.001491			
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/./case_4_tractography_p.vtk								
00495	0.000419	0.000316	0.145545	0.272013	0.436303	0.001484		
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/./case_5_CC_extracted.vtk								
0.000410	0.000306	0.128348	0.342897	0.365993	0.001593			
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/./case_5_tractography_p.vtk								
00530	0.000441	0.000328	0.145413	0.289454	0.415943	0.001589		

```
Finished!
[31-35-120: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
```

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/Slicer.app/Contents/Extensions-26813/SlicerDMRI/lib/Slicer-4.8/cli-modules/
FiberBundleLabelSelect ./case_1_CC_label.nrrd ./case_1_tractography_p.vtk ./case_1_CC_extracted.vtk -p 1
Sampling Distance: 0.3
Total number of fibers before selection: 9536
Total number of fibers after selection: 1083
#Fiber bundle selection from CC of case_2
```

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/Slicer.app/Contents/Extensions-26813/SlicerDMRI/lib/Slicer-4.8/cli-modules/
FiberTractMeasurements --inputtype Fibers_File_Folder --format Column_Hierarchy --separator Tab --printAllStatistics --in
putdirectory . --outputfile ./tractmeasurements.txt
```

Name	Num_Points	Num_Fibers	Mean_Length	Tensors_.FractionalAnisotropy.Mean	Tensors_.LinearMeasure.M
ean	Tensors_.MaxEigenvalue.Mean	Tensors_.MeanDiffusivity.Mean	Tensors_.MidEigenvalue.Mean	Tensors_.MinE	
igenvalue.Mean	Tensors_.PlanarMeasure.Mean	Tensors_.RelativeAnisotropy.Mean	Tensors_.SphericalMeasure.Mean		
	Tensors_.Trace.Mean				
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/./case_1_CC_extracted.vtk				127684.000000	1083.000
000	79.988488	0.461613	0.455960	0.001415	0.000907
588	0.308867	0.410402	0.002762	0.000740	0.000566
					0.138

Output

```
Last login: Fri Jan 12 11:56:04 on ttys001
-bash: pyenv: command not found
31-35-120:cli_data fan$ ls
case_1_CC_extracted.vtk      case_3_CC_extracted.vtk      case_5_CC_extracted.vtk
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_extracted.vtk      case_4_CC_extracted.vtk      cli_tutorial_script.sh
case_2_CC_label.nrrd        case_4_CC_label.nrrd        tractmeasurements.txt
case_2_baseline.nrrd        case_4_baseline.nrrd
case_2_tractography_p.vtk    case_4_tractography_p.vtk
31-35-120:cli_data fan$
```

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

The screenshot shows the 3D Slicer 4.8.1 application window. On the left, the 'cli_data' directory is expanded in the file browser, showing a list of files. A red arrow points to the file 'case_2_CC...tracted.vtk'. A yellow box with the text 'Locate the selected CC tracts.' and 'Drag and drop the file onto the viewer of the Slicer application' is positioned over the file list. Below the file list, a 'Choose File(s) to Add' dialog box is open, showing the same file selected. A red arrow points to the 'FiberBundle' dropdown menu in the dialog. A yellow box with the text 'Load the tractography as FiberBundle' is positioned over the dialog. At the bottom, a yellow box with the text 'Click OK to load the dataset to Slicer' has a red arrow pointing to the 'OK' button in the dialog box.

3D Slicer 4.8.1

Modules: Welcome to Slicer

cli_data

Name	Date Modified	Size
case_1_baseline.nrrd	Mar 29, 2011, 9:03 PM	2.8 MB
case_1_CC...tracted.vtk	Today, 11:57 AM	6.6 MB
case_1_CC_label.nrrd	Mar 5, 2016, 11:34 PM	7 KB
case_1_tra...raphy_p.vtk	Mar 6, 2016, 9:30 AM	46.2 MB
case_2_baseline.nrrd	Mar 6, 2016, 12:17 AM	1.8 MB
case_2_CC...tracted.vtk	Today, 11:57 AM	16.4 MB
case_2_CC_label.nrrd	Mar 6, 2016, 12:33 AM	4 KB
case_2_tra...raphy_p.vtk	Mar 6, 2016, 9:34 AM	52.9 MB
case_3_baseline.nrrd	Mar 6, 2016, 12:29 AM	2.1 MB
case_3_CC...tracted.vtk	Today, 11:57 AM	19.2 MB
case_3_CC_label.nrrd	Mar 6, 2016, 12:34 AM	8 KB
case_3_tra...raphy_p.vtk	Mar 6, 2016, 9:35 AM	60.4 MB
case_4_baseline.nrrd	Mar 6, 2016, 12:29 AM	2.4 MB
case_4_CC...tracted.vtk	Today, 11:57 AM	19.6 MB
case_4_CC_label.nrrd	Mar 6, 2016, 12:37 AM	
case_4_tra...raphy_p.vtk	Mar 6, 2016, 9:38 AM	
case_5_baseline.nrrd	Mar 6, 2016, 12:37 AM	

Locate the selected CC tracts.

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

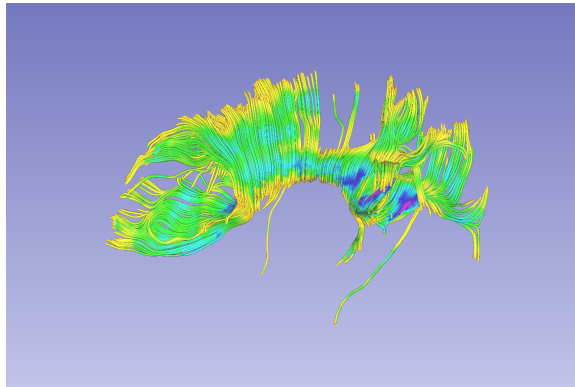
Choose Directory to Add Choose File(s) to Add

File	Description	Options
/Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials/cli_data/case_2_CC_extracted.vtk	FiberBundle	

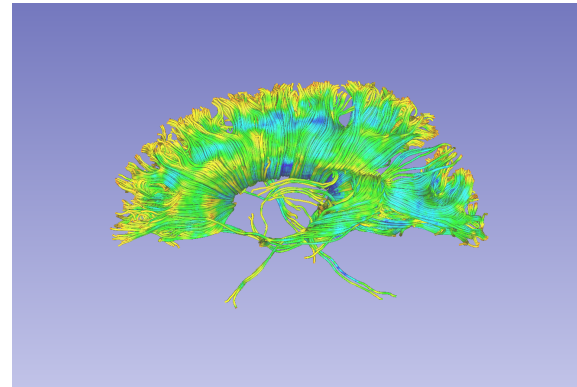
OK Cancel

Selection result

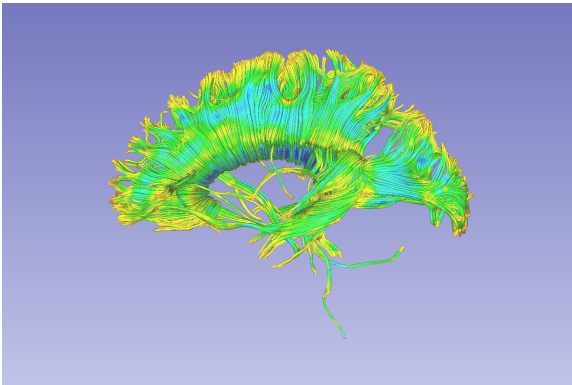
Selected fiber bundles from CC of the 5 cases.



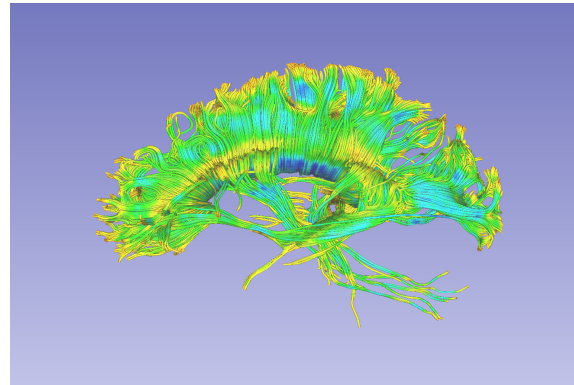
Case 1



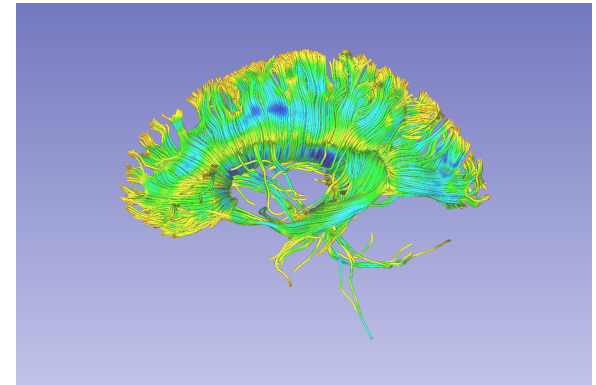
Case 2



Case 3



Case 4



Case 5

Measurement result

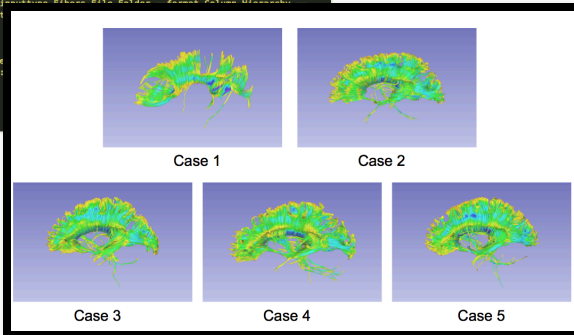
The txt file (tractmeasurements.txt) lists the mean scalar value (such as FA and Trace) of all fiber tracts, including the whole brain tractography and CC fiber bundles.

	A	B	C	D	E	F	G	H	I	J	K
1	Name	Num_Points	Num_Fibers	Mean_Length	Tensors_.FractionalAnisotropy.Mean	Tensors_.LinearMeasure.Mean	Tensors_.MaxEigenvalue.Mean	Tensors_.M	Tensors_.Mi	Tensors_.Mi	Tensors_.
2	/Users/fan/D	127684	1083	79.988488	0.461613	0.45596	0.001415	0.000907	0.00074	0.000566	0.1385
3	/Users/fan/D	888495	9536	68.984782	0.384181	0.369968	0.001214	0.000844	0.000748	0.00057	0.1565
4	/Users/fan/D	314367	2094	111.762935	0.529715	0.510843	0.001214	0.000724	0.000561	0.000398	0.1449
5	/Users/fan/D	1016977	9623	78.431251	0.453874	0.430557	0.001087	0.000701	0.000593	0.000424	0.1643
6	/Users/fan/D	369944	1976	116.335053	0.493159	0.485808	0.000807	0.0005	0.000398	0.000295	0.1343
7	/Users/fan/D	1160275	8991	79.986268	0.432076	0.424927	0.000768	0.000505	0.000427	0.000321	0.1433
8	/Users/fan/D	376520	1957	119.564865	0.480953	0.476209	0.000795	0.000497	0.000396	0.000301	0.1293
9	/Users/fan/D	1268505	9979	78.77571	0.42697	0.418042	0.000749	0.000495	0.000419	0.000316	0.1455
10	/Users/fan/D	359844	1932	115.734983	0.512674	0.505656	0.000877	0.000531	0.00041	0.000306	0.1283
11	/Users/fan/D	1214516	9385	80.211446	0.449067	0.438463	0.00082	0.00053	0.000441	0.000328	0.1454

Conclusion

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

```
4 ➤ 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 fiberbundeselectCLI $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 ${vtkfile}~23:6)
12
13     wholebraintractography-$datafolder/$caseid_tractography_p.vtk
14     CClabelmap-$datafolder/$caseid_CC_label.nrrd
15     extractedCC-$datafolder/$caseid_CC_extracted.vtk
16     clicommand="$fiberbundeselectCLI $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 fiberbundeselectCLI $slicerpath/lib/Slicer-4.5/cli-modules/FiberTractMeasurements
29 echo "Step 2: Conducting fiber tract scalar measurement"
30
31 tractfolder=$datafolder # Use datafolder as input to measure the tractography we just obtained (
32 both whole brain and CC)
33 measurefile="$datafolder/tractmeasurements.txt"
34 clicommand="$fiberbundeselectCLI -j $tractfolder $measurefile -s $slicerpath/lib/Slicer-4.5/cli-modules/FiberTractMeasurements"
35 separator Tab --inputdirectory $tractfolder
36
37 echo "#Scalar measurements from both"
38 echo "  - Input folder: $tractfolder"
39 echo "  - Output measurement: $measurefile"
40 echo "  - CLI command of this process: $clicommand"
41 $clicommand
42 echo "Finished!"
```



	A	B	C	D	E	F	G	H	I	J	K
1	Name	Num_Points	Num_Fibers	Mean_Length	Tensors_FractionalAnisotropy.Mean	Tensors_LinearMeasure.Mean	Tensors_MaxEigenvalue.Mean	Tensors_Mi	Tensors_Mi	Tensors_Mi	Tensors_L
2	/Users/fan/C	127684	1083	79.988488	0.461613	0.45596	0.001415	0.000907	0.00074	0.000566	0.13858
3	/Users/fan/C	888495	9536	68.984782	0.384181	0.369968	0.001214	0.000844	0.000748	0.00057	0.15656
4	/Users/fan/C	314367	2094	111.762935	0.529715	0.510843	0.001214	0.000724	0.000561	0.000398	0.1449
5	/Users/fan/C	1016977	9623	78.431251	0.453874	0.430557	0.001087	0.000701	0.000593	0.000424	0.16433
6	/Users/fan/C	369944	1976	116.335053	0.493159	0.485808	0.000807	0.0005	0.000398	0.000295	0.13433
7	/Users/fan/C	1160275	8991	79.986268	0.432076	0.424927	0.000768	0.000505	0.000427	0.000321	0.14333
8	/Users/fan/C	376520	1957	119.564865	0.480953	0.476209	0.000795	0.000497	0.000396	0.000301	0.12934
9	/Users/fan/C	1268505	9979	78.77571	0.42697	0.418042	0.000749	0.000495	0.000419	0.000316	0.14554
10	/Users/fan/C	359844	1932	115.734983	0.512674	0.505656	0.000877	0.000531	0.00041	0.000306	0.12834
11	/Users/fan/C	1214516	9385	80.211446	0.449067	0.438463	0.00082	0.00053	0.000441	0.000328	0.14541

Acknowledgments

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