

# Fiber Bundle Selection And Scalar Measurement

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BWH

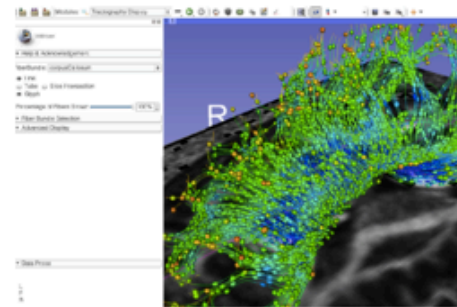
# Pre-requisite

- This tutorial is a follow-up tutorial of the Diffusion Tensor Imaging Tutorial. 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 4.4
- 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 contains a 'Modules' section with 'Welcome to Slicer' and a 'Data' section with a file browser. The file browser lists several files, with 'diffusiontutorialdata.mrml' selected. A red arrow points from this file to a yellow text box. Below the file browser, there is a 'Data Probe' section with a 'Show Zoom' checkbox. A dialog box titled 'Add data into the scene' is open in the foreground, showing a list of files to be added. The file '...easurement\_TutorialContestWinter2016/diffusiontutorialdata.mrml' is selected in the list. A red arrow points from the 'OK' button in the dialog box to a yellow text box. The bottom of the interface shows a 3D view with a 5 cm scale bar.

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>	<b>Dec 31, 2015, 1:48 PM</b>	<b>731 B</b>
dti.nrrd	Dec 31, 2015, 1:37 PM	10.4 M
dwi_mask.nrrd	Dec 31, 2015, 1:38 PM	28 M
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 B

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

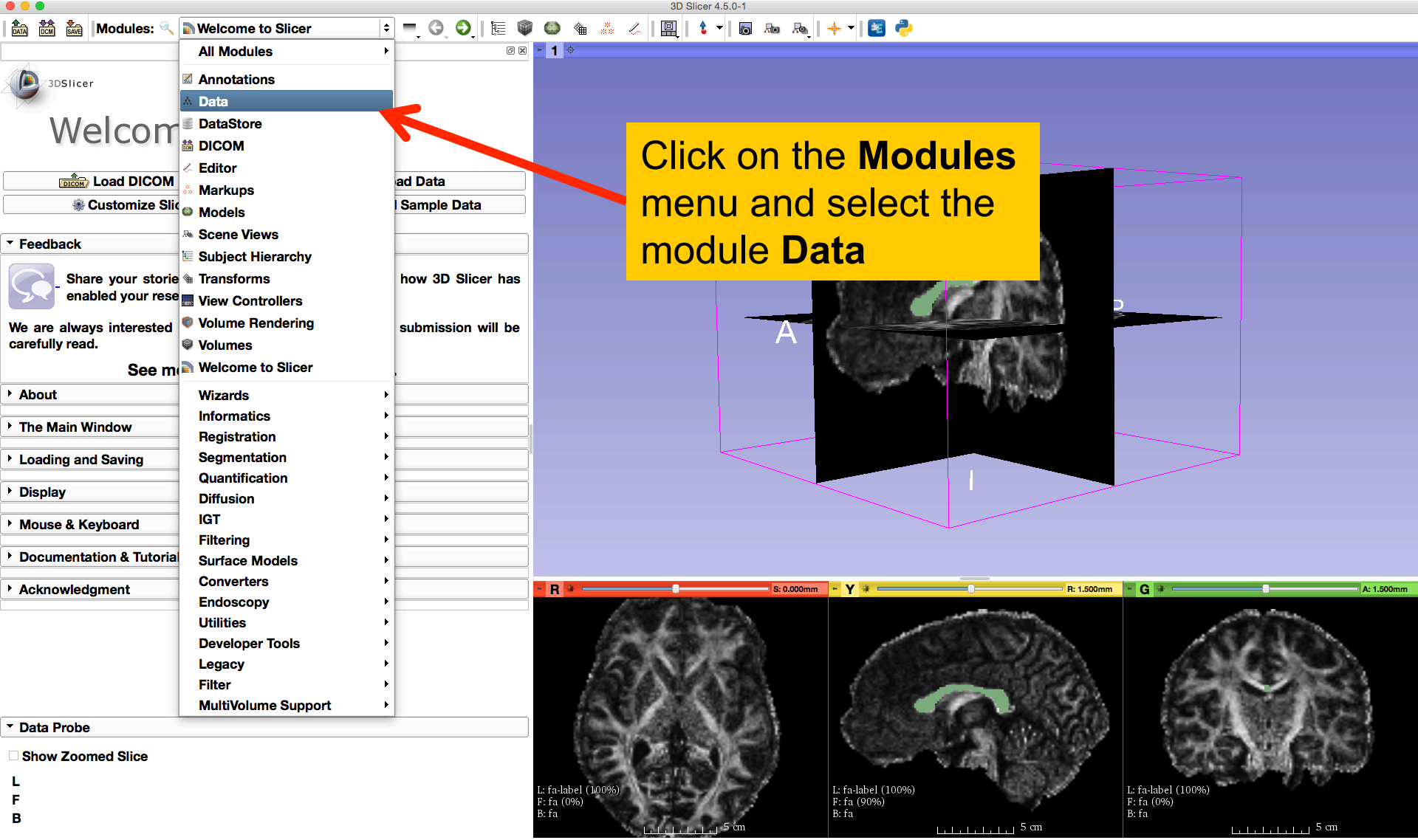
Click **OK** to load the dataset to Slicer

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

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

Scene Model: Transform

Filter:

MRML Node Inspector

Data Probe

Show Zoomed Slice

L  
F  
B

Select the module **Editor**

A  
I  
B

R: 0.000mm Y: 1.500mm G: 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

# Edit Multiple Labels

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

Select the **Yellow slice only** layout

Undo/Redo: [Undo] [Redo]

Active Tool: DefaultTool

Label: tissue 1

R 1.500mm G 1.500mm A 1.500mm

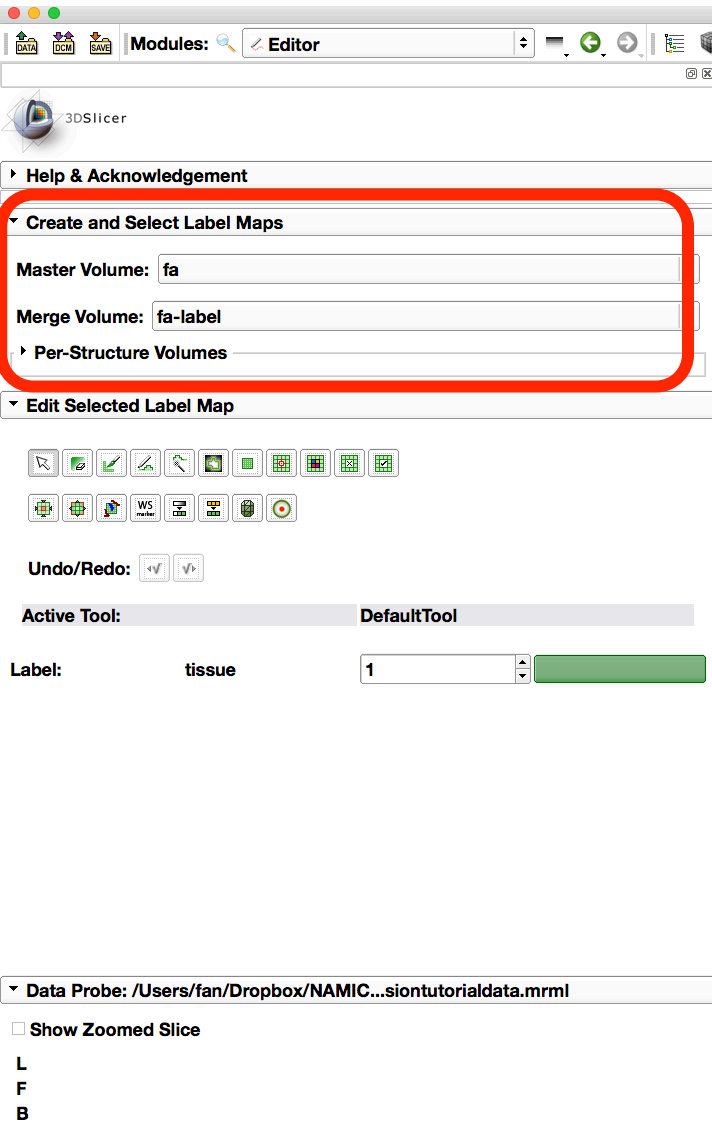
L: fa-label (100%)  
F: fa (90%)  
B: fa

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

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

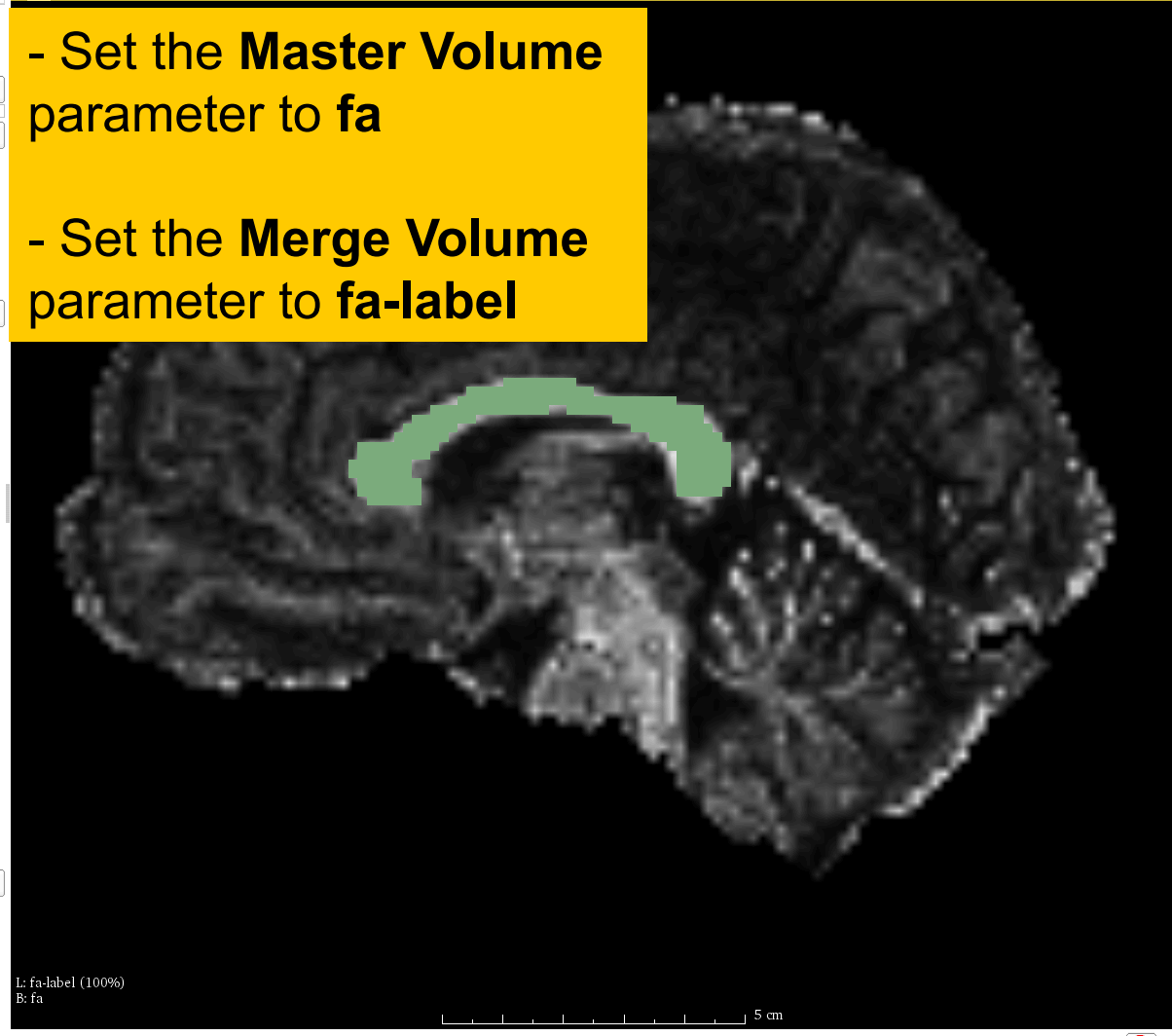
5 cm 5 cm 5 cm

# 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 Editor interface. The main window displays a brain MRI slice. 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

At the bottom left, the legend shows: L: fa-label (100%), B: fa. A scale bar at the bottom right indicates 5 cm. The top right corner shows "R: 6.000mm".

Yellow callout boxes with red arrows provide instructions:

- Slide right to the next slice**: An arrow points to the right edge of the slice view.
- Select the DrawEffect tool**: An arrow points to the DrawEffect tool icon in the toolbar.
- Set the Label to 2**: An arrow points to the label dropdown menu.

# 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 label '3' (brown) drawn on 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 the text 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 "Data Probe: /Users/fan/Dropbox/NAMIC...siontutorialdata.mrml" and "Yellow RAS: ( 7.5, 5.2, 46.2) Sagittal Sp: 1.5".

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%)

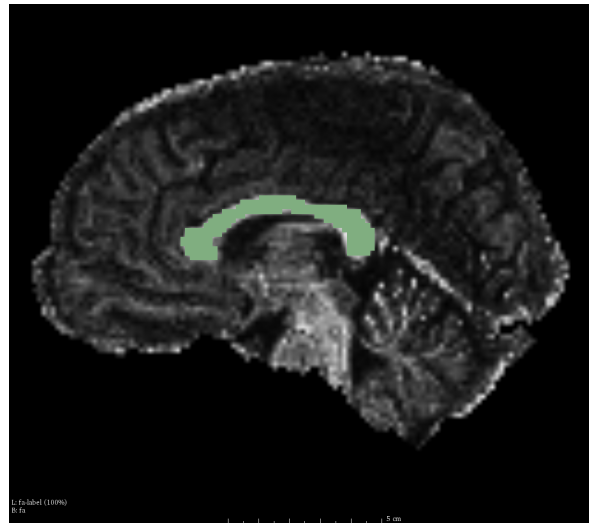
B: fa

5 cm

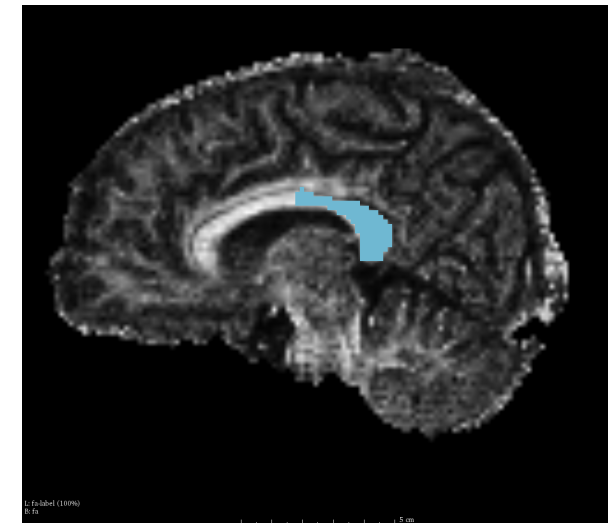
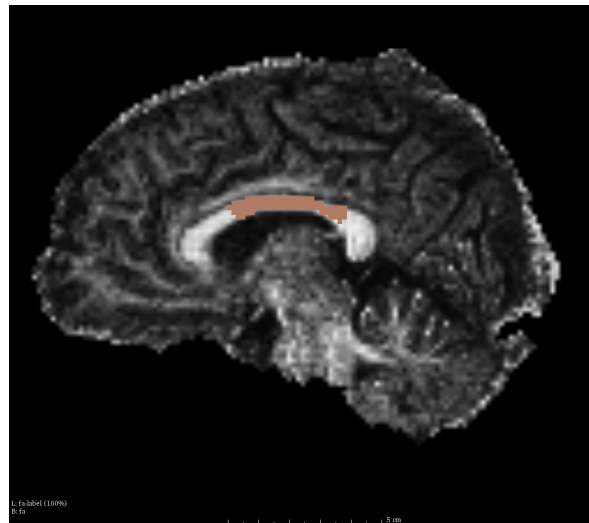
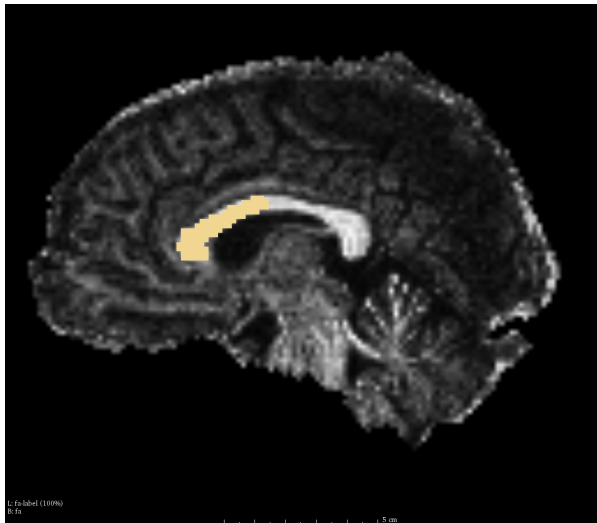
# Edit Multiple Labels

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.





# Whole Brain Tractography

The image shows the 3D Slicer 4.5.0-1 interface. The 'Editor' menu is open, and the 'Diffusion' sub-menu is selected. Within 'Diffusion', the 'Tractography' option is highlighted, and its sub-menu is open, showing 'Tractography Label Map Seeding' as the selected option. A red arrow points from a yellow callout box to the 'Tractography Label Map Seeding' option. Another yellow callout box with a red arrow points to the 'Conventional' layout icon in the top toolbar. The main 3D view shows a brain slice with a green tract. Below the main view are three zoomed-in slices of the brain, each with a 5 cm scale bar. The bottom left shows the 'Data Probe' and 'Show Zoomed Slice' options.

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

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

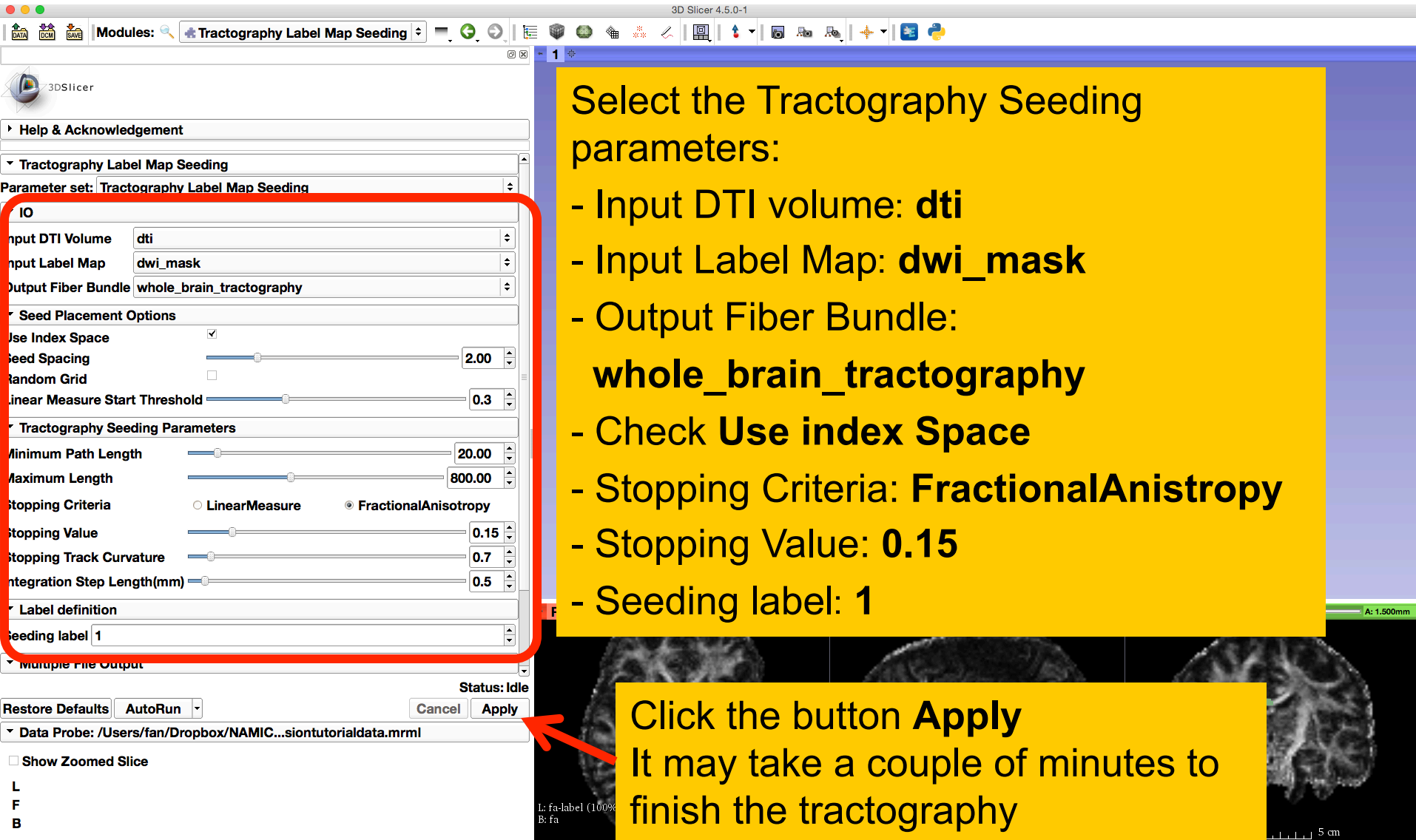
L: fa-label (100%)  
B: fa

5 cm

5 cm

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.mrml

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

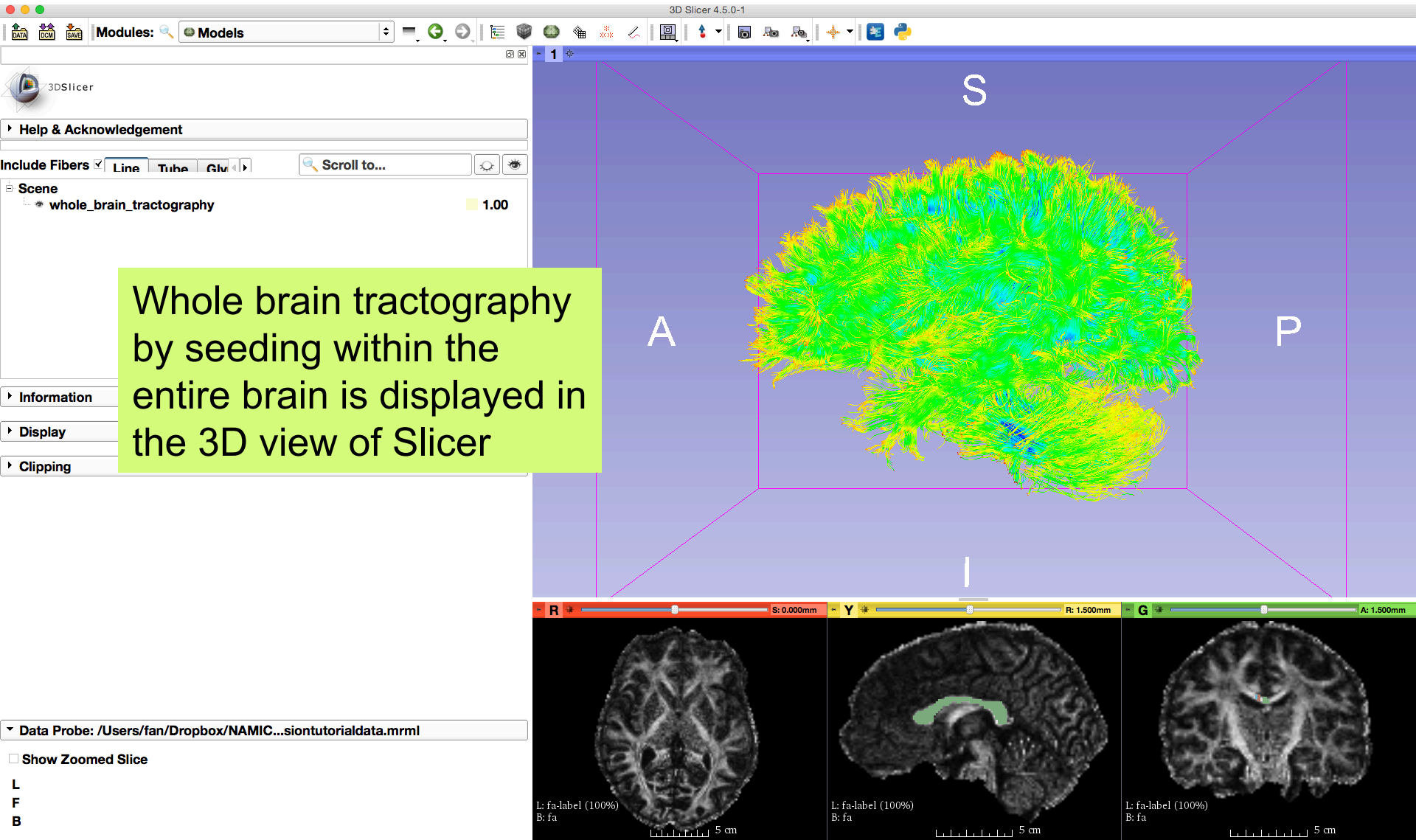
L: fa-label (100%)  
B: fa

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

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

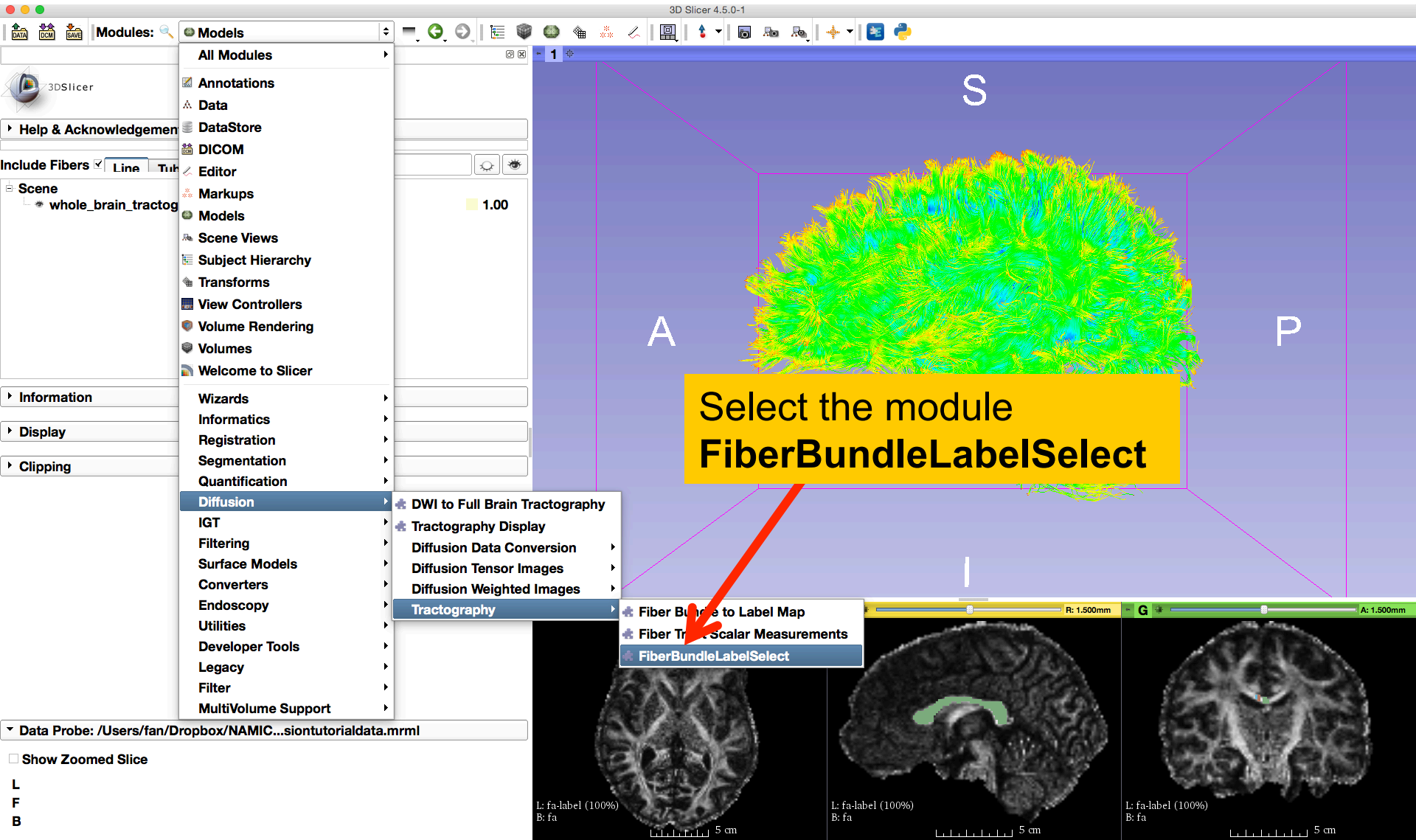
5 cm 5 cm 5 cm

# Whole Brain Tractography



Whole brain tractography by seeding within the entire brain is displayed in the 3D view of Slicer

# 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 following parameters:

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

Below the highlighted parameters, there are options for "Combine include labels" (radio buttons for OR and AND) and "Labels to exclude" (text input field). At the bottom of the sidebar, there are buttons for "Restore Defaults", "AutoRun", "Cancel", and "Apply".

The main 3D view shows three brain slices (axial, sagittal, and coronal) with fiber bundles overlaid. A yellow box with a red arrow points to the "Apply" button, with the text "Click the button Apply".

**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**

# Single Label Selection

The image shows the 3D Slicer 4.5.0-1 interface. The main 3D view displays a brain with a fiber bundle highlighted in green and blue, with anatomical planes labeled S (Superior), A (Anterior), R (Right), and P (Posterior). The left sidebar shows the 'Scene' panel with 'whole\_brain\_tractography' and 'bundle\_label1\_include' listed. A red arrow points to the 'Models' module in the top toolbar. Another red arrow points to the 'bundle\_label1\_include' entry in the Scene panel. The bottom panel shows a zoomed-in slice of the fiber bundle, with a green text box overlaid on the right side.

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

3D Slicer 4.5.0-1

Modules: Models

3DSlicer

Help & Acknowledg

Include Fibers Line Tube GLV Scroll to...

Scene

- whole\_brain\_tractography 1.00
- bundle\_label1\_include 1.00

Clipping

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

Show Zoomed Slice

L  
F  
B

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

5 cm

5 cm

5 cm

# Single Label Selection

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\_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

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

R S I  
Y G A

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

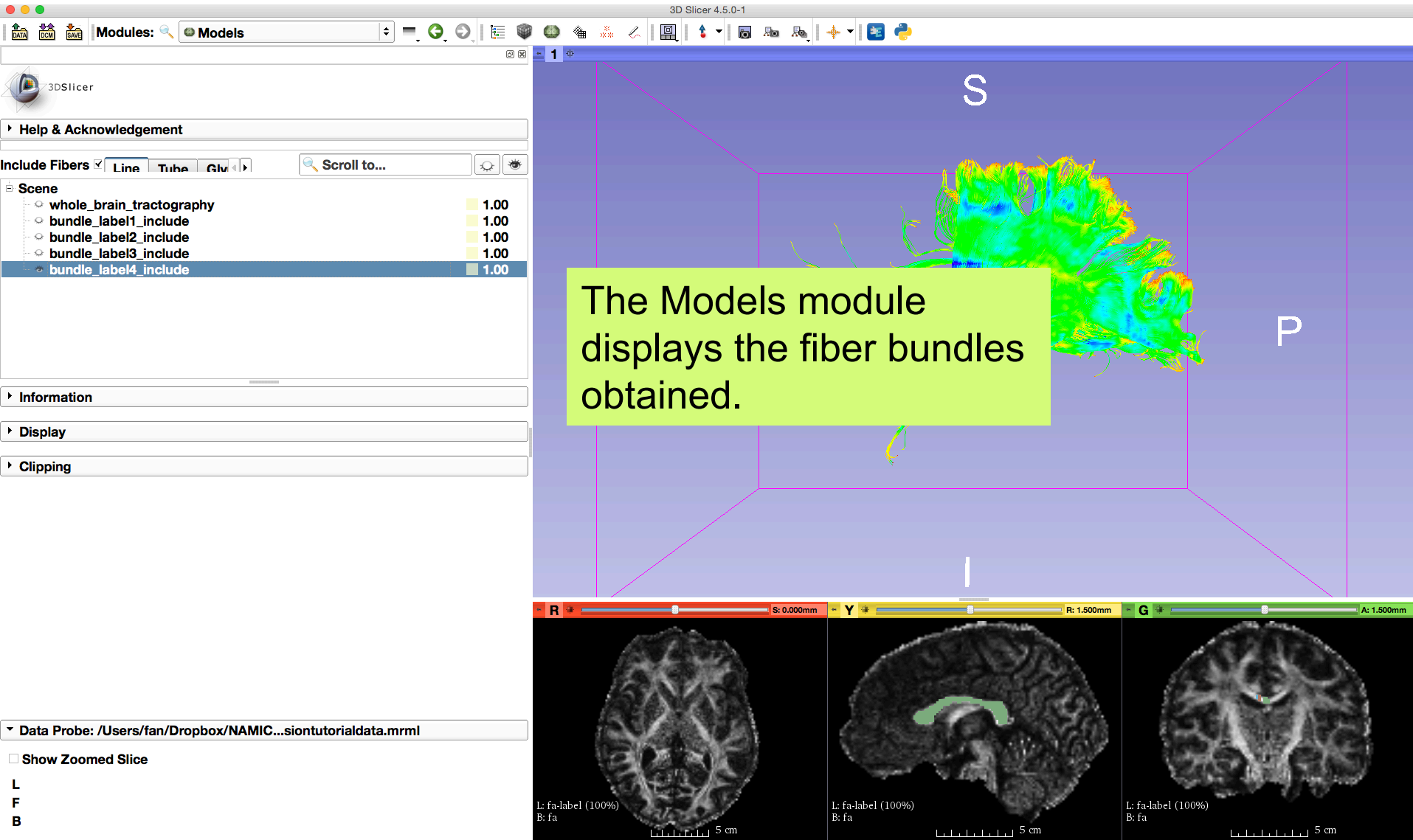
L: fa-label (100%)  
B: fa

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

5 cm

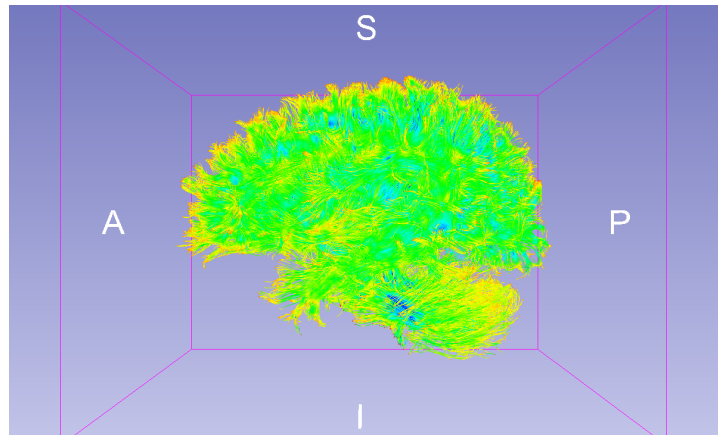


# Single Label Selection

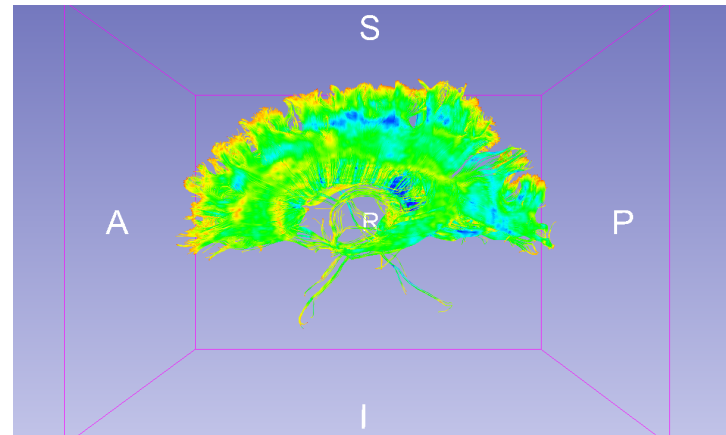


# Single Label Selection

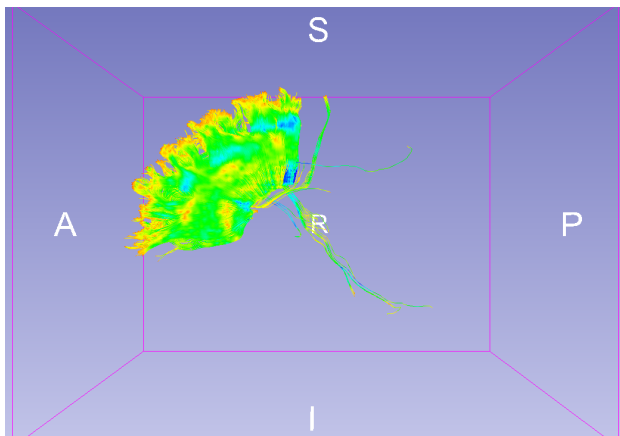
Whole Brain



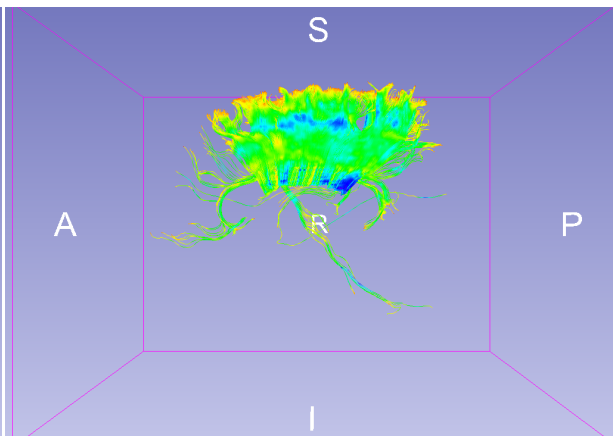
Label 1



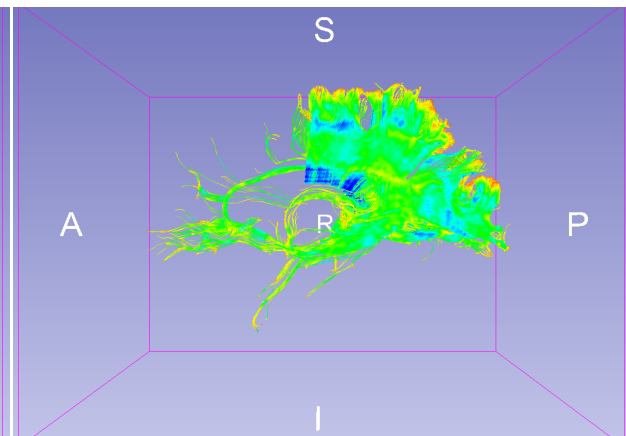
Label 2



Label 3



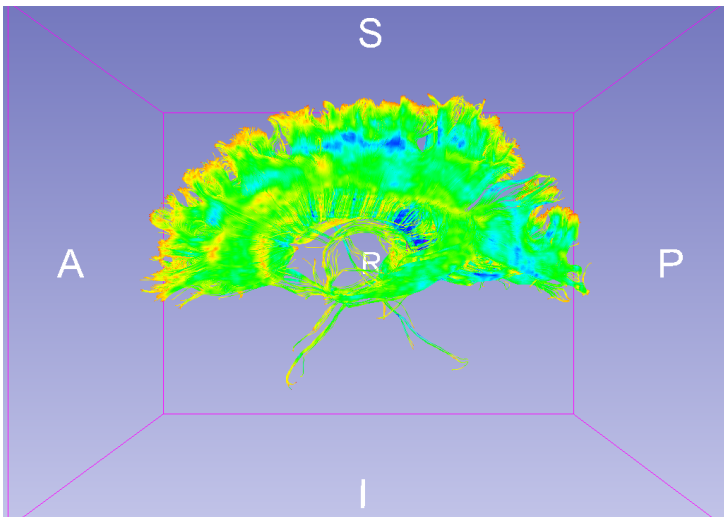
Label 4



# Single Label Selection

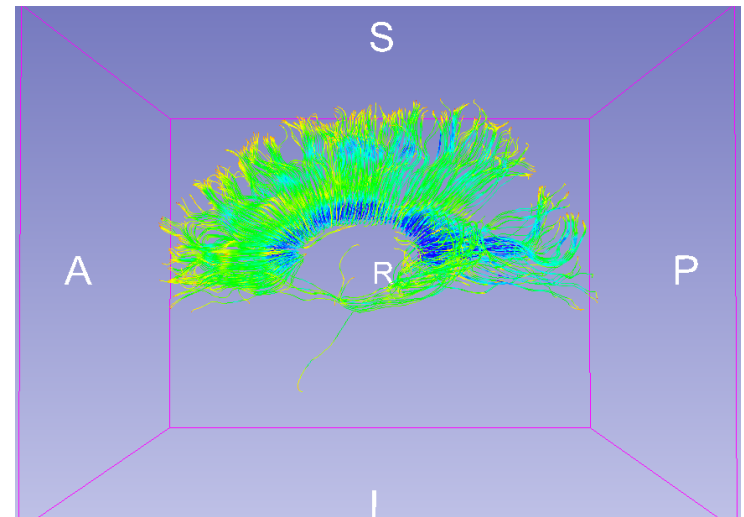
Notice that whole brain seeding creates a denser fiber bundle than seeding from the label 1.

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

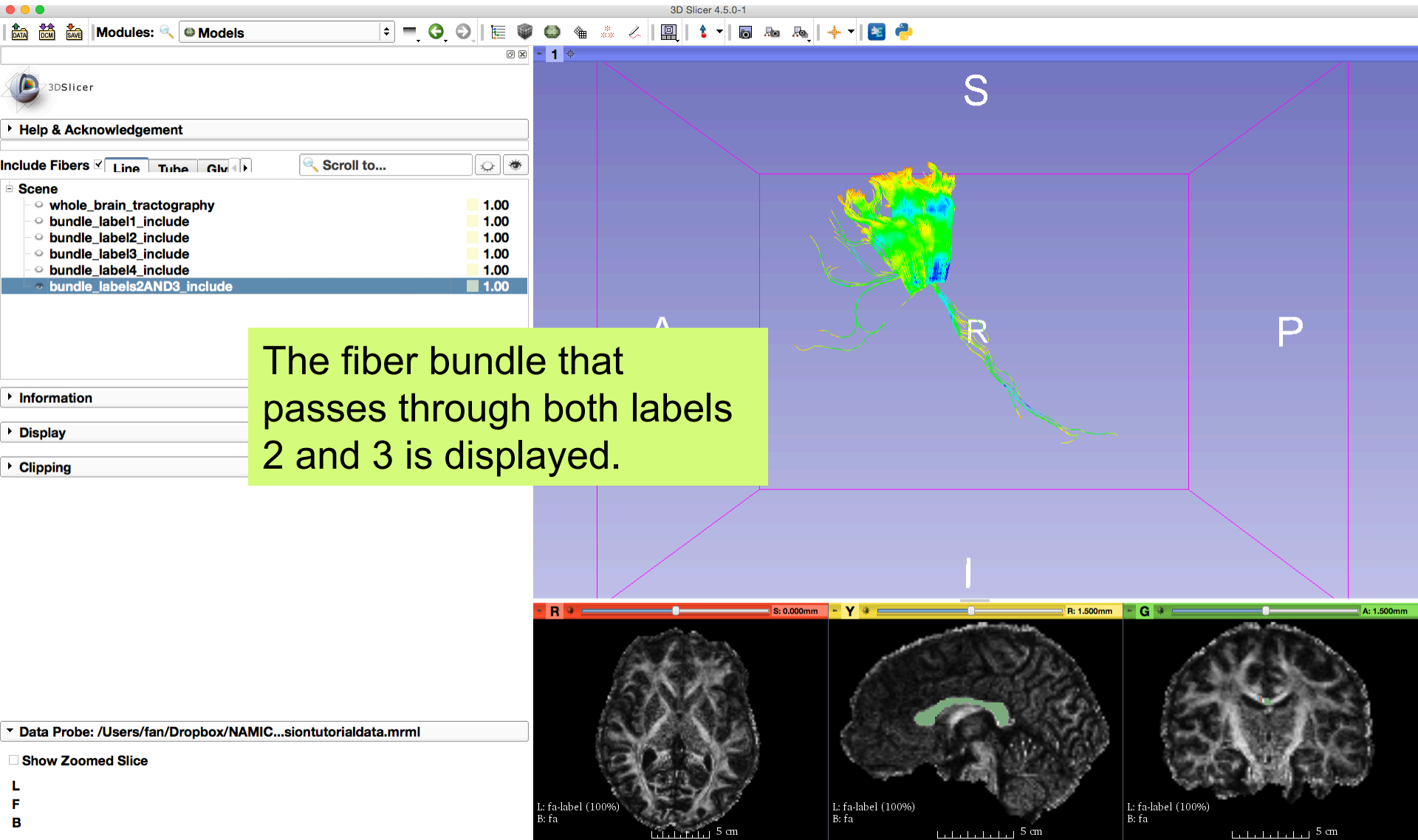
Set the FiberBundleLabelSelection parameters:

- 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 is as follows:

- Parameter set: FiberBundleLabelSelect
- IO
  - Input Label Map: fa-label
  - Input Fiber Bundle: whole\_brain\_tractography
  - Output Fiber Bundle: bundle\_labels2OR3\_include
- Label regions definition
  - Labels to include: 2,3
  - Combine include labels:  OR  AND
  - Labels to exclude: (empty)
  - Combine exclude labels:  OR  AND

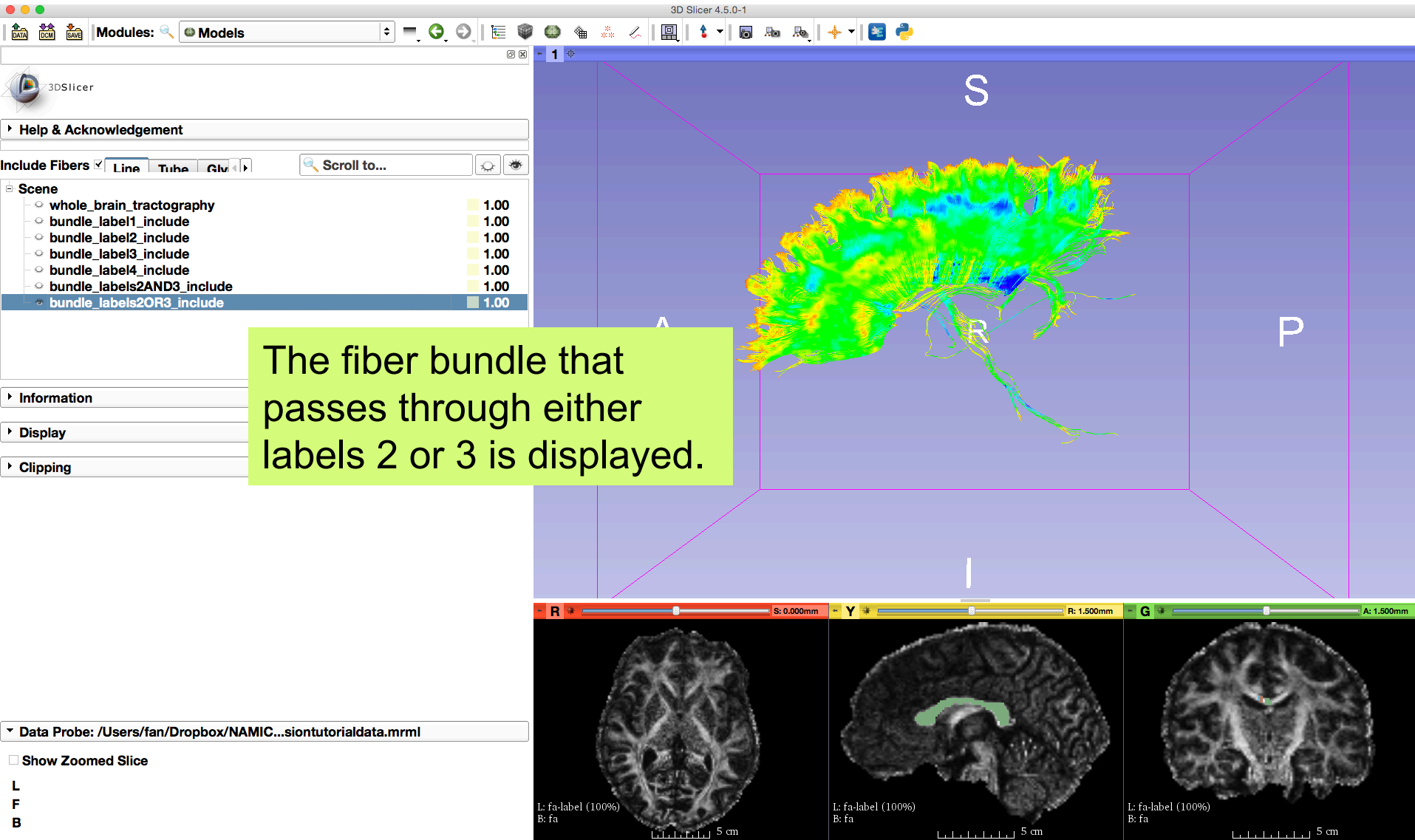
The 3D view shows a brain slice with fiber bundles. A yellow box highlights the text: "Repeat the above steps to select the fiber bundle that passes through labels 2 or 3 and obtain the selection result of bundle\_labels2OR3\_include".

A yellow box with an arrow pointing to the "Combine include labels" radio buttons contains the text: "Set Combine include labels to OR".

At the bottom, the status bar shows "Status: Completed 100%". A yellow box with an arrow pointing to the "Apply" button contains the text: "Click the button Apply".

Three axial brain slices are shown at the bottom, each with a 5 cm scale bar. The left slice is labeled "L: fa-label (100%) B: fa". The middle slice is labeled "L: fa-label (100%) B: fa". The right slice is labeled "L: fa-label (100%) B: fa".

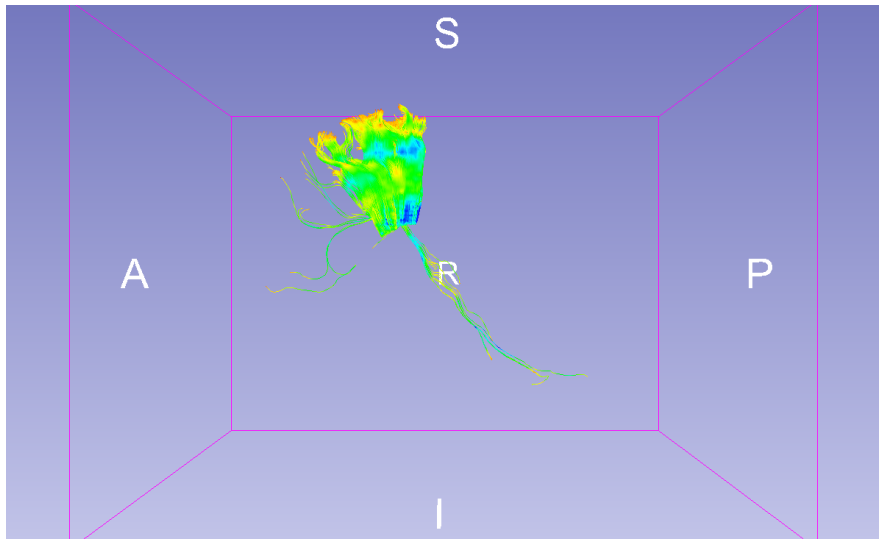
# Multiple Labels Selection (OR)



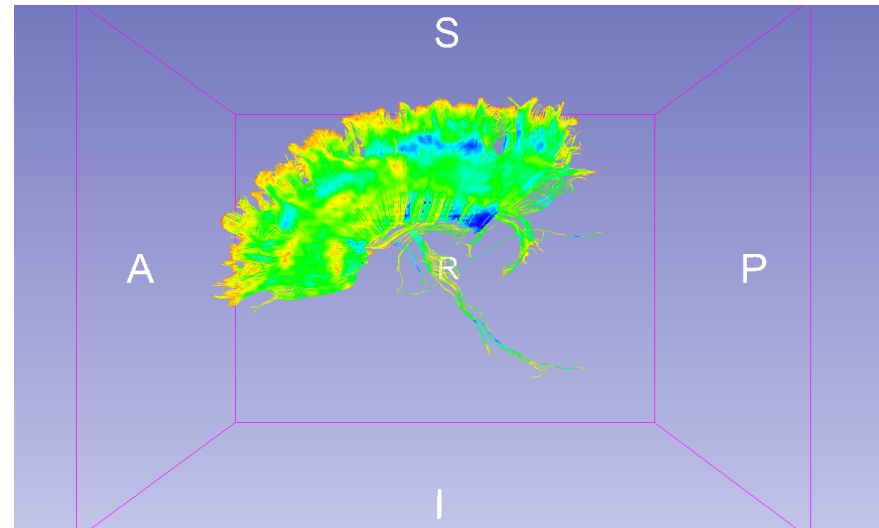


# Multiple Labels Selection

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
- Slicer Data Bundle Scene View.png

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 axes are labeled S (Superior), A (Anterior), and P (Posterior). 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

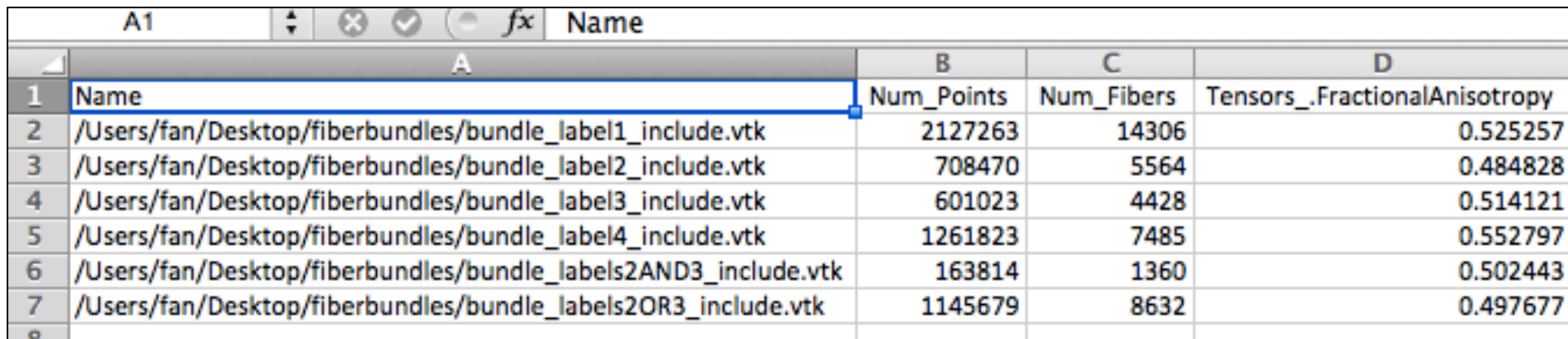
Set the FiberTractScalarMeasurements parameters:

- 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

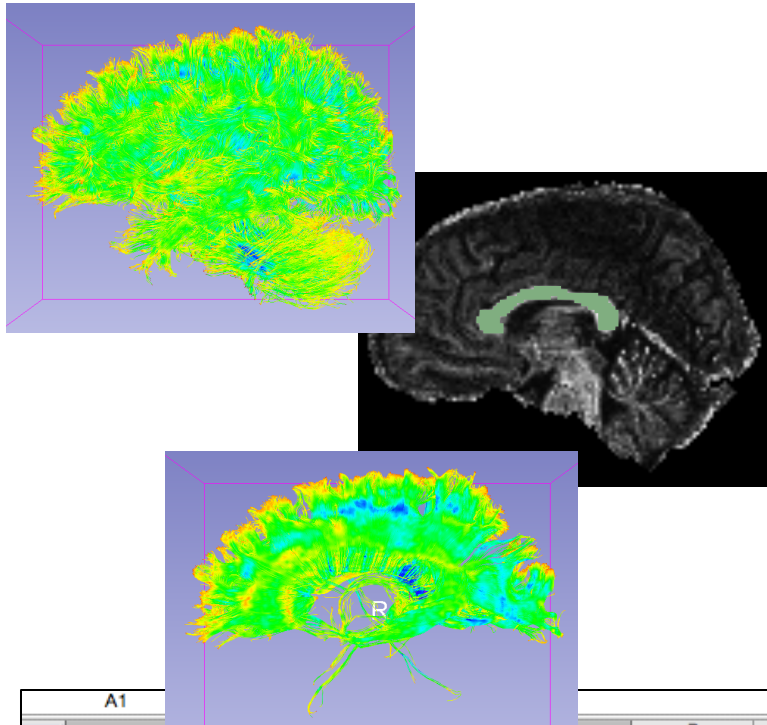
The module outputted a CSV file listing the mean scalar value (such as FA and Trace) of each fiber bundle in the folder



A screenshot of a spreadsheet application showing a table with 4 columns and 8 rows. The columns are labeled A, B, C, and D. The rows contain data for fiber bundles, including their names, number of points, number of fibers, and fractional anisotropy values.

	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	

# Acknowledgments

**Open Source Diffusion MRI Technology For Brain Cancer Research**

U01CA199459

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**Neuroimage Analysis Center (NAC)**

P41EB015902