

Fiber Bundle Selection And Scalar Measurement

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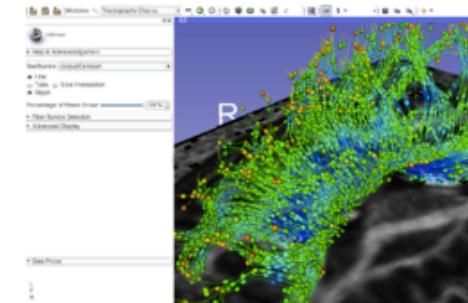
Pre-requisite

- 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/4.5/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 4.5.0-1 Stable Release) software available at

<http://download.slicer.org>

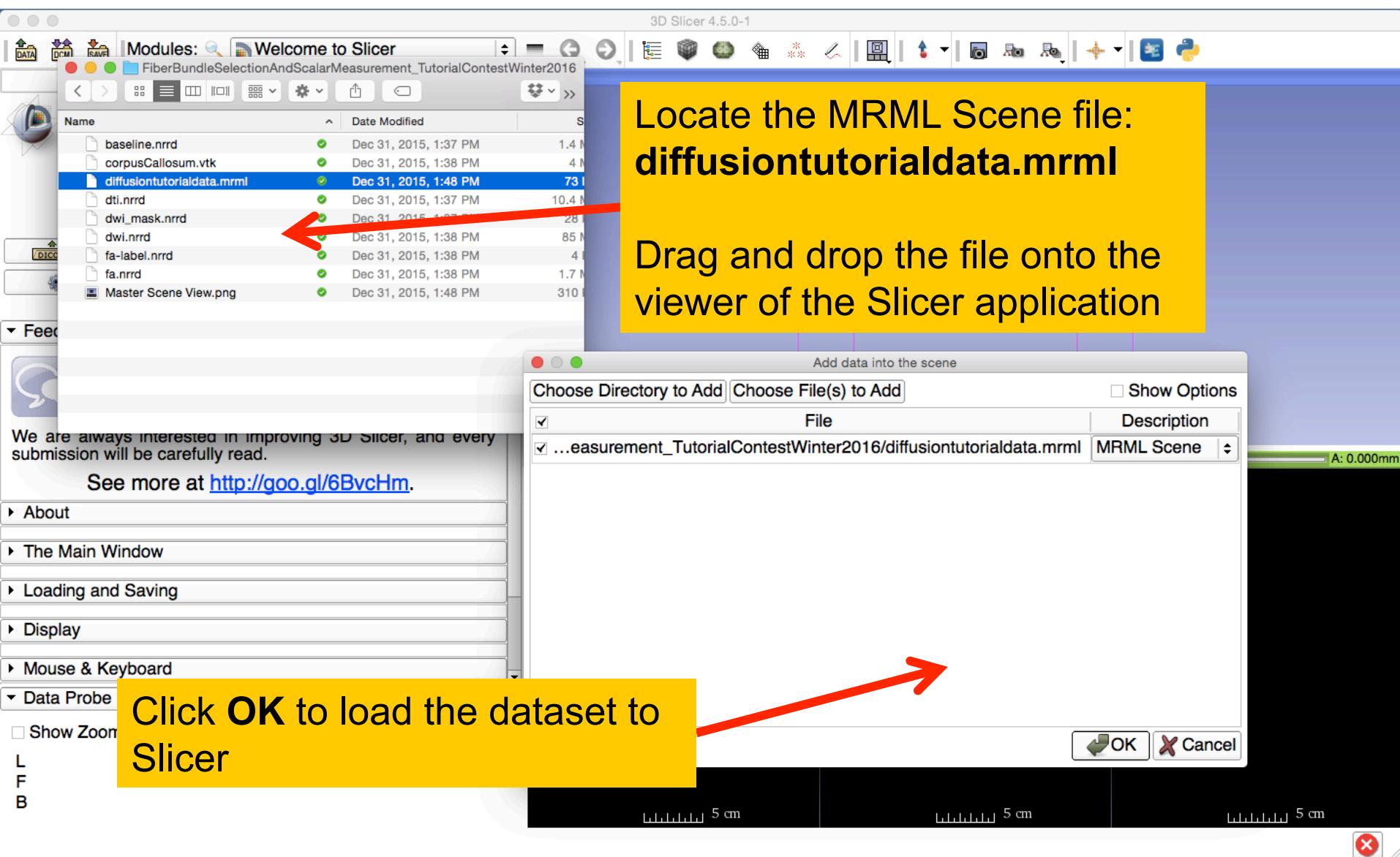
Data available at

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

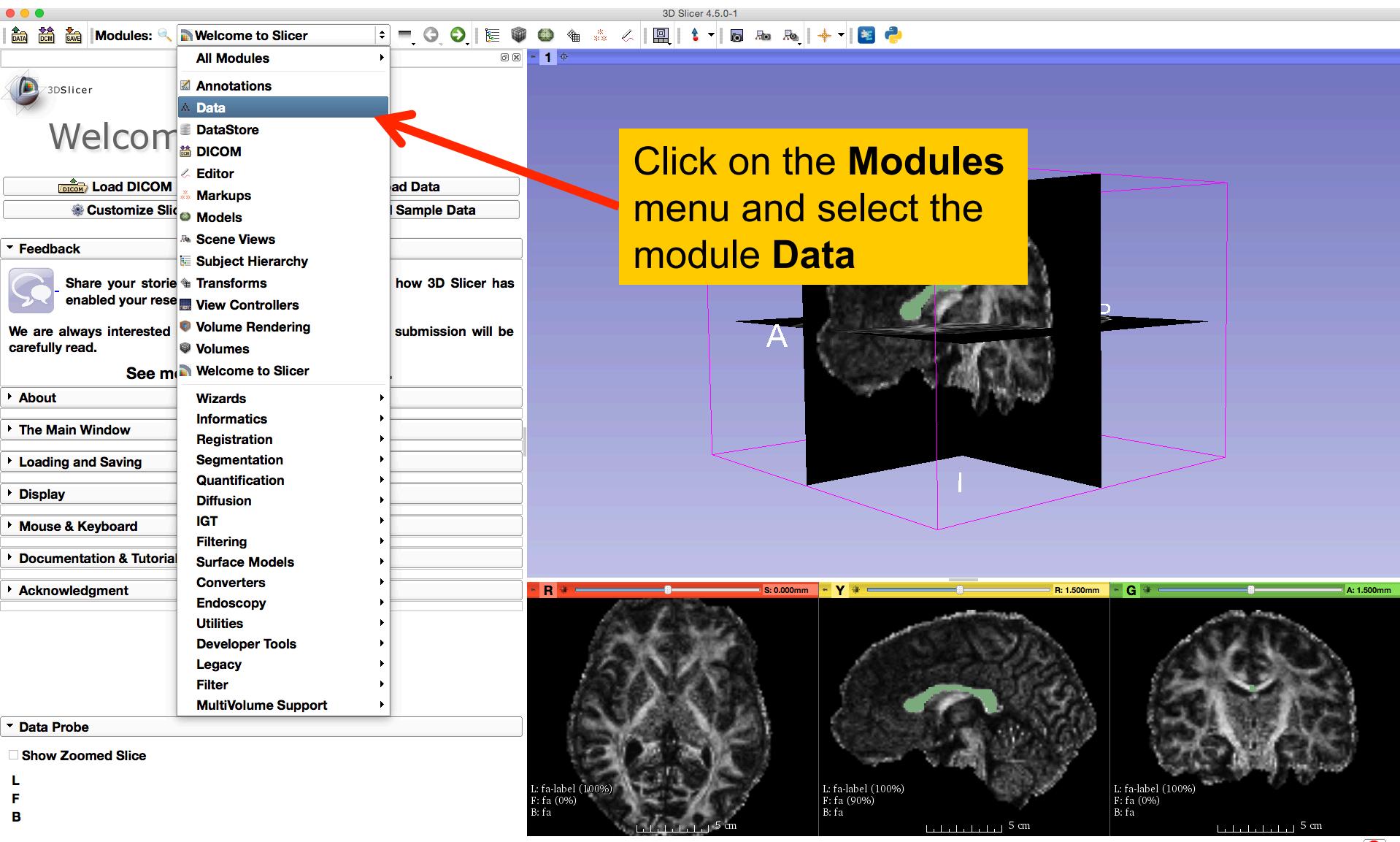
Disclaimer

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.

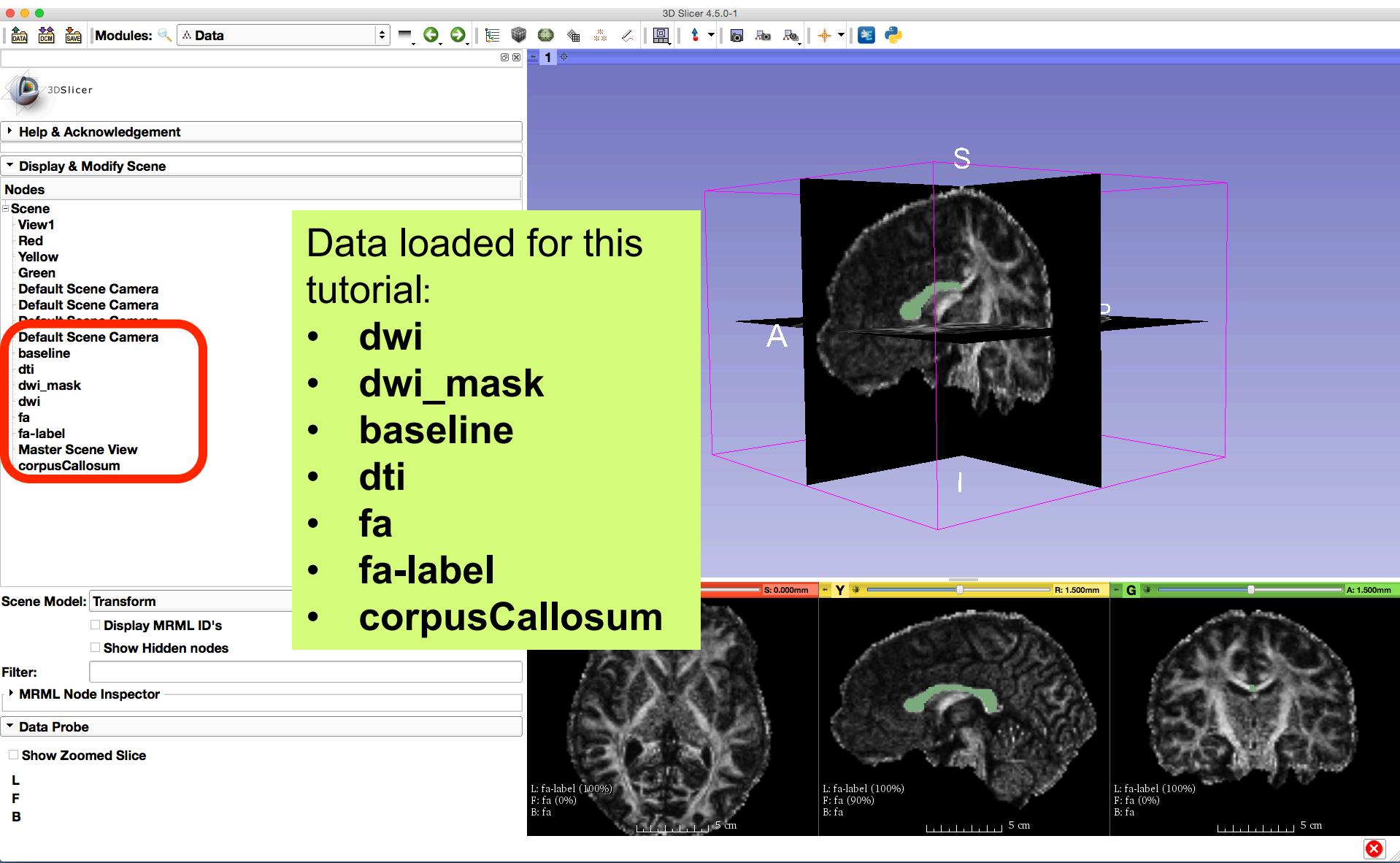
Load MRML Data



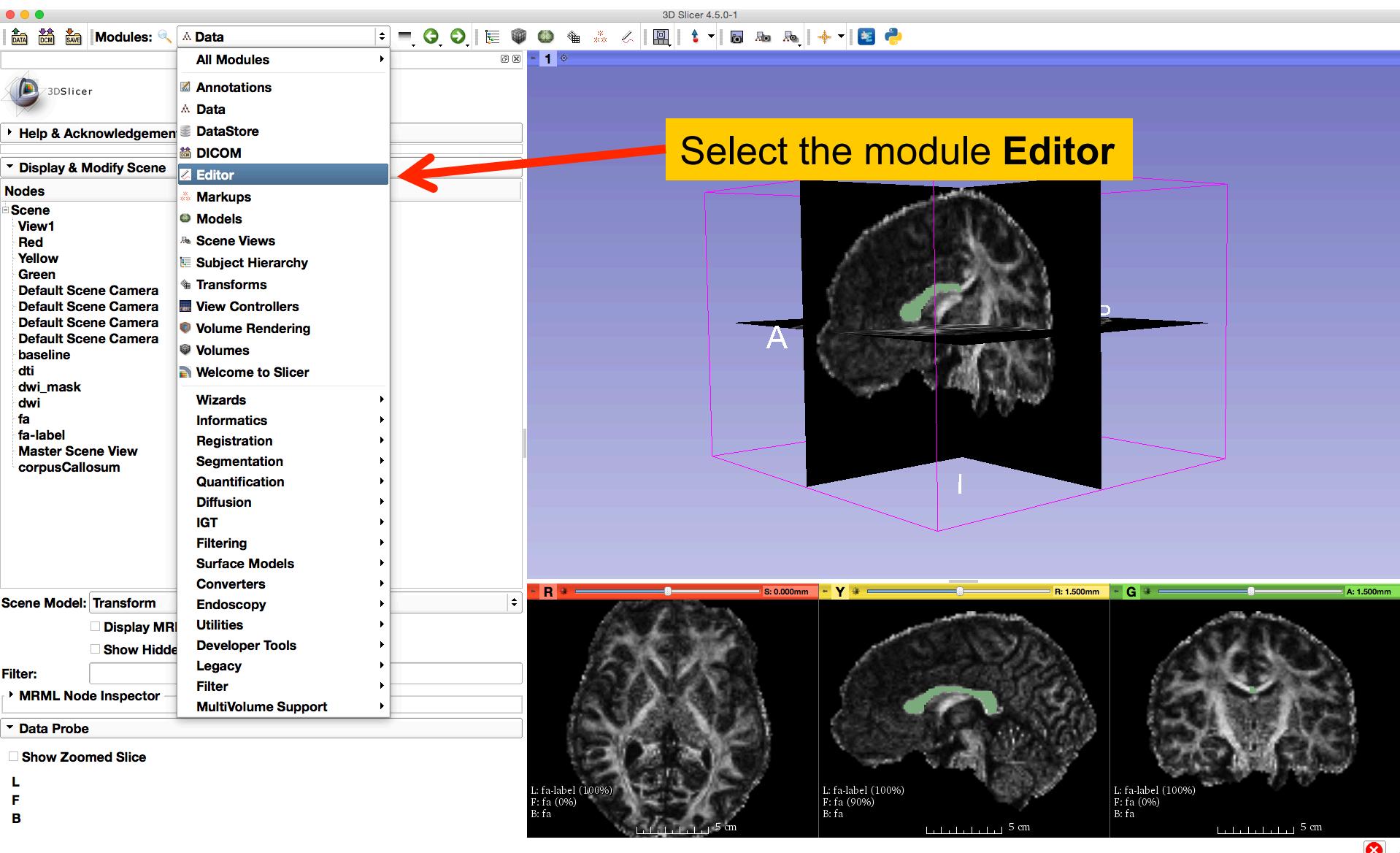
Load MRML Data



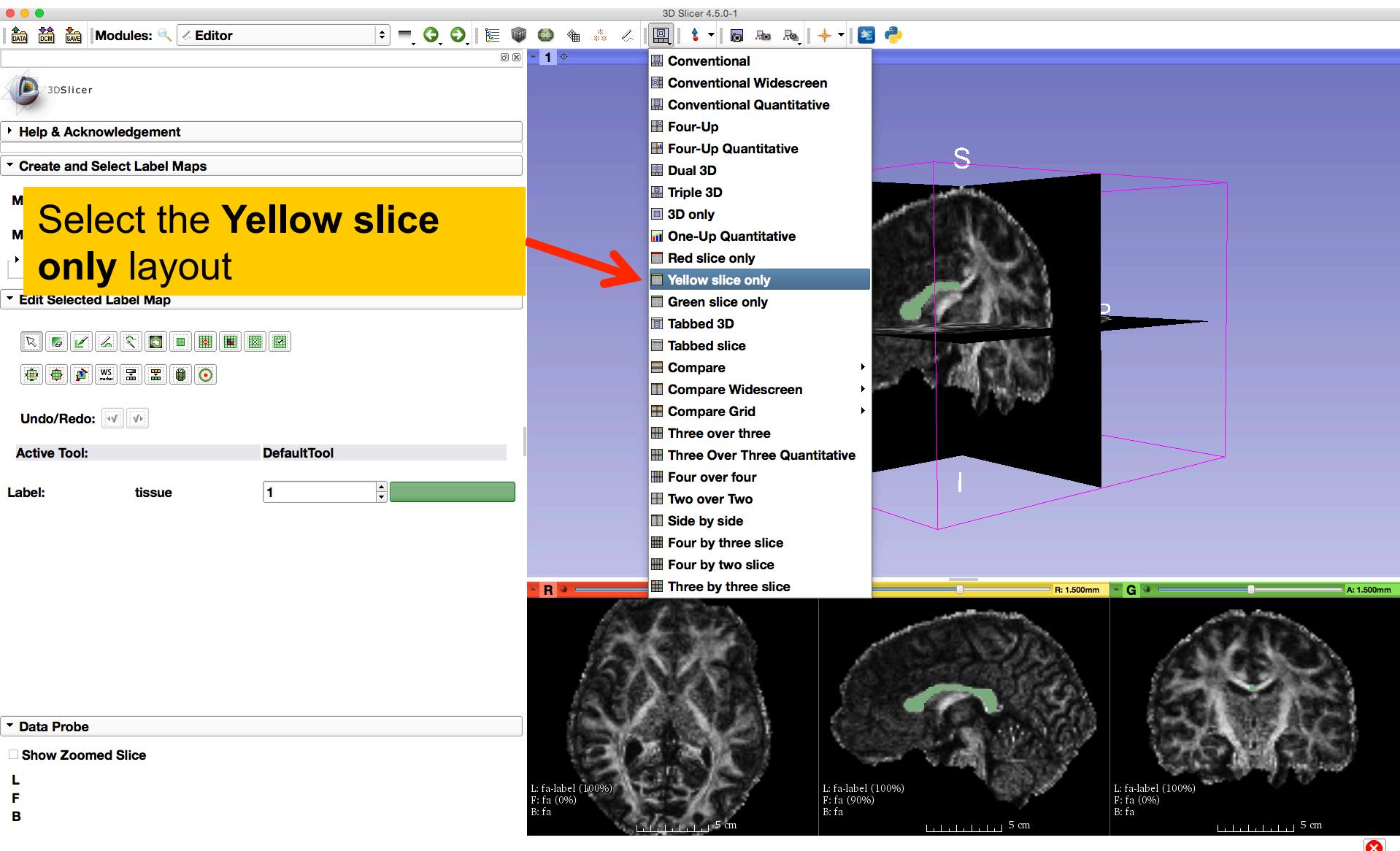
Load MRML Data



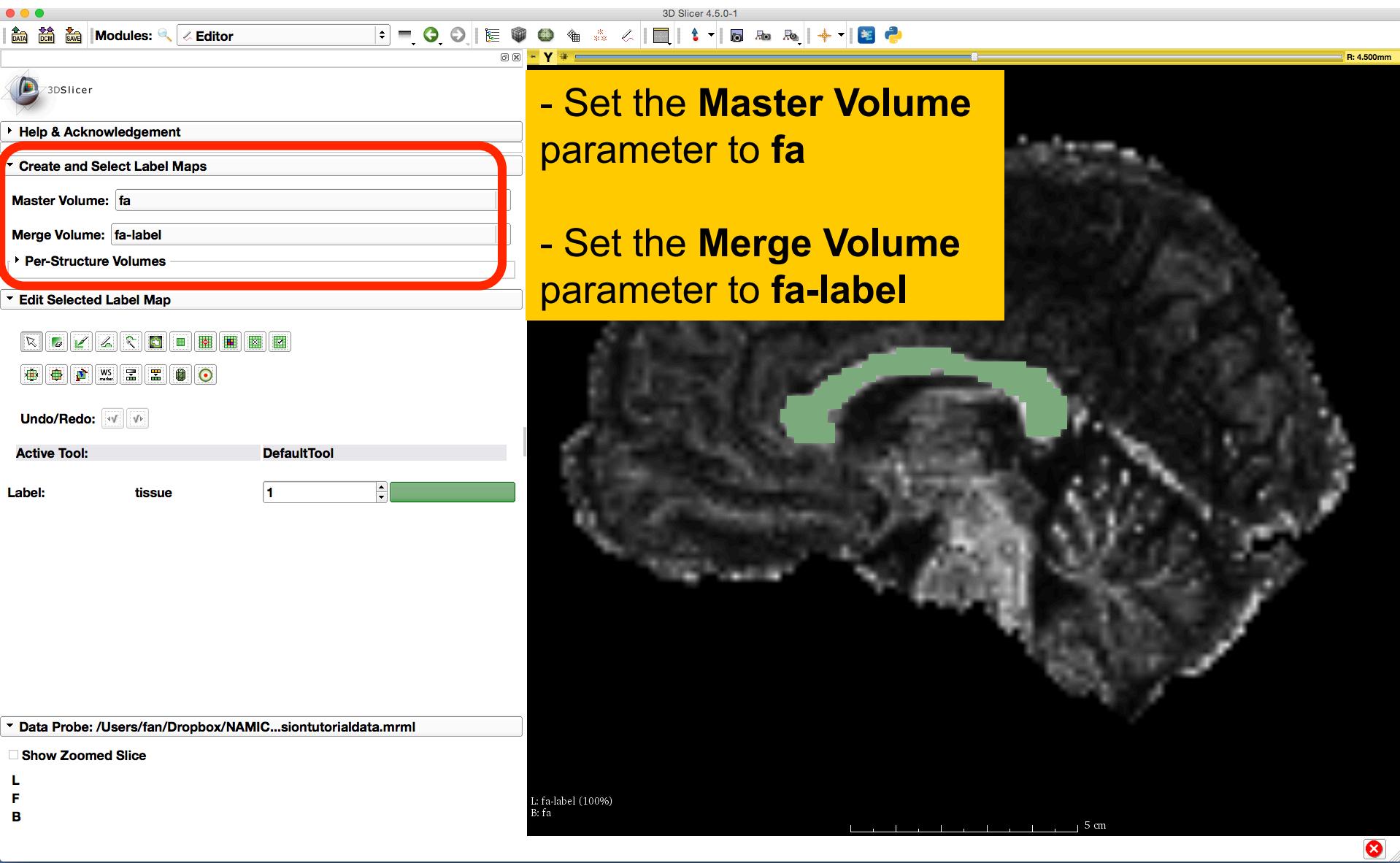
Edit Multiple Labels



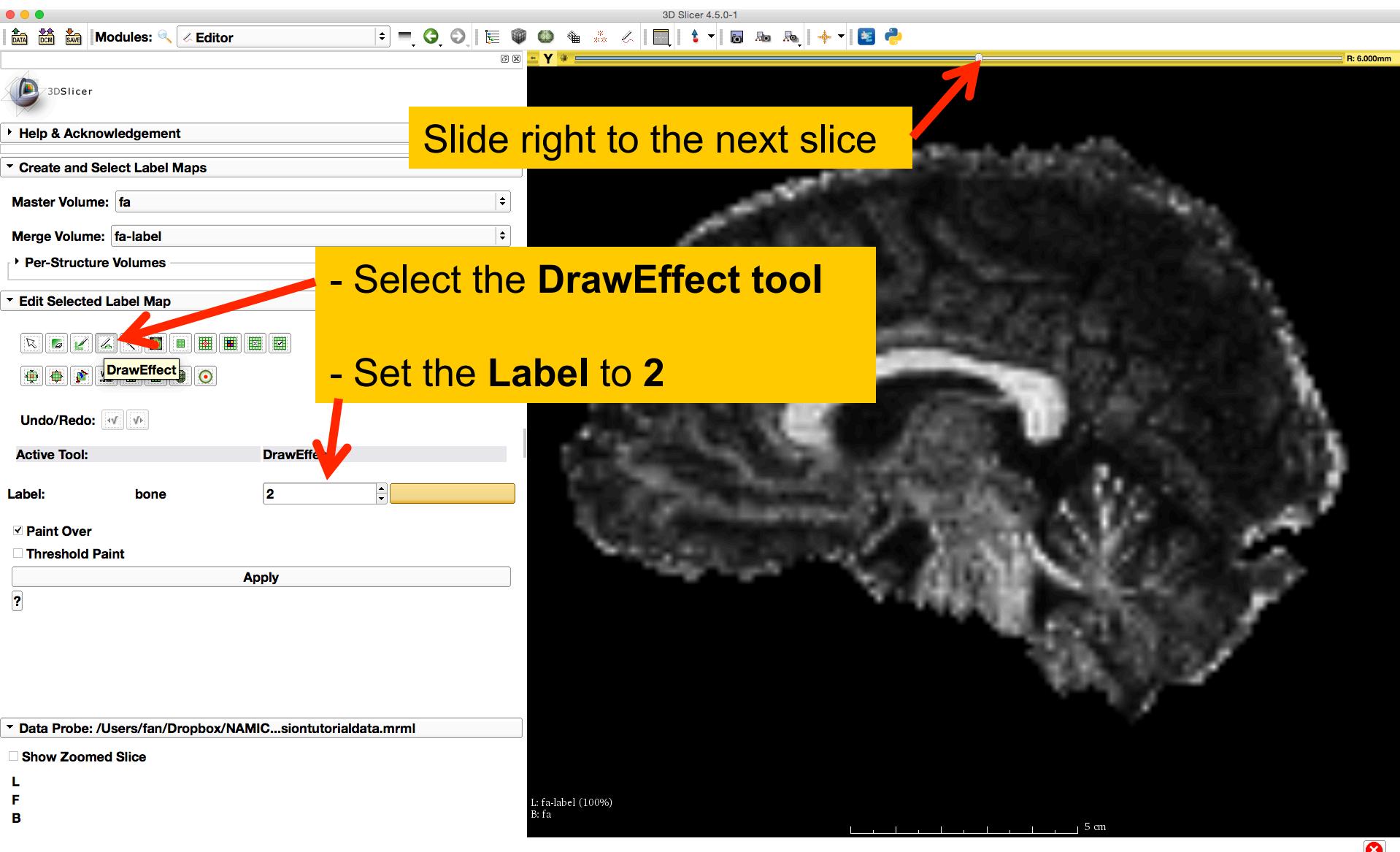
Edit Multiple Labels



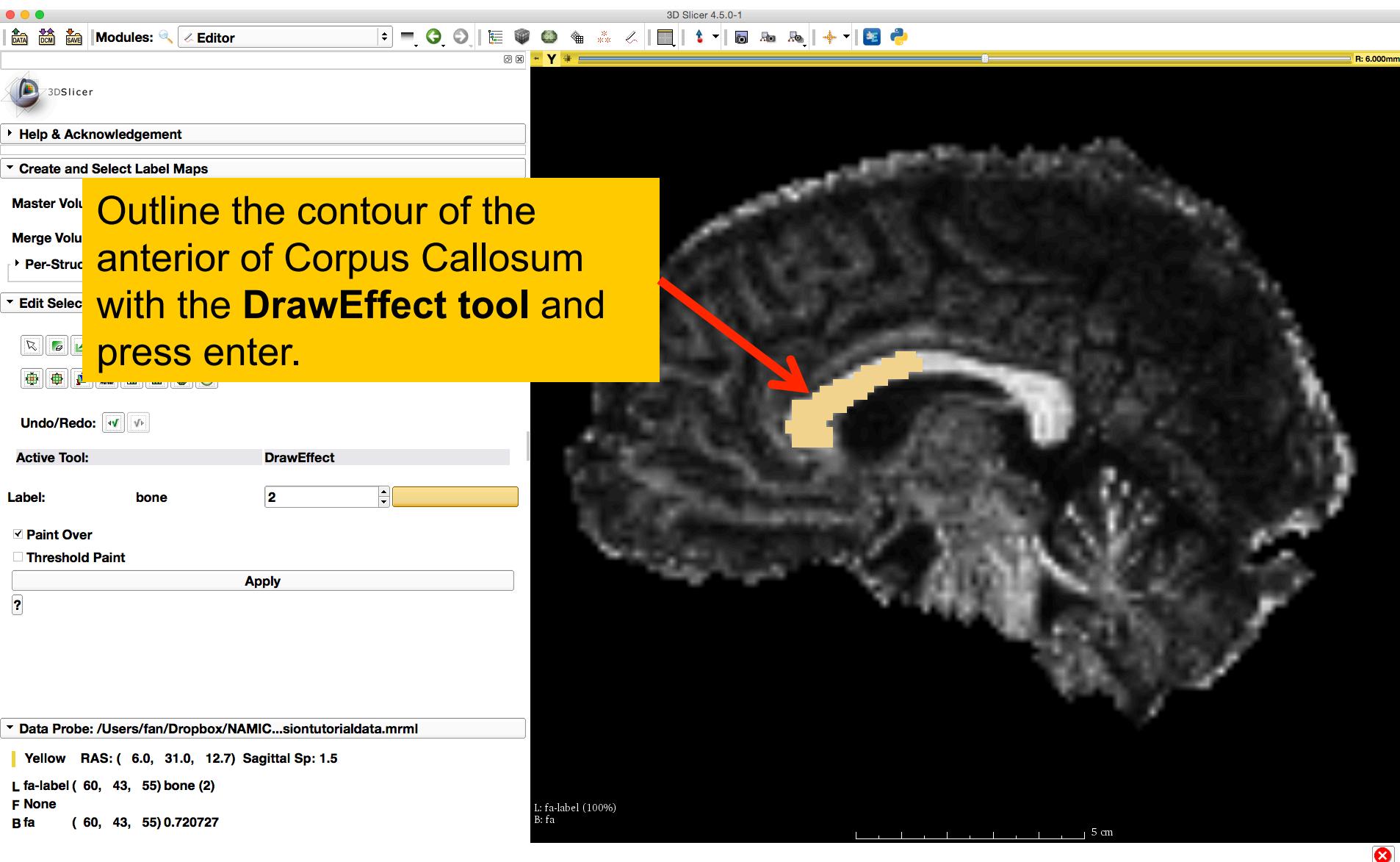
Edit Multiple Labels



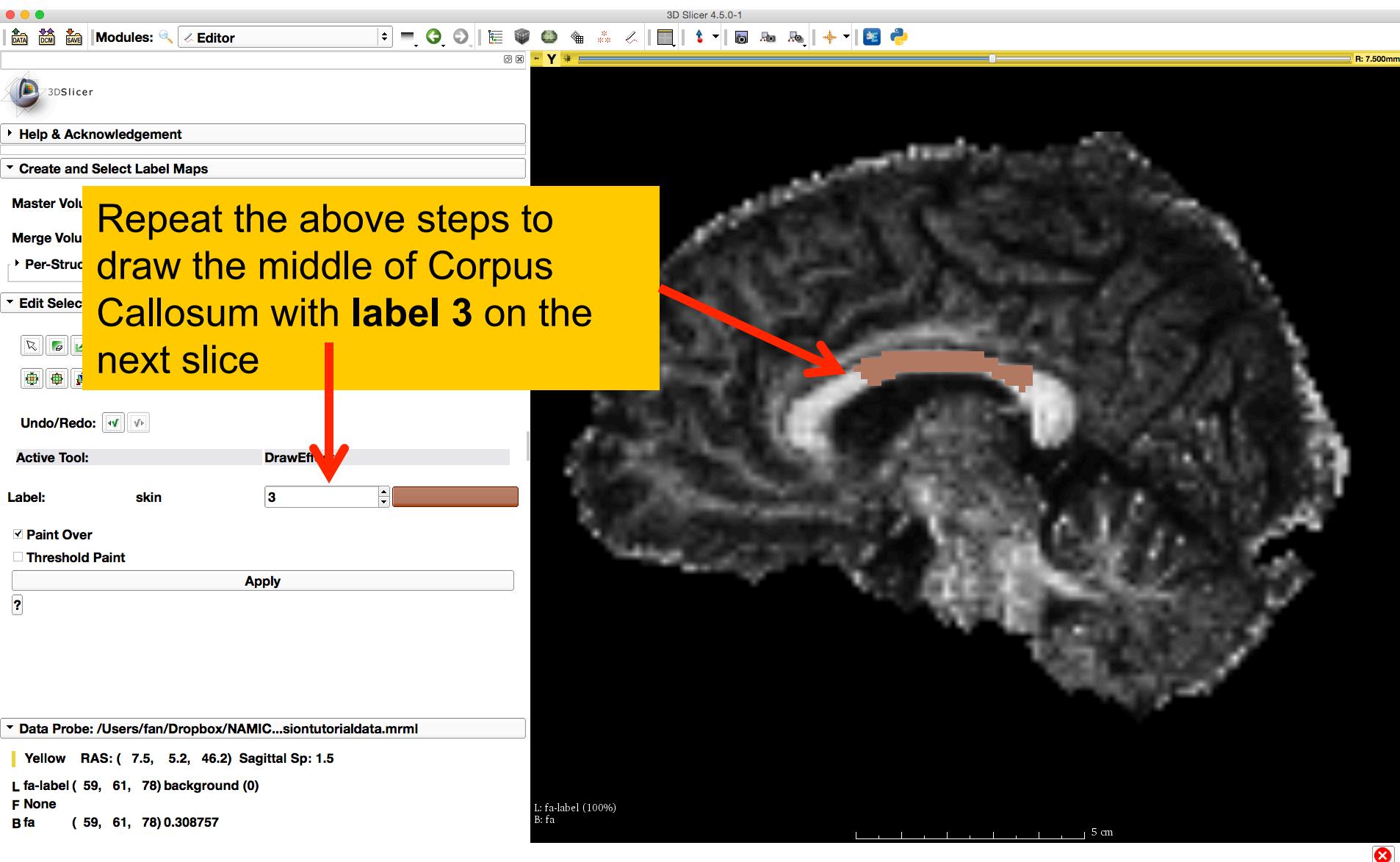
Edit Multiple Labels



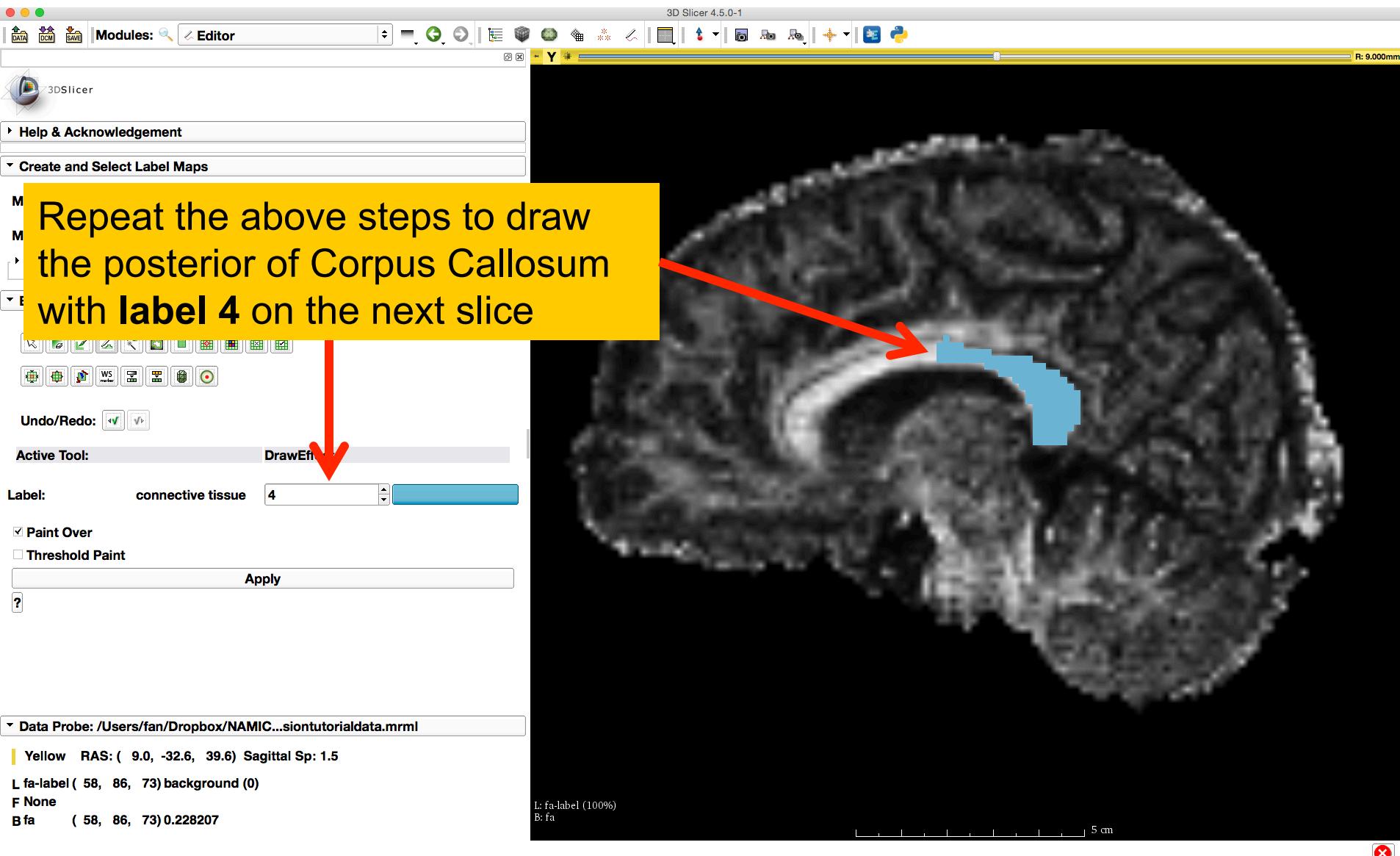
Edit Multiple Labels



Edit Multiple Labels



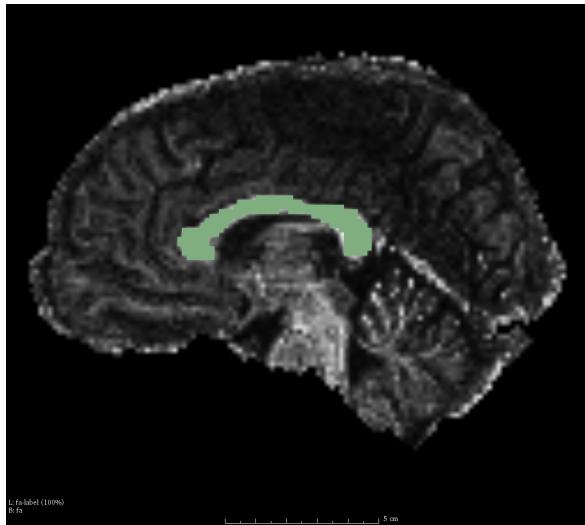
Edit Multiple Labels



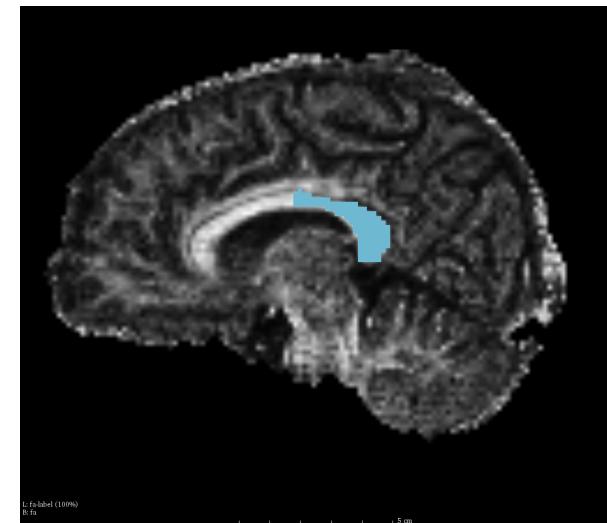
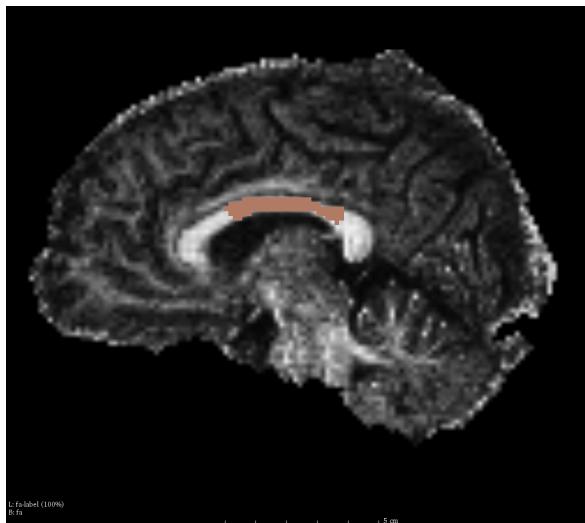
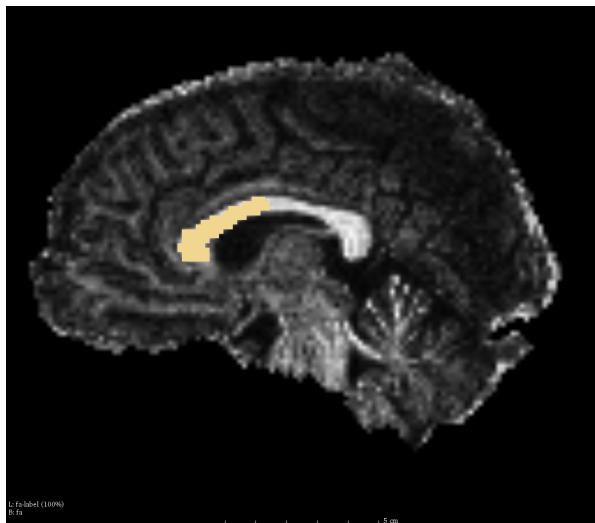
Edit Multiple Labels

Label map on individual slice, with :

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

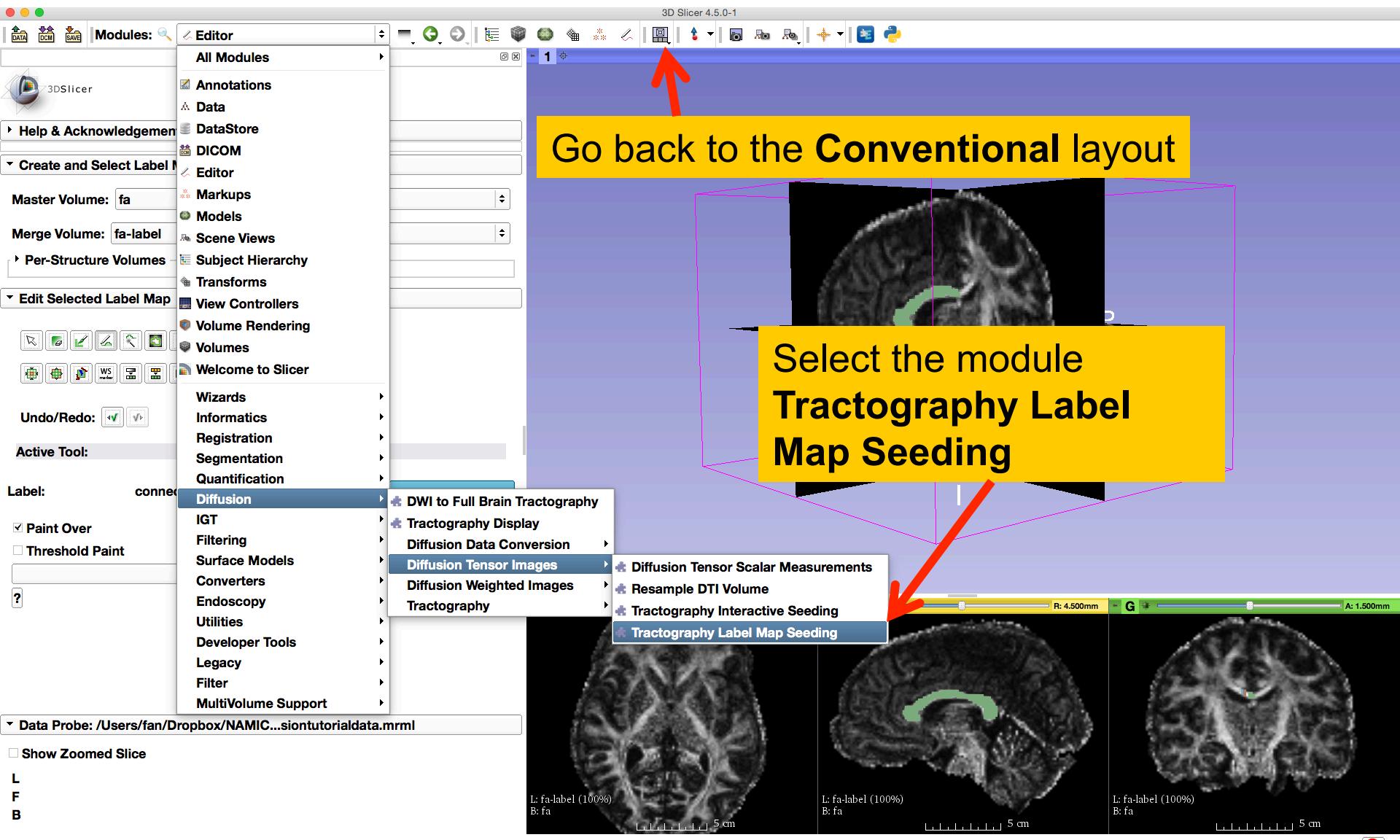


Notice that there are overlaps between different labeled regions*, which will be used to investigate the fiber bundle selection.



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

Whole Brain Tractography



Whole Brain Tractography

3D Slicer 4.5.0-1

Modules: Tractography Label Map Seeding

Help & Acknowledgement

Tractography Label Map Seeding

Parameter set: Tractography Label Map Seeding

IO

Input DTI Volume: dti

Input Label Map: dwi_mask

Output Fiber Bundle: whole_brain_tractography

Seed Placement Options

Use Index Space:

Seed Spacing: 2.00

Random Grid:

Linear Measure Start Threshold: 0.3

Tractography Seeding Parameters

Minimum Path Length: 20.00

Maximum Length: 800.00

Stopping Criteria: LinearMeasure FractionalAnisotropy

Stopping Value: 0.15

Stopping Track Curvature: 0.7

Integration Step Length(mm): 0.5

Label definition

Seeding label: 1

Multiple File Output

Status: Idle

Restore Defaults AutoRun

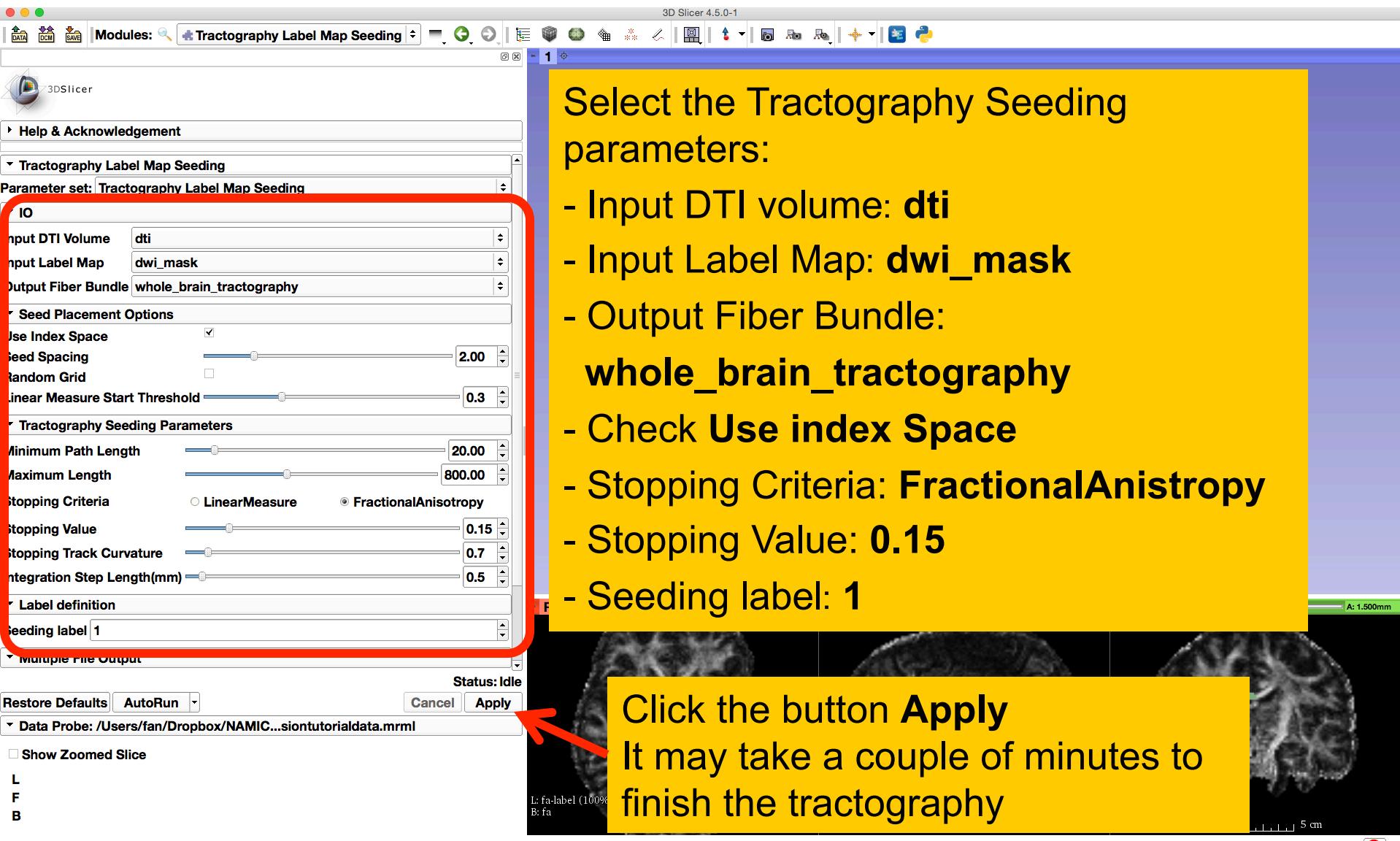
Data Probe: /Users/fan/Dropbox/NAMIC...siontutorialdata.mrml

Show Zoomed Slice L F B

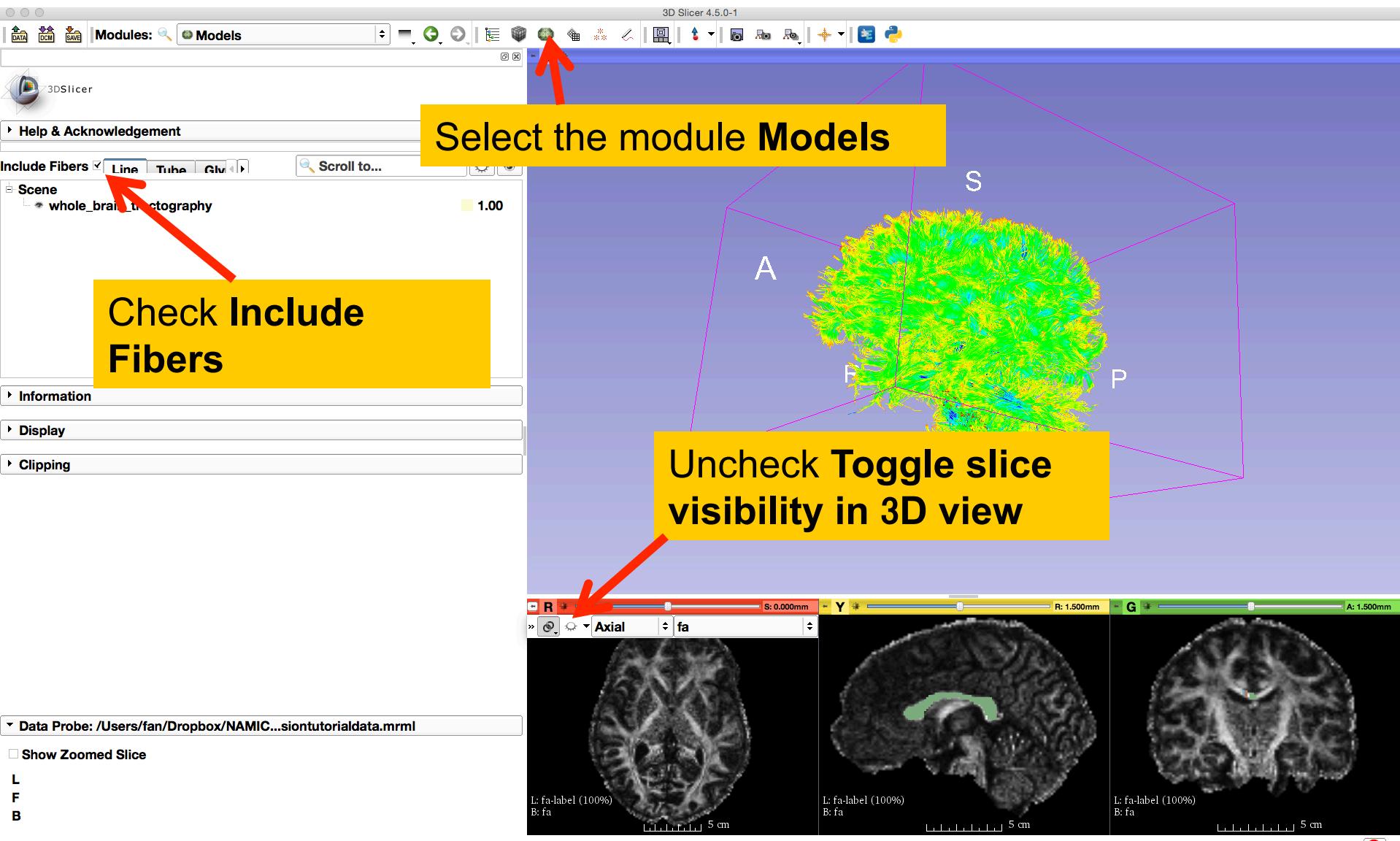
Select the Tractography Seeding parameters:

- Input DTI volume: **dti**
- Input Label Map: **dwi_mask**
- Output Fiber Bundle:
whole_brain_tractography
- Check **Use index Space**
- Stopping Criteria: **FractionalAnisotropy**
- Stopping Value: **0.15**
- Seeding label: **1**

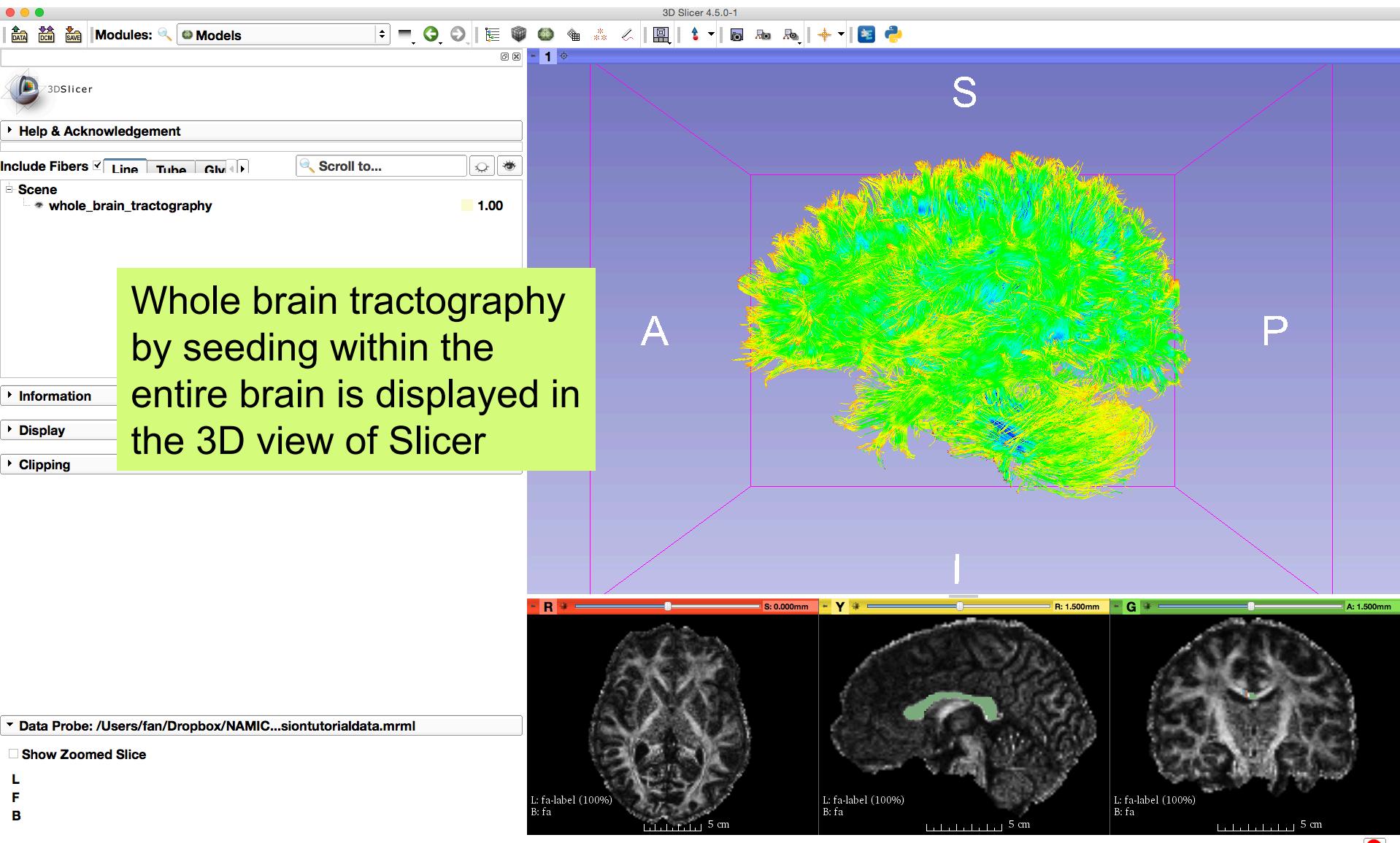
Click the button **Apply**
It may take a couple of minutes to finish the tractography



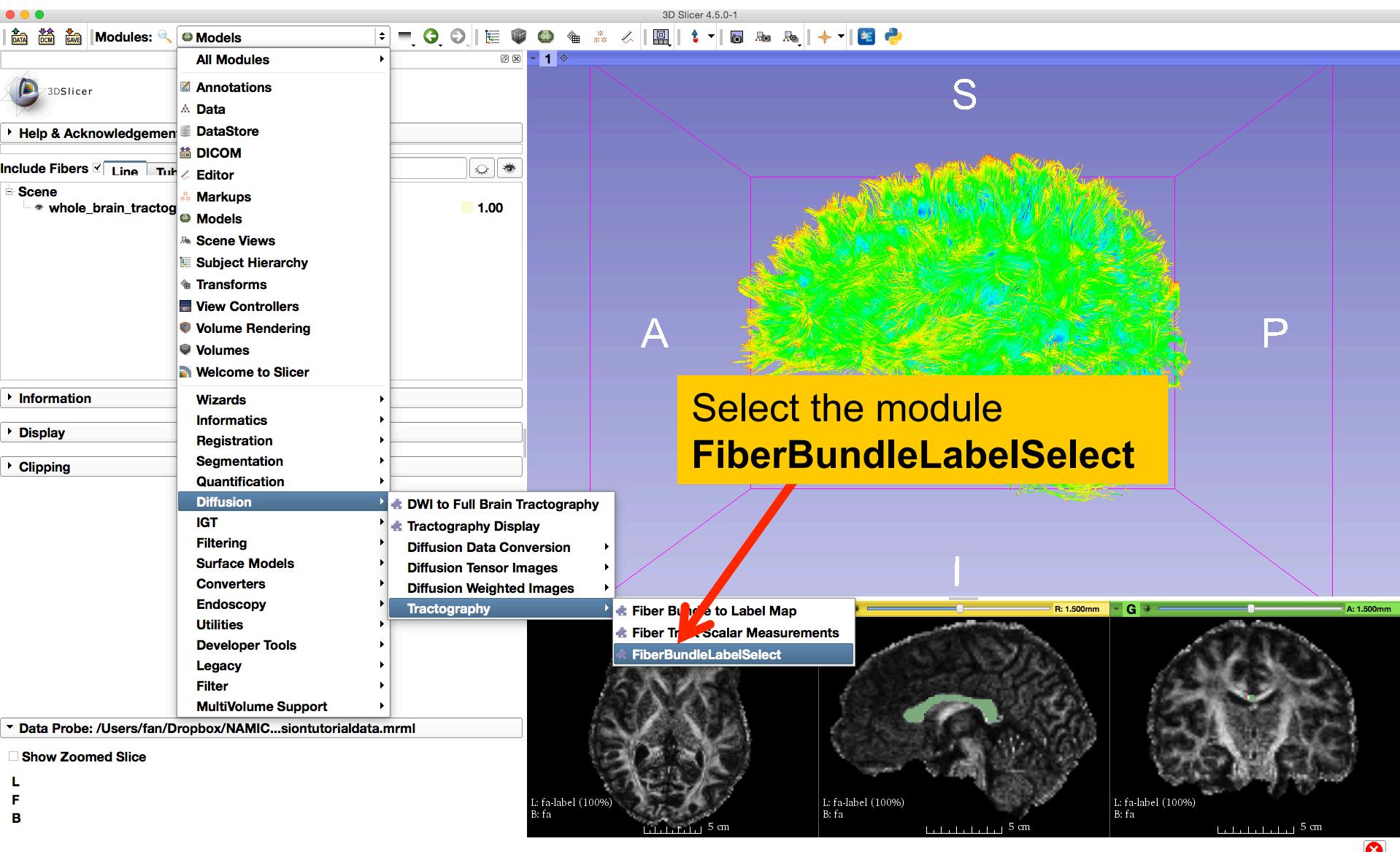
Whole Brain Tractography



Whole Brain Tractography



Fiber Bundle Label Selection



Single Label Selection

3D Slicer 4.5.0-1

Modules: FiberBundleLabelSelect

Help & Acknowledgement

FiberBundleLabelSelect

Parameter set: FiberBundleLabelSelect

Input Label Map: fa-label

Input Fiber Bundle: whole_brain_tractography

Output Fiber Bundle: bundle_label1_include

Labels to include: 1

Combine include labels: OR AND

Labels to exclude:

Combine exclude labels: OR AND

Status: Idle

Cancel Apply

Data Probe: /Users/fan/Dropbox/NAMIC...siontutorialdata.mrml

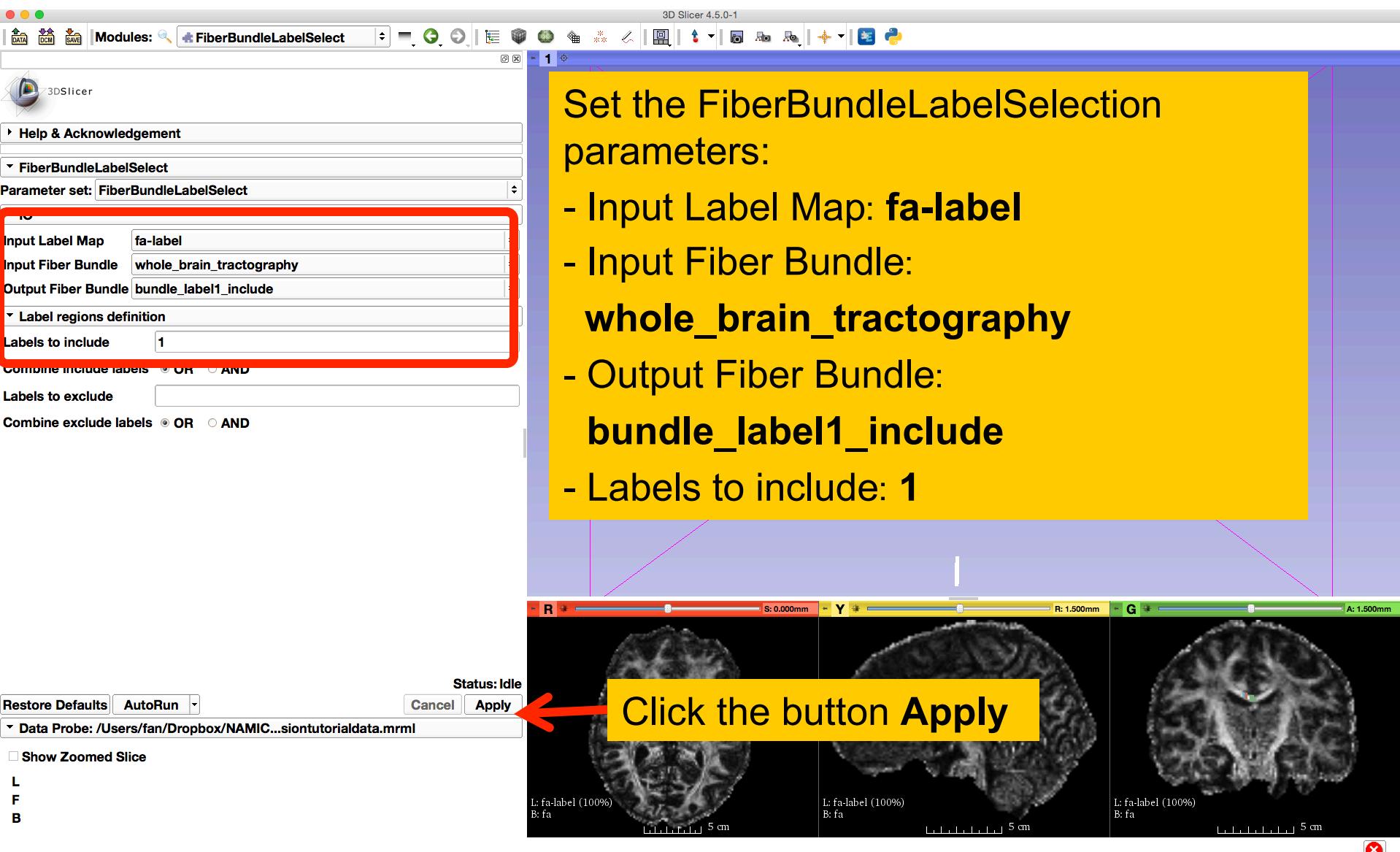
Show Zoomed Slice

L F B

Set the FiberBundleLabelSelection parameters:

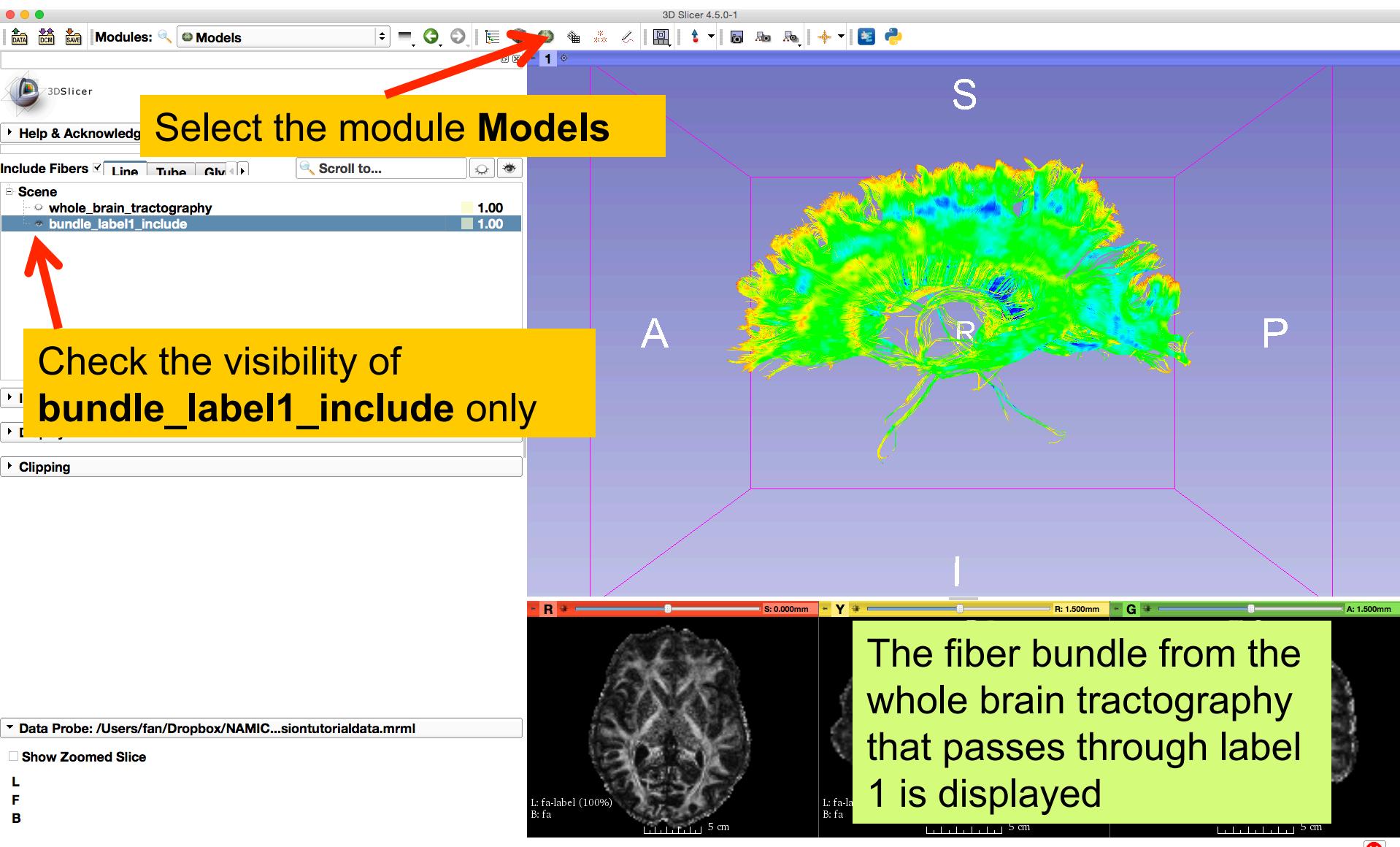
- Input Label Map: **fa-label**
- Input Fiber Bundle:
whole_brain_tractography
- Output Fiber Bundle:
bundle_label1_include
- Labels to include: 1

Click the button **Apply**

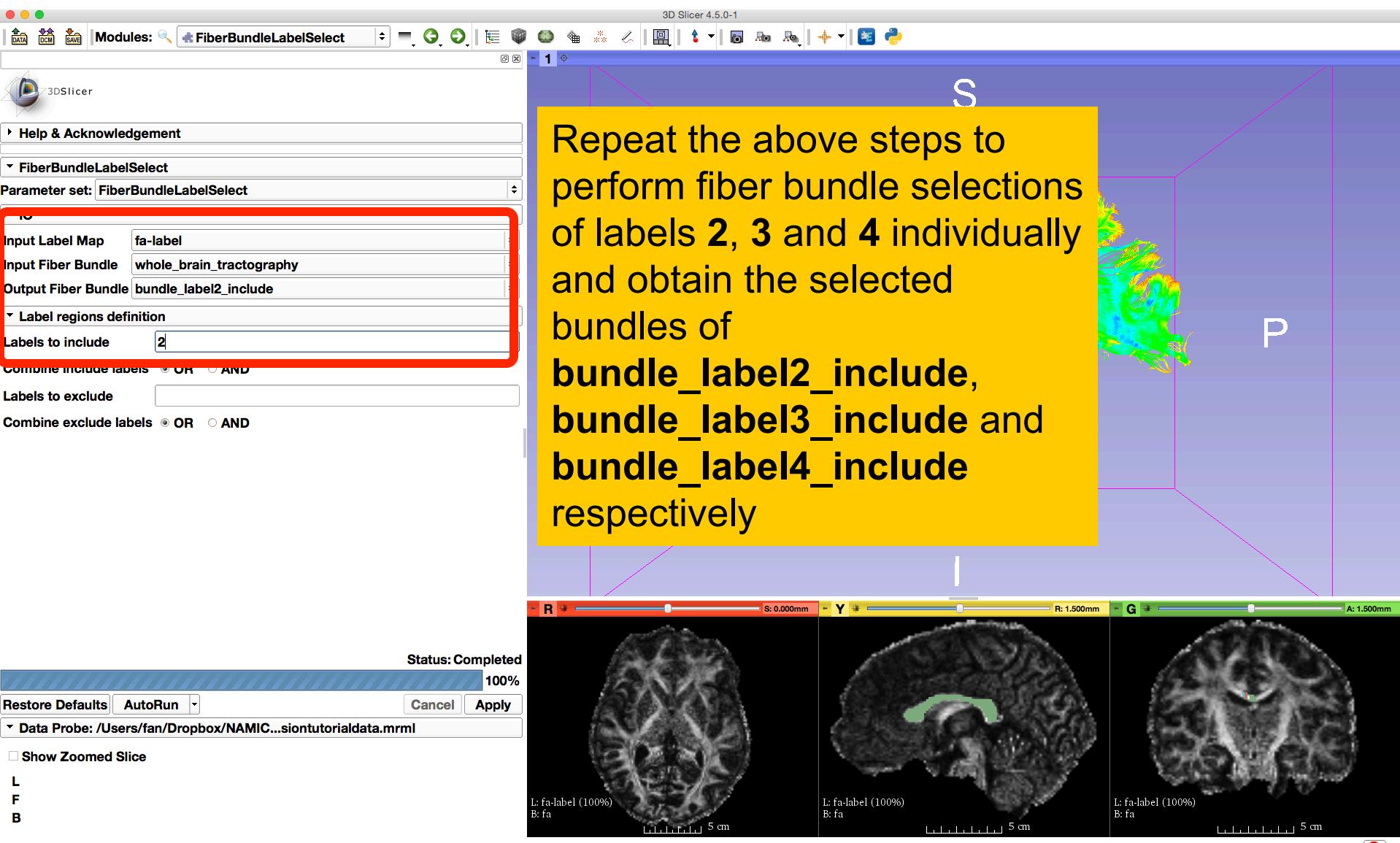


The image shows the 3D Slicer software interface. On the left, the 'FiberBundleLabelSelect' module parameters are displayed. A red box highlights the 'Input Label Map' field containing 'fa-label'. Below it are 'Input Fiber Bundle' (set to 'whole_brain_tractography') and 'Output Fiber Bundle' (set to 'bundle_label1_include'). Under 'Label regions definition', 'Labels to include' is set to '1'. At the bottom of the module panel, there are buttons for 'Status: Idle', 'Cancel', and 'Apply'. A large yellow callout box points to the 'Apply' button with the instruction 'Click the button **Apply**'. On the right side of the interface, three axial brain slices are shown. The top slice has a yellow box around its central region with the text 'L: fa-label (100%) B: fa'. The bottom slices also show similar labeling. The overall background is light blue.

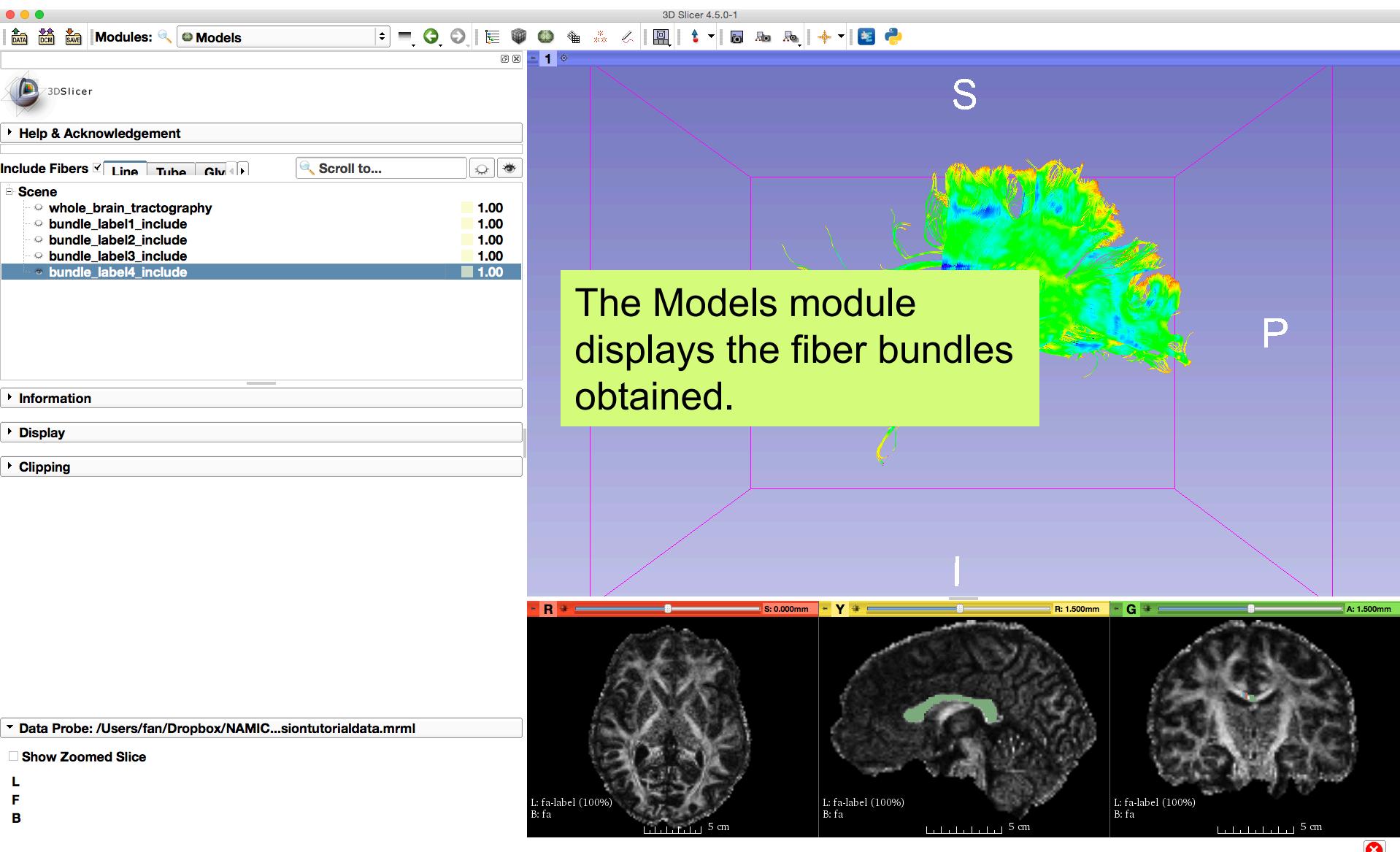
Single Label Selection



Single Label Selection

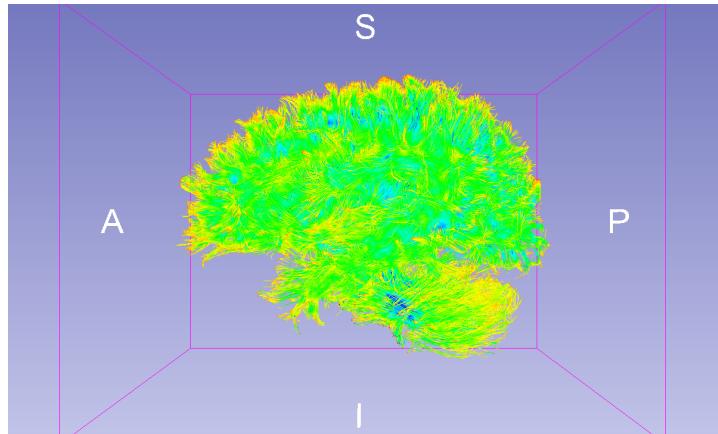


Single Label Selection

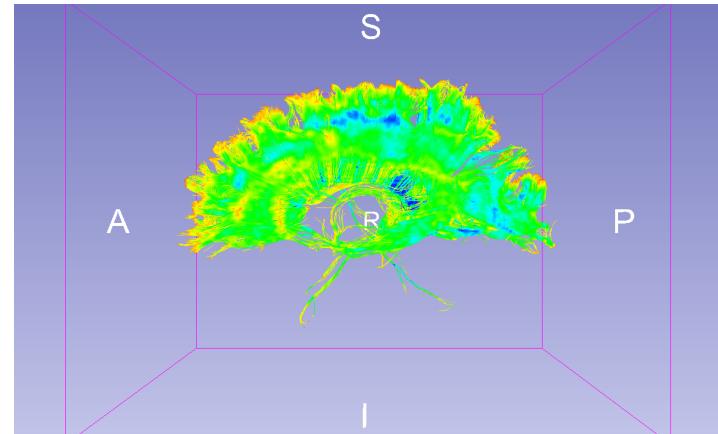


Single Label Selection

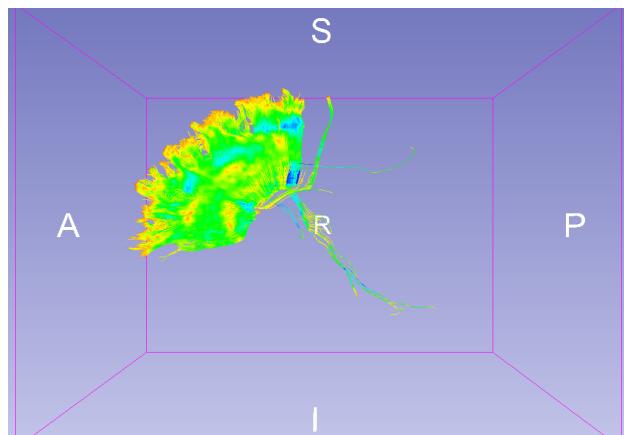
Whole Brain



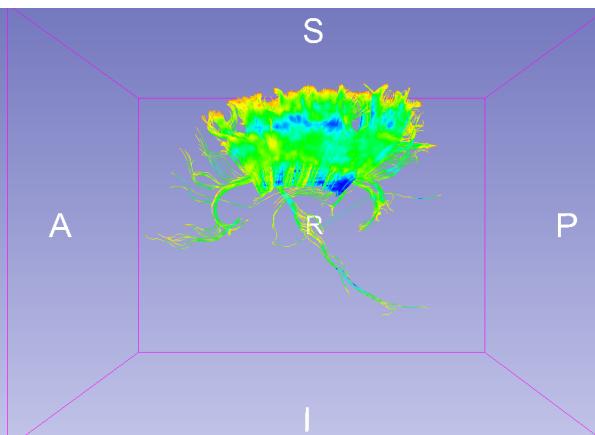
Label 1



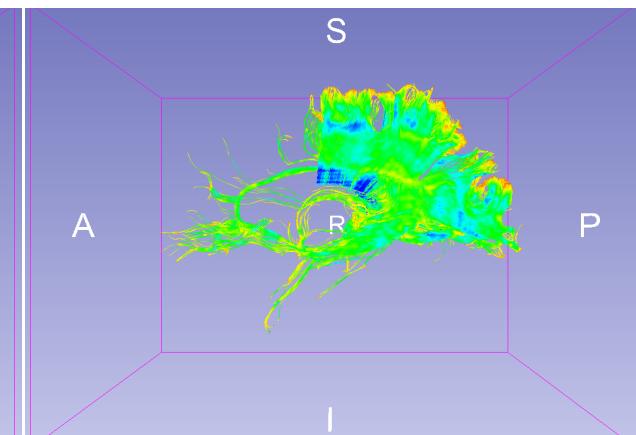
Label 2



Label 3



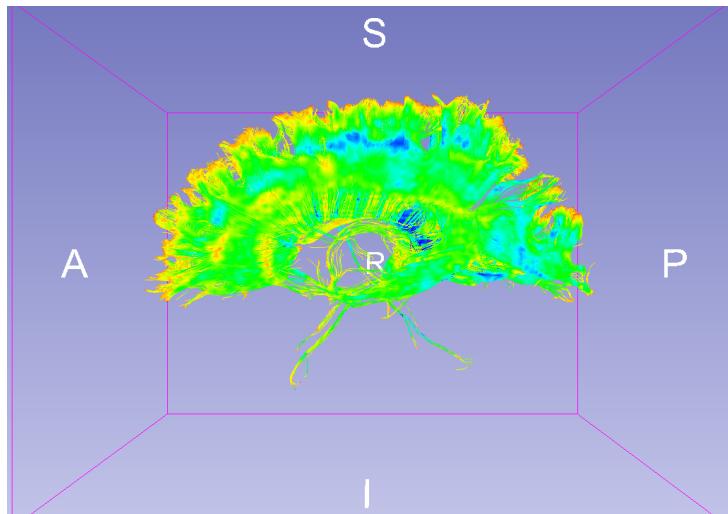
Label 4



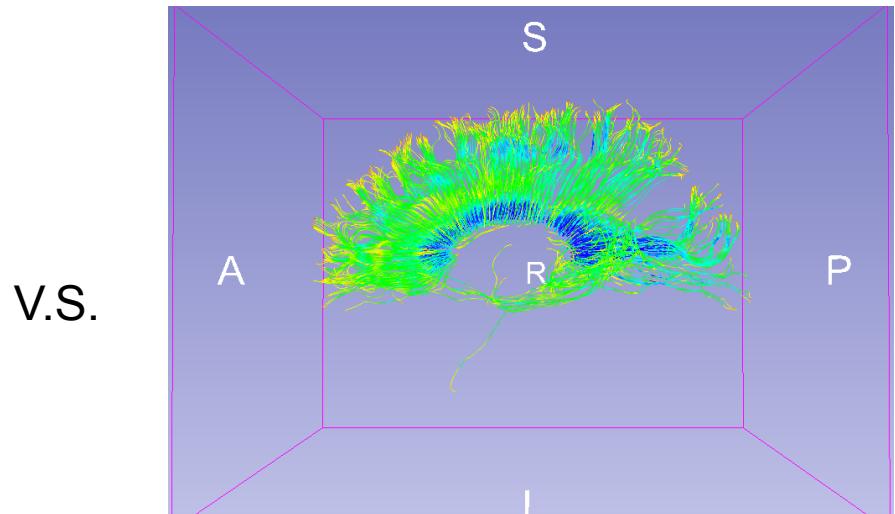
Single Label Selection

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

▼ Label regions definition

Labels to include

2,3

Combine include labels

OR

AND

Labels to exclude

And or Or logical
operation used to
combine include
labels

AND

Multiple Labels Selection (AND)

Set the FiberBundleLabelSelection parameters:

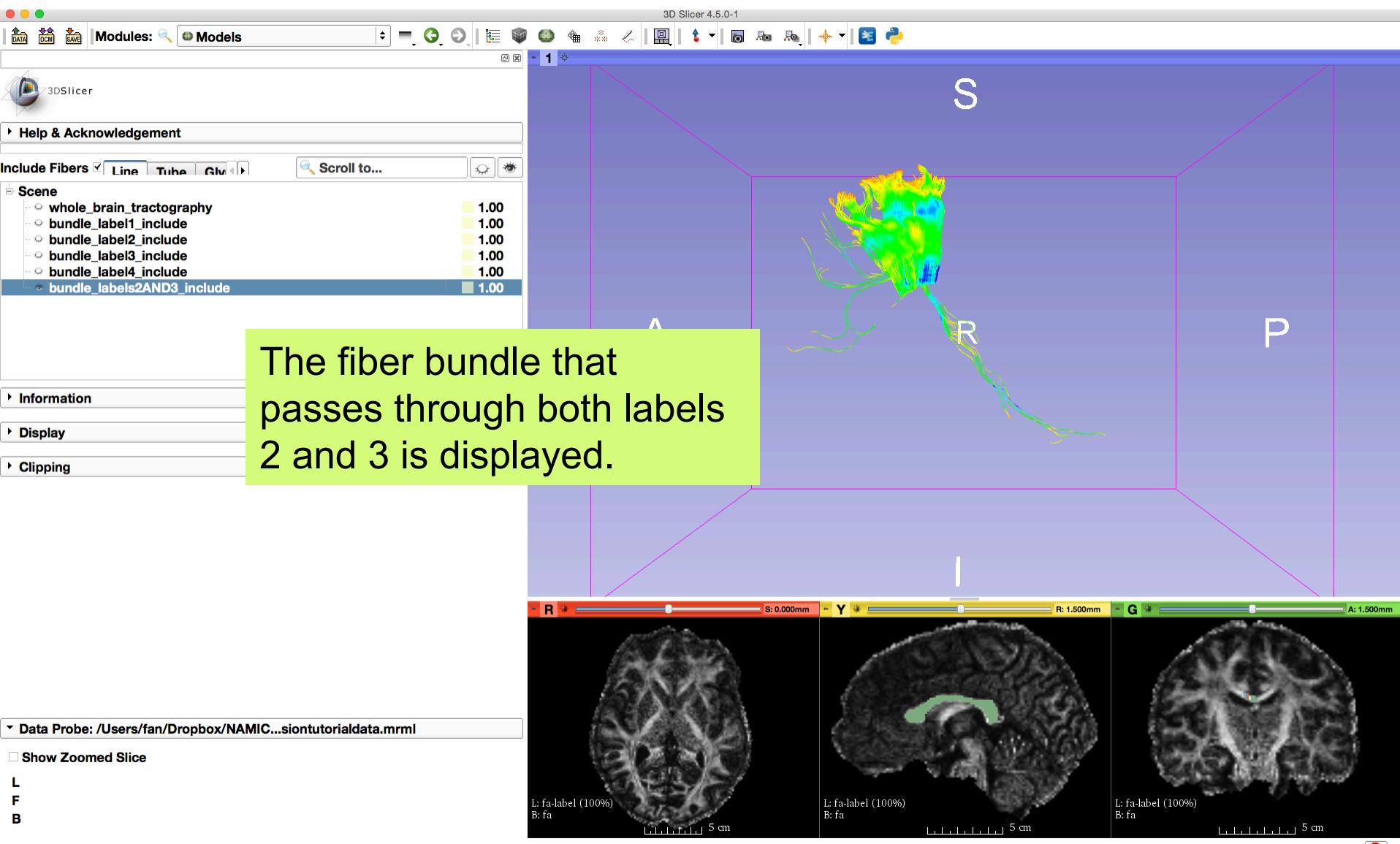
- Input Label Map: **fa-label**
- Input Fiber Bundle: **whole_brain_tractography**
- Output Fiber Bundle: **bundle_labels2AND3_include**
- Labels to include: **2,3**
- Combine include labels AND
- Labels to exclude
- Combine exclude labels OR AND

Set **Combine include labels** to **AND**

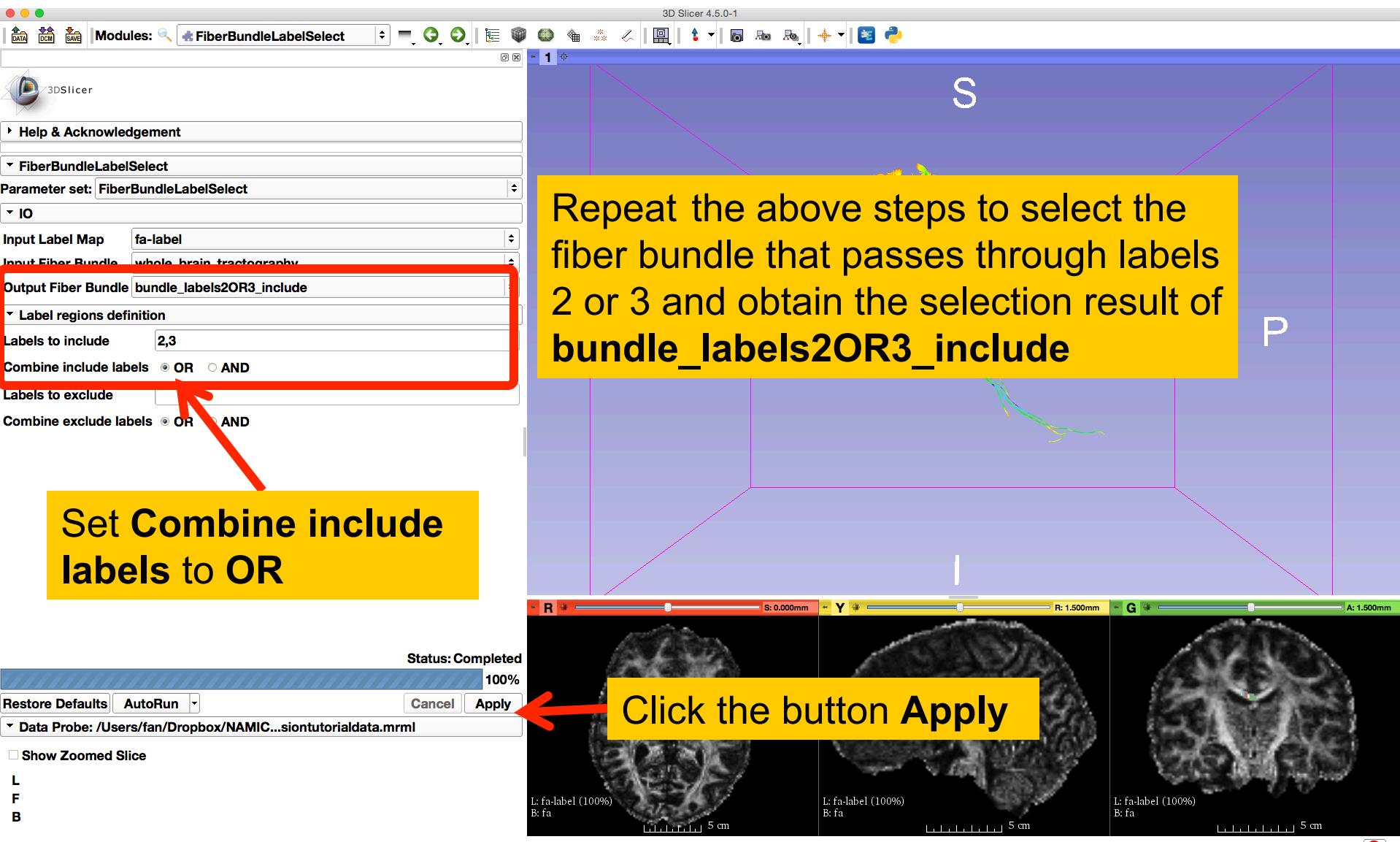
Click the button **Apply**

The screenshot shows the 3D Slicer interface with the 'FiberBundleLabelSelect' module open. A red box highlights the 'Labels to include' field set to '2,3' and the 'Combine include labels' radio button set to 'AND'. A yellow box with a black border contains the instructions. Another yellow box with a black border at the bottom right of the slice image contains the 'Click the button Apply' instruction. The 3D brain slice shows white tracts against a black background, with three orthogonal slices (R, Y, G) and a status bar indicating 'Status: Completed' and '100%'. A legend at the bottom left identifies the labels: L: fa-label (100%), B: fa.

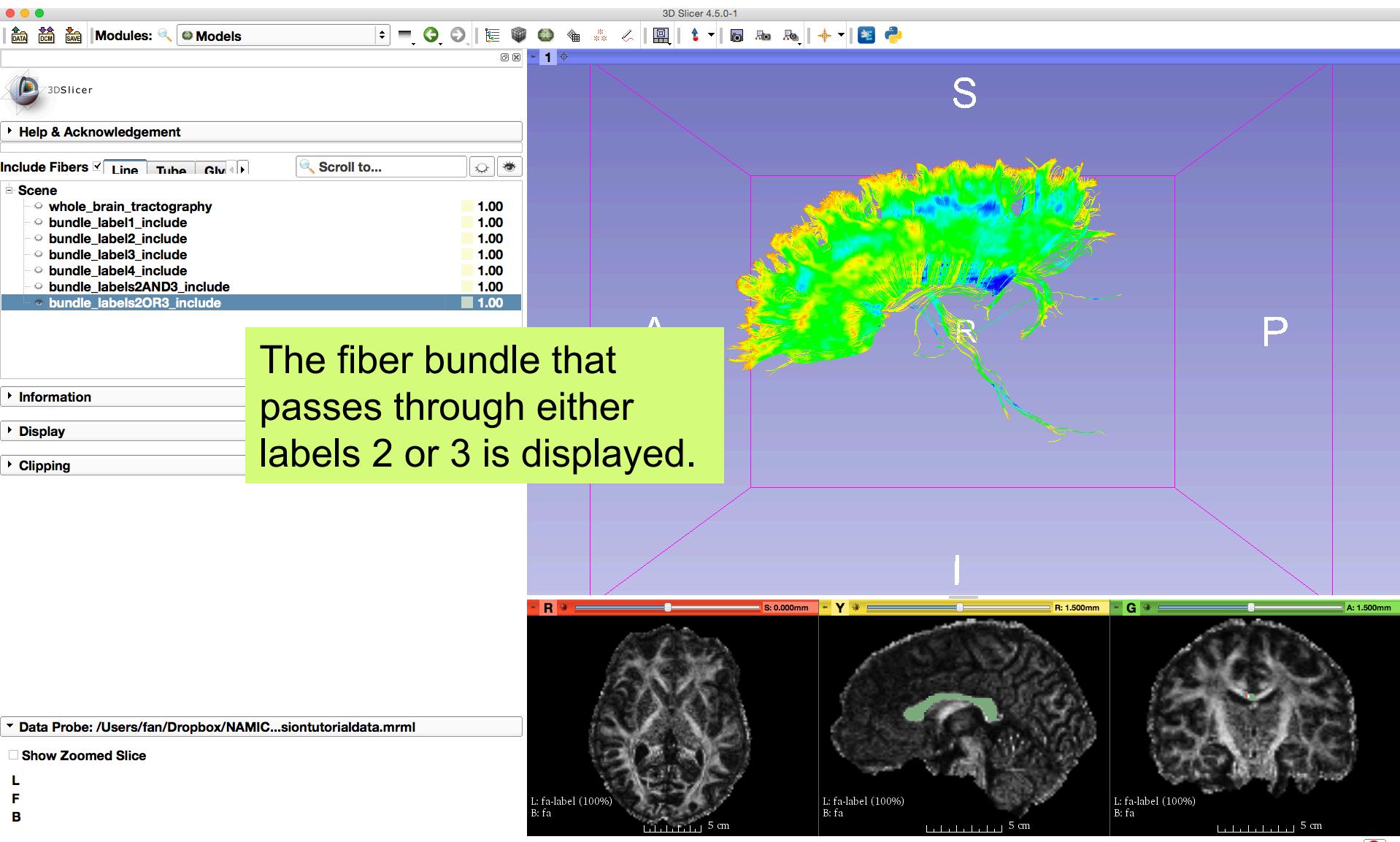
Multiple Labels Selection (AND)



Multiple Labels Selection (OR)

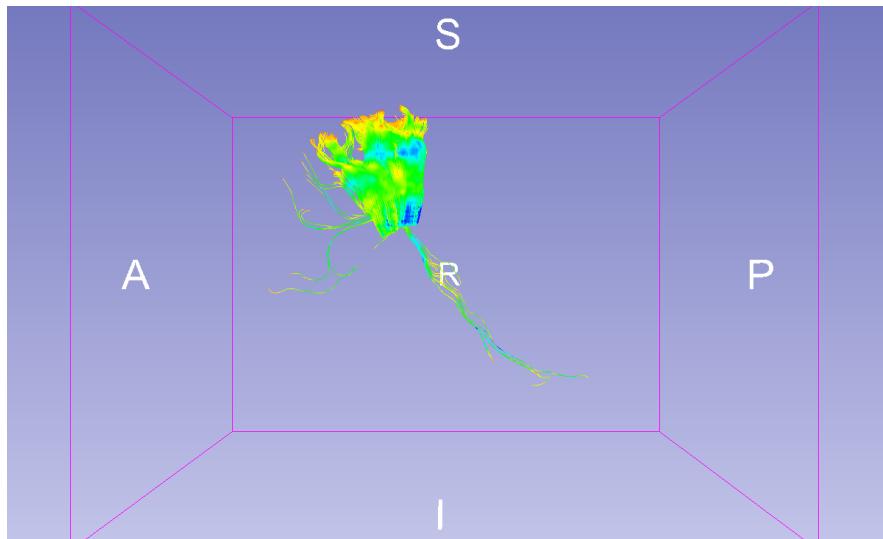


Multiple Labels Selection (OR)

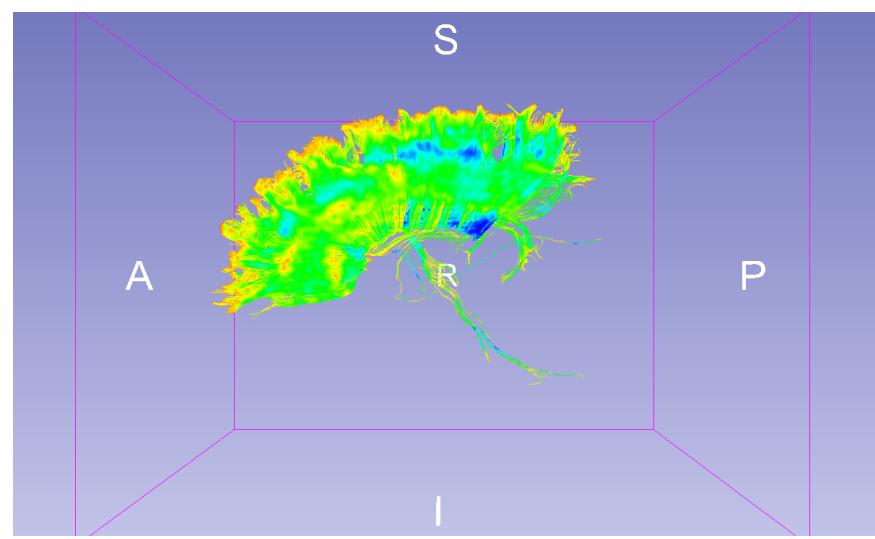


Multiple Labels Selection

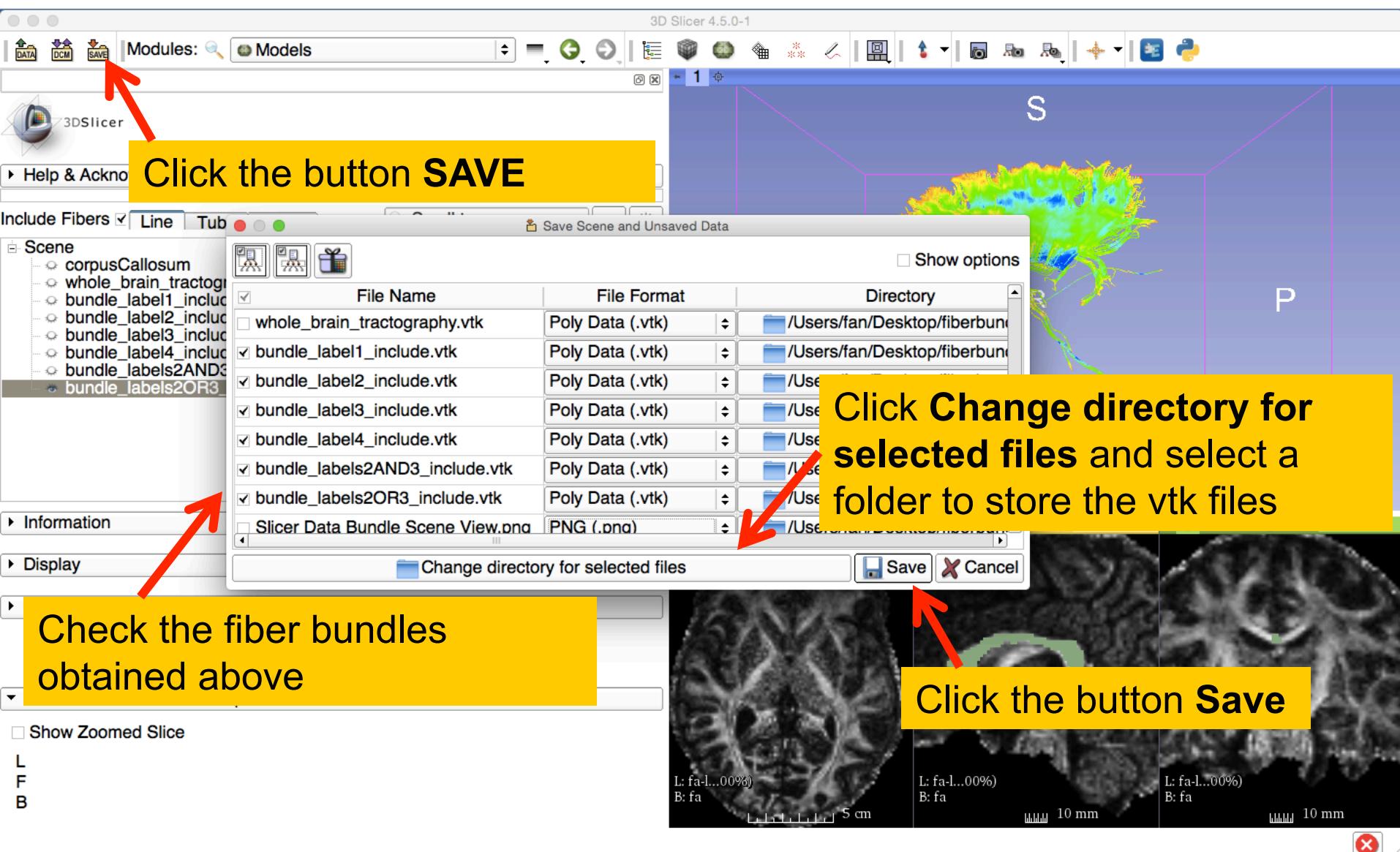
Labels 2 and 3



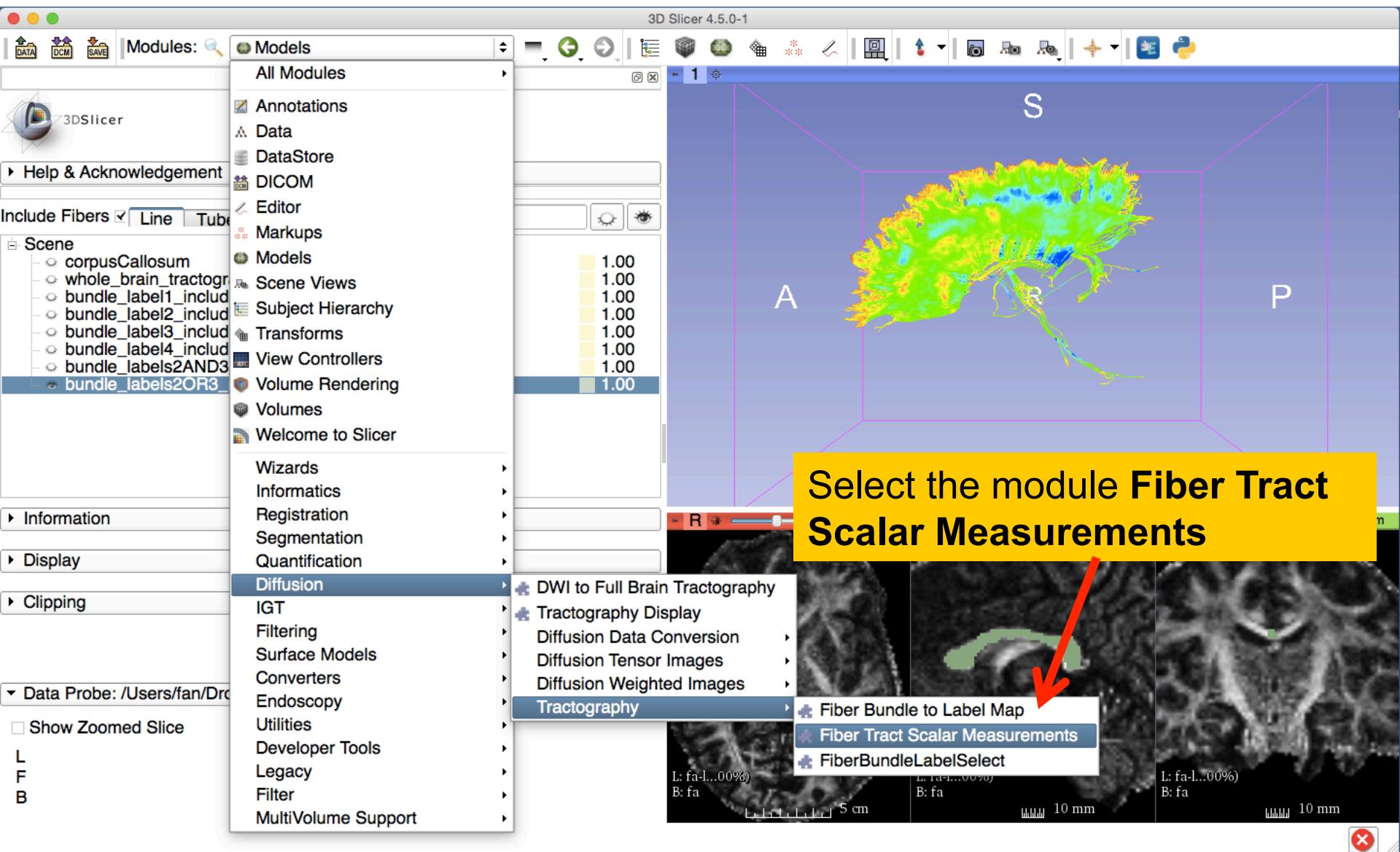
Labels 2 or 3



Save Fiber Bundles



Fiber Tract Scalar Measurements



Fiber Tract Scalar Measurements

The screenshot shows the 3D Slicer 4.5.0-1 interface. The top menu bar includes 'DATA', 'DCM', 'SAVE', 'Modules' (with 'Fiber Tract Scalar Measurements' selected), and various tool icons. The left sidebar has sections for 'Help & Acknowledgement' and 'Fiber Tract Scalar Measurements'. The main window displays the 'Fiber Tract Scalar Measurements' module parameters. A red box highlights the 'Parameter set: Fiber Tract Scalar Measurements' section and the 'Select Input Type' dropdown. The 'Select Input Type' dropdown is set to 'Fibers_File_Folder' (radio button selected). Below it is a 'Select a ModelHierarchy' dropdown containing '/Users/fan/Desktop/fiberbundles'. The 'Output Text File' field is set to 'desktop/fiberbundles/measurements.csv'. The 'Select Output Format' dropdown is set to 'Column_Hierarchy' (radio button selected). The 'Output Field Separator' dropdown is set to 'Tab' (radio button selected). At the bottom of the module window are 'Status: Idle', 'Cancel', and 'Apply' buttons. A red arrow points from a yellow box labeled 'Click the button Apply' to the 'Apply' button.

3D Slicer 4.5.0-1

Modules: Fiber Tract Scalar Measurements

3DSlicer

Help & Acknowledgement

Fiber Tract Scalar Measurements

Parameter set: Fiber Tract Scalar Measurements

IO

Select Input Type

Fibers Hierarchy

Fibers File Folder

Output Text File

Select Output Format

Output Field Separator

Status: Idle

Cancel

Apply

Restore Defaults

AutoRun

Data Probe

Show Zoomed Slice

L

F

B

S

Set the FiberTractScalarMeasurements 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**

5 cm

5 cm

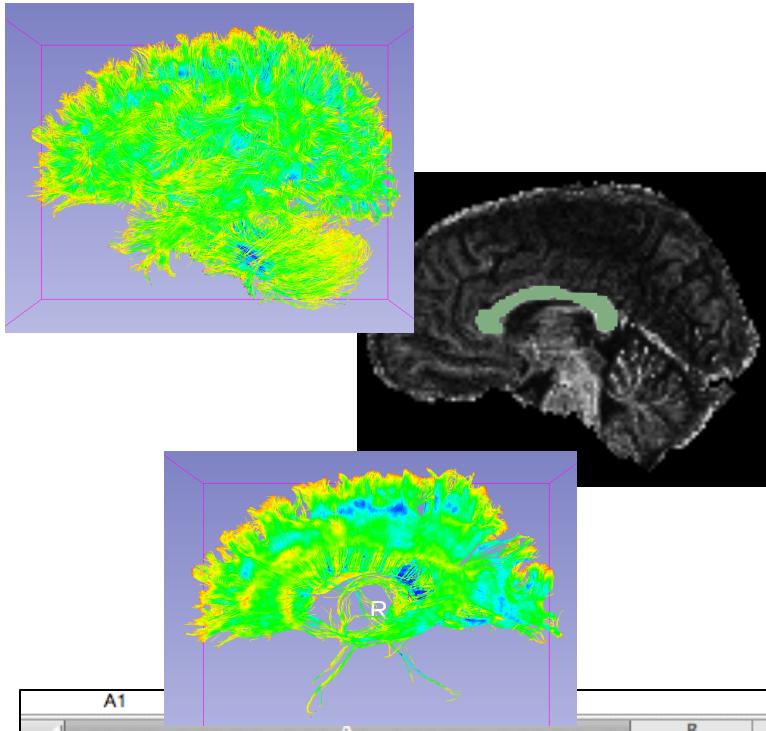
5 cm

Fiber Tract Scalar 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 U01CA199459

National Center for Image Guided Therapy (NCIGT)

NIH P41EB015898

Neuroimage Analysis Center (NAC)

NIH P41EB015902