

Fiber Bundle Selection And Scalar Measurement

Fan Zhang, PhD

Brigham and Women's Hospital

Harvard Medical School

fzhang@bwh.harvard.edu

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 4.8.1, revision 26813, Stable Release) software available at:

<http://download.slicer.org>

Data used in this tutorial is available at:

<https://namic.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>

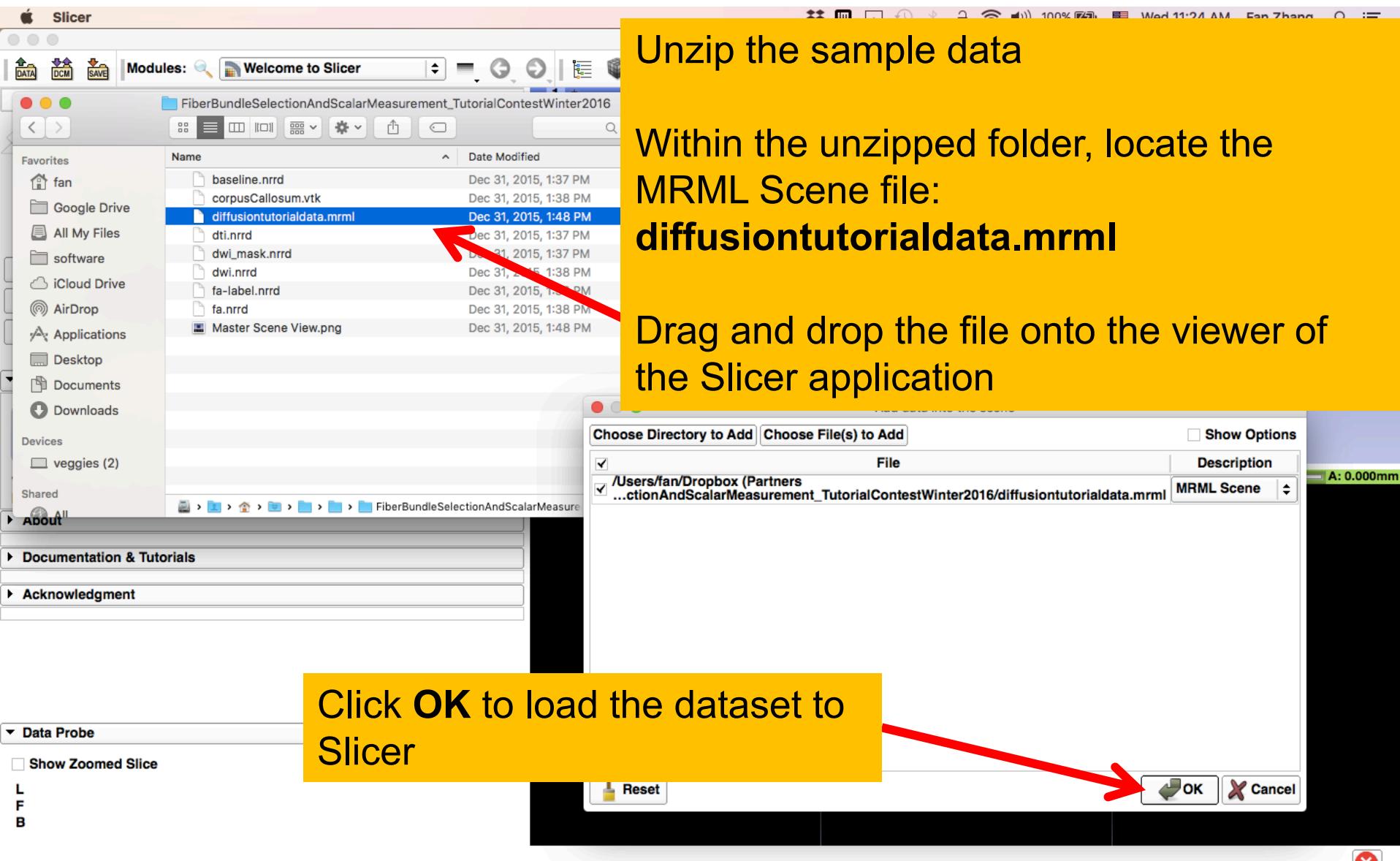
Load MRML Data

Unzip the sample data

Within the unzipped folder, locate the MRML Scene file:
diffusiontutorialdata_mrml

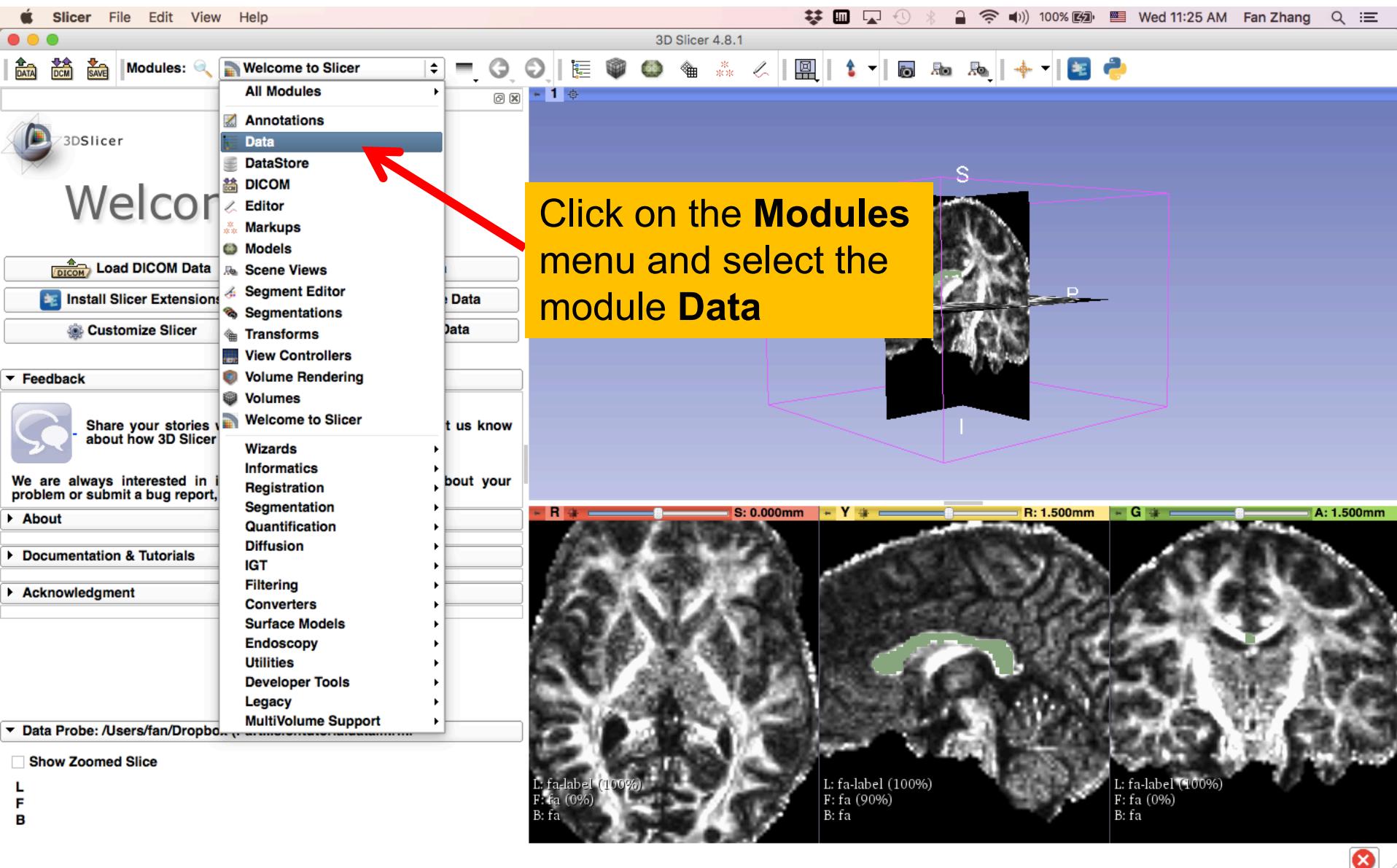
Drag and drop the file onto the viewer of the Slicer application

Click OK to load the dataset to Slicer



The screenshot shows the Slicer application interface. On the left is a file browser window titled 'FiberBundleSelectionAndScalarMeasurement_TutorialContestWinter2016'. It lists several files: baseline.nrrd, corpusCallosum.vtk, diffusiontutorialdata_mrml, dti.nrrd, dwi_mask.nrrd, dwi.nrrd, fa-label.nrrd, fa.nrrd, and Master Scene View.png. A red arrow points to the 'diffusiontutorialdata_mrml' file. To the right of the browser is a 'Choose File(s) to Add' dialog box. It has two tabs: 'Choose Directory to Add' (selected) and 'Choose File(s) to Add'. Under 'File', it shows '/Users/fan/Dropbox (Partners) ...ctionAndScalarMeasurement_TutorialContestWinter2016/diffusiontutorialdata_mrml'. Under 'Description', it says 'MRML Scene'. At the bottom right of the dialog are 'OK' and 'Cancel' buttons. A red arrow points from the text 'Click OK to load the dataset to Slicer' to the 'OK' button.

Load MRML Data



Load MRML Data

Slicer File Edit View Help

3D Slicer 4.8.1

DATA DCM SAVE Modules: Data

3DSlicer

Help & Acknowledgement

Subject hierarchy Transform hierarchy All nodes

Node

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

Show transforms Show MRML Subject hierarchy item information

Filter: MRML node information

Data Probe: /Users/fan/Dropbox (Part...siontutorialdata.mrml)

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 segmentation mask of the corpus callosum. The interface includes a 3D view with axes (S, A, R, P, I) and three 2D axial slices below.

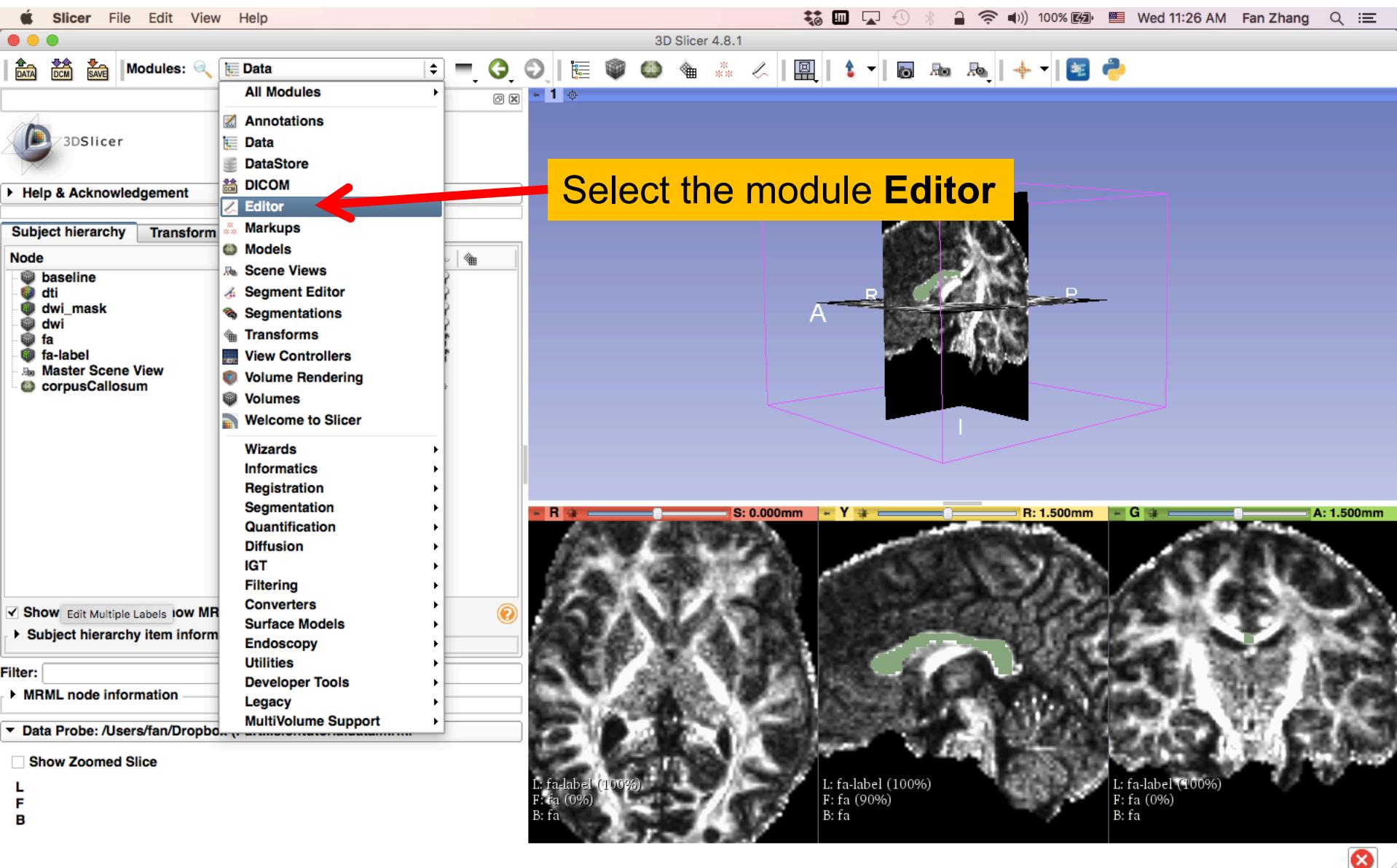
3D View (Top):

- S: 0.000mm
- R: 1.500mm
- A: 1.500mm

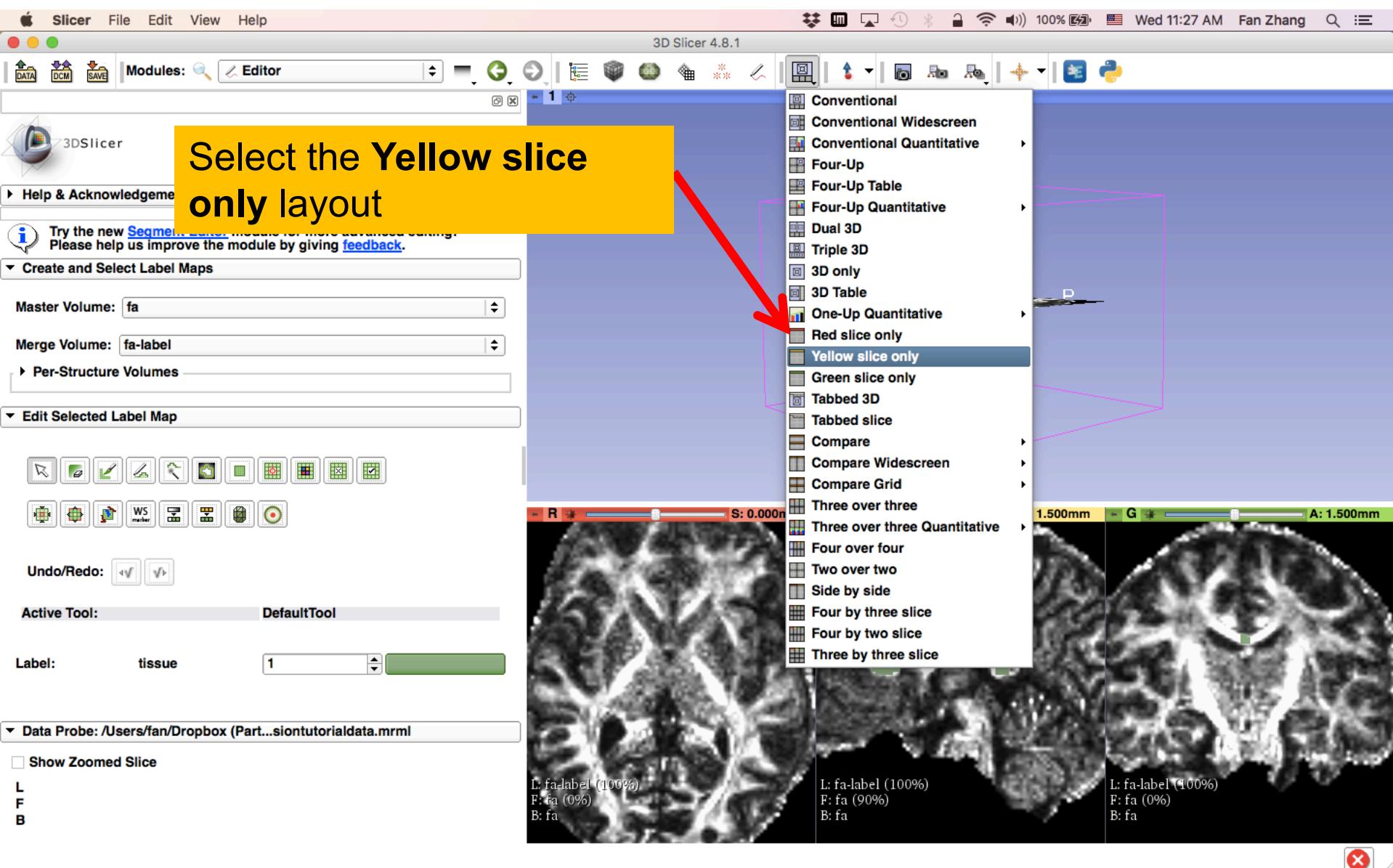
2D Slices (Bottom):

- L: fa-label (100%) F: fa (0%) B: fa
- L: fa-label (100%) F: fa (90%) B: fa
- L: fa-label (100%) F: fa (0%) B: fa

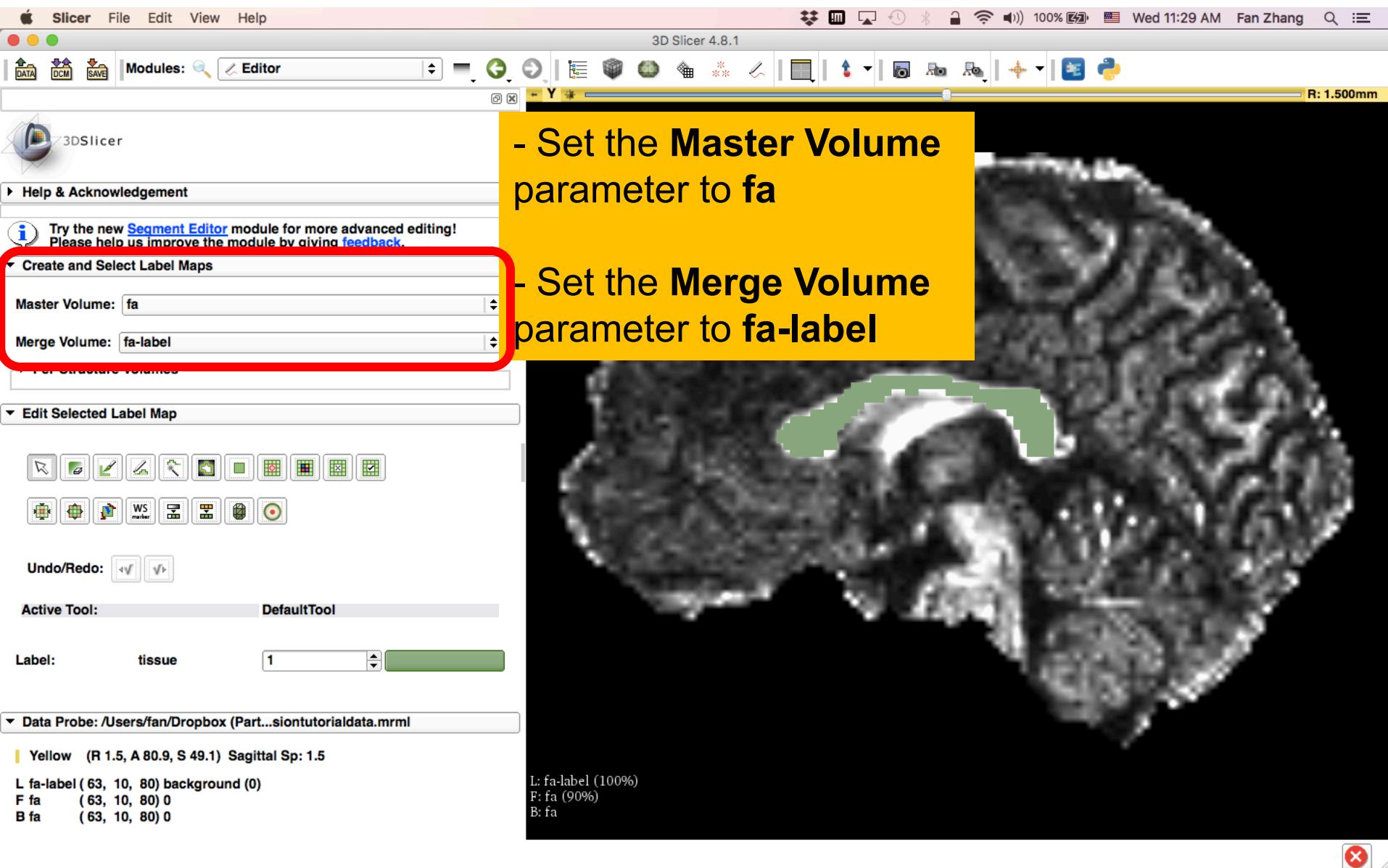
Edit Multiple Labels



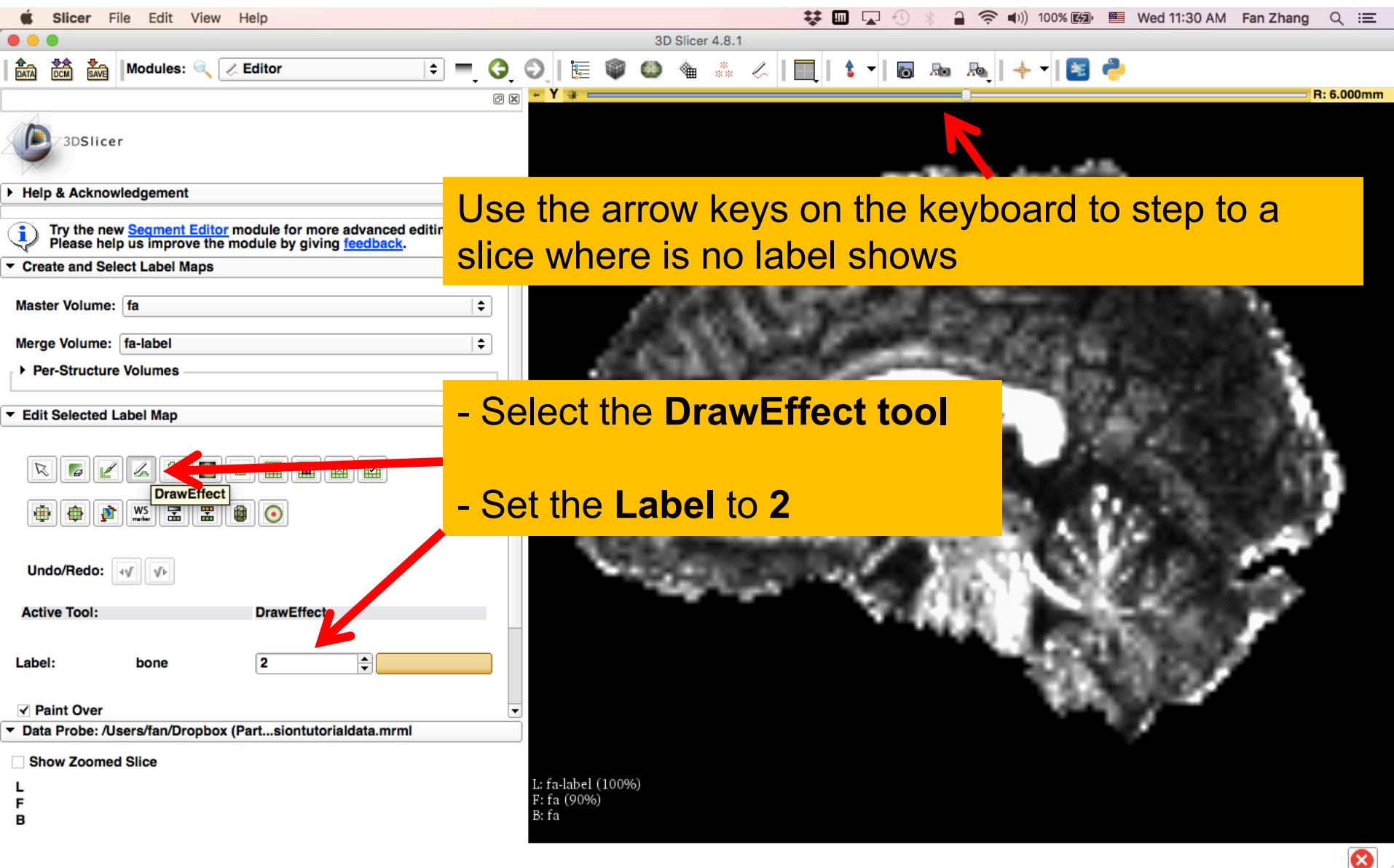
Edit Multiple Labels



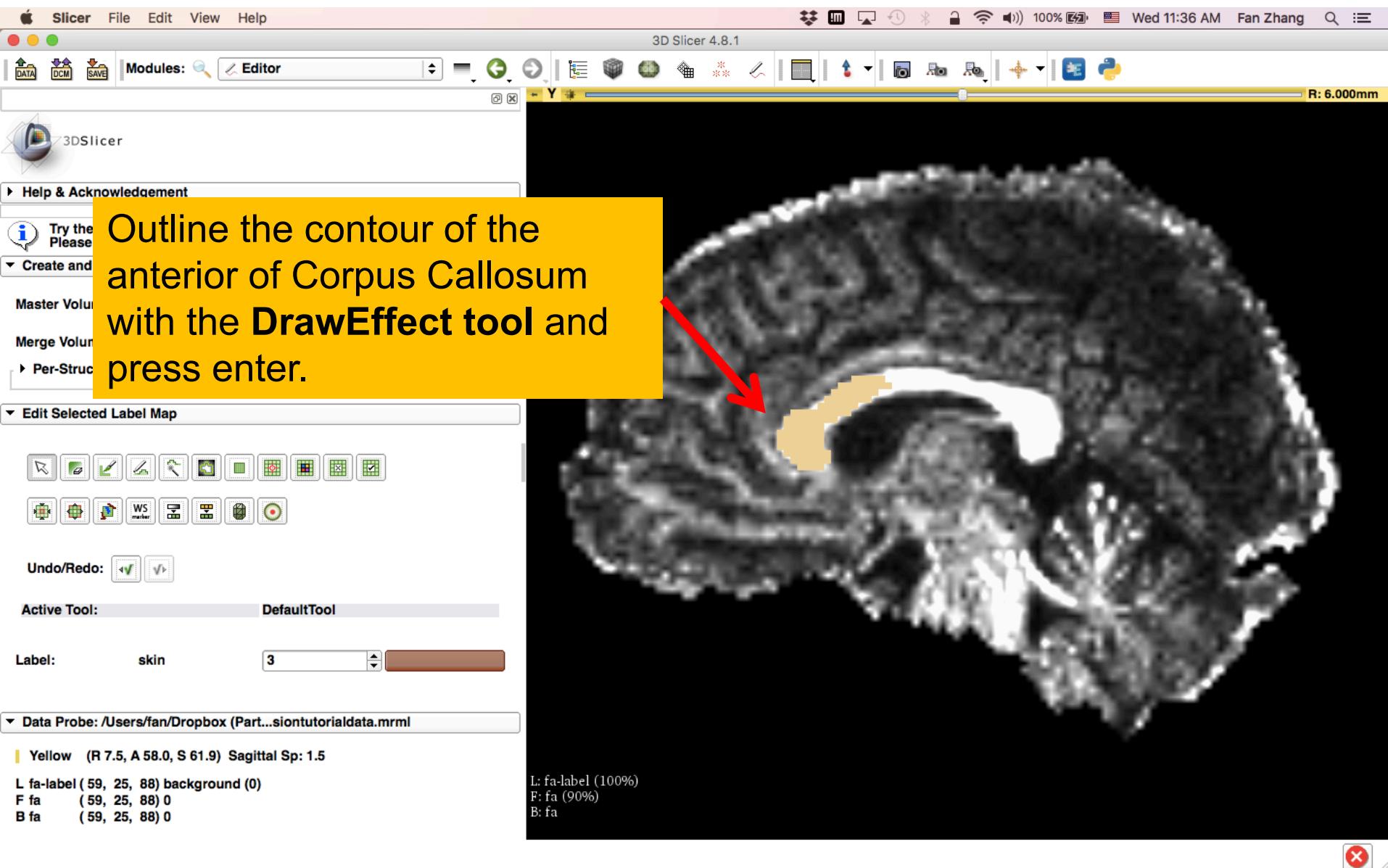
Edit Multiple Labels



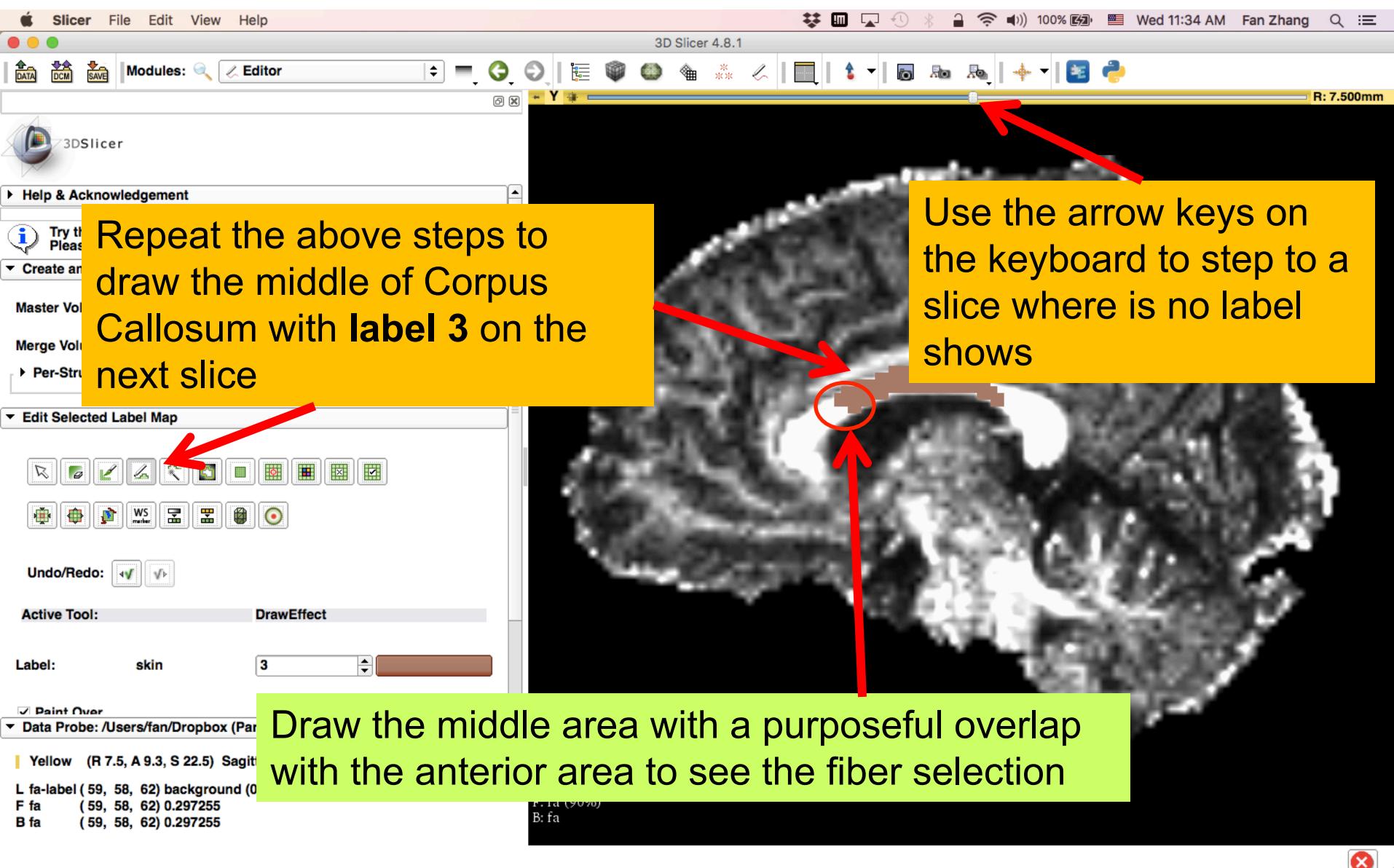
Edit Multiple Labels



Edit Multiple Labels



Edit Multiple Labels



Edit Multiple Labels

The screenshot shows the 3D Slicer interface version 4.8.1. On the left, there's a panel titled "Edit Selected Label Map" with various segmentation tools like "Paint Over" and "Data Probe". The main window displays a grayscale brain scan with blue regions representing segmented areas. A red arrow points to the top right of the screen, indicating the keyboard arrow keys for navigating slices.

Repeat the above steps to draw the posterior of Corpus Callosum with **label 4** on the next slice

Use the arrow keys on the keyboard to step to a slice where no label shows

Draw the posterior area with a purposeful overlap with the middle area to see the fiber selection

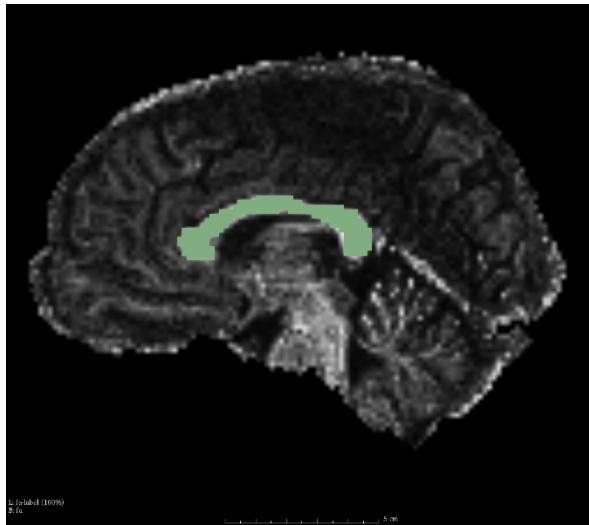
Labels:

- Yellow (R 9.0, P 6.3, I 5.1) Sagittal Sp: 1.5
- L fa-label (58, 68, 44) background (0)
- F fa (58, 68, 44) 0.243663
- B fa (58, 68, 44) 0.243663

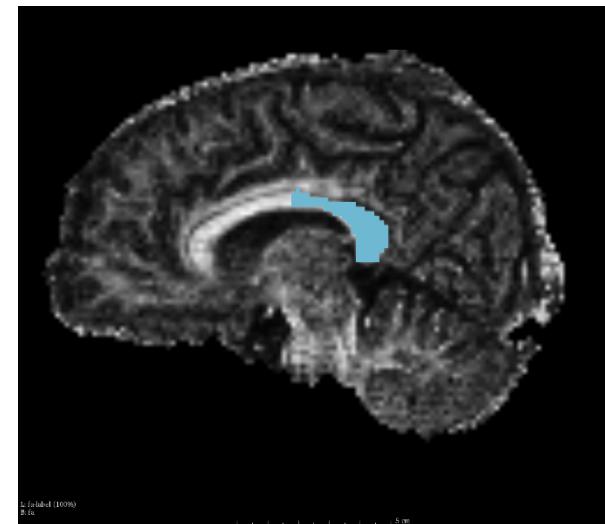
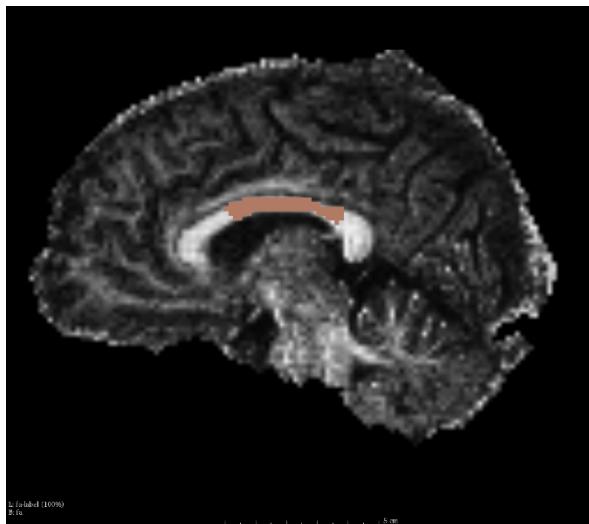
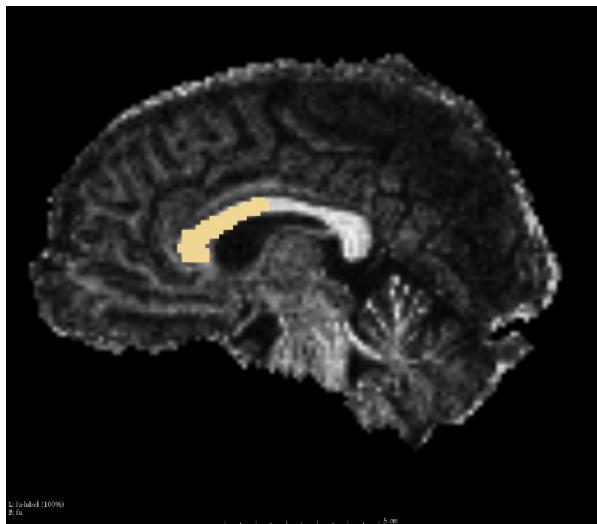
Edit Multiple Labels

Label map on individual slice, with :

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

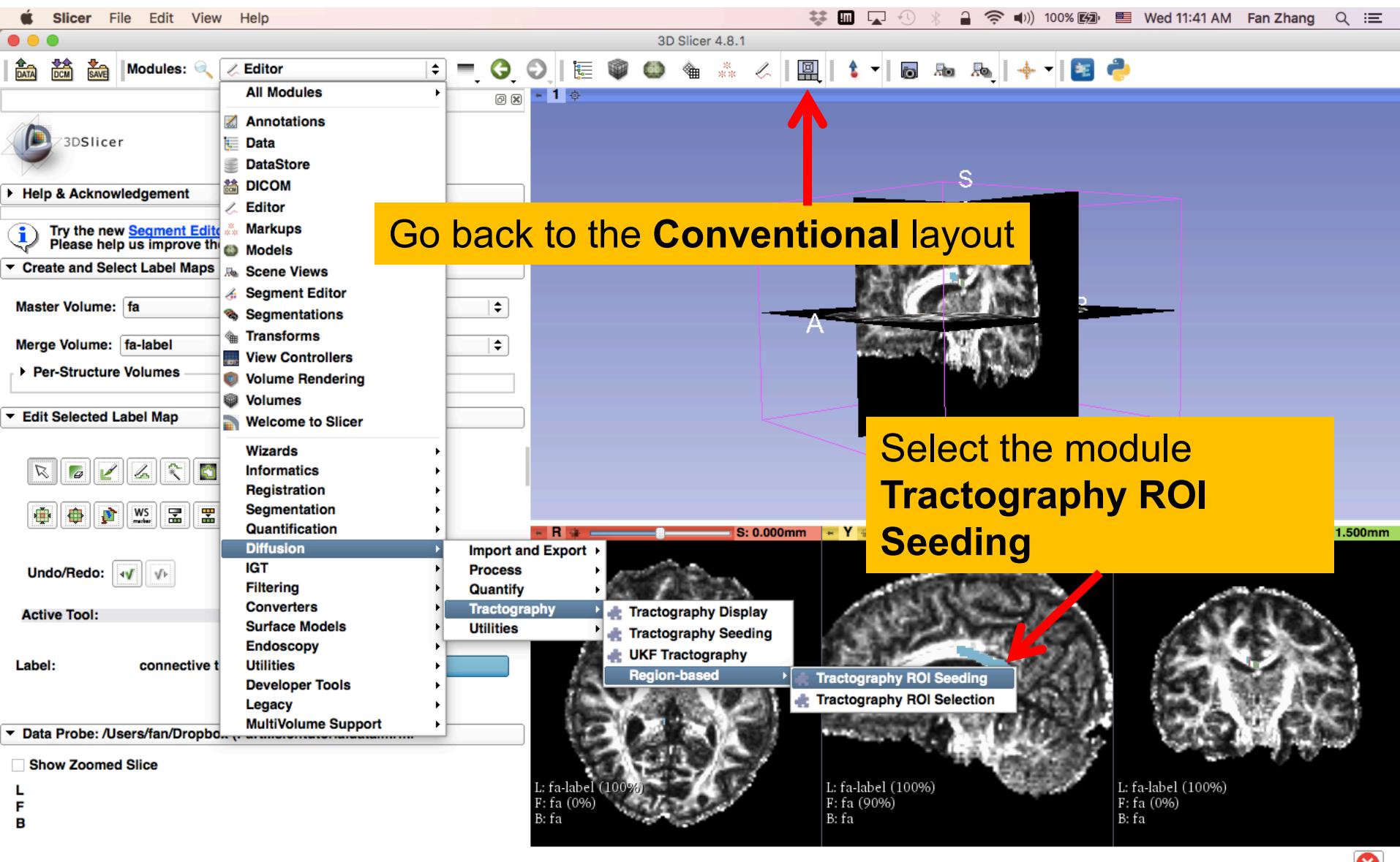


Notice that there are overlaps between different labeled regions*, which will be used to investigate the fiber bundle selection.



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

Whole Brain Tractography



Whole Brain Tractography

Slicer File Edit View Help

3D Slicer 4.8.1

DATA DCM SAVE Modules: Tractography ROI Seeding

3DSlicer

Help & Acknowledgement

Tractography ROI Seeding

Parameter set: Tractography ROI Seeding

IO

Input DTI Volume: dti
Input Label Map: dwi_mask
Output Fiber Bundle: whole_brain_tractography

Seeding Options

Start Threshold: 0.15

Tractography Seeding Parameters

Minimum Length: 20.00
Maximum Length: 800.00

Stopping Criteria

LinearMeasure
 FractionalAnisotropy

Stopping Value: 0.25

Stopping Track Curvature: 0.7

Integration Step Length(mm): 0.5

Label definition

Seeding label: 1

Advanced

Status: Idle

Cancel Apply

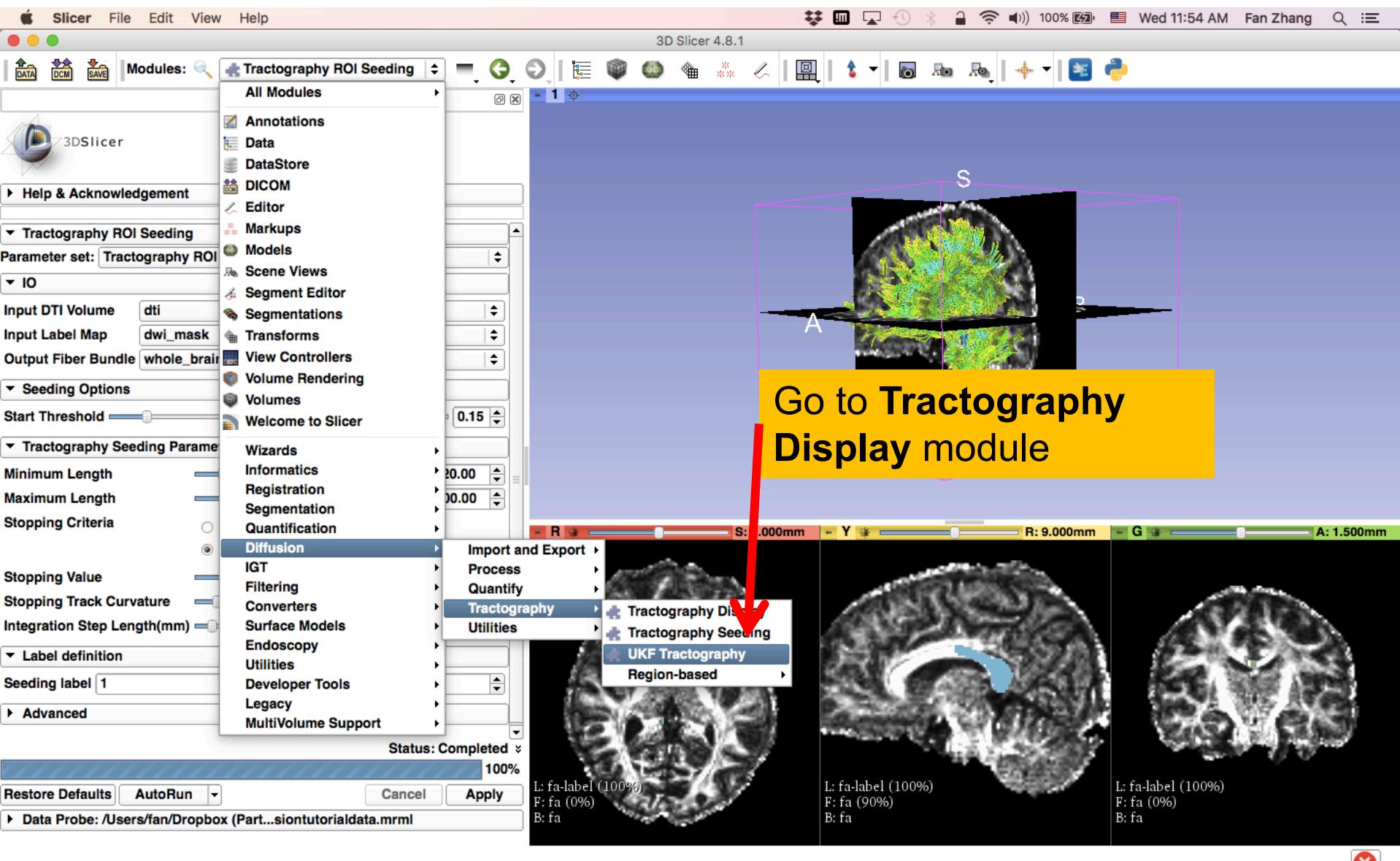
Data Probe: /Users/fan/Dropbox (Part...siontutorialdata.mrml)

Select the Tractography Seeding parameters:

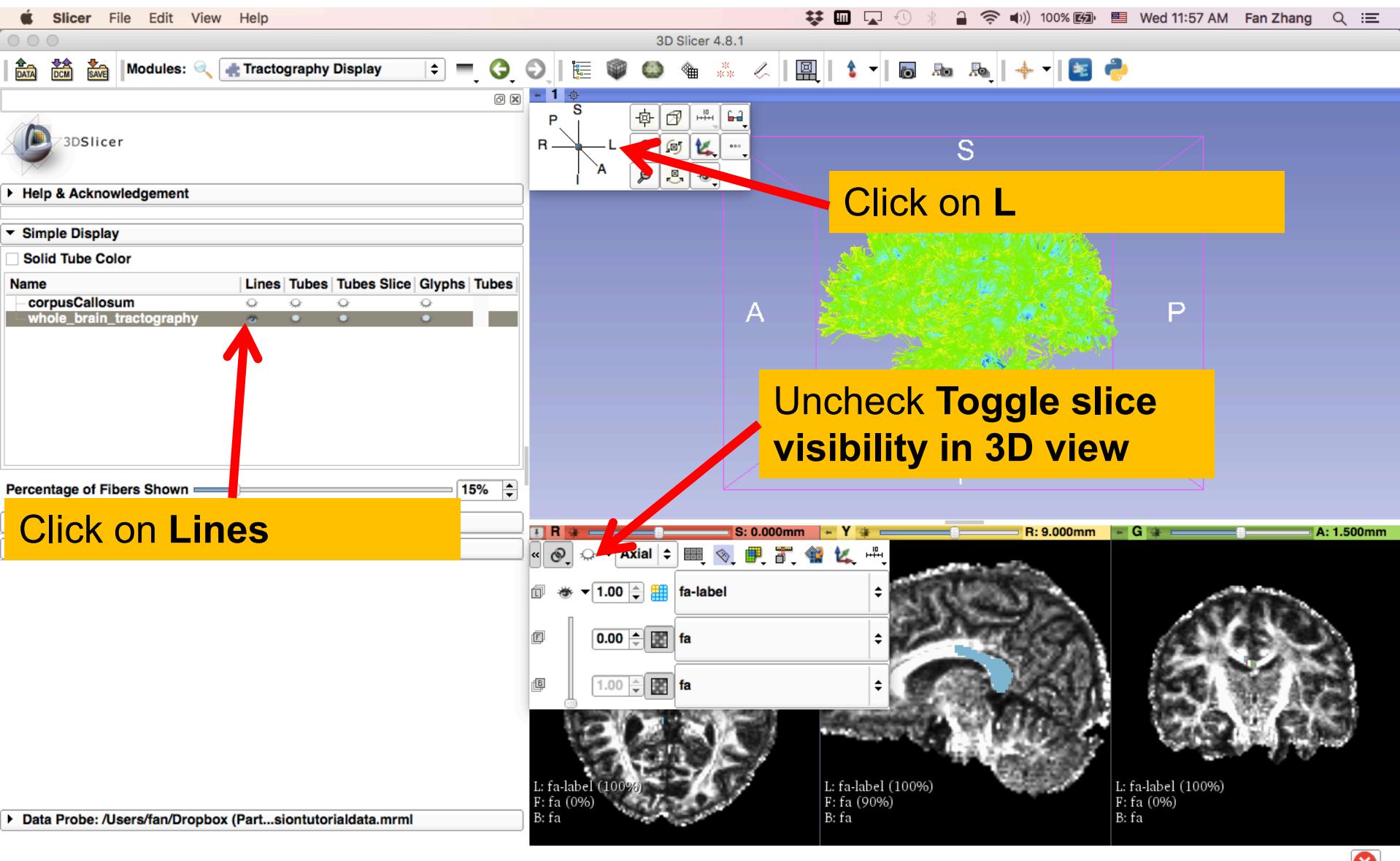
- Input DTI volume: **dti**
- Input Label Map: **dwi_mask**
- Click Output Fiber Bundle and Create new FiberBundle as:
whole_brain_tractography
- Stopping Criteria: **FractionalAnisotropy**
- Stopping Value: **0.15**
- Seeding label: **1**

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

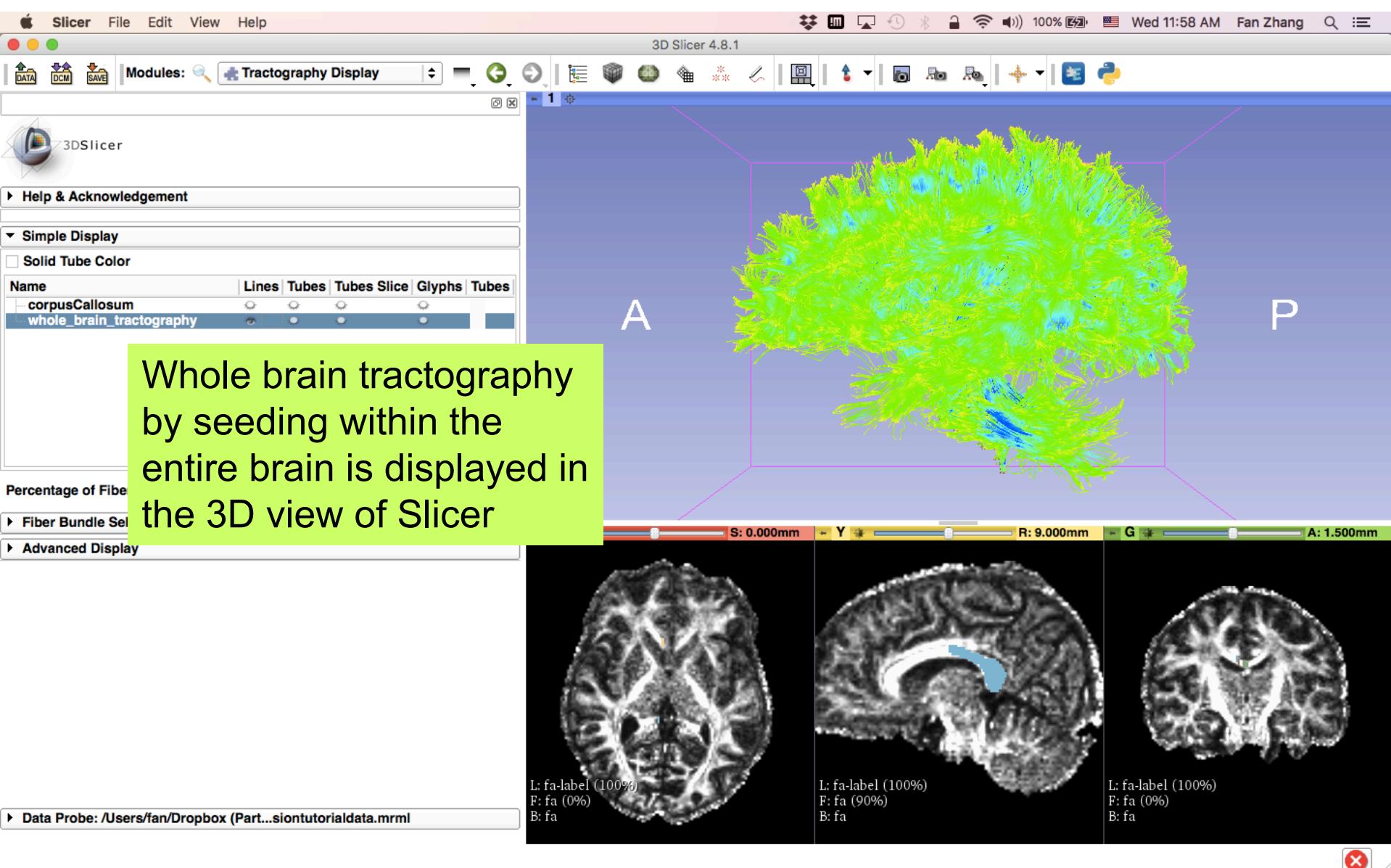
Whole Brain Tractography



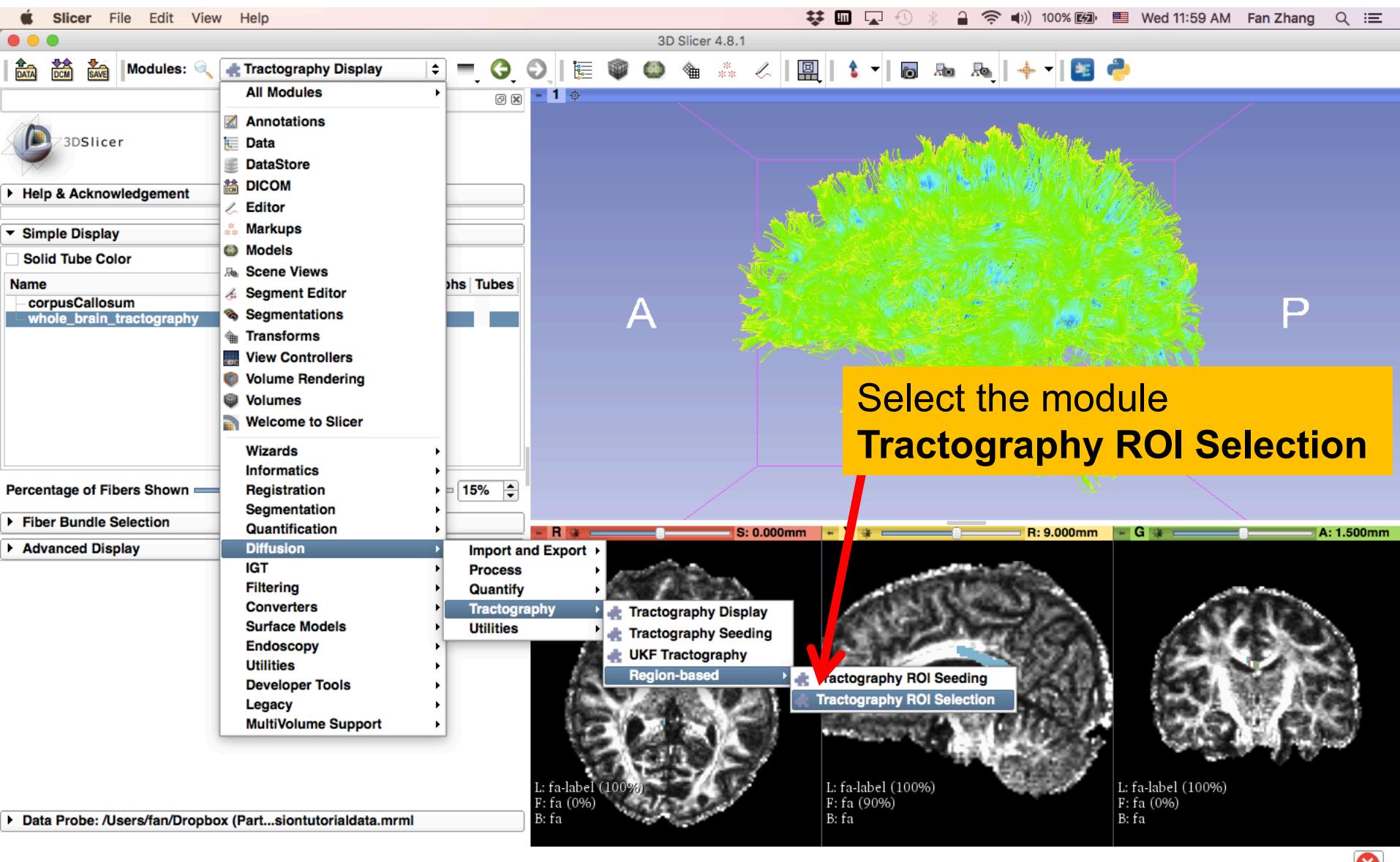
Whole Brain Tractography



Whole Brain Tractography



Tractography ROI Selection



Single Label Selection

Slicer File Edit View Help

3D Slicer 4.8.1

DATA DCM SAVE Modules: Tractography ROI Selection

3DSlicer

Help & Acknowledgement

Tractography ROI Selection

Parameter set: Tractography ROI Selection

IO

Selection Region Label Map fa-label

Input Fiber Bundle whole_brain_tractography

Output Fiber Bundle bundle_label1_include

Tract selection region labels

Inclusion labels (comma-separated) 1

Inclusion label combination logic OR AND

Exclusion label combination logic OR AND

Advanced Settings

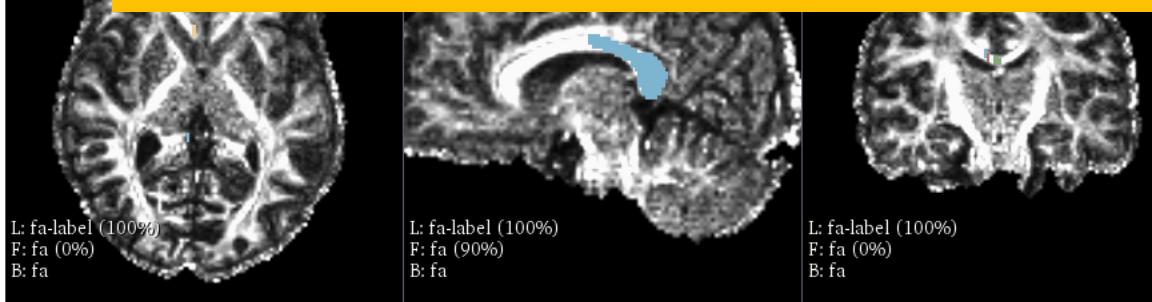
Click the button **Apply**

Restore Defaults AutoRun Cancel Apply

Data Probe: /Users/fan/Dropbox (Part...siontutorialdata.mrml)

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**

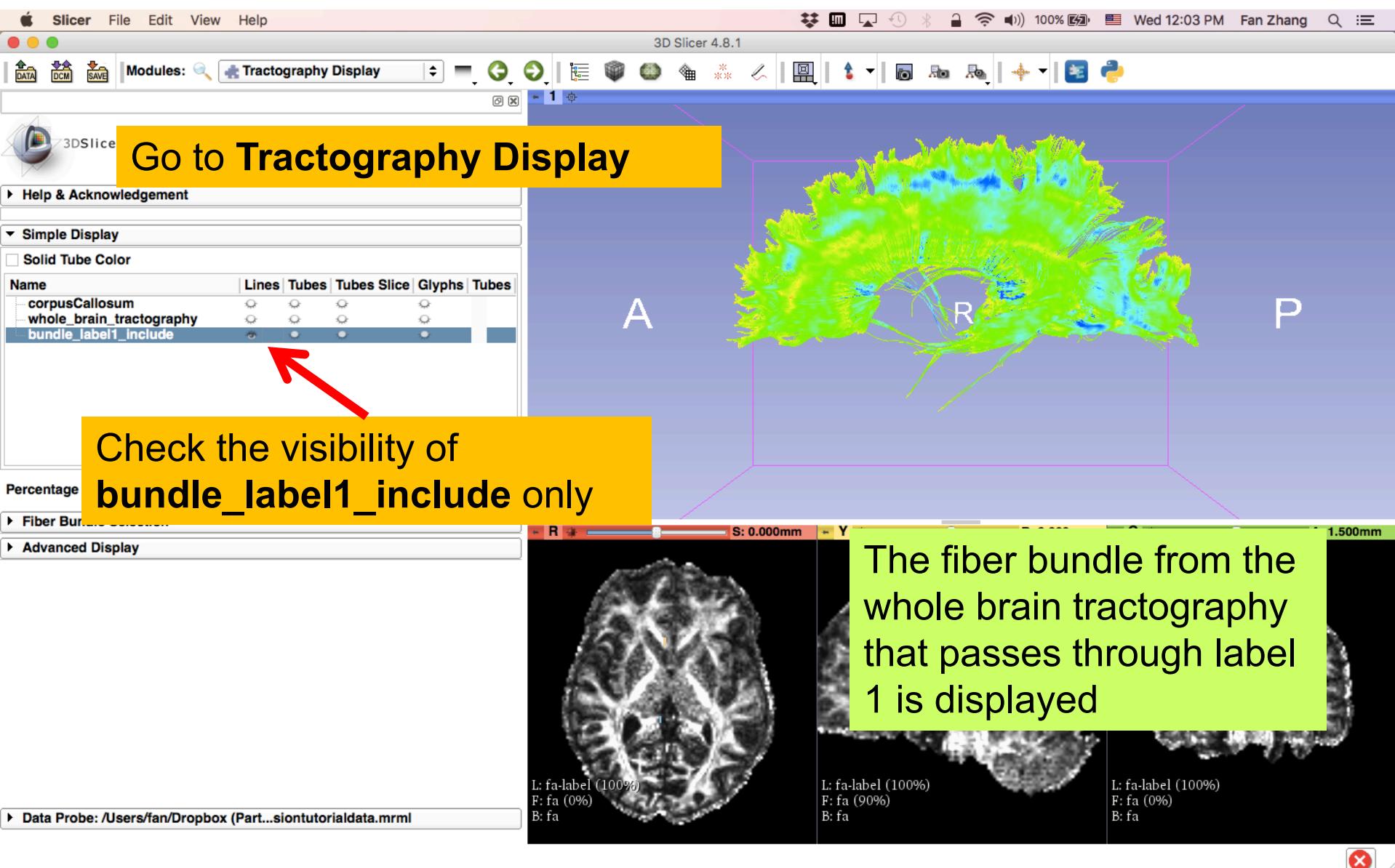


L: fa-label (100%)
F: fa (0%)
B: fa

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

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

Single Label Selection



Single Label Selection

Slicer File Edit View Help

3D Slicer 4.8.1

DATA DCM SAVE Modules: Tractography ROI Selection

3DSlicer

Help & Acknowledgement

Tractography ROI Selection

Parameter set: Tractography ROI Selection

IO

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)

Advanced Settings

Status: Scheduled

Restore Defaults AutoRun Cancel Apply

Data Probe: /Users/fan/Dropbox (Part...siontutorialdata.mrml)

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

P

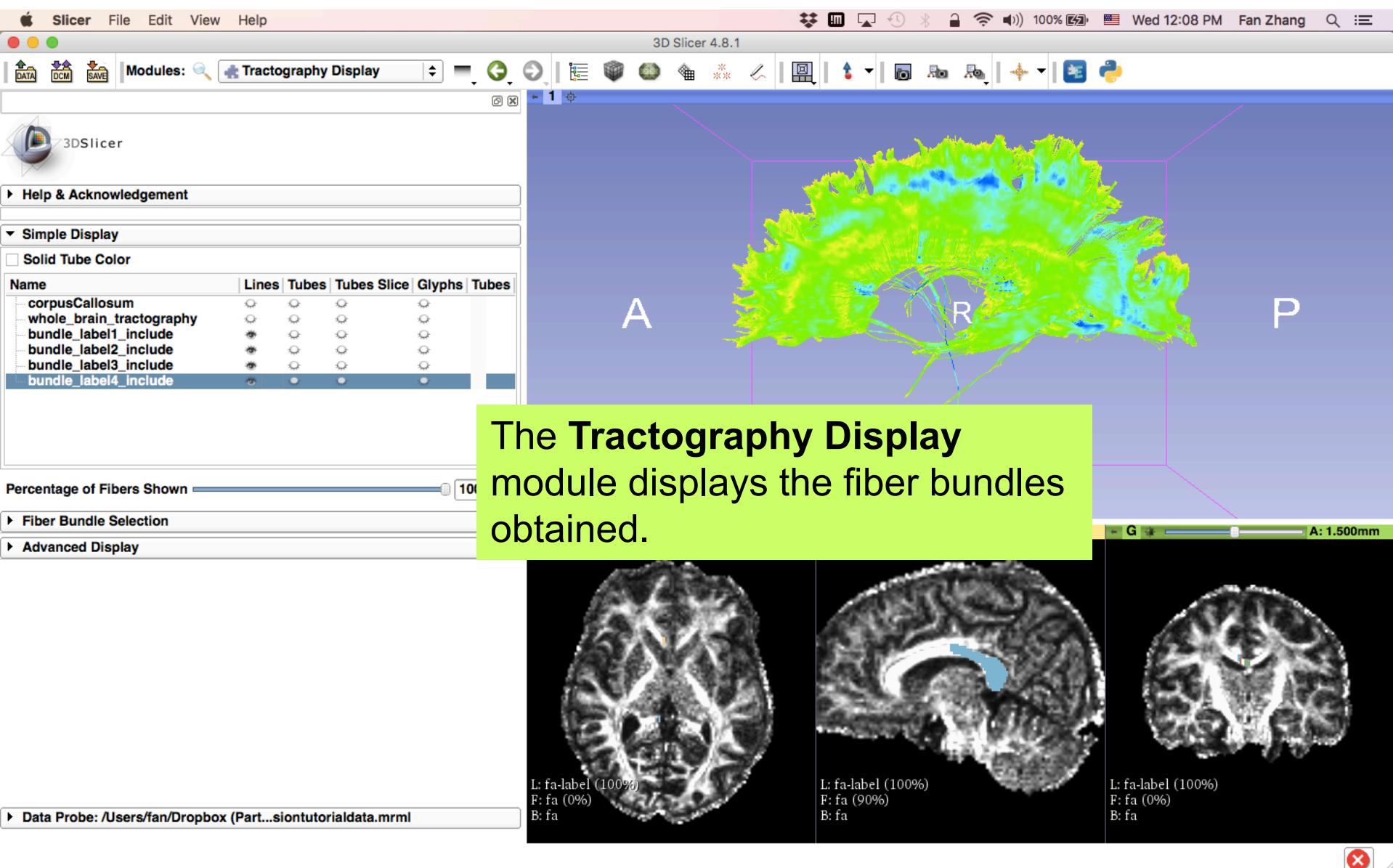
A: 1.500mm

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

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

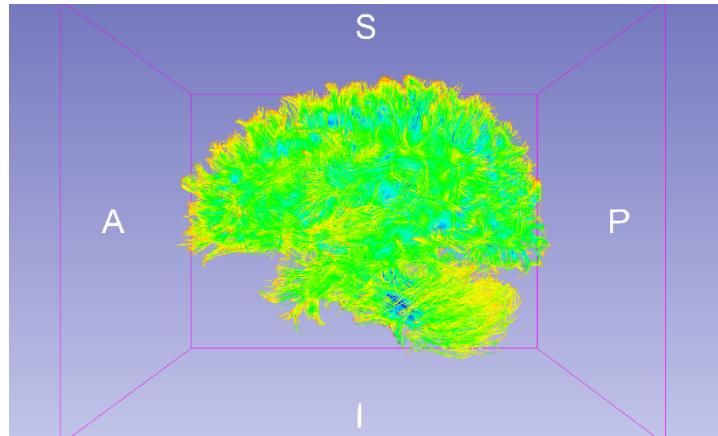
L: fa-label (100%)
F: fa (0%)
B: fa

Single Label Selection

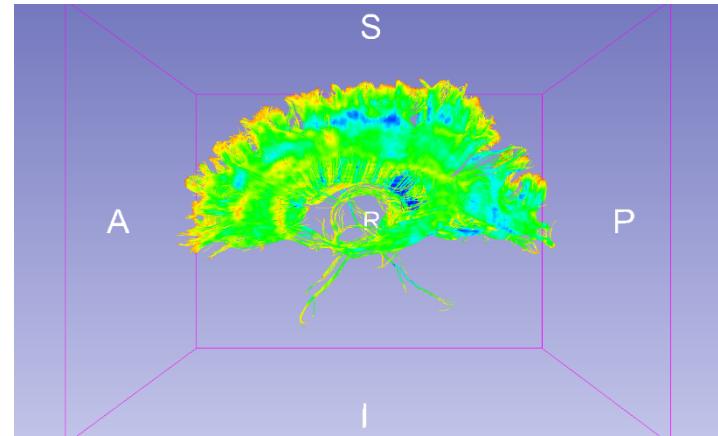


Single Label Selection

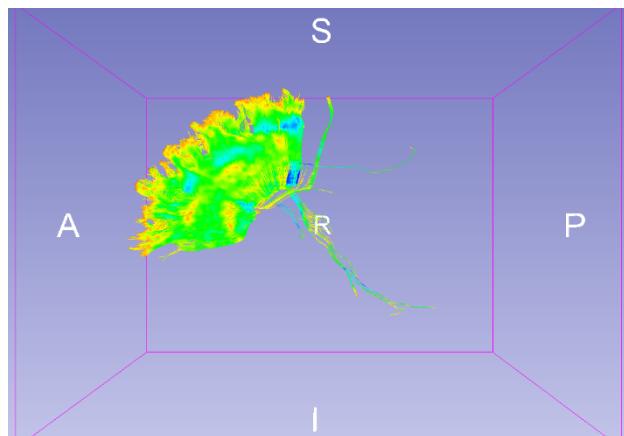
Whole Brain



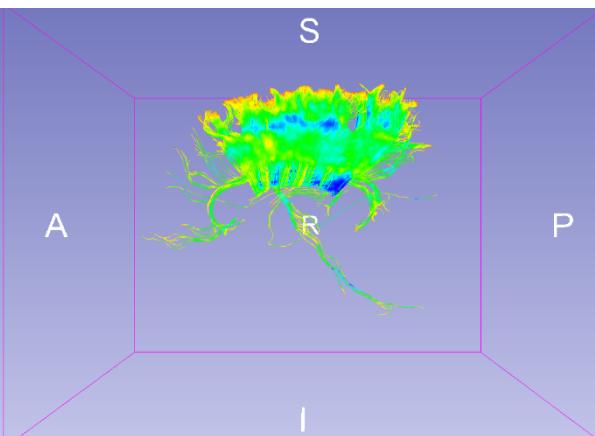
Label 1



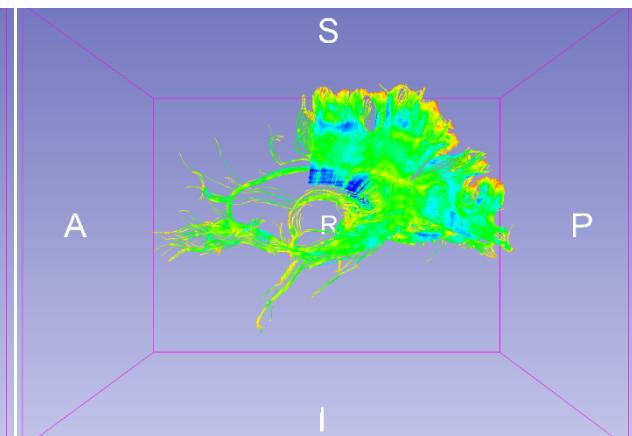
Label 2



Label 3



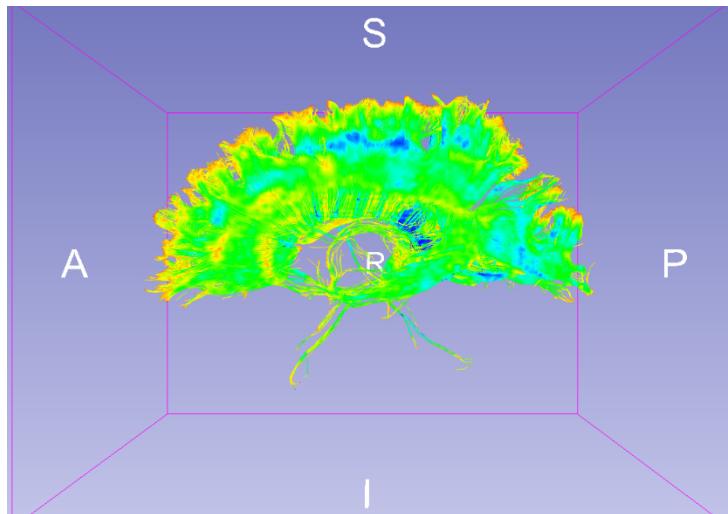
Label 4



Single Label Selection

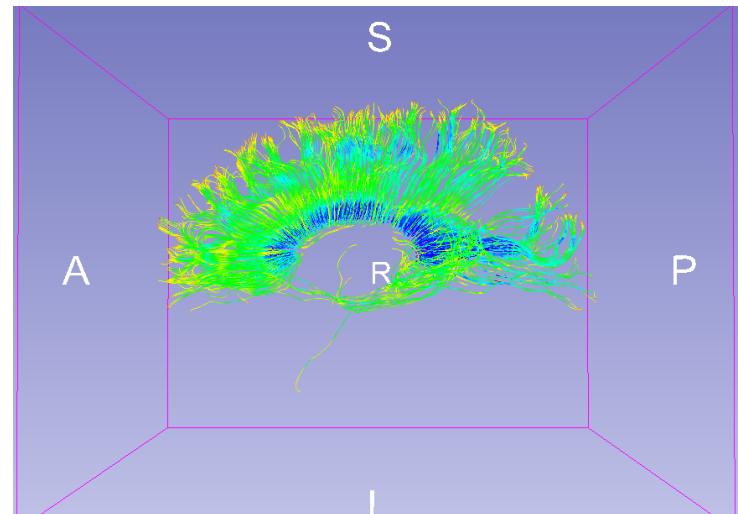
Notice that whole brain seeding creates a denser fiber bundle than seeding from the label 1.

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)

Slicer File Edit View Help

3D Slicer 4.8.1

DATA DCM SAVE Modules: Tractography ROI Selection

3DSlicer

Help & Acknowledgement

Tractography ROI Selection

Parameter set: Tractography ROI Selection

IO

Selection Region Label Map fa-label

Input Fiber Bundle whole_brain_tractography

Output Fiber Bundle bundle_labels2AND3_include

Tract selection region labels

Inclusion labels (comma-separated) 2,3

Inclusion label combination logic OR AND

Exclusion labels (comma-separated)

Exclusion label combination logic OR AND

Advanced Settings

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

Data Probe: /Users/fan/Dropbox (Part...siontutorialdata.mrml)

Set Combine include labels to 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

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

Multiple Labels Selection (AND)

The fiber bundle that passes through both labels 2 and 3 is displayed.

This screenshot shows the 3D Slicer interface version 4.8.1. The main window displays a 3D brain model with a green and yellow fiber bundle tractography. The tractography is labeled with 'A' (Anterior), 'R' (Right), and 'P' (Posterior). The interface includes a toolbar at the top, a 3D Slicer logo, and a status bar showing '100%' battery, 'Wed 12:12 PM', and 'Fan Zhang'. On the left, the 'Tractography Display' module is selected in the 'Modules' list. The 'Solid Tube Color' panel lists various fiber bundles with checkboxes for 'Lines', 'Tubes', 'Tubes Slice', 'Glyphs', and 'Tubes'. The checkbox for 'bundle_labels2AND3_include' is checked. A green callout box highlights this selection. Below the list is a slider for 'Percentage of Fibers Shown' and sections for 'Fiber Bundle Selection' and 'Advanced Display'. At the bottom, three axial MRI slices show the brain with colored regions indicating label presence: L: fa-label (100%), F: fa (0%), B: fa; L: fa-label (100%), F: fa (90%), B: fa; and L: fa-label (100%), F: fa (0%), B: fa. A data probe path is indicated in the bottom left.

3DSlicer

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_labels2AND3_include	●	●	●	●	●

Percentage of Fibers Shown

Fiber Bundle Selection

Advanced Display

Data Probe: /Users/fan/Dropbox (Part...siontutorialdata.mrml)

3D Slicer 4.8.1

R: 9.000mm G: 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 (0%)
B: fa

Multiple Labels Selection (OR)

The screenshot shows the 3D Slicer 4.8.1 interface. The top menu bar includes Apple, Slicer, File, Edit, View, Help, and a status bar showing 100%, Wed 12:12 PM, Fan Zhang, and a search icon. The toolbar has various icons for data management and analysis. The main window displays a 3D brain volume with a green fiber bundle highlighted. Below the 3D view are three 2D axial slices of the brain. A yellow callout box on the right side of the interface contains the text: "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**". On the left, the "Tractography ROI Selection" module panel is open, showing parameters for "Selection Region Label Map" (fa-label), "Input Fiber Bundle" (whole_brain_tractography), and "Output Fiber Bundle" (bundle_labels2OR3_include). A red box highlights the "Inclusion labels (comma-separated)" field containing "2,3" and the "Inclusion label combination logic" radio button set to "OR". A red arrow points from the text "Set Combine include labels to OR" to the "OR" radio button. Another red arrow points from the text "Click the button Apply" to the "Apply" button at the bottom of the module panel. The status bar at the bottom indicates "Status: Completed" and "100%". The data probe shows "L: fa-label (100%)", "F: fa (0%)", and "B: fa".

3D Slicer 4.8.1

DATA DCM SAVE Modules: Tractography ROI Selection 1

Help & Acknowledgement

Tractography ROI Selection Parameter set: Tractography ROI Selection

Selection Region Label Map fa-label

Inclusion labels (comma-separated) 2,3

Inclusion label combination logic OR AND

Exclusion labels (comma-separated)

Exclusion label combination logic OR AND

Advanced Settings

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

Data Probe: /Users/fan/Dropbox (Part...siontutorialdata.mrml)

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

Set Combine include labels to OR

Click the button Apply

P

Multiple Labels Selection (OR)

Slicer File Edit View Help

3D Slicer 4.8.1

DATA DCM SAVE Modules: Tractography Display

3DSlicer

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_labels2AND3_include	○	○	○	○	○
bundle_labels2OR3_include	●	●	●	●	●

Percentage of Fibers Shown

Fiber Bundle Selection

Advanced Display

Data Probe: /Users/fan/Dropbox (Part...siontutorialdata.mrml)

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

A R P

This figure displays the 3D Slicer software interface for tractography analysis. The main window shows a 3D reconstruction of a brain with colored fiber tracts. The labels A, R, and P indicate the anterior-posterior, right-left, and dorsal-ventral axes respectively. Below the 3D view are three corresponding axial slices of the brain, each showing a highlighted region of fibers. The slices are labeled with their respective coordinates: R: 9.000mm, G, A: 1.500mm. A callout box contains the text: "The fiber bundle that passes through either labels 2 or 3 is displayed." On the left side of the interface, there is a table titled "Solid Tube Color" which lists various tractography components and their selection status. One row, "bundle_labels2OR3_include", is highlighted with a blue background, indicating it is the selected label for the current visualization. The bottom left corner shows the data probe path: "/Users/fan/Dropbox (Part...siontutorialdata.mrml)".

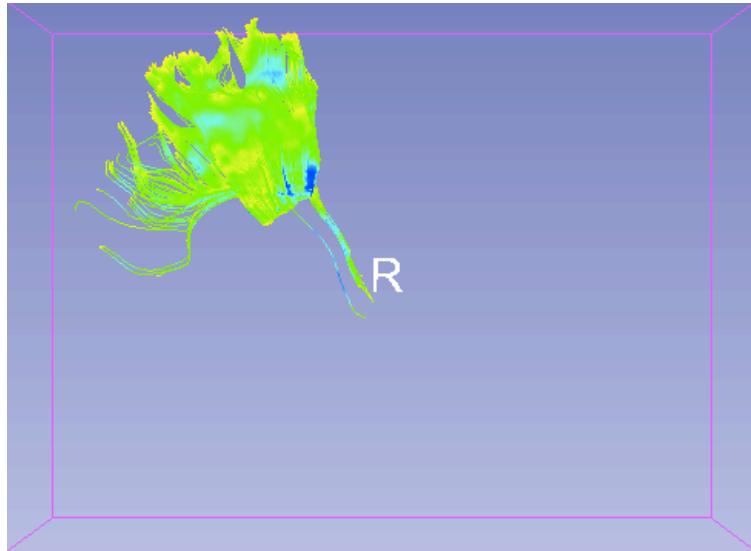
L: fa-label (100%)
F: fa (0%)
B: fa

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

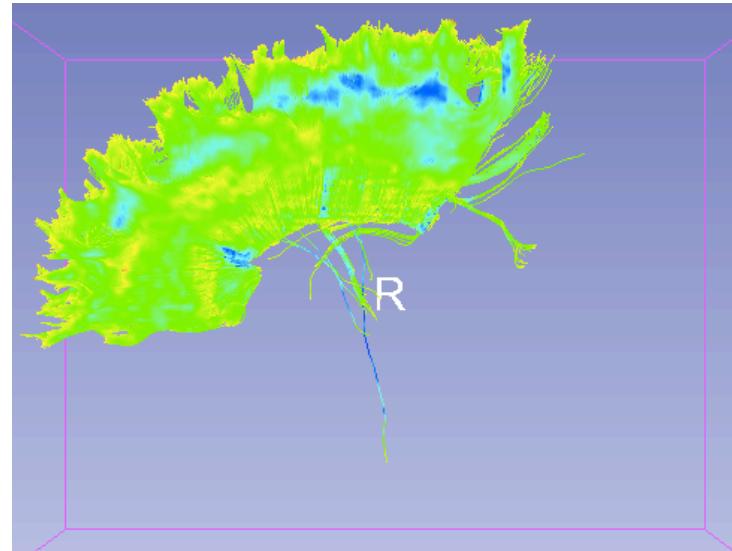
L: fa-label (100%)
F: fa (0%)
B: fa

Multiple Labels Selection

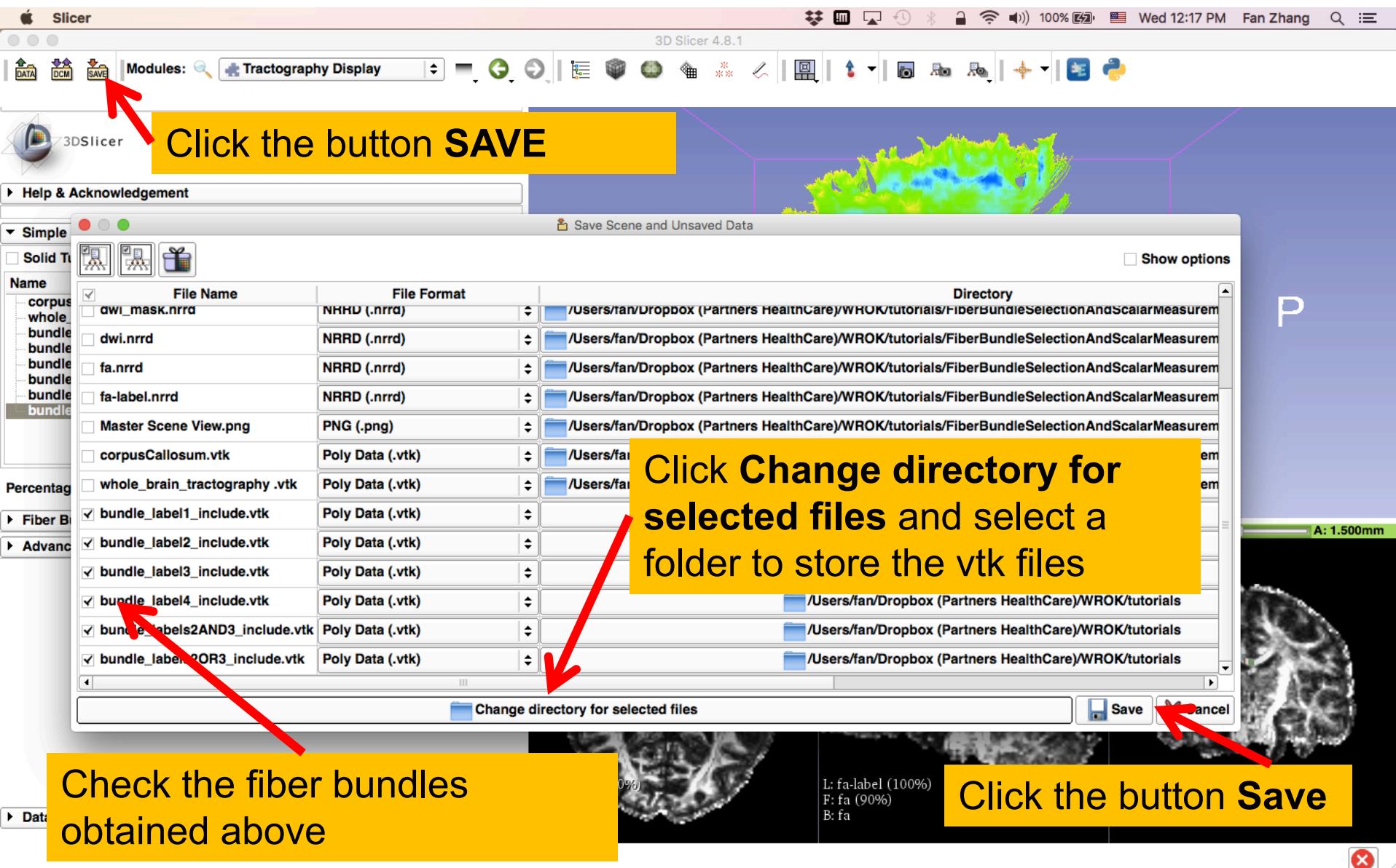
Labels 2 **and** 3



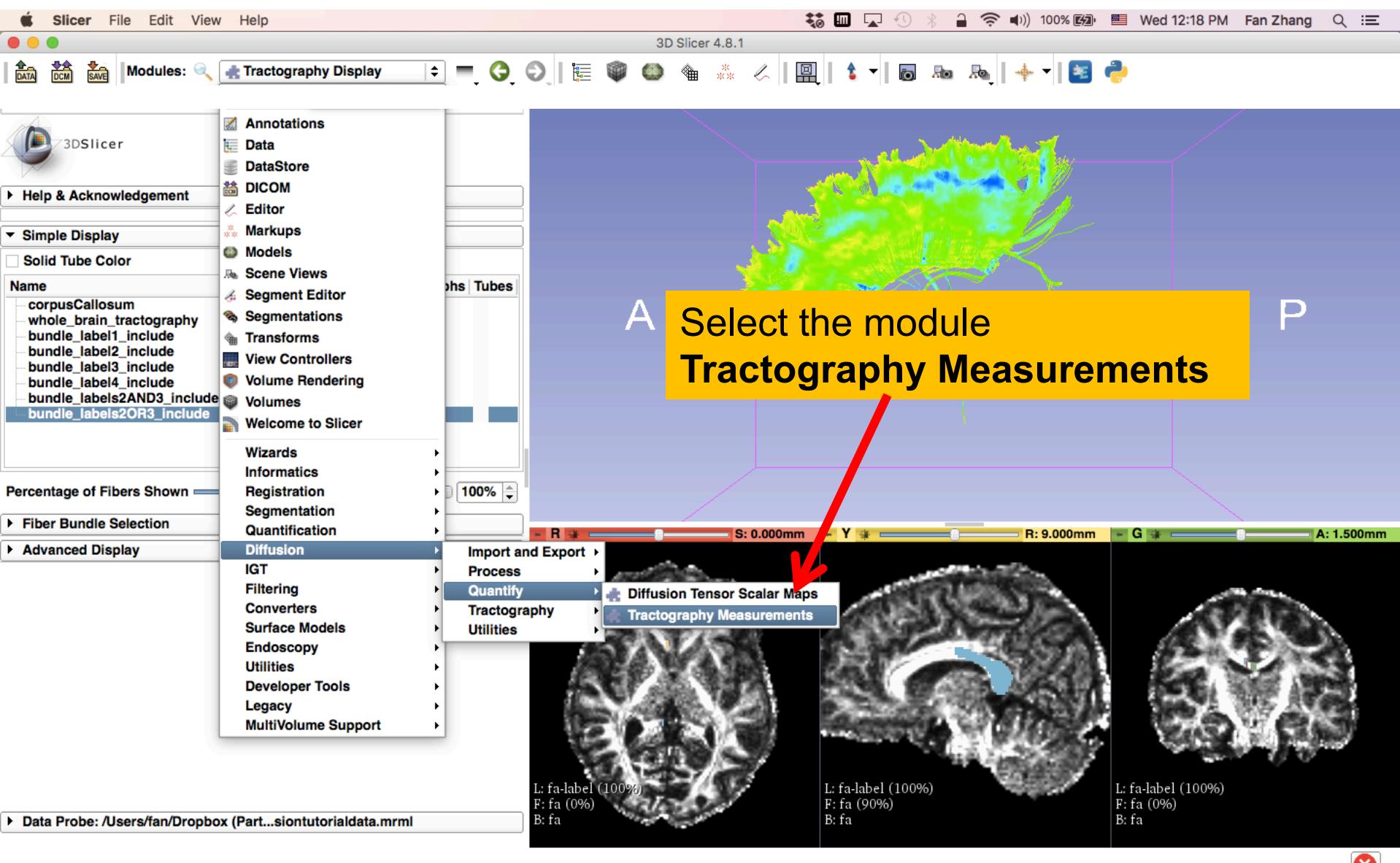
Labels 2 **or** 3



Save Fiber Bundles



Tractography Measurements



Tractography Measurements

Slicer File Edit View Help

3D Slicer 4.9.1

DATA DCM SAVE Modules: Tractography Measurements

Help & Acknowledgement

Tractography Measurements

Parameter set: Tractography Measurements

IO

Select Input Type: Fibers_Hierarchy (radio button) Fibers_File_Folder (radio button) None /Users/fan/Dropbox (Partners HealthCare)/WROK/tutorials x (Partners HealthCare)/WROK/tutorials/measurements.csv Row_Hierarchy (radio button) Column_Hierarchy (radio button) Comma Space Tab

Fibers Hierarchy

Fibers File Folder

Output Text File

Select Output Format

Output Field Separator

Print statistics for all clusters and children.

Advanced Settings

Output more statistics

Click the button **Apply**

Status: Idle

Cancel Apply

Data Probe: /Users/fan/Dropbox (Part...siontutorialdata.mrml)

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**

L: fa..., 0%
F: fa (0%)
B: fa

L: fa..., 0%
F: fa (90%)
B: fa

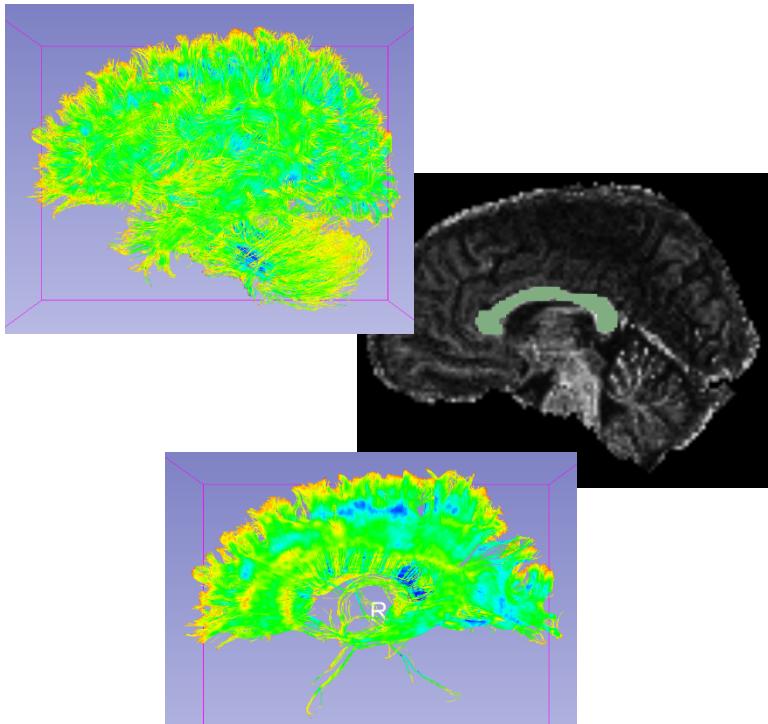
L: fa..., 0%
F: fa (0%)
B: fa

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	Name	B	C	D	E	F	G	H
1		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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