

# Fiber Bundle Selection And Scalar Measurement

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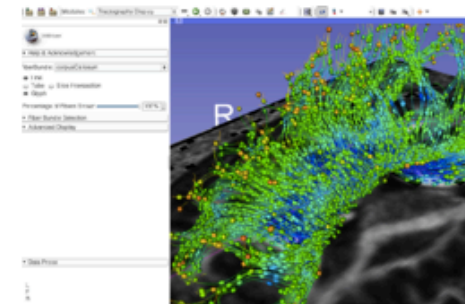
# Pre-requisite

- 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](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

The screenshot shows the 3D Slicer 4.5.0-1 application interface. The top toolbar includes various icons for file operations and viewing. The left sidebar shows the 'Data' panel with a file browser. The main window displays a 3D view of a brain scan. A yellow callout box highlights the file 'diffusiontutorialdata.mrml' in the file browser, with a red arrow pointing to it. Another yellow callout box points to the 'diffusiontutorialdata.mrml' entry in the 'Add data into the scene' dialog, which is open over the 3D view. The dialog shows the file selected and ready to be added to the scene.

3D Slicer 4.5.0-1

Modules: Welcome to Slicer

FiberBundleSelectionAndScalarMeasurement\_TutorialContestWinter2016

Name	Date Modified	Size
baseline.nrrd	Dec 31, 2015, 1:37 PM	1.4 M
corpusCallosum.vtk	Dec 31, 2015, 1:38 PM	4 M
<b>diffusiontutorialdata.mrml</b>	Dec 31, 2015, 1:48 PM	73 K
dti.nrrd	Dec 31, 2015, 1:37 PM	10.4 M
dwi_mask.nrrd	Dec 31, 2015, 1:38 PM	28 K
dwi.nrrd	Dec 31, 2015, 1:38 PM	85 M
fa-label.nrrd	Dec 31, 2015, 1:38 PM	4 M
fa.nrrd	Dec 31, 2015, 1:38 PM	1.7 M
Master Scene View.png	Dec 31, 2015, 1:48 PM	310 K

Locate the MRML Scene file:  
**diffusiontutorialdata.mrml**

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

Add data into the scene

Choose Directory to Add | Choose File(s) to Add |  Show Options

File	Description
<input checked="" type="checkbox"/> ...easurement_TutorialContestWinter2016/diffusiontutorialdata.mrml	MRML Scene

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

See more at <http://goo.gl/6BvcHm>

▶ About

▶ The Main Window

▶ Loading and Saving

▶ Display

▶ Mouse & Keyboard

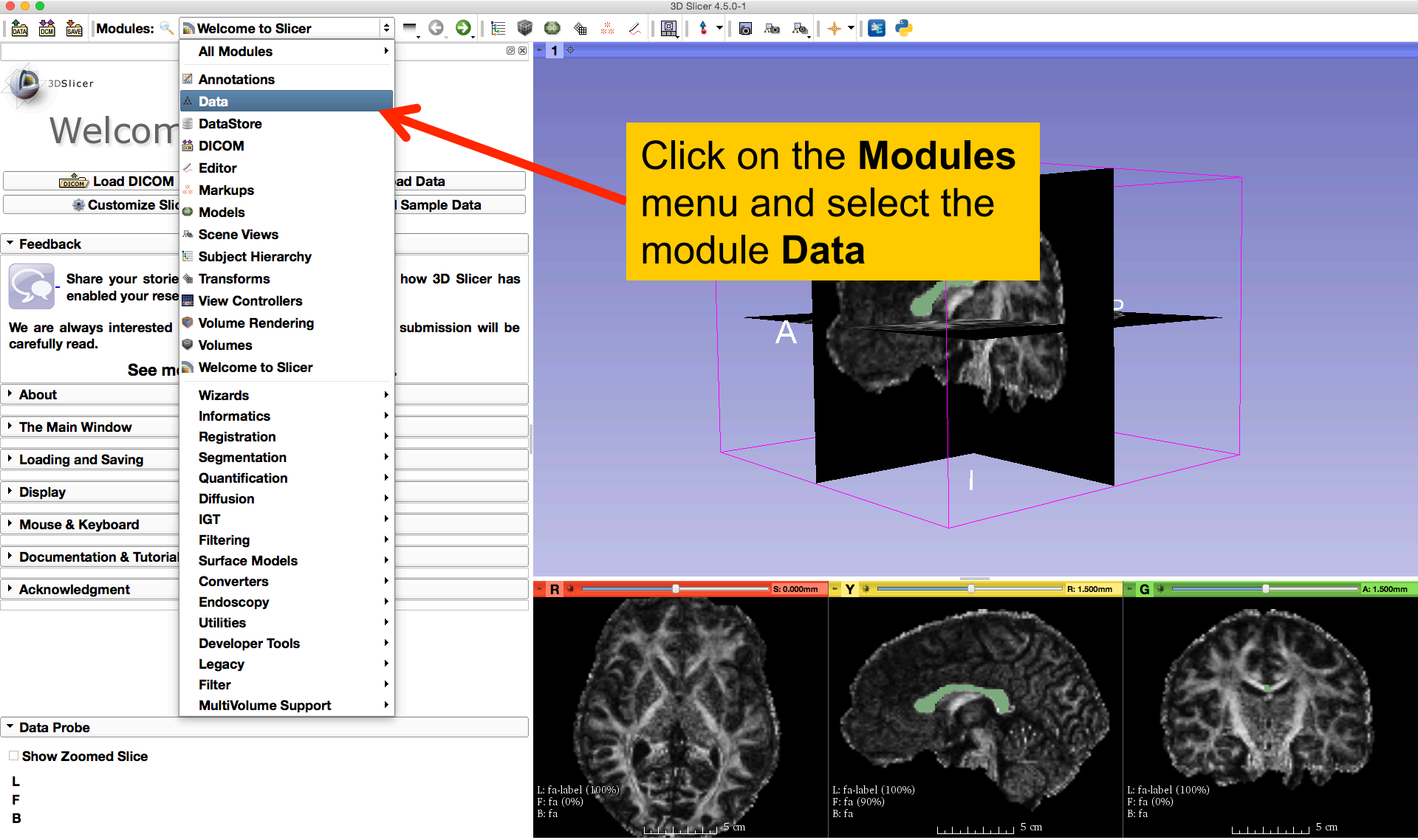
▶ Data Probe

Show Zoom

L  
F  
B

5 cm 5 cm 5 cm

# Load MRML Data



# Load MRML Data

3D Slicer 4.5.0-1

Modules: Data

Help & Acknowledgement

Display & Modify Scene

Nodes

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

Scene Model: Transform

- Display MRML ID's
- Show Hidden nodes

Filter:

MRML Node Inspector

Data Probe

- Show Zoomed Slice

L  
F  
B

S  
A  
I

S: 0.000mm Y R: 1.500mm 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

5 cm

5 cm

5 cm

Data loaded for this tutorial:

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

# Edit Multiple Labels

3D Slicer 4.5.0-1

Modules: Data

- All Modules
- Annotations
- Data
- DataStore
- DICOM
- Editor**
- Markups
- Models
- Scene Views
- Subject Hierarchy
- Transforms
- View Controllers
- Volume Rendering
- Volumes
- Welcome to Slicer
- Wizards
- Informatics
- Registration
- Segmentation
- Quantification
- Diffusion
- IGT
- Filtering
- Surface Models
- Converters
- Endoscopy
- Utilities
- Developer Tools
- Legacy
- Filter
- MultiVolume Support

Help & Acknowledgements

Display & Modify Scene

Nodes

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

Scene Model: Transform

Display MRI

Show Hidden

Filter:

MRML Node Inspector

Data Probe

Show Zoomed Slice

L  
F  
B

Select the module Editor

A

I

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

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

5 cm

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

5 cm

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

5 cm

# Edit Multiple Labels

The screenshot displays the 3D Slicer 4.5.0-1 interface. On the left, the 'Editor' module is active, showing a 'Data Probe' section with 'tissue' selected and '1' in the dropdown. A yellow box with the text 'Select the Yellow slice only layout' has a red arrow pointing to the 'Yellow slice only' option in the View menu. The View menu is open, listing various display styles, with 'Yellow slice only' highlighted. The main 3D view shows a brain slice with a green label, and the bottom panel shows three orthogonal views (L, F, B) with a 5 cm scale bar. The status bar at the bottom indicates 'R: 1.500mm' and 'G: 1.500mm'.

3D Slicer 4.5.0-1

Modules: Editor

1

Conventional  
Conventional Widescreen  
Conventional Quantitative  
Four-Up  
Four-Up Quantitative  
Dual 3D  
Triple 3D  
3D only  
One-Up Quantitative  
Red slice only  
**Yellow slice only**  
Green slice only  
Tabbed 3D  
Tabbed slice  
Compare  
Compare Widescreen  
Compare Grid  
Three over three  
Three Over Three Quantitative  
Four over four  
Two over Two  
Side by side  
Four by three slice  
Four by two slice  
Three by three slice

3DSlicer

Help & Acknowledgement

Create and Select Label Maps

Select the Yellow slice only layout

Edit Selected Label Map

Undo/Redo:

Active Tool: DefaultTool

Label: tissue 1

Data Probe

Show Zoomed Slice

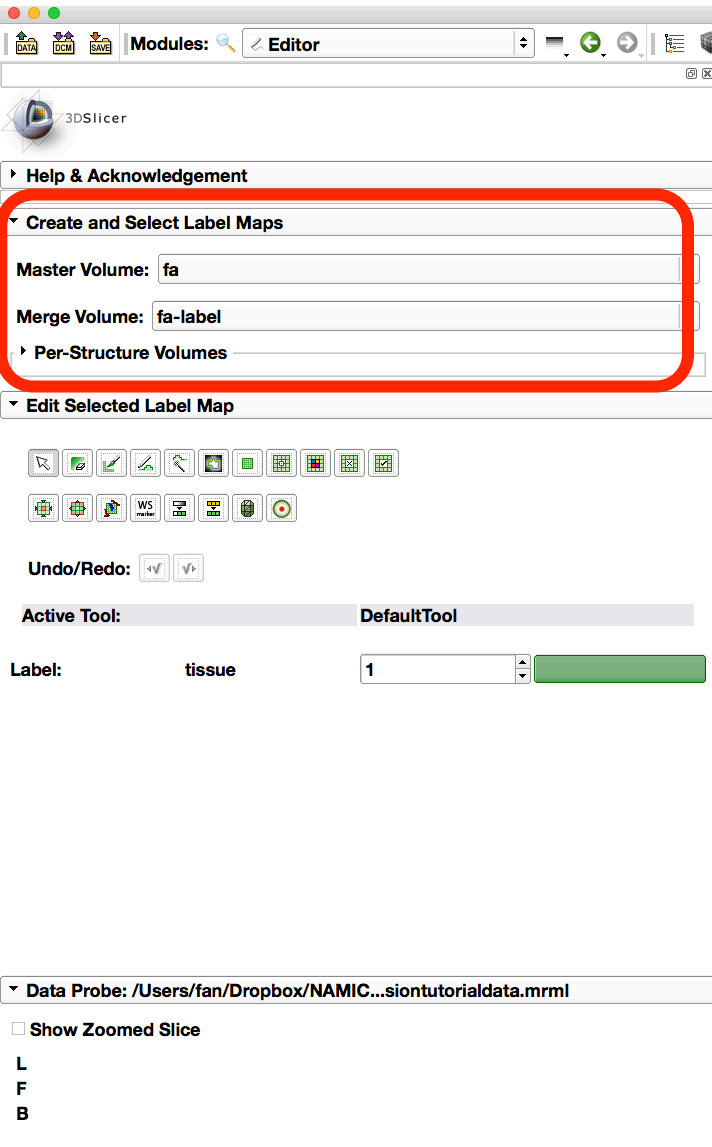
L: fa-label (100%)  
F: fa (0%)  
B: fa

R: 1.500mm

G: 1.500mm

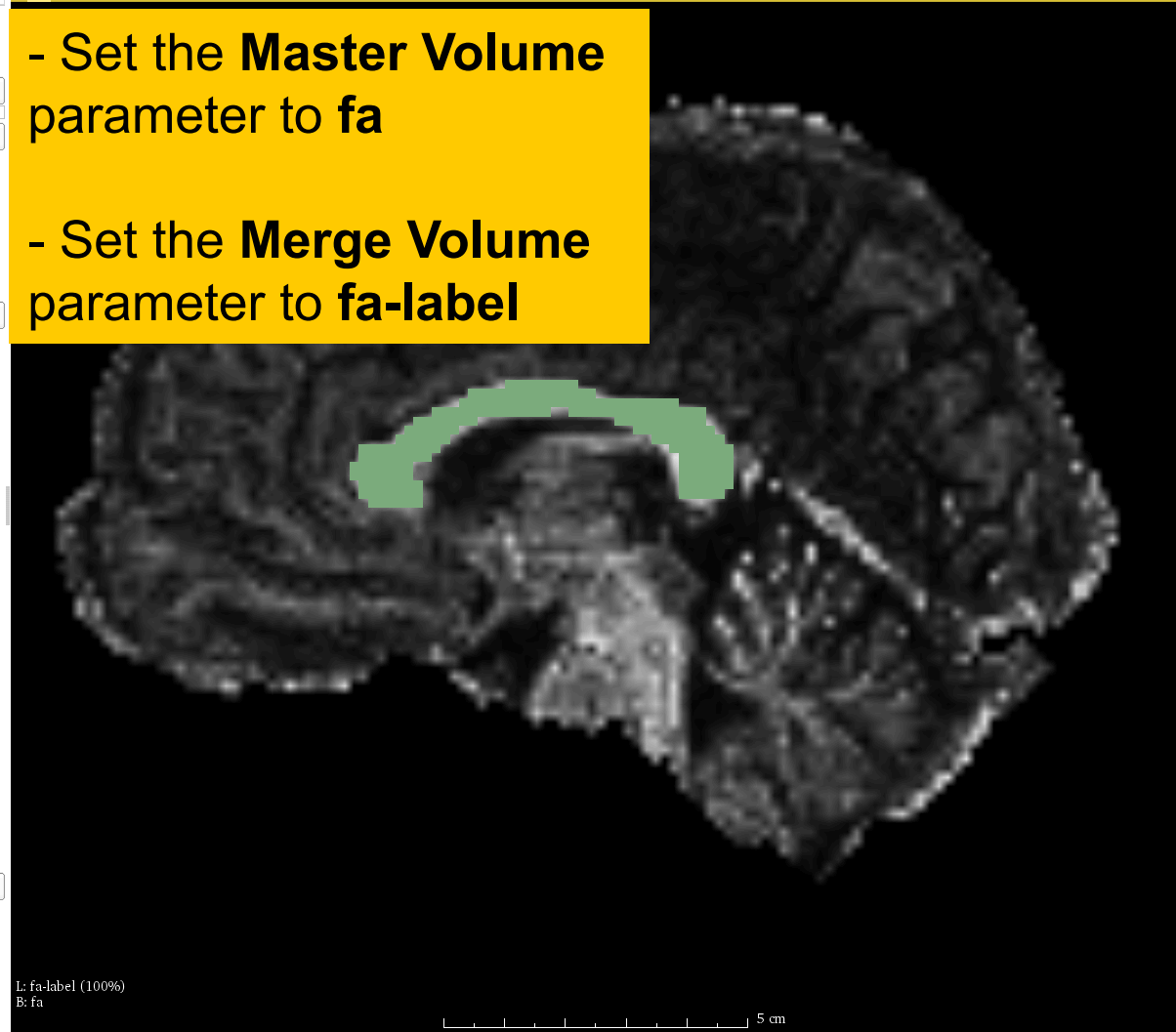
5 cm

# Edit Multiple Labels



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

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



# Edit Multiple Labels

The screenshot shows the 3D Slicer 4.5.0-1 interface with the Editor module active. The main window displays a coronal slice of a brain MRI. The left sidebar contains the following sections:

- Help & Acknowledgement**
- Create and Select Label Maps**
  - Master Volume: fa
  - Merge Volume: fa-label
  - Per-Structure Volumes
- Edit Selected Label Map**
  - Tools: A toolbar with various icons, including the **DrawEffect** tool (a red square icon) which is highlighted with a red arrow.
  - Undo/Redo: [Undo] [Redo]
  - Active Tool: DrawEffect
  - Label: bone, 2 (with a dropdown arrow)
  - Paint Over
  - Threshold Paint
  - Apply
- Data Probe: /Users/fan/Dropbox/NAMIC...siontutorialdata.mrml**
  - Show Zoomed Slice
  - L
  - F
  - B

Annotations on the image:

- A yellow box with the text "Slide right to the next slice" has a red arrow pointing to the right edge of the slice view.
- A yellow box with the text "- Select the DrawEffect tool" has a red arrow pointing to the DrawEffect tool icon in the toolbar.
- A yellow box with the text "- Set the Label to 2" has a red arrow pointing to the label dropdown menu.

At the bottom left of the slice view, the legend indicates: L: fa-label (100%), B: fa. A 5 cm scale bar is visible at the bottom right.



# Edit Multiple Labels

3D Slicer 4.5.0-1

Modules: Editor

3DSlicer

- Help & Acknowledgement
- Create and Select Label Maps
  - Master Volume
  - Merge Volume
  - Per-Structure
  - Edit Selection

Undo/Redo: [Undo] [Redo]

Active Tool: DrawEffect

Label: bone 2

Paint Over  
 Threshold Paint

Apply

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

Yellow RAS: ( 6.0, 31.0, 12.7) Sagittal Sp: 1.5

L fa-label ( 60, 43, 55) bone (2)  
F None  
B fa ( 60, 43, 55) 0.720727

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

5 cm

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

# Edit Multiple Labels

The screenshot shows the 3D Slicer 4.5.0-1 Editor interface. The main window displays a sagittal brain slice with a brown label '3' applied to a region in the corpus callosum. A yellow box with black text contains the instruction: "Repeat the above steps to draw the middle of Corpus Callosum with **label 3** on the next slice". A red arrow points from this box to the label in the brain slice. The interface includes a top toolbar, a left sidebar with menu items like "Help & Acknowledgement", "Create and Select Label Maps", and "Edit Selection", and a bottom status bar showing the current tool as "DrawEff" and the label as "3".

3D Slicer 4.5.0-1

Modules: Editor

3DSlicer

Help & Acknowledgement

Create and Select Label Maps

Master Volume

Merge Volume

Per-Structure

Edit Selection

Undo/Redo: [Undo] [Redo]

Active Tool: DrawEff

Label: skin 3

Paint Over

Threshold Paint

Apply

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

Yellow RAS: ( 7.5, 5.2, 46.2) Sagittal Sp: 1.5

L fa-label ( 59, 61, 78) background ( 0)

F None

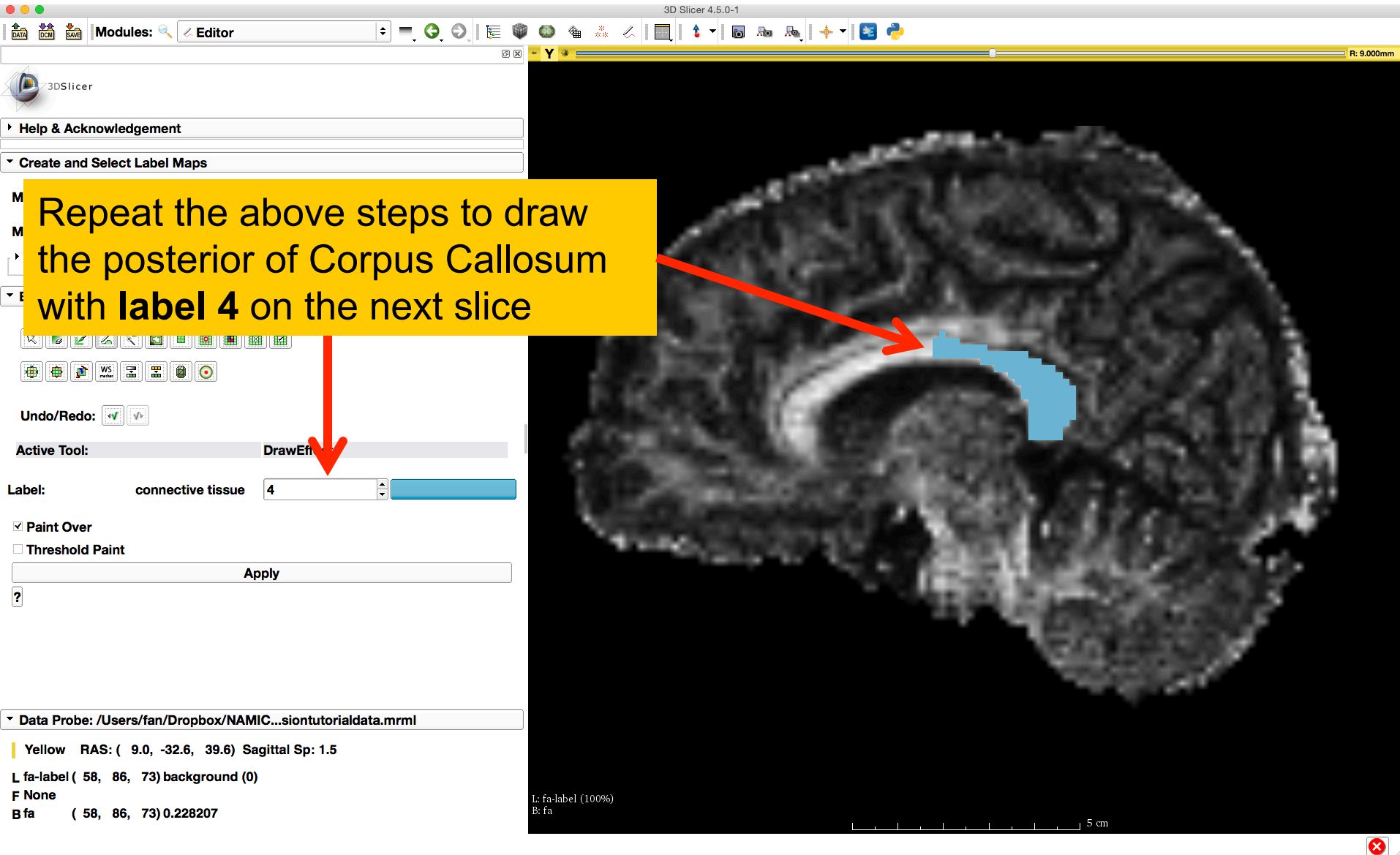
B fa ( 59, 61, 78) 0.308757

L: fa-label (100%)

B: fa

5 cm

# Edit Multiple Labels



3D Slicer 4.5.0-1

Modules: Editor

Help & Acknowledgement

Create and Select Label Maps

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

Active Tool: DrawEff

Label: connective tissue 4

Paint Over

Threshold Paint

Apply

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

Yellow RAS: ( 9.0, -32.6, 39.6) Sagittal Sp: 1.5

L fa-label ( 58, 86, 73) background (0)

F None

B fa ( 58, 86, 73) 0.228207

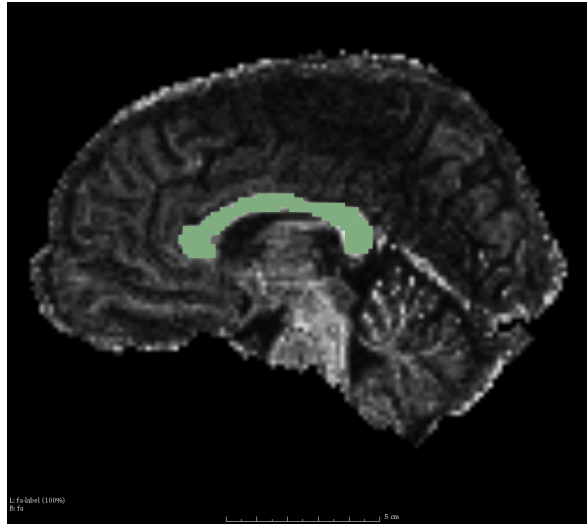
L: fa-label (100%)  
B: fa

5 cm

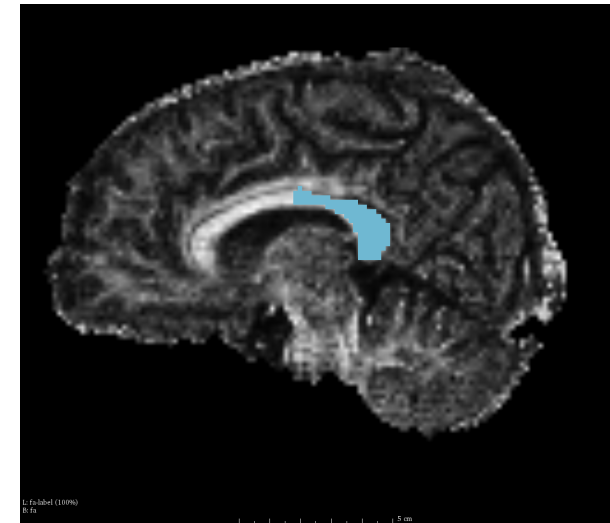
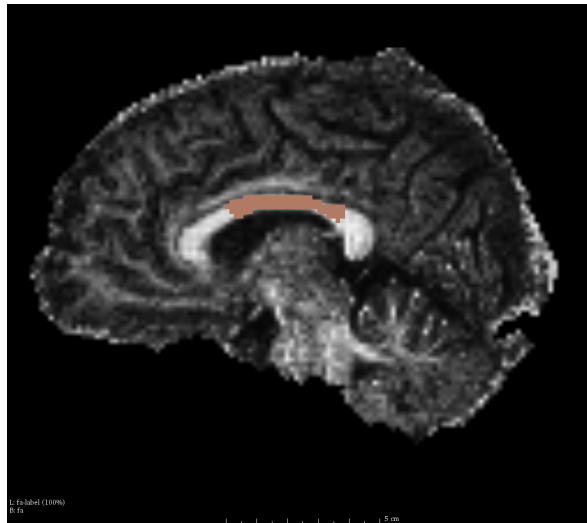
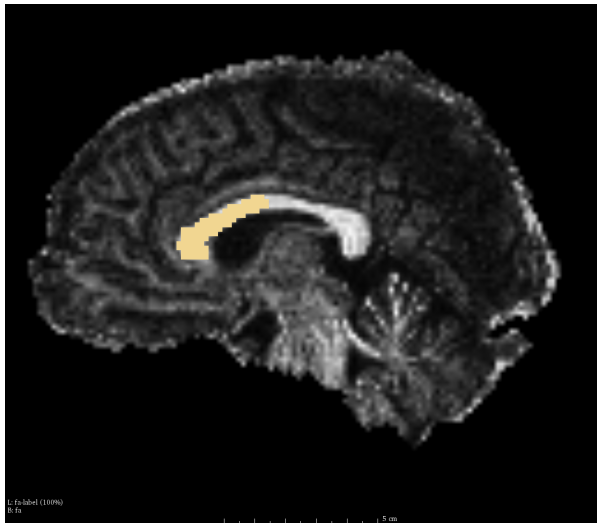
# Edit Multiple Labels

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

The image shows the 3D Slicer 4.5.0-1 interface. The 'Editor' menu is open, and the path 'Diffusion' > 'Tractography' > 'Tractography Label Map Seeding' is highlighted. A red arrow points to the 'Tractography Label Map Seeding' option. A yellow callout box with the text 'Go back to the Conventional layout' has a red arrow pointing to the 'Conventional' icon in the top toolbar. Another yellow callout box with the text 'Select the module Tractography Label Map Seeding' has a red arrow pointing to the 'Tractography Label Map Seeding' option in the menu. The main view displays three orthogonal slices of a brain with a green tractography line. The bottom status bar shows 'L: fa-label (100%) B: fa' and a 5 cm scale bar.

3D Slicer 4.5.0-1

Go back to the **Conventional** layout

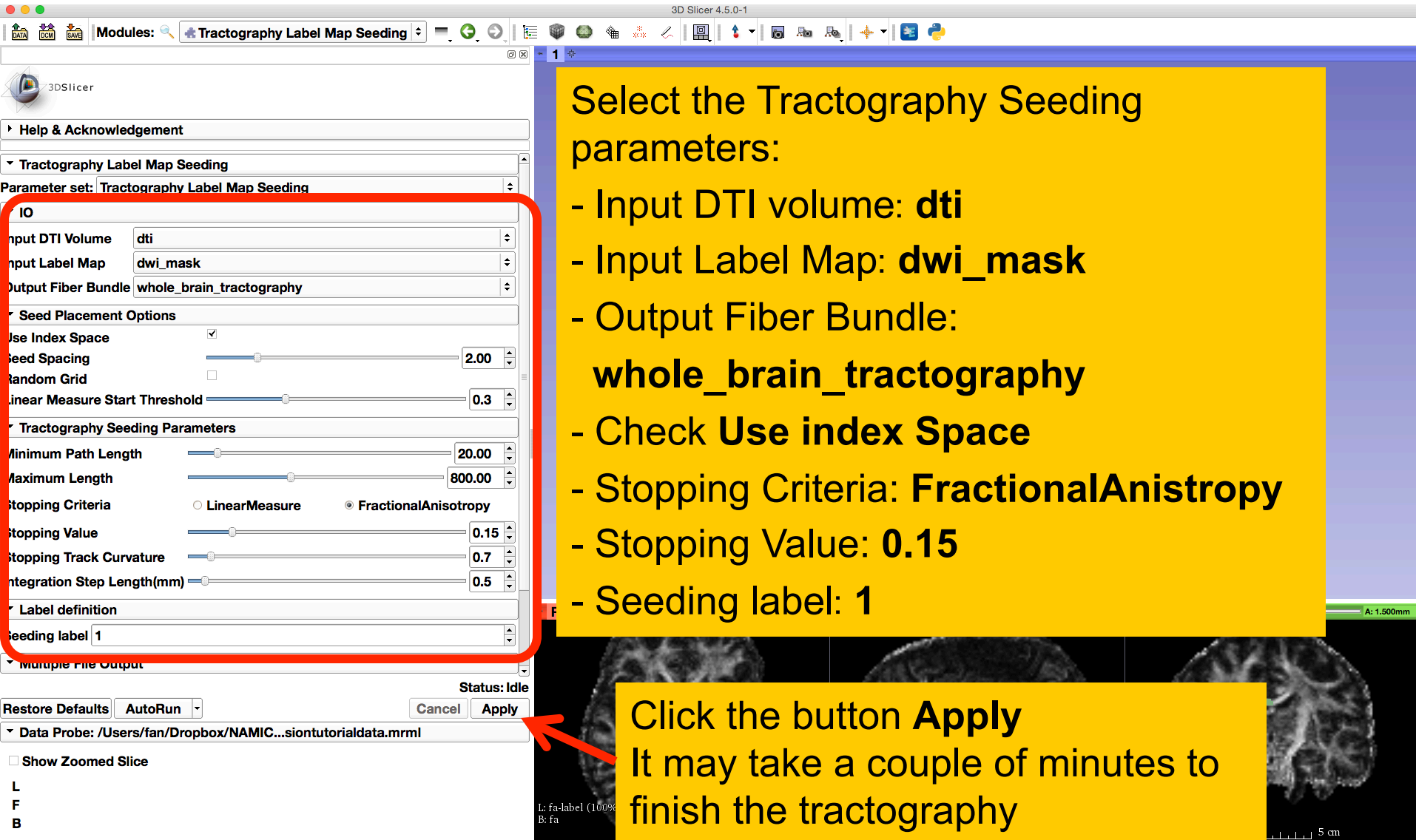
Select the module **Tractography Label Map Seeding**

- Diffusion
  - DWI to Full Brain Tractography
  - Tractography Display
  - Diffusion Data Conversion
    - Diffusion Tensor Images
      - Diffusion Tensor Scalar Measurements
      - Resample DTI Volume
    - Diffusion Weighted Images
    - Tractography
      - Tractography Interactive Seeding
      - Tractography Label Map Seeding**

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

5 cm

# Whole Brain Tractography



3D Slicer 4.5.0-1

Modules: 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 Cancel Apply

Data Probe: /Users/fan/Dropbox/NAMIC...siontutorialdata.mrm1

Show Zoomed Slice

L  
F  
B

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

5 cm

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

3D Slicer 4.5.0-1

Modules: Models

3DSlicer

Help & Acknowledgement

Include Fibers  Line Tube GLM

Scene

whole\_brain\_tractography 1.00

Information

Display

Clipping

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

Show Zoomed Slice

L  
F  
B

**Select the module Models**

**Check Include Fibers**

**Uncheck Toggle slice visibility in 3D view**

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

Axial fa

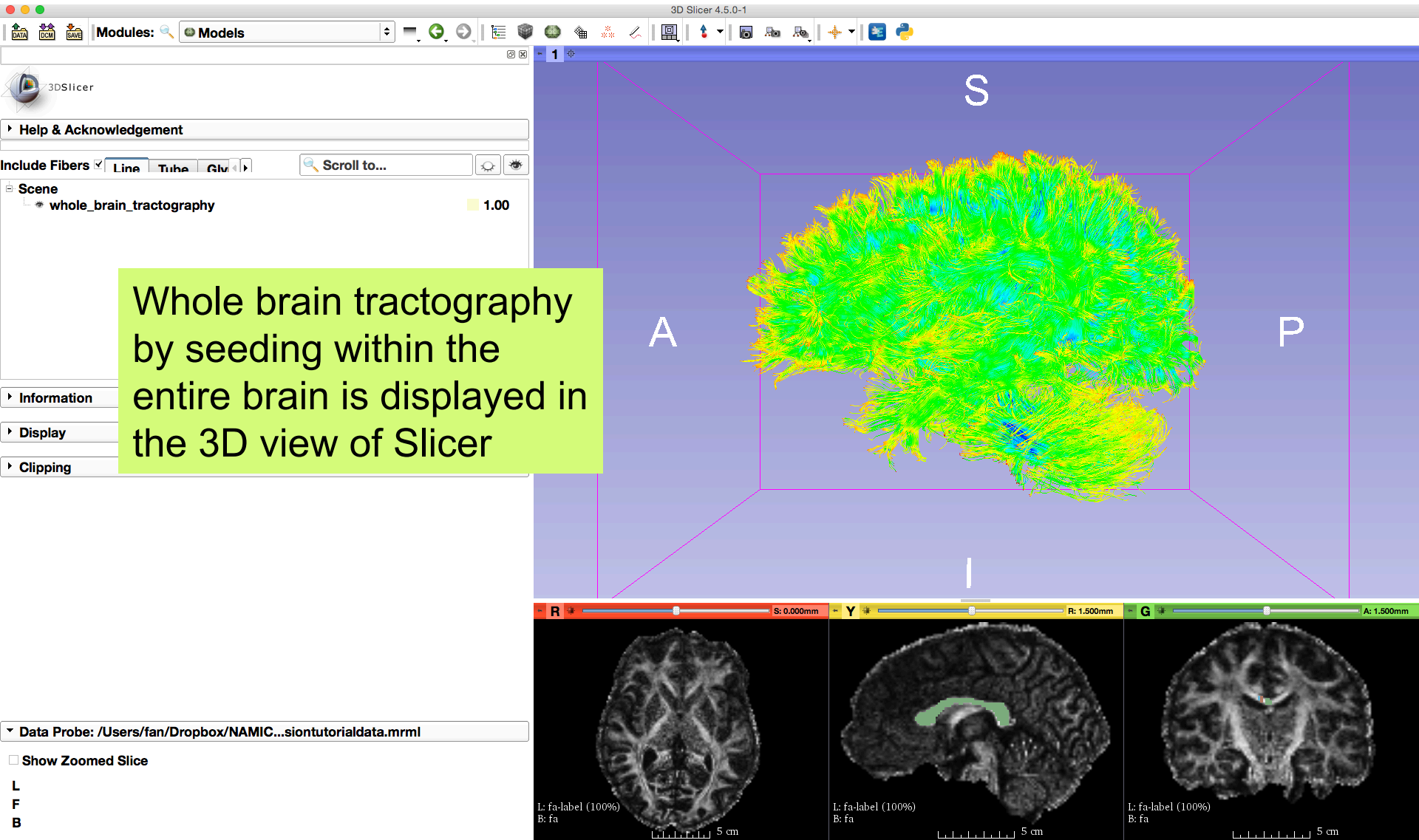
L: fa-label (100%)  
B: fa

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

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

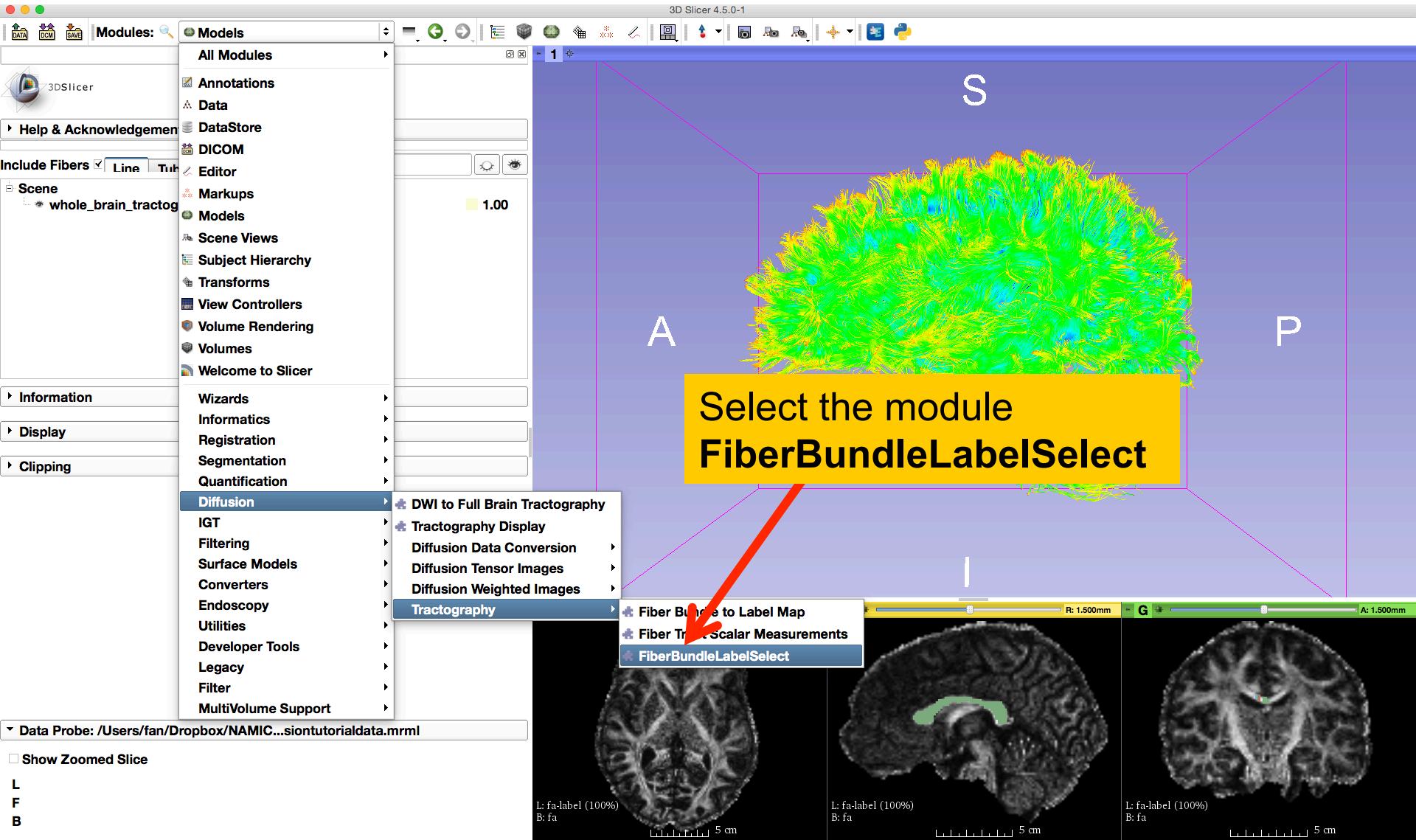
5 cm 5 cm 5 cm

# Whole Brain Tractography





# Fiber Bundle Label Selection



# Single Label Selection

The screenshot shows the 3D Slicer 4.5.0-1 interface. The 'FiberBundleLabelSelect' module is active, and its parameters are displayed in the left sidebar. A red box highlights the 'Input Label Map', 'Input Fiber Bundle', 'Output Fiber Bundle', and 'Labels to include' fields. The 'Labels to include' field contains the value '1'. Below the parameters, there are radio buttons for 'Combine include labels' (OR selected) and 'Combine exclude labels' (OR selected). At the bottom of the sidebar, there are buttons for 'Restore Defaults', 'AutoRun', 'Cancel', and 'Apply'. The 'Apply' button is highlighted with a red arrow pointing to a yellow callout box that says 'Click the button Apply'. The main 3D view shows three brain slices in the R, Y, and G planes. The status bar at the bottom indicates 'Status: Idle'.

3D Slicer 4.5.0-1

Modules: 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

Restore Defaults AutoRun Cancel Apply

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

Show Zoomed Slice

L F B

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

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

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

5 cm 5 cm 5 cm

Click the button Apply

- Input Label Map: **fa-label**
- Input Fiber Bundle: **whole\_brain\_tractography**
- Output Fiber Bundle: **bundle\_label1\_include**
- Labels to include: **1**

# Single Label Selection

The screenshot displays the 3D Slicer 4.5.0-1 interface. The top toolbar contains various icons, with a red arrow pointing to the 'Models' icon. The left sidebar shows the 'Scene' panel with a tree view containing 'whole\_brain\_tractography' and 'bundle\_label1\_include'. A red arrow points to the 'bundle\_label1\_include' entry. The main 3D view shows a fiber bundle visualization in a color gradient (green to blue) within a purple wireframe box. The box is labeled with 'S' at the top, 'A' on the left, 'P' on the right, and 'I' at the bottom. Below the 3D view are three orthogonal slice windows: 'R' (axial), 'Y' (sagittal), and 'G' (coronal). The 'R' window shows a zoomed-in view of the fiber bundle. A green text box is overlaid on the 'R' and 'G' windows.

**Select the module Models**

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

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

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

Show Zoomed Slice

L  
F  
B

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

5 cm

# Single Label Selection

3D Slicer 4.5.0-1

Modules: FiberBundleLabelSelect

3DSlicer

Help & Acknowledgement

FiberBundleLabelSelect

Parameter set: FiberBundleLabelSelect

Input Label Map: fa-label

Input Fiber Bundle: whole\_brain\_tractography

Output Fiber Bundle: bundle\_label2\_include

Label regions definition

Labels to include: 2

Combine include labels:  OR  AND

Labels to exclude:

Combine exclude labels:  OR  AND

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

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

Show Zoomed Slice

L  
F  
B

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

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

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

5 cm

5 cm

5 cm

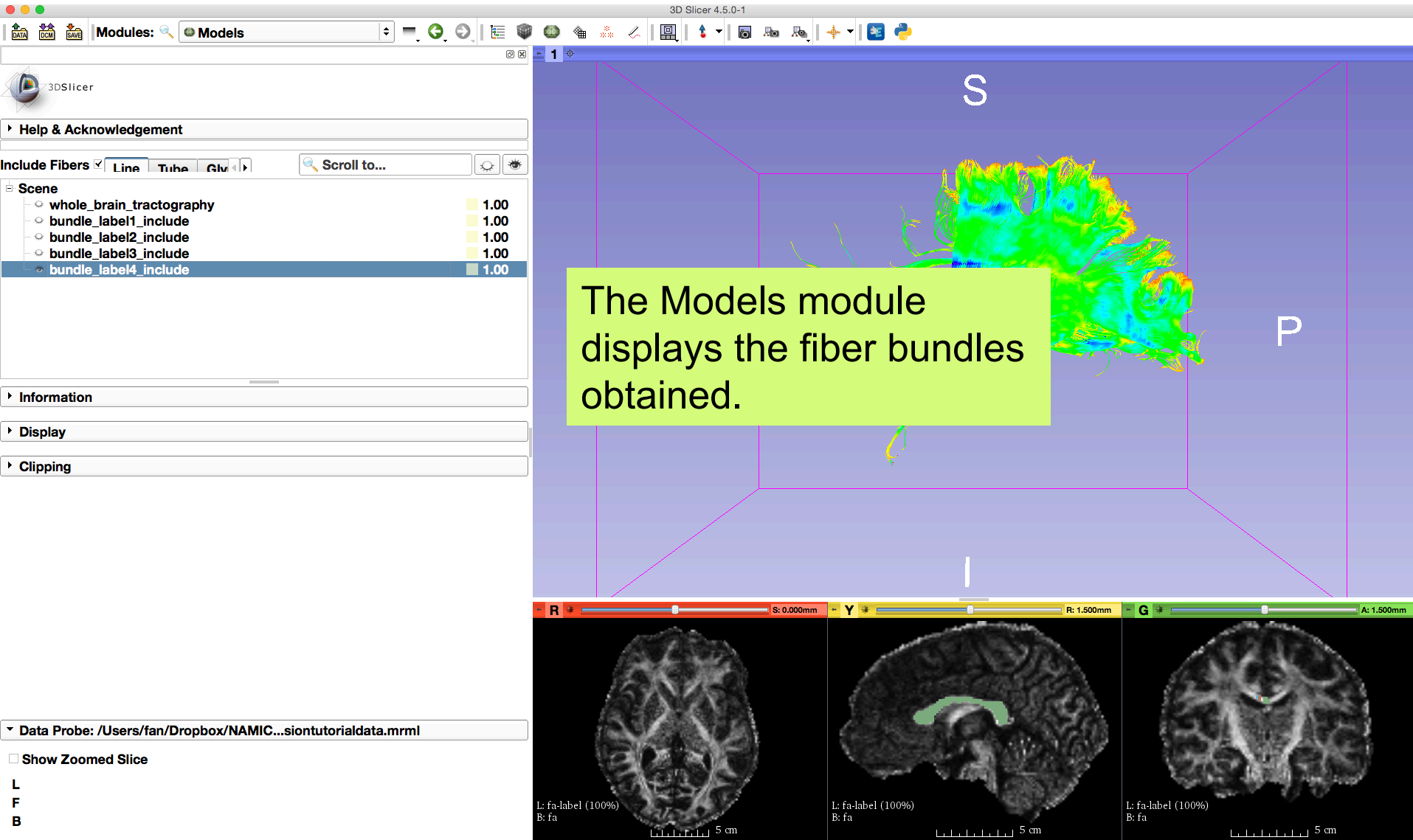
S

P

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

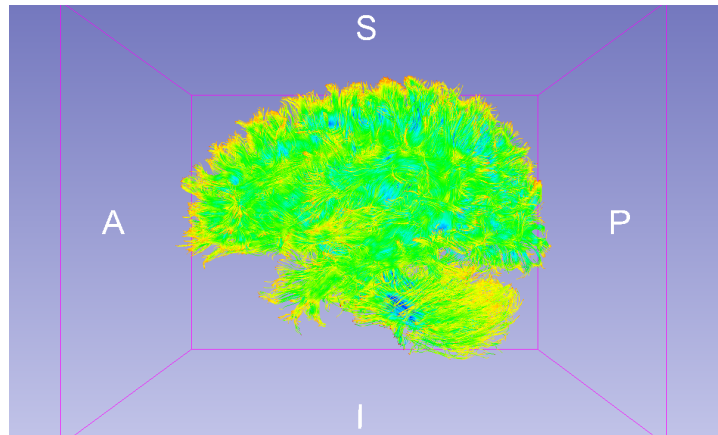
Repeat the above steps to perform fiber bundle selections of labels 2, 3 and 4 individually and obtain the selected bundles of **bundle\_label2\_include**, **bundle\_label3\_include** and **bundle\_label4\_include** respectively

# Single Label Selection

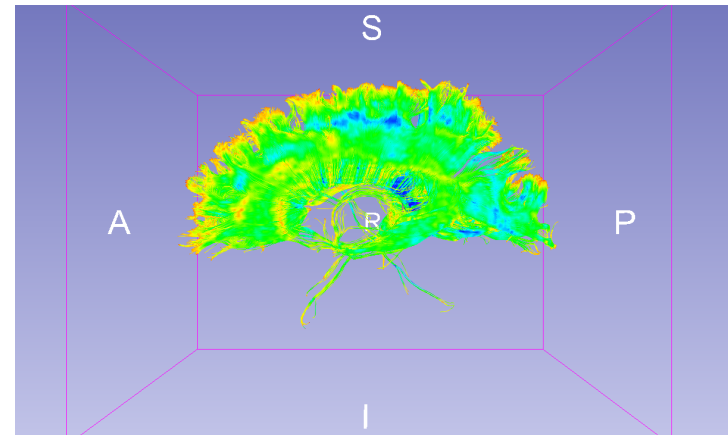


# Single Label Selection

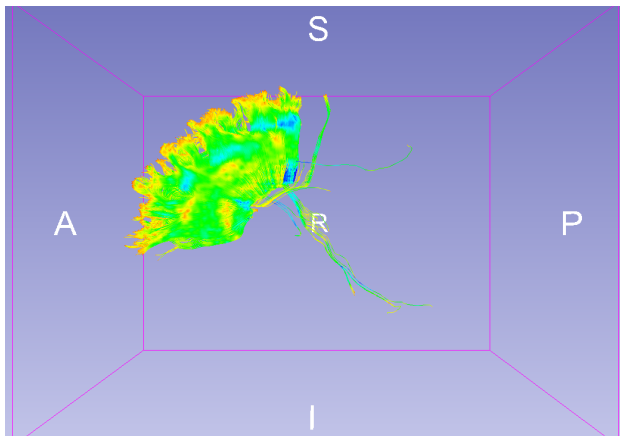
Whole Brain



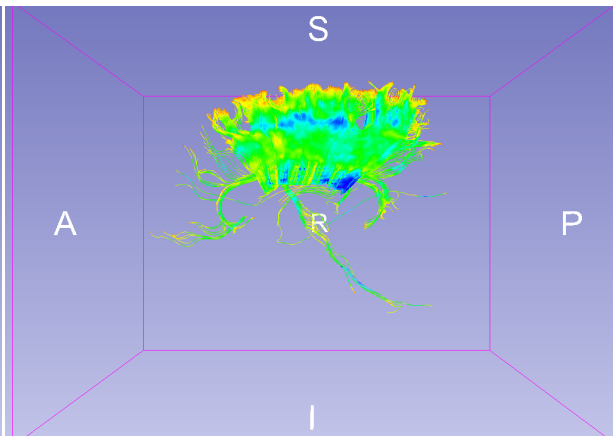
Label 1



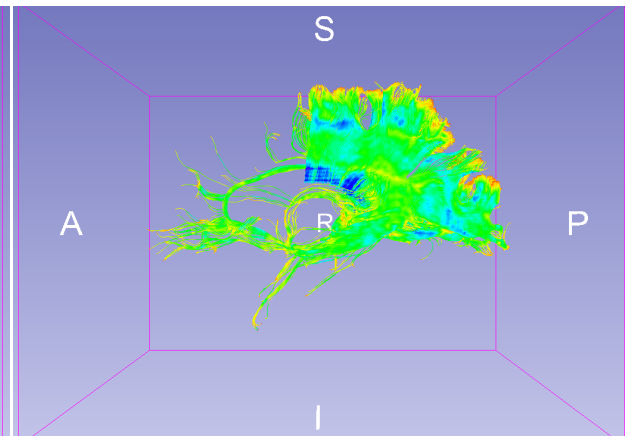
Label 2



Label 3



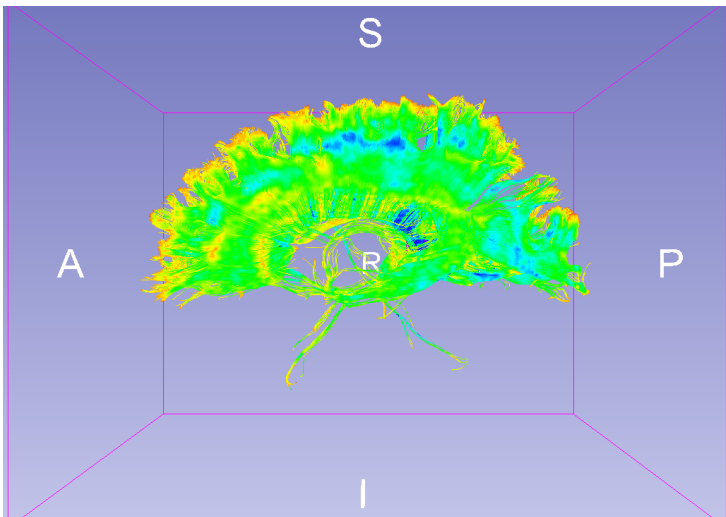
Label 4



# Single Label Selection

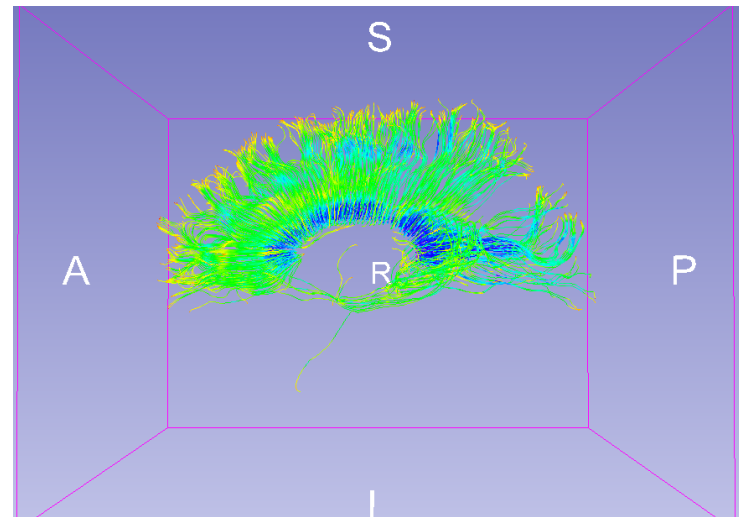
Notice that whole brain seeding creates a denser fiber bundle than seeding from the label 1.

Fiber Bundle Selection of Label 1  
from the Whole Brain Tractography



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

▼ Label regions definition

Labels to include

Combine include labels  OR  AND

Labels to exclude

Combine exclude labels  AND

And or Or logical operation used to combine include labels



# Multiple Labels Selection (AND)

3D Slicer 4.5.0-1

Modules: FiberBundleLabelSelect

Parameter set: FiberBundleLabelSelect

Input Label Map: fa-label

Input Fiber Bundle: whole\_brain\_tractography

Output Fiber Bundle: bundle\_labels2AND3\_include

Label regions definition

Labels to include: 2,3

Combine include labels:  OR  AND

Labels to exclude:

Combine exclude labels:  OR  AND

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

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

Show Zoomed Slice

L F B

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

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

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

5 cm 5 cm 5 cm

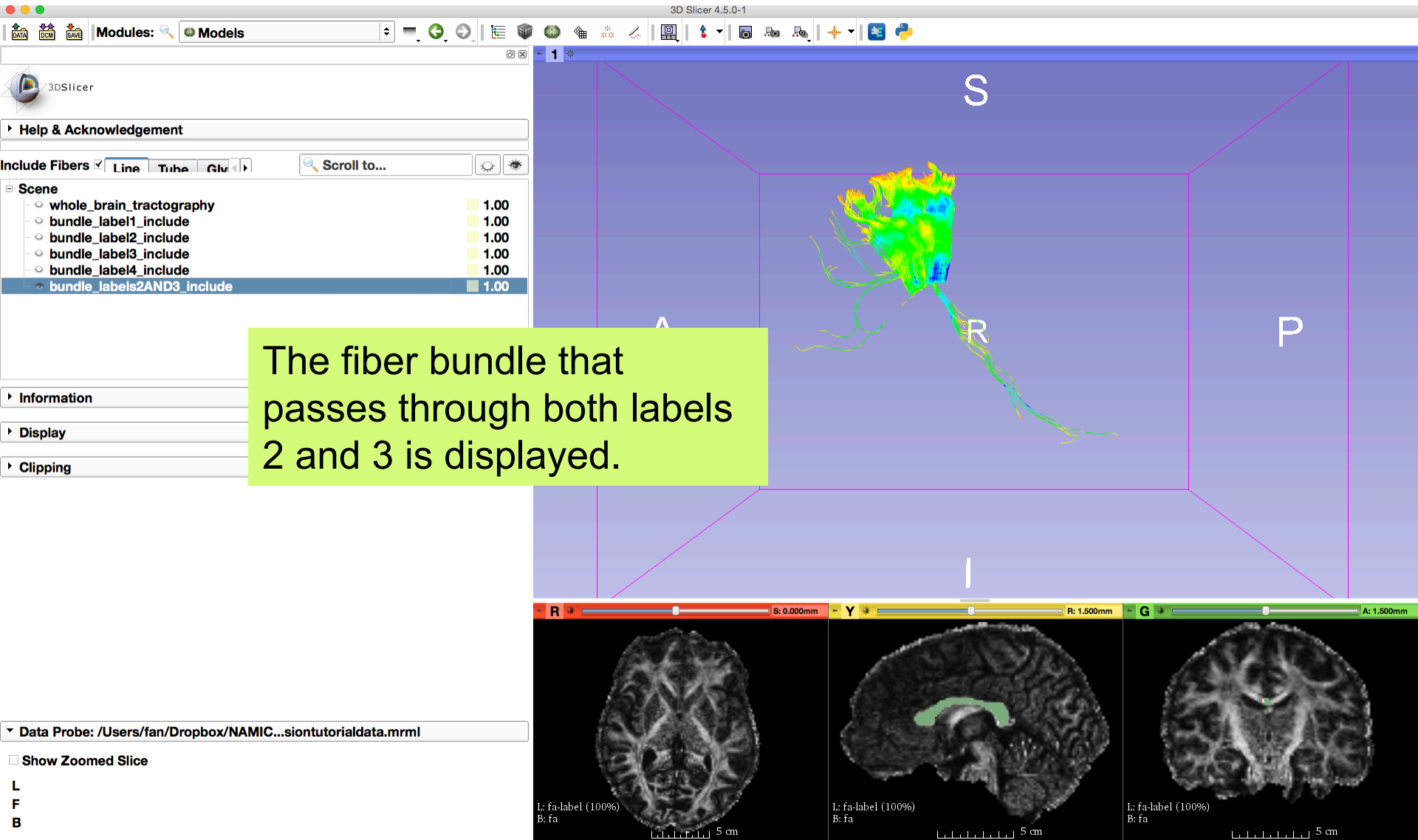
Set the FiberBundleLabelSelection parameters:

- Input Label Map: **fa-label**
- Input Fiber Bundle: **whole\_brain\_tractography**
- Output Fiber Bundle: **bundle\_labels2AND3\_include**
- Labels to include: **2,3**

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

Click the button **Apply**

# Multiple Labels Selection (AND)



# Multiple Labels Selection (OR)

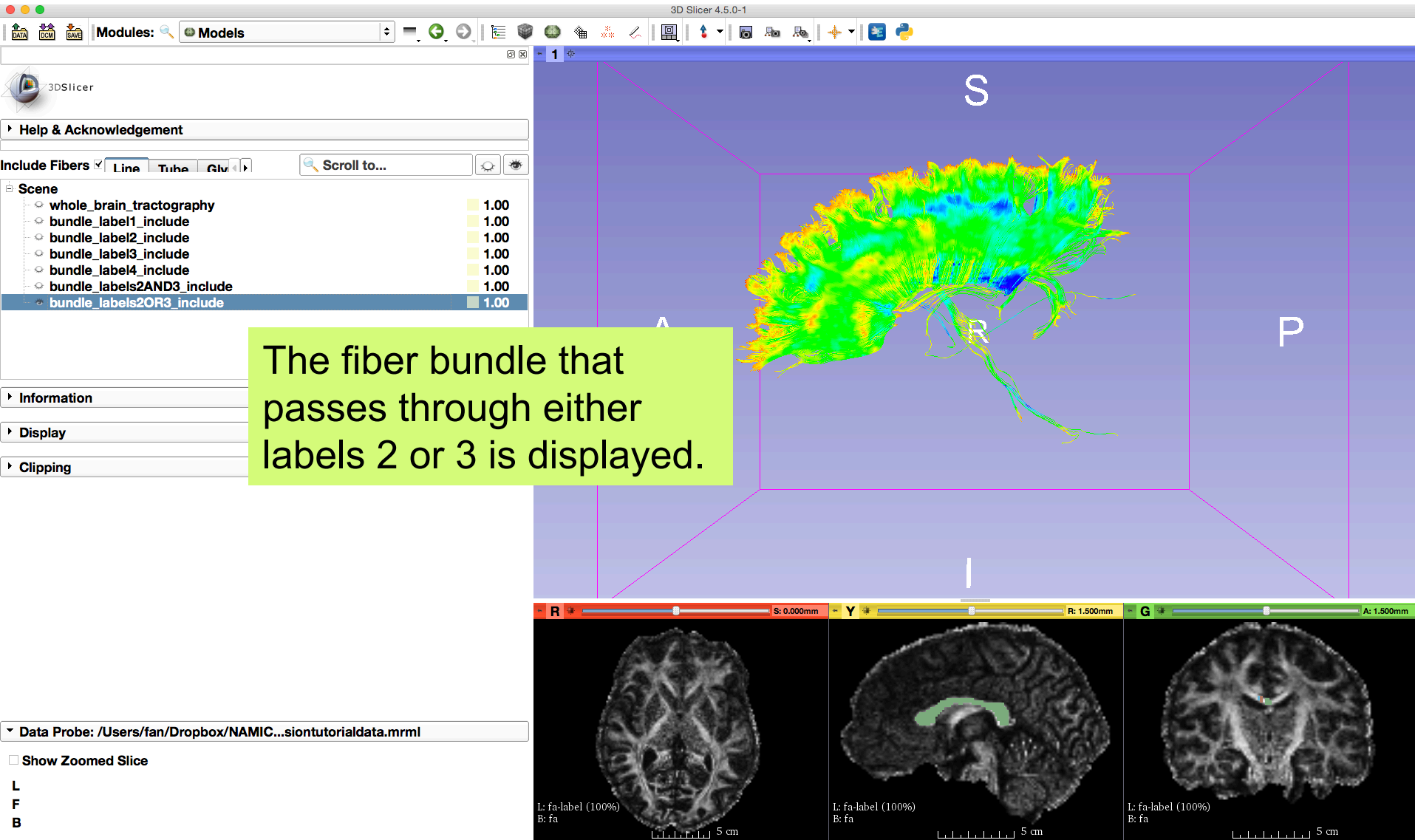
The screenshot shows the 3D Slicer 4.5.0-1 interface. The **FiberBundleLabelSelect** module is active. The configuration panel on the left is highlighted with a red box, and a red arrow points to the **Combine include labels** radio button, which is set to **OR**. A yellow callout box points to this button with the text: "Set **Combine include labels** to **OR**".

The 3D view shows a brain slice with fiber bundles. A yellow callout box with 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**" is overlaid on the 3D view.

At the bottom, the **Apply** button is highlighted with a red arrow and a yellow callout box with the text: "Click the button **Apply**".

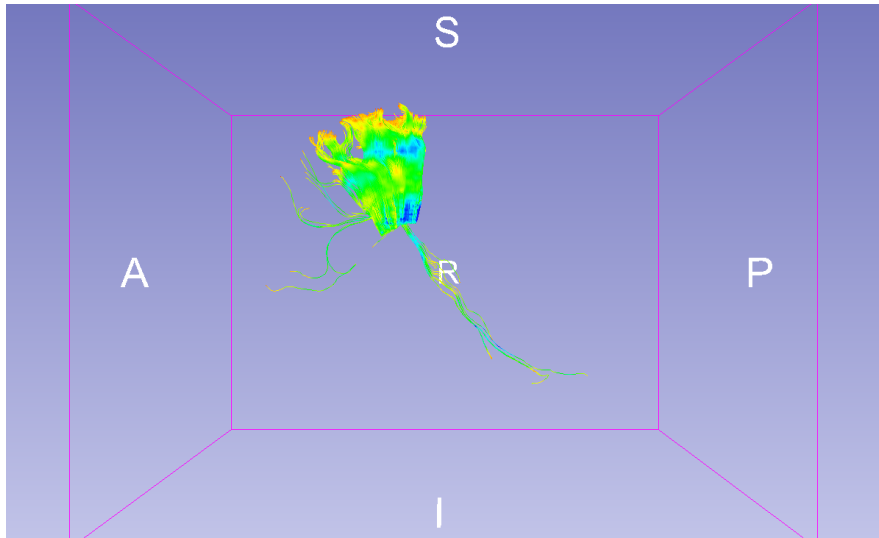
The status bar at the bottom shows "Status: Completed" and "100%". The bottom right corner shows three axial brain slices with fiber bundles, labeled "L: fa-label (100%) B: fa".

# Multiple Labels Selection (OR)

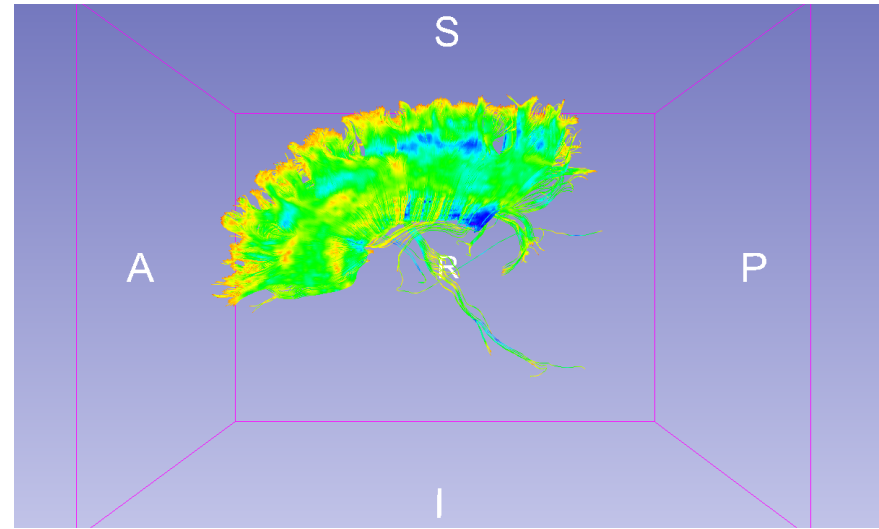


# Multiple Labels Selection

Labels 2 and 3



Labels 2 or 3



# Save Fiber Bundles

3D Slicer 4.5.0-1

Modules: Models

3DSlicer

Help & Ackno

Click the button **SAVE**

Include Fibers  Line Tub

Scene

- corpusCallosum
- whole\_brain\_tractography
- bundle\_label1\_include.vtk
- bundle\_label2\_include.vtk
- bundle\_label3\_include.vtk
- bundle\_label4\_include.vtk
- bundle\_labels2AND3\_include.vtk
- bundle\_labels2OR3\_include.vtk

File Name	File Format	Directory
<input type="checkbox"/> whole_brain_tractography.vtk	Poly Data (.vtk)	/Users/fan/Desktop/fiberbund
<input checked="" type="checkbox"/> bundle_label1_include.vtk	Poly Data (.vtk)	/Users/fan/Desktop/fiberbund
<input checked="" type="checkbox"/> bundle_label2_include.vtk	Poly Data (.vtk)	/Use
<input checked="" type="checkbox"/> bundle_label3_include.vtk	Poly Data (.vtk)	/Use
<input checked="" type="checkbox"/> bundle_label4_include.vtk	Poly Data (.vtk)	/Use
<input checked="" type="checkbox"/> bundle_labels2AND3_include.vtk	Poly Data (.vtk)	/Use
<input checked="" type="checkbox"/> bundle_labels2OR3_include.vtk	Poly Data (.vtk)	/Use
<input type="checkbox"/> Slicer Data Bundle Scene View.png	PNG (.png)	/Use

Change directory for selected files

Save Cancel

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**

Information

Display

Show Zoomed Slice

L  
F  
B

L: fa-l...00%)  
B: fa

L: fa-l...00%)  
B: fa

L: fa-l...00%)  
B: fa

5 cm

10 mm

10 mm

# Fiber Tract Scalar Measurements

The image shows the 3D Slicer 4.5.0-1 interface. The main window displays a 3D brain model with fiber tracts, color-coded by scalar measurements. The model is oriented with S (Superior), A (Anterior), and P (Posterior) axes. A yellow callout box with a red arrow points to the 'Fiber Tract Scalar Measurements' option in the 'Tractography' sub-menu of the 'Diffusion' module.

**Select the module Fiber Tract Scalar Measurements**

- Modules
  - All Modules
    - Annotations
    - Data
    - DataStore
    - DICOM
    - Editor
    - Markups
    - Models
      - 1.00
      - 1.00
      - 1.00
      - 1.00
      - 1.00
      - 1.00
      - 1.00
      - 1.00
      - 1.00
      - 1.00
      - 1.00
    - Scene Views
    - Subject Hierarchy
    - Transforms
    - View Controllers
    - Volume Rendering
    - Volumes
    - Welcome to Slicer
  - Wizards
  - Informatics
  - Registration
  - Segmentation
  - Quantification
  - Diffusion
    - DWI to Full Brain Tractography
    - Tractography Display
    - Diffusion Data Conversion
    - Diffusion Tensor Images
    - Diffusion Weighted Images
    - Tractography
      - Fiber Bundle to Label Map
      - Fiber Tract Scalar Measurements**
      - FiberBundleLabelSelect
  - IGT
  - Filtering
  - Surface Models
  - Converters
  - Endoscopy
  - Utilities
  - Developer Tools
  - Legacy
  - Filter
  - MultiVolume Support

Information

Display

Clipping

Data Probe: /Users/fan/Dr...

Show Zoomed Slice

L  
F  
B

5 cm  
10 mm  
10 mm

# Fiber Tract Scalar Measurements

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

Fibers Hierarchy Select a ModelHierarchy

Fibers File Folder /Users/fan/Desktop/fiberbundles

Output Text File esktop/fiberbundles/measurements.csv

Select Output Format  Row\_Hierarchy  Column\_Hierarchy

Output Field Separator  Comma  Space  Tab

Status: Idle

Restore Defaults AutoRun

Cancel Apply

Data Probe

Show Zoomed Slice

L  
F  
B

5 cm 5 cm 5 cm

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**

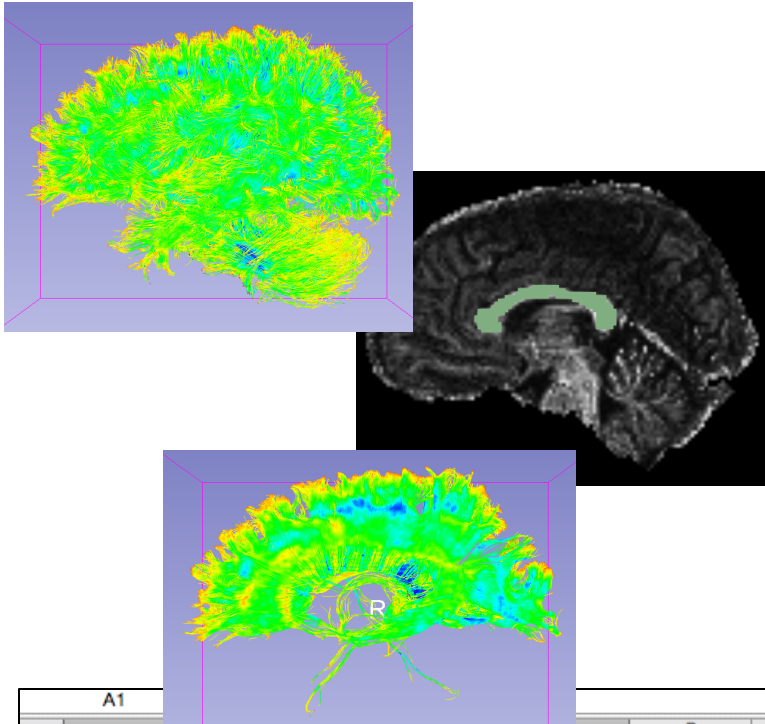


# Fiber Tract Scalar Measurements

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

	A	B	C	D
1	Name	Num_Points	Num_Fibers	Tensors_.FractionalAnisotropy
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	A	Num_Points	Num_Fibers	Tensors_FractionalAnisotropy	Tensors_LinearMeasurement	Tense
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	

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**Neuroimage Analysis Center (NAC)**

NIH P41EB015902