

CLI Application

Tractography selection and measurements

Fan Zhang, Sonia Pujol,

Lauren J. O'Donnell

Brigham and Women's Hospital

Harvard Medical School

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/DiffusionMRIanalysis.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/DiffusionMRIanalysis.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

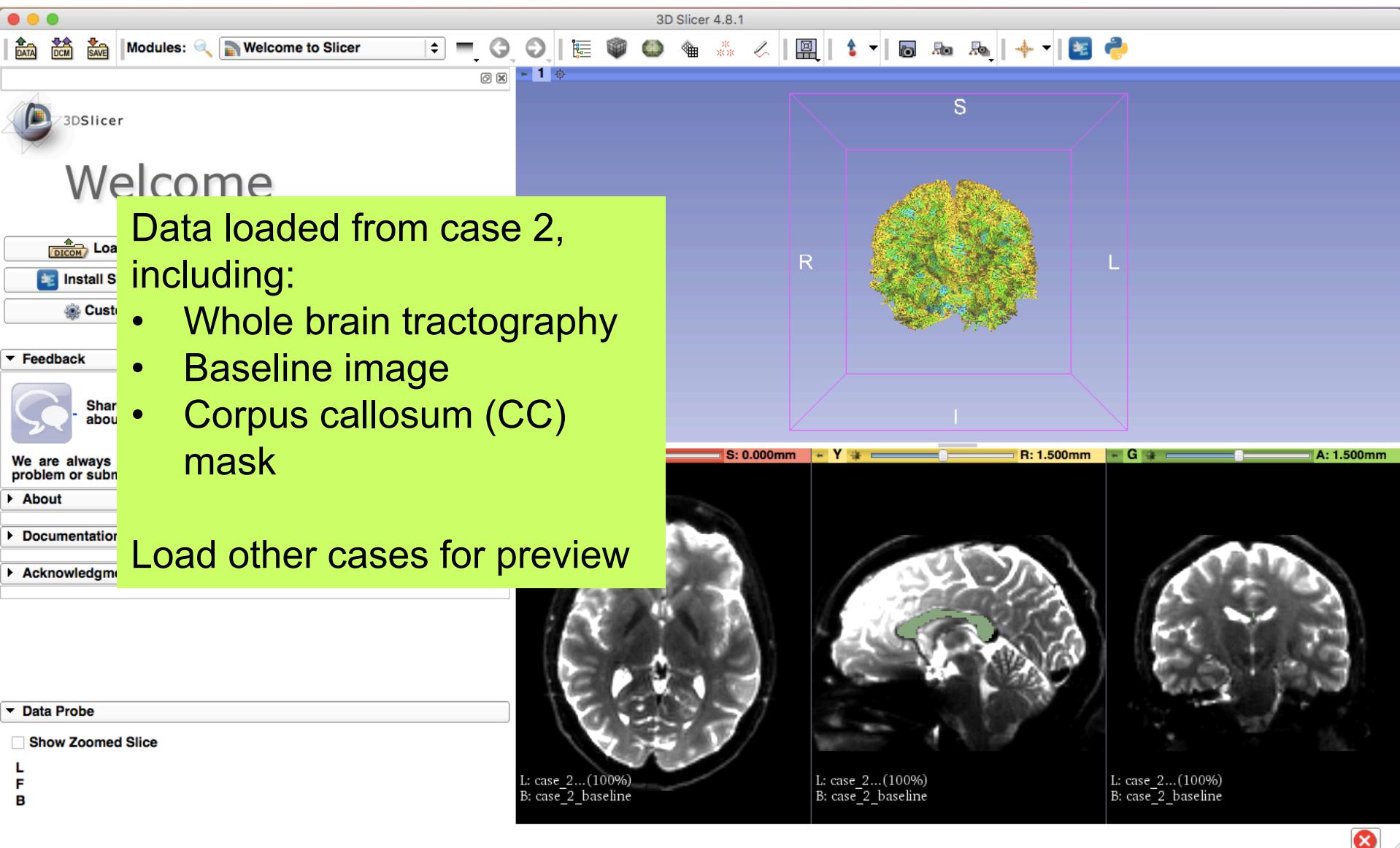
Load the tractography as FiberBundle

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.

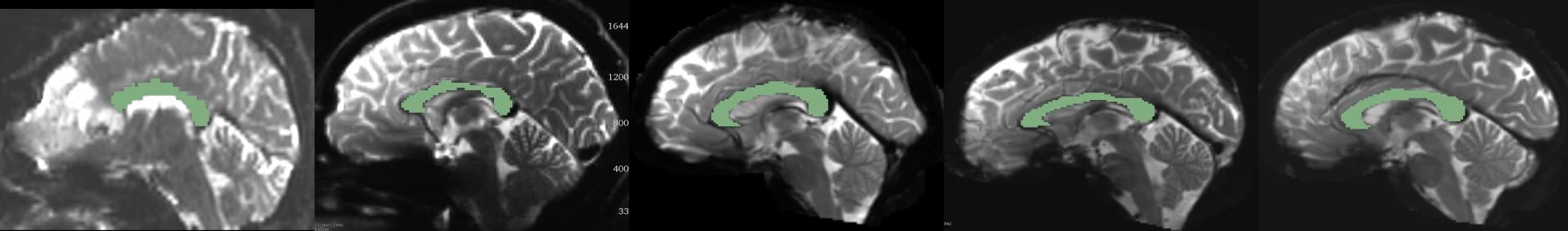
OK Cancel

Data preview

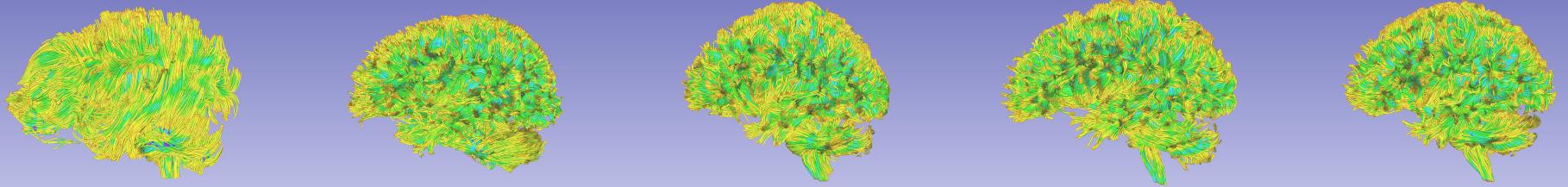


Data preview

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

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
```

```
# 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!"
```

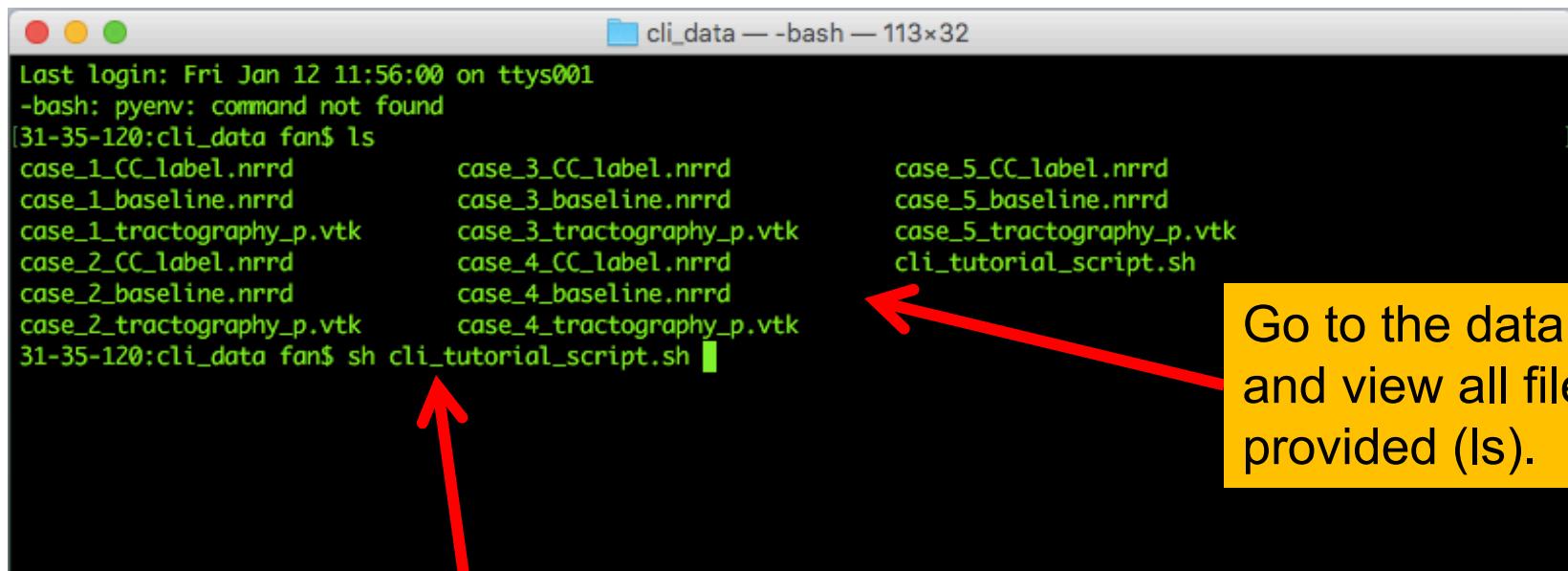
Copy the code here into a file, name it to **cli_tutorial_script.sh** and put the sh file in the data folder.

Fiber Bundle Selection

Fiber Tract Measurement

Run script

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



The screenshot shows a terminal window titled "cli_data — -bash — 113x32". The window contains the following text:

```
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_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
31-35-120:cli_data fan$ sh cliTutorial_script.sh
```

A red arrow points from the text "Execute the script (sh cliTutorial_script.sh)" in the yellow box at the bottom left to the command "sh cliTutorial_script.sh" in the terminal window. Another red arrow points from the text "Go to the data folder and view all files provided (ls)." in the yellow box at the bottom right to the "ls" command in the terminal window.

Execute the script (sh cliTutorial_script.sh)

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

Run script

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
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

cli_data — bash — 204x52

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 --separat
or 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   Tensors_.MinEigenvalue.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   1083.000000   79.988488   0.461613   0.455960   0.001415   0.000907
/0.000740      0.000566   0.138588   0.308867   0.410402   0.002762
/0.000748      0.000570   0.156563   0.242185   0.473954   0.002540
/0.000561      0.000398   0.144940   0.360300   0.344502   0.002175
/0.000593      0.000424   0.164333   0.294700   0.404446   0.002106
/0.000398      0.000295   0.134339   0.324726   0.379850   0.001500
/0.000505      0.000427   0.000321   0.143339   0.275661   0.431493   0.001517
/0.000396      0.000301   0.129342   0.316401   0.394448   0.001491
/0.000495      0.000419   0.000316   0.145545   0.272013   0.436303   0.001484
/0.000410      0.000306   0.128348   0.342897   0.365993   0.001593
/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      cliTutorial_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
31-35-120:cli_data fan$ ]
```

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      0.000740      0.000566      0.138
588      0.308867      0.410402      0.002762

```

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      cliTutorial_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$
```

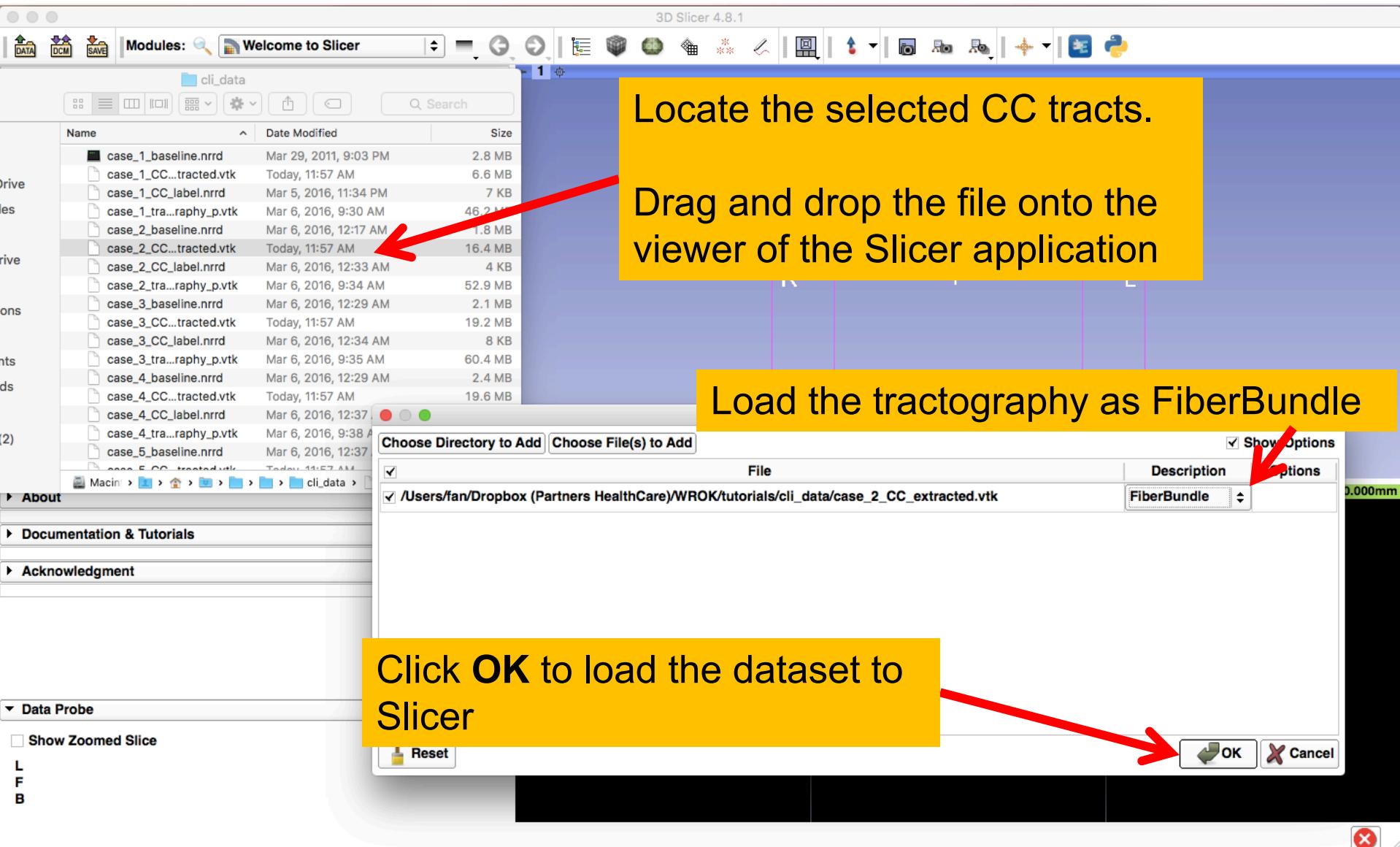
Selected fiber bundles from CC

- 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:

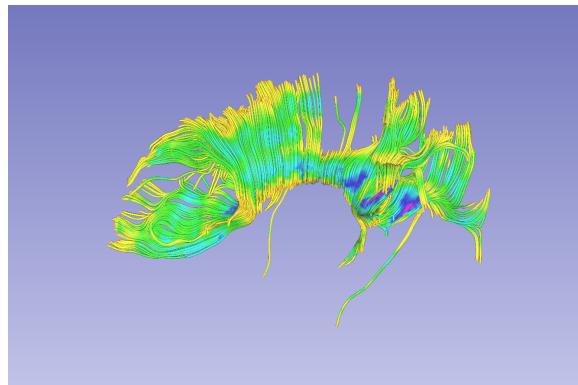
- tractmeasurements.txt

Selection result

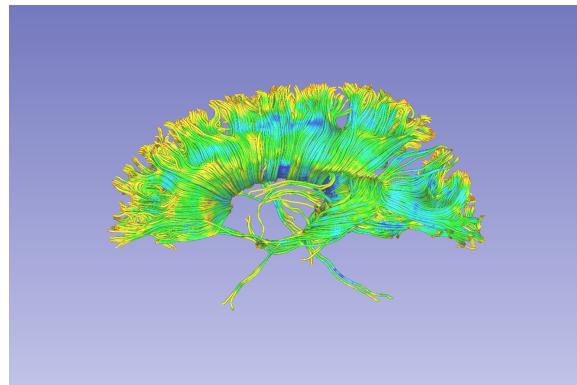


Selection result

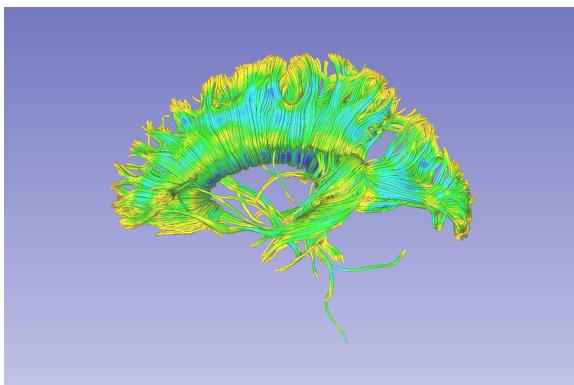
Selected fiber bundles from CC of the 5 cases.



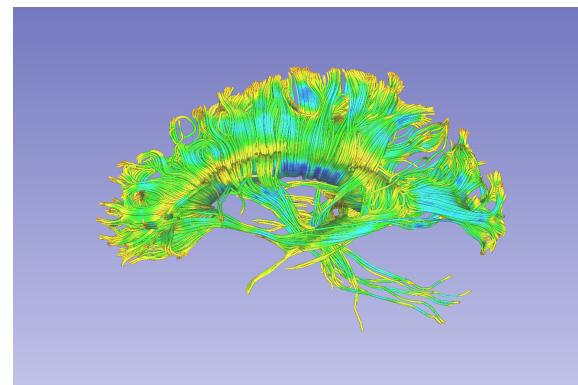
Case 1



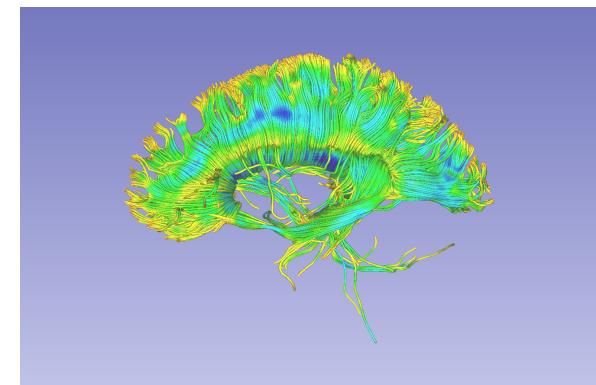
Case 2



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_.Mi	Tensors_.Mi	Tensors_.Mi	Tensors_.Mi
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.



A	B	C	D	E	F	G	H	I	J	K
Name	Num_Points	Num_Fibers	Mean_Length	Tensors_.FractionalAnisotropy.Mean	Tensors_.LinearMeasure.Mean	Tensors_.MaxEigenvalue.Mean	Tensors_.Mi	Tensors_.Mi	Tensors_.Mi	Tensors_.Mi
1 /Users/fan/C	127684	1083	79.988488	0.461613	0.45596	0.001415	0.000907	0.00074	0.000566	0.13858
2 /Users/fan/C	888495	9536	68.984782	0.384181	0.369968	0.001214	0.000844	0.000748	0.00057	0.15656
3 /Users/fan/C	314367	2094	111.762935	0.529715	0.510843	0.001214	0.000724	0.000561	0.000398	0.14449
4 /Users/fan/C	1016977	9623	78.431251	0.453874	0.430557	0.001087	0.000701	0.000593	0.000424	0.16433
5 /Users/fan/C	369944	1976	116.335053	0.493159	0.485808	0.000807	0.0005	0.000398	0.000295	0.13433
6 /Users/fan/C	1160275	8991	79.986268	0.432076	0.424927	0.000768	0.000505	0.000427	0.000321	0.14333
7 /Users/fan/C	376520	1957	119.564865	0.480953	0.476209	0.000795	0.000497	0.000396	0.000301	0.12934
8 /Users/fan/C	1268505	9979	78.77571	0.42697	0.418042	0.000749	0.000495	0.000419	0.000316	0.14554
9 /Users/fan/C	359844	1932	115.734983	0.512674	0.505656	0.000877	0.000531	0.00041	0.000306	0.12834
10 /Users/fan/C	1214516	9385	80.211446	0.449067	0.438463	0.00082	0.00053	0.000441	0.000328	0.14541

Acknowledgments

Open Source Diffusion MRI Technology For Brain Cancer Research
NIH U01CA199459

National Center for Image Guided Therapy (NCIGT)
NIH P41EB015898

Neuroimage Analysis Center (NAC)
NIH P41EB015902

The University of Sydney, APA/IPRS/ARC
International Postgraduate Research Scholarships
Australian Postgraduate Award
Australian Research Council