

Fiber Bundle Selection And Scalar Measurement

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Learning Objectives

Following this tutorial, you'll be able to:

- 1) select fiber bundles passing through region(s) of interest, and
- 1) calculate scalar measurements (such as FA and trace) from the fiber bundles.

Tutorial Outline

- Editing multiple labels
- Whole brain tractography
- Fiber bundle selection
- Fiber bundle scalar measurements

3D Slicer

The tutorial uses the 3D Slicer (Version 4.10, Stable Release) software available at:

<http://download.slicer.org>

Data used in this tutorial is available at:

<https://na-mic.org/w/images/d/d6/FiberBundleSelectionAndScalarMeasurementTutorialContestWinter2016.zip>

Download sample data

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

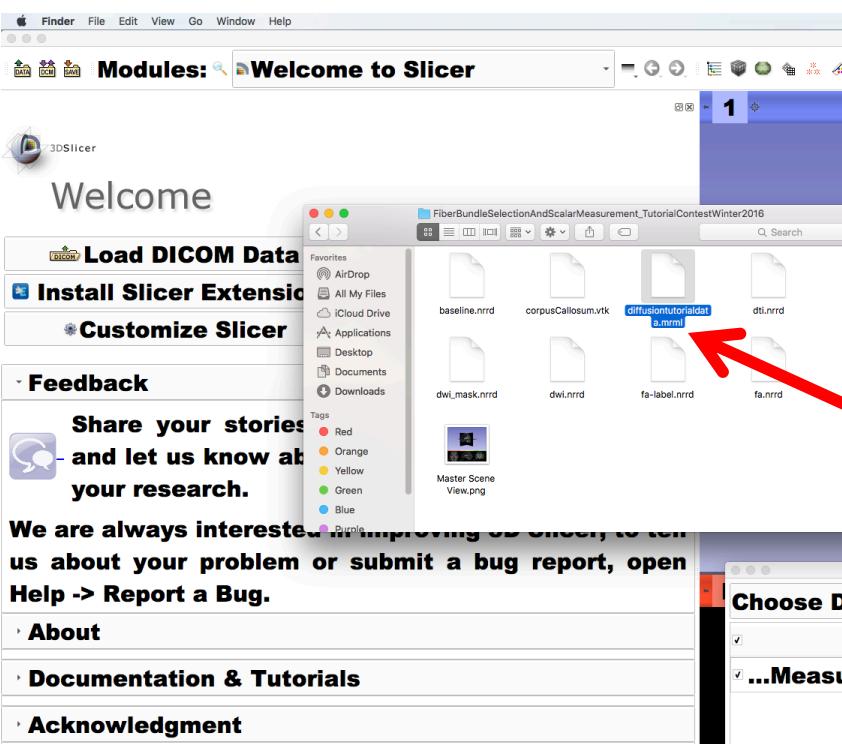
An open-source project to improve and extend diffusion magnetic resonance imaging software in 3D Slicer:

<http://dmri.slicer.org>

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

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

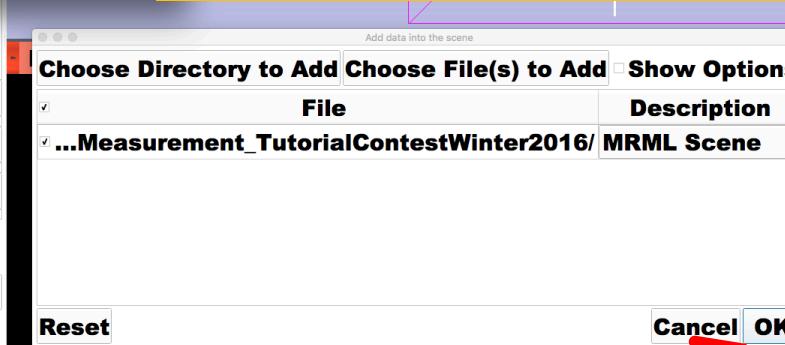
Load MRML Data



Unzip the sample data

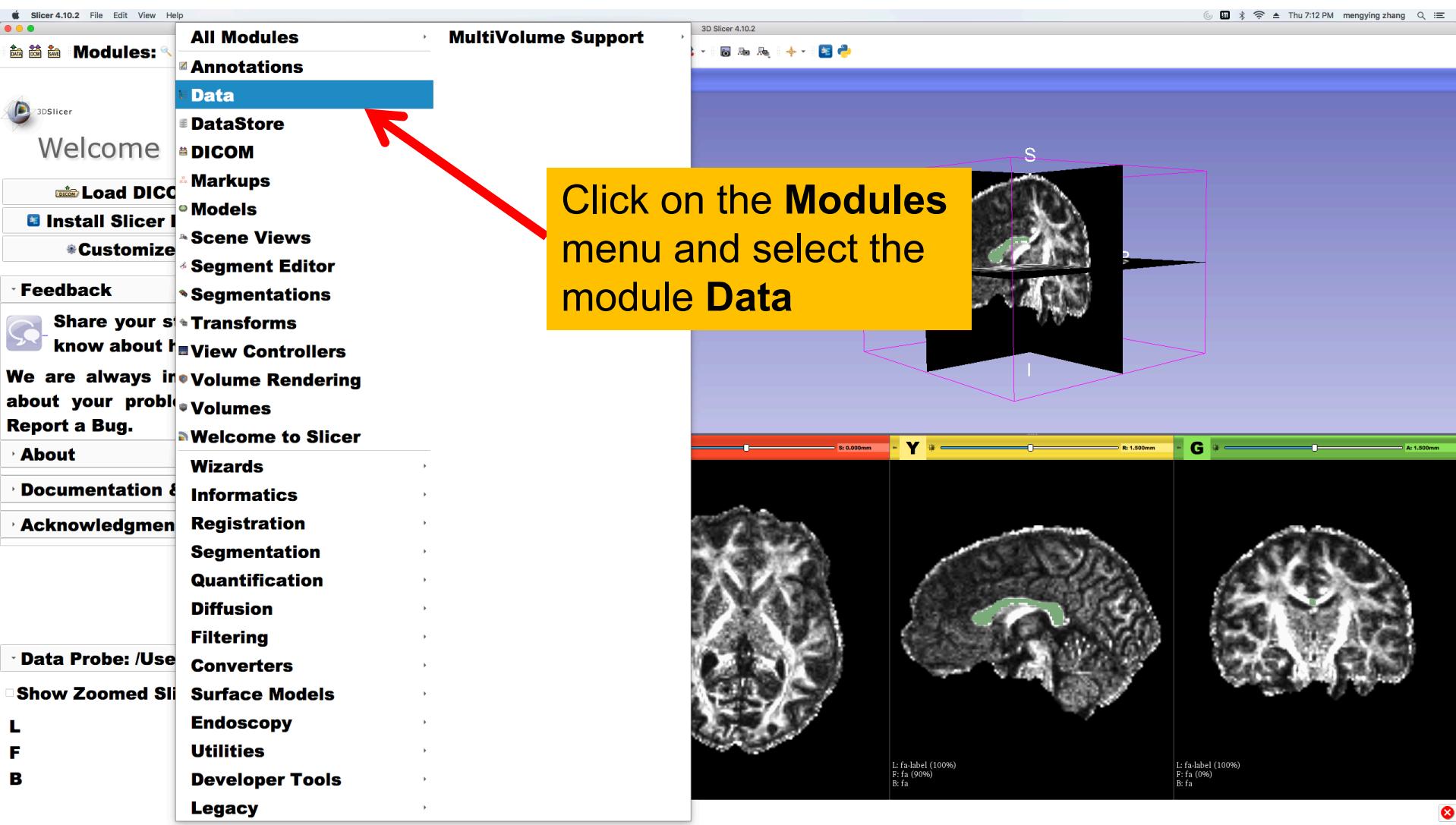
Within the unzipped folder, locate the
MRML Scene file:
diffusiontutorialdata.mrml

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



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

Load MRML Data



Load MRML Data

Slicer 4.10.2 File Edit View Help

3D Slicer 4.10.2

Thu 7:12 PM mengying zhang

Modules: Data

Help & Acknowledgement

Subject hierarchy Transform hierarchy All nodes

Node

- baseline
- dti
- dwi_mask
- dwi
- fa
- fa-label
- Master Scene View
- corpusCallosum

Show transforms Show

Filter:

Data Probe: /Users/meng...
Show Zoomed Slice

L F B

Data loaded for this tutorial:

- dwi
- dwi_mask
- baseline
- dti
- fa
- fa-label
- corpusCallosum

3D Slicer interface showing a brain scan with a green highlighted region. A 3D coordinate system (A-P, S-I, R-L) is overlaid on the brain. Below are three 2D axial slices showing the same region with a green outline. The bottom slices have status bars: L: fa-label (100%) F: fa (0%) B: fa; F: fa (90%) B: fa; L: fa-label (100%) F: fa (0%) B: fa.

Edit Multiple Labels

The screenshot shows the Slicer 4.10.2 application window. At the top, there is a menu bar with options: File, Edit, View, Help. Below the menu bar is a large list of modules. A red arrow points from a yellow callout box to the "Editor" module in the list. The yellow callout box contains the text: "Go to All modules and select the module Editor". The "Editor" module is highlighted with a blue background.

- ACPC Transform
- Add Scalar Volumes
- Annotations
- BRAINS Strip Rotation
- BRAINS Transform Convert
- BRAINSDWICleanup
- Cameras
- Cast Scalar Volume
- CheckerBoard Filter
- Colors
- Compare Volumes
- ConvertVTK
- Create a DICOM Series
- Crop Volume
- Curvature Anisotropic Diffusion
- Data
- DataProbe
- DataStore
- Demon Registration (BRAINS)
- DICOM
- DICOM Diffusion Volume Plugin
- DICOM Patcher
- DICOM Scalar Volume Plugin
- Diffusion Brain Masking
- Diffusion Tensor Estimation
- Diffusion Tensor Scalar Maps
- Diffusion-weighted DICOM Import (DWIConvert)
- DWI to Full Brain Tractography

Editor

- Endoscopy
- Event Broker
- Execution Model Tour
- Expert Automated Registration
- Export tractography to PLY (mesh)
- Export tractography to VTK
- Expert Label Map
- Expert Label Statistics
- Expert Label Smoothing
- Expert Label Statistics (BRAINS)
- Expert Landmark Registration
- Expert Markups
- Expert Mask Scalar Volume
- Expert Median Image Filter
- Expert Merge Models

- Metric Test
- Model Maker
- Model To Label Map
- Models
- Multiply Scalar Volumes
- MultiVolumeExplorer
- MultiVolumeImporter
- N4ITK MRI Bias correction
- Orient Scalar Volume
- PET Standard Uptake Value Computation
- Plots
- Probe Volume With Model
- Reformat
- Resample DTI Volume
- Resample Image (BRAINS)
- Resample Scalar Volume
- Resample Scalar/Vector/DWI Volume
- Resize Image (BRAINS)
- Robust Statistics Segmente
- Sample Data
- Scene Views
- Screen Capture
- Segment Editor
- Segment Statistics
- Segmentations
- Simple Filters
- Simple Region Growing Segmentation
- Subtract Scalar Volumes

Edit Multiple Labels

Select the Yellow slice only layout

Modules: Editor

Help & Acknowledgments

Try the new Segmentation Editor

Please help us improve Slicer

Create and Select Label Maps

Master Volume: fa

Merge Volume: fa-label

Per-Structure Volumes

Edit Selected Label Map

Undo/Redo:

Active Tool: DefaultTool

Label: tissue 1

Data Probe: /Users/mengyingzhang/Dow...siontutorialdata.mrml

Show Zoomed Slice

L F B

Conventional

Conventional Widescreen

Conventional Quantitative

Two-up

Two-up Table

Two-up Quantitative

Three over three

Triple 3D

3D only

3D Table

One-Up Quantitative

Red slice only

Yellow slice only

Green slice only

Tabbed 3D

Tabbed slice

Compare

Compare Widescreen

Compare Grid

Three over three

Three over three Quantitative

Four over four

Two over two

Side by side

Four by three slice

Four by two slice

Three by three slice

S

R: 1.000mm G: 1.000mm

L: fa-label (100%) F: fa (0%) B: fa

Edit Multiple Labels

Slicer 4.10.2 File Edit View Help

3D Slicer 4.10.2

Modules: Editor

Help & Acknowledgement

Try the new [Segment Editor](#) module for more advanced segmentation. Please help us improve the module by giving [feedback](#).

Master Volume: fa

Merge Volume: fa-label

Per-Structure volumes

Edit Selected Label Map

Undo/Redo:

Active Tool: DefaultTool

Label: tissue 1

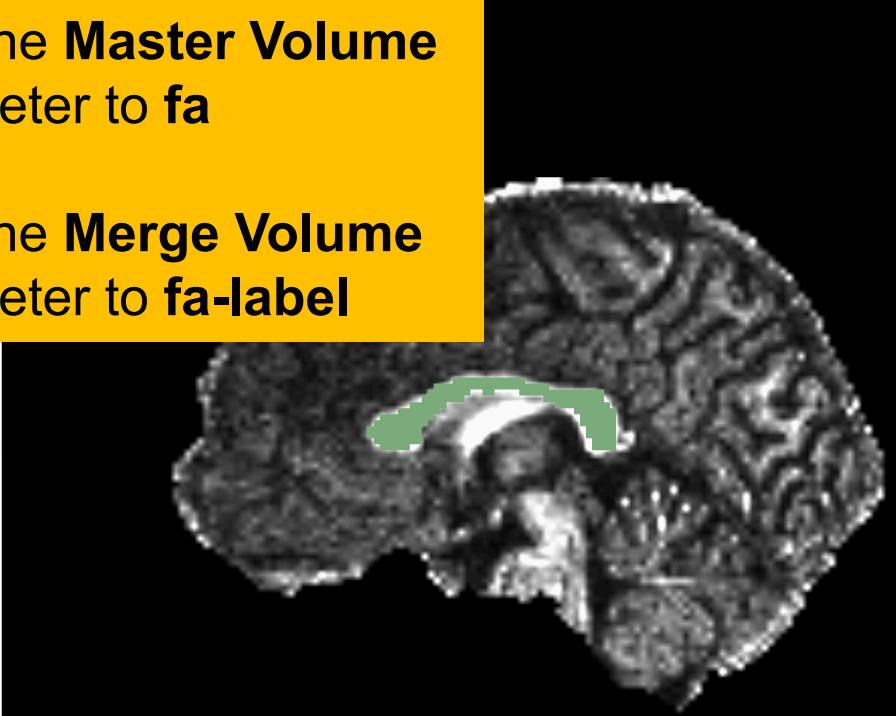
Data Probe: /Users/mengyingzhang/Dow...siontutorialdata.mrml

Show Zoomed Slice

L F B

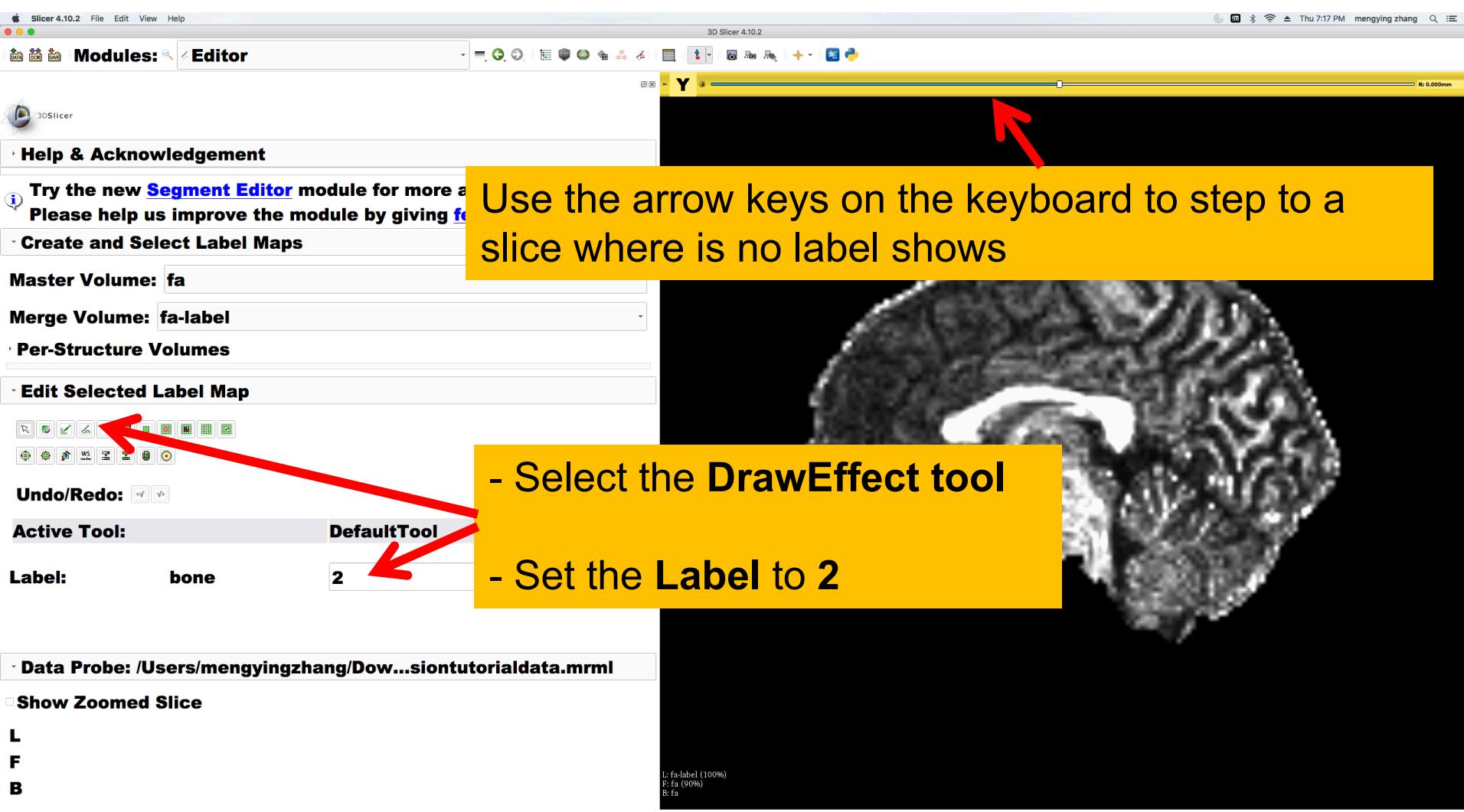
- Set the **Master Volume** parameter to **fa**

- Set the **Merge Volume** parameter to **fa-label**

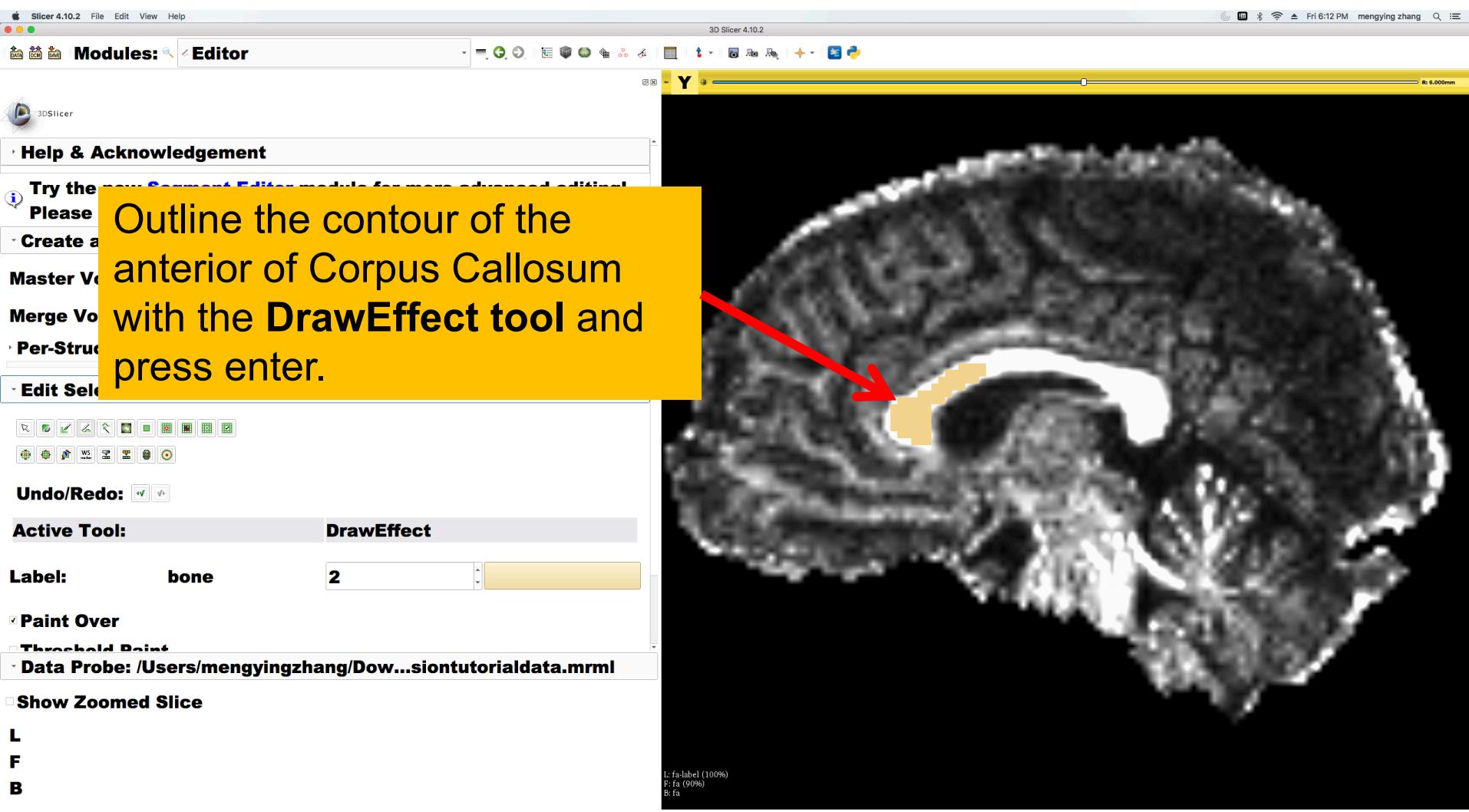


L: fa-label (100%)
F: fa (90%)
B: fa

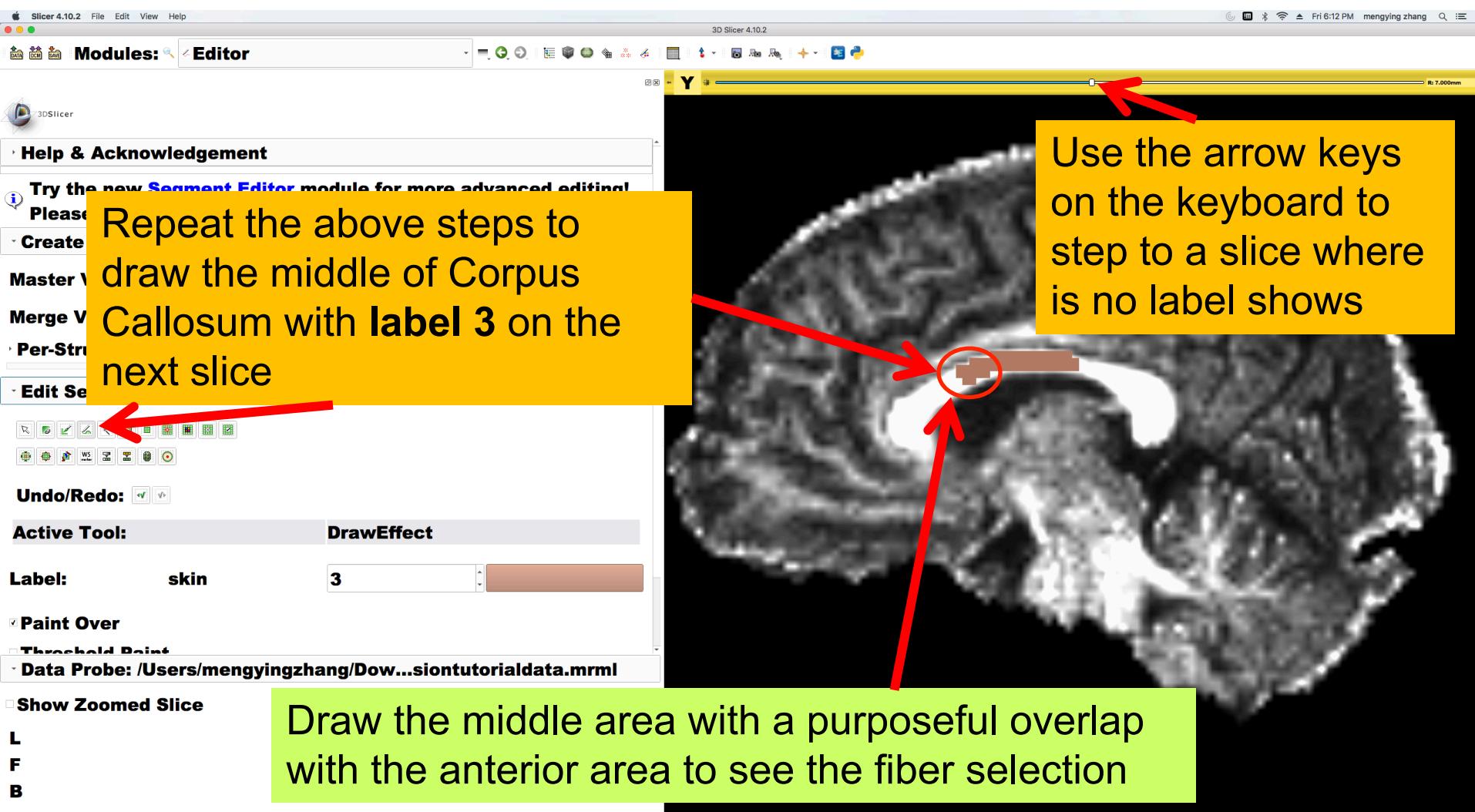
Edit Multiple Labels



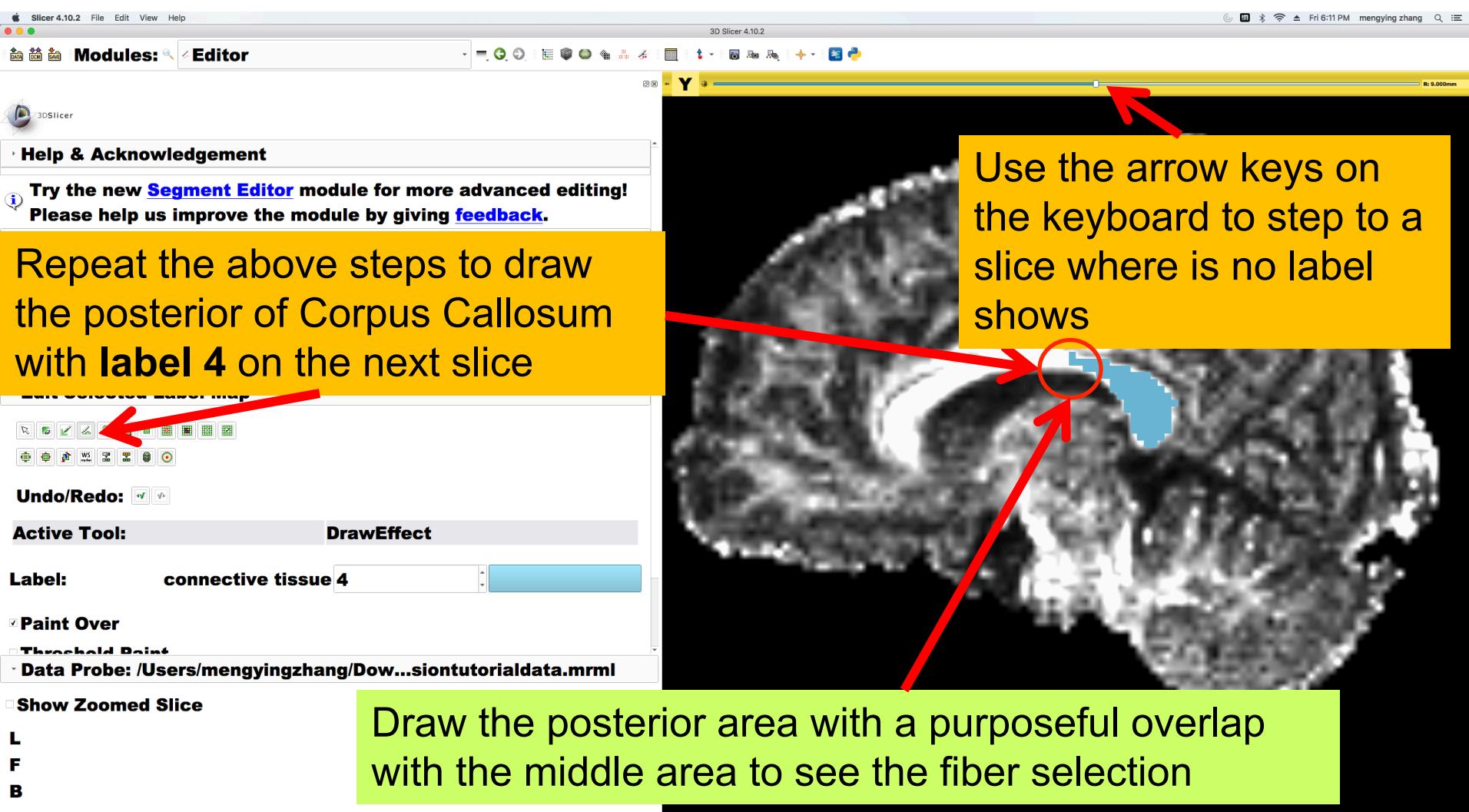
Edit Multiple Labels



Edit Multiple Labels



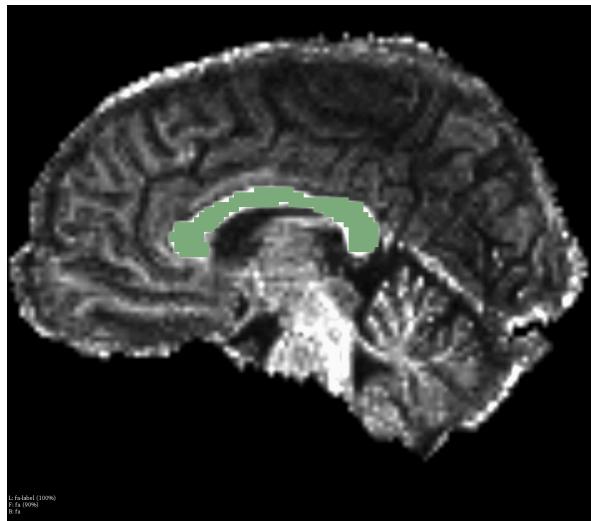
Edit Multiple Labels



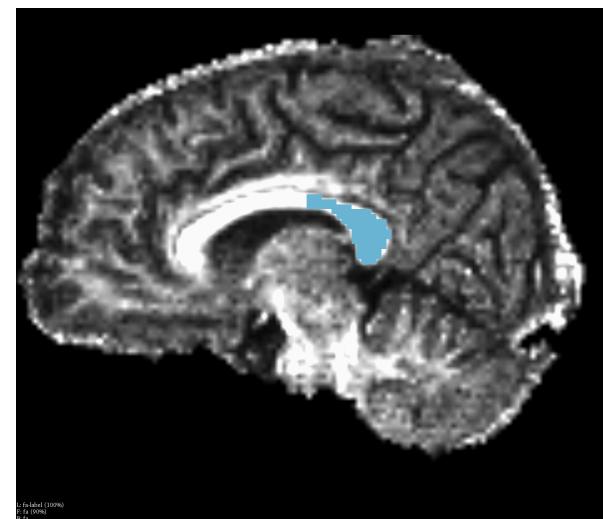
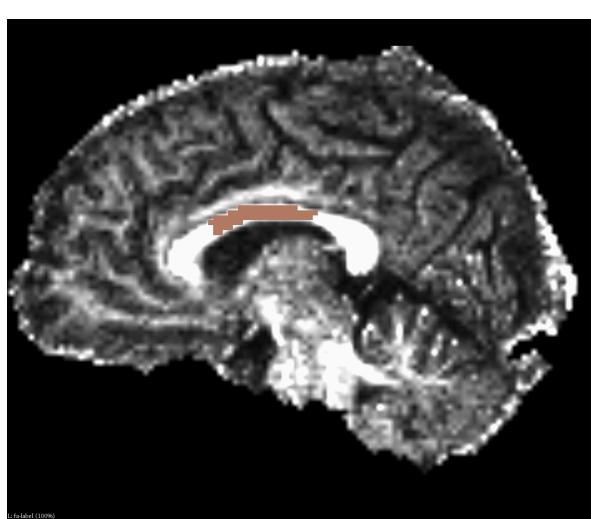
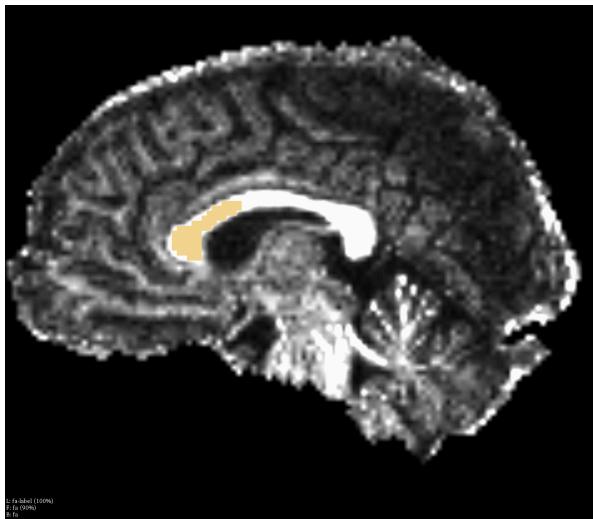
Edit Multiple Labels

Label map on individual slice, with :

- **1 - entire CC**
- **2 - anterior CC**
- **3 - middle CC**
- **4 - posterior CC**



Notice that there are overlaps between different labeled regions*, which will be used to investigate the fiber bundle selection.



* For details of CC segments: http://adessowiki.fee.unicamp.br/adesso/wiki/DTI/proj_cc/view/

Whole Brain Tractography

The screenshot shows the 3D Slicer application interface. On the left, the 'Modules' panel is open, displaying a tree view of available modules. A red arrow points upwards from the 'Tractography ROI Seeding' module in the 'Tractography' submenu towards the top of the screen. A yellow box contains the text 'Go back to the Conventional layout'. In the center, a 3D brain volume is shown with a pink translucent cube highlighting a region. Labels A, P, S, and I are visible on the cube. Below the brain volume, three axial slices of the brain are displayed. A red arrow points downwards from the 'Tractography ROI Seeding' module in the 'Tractography' submenu towards the bottom right of the screen. A yellow box contains the text 'Select the module Tractography ROI Seeding'. The 'Tractography' submenu is expanded, showing several options: Interactive UKF, Tractography Display, Tractography Seeding, UKF Tractography, Region-based, and Tractography ROI Seeding (which is highlighted).

3D Slicer 4.10.2 File Edit View Help

All Modules > MultiVolume Support

3D Slicer

Modules:

- Annotations
- Data
- DataStore
- DICOM
- Markups
- Models
- Scene Views
- Segment Editor
- Segmentations
- Transforms
- View Controllers
- Volume Rendering
- Volumes
- Welcome to Slicer

Help & Acknowledgments

Please help us!

Try the new Segmentation

Create and Select

Master Volume: fa

Merge Volume: fa

Per-Structure Volume

Edit Selected Label

Undo/Redo:

Active Tool:

Label:

Paint Over

Show Zoomed Slice

L F B

Diffusion

Filtering

Converters

Surface Models

Endoscopy

Utilities

Developer Tools

Legacy

Import and Export

Process

Quantify

Tractography

- Interactive UKF
- Tractography Display
- Tractography Seeding
- UKF Tractography
- Region-based

Tractography ROI Seeding

Tractography ROI Selection

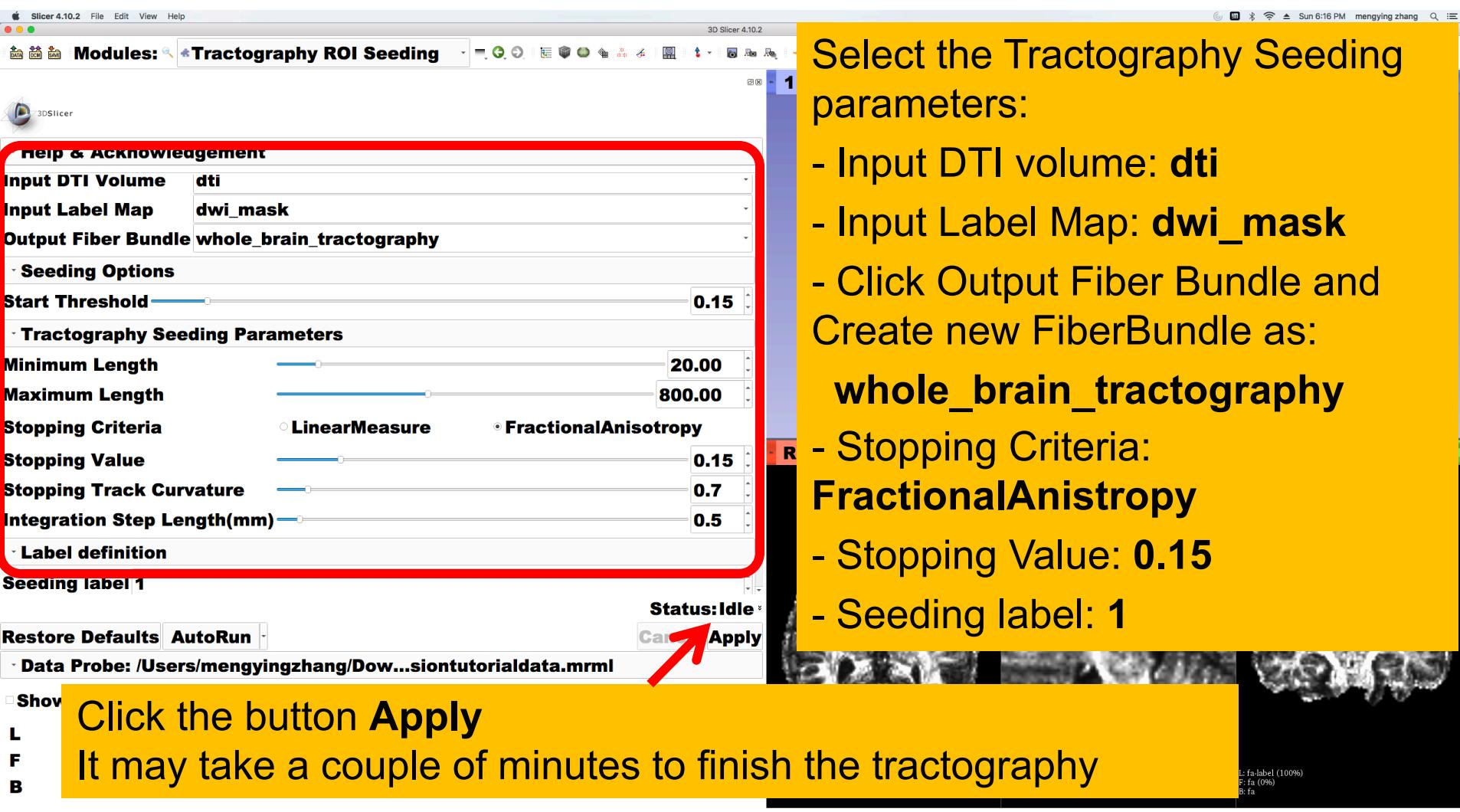
Go back to the Conventional layout

S

A P I

Select the module
Tractography ROI
Seeding

Whole Brain Tractography



Select the Tractography Seeding parameters:

- Input DTI volume: **dti**
- Input Label Map: **dwi_mask**
- Click Output Fiber Bundle and Create new FiberBundle as:
whole_brain_tractography
- Stopping Criteria:
FractionalAnisotropy
- Stopping Value: **0.15**
- Stopping Track Curvature: **0.7**
- Integration Step Length(mm): **0.5**
- Seeding label: **1**

Click the button **Apply**
It may take a couple of minutes to finish the tractography

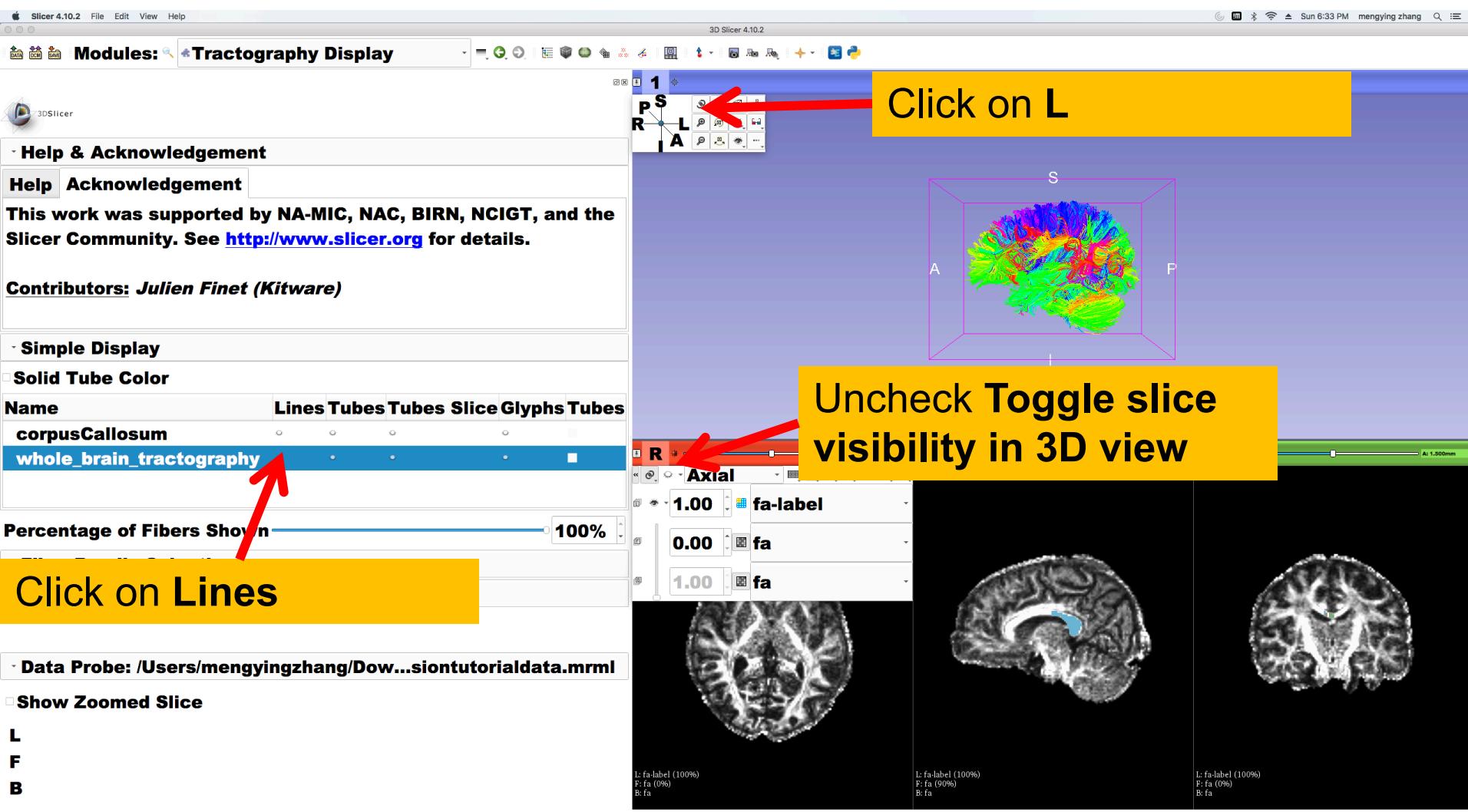
Whole Brain Tractography

The screenshot shows the 3D Slicer 4.10.2 interface. The top menu bar includes File, Edit, View, Help, and a Python icon. The left sidebar lists various modules: Annotations, Data, DataStore, DICOM, Markups, Models, Scene Views, Segment Editor, Segmentations, Transforms, View Controllers, Volume Rendering, Volumes, Welcome to Slicer, Wizards, Informatics, Registration, Segmentation, Quantification, Diffusion (selected), Filtering, Converters, Surface Models, Endoscopy, Utilities, Developer Tools, and Legacy. A yellow callout box with a red arrow points to the "Tractography Display" option in the Diffusion module's dropdown menu. The main window displays a 3D brain volume with a pink coordinate system (A-P, S-I, R-L) and a central slice showing white matter tracts. Below the main view are three smaller 2D brain slices. A status bar at the bottom right shows "A: 1.500mm". The title bar indicates "3D Slicer 4.10.2" and the system status "Sun 6:19 PM mengying zhang".

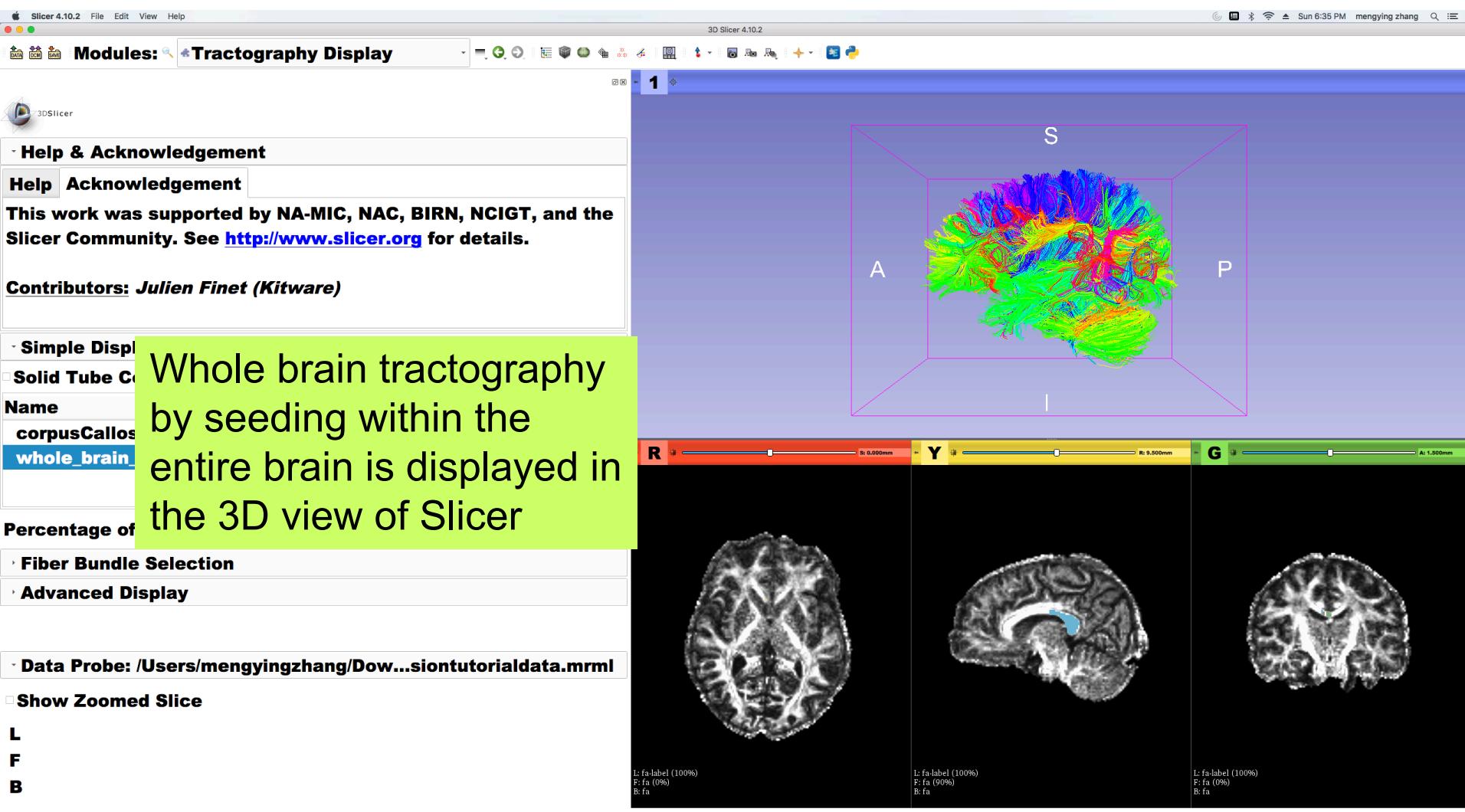
Go to Tractography Display module

- Diffusion
 - Import and Export
 - Process
 - Quantify
 - Tractography
 - Utilities
- Utilities
 - Interactive UKF
 - Tractography Display
 - Tractography Seeding
 - UKF Tractography
 - Region-based

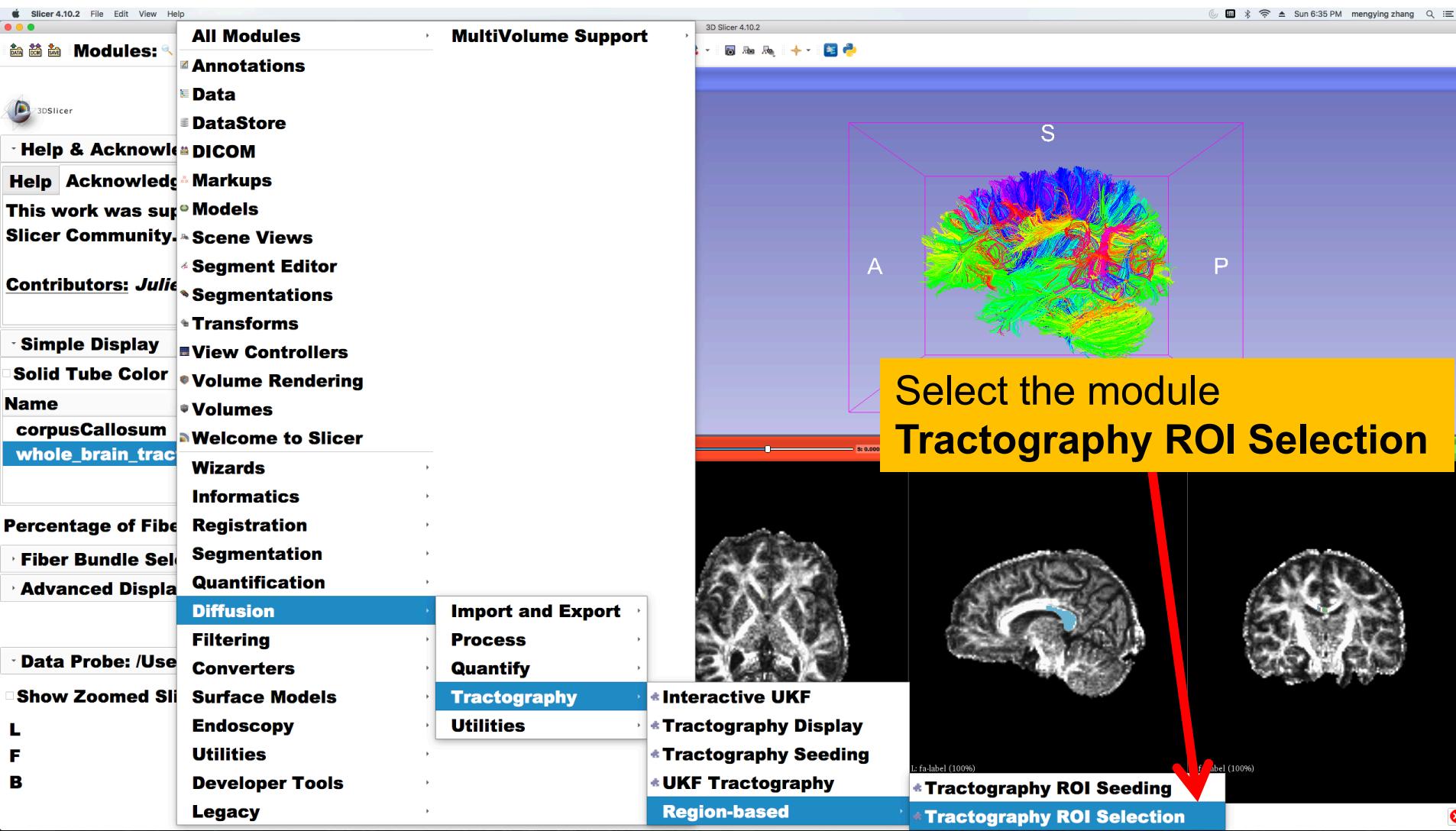
Whole Brain Tractography



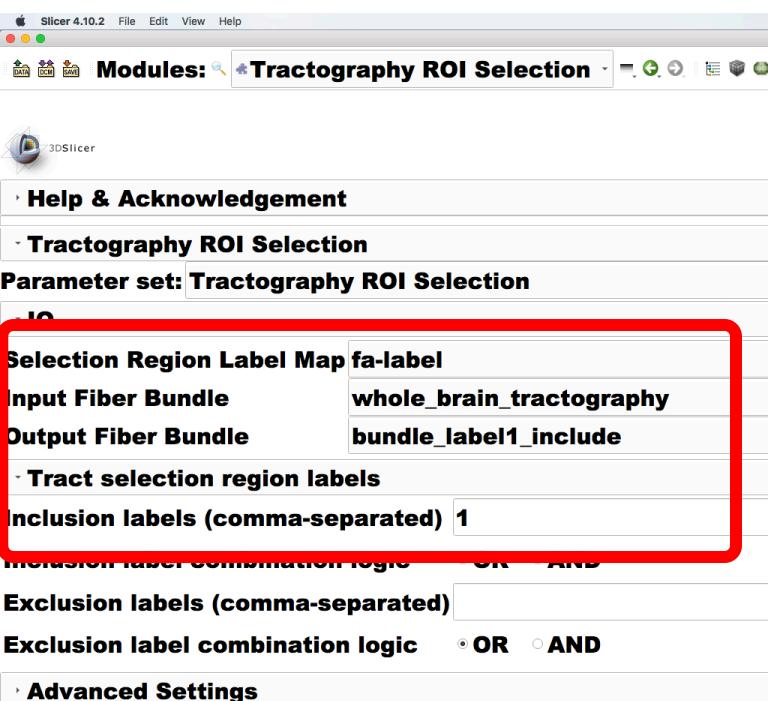
Whole Brain Tractography



Tractography ROI Selection

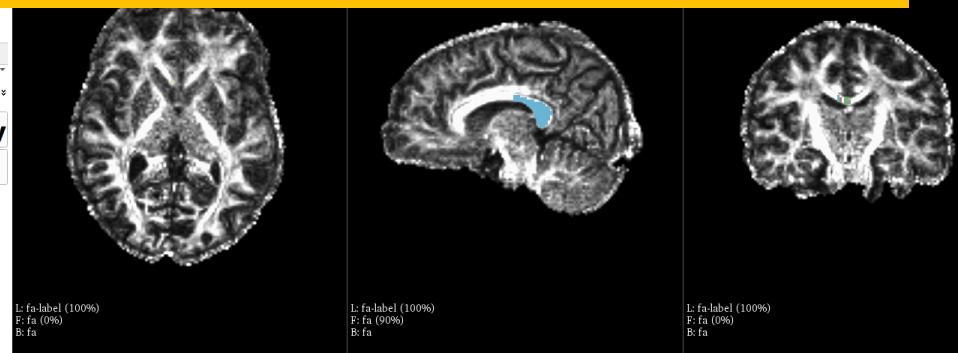
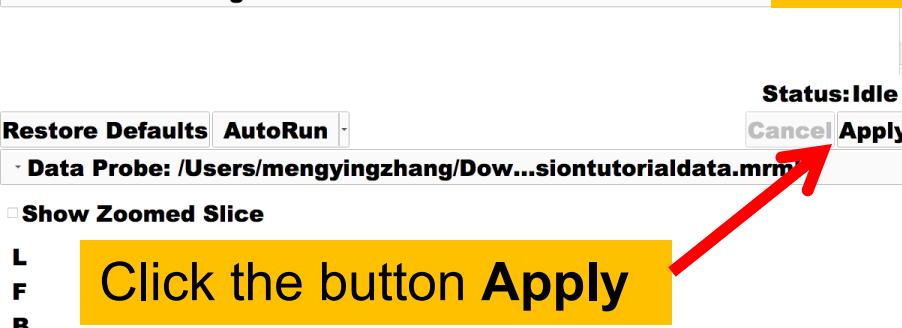


Single Label Selection



Set the Tractography ROI Selection parameters:

- Input Label Map: **fa-label**
- Input Fiber Bundle:
whole_brain_tractography
- Click Output Fiber Bundle and Create new FiberBundle as:
bundle_label1_include
- Labels to include: **1**



Single Label Selection

Slicer 4.10.2 File Edit View Help 3D Slicer 4.10.2 Sun 6:43 PM mengying zhang

Modules: Tractography Display

Go to Tractography Display

Help & Acknowledgement

Simple Display

Solid Tube Color

Name	Lines	Tubes	Tubes	Slice	Glyphs	Tubes
corpusCallosum	○	○	○	○		
whole_brain_tractography	○	○	○	○		
bundle_label1_include	●	●	●	●	■	

Percentage of Fibers Shown 48%

Fiber B

Advanced

Data Probe: /Users/mengyingzhang/Dow...siontutorialdata.mrml

Show Zoomed Slice

L F B

The fiber bundle from the whole brain tractography that passes through label 1 is displayed

Single Label Selection

Sun 6:45 PM mengying zhang

Modules: Tractography ROI Selection

Parameters: Tractography ROI Selection

10

Selection Region Label Map fa-label

Input Fiber Bundle whole_brain_tractography

Output Fiber Bundle bundle_label2_include

Tract selection region labels

Inclusion labels (comma-separated) 2

Inclusion label combination logic OR AND

Exclusion labels (comma-separated)

Exclusion label combination logic OR AND

Advanced Settings

Status: Com

100%

Restore Defaults AutoRun

Data Probe: /Users/mengyingzhang/Dow...siontutorialdata.mrml

Show Zoomed Slice

L F B

S

P

G

A: 1.500mm

Repeat the above steps to perform fiber bundle selections of labels **2**, **3** and **4** individually and obtain the selected bundles of **bundle_label2_include**, **bundle_label3_include** and **bundle_label4_include** respectively

L: fa-label (100%)
F: fa (0%)
B: fa

L: fa-label (100%)
F: fa (90%)
B: fa

L: fa-label (100%)
F: fa (9%)
B: fa

Single Label Selection

Slicer 4.10.2 File Edit View Help

3D Slicer 4.10.2 Sun 6:46 PM mengying zhang

Modules: Tractography Display

Help & Acknowledgement

Simple Display

Solid Tube Color

Name	Lines	Tubes	Tubes	Slice	Glyphs	Tubes
corpusCallosum	○	○	○	○	○	○
whole_brain_tractography	○	○	○	○	○	○
bundle_label1_include	○	○	○	○	○	○
bundle_label2_include	●	●	●	●	●	●

Percentage of Fibers Shown

Fiber Bundle Selection

Advanced Display

Data Probe: /Users/mengyingzhang/Dow...siontutorialdata.mrml

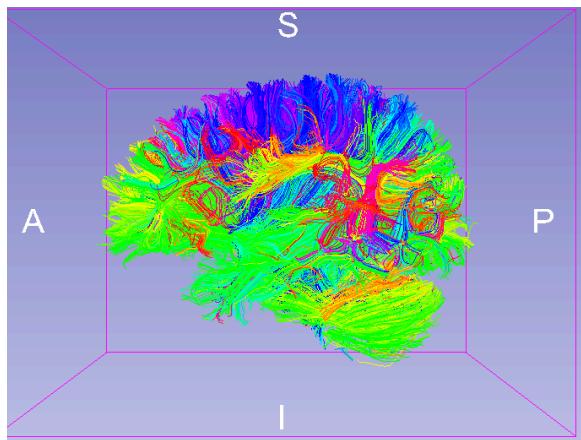
Show Zoomed Slice

L F B

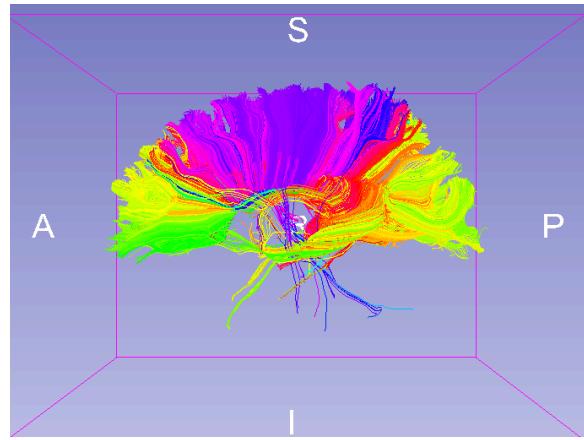
The Tractography Display module displays the fiber bundles obtained.

Single Label Selection

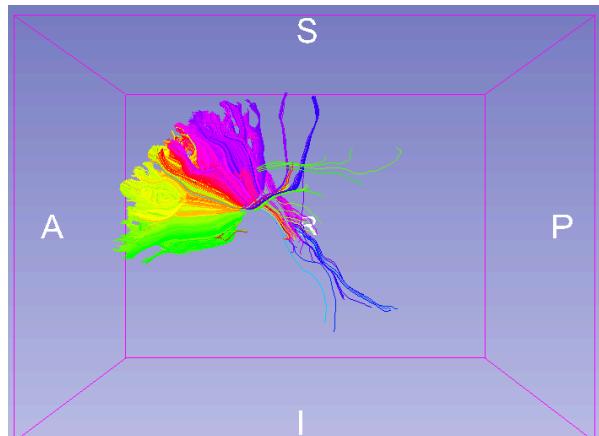
Whole Brain



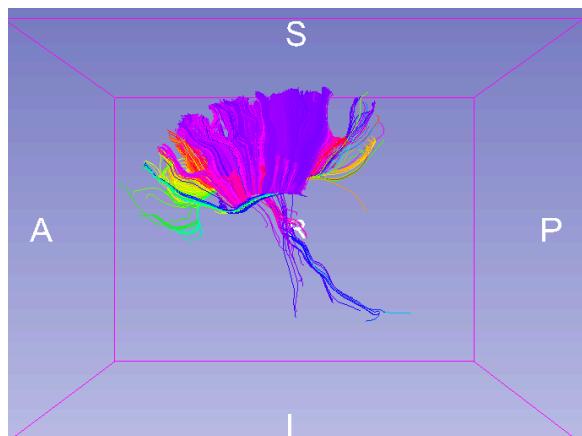
Label 1



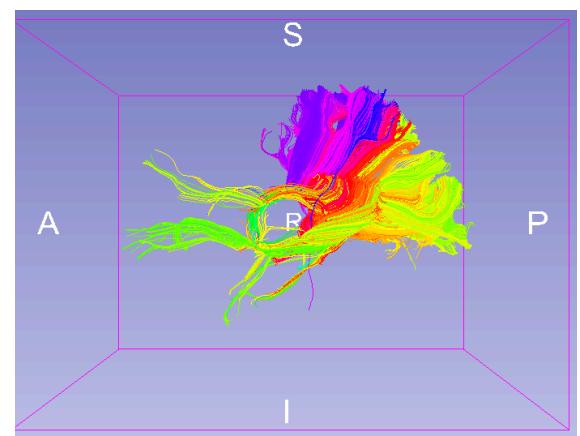
Label 2



Label 3



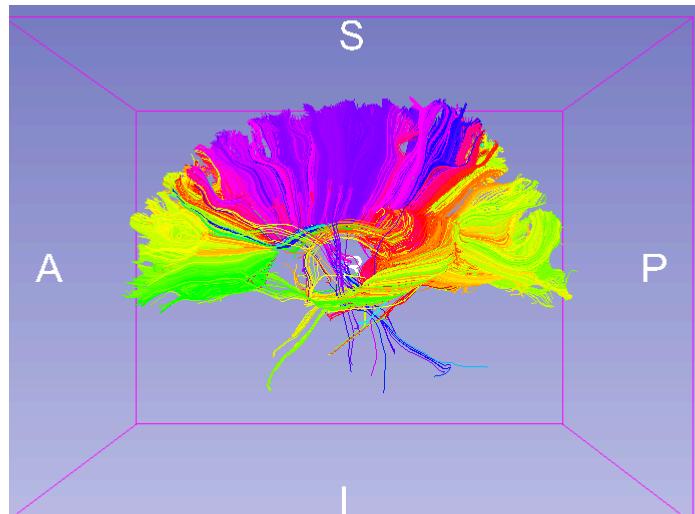
Label 4



Single Label Selection

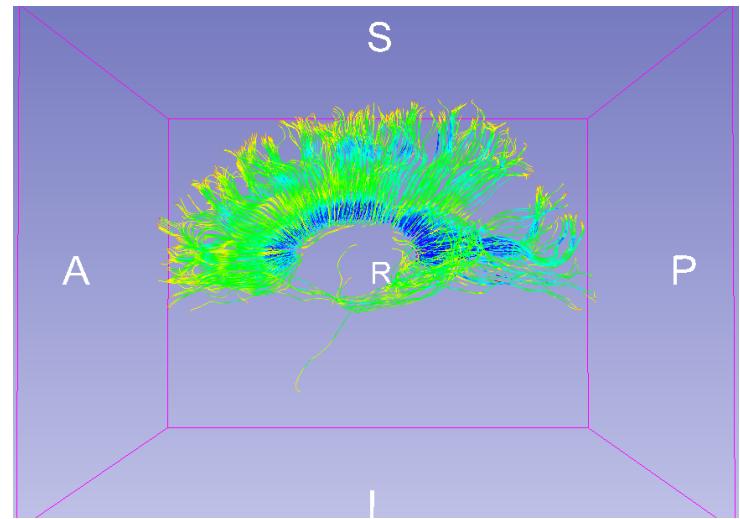
Notice that whole brain seeding creates a denser fiber bundle than seeding from the label 1.

Fiber Bundle Selection of Label 1
from the Whole Brain Tractography



Fiber Bundle Obtained by
Seeding within Label 1

V.S.



By viewing **corpusCallosum**
loaded in the MRML file

Multiple Labels Selection

FiberBundleLabelSelect allows users to perform multiple labels selection by providing a list of labels and selecting one logical operation:

- **OR**: fiber bundles that pass through **any label** in the list
- **AND**: fiber bundles that pass through **all labels** in the list

▼ Tract selection region labels

Inclusion labels (comma-separated)

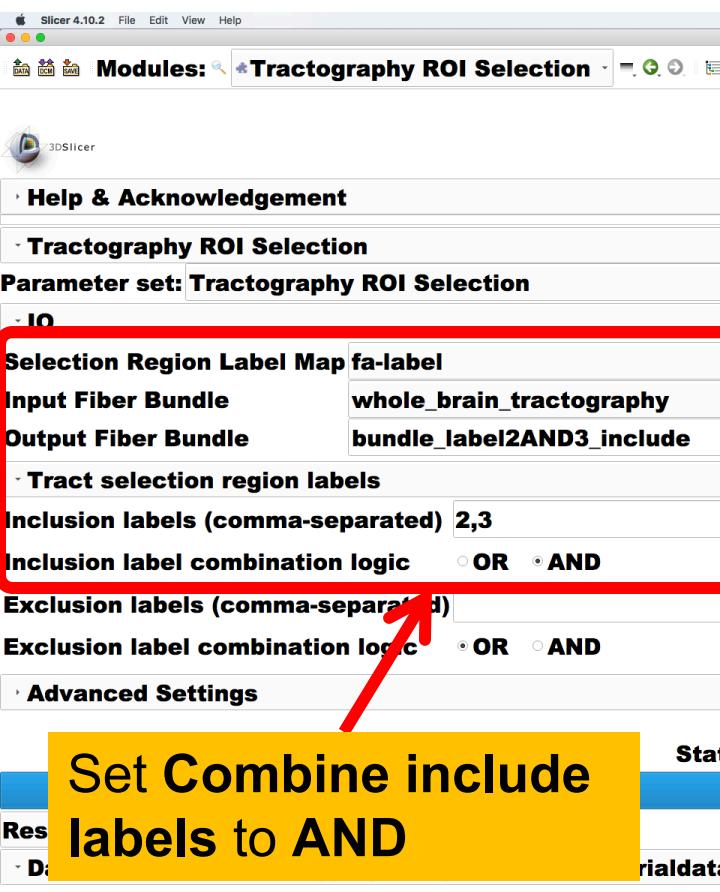
Inclusion label combination logic OR AND

Exclusion labels (comma-separated)

Exclusion label combination logic

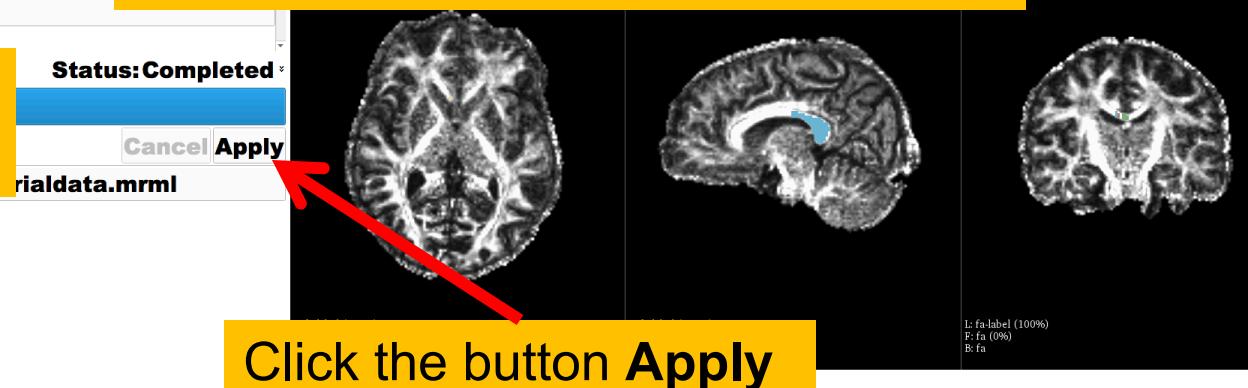
AND: Fiber must pass through all specified labels.
OR: Fiber must pass through any specified label (at least one).

Multiple Labels Selection (AND)



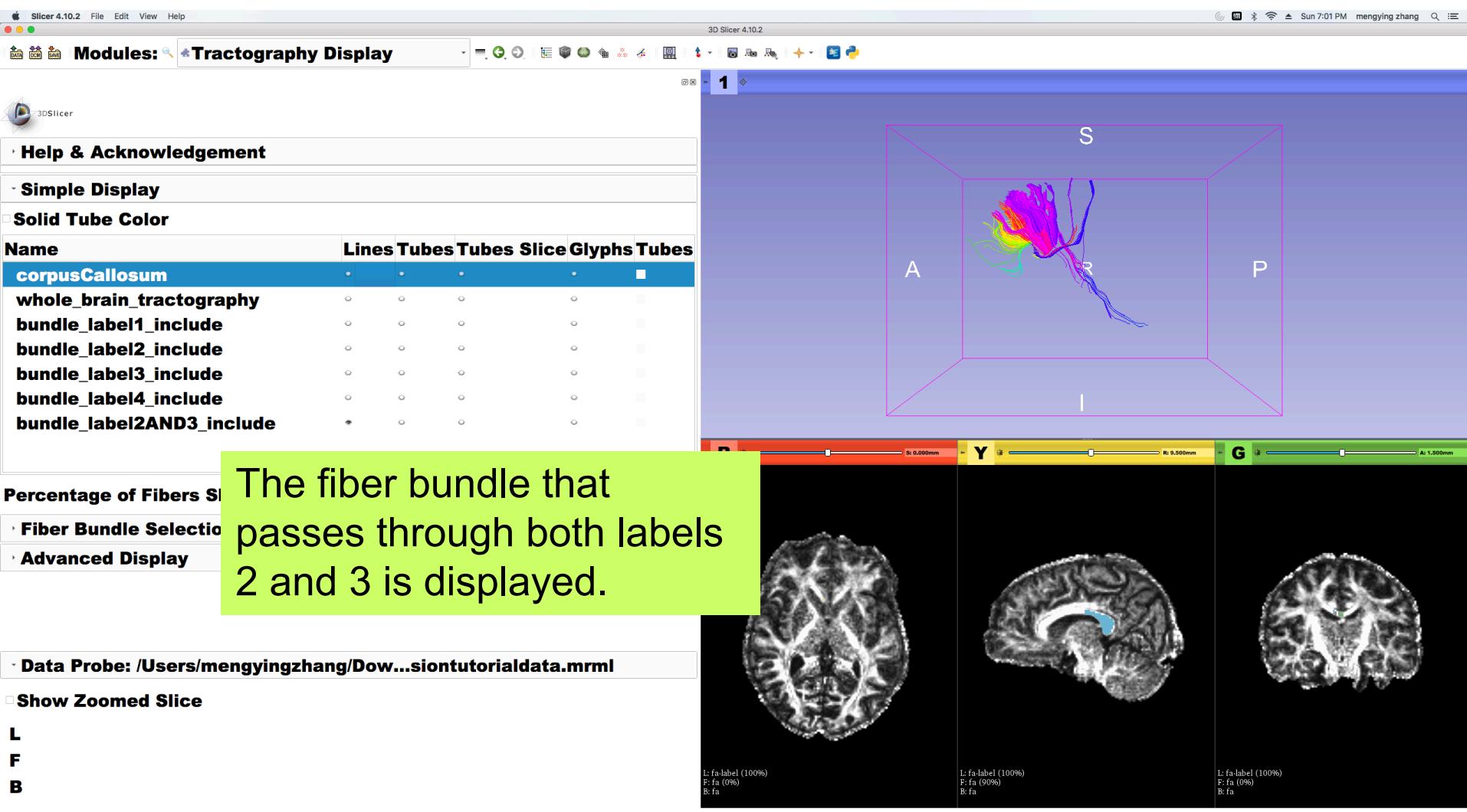
Set the Tractography ROI Selection parameters:

- Input Label Map: **fa-label**
- Input Fiber Bundle:
whole_brain_tractography
- Create and rename Output Fiber Bundle:
bundle_labels2AND3_include
- Labels to include: 2,3



Click the button **Apply**

Multiple Labels Selection (AND)



Multiple Labels Selection (OR)

The screenshot shows the 3D Slicer interface with the 'Tractography ROI Selection' module open. The parameter set is 'Tractography ROI Selection'. The 'Input Fiber Bundle' is set to 'whole_brain_tractography' and the 'Output Fiber Bundle' is set to 'bundle_label2OR3_include'. The 'Inclusion labels (comma-separated)' field contains '2,3'. The 'Inclusion label combination logic' is set to 'OR'. The 'Exclusion labels (comma-separated)' field is empty. The 'Exclusion label combination logic' is set to 'OR'. A red box highlights the 'Inclusion labels' and 'Inclusion label combination logic' fields. A yellow box with a red arrow points to the 'Exclusion labels' field with the text 'Set Combine include labels to OR'. A yellow box at the bottom right with a red arrow points to the 'Apply' button with the text 'Click the button Apply'. The 3D view shows a brain with a highlighted fiber bundle.

Repeat the above steps to select the fiber bundle that passes through labels 2 or 3 and obtain the selection result of **bundle_labels2OR3_include**

Set Combine include labels to OR

Click the button **Apply**

Multiple Labels Selection (OR)

Slicer 4.10.2 File Edit View Help

3D Slicer 4.10.2 Sun 7:05 PM mengying zhang

Modules: Tractography Display

Help & Acknowledgement

Simple Display

Solid Tube Color

Name	Lines	Tubes	Tubes	Slice	Glyphs	Tubes
corpusCallosum	○	○	○	○		
whole_brain_tractography	○	○	○	○		
bundle_label1_include	○	○	○	○		
bundle_label2_include	○	○	○	○		
bundle_label3_include	○	○	○	○		
bundle_label4_include	○	○	○	○		
bundle_label2AND3_include	○	○	○	○		
bundle_label2OR3_include	●	●	●	●	●	●

Percentage of Fibers Shown

Fiber Bundle Selection

Advanced Display

Data Probe: /Users/mengyingzhang/Dow...siontutorialdata.mrml

Show Zoomed Slice

L

F

B

The fiber bundle that passes through either labels 2 or 3 is displayed.

R: 0.000mm S: 0.000mm

Y: 9.500mm R: 9.500mm

G: 1.500mm A: 1.500mm

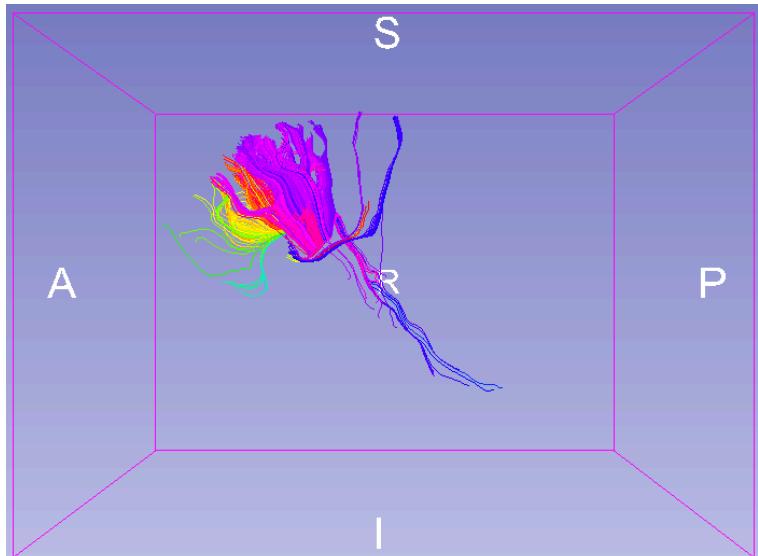
L: fa-label (100%)
F: fa (0%)
B: fa

L: fa-label (100%)
F: fa (90%)
B: fa

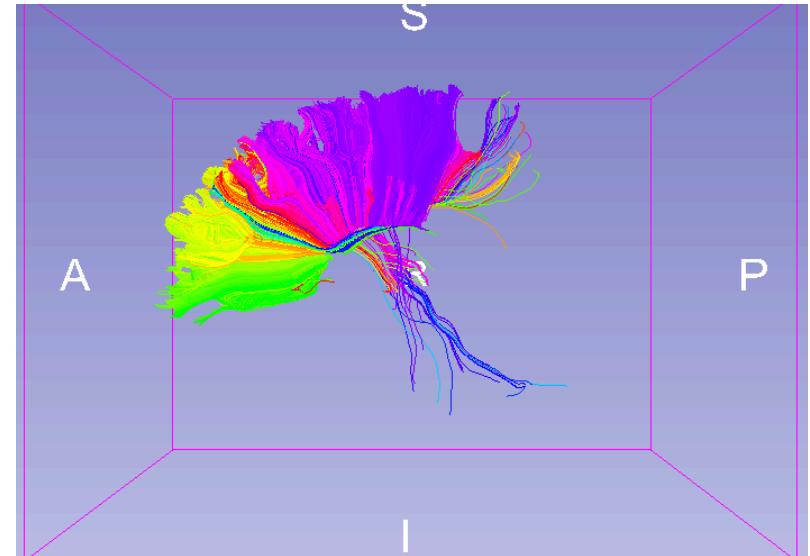
L: fa-label (100%)
F: fa (9%)
B: fa

Multiple Labels Selection

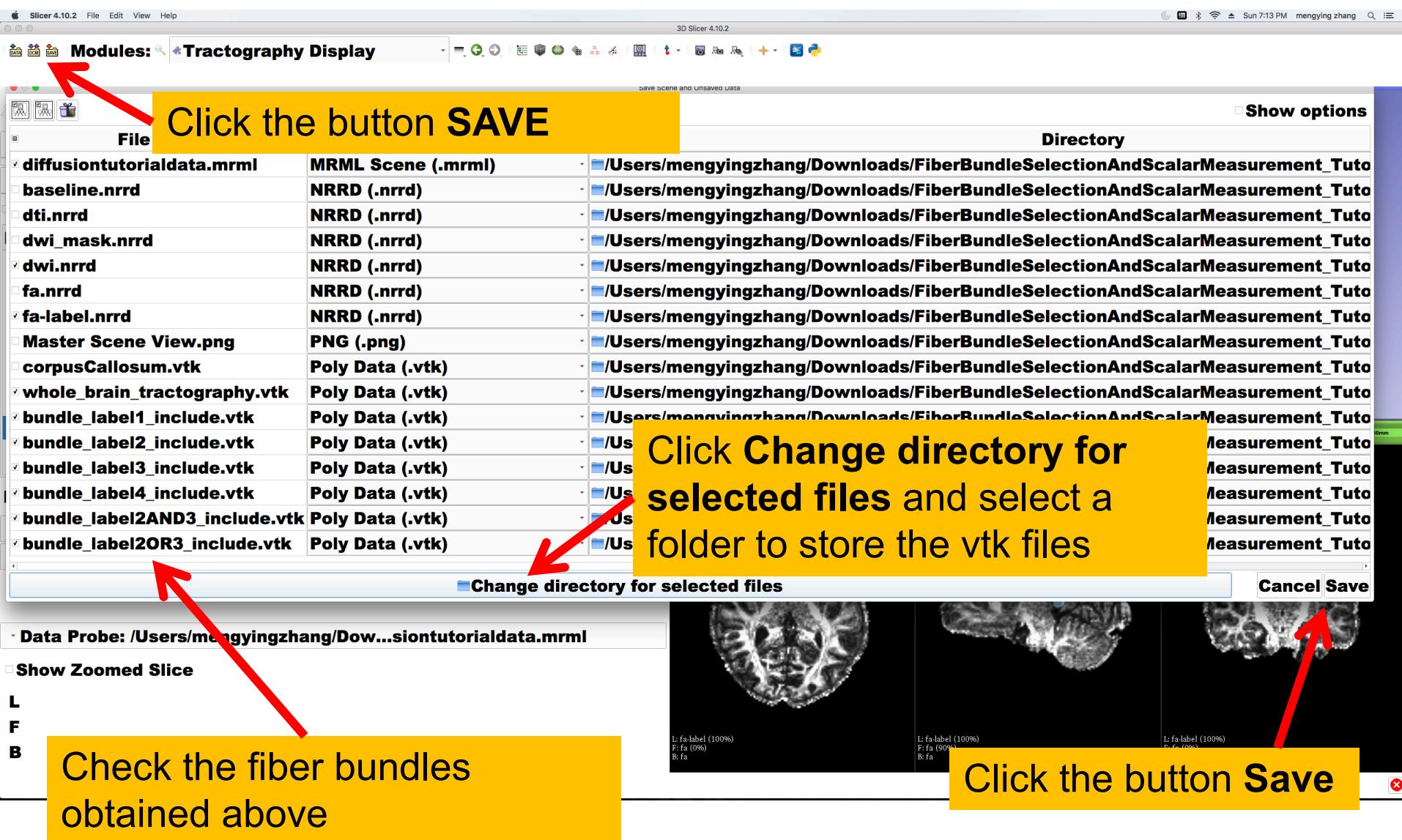
Labels 2 **and** 3



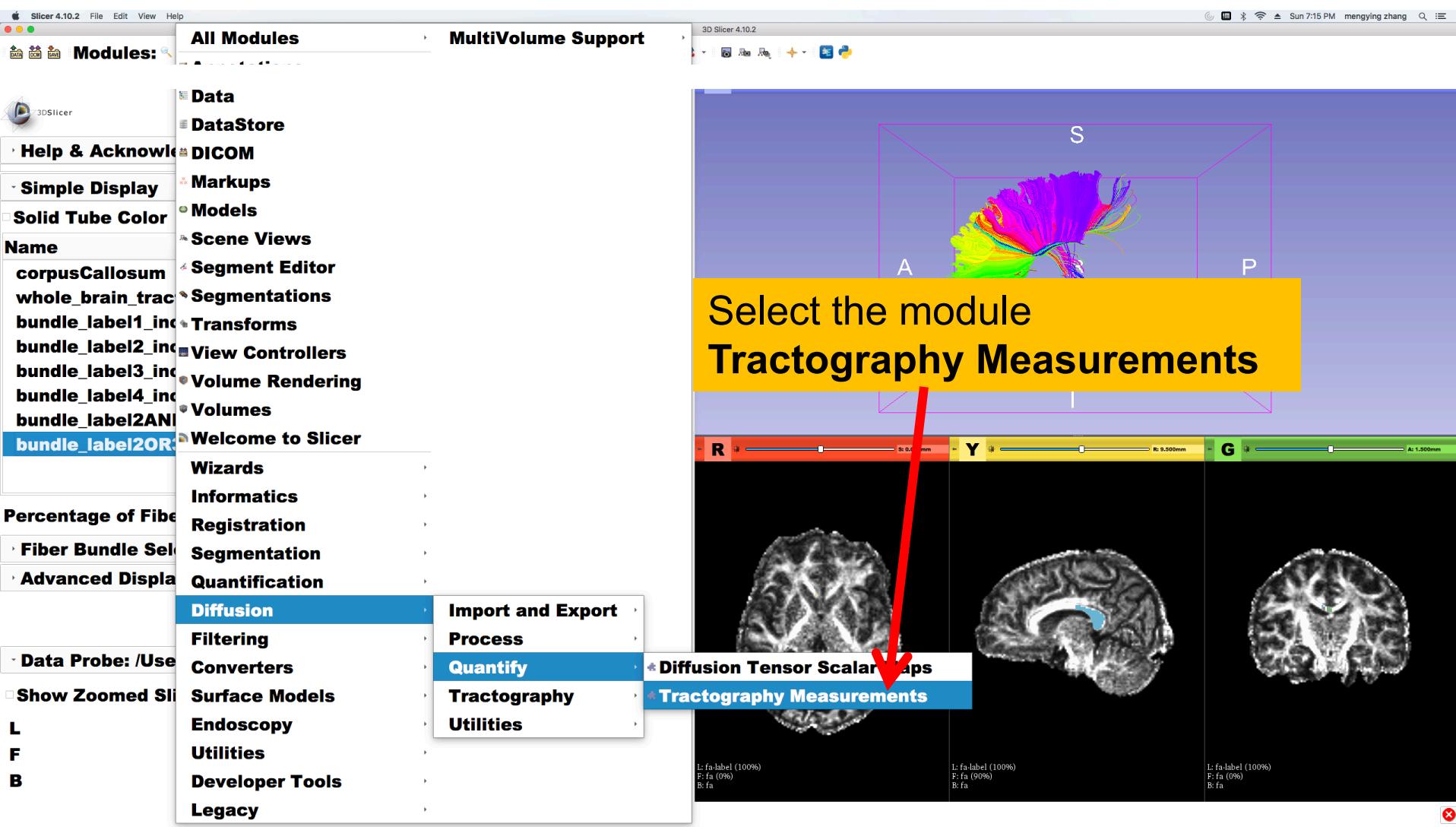
Labels 2 **or** 3



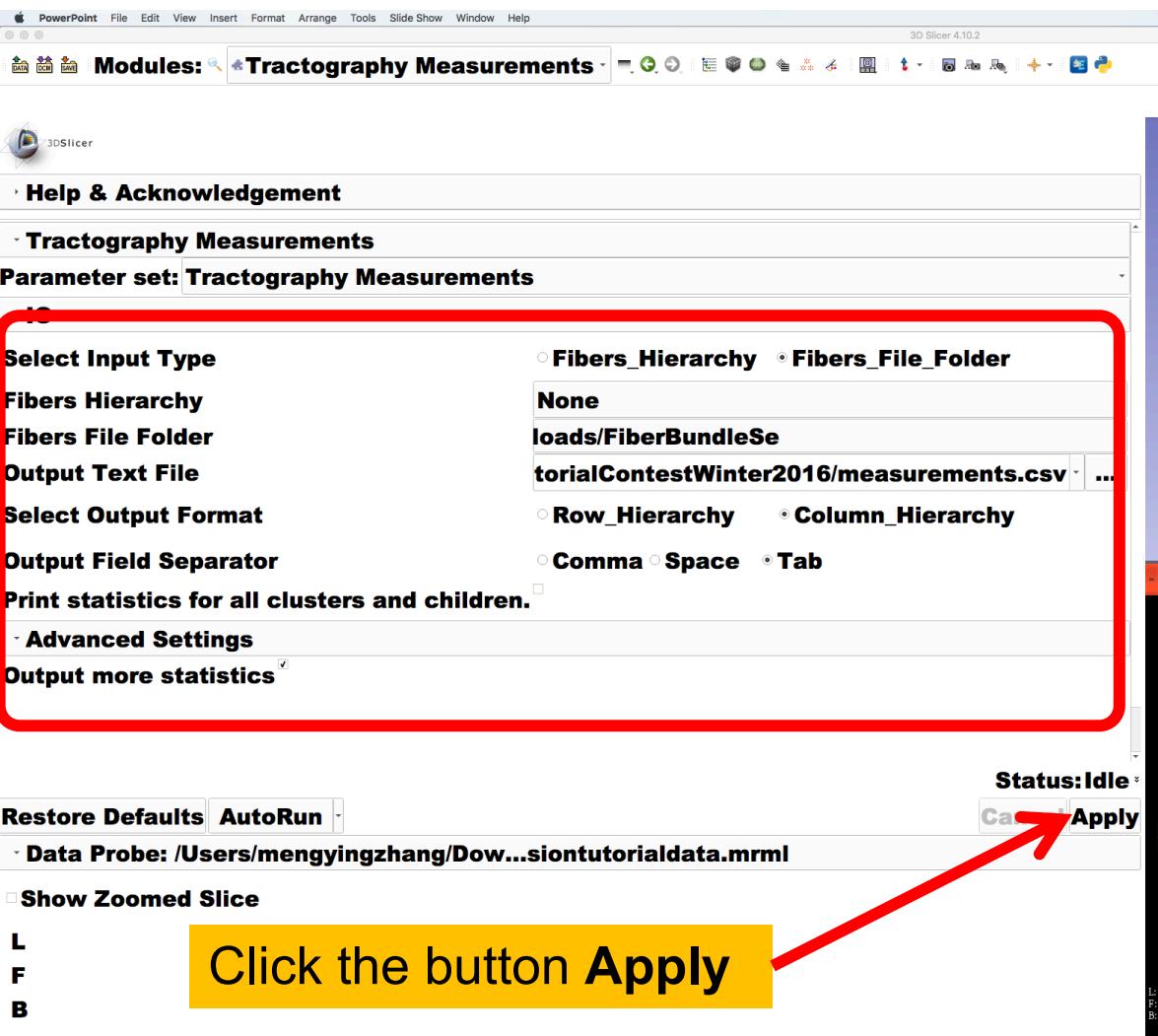
Save Fiber Bundles



Tractography Measurements



Tractography Measurements



Set the Tractography Measurements parameters:

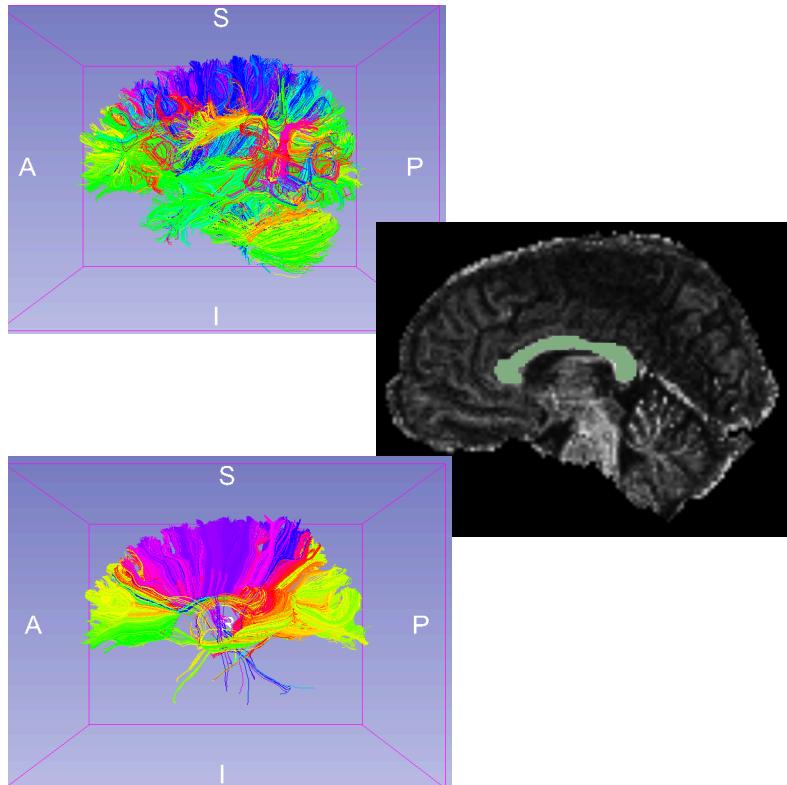
- Select Input Type: **Fibers_File_Folder**
- Fibers File Folder: **XXX/**
- Output Text File: **XXX/measurements.csv**
- Select Output Format: **Column_Hierarchy**
- Output Field Separator: **Tab**
- Check **Output more statistics**

Tractography Measurements

The module outputted a CSV file listing the mean scalar value (such as FA and Trace) of each fiber bundle in the folder

A	B	C	D	E	F	G	H	
1	Name	Num_Points	Num_Fibers	Mean_Length	Num_Clamp_Excluded	Tensors_.FractionalAnisotropy.Max	Tensors_.FractionalAnisotropy.Mean	Tensors_.FractionalAnisotropy.Median
2	bundle_label1_include.vtk	2151800	16140	99.185761	1955	1	0.552109	0.529033
3	bundle_label2_include.vtk	617185	5483	83.621564	0	0.997704	0.512498	0.479581
4	bundle_label3_include.vtk	651843	5598	86.535613	0	0.997704	0.528475	0.512219
5	bundle_label4_include.vtk	1346359	8972	111.736367	1957	1	0.57416	0.55411
6	bundle_labels2AND3_include.vtk	171716	1630	78.215332	0	0.997704	0.518245	0.487751
7	bundle_labels2OR3_include.vtk	1097312	9451	86.280013	0	0.997704	0.521089	0.498575

Conclusion



This tutorial guided you through the fiber bundle label selection and fiber tract scalar measurements for conducting further tractography processing.

A	B	C	D	E	F	G	H	
1	Name	Num_Points	Num_Fibers	Mean_Length	Num_Clamp_Excluded	Tensors_FractionalAnisotropy.Max	Tensors_FractionalAnisotropy.Mean	Tensors_FractionalAnisotropy.Median
2	bundle_label1_include.vtk	2151800	16140	99.185761	1955	1	0.552109	0.529033
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