

# 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 4.8.1, revision 26813, 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

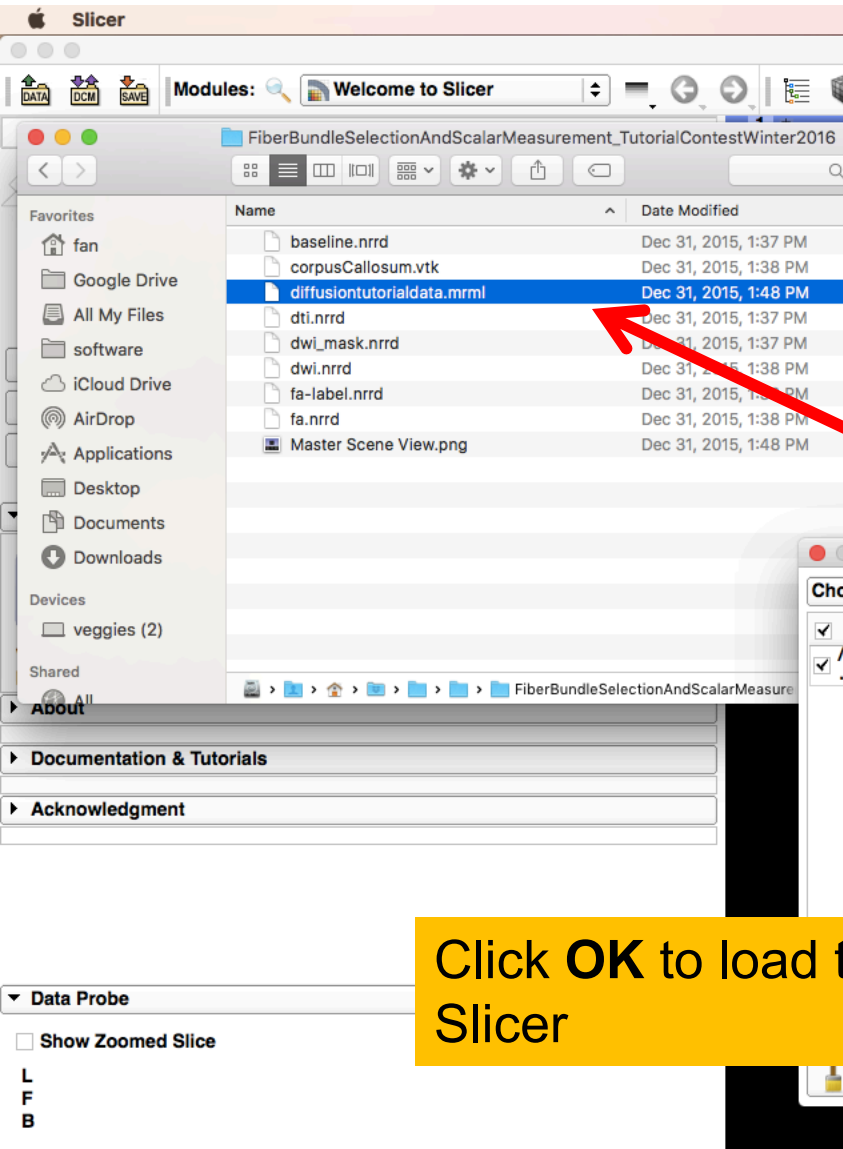
An open-source project to improve and extend diffusion magnetic resonance imaging software in 3D Slicer:

<http://dmri.slicer.org>

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

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

# Load MRML Data



Unzip the sample data

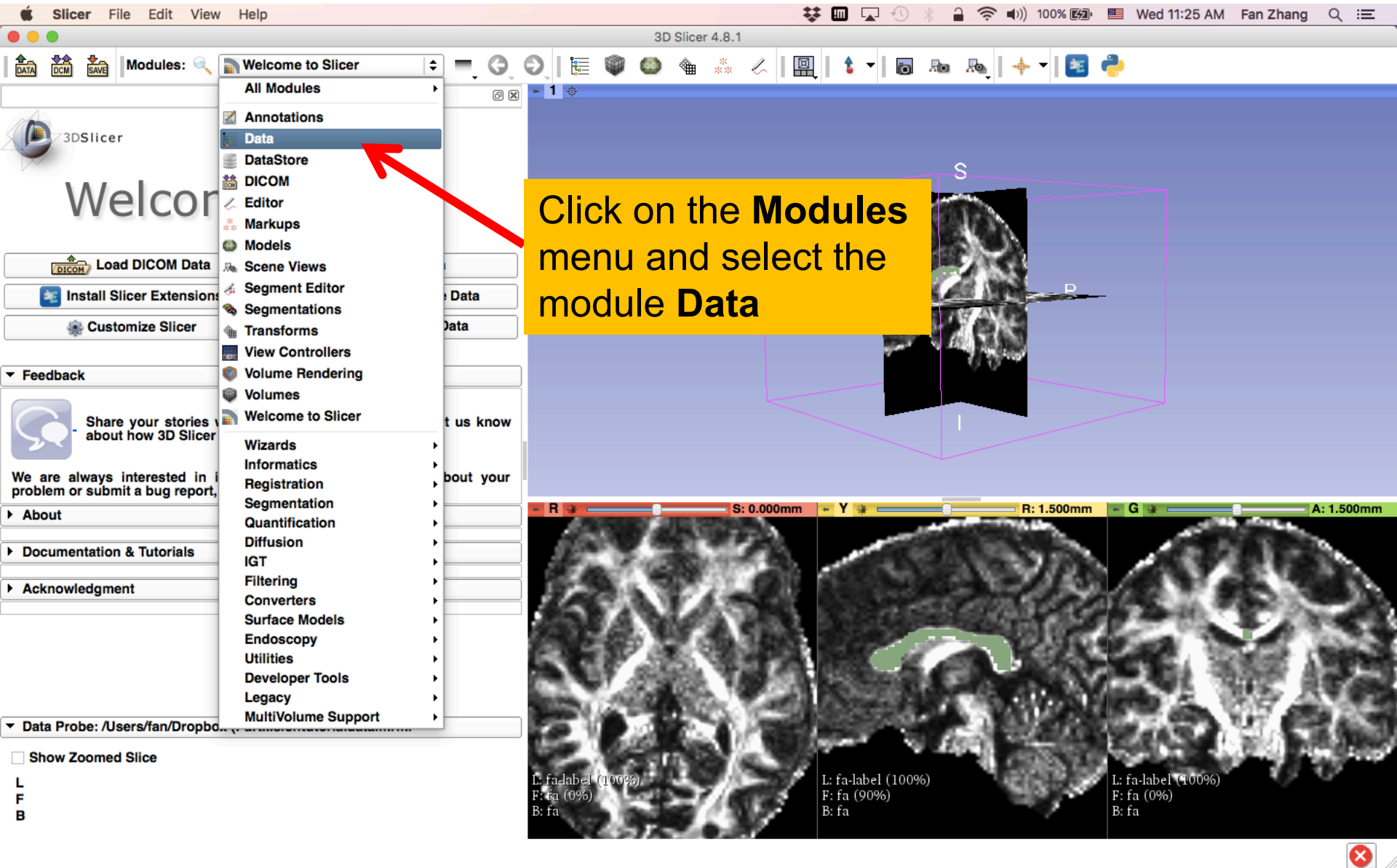
Within the unzipped folder, locate the MRML Scene file:

**diffusiontutorialdata.mrml**

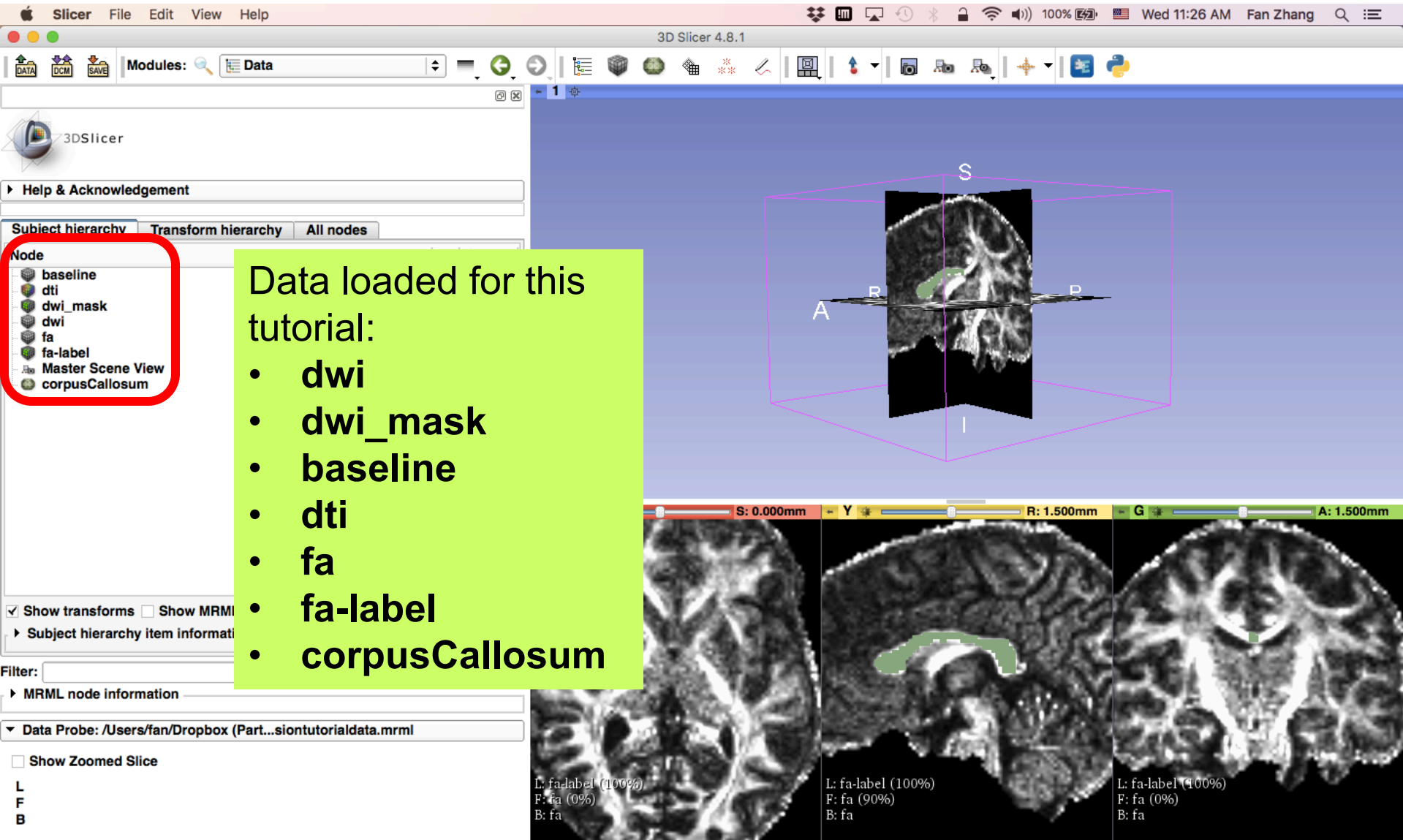
Drag and drop the file onto the viewer of the Slicer application

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

# Load MRML Data



# Load MRML Data



The screenshot displays the 3D Slicer 4.8.1 application window. The top menu bar includes 'Slicer', 'File', 'Edit', 'View', and 'Help'. The status bar at the top right shows 'Wed 11:26 AM' and 'Fan Zhang'. The 'Modules' panel on the left has 'Data' selected. The 'Subject hierarchy' panel is open, showing a list of nodes: 'baseline', 'dti', 'dwi\_mask', 'dwi', 'fa', 'fa-label', 'Master Scene View', and 'corpusCallosum'. The 'fa-label' node is highlighted with a red box. A green box is overlaid on the center of the screen, containing the text 'Data loaded for this tutorial:' followed by a bulleted list of the loaded data: 'dwi', 'dwi\_mask', 'baseline', 'dti', 'fa', 'fa-label', and 'corpusCallosum'. The main 3D view shows a brain model with a green overlay. The bottom panel displays three axial slices of the brain, with the middle slice showing the green overlay. The bottom status bar shows the coordinates 'S: 0.000mm', 'Y: 1.500mm', 'R: 1.500mm', and 'A: 1.500mm'.

3D Slicer 4.8.1

Modules: Data

Subject hierarchy

Node

- baseline
- dti
- dwi\_mask
- dwi
- fa
- fa-label
- Master Scene View
- corpusCallosum

Help & Acknowledgement

Transform hierarchy

All nodes

Filter:

MRML node information

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

Show transforms Show MRML Subject hierarchy item informati

Show Zoomed Slice

L F B

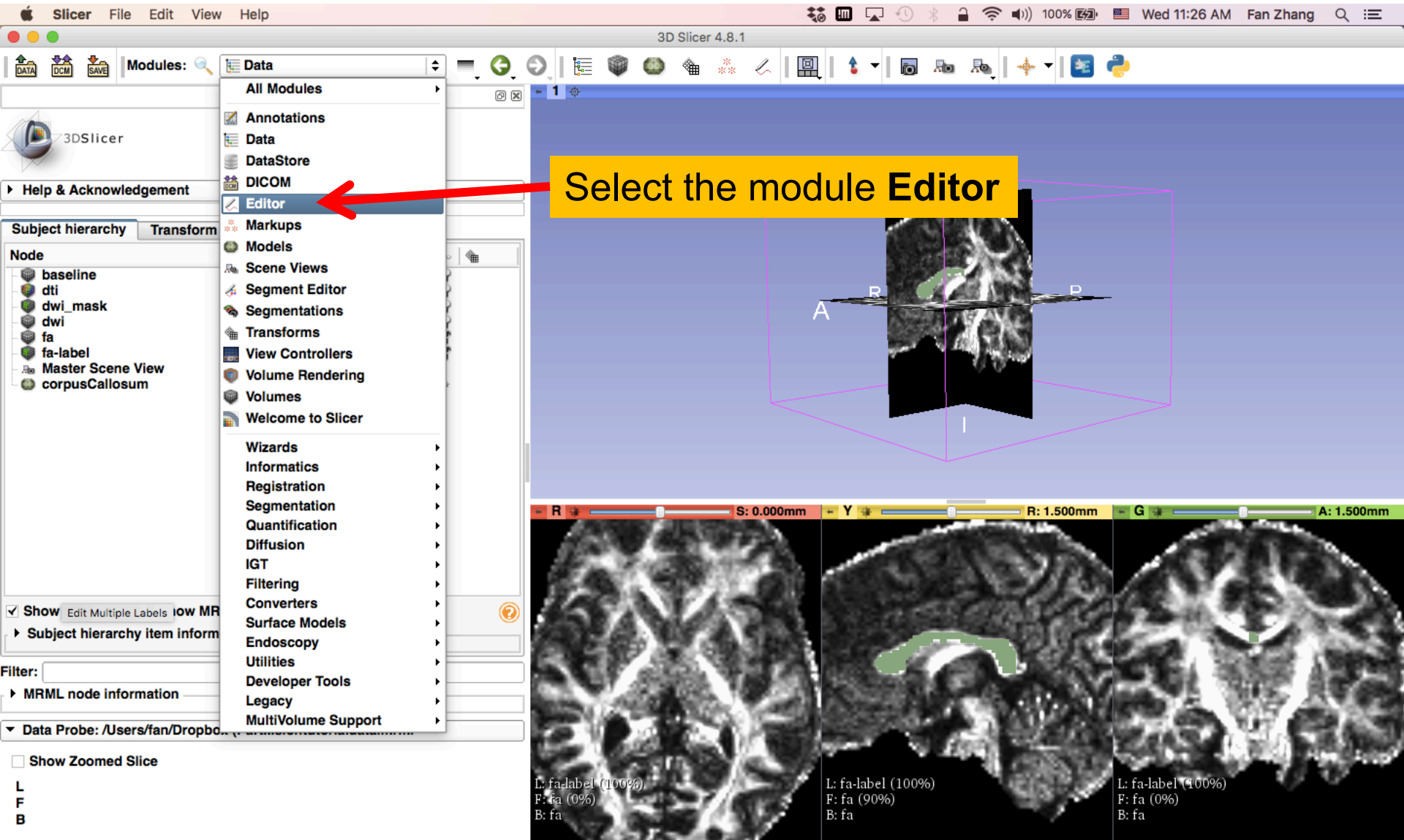
L: fa-label (100%)  
F: fa (0%)  
B: fa

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

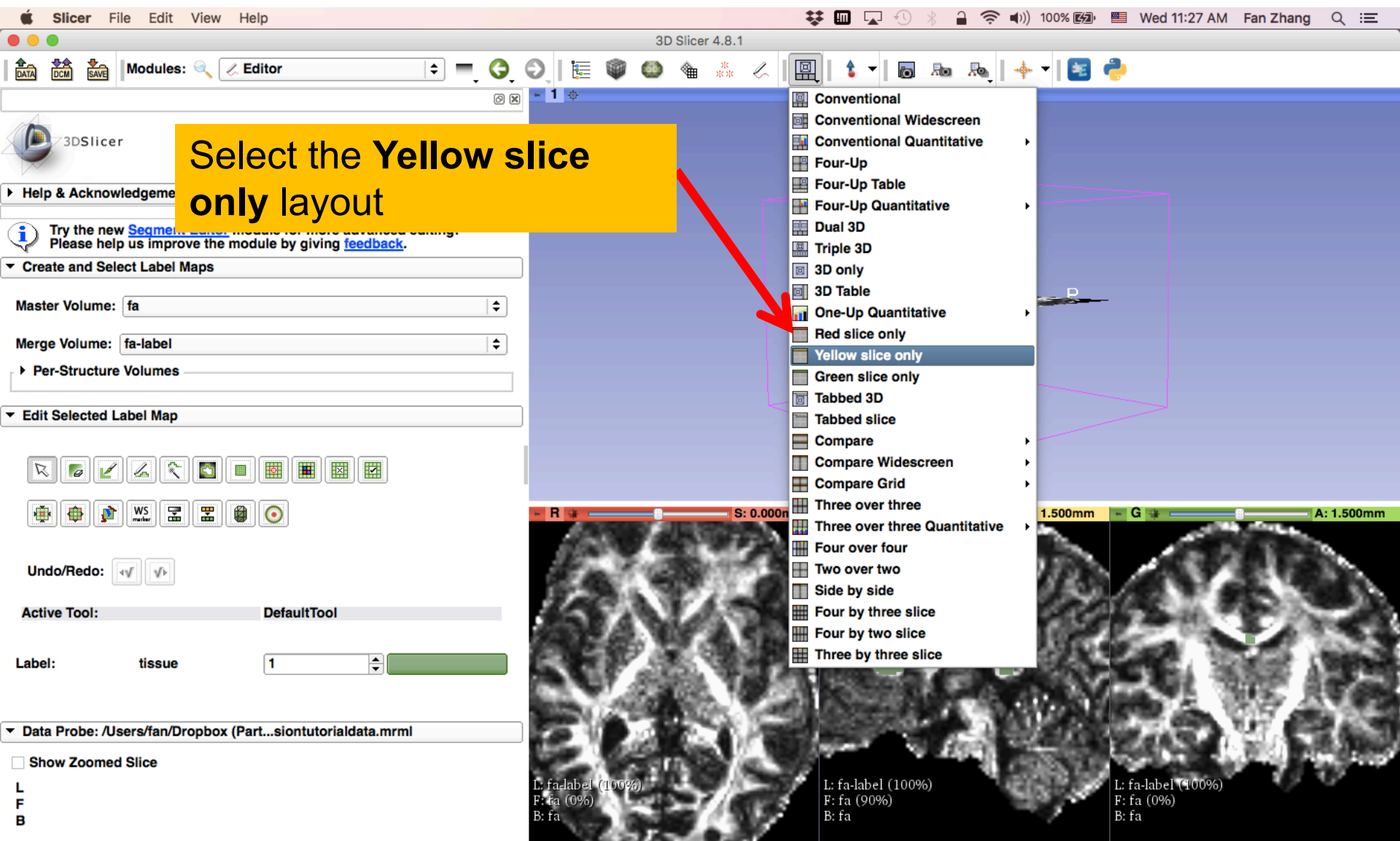
L: fa-label (100%)  
F: fa (0%)  
B: fa

S: 0.000mm Y R: 1.500mm G A: 1.500mm

# Edit Multiple Labels



# Edit Multiple Labels





# Edit Multiple Labels

The screenshot shows the 3D Slicer 4.8.1 interface. The 'Create and Select Label Maps' panel is highlighted with a red rectangle. It contains the following settings:

- Master Volume: fa
- Merge Volume: fa-label

Two yellow callout boxes provide instructions:

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

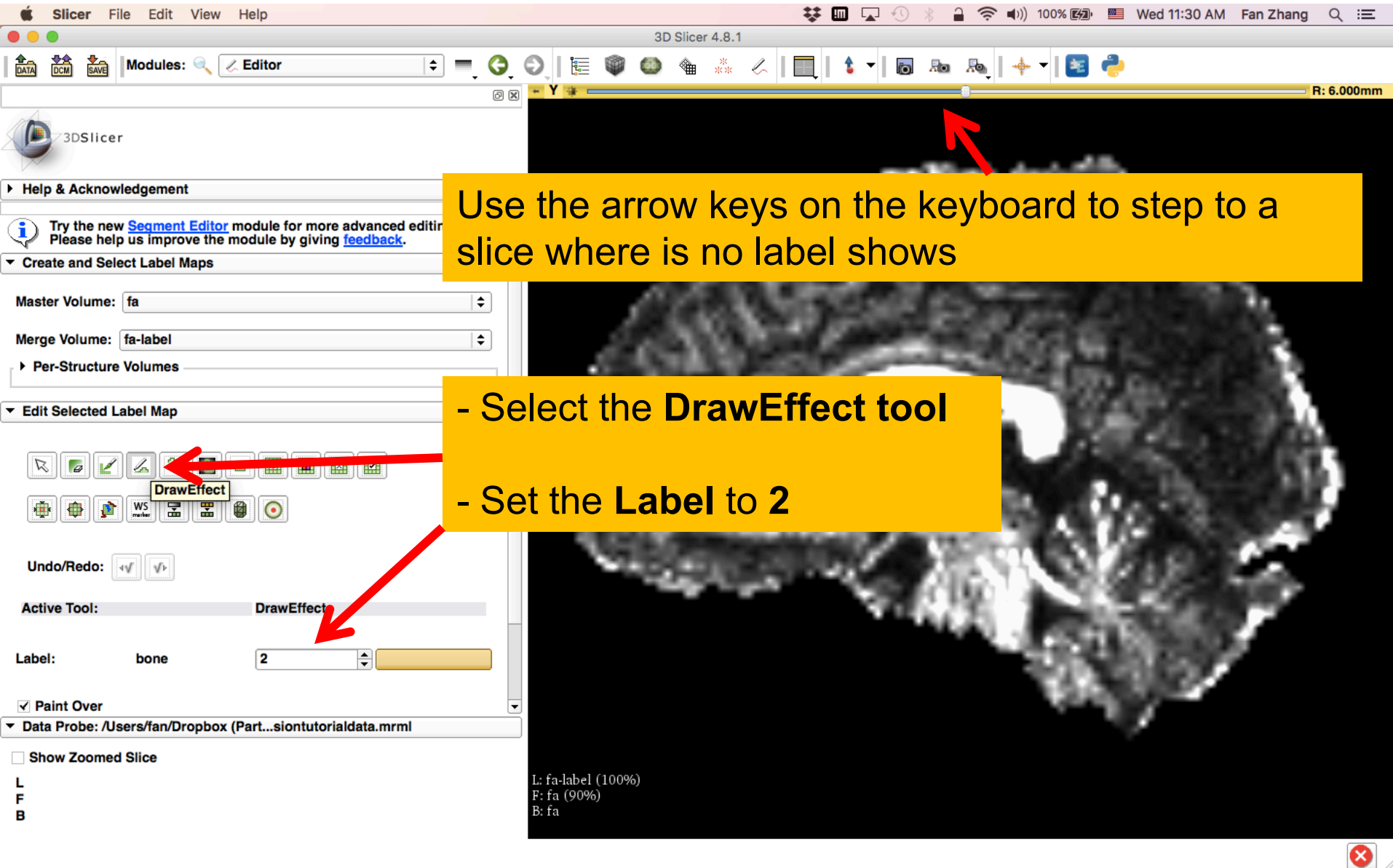
The 'Edit Selected Label Map' panel shows the 'tissue' label with a value of 1. The 'Data Probe' shows the following information:

Yellow (R 1.5, A 80.9, S 49.1) Sagittal Sp: 1.5

L: fa-label (63, 10, 80) background (0)  
F: fa (63, 10, 80) 0  
B: fa (63, 10, 80) 0

The main 3D view displays a sagittal slice of a brain with a green overlay. The status bar at the bottom right indicates 'R: 1.500mm'.

# Edit Multiple Labels



The screenshot shows the 3D Slicer 4.8.1 interface. The top menu bar includes Apple logo, Slicer, File, Edit, View, and Help. The status bar at the top right shows system icons, 100% zoom, and the date/time: Wed 11:30 AM, Fan Zhang. The main window is titled '3D Slicer 4.8.1' and displays a brain MRI slice. The left sidebar contains the 'Modules' panel with 'Editor' selected. Below it are sections for 'Help & Acknowledgement', 'Create and Select Label Maps', and 'Edit Selected Label Map'. The 'Edit Selected Label Map' section shows the 'DrawEffect' tool selected in the 'Active Tool' dropdown, and the 'Label' dropdown set to '2'. A red arrow points from the 'DrawEffect' tool icon to the 'Active Tool' dropdown. Another red arrow points from the 'Label' dropdown to the '2' value. A third red arrow points from the top of the main window to a yellow callout box. A fourth red arrow points from the 'DrawEffect' tool icon to the 'Label' dropdown. The main window displays a brain MRI slice with a white label '2' on a dark background. A yellow callout box with black text says: 'Use the arrow keys on the keyboard to step to a slice where is no label shows'. The bottom status bar shows 'L: fa-label (100%)', 'F: fa (90%)', and 'B: fa'.

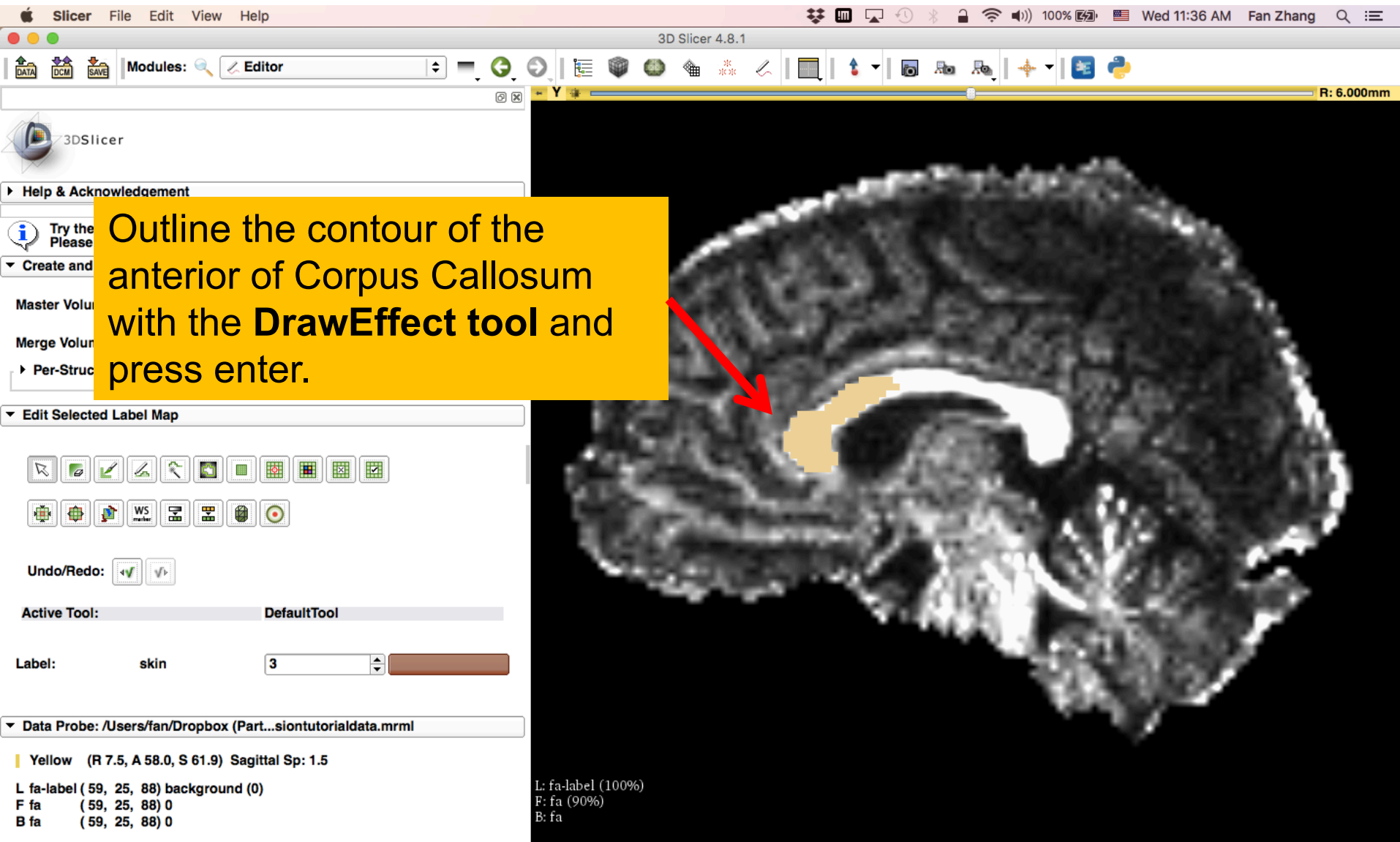
Use the arrow keys on the keyboard to step to a slice where is no label shows

- Select the **DrawEffect** tool
- Set the **Label** to 2

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



# Edit Multiple Labels



Outline the contour of the anterior of Corpus Callosum with the **DrawEffect** tool and press enter.

3D Slicer 4.8.1

Modules: Editor

Help & Acknowledgement

Try the Please

Create and

Master Volume

Merge Volume

Per-Structure

Edit Selected Label Map

Undo/Redo:

Active Tool: DefaultTool

Label: skin 3

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

Yellow (R 7.5, A 58.0, S 61.9) Sagittal Sp: 1.5

L: fa-label (59, 25, 88) background (0)  
F: fa (59, 25, 88) 0  
B: fa (59, 25, 88) 0

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

# Edit Multiple Labels

The screenshot shows the 3D Slicer 4.8.1 interface. The main window displays a brain MRI slice. A red circle highlights a specific area in the center of the slice. A red arrow points from the 'Edit Selected Label Map' panel to the 'DrawEffect' tool. Another red arrow points from the 'Data Probe' panel to the same area. A yellow box contains text about repeating steps to draw the middle of the Corpus Callosum with label 3. A green box contains text about drawing the middle area with a purposeful overlap with the anterior area to see the fiber selection. The 'Edit Selected Label Map' panel shows various drawing tools and the 'Active Tool' is set to 'DrawEffect'. The 'Data Probe' panel shows the 'Label' as 'skin' and the value '3'. The 'Data Probe' panel also shows the 'Paint Over' checkbox and the 'Data Probe' path. The 'Data Probe' panel shows the 'Data Probe' path as '/Users/fan/Dropbox (Par'.

Repeat the above steps to draw the middle of Corpus Callosum with **label 3** on the next slice

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

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

3D Slicer 4.8.1

Modules: Editor

Help & Acknowledgement

Try the Please

Create an

Master Vol

Merge Vol

Per-Stru

Edit Selected Label Map

Undo/Redo:

Active Tool: DrawEffect

Label: skin 3

Paint Over

Data Probe: /Users/fan/Dropbox (Par

Yellow (R 7.5, A 9.3, S 22.5) Sagit

L fa-label ( 59, 58, 62) background (0

F fa ( 59, 58, 62) 0.297255

B fa ( 59, 58, 62) 0.297255

R: 7.500mm

# Edit Multiple Labels

3D Slicer 4.8.1

Modules: Editor

Help & Acknowledgement

Try the new [Segment Editor](#) module for more advanced editing!

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 is no label shows

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

3DSlicer

▼ Edit Selected Label Map

Undo/Redo: [Undo] [Redo]

Active Tool: DrawEffect

Label: connective tissue 4

✓ Paint Over

▼ Data Probe: /Users/fan/Dropbox (Part...siontuto

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

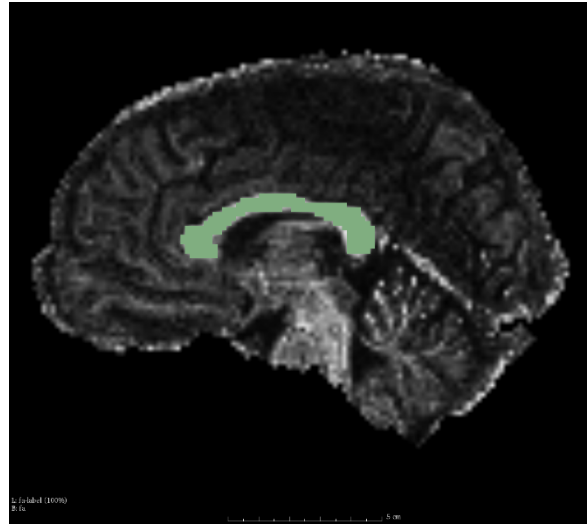
B fa ( 58, 68, 44) 0.243663

B: fa

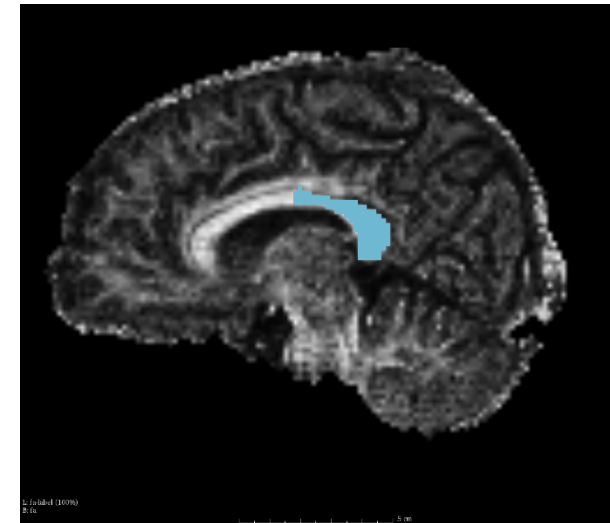
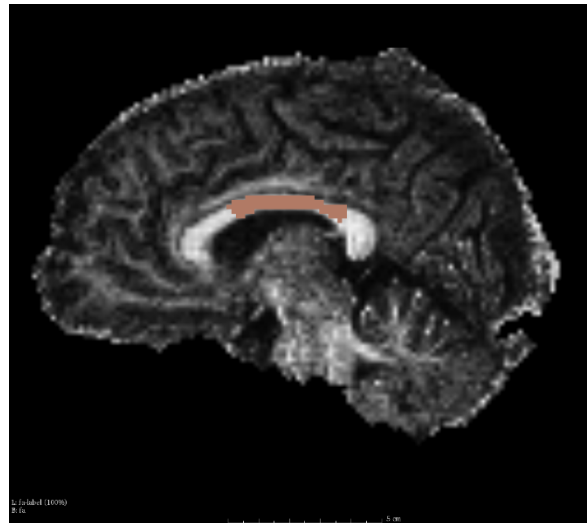
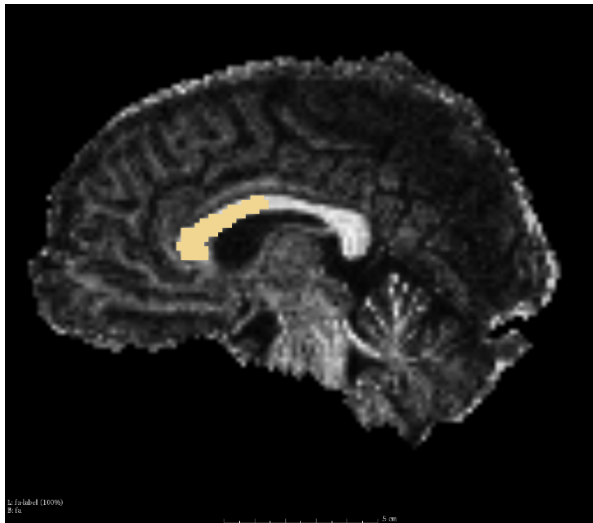
# Edit Multiple Labels

Label map on individual slice, with :

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

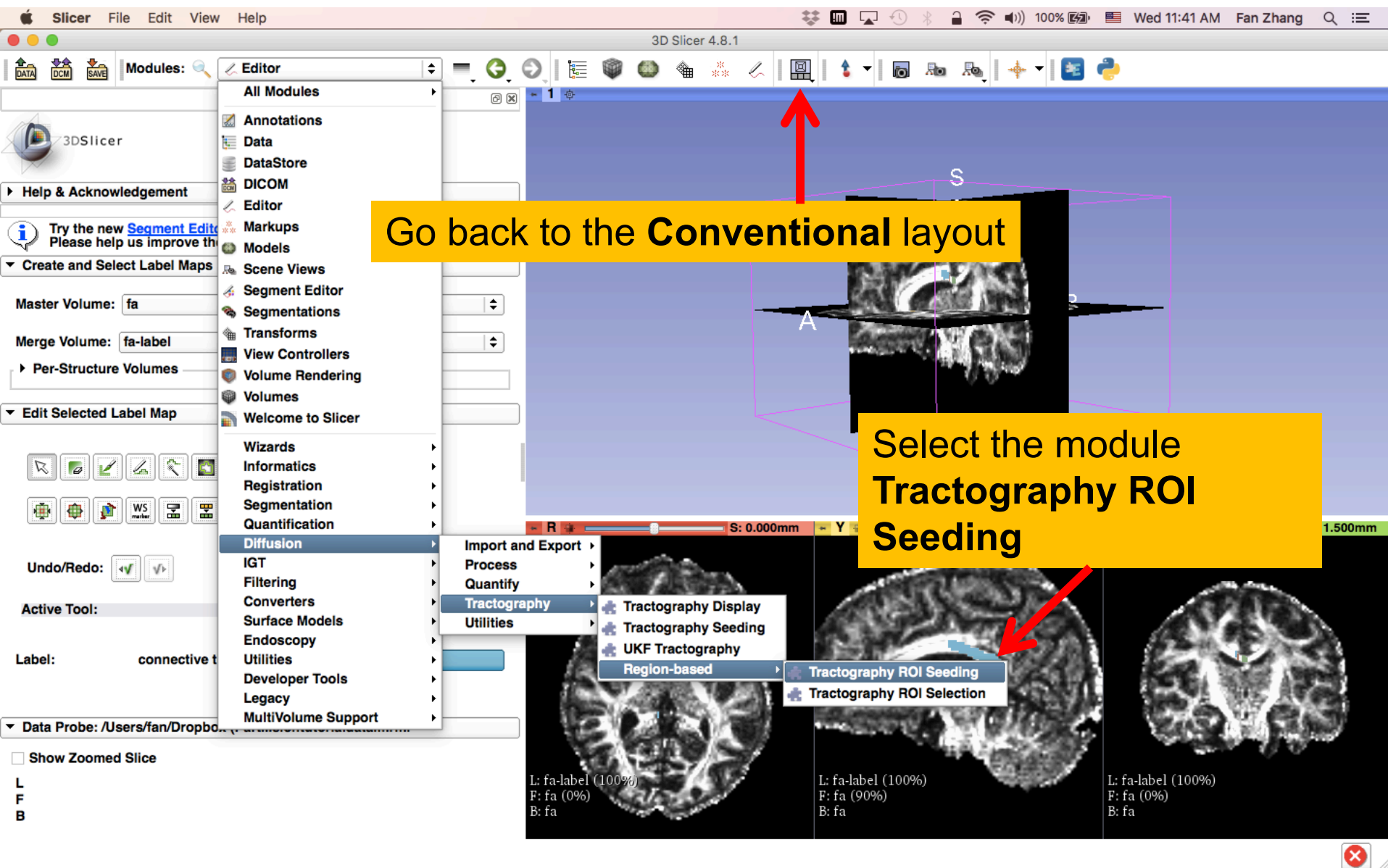


Notice that there are overlaps between different labeled regions\*, which will be used to investigate the fiber bundle selection.



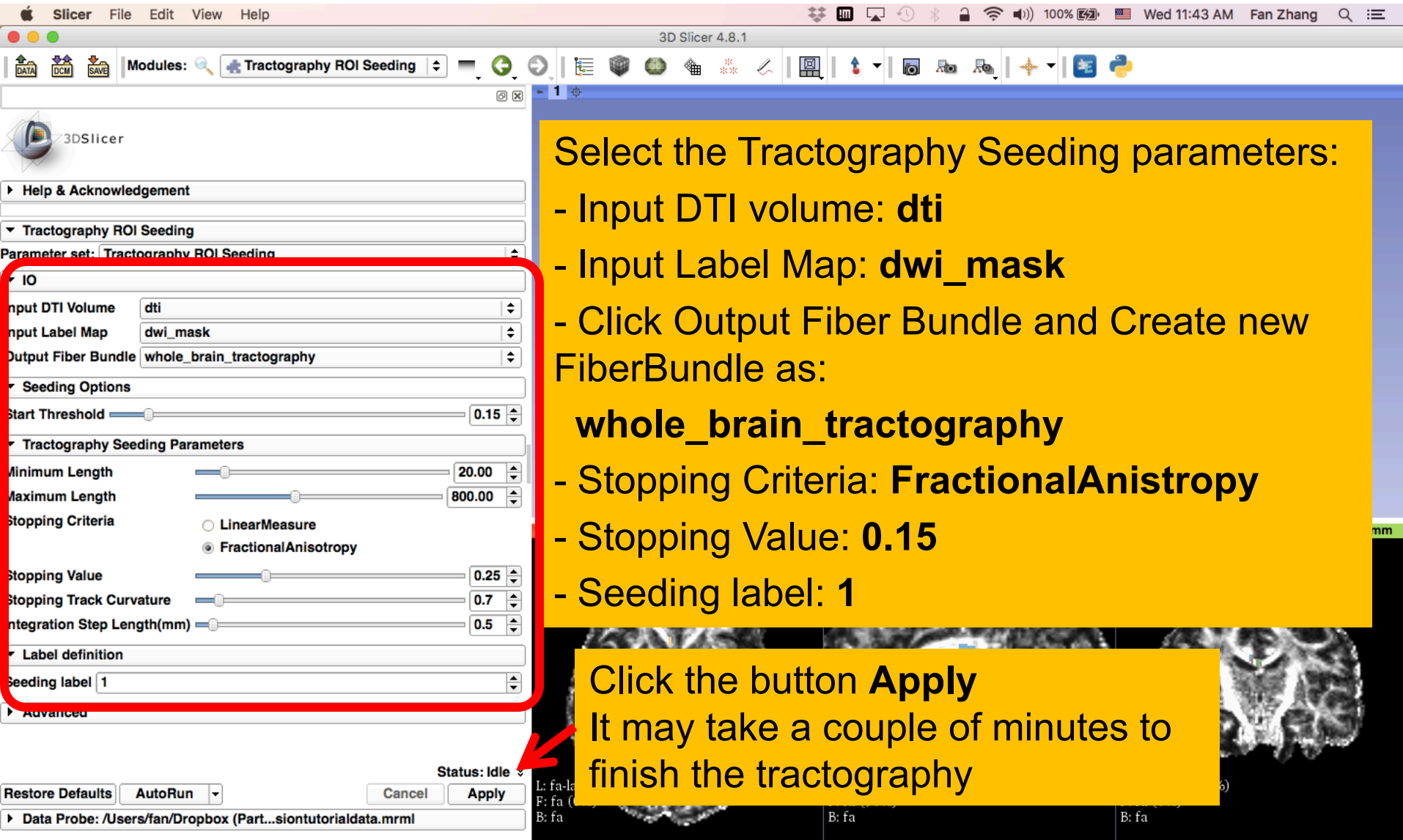
\* For details of CC segments: [http://adessowiki.fee.unicamp.br/adesso/wiki/DTI/proj\\_cc/view/](http://adessowiki.fee.unicamp.br/adesso/wiki/DTI/proj_cc/view/)

# Whole Brain Tractography





# Whole Brain Tractography



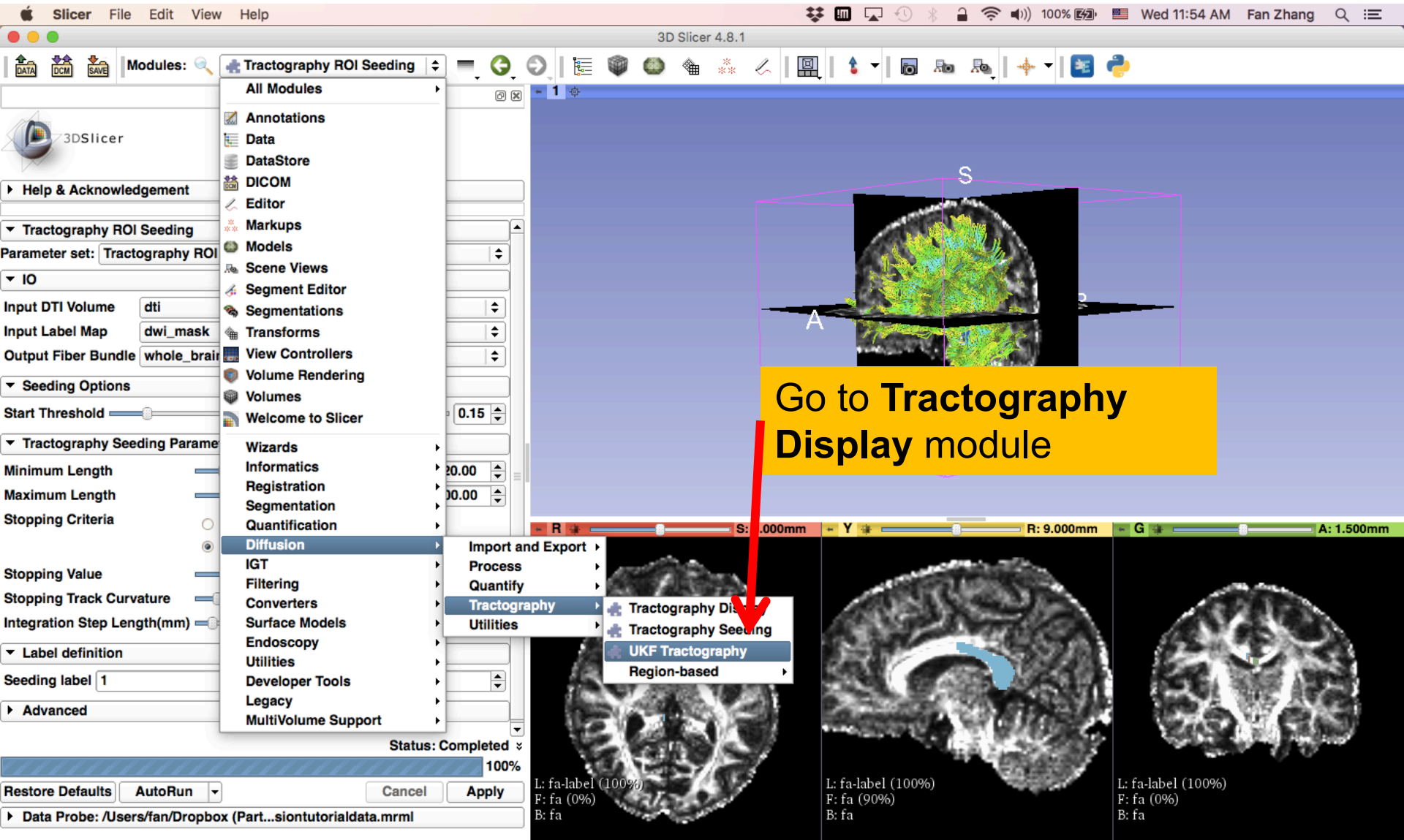
The screenshot shows the 3D Slicer 4.8.1 interface. The 'Tractography ROI Seeding' module is active, and its parameters are displayed in the left sidebar. A red box highlights the 'IO' and 'Seeding Options' sections. The 'IO' section shows 'Input DTI Volume' set to 'dti', 'Input Label Map' set to 'dwi\_mask', and 'Output Fiber Bundle' set to 'whole\_brain\_tractography'. The 'Seeding Options' section shows 'Start Threshold' set to 0.15. The 'Tractography Seeding Parameters' section shows 'Minimum Length' set to 20.00, 'Maximum Length' set to 800.00, 'Stopping Criteria' set to 'FractionalAnisotropy', 'Stopping Value' set to 0.25, 'Stopping Track Curvature' set to 0.7, and 'Integration Step Length(mm)' set to 0.5. The 'Label definition' section shows 'Seeding label' set to 1. At the bottom, the 'Apply' button is highlighted with a red arrow. The status bar at the bottom indicates 'Status: Idle'.

Select the Tractography Seeding parameters:

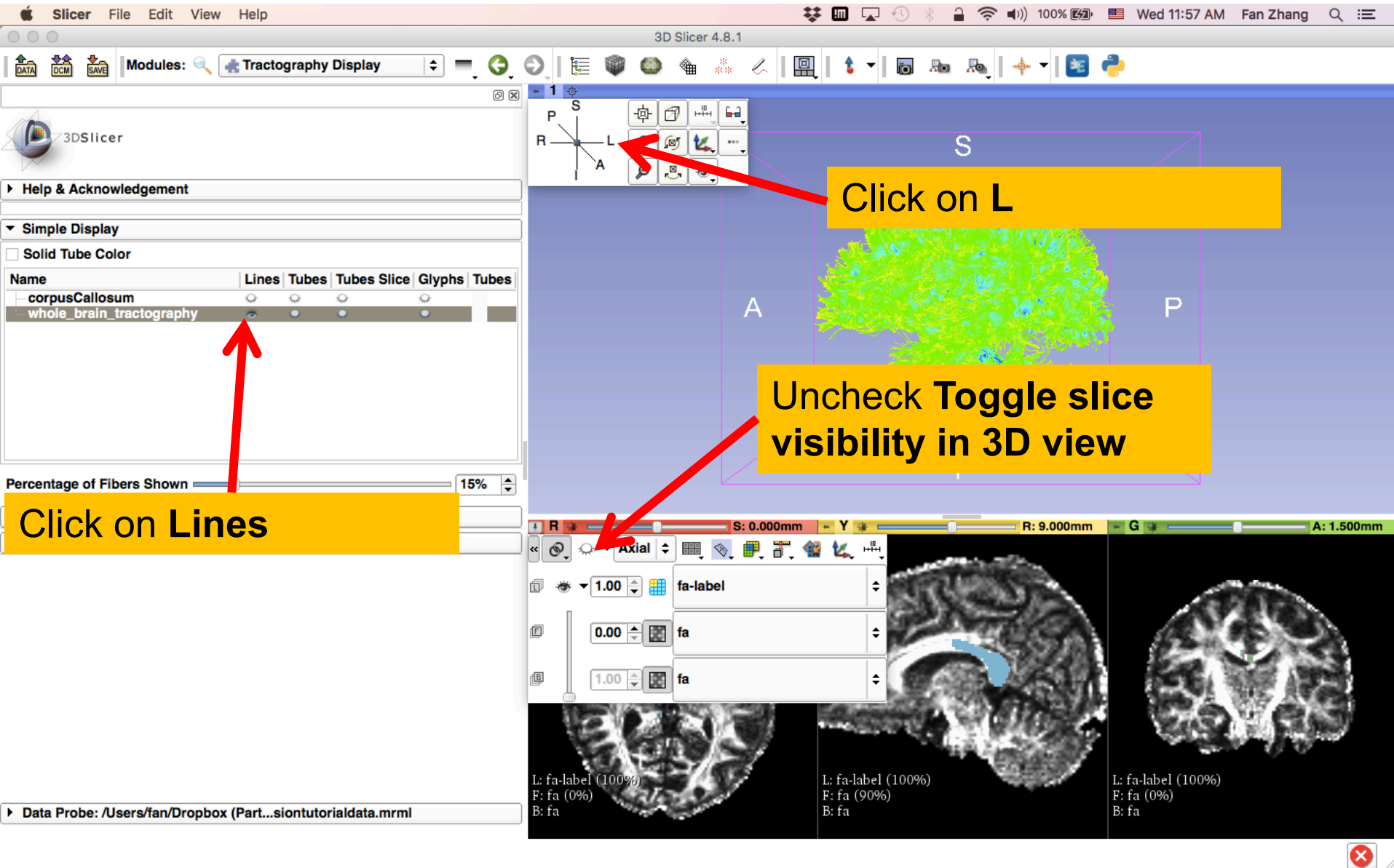
- Input DTI volume: **dti**
- Input Label Map: **dwi\_mask**
- Click Output Fiber Bundle and Create new FiberBundle as:  
**whole\_brain\_tractography**
- Stopping Criteria: **FractionalAnisotropy**
- Stopping Value: **0.15**
- Seeding label: **1**

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

# Whole Brain Tractography

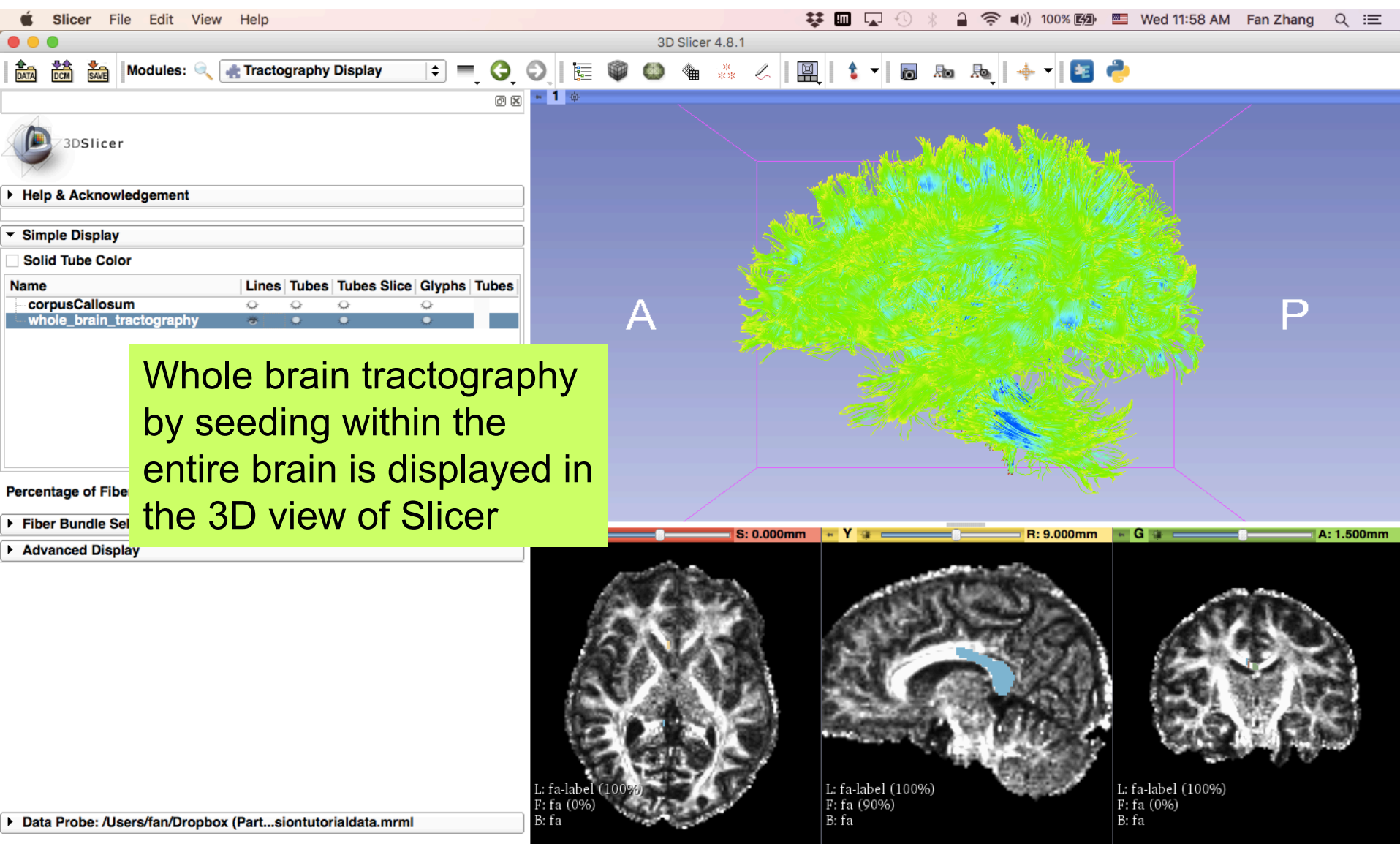


# Whole Brain Tractography

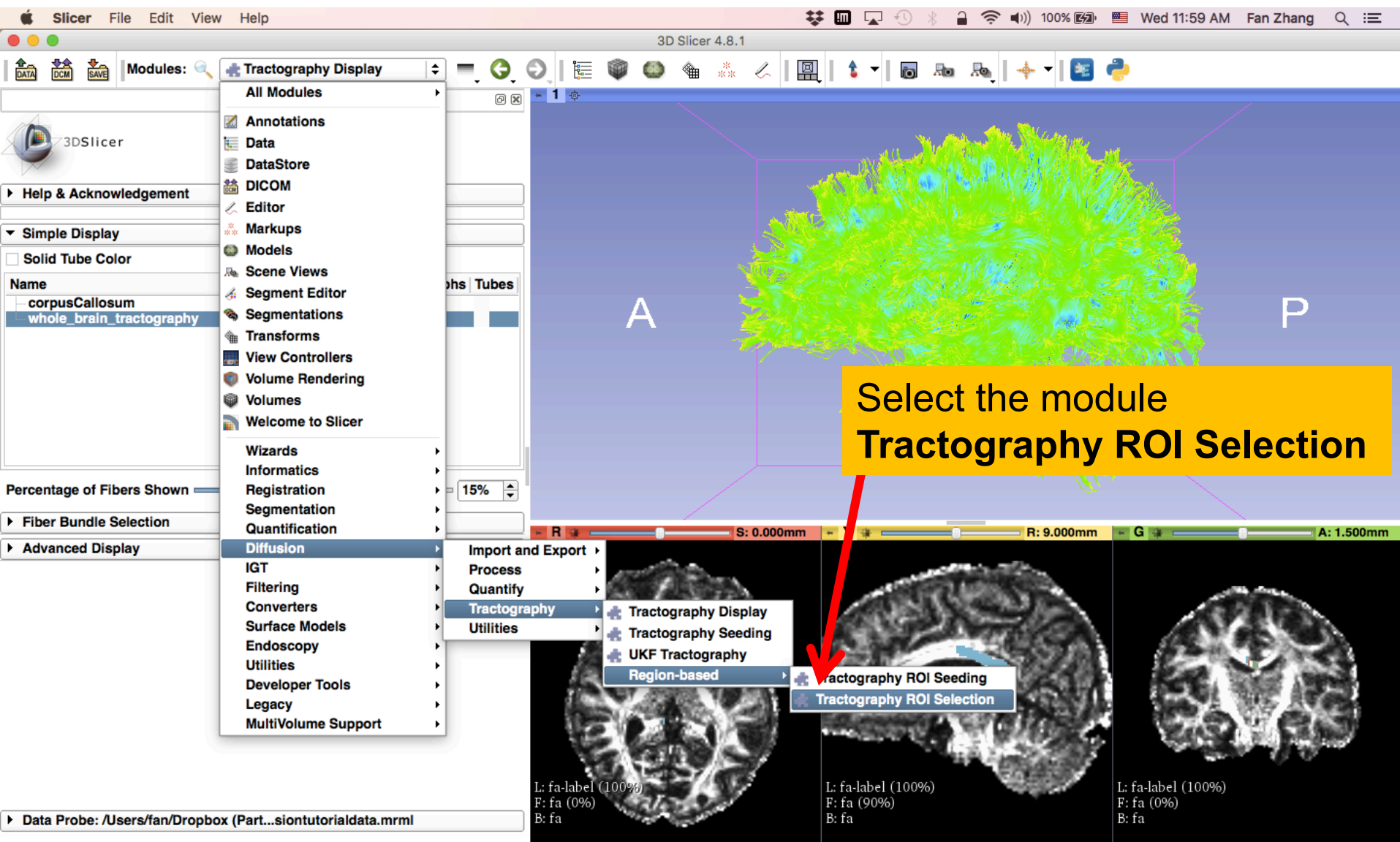




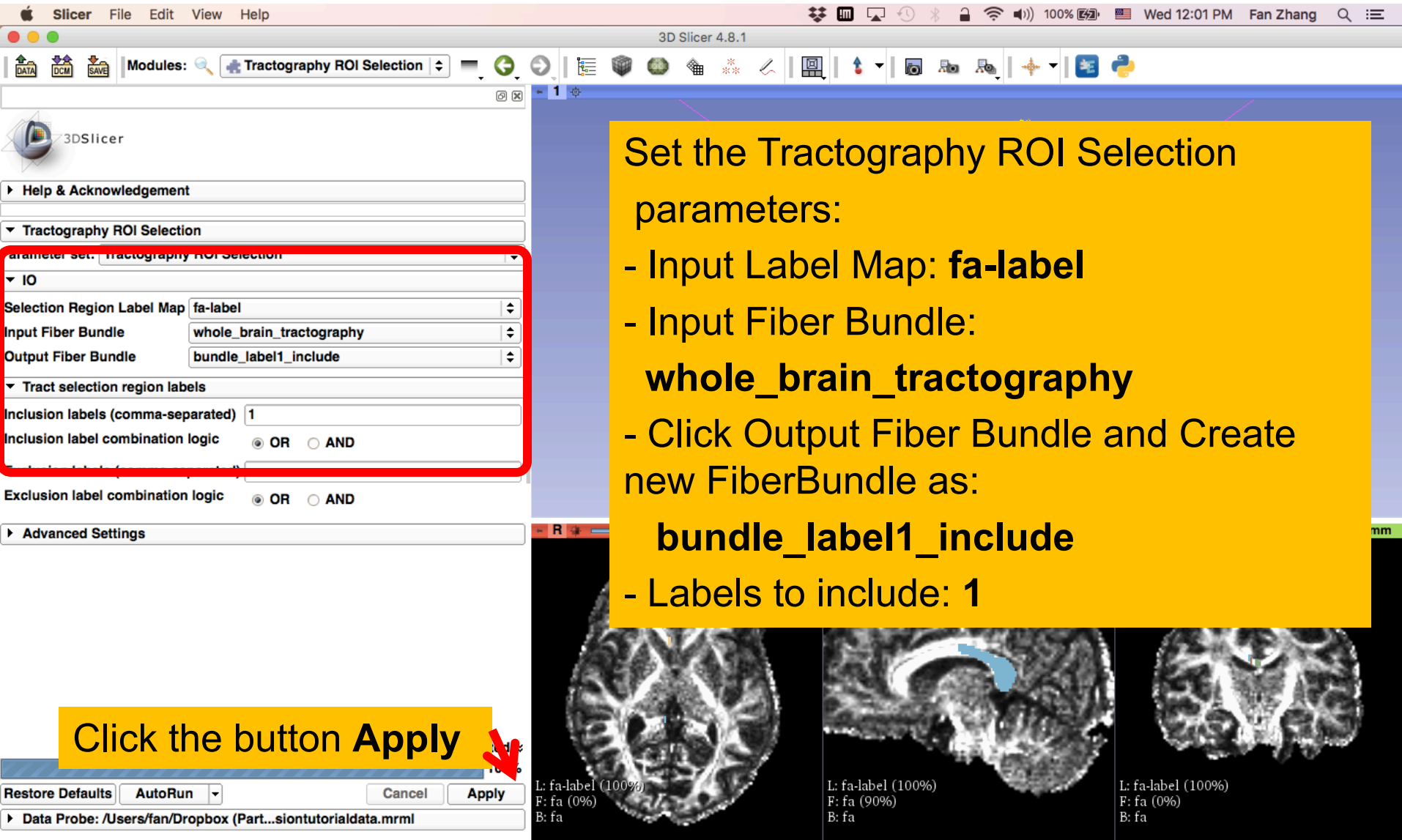
# Whole Brain Tractography



# Tractography ROI Selection



# Single Label Selection



3D Slicer 4.8.1

Modules: 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**

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**

Restore Defaults AutoRun Cancel Apply

Data Probe: /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

# Single Label Selection

The screenshot shows the 3D Slicer 4.8.1 interface. The main 3D view displays a brain with fiber tractography. A yellow box with the text "Go to Tractography Display" points to the "Tractography Display" module in the left sidebar. Below this, the "Simple Display" section shows a table of fiber bundles. A red arrow points to the "bundle\_label1\_include" row, which is highlighted. A yellow box with the text "Check the visibility of bundle\_label1\_include only" is positioned next to the arrow. The bottom of the interface shows three orthogonal views (axial, sagittal, and coronal) of the brain. A green box with the text "The fiber bundle from the whole brain tractography that passes through label 1 is displayed" points to the fiber bundle in the sagittal view. The status bar at the bottom indicates the data probe is "/Users/fan/Dropbox (Part...siontutorialdata.mrml)".

Go to Tractography Display

Check the visibility of **bundle\_label1\_include** only

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

Name	Lines	Tubes	Tubes Slice	Glyphs	Tubes
corpusCallosum	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
whole_brain_tractography	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
bundle_label1_include	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

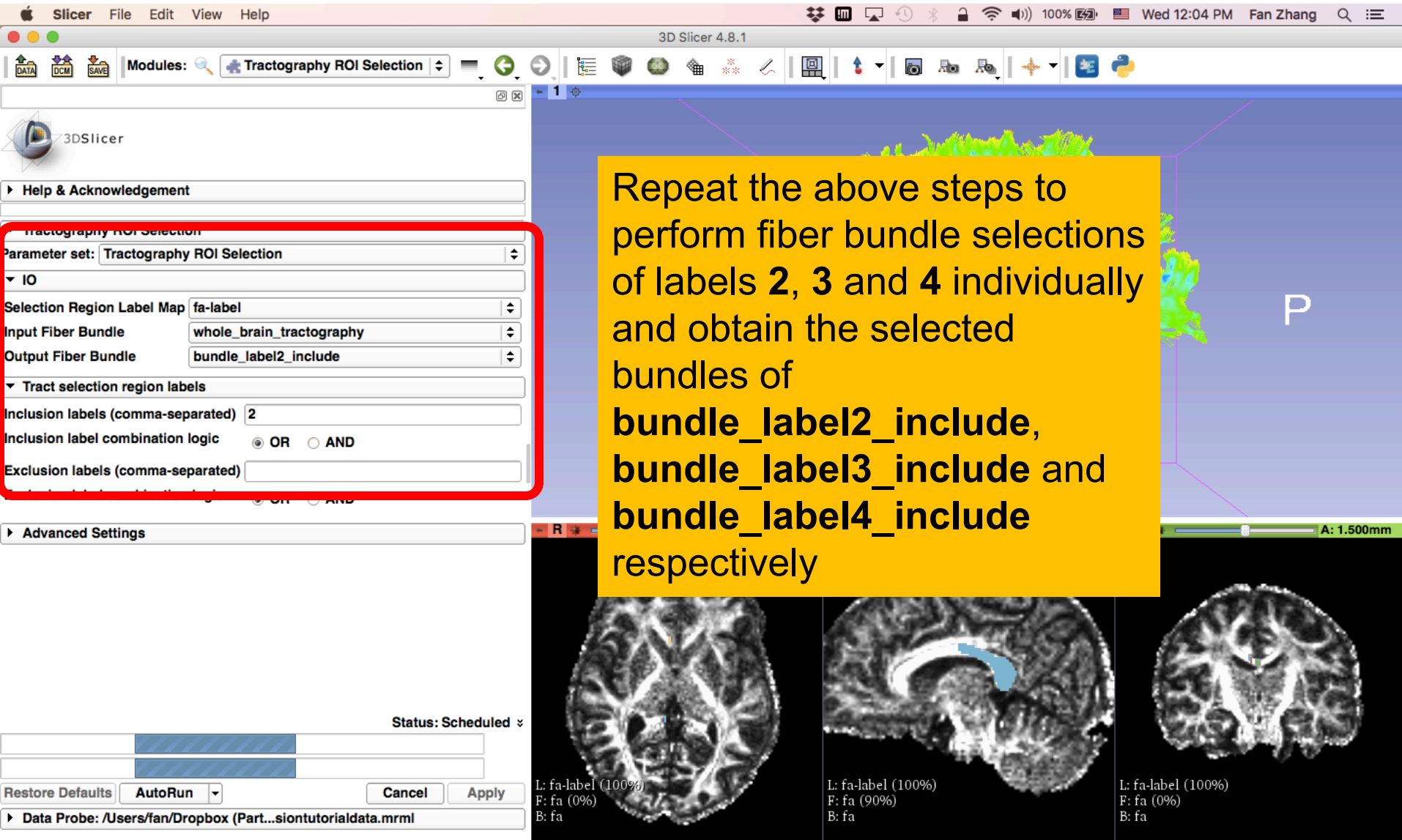
L: fa-label (100%)  
F: fa (0%)  
B: fa

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

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



# Single Label Selection



3D Slicer 4.8.1

Modules: 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

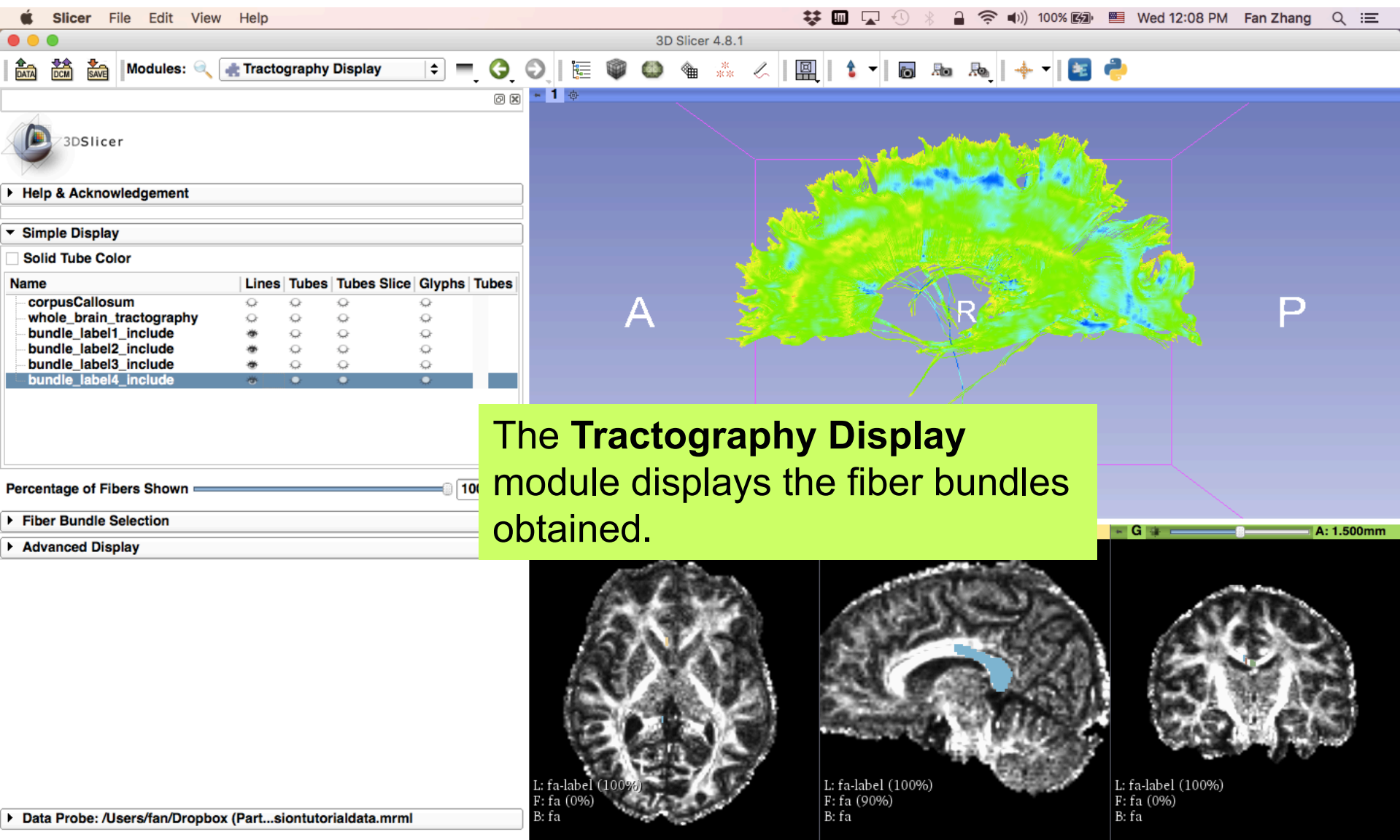
A: 1.500mm

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



3D Slicer 4.8.1

Modules: Tractography Display

Help & Acknowledgement

Simple Display

☐ Solid Tube Color

Name	Lines	Tubes	Tubes Slice	Glyphs	Tubes
corpusCallosum	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
whole_brain_tractography	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
bundle_label1_include	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
bundle_label2_include	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
bundle_label3_include	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
bundle_label4_include	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Percentage of Fibers Shown: 100

Fiber Bundle Selection

Advanced Display

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

The Tractography Display module displays the fiber bundles obtained.

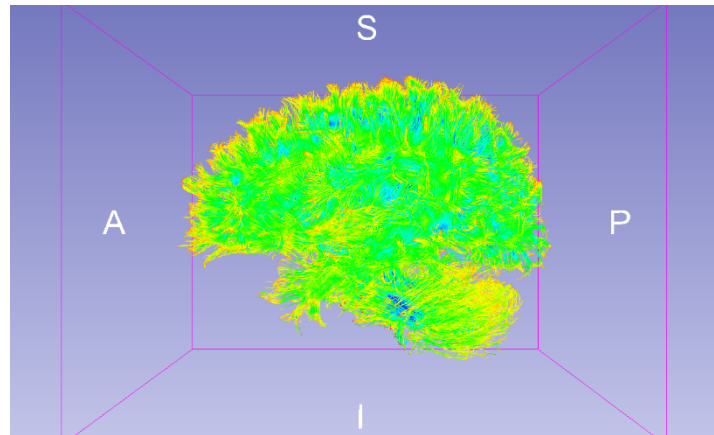
L: fa-label (100%)  
F: fa (0%)  
B: fa

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

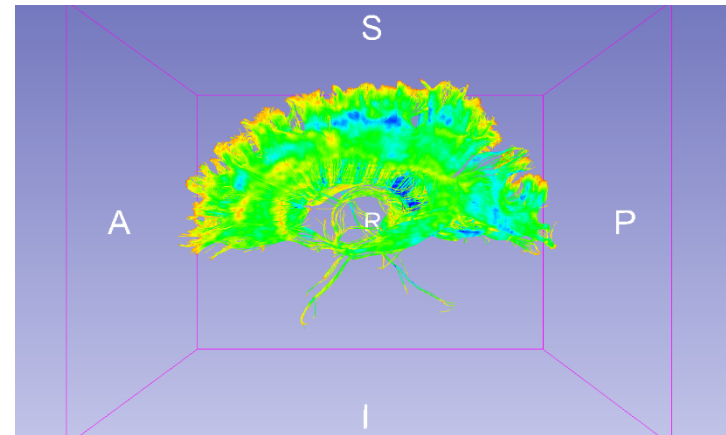
L: fa-label (100%)  
F: fa (0%)  
B: fa

# Single Label Selection

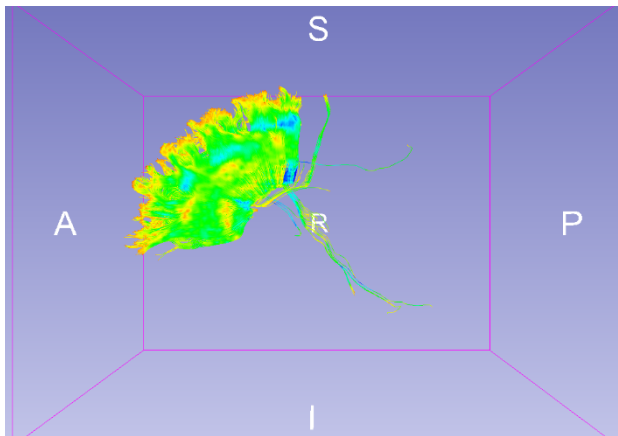
Whole Brain



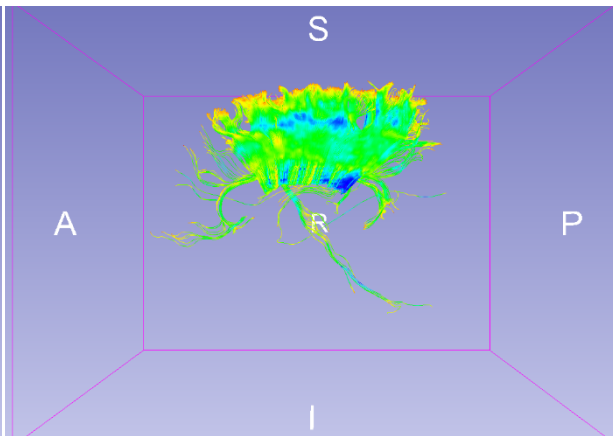
Label 1



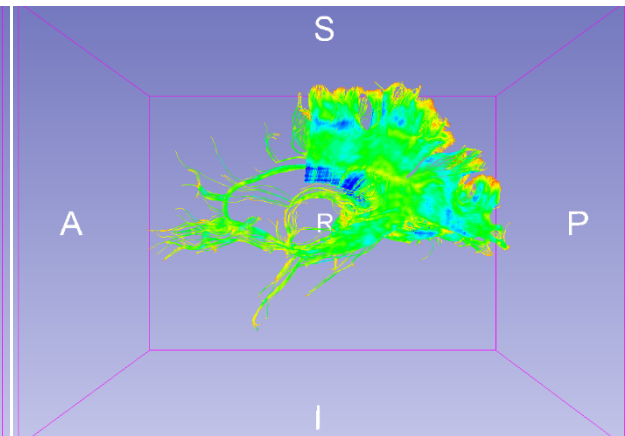
Label 2



Label 3



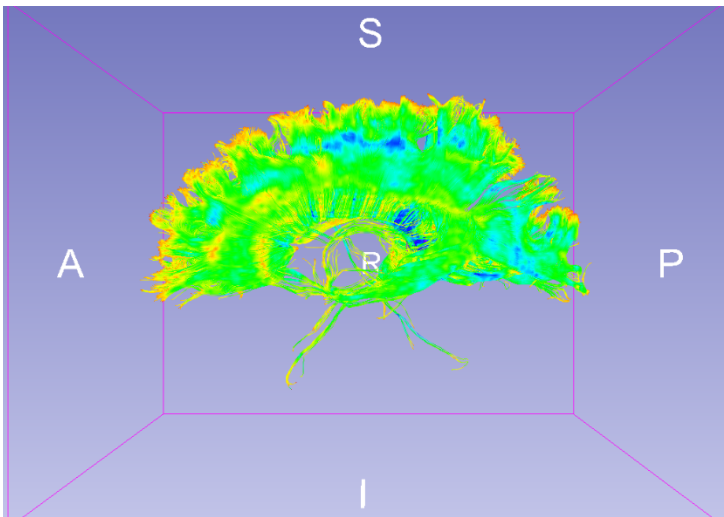
Label 4



# Single Label Selection

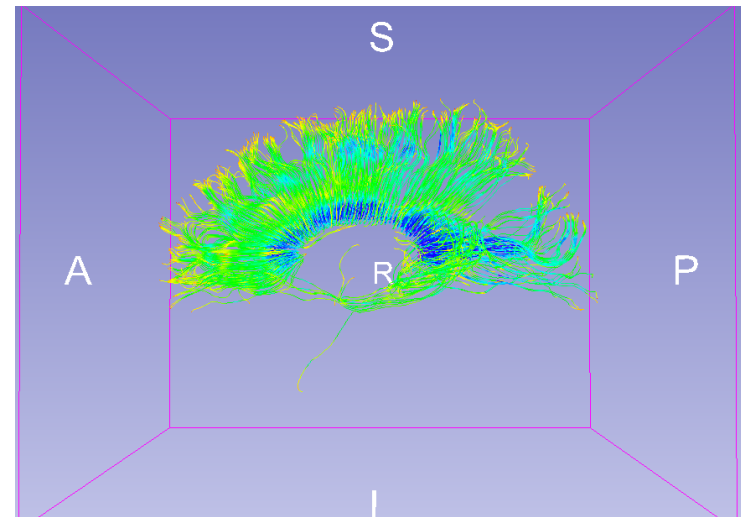
Notice that whole brain seeding creates a denser fiber bundle than seeding from the label 1.

Fiber Bundle Selection of Label 1  
from the Whole Brain Tractography



V.S.

Fiber Bundle Obtained by  
Seeding within Label 1



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

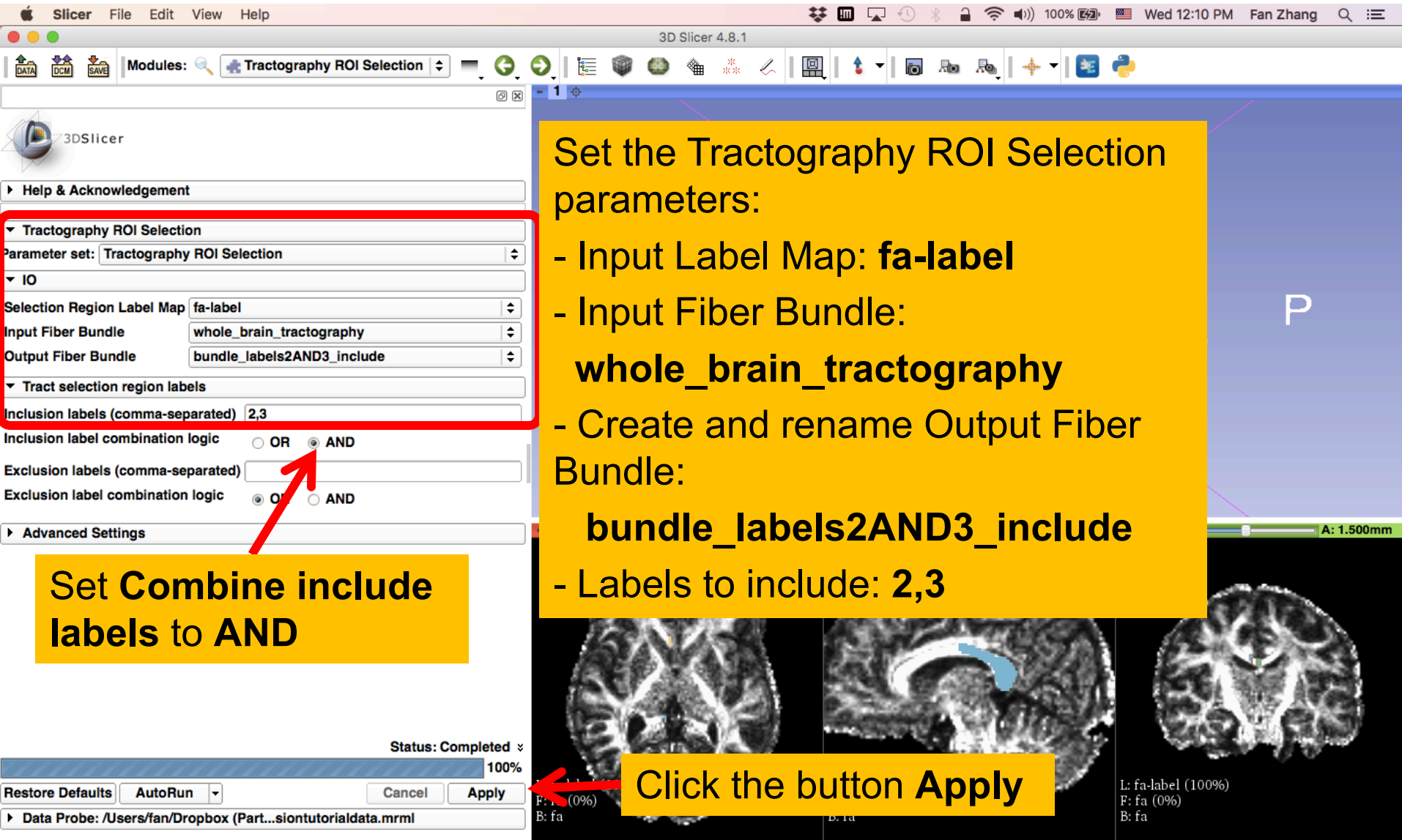
Inclusion labels (comma-separated)

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)



The screenshot shows the 3D Slicer 4.8.1 interface. The 'Tractography ROI Selection' module is active, and its settings are displayed in the left sidebar. A red box highlights the 'IO' and 'Tract selection region labels' sections. A red arrow points to the 'AND' radio button under 'Inclusion label combination logic'. Another red arrow points to the 'Apply' button at the bottom right of the interface.

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**

Set **Combine include labels to AND**

Click the button **Apply**

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

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

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

# Multiple Labels Selection (AND)

The screenshot shows the 3D Slicer 4.8.1 interface. The main 3D view displays a fiber bundle visualization in a 3D coordinate system with axes labeled A (Anterior), R (Right), and P (Posterior). The bundle is colored with a gradient from blue to yellow. The left sidebar contains the 'Modules' panel with 'Tractography Display' selected, and the 'Simple Display' panel with 'Solid Tube Color' checked. Below this is a table with columns: Name, Lines, Tubes, Tubes Slice, Glyphs, and Tubes. The table lists several bundles, with 'bundle\_labels2AND3\_include' selected. At the bottom, there are three 2D slice views (axial, sagittal, and coronal) showing the fiber bundle in the context of the brain MRI. The status bar at the bottom indicates the data probe path: /Users/fan/Dropbox (Part...siontutorialdata.mrml).

Name	Lines	Tubes	Tubes Slice	Glyphs	Tubes
corpusCallosum	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
whole_brain_tractography	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
bundle_label1_include	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
bundle_label2_include	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
bundle_label3_include	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
bundle_label4_include	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
bundle_labels2AND3_include	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	

Percentage of Fibers Shown:

Fiber Bundle Selection: ☐

Advanced Display: ☐

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

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

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

# Multiple Labels Selection (OR)

3D Slicer 4.8.1

Modules: Tractography ROI Selection

Selection Region Label Map: **fa-label**

Input Fiber Bundle: **whole\_brain\_tractography**

Output Fiber Bundle: **bundle\_labels2OR3\_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)

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**

P

R S: 0.000mm Y R: 9.000mm G A: 1.500mm

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

# Multiple Labels Selection (OR)

3D Slicer 4.8.1

Modules: Tractography Display

Help & Acknowledgement

Simple Display

☐ Solid Tube Color

Name	Lines	Tubes	Tubes Slice	Glyphs	Tubes
corpusCallosum	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
whole_brain_tractography	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
bundle_label1_include	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
bundle_label2_include	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
bundle_label3_include	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
bundle_label4_include	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
bundle_labels2AND3_include	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	
bundle_labels2OR3_include	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>

Percentage of Fibers Shown

Fiber Bundle Selection

Advanced Display

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

A R P

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

R: 9.000mm G A: 1.500mm

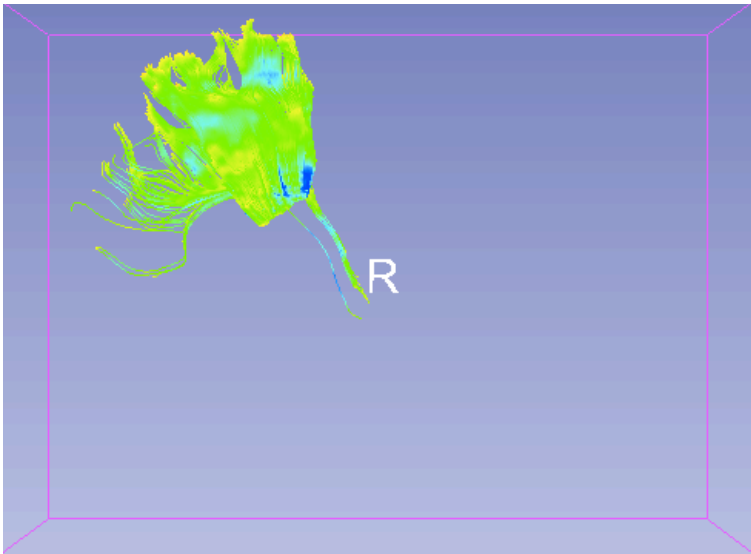
L: fa-label (100%)  
F: fa (0%)  
B: fa

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

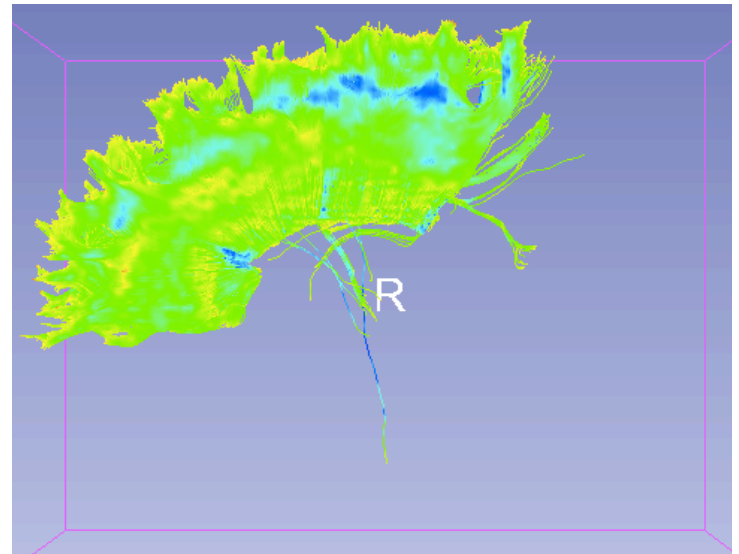
L: fa-label (100%)  
F: fa (0%)  
B: fa

# Multiple Labels Selection

Labels 2 and 3



Labels 2 or 3





# Save Fiber Bundles

The screenshot shows the 3D Slicer 4.8.1 interface. At the top, the 'Modules' dropdown is set to 'Tractography Display'. A red arrow points to the 'SAVE' button in the top toolbar. A yellow box with the text 'Click the button **SAVE**' is overlaid on the toolbar. Below the toolbar, a file save dialog is open, titled 'Save Scene and Unsaved Data'. The dialog has a table with columns: 'File Name', 'File Format', and 'Directory'. The table lists several files, including 'dwi\_mask.nrrd', 'dwi.nrrd', 'fa.nrrd', 'fa-label.nrrd', 'Master Scene View.png', 'corpusCallosum.vtk', 'whole\_brain\_tractography.vtk', and several 'bundle\_label' files. The 'bundle\_label' files are checked. A red arrow points to the 'bundle\_label1\_include.vtk' row. Another red arrow points to the 'Change directory for selected files' button at the bottom of the dialog. A yellow box with the text 'Click **Change directory** for selected files and select a folder to store the vtk files' is overlaid on the dialog. At the bottom right of the dialog, there are 'Save' and 'Cancel' buttons. A red arrow points to the 'Save' button. A yellow box with the text 'Click the button **Save**' is overlaid on the 'Save' button. In the bottom left corner, a yellow box with the text 'Check the fiber bundles obtained above' is overlaid on the 'Fiber Bundle' panel. The 'Fiber Bundle' panel shows a list of fiber bundles with checkboxes. The 'bundle\_label' files are checked. A red arrow points to the 'bundle\_label1\_include.vtk' row. In the bottom right corner, a yellow box with the text 'Click the button **Save**' is overlaid on the 'Save' button.

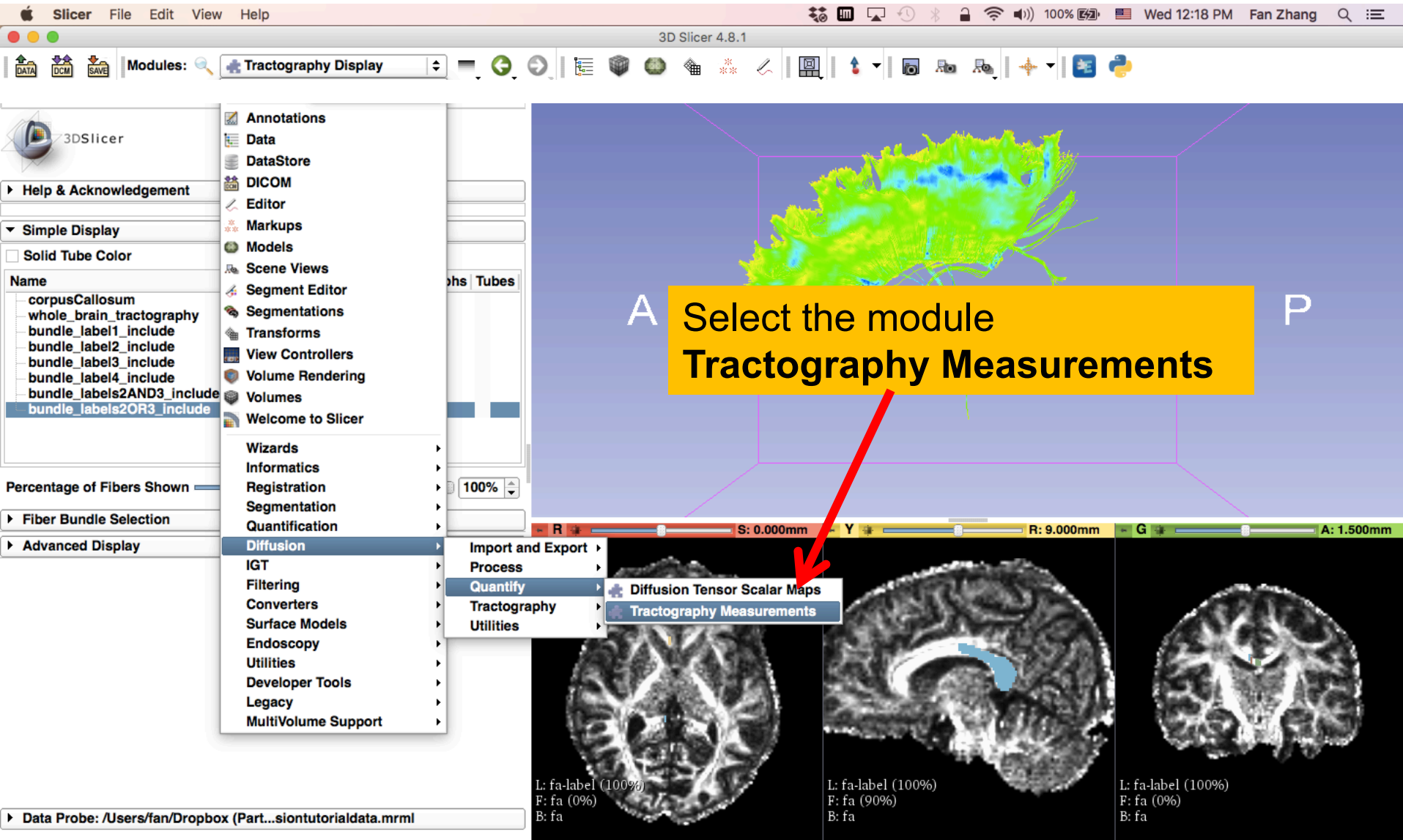
Click the button **SAVE**

Click **Change directory** for selected files and select a folder to store the vtk files

Check the fiber bundles obtained above

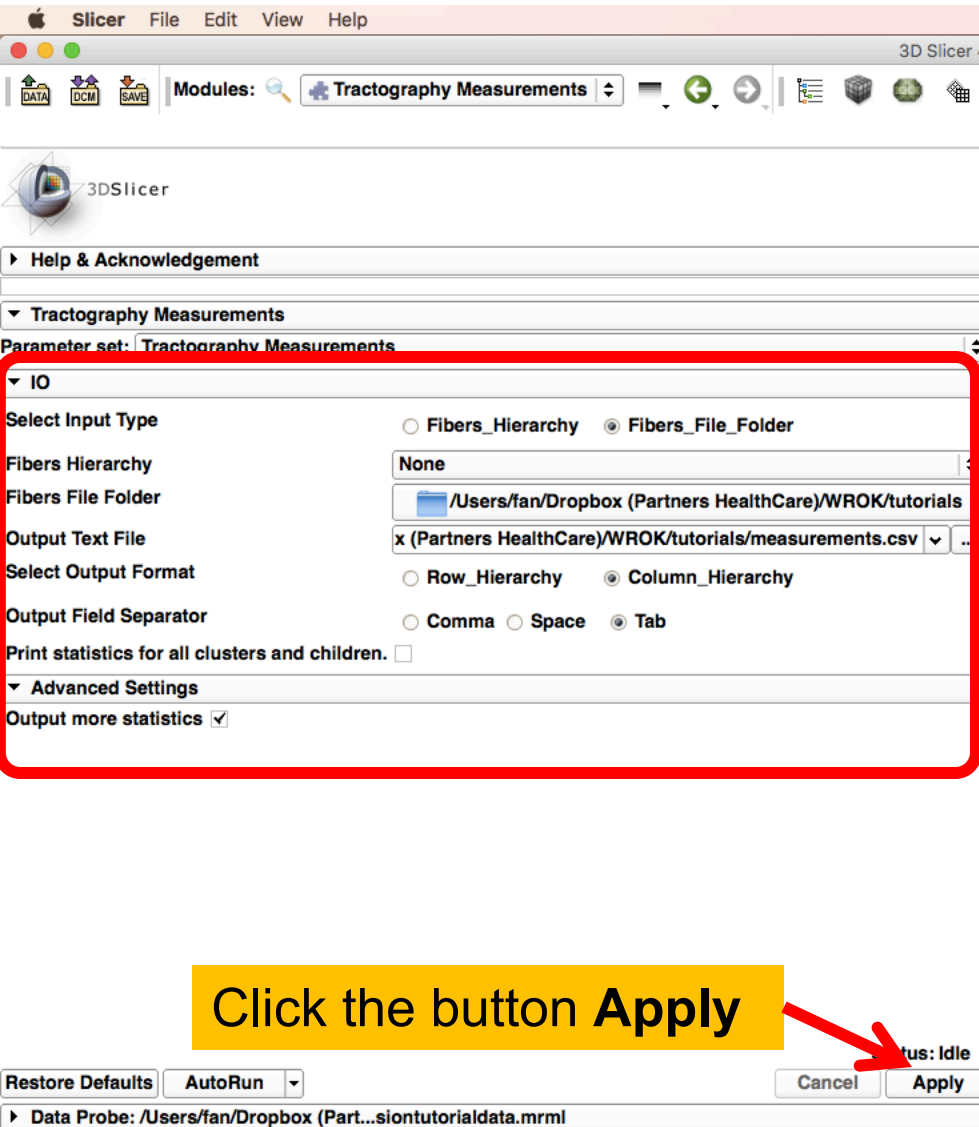
Click the button **Save**

# Tractography Measurements



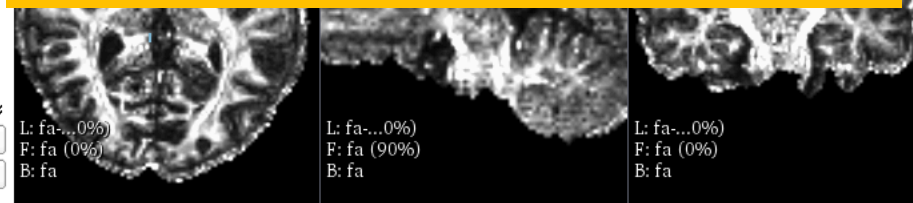


# Tractography Measurements



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**

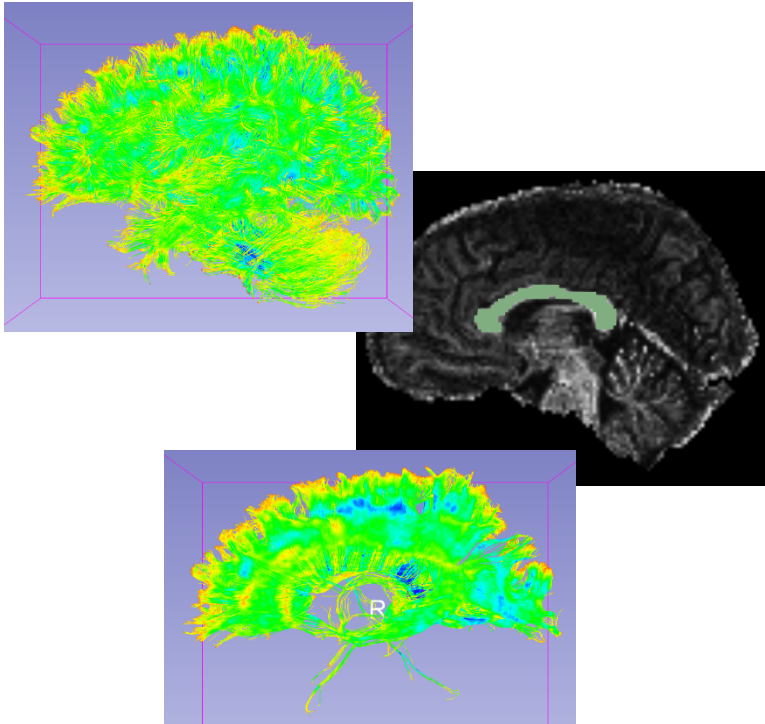


# Tractography Measurements

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
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

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