

# Fiber Bundle Selection And Scalar Measurement

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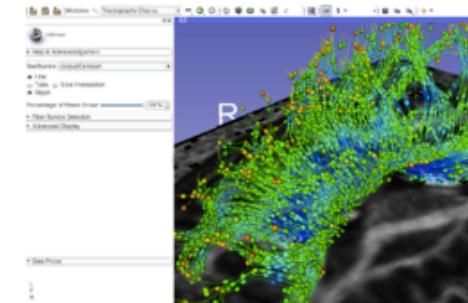
# Pre-requisite

- This tutorial is a follow-up tutorial of the “Diffusion Tensor Imaging Tutorial” by Sonia Pujol, PhD. Please go through this ahead, which is available at:

[https://www.slicer.org/slicerWiki/index.php/Documentation/4.6/Training#Slicer4\\_Diffusion\\_Tensor\\_Imaging\\_Tutorial](https://www.slicer.org/slicerWiki/index.php/Documentation/4.6/Training#Slicer4_Diffusion_Tensor_Imaging_Tutorial)

## Slicer4 Diffusion Tensor Imaging Tutorial

- The [Diffusion Tensor Imaging Tutorial](#) course guides through the basics of loading Diffusion Weighted images in Slicer, estimating tensors and generating fiber tracts.
- Author: Sonia Pujol, Ph.D.
- Audience: End-users and developers
- Modules: Data, Volumes, DWI to DTI Estimation, Diffusion Tensor Scalar Measurements, Editor, Markups, Tractography Label Map Seeding, Tractography Interactive Seeding
- Based on: 3D Slicer version 4.5
- The [DTI dataset](#) contains an MR Diffusion Weighted Imaging scan of the brain.



# Learning Objectives

Following this tutorial, you'll be able to:

- 1) select fiber bundles passing through region(s) of interest, and
- 2) 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

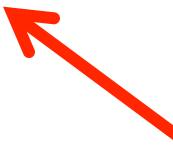
# Tutorial Software

The tutorial uses the 3DSlicer (Version 4.6.2 Stable Release) software available at

<http://download.slicer.org>

Data available at

[http://www.na-mic.org/Wiki/index.php/  
FiberBundleSelectionAndScalarMeasurement\\_TutorialContest  
Winter2016](http://www.na-mic.org/Wiki/index.php/FiberBundleSelectionAndScalarMeasurement_TutorialContest_Winter2016)

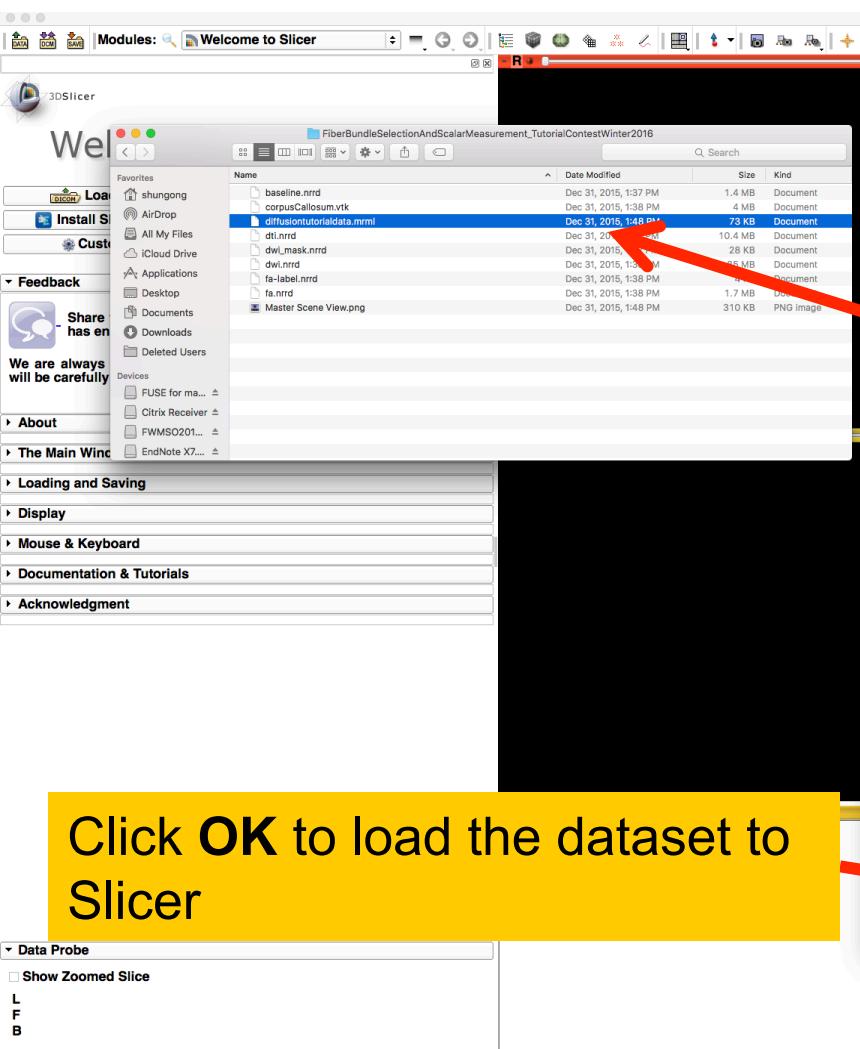


Download sample data

## *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.

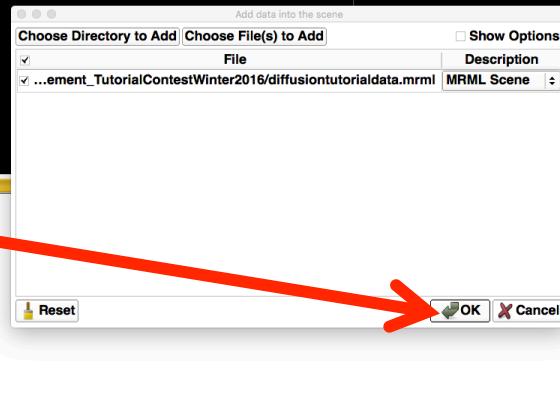
# Load MRML Data



Unzip the sample data

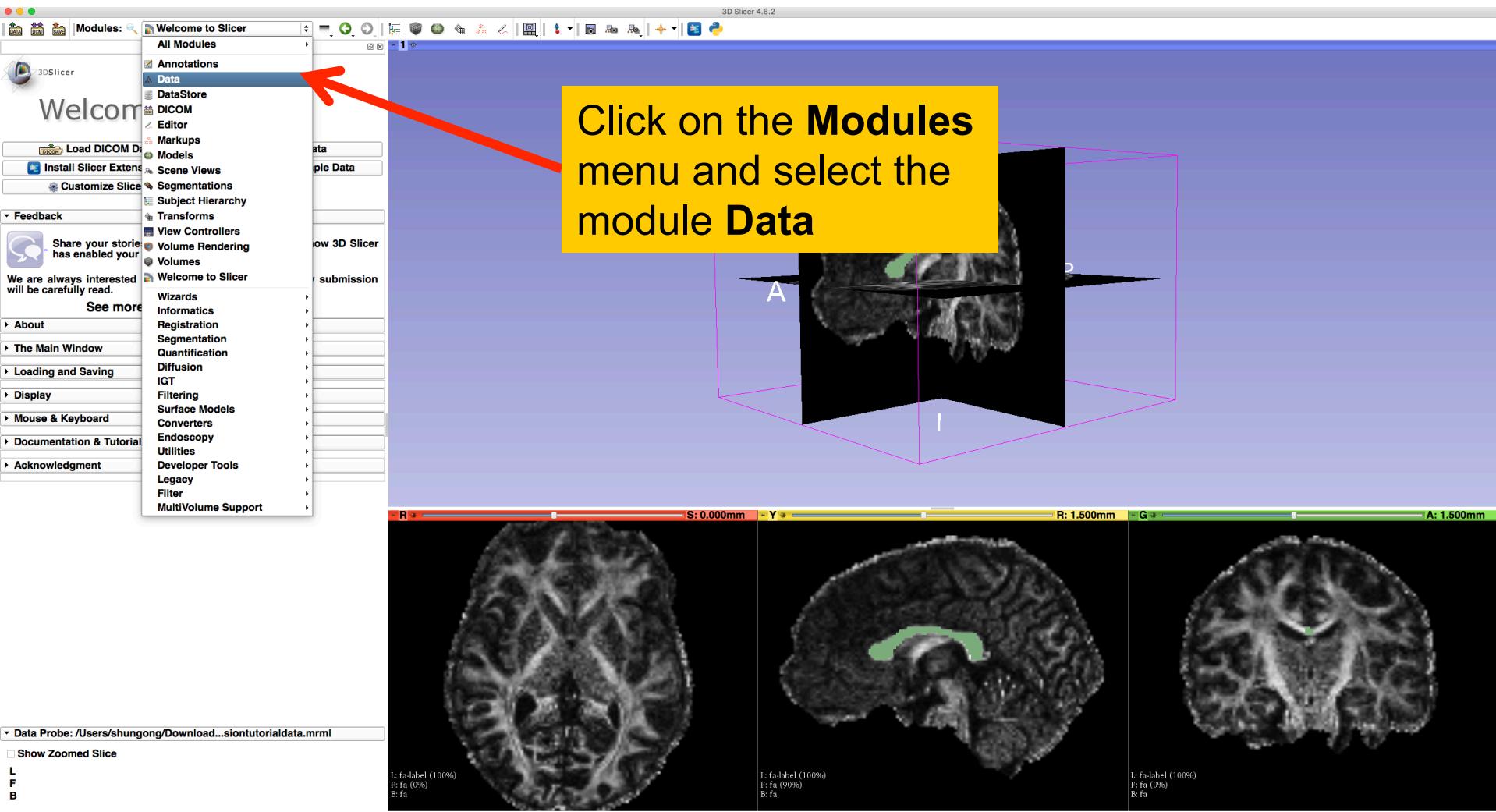
Within the unzipped folder, locate the  
MRML Scene file:  
**diffusiontutorialdata.mrml**

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

3D Slicer 4.6.2

Modules: Data

Help & Acknowledgement

Display & Modify Scene

Nodes

- Scene
- View1
- Red
- Yellow
- Green
- Default Scene Camera
- TableView1
- Default Scene Camera
- baseline
- dwi
- dwi\_mask
- fa
- fa-label
- Master Scene View

Data loaded for this tutorial:

- dwi
- dwi\_mask
- baseline
- dti
- fa
- fa-label
- corpusCallosum

Scene Model: Transform

- Display MRML ID's
- Show Hidden nodes

Filter:

MRML Node Inspector

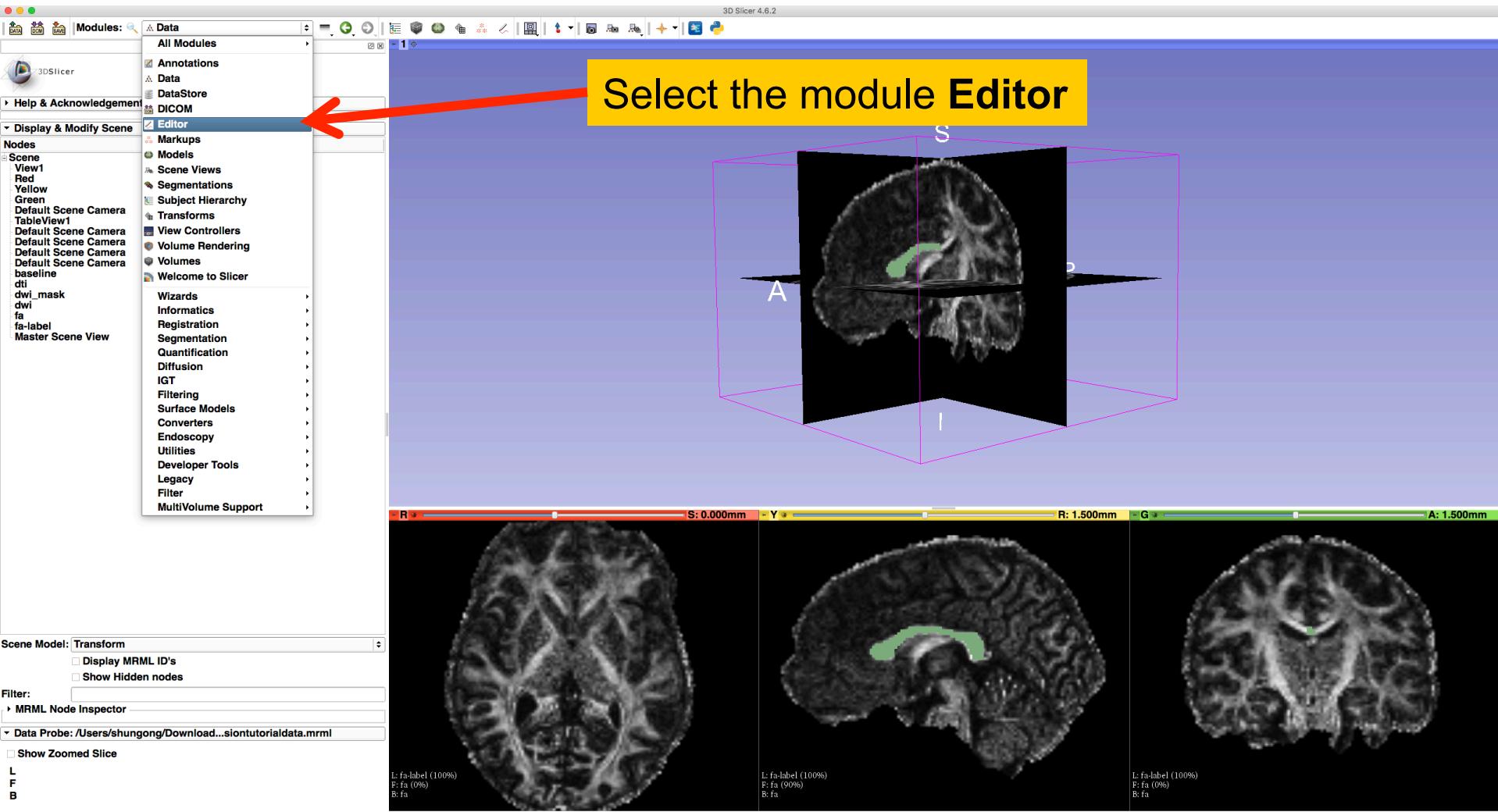
Data Probe: /Users/shungong/Download...siontutorialdata.mrml

Show Zoomed Slice

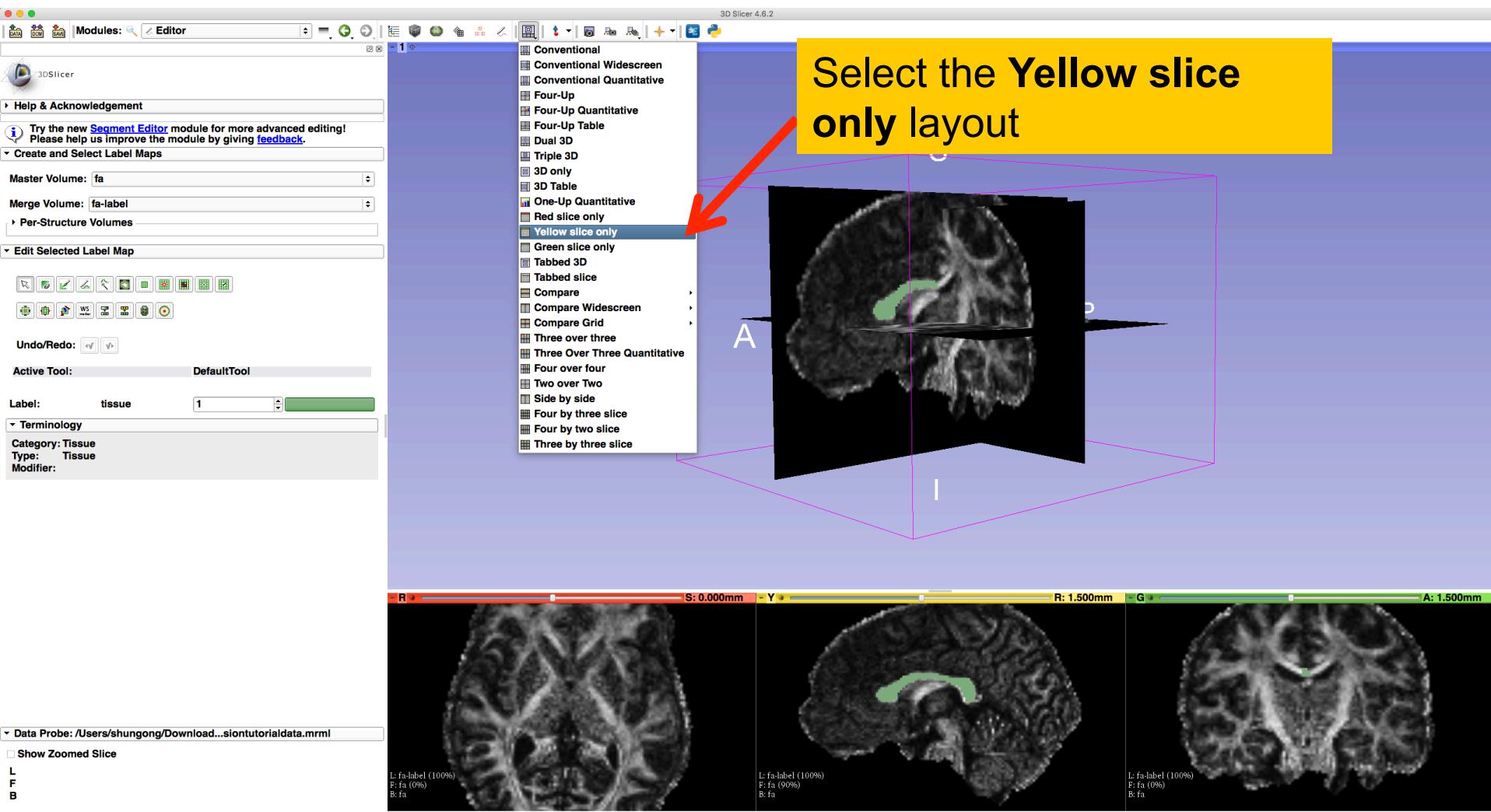
L F B

The image shows the 3D Slicer software interface. On the left, a red box highlights the 'Nodes' panel where several data sets are listed. A large yellow box on the left side of the main window contains a list of loaded data sets. In the center, a 3D brain model is displayed with a green highlighted region representing the 'corpusCallosum'. The brain is shown from a lateral perspective with anatomical axes (Sagittal S, Coronal C, Axial I). Below the 3D view are three 2D axial slices of the brain, each with a green highlighted region. The bottom right corner of the image has a small red '3' indicating there are three more slides.

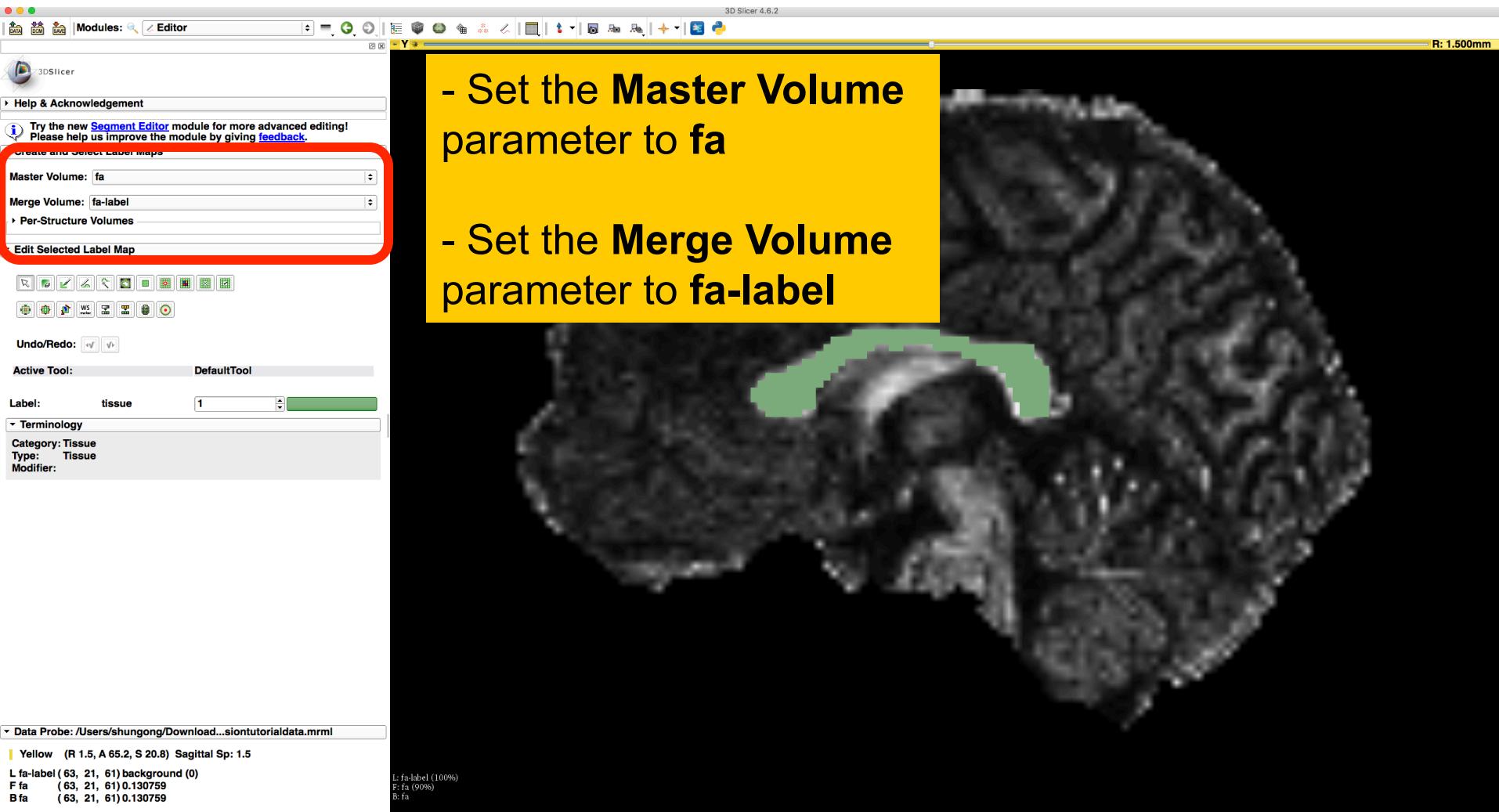
# Edit Multiple Labels



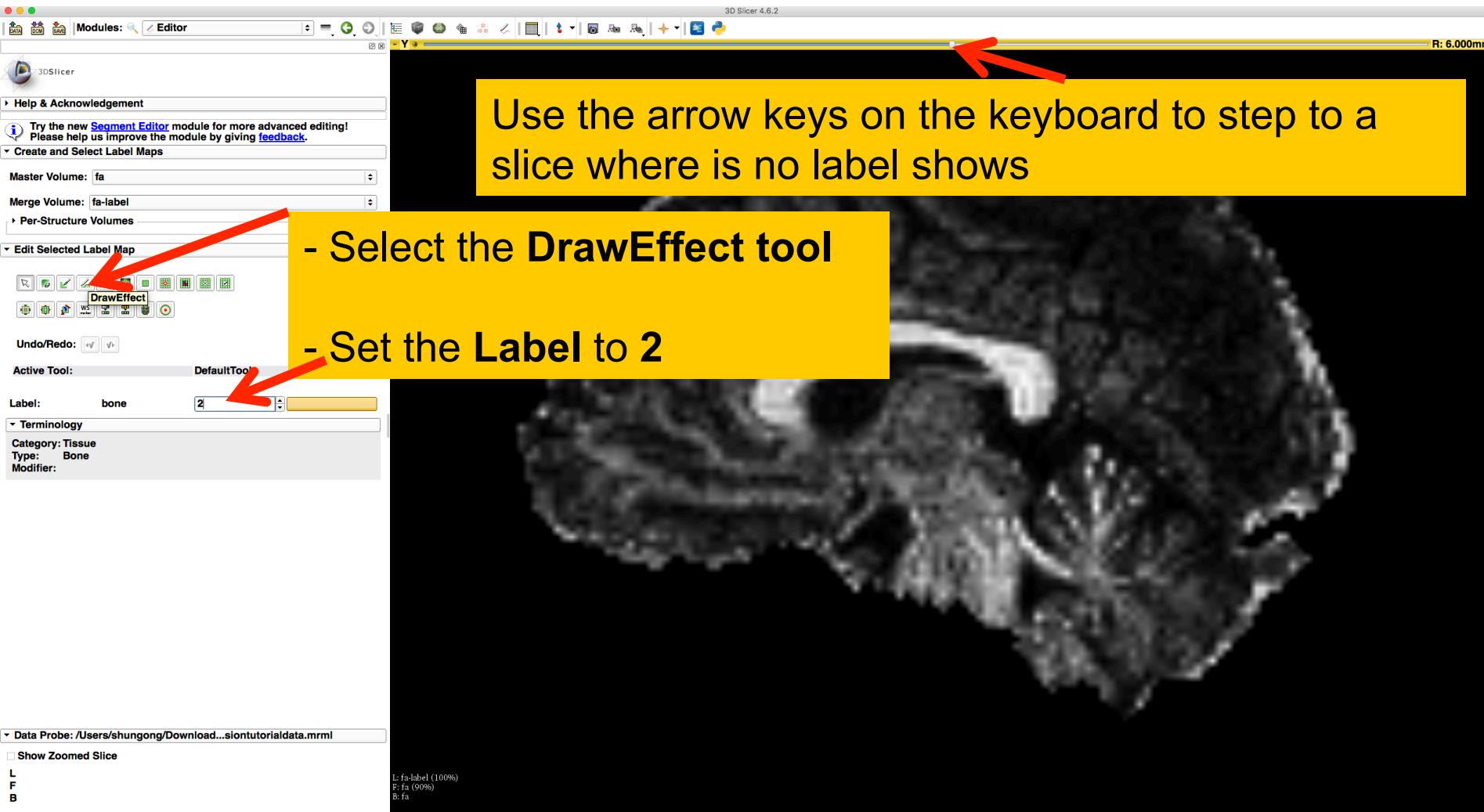
# Edit Multiple Labels



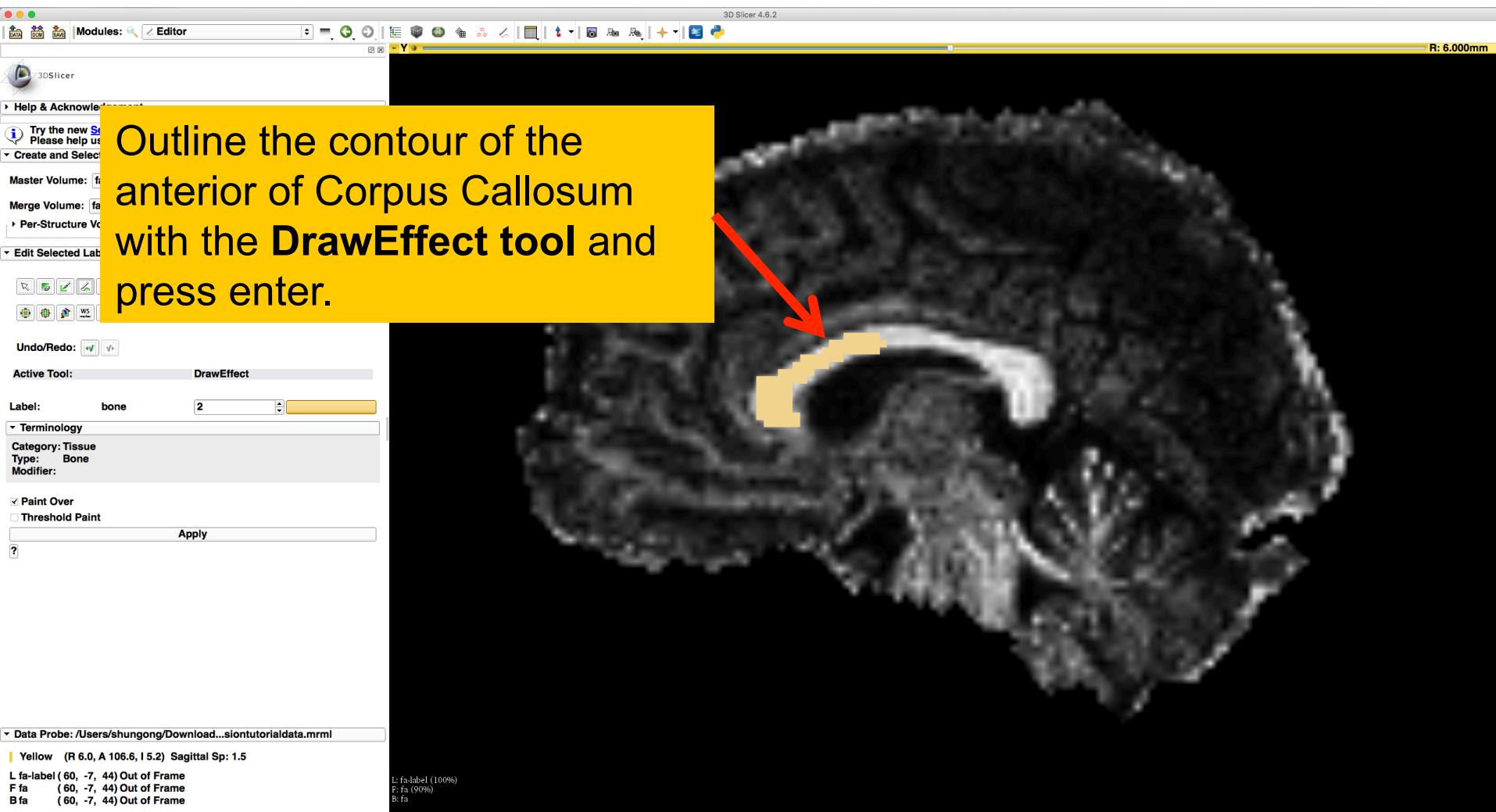
# Edit Multiple Labels



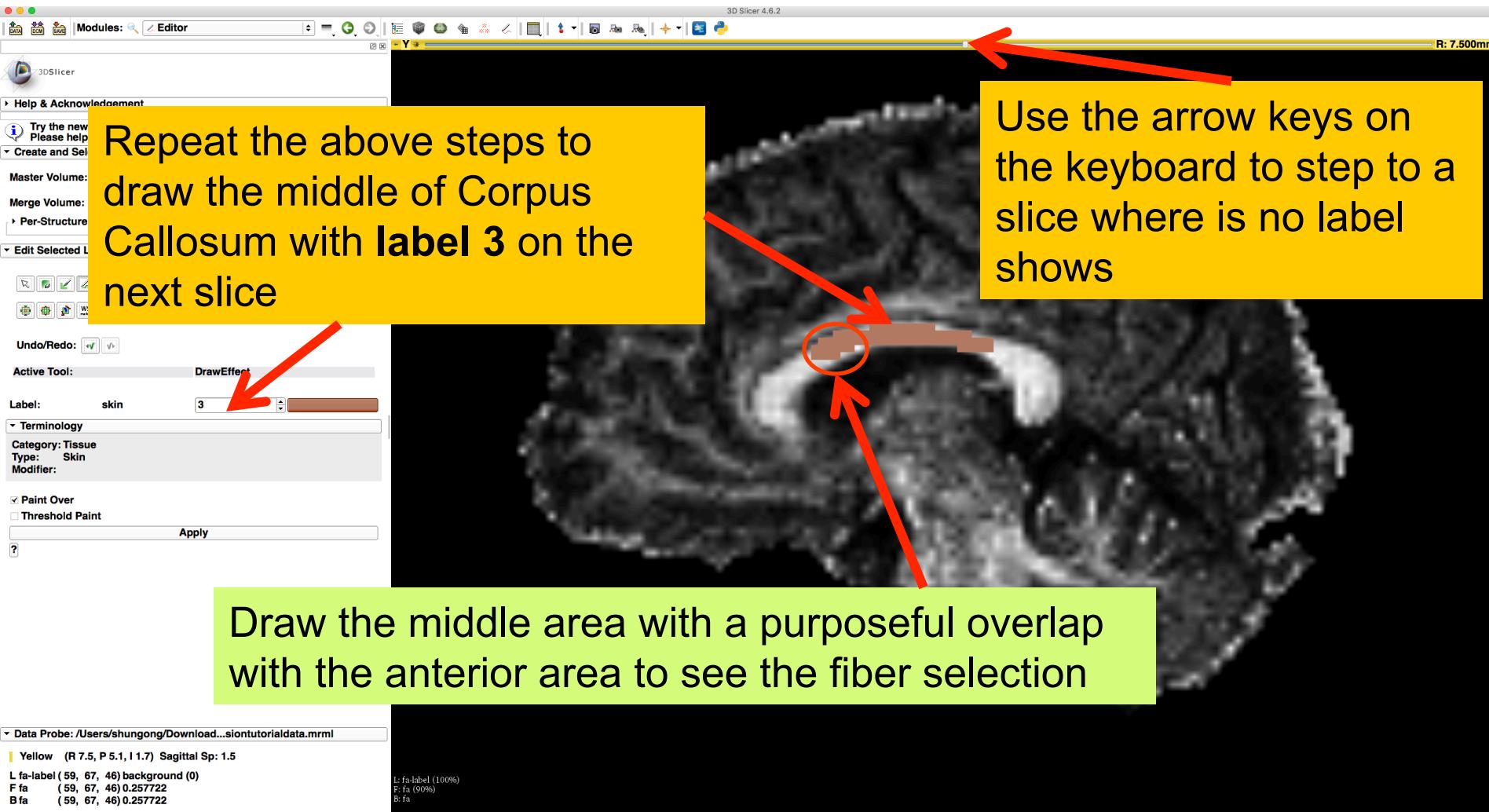
# Edit Multiple Labels



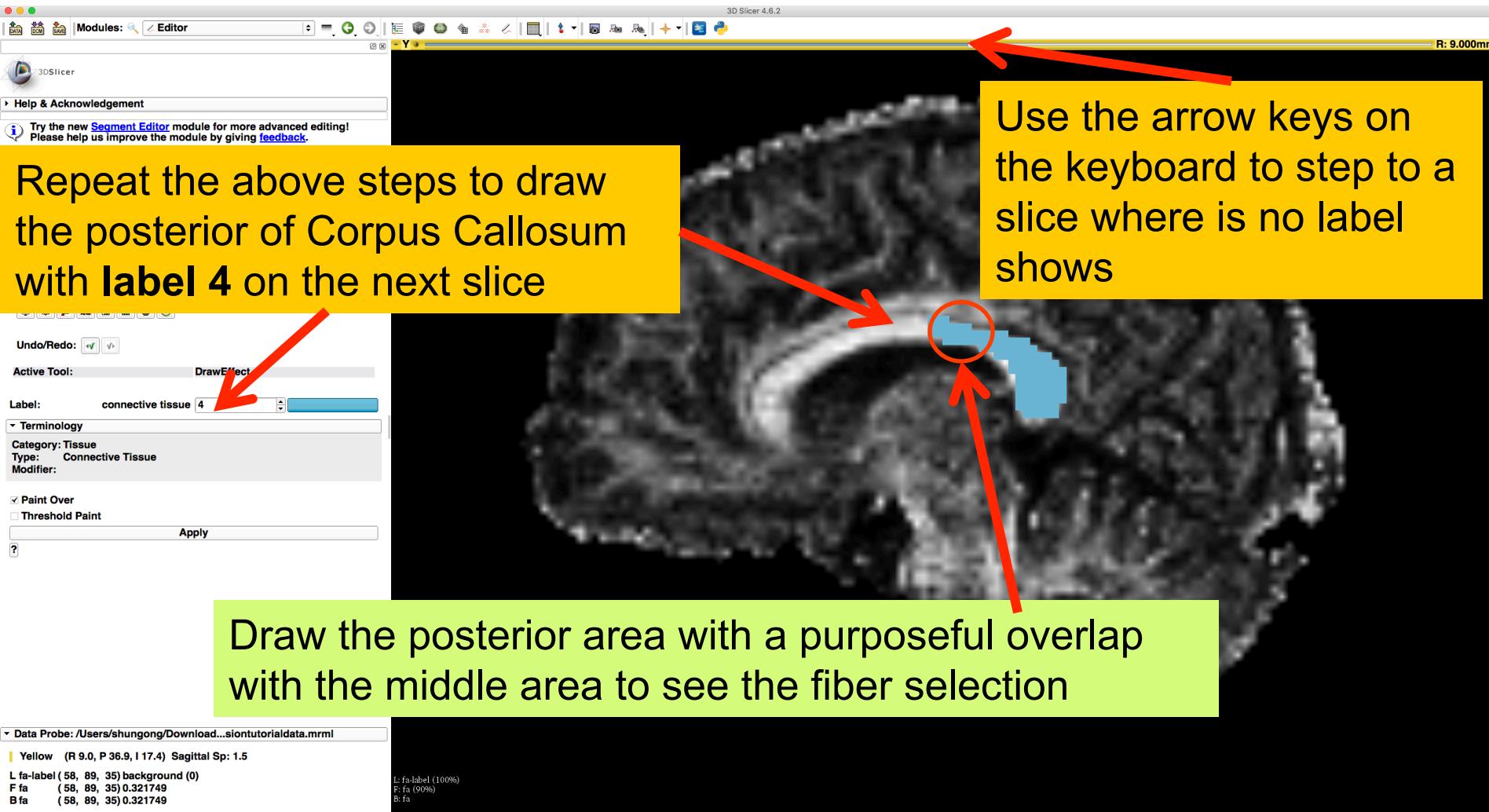
# Edit Multiple Labels



# Edit Multiple Labels



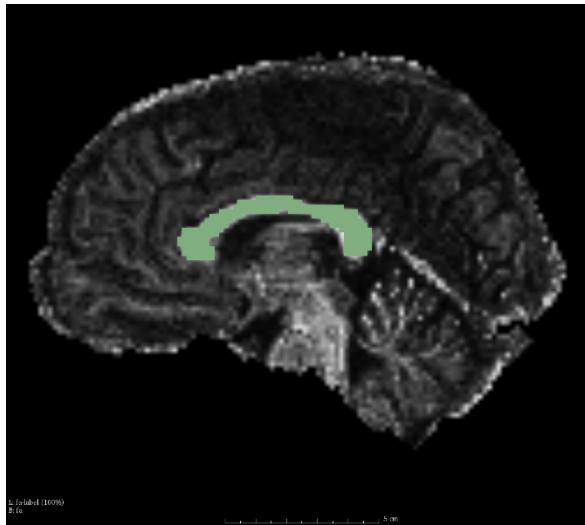
# Edit Multiple Labels



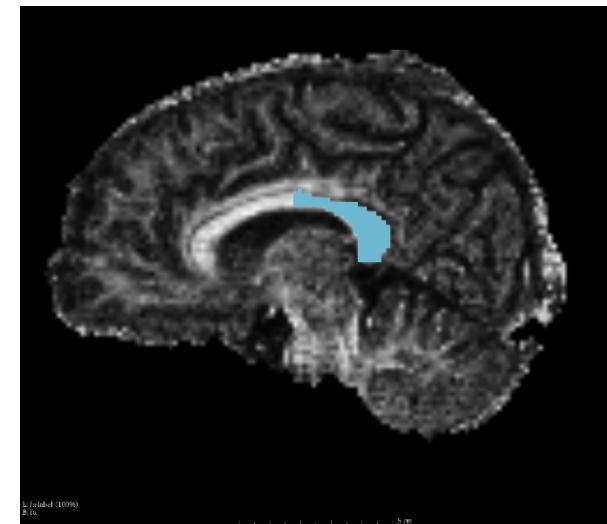
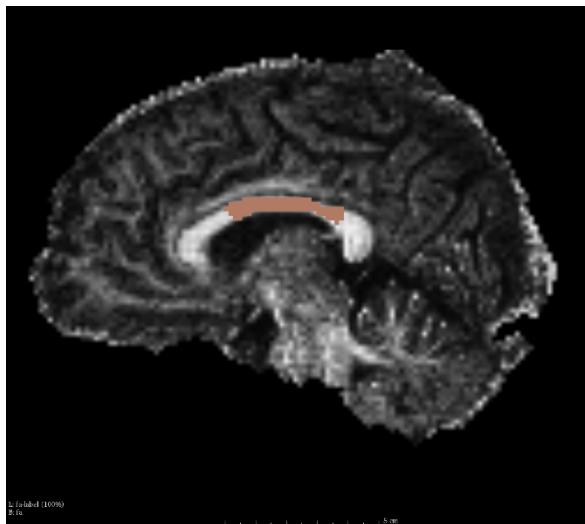
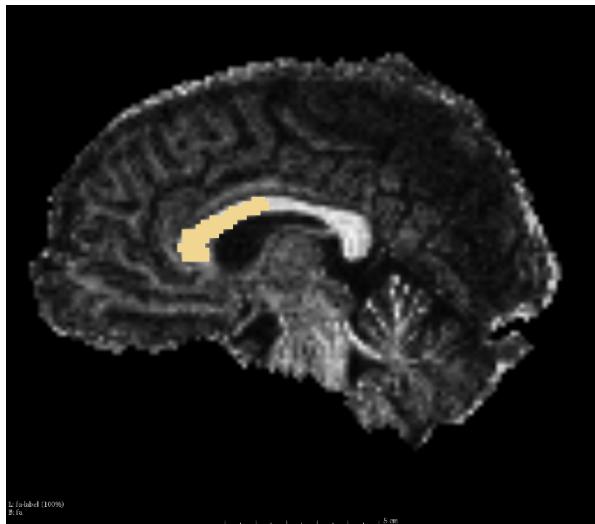
# Edit Multiple Labels

Label map on individual slice, with :

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

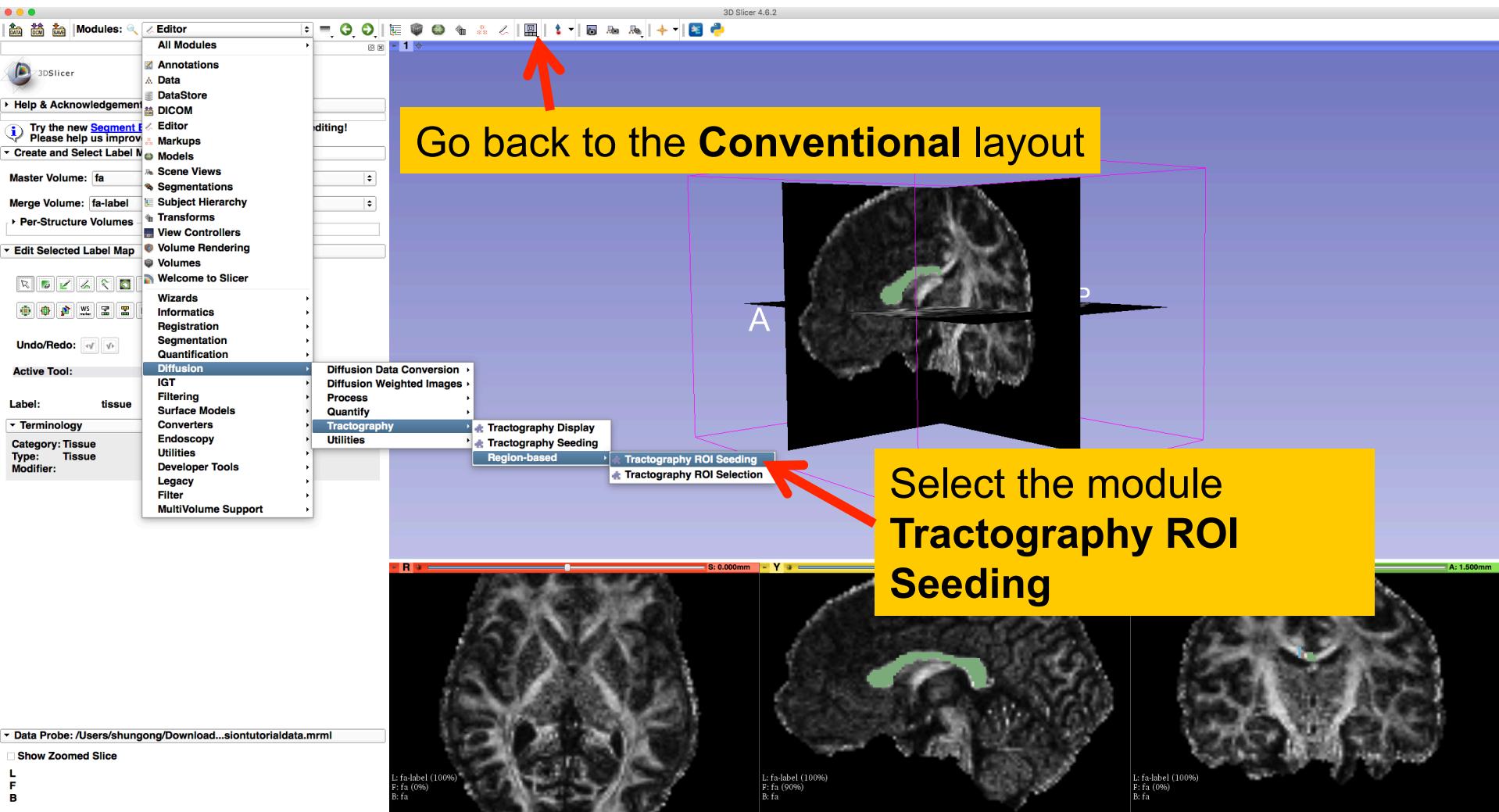


Notice that there are overlaps between different labeled regions\*, which will be used to investigate the fiber bundle selection.



\* For details of CC segments: [http://adessowiki.fee.unicamp.br/adesso/wiki/DTI/proj\\_cc/view/](http://adessowiki.fee.unicamp.br/adesso/wiki/DTI/proj_cc/view/)

# Whole Brain Tractography

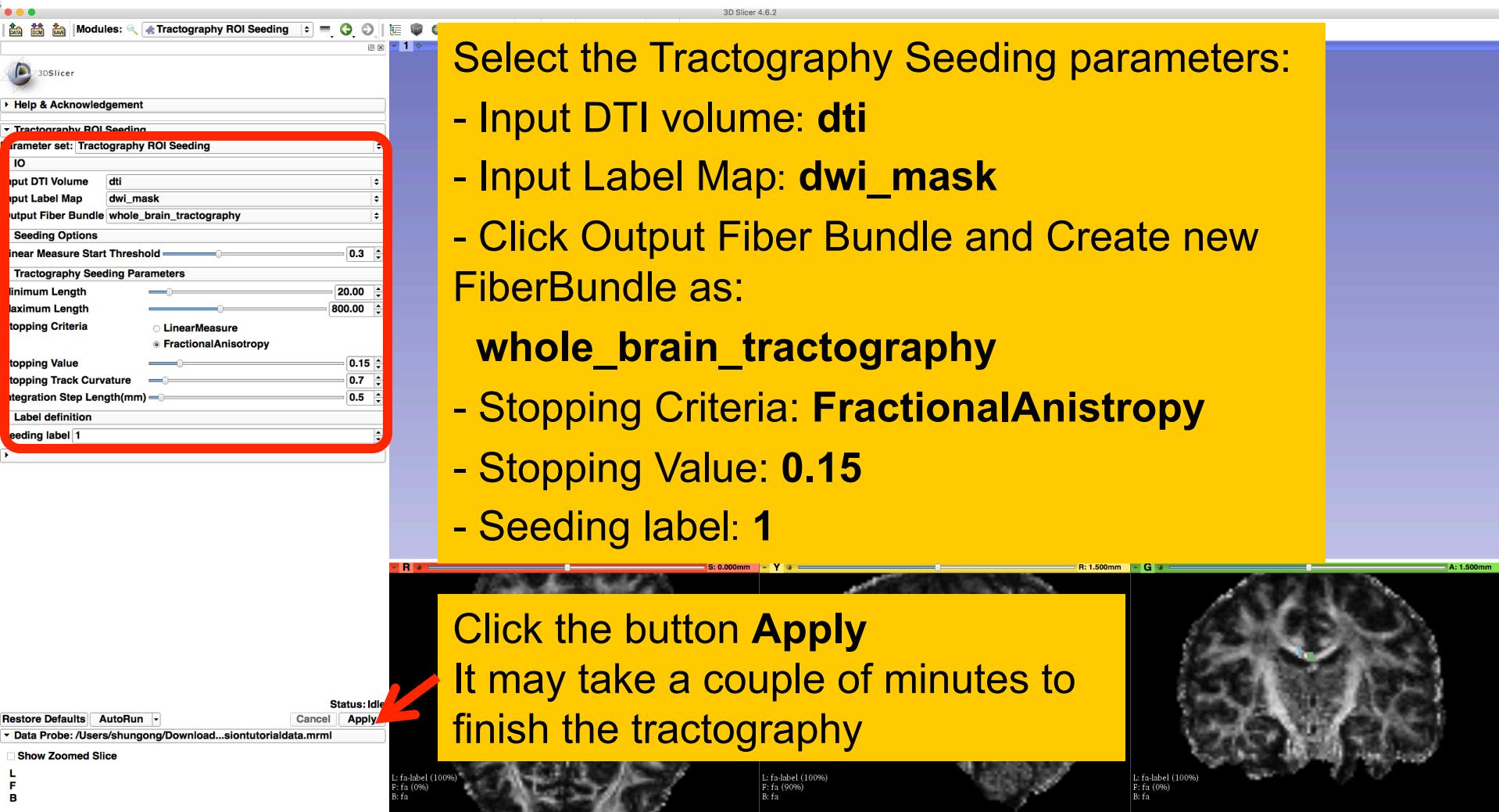


# Whole Brain Tractography

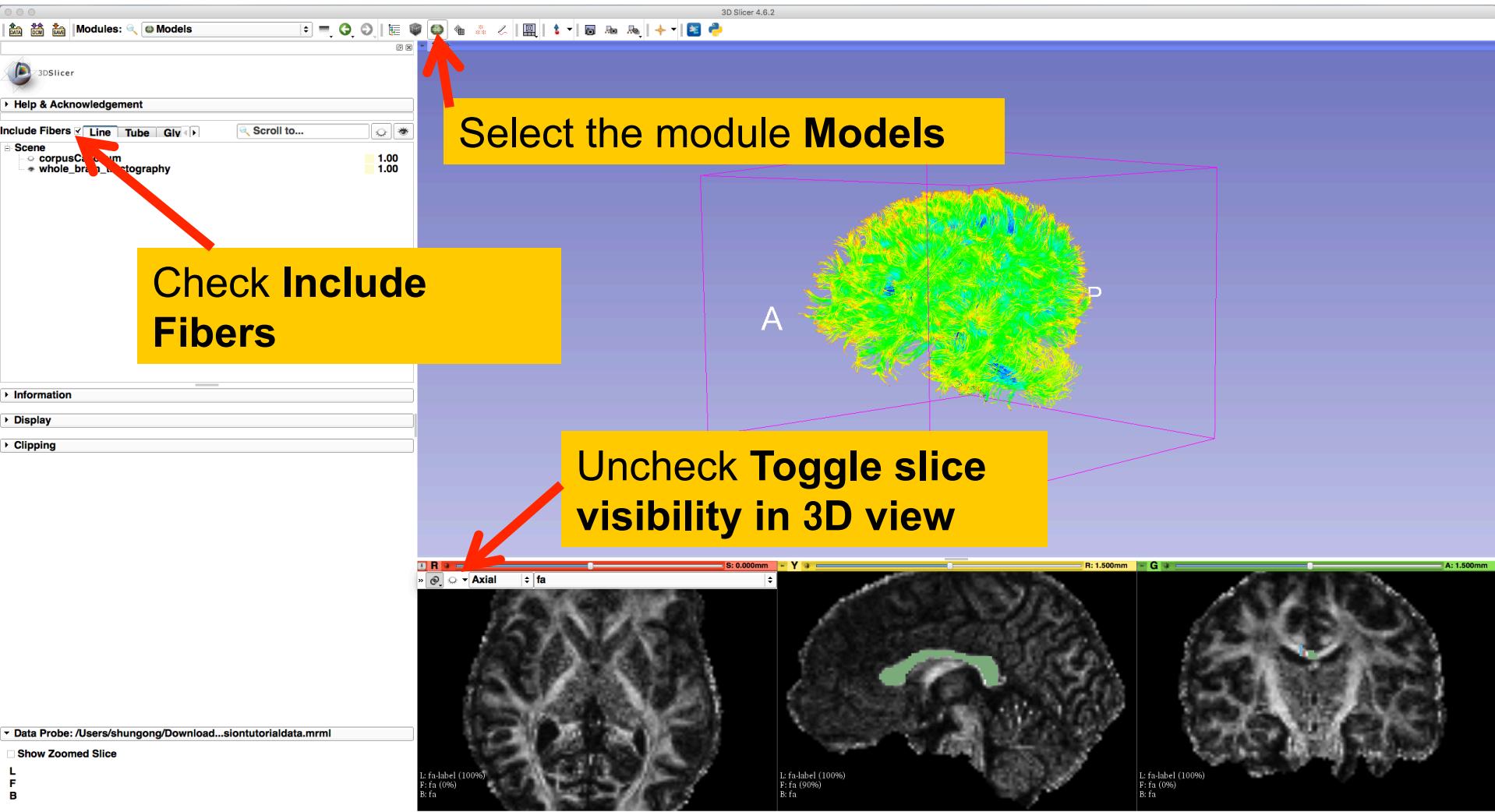
Select the Tractography Seeding parameters:

- 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**
- Seeding label: **1**

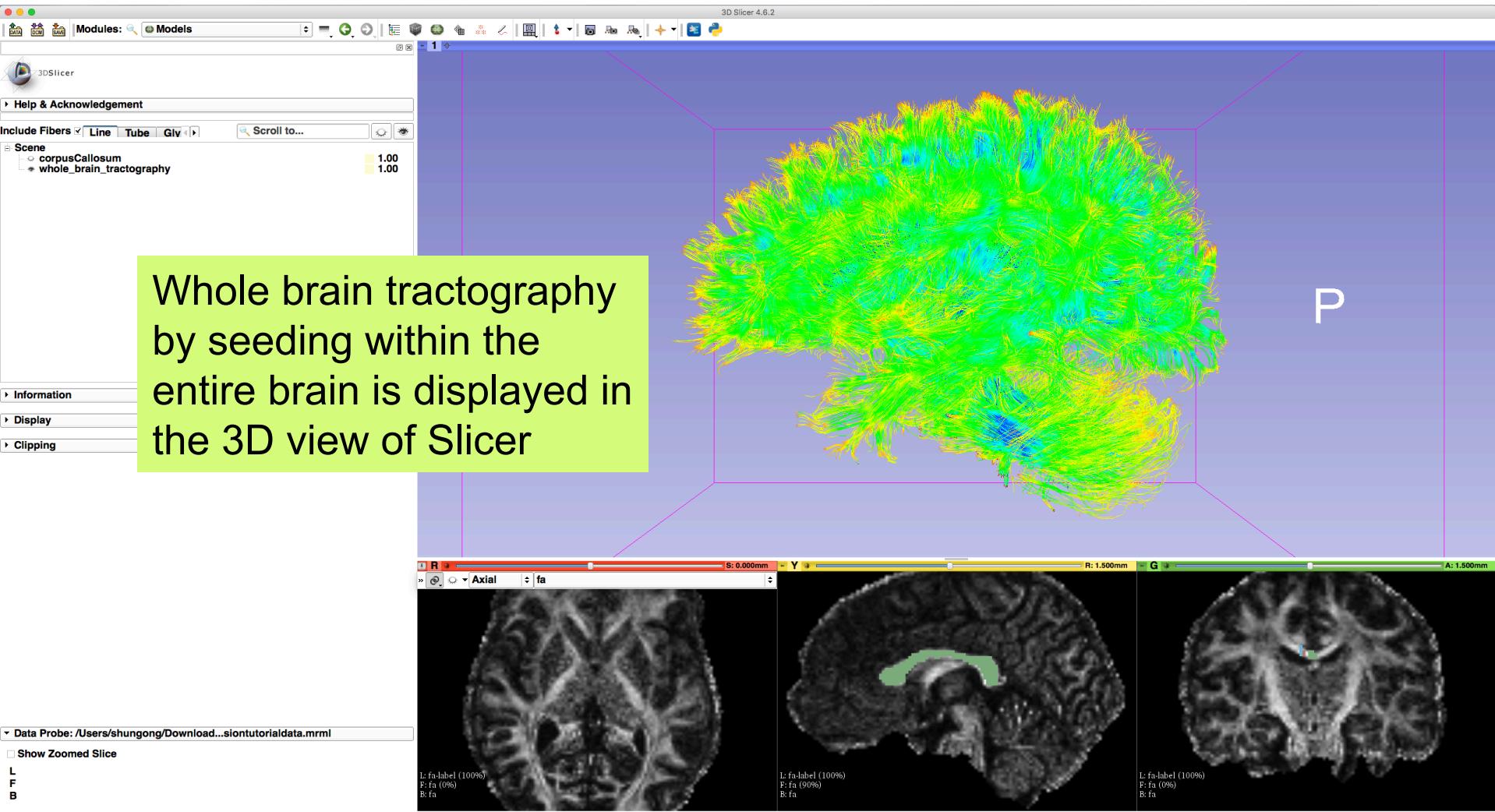
Click the button **Apply**  
It may take a couple of minutes to finish the tractography



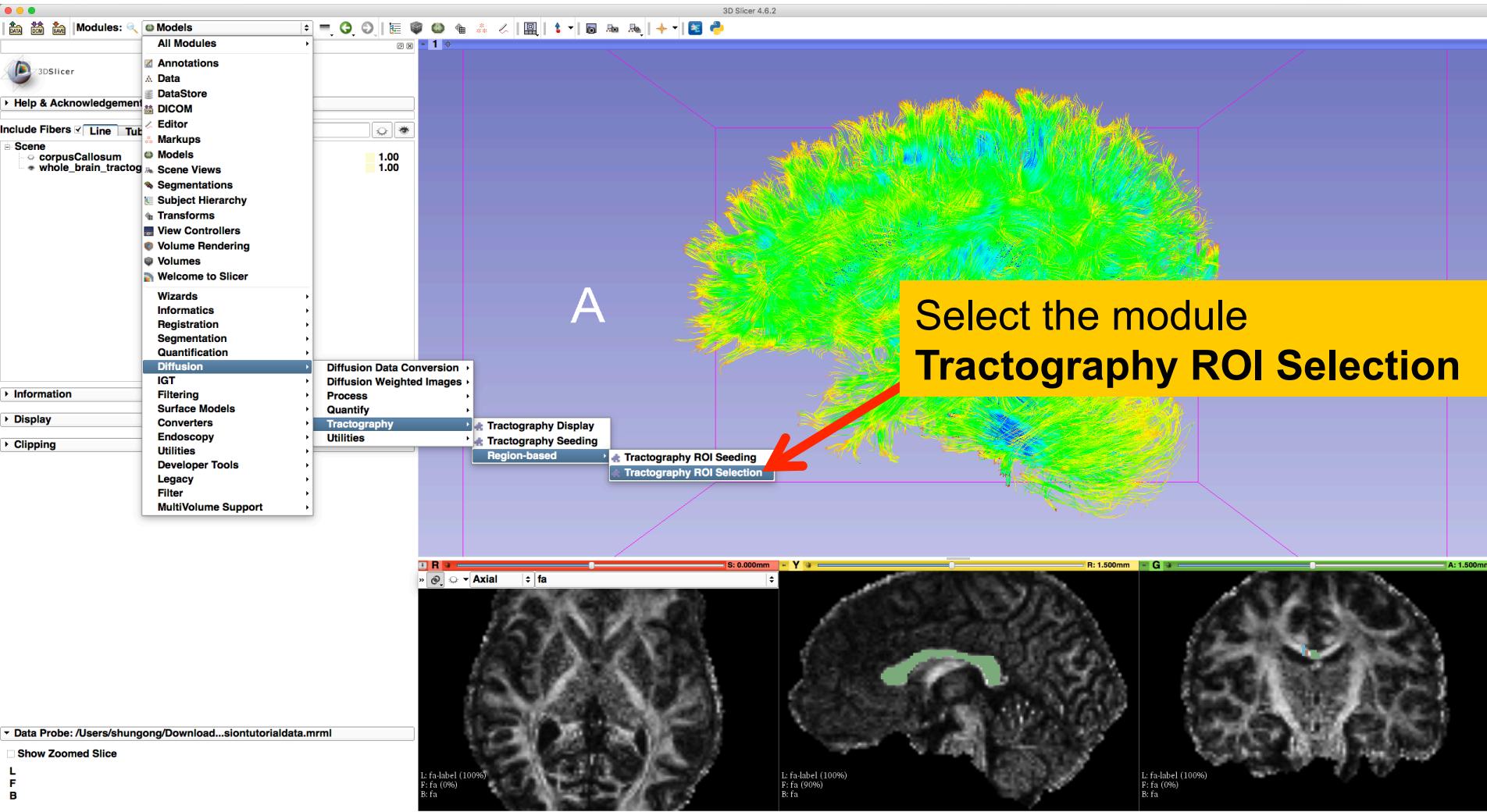
# Whole Brain Tractography



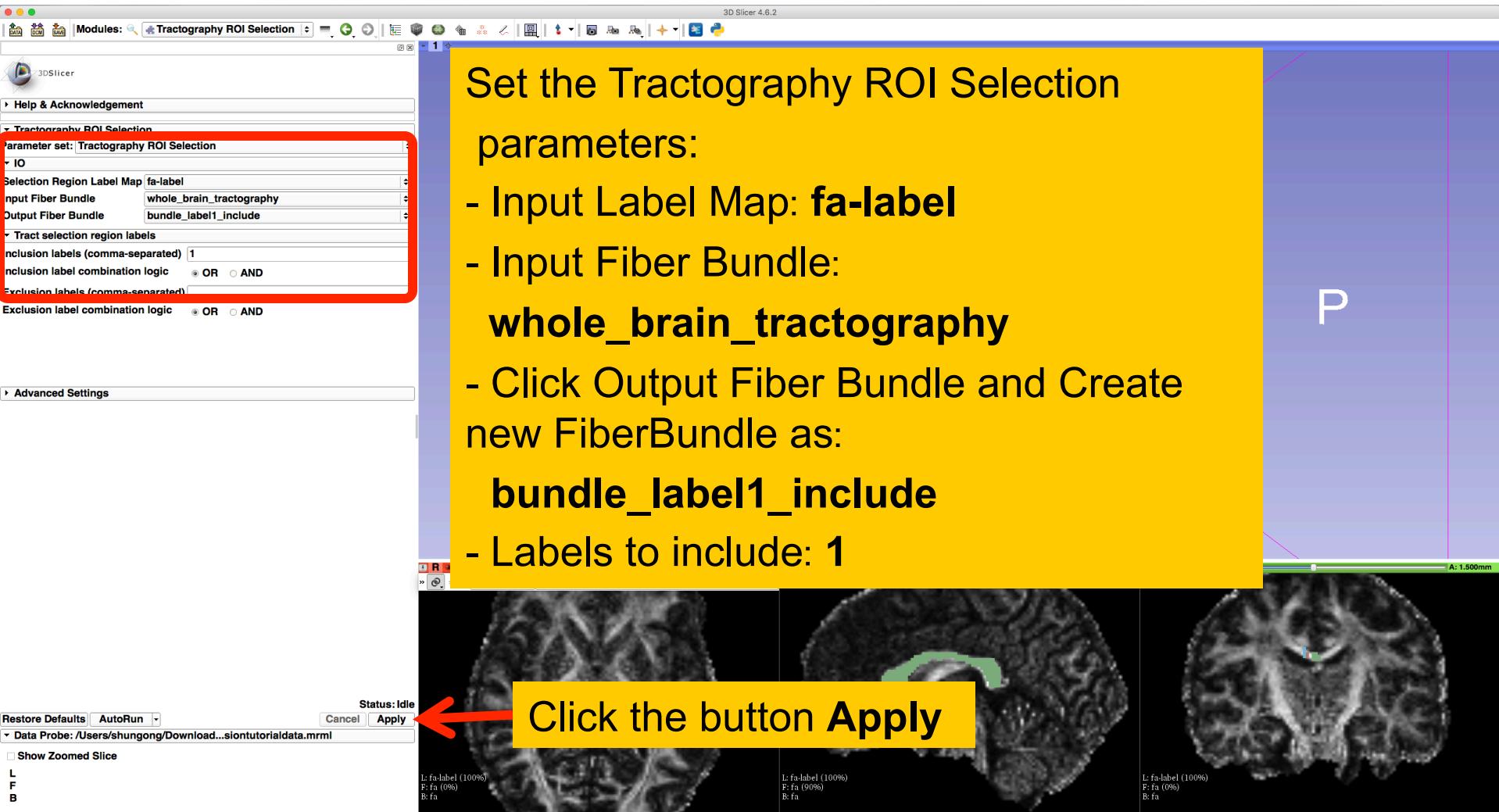
# Whole Brain Tractography



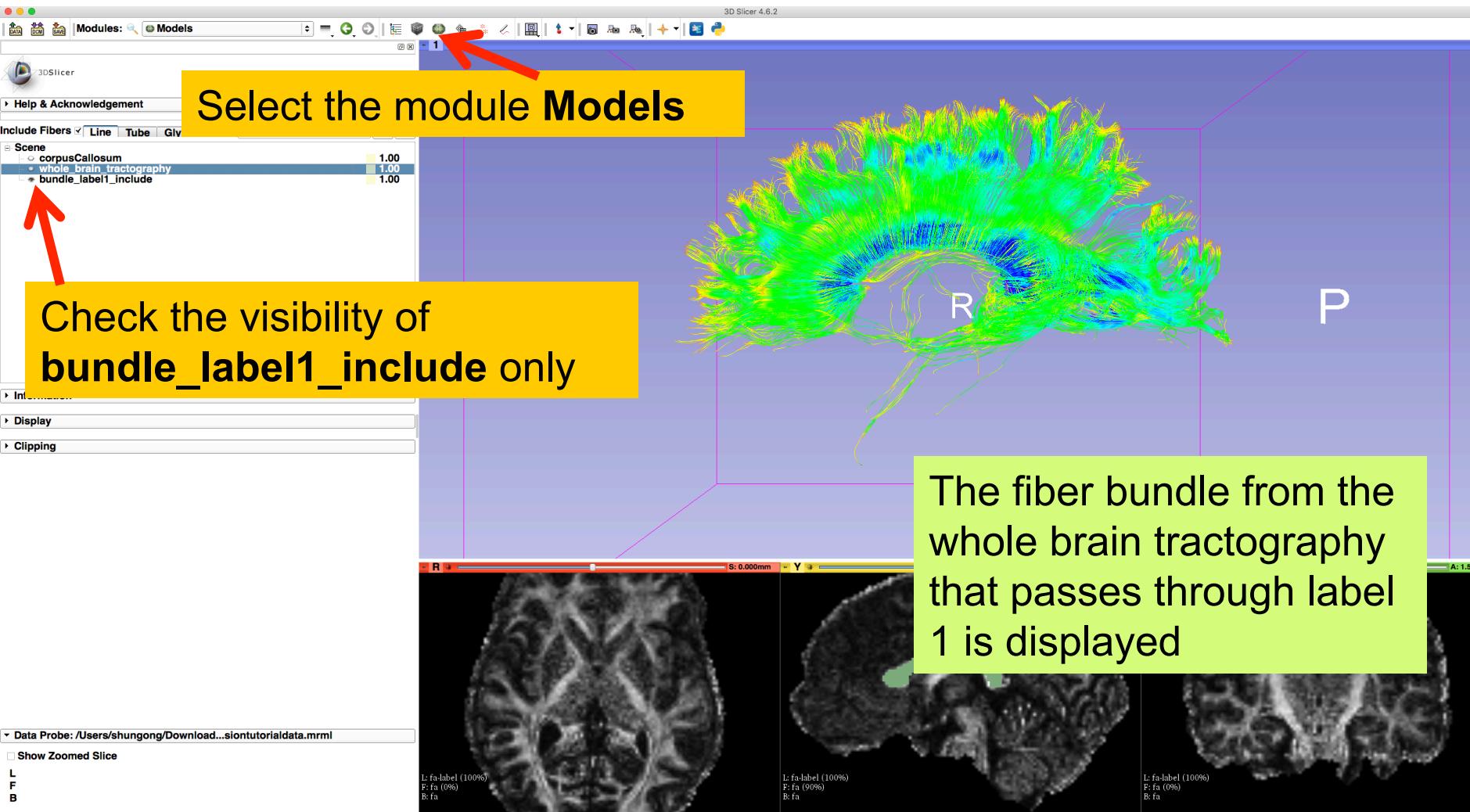
# Tractography ROI Selection



# Single Label Selection



# Single Label Selection



# Single Label Selection

A

P

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

3D Slicer 4.6.2

Modules: Tractography ROI Selection

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):

Exclusion label combination logic: OR  AND

Advanced Settings

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

Data Probe: /Users/shungong/Downloads/siontutorialdata.mrml

Red (L 71.0, A 50.6, S 0.0) Axial Sp: 1.5

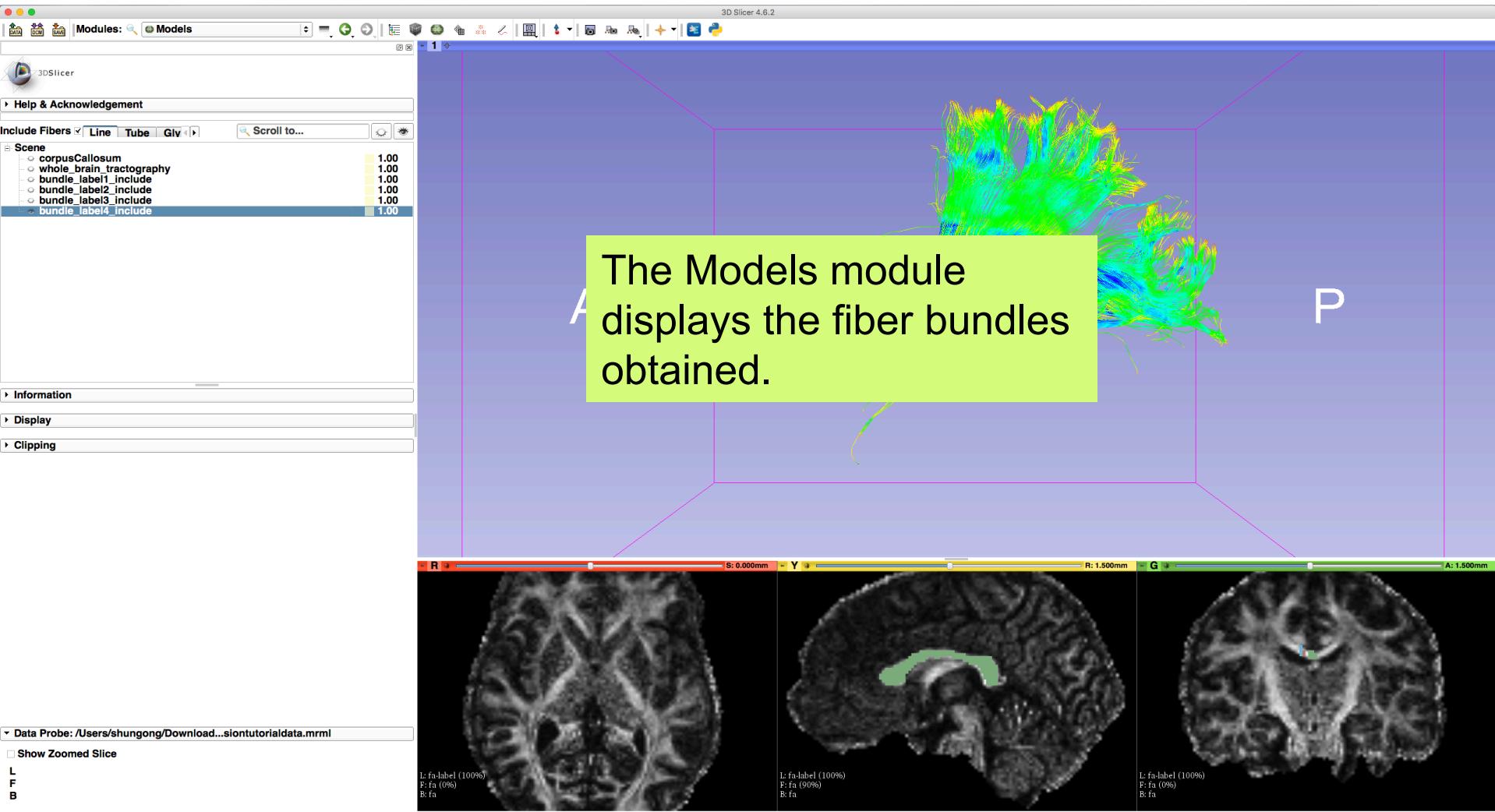
L: fa-label (111, 30, 47) background (0)  
F: fa (111, 30, 47) 0  
R: fa (111, 30, 47) 0

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

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

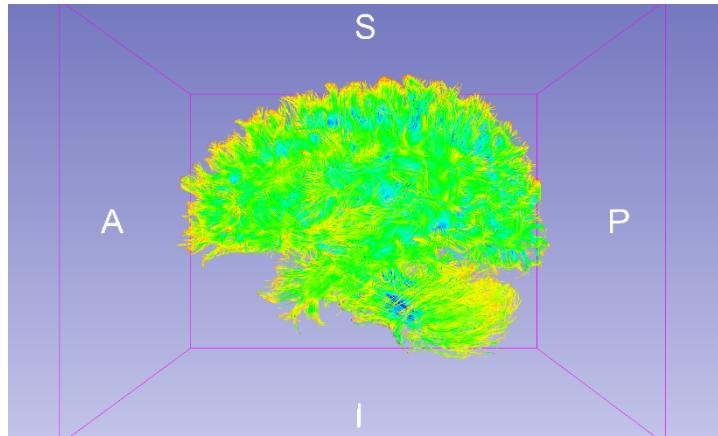
L: fa-label (100%)  
F: fa (0%)  
R: fa

# Single Label Selection

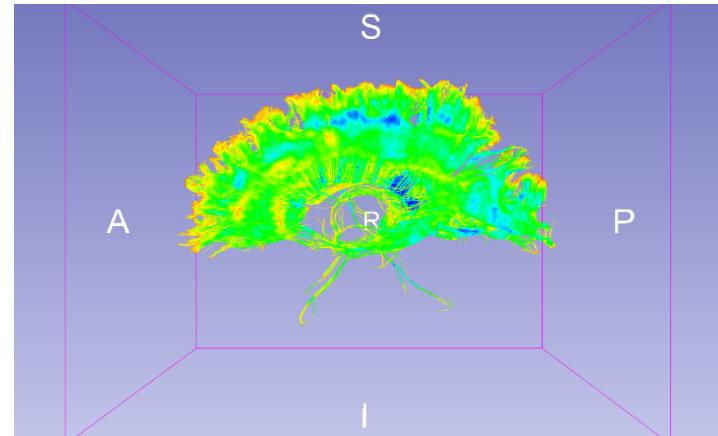


# Single Label Selection

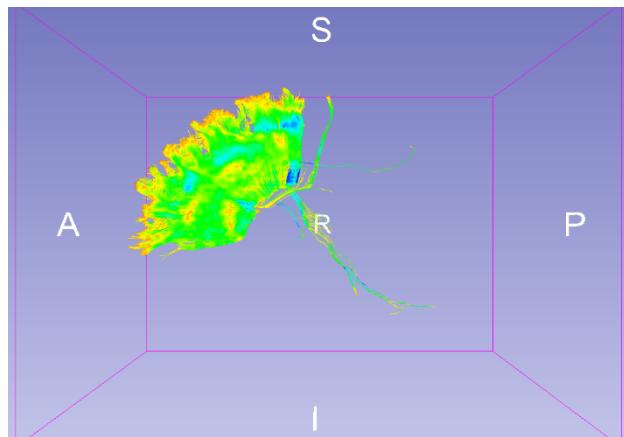
Whole Brain



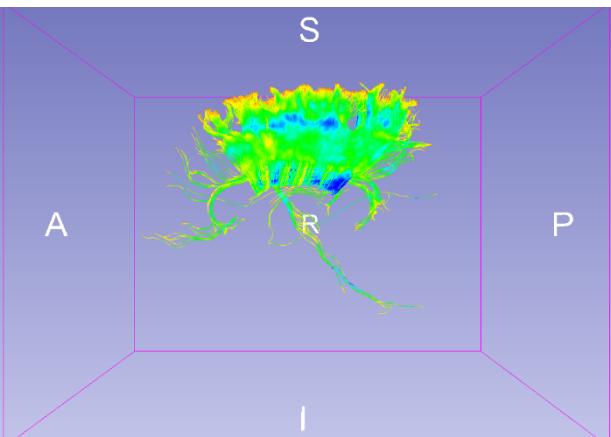
Label 1



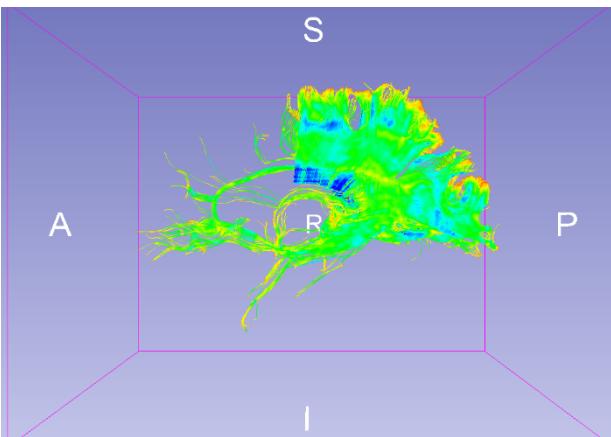
Label 2



Label 3



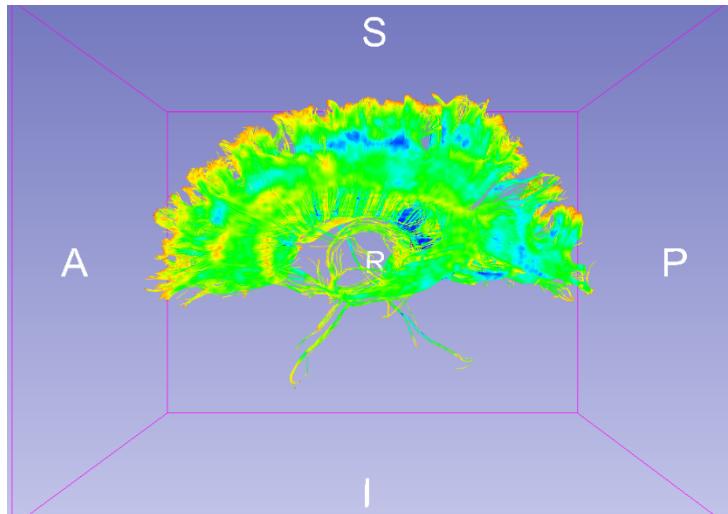
Label 4



# Single Label Selection

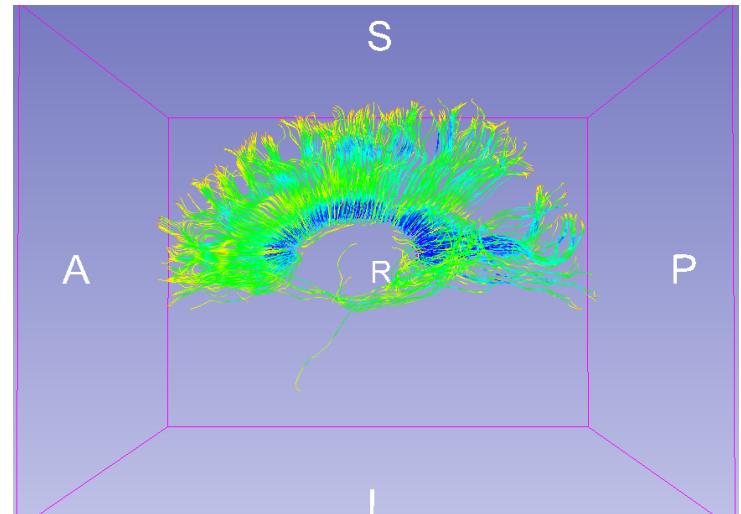
Notice that whole brain seeding creates a denser fiber bundle than seeding from the label 1.

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)

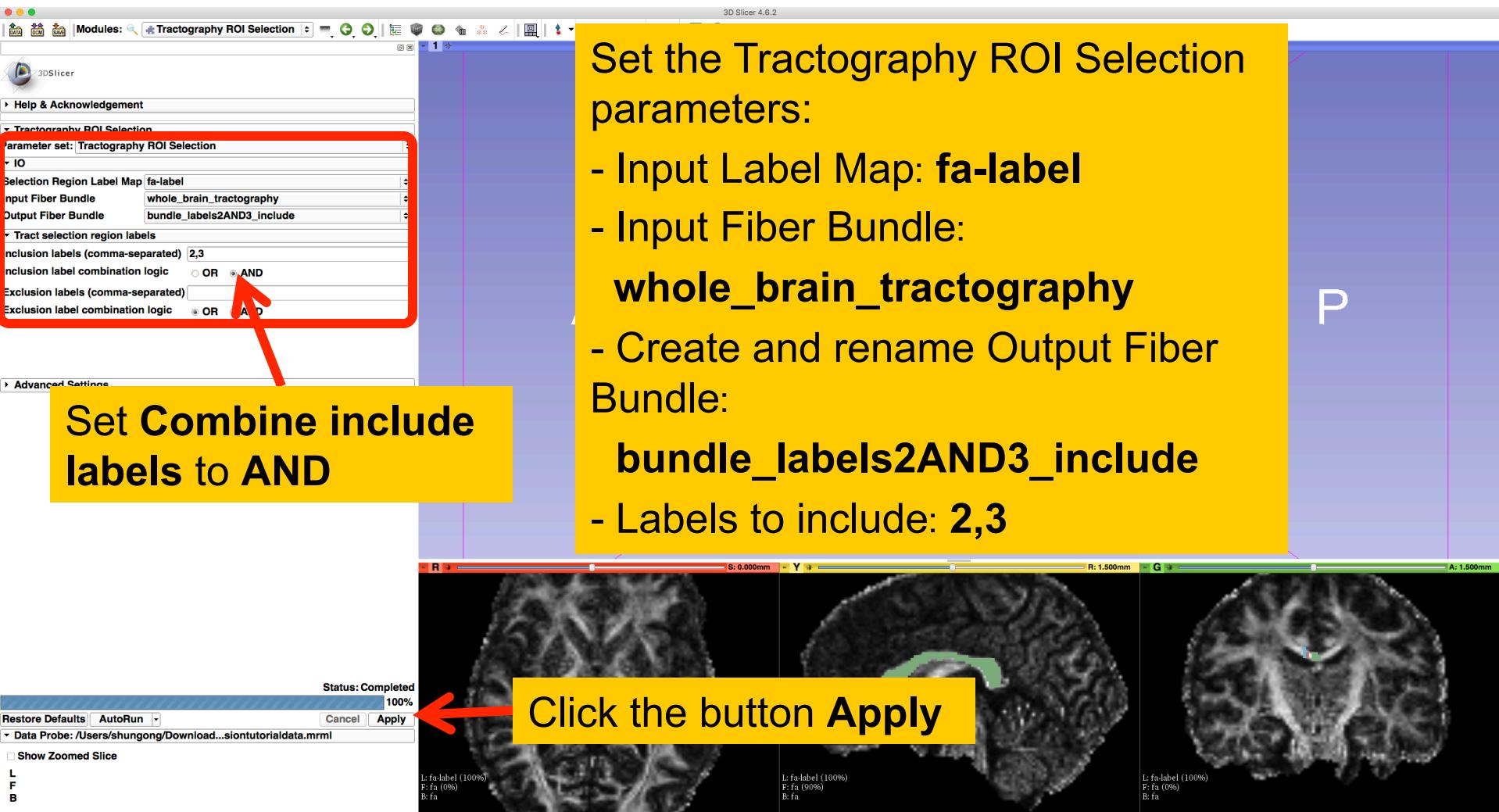
Inclusion label combination logic  OR  AND

Exclusion labels (comma-separated)

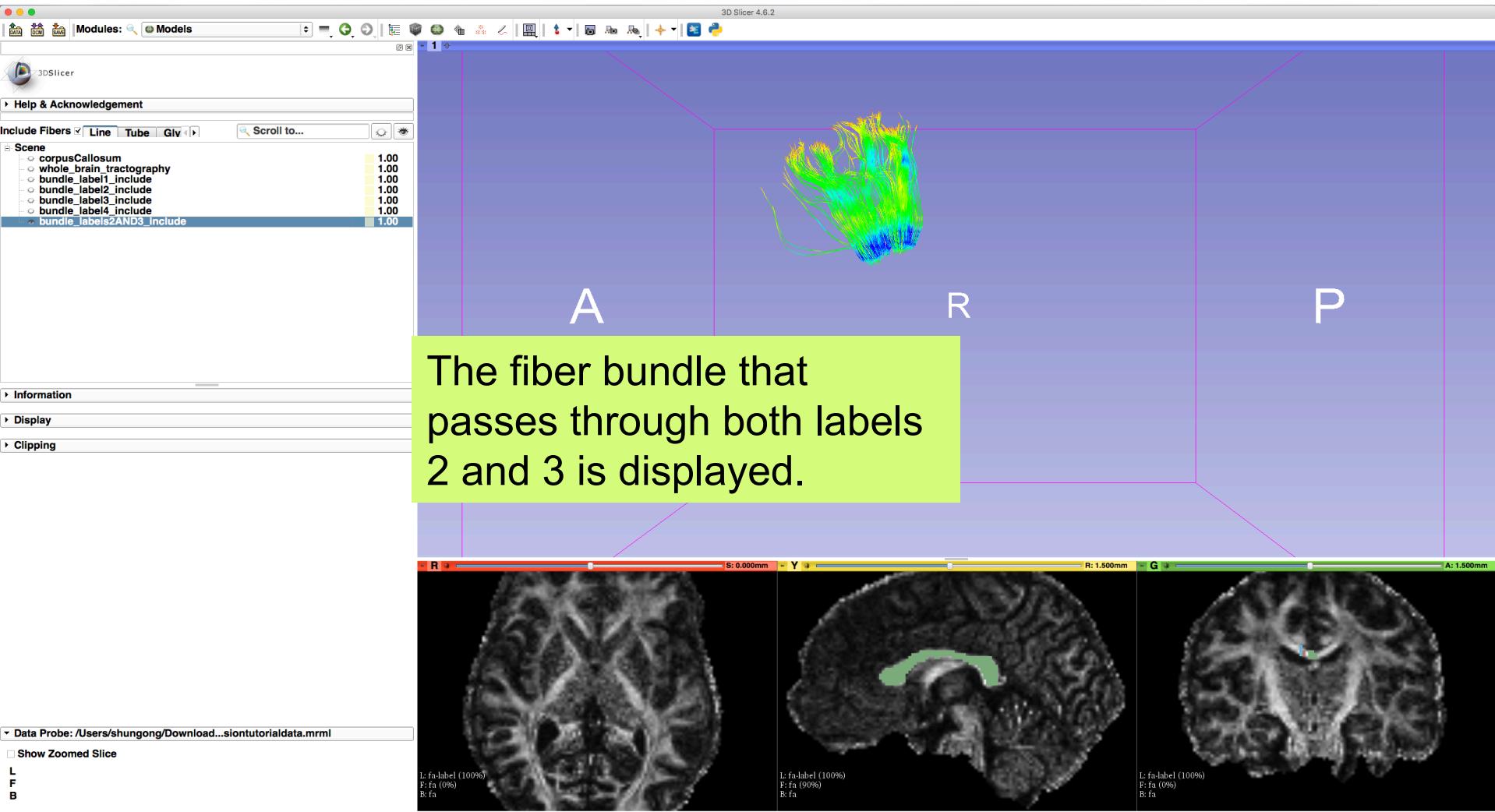
Exclusion label combination logic

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

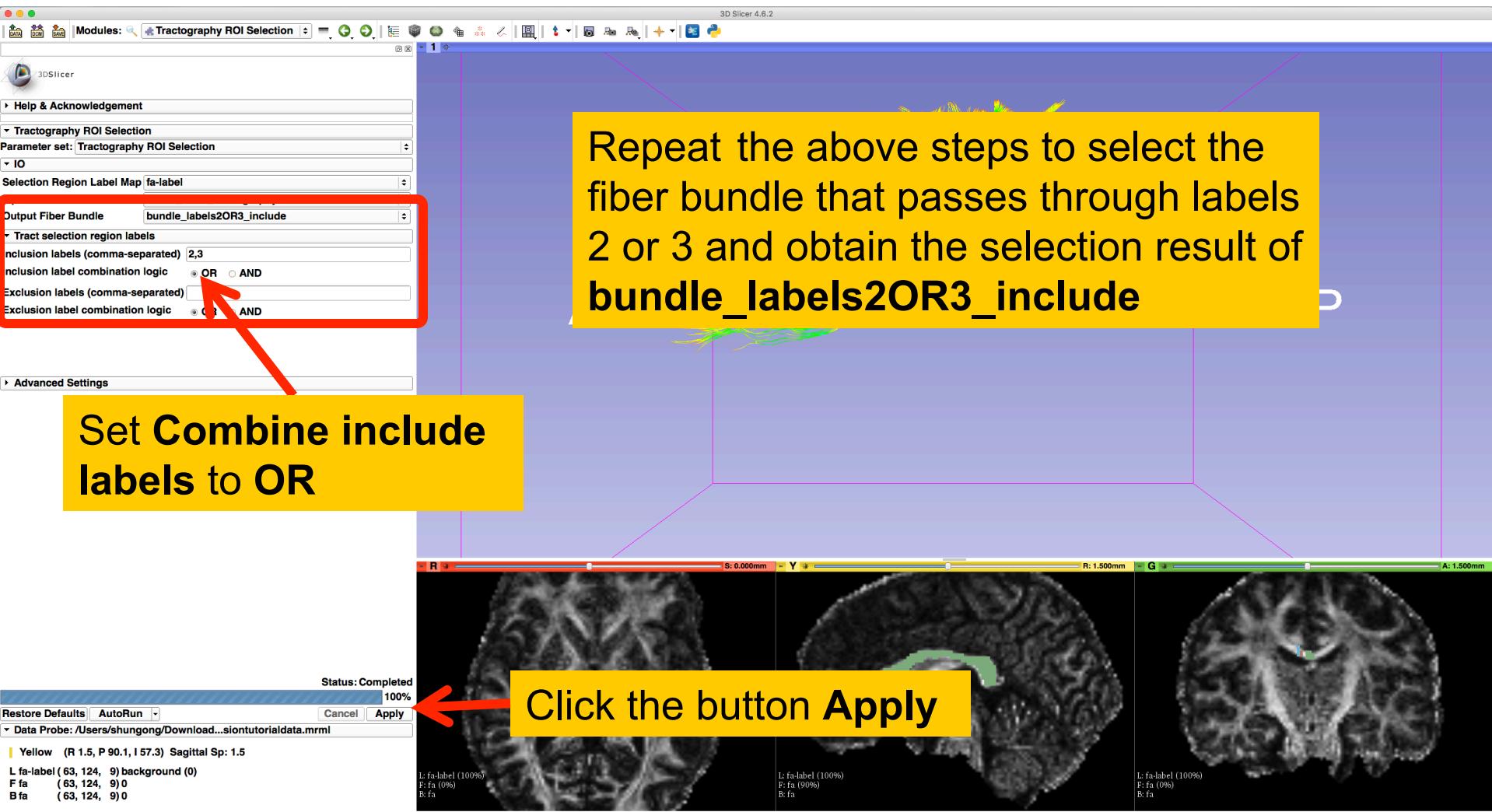
# Multiple Labels Selection (AND)



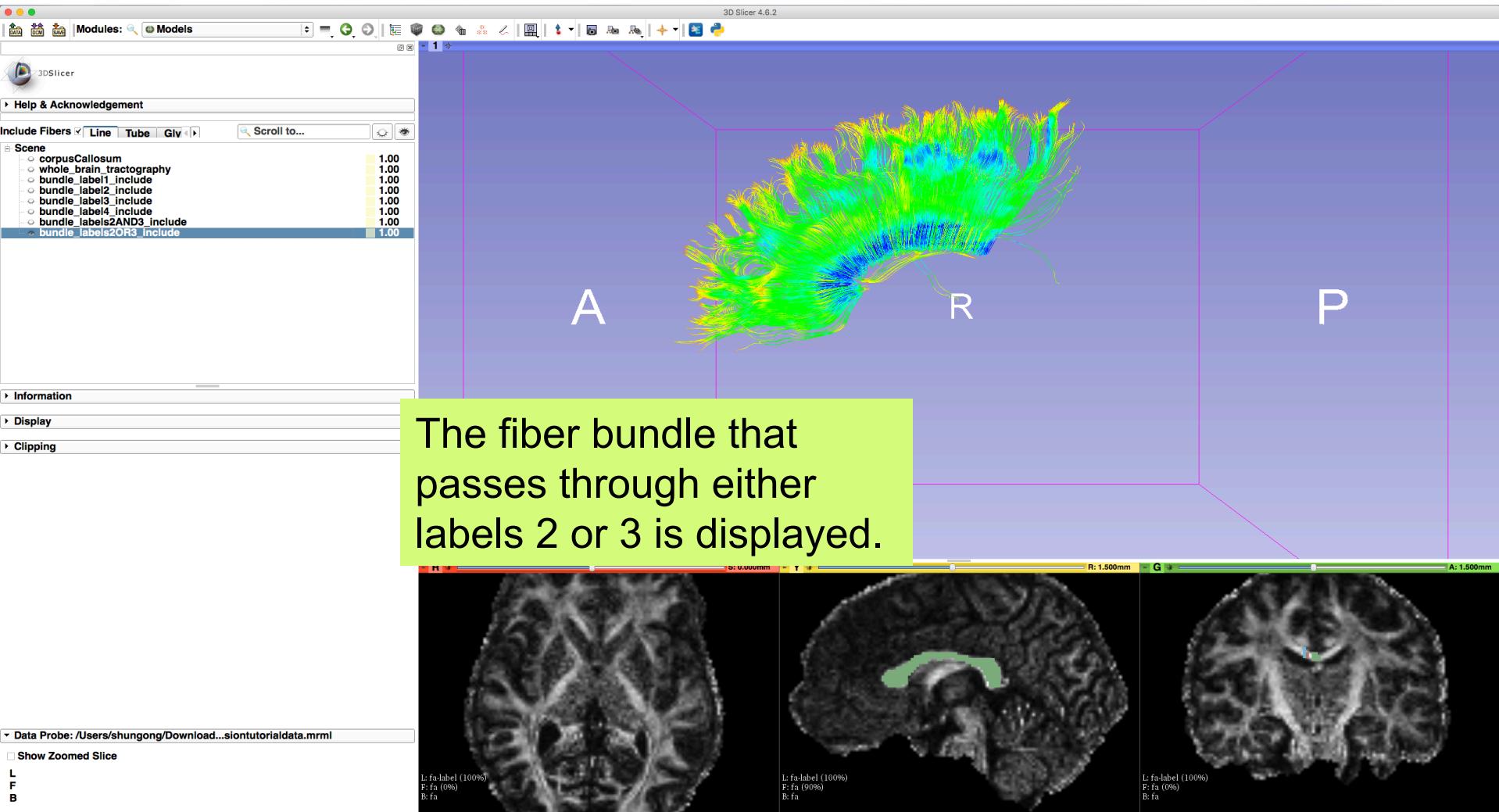
# Multiple Labels Selection (AND)



# Multiple Labels Selection (OR)

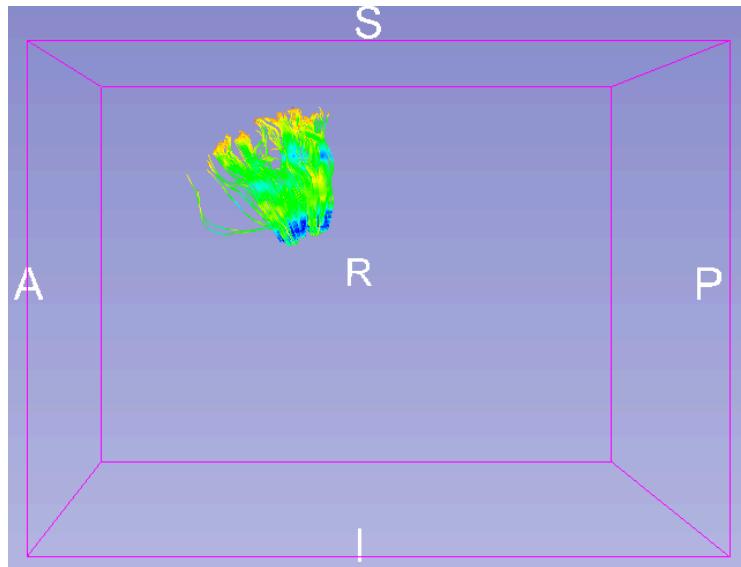


# Multiple Labels Selection (OR)

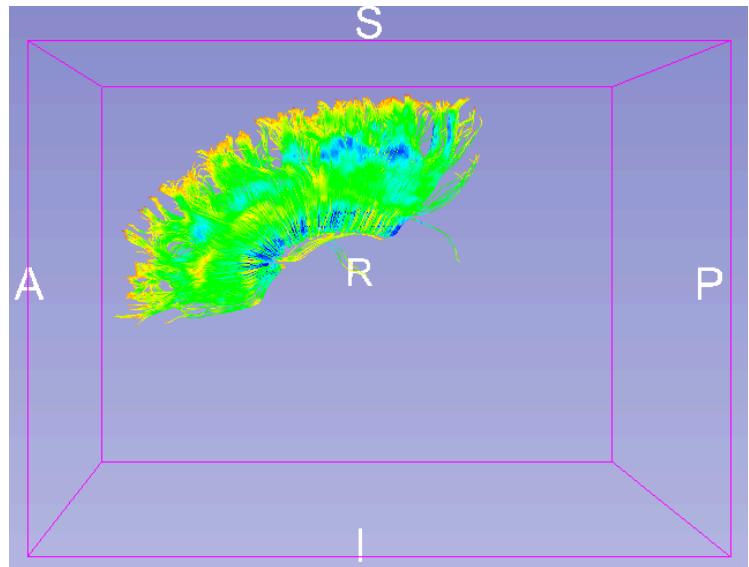


# Multiple Labels Selection

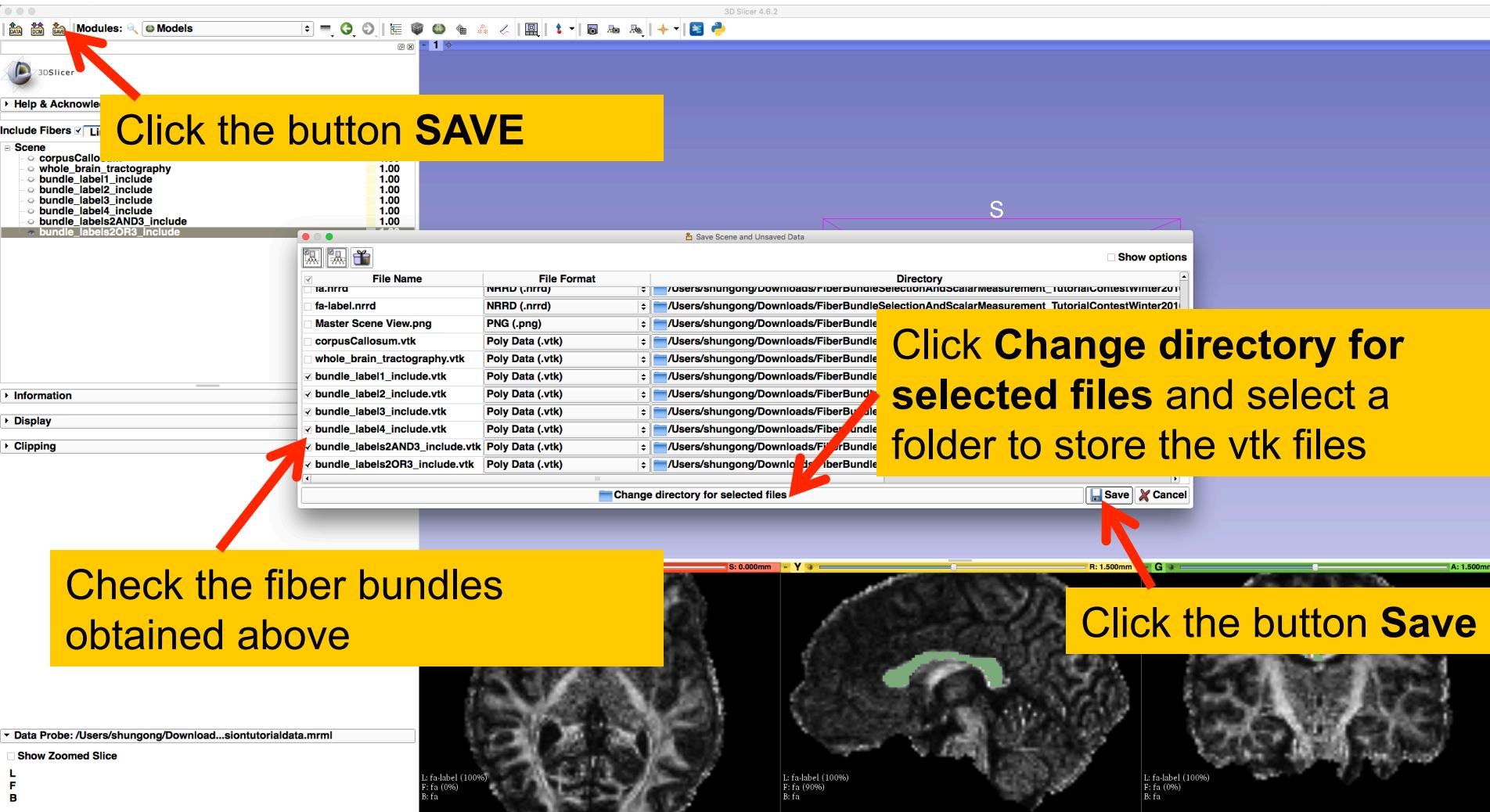
Labels 2 and 3



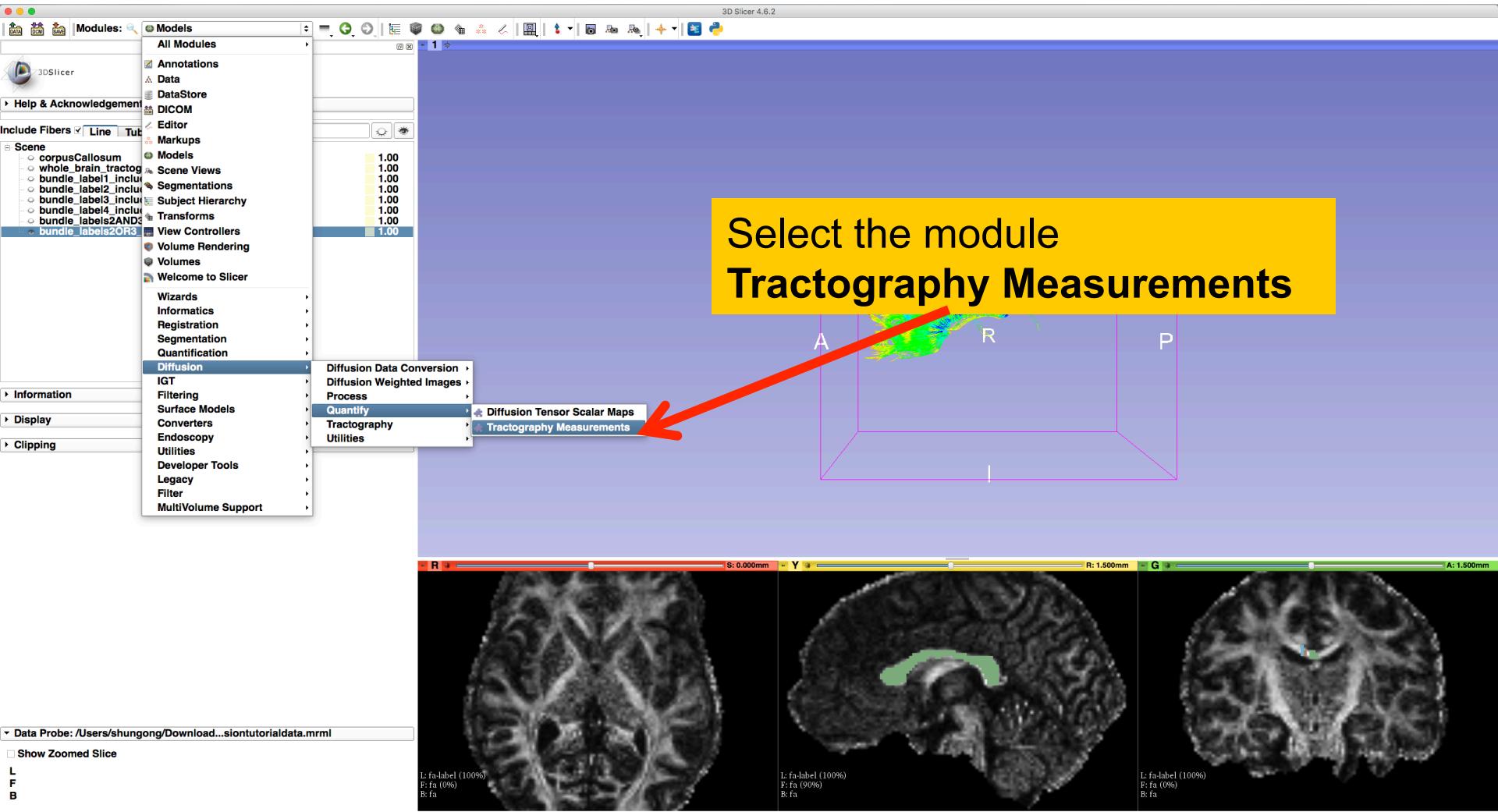
Labels 2 or 3



# Save Fiber Bundles



# Tractography Measurements

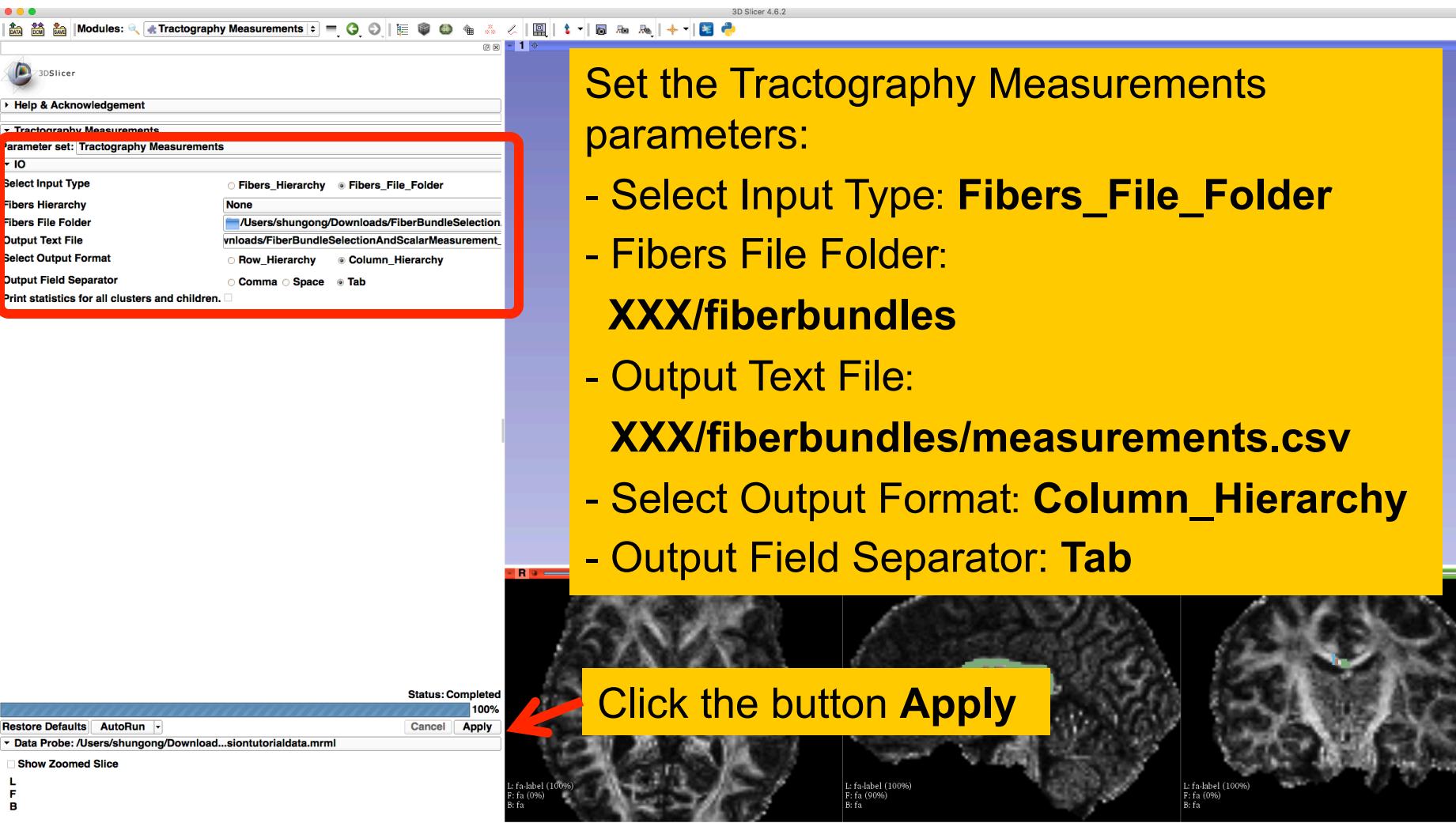


# Tractography Measurements

Set the Tractography Measurements parameters:

- Select Input Type: **Fibers\_File\_Folder**
- Fibers File Folder:  
**XXX/fiberbundles**
- Output Text File:  
**XXX/fiberbundles/measurements.csv**
- Select Output Format: **Column\_Hierarchy**
- Output Field Separator: **Tab**

Click the button **Apply**

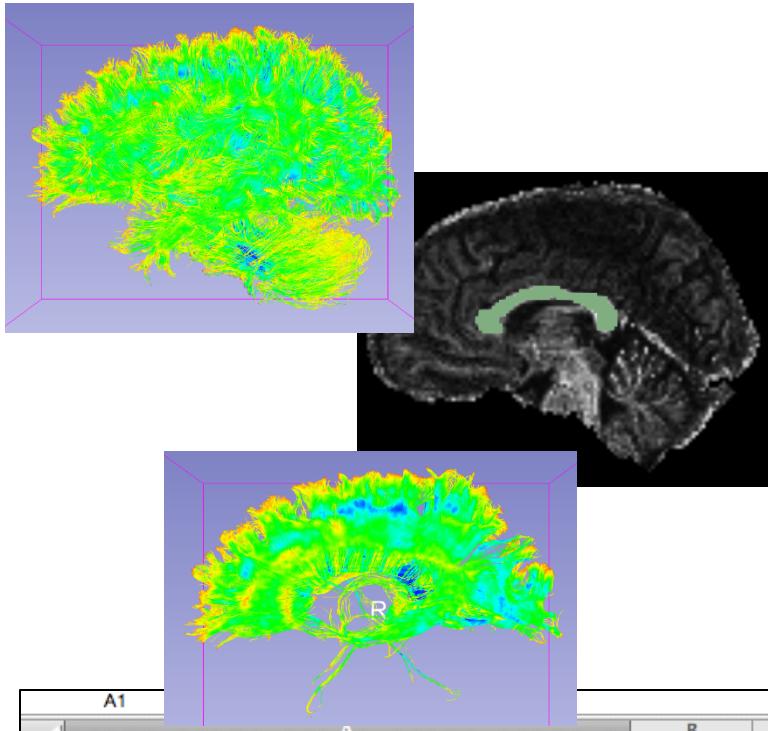


# Tractography Measurements

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

	A1				
1	Name	B	C	D	
2	/Users/fan/Desktop/fiberbundles/bundle_label1_include.vtk	2127263	14306	0.525257	
3	/Users/fan/Desktop/fiberbundles/bundle_label2_include.vtk	708470	5564	0.484828	
4	/Users/fan/Desktop/fiberbundles/bundle_label3_include.vtk	601023	4428	0.514121	
5	/Users/fan/Desktop/fiberbundles/bundle_label4_include.vtk	1261823	7485	0.552797	
6	/Users/fan/Desktop/fiberbundles/bundle_labels2AND3_include.vtk	163814	1360	0.502443	
7	/Users/fan/Desktop/fiberbundles/bundle_labels2OR3_include.vtk	1145679	8632	0.497677	
8					

# Conclusion



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

A1	B	C	D	E		
1	Name	Num_Points	Num_Fibers	Tensors_.FractionalAnisotropy	Tensors_.LinearMeasurement	Tenso
2	/Users/fan/Desktop/fiberbundles/bundle_label1_include.vtk	2127263	14306	0.525257	0.505662	
3	/Users/fan/Desktop/fiberbundles/bundle_label2_include.vtk	708470	5564	0.484828	0.471678	
4	/Users/fan/Desktop/fiberbundles/bundle_label3_include.vtk	601023	4428	0.514121	0.490995	
5	/Users/fan/Desktop/fiberbundles/bundle_label4_include.vtk	1261823	7485	0.552797	0.528861	
6	/Users/fan/Desktop/fiberbundles/bundle_labels2AND3_include.vtk	163814	1360	0.502443	0.490922	
7	/Users/fan/Desktop/fiberbundles/bundle_labels2OR3_include.vtk	1145679	8632	0.497677	0.47906	
8						

# Acknowledgments

**The University of Sydney, APA/IPRS/ARC**

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Australian Research Council

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NIH P41EB015898

**Neuroimage Analysis Center (NAC)**

NIH P41EB015902