

# Fiber Bundle Selection And Scalar Measurement

Fan Zhang

# 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

# 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)

# Tutorial Software

The tutorial uses the 3DSlicer (Version 4.5.0-1 Stable Release) software available at

<http://download.slicer.org>

## *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

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	731 K
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 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

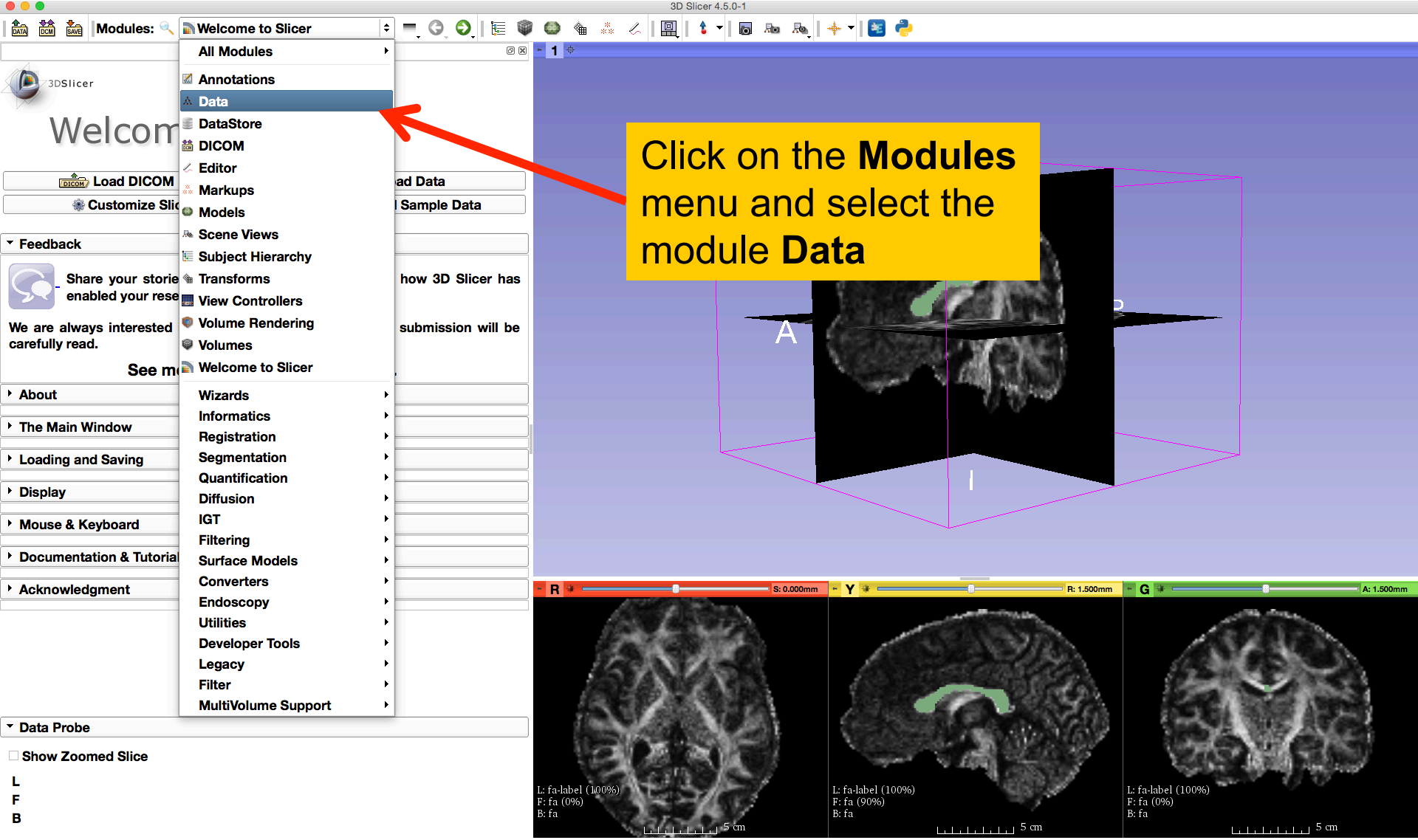
Click **OK** to load the dataset to Slicer

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:

- **baseline**
- **dti**
- **dwi\_mask**
- **dwi**
- **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

Display MRI

Show Hidden

Filter:

MRML Node Inspector

Data Probe

Show Zoomed Slice

L  
F  
B

Select the module **Editor**

A

B

I

R: 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. The 'Editor' module is active, showing a central 3D view of a brain slice with a green label. A red arrow points from a yellow text box on the left to the 'Yellow slice only' option in a layout selection menu. The menu lists various layout options, with 'Yellow slice only' highlighted. The interface includes a top toolbar, a left sidebar with 'Help & Acknowledgement', 'Create and Select Label Maps', and 'Edit Selected Label Map' sections. The 'Edit Selected Label Map' section shows a 'Label: tissue' dropdown set to '1'. The bottom of the interface features a 'Data Probe' section with 'Show Zoomed Slice' checked and three zoomed-in views of the brain slice, each with a 5 cm scale bar and labels for 'L: fa-label (100%)', 'F: fa (90%)', and 'B: fa'.

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:

Active Tool: DefaultTool

Label: tissue 1

Data Probe

Show Zoomed Slice

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

3D Slicer 4.5.0-1

Modules: Editor

3DSlicer

- Help & Acknowledgement
- Create and Select Label Maps**
  - Master Volume: fa
  - Merge Volume: fa-label
- Per-Structure Volumes
- Edit Selected Label Map

Undo/Redo: [Undo] [Redo]

Active Tool: DefaultTool

Label: tissue 1

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

Show Zoomed Slice

L  
F  
B

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

5 cm

R: 4.500mm

**- 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. A yellow callout box with a red arrow pointing to the right edge of the slice contains the text: "Slide right to the next slice". Another yellow callout box with a red arrow pointing to the "DrawEffect" tool in the "Edit Selected Label Map" panel contains the text: "- Select the DrawEffect tool" and "- Set the Label to 2". The "Edit Selected Label Map" panel shows the "Active Tool" set to "DrawEffect" and the "Label" set to "2". The "Label" dropdown menu is open, showing "2" selected. The "Paint Over" checkbox is checked. The "Apply" button is visible. The "Data Probe" section shows the path: "/Users/fan/Dropbox/NAMIC...siontutorialdata.mrml". The "Show Zoomed Slice" checkbox is unchecked. The "L", "F", and "B" checkboxes are checked. The "L: fa-label (100%)" and "B: fa" labels are visible in the bottom left corner. A 5 cm scale bar is visible in the bottom right corner.

Slide right to the next slice

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

3D Slicer 4.5.0-1

Modules: Editor

3DSlicer

Help & Acknowledgement

Create and Select Label Maps

Master Volume: fa

Merge Volume: fa-label

Per-Structure Volumes

Edit Selected Label Map

DrawEffect

Undo/Redo:

Active Tool: DrawEffect

Label: bone 2

Paint Over

Threshold Paint

Apply

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

Show Zoomed Slice

L

F

B

L: fa-label (100%)

B: fa

5 cm

# 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 Selected Labels

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 of 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 left sidebar shows the 'Edit Selection' panel with the 'Active Tool' set to 'DrawEff' and the 'Label' set to '3'. The 'Paint Over' checkbox is checked. The bottom status bar shows the current slice is 'fa-label (100%)' and the background is 'None'.

3D Slicer 4.5.0-1

Modules: Editor

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

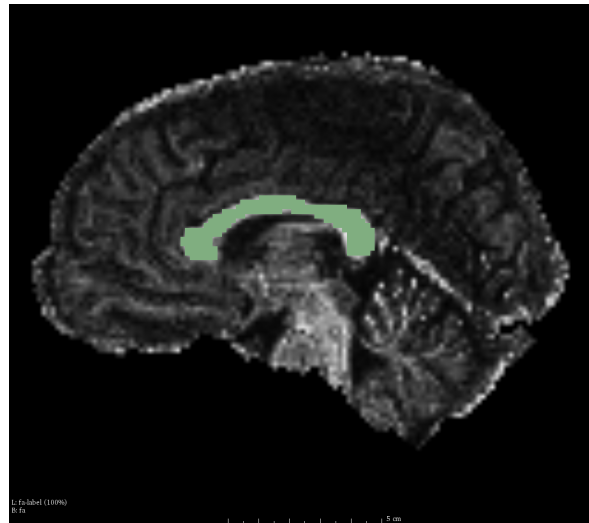
L: fa-label (100%)  
B: fa

5 cm

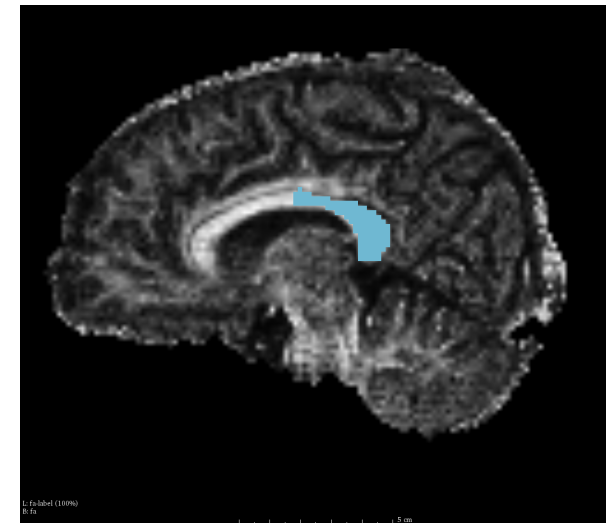
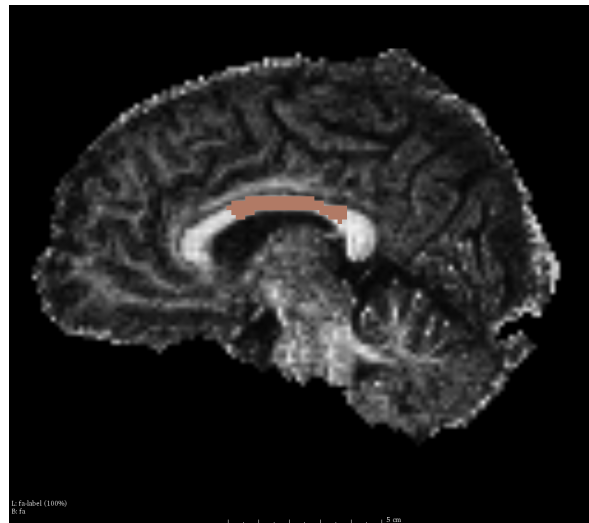
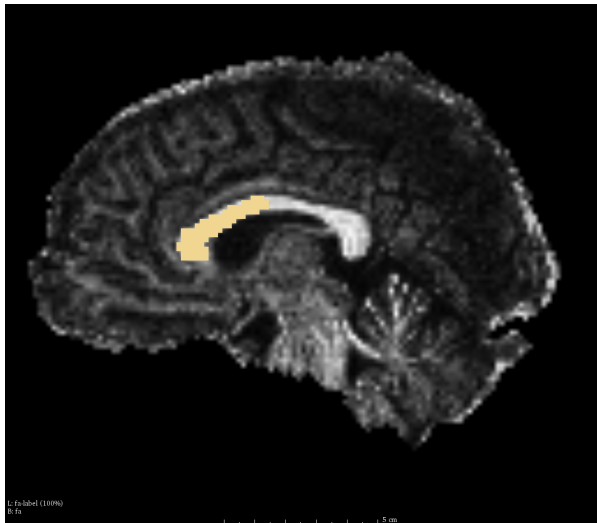
# Edit Multiple Labels

Label map on individual slice, with :

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

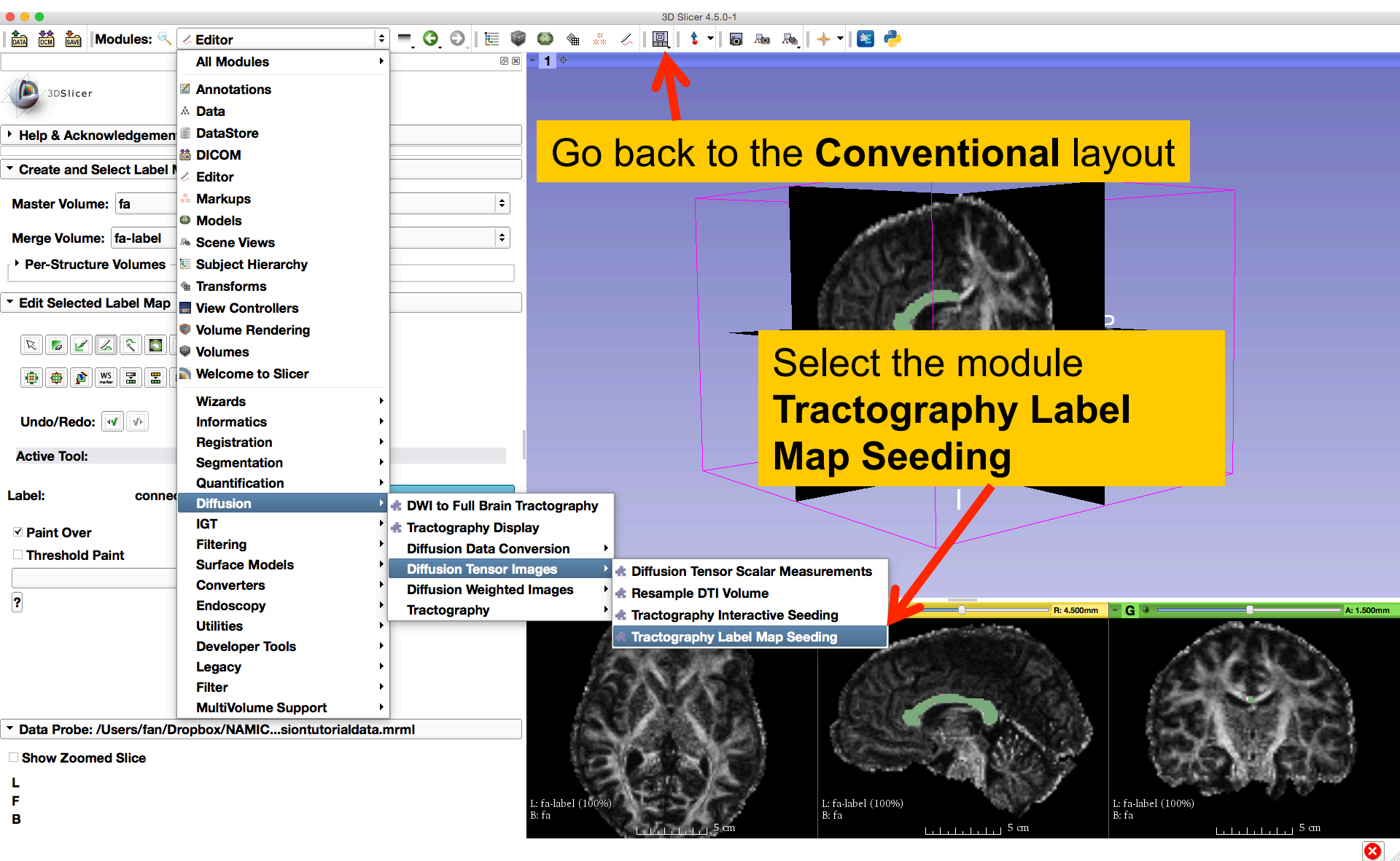


Notice that there are overlaps between different labeled regions, which will be used to investigate the fiber bundle selection.

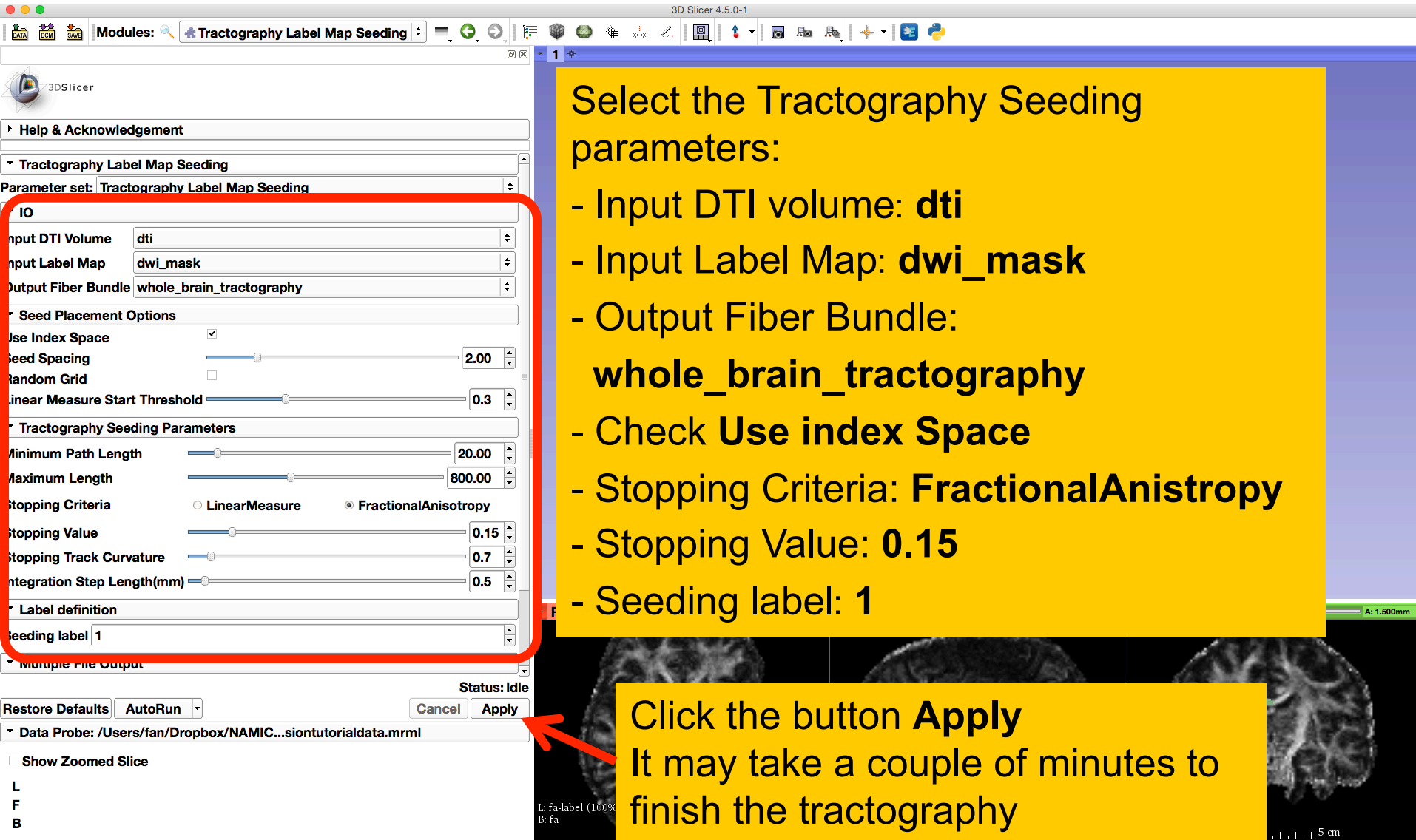




# Whole Brain Tractography



# 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

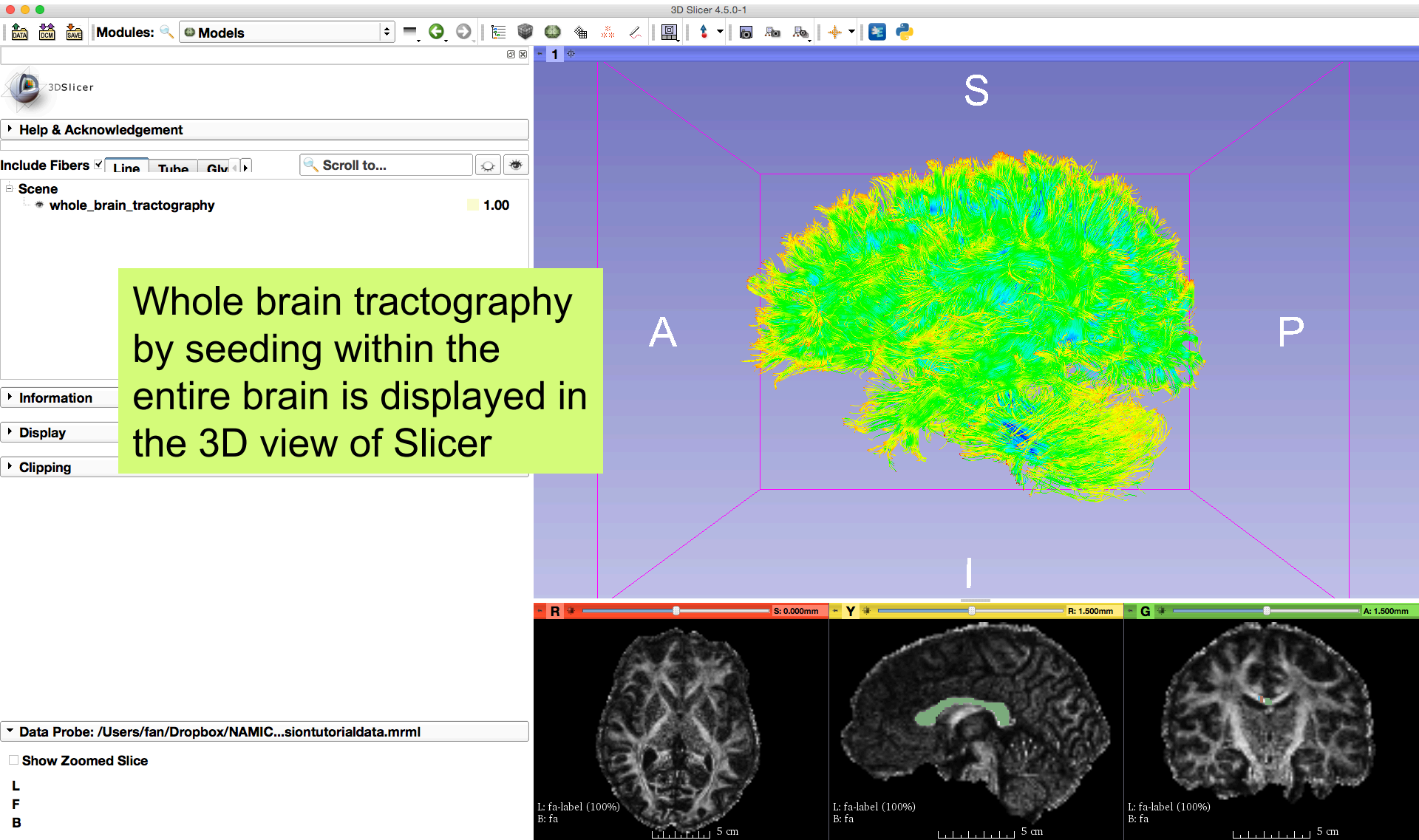
L: fa-label (100%)  
B: fa

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

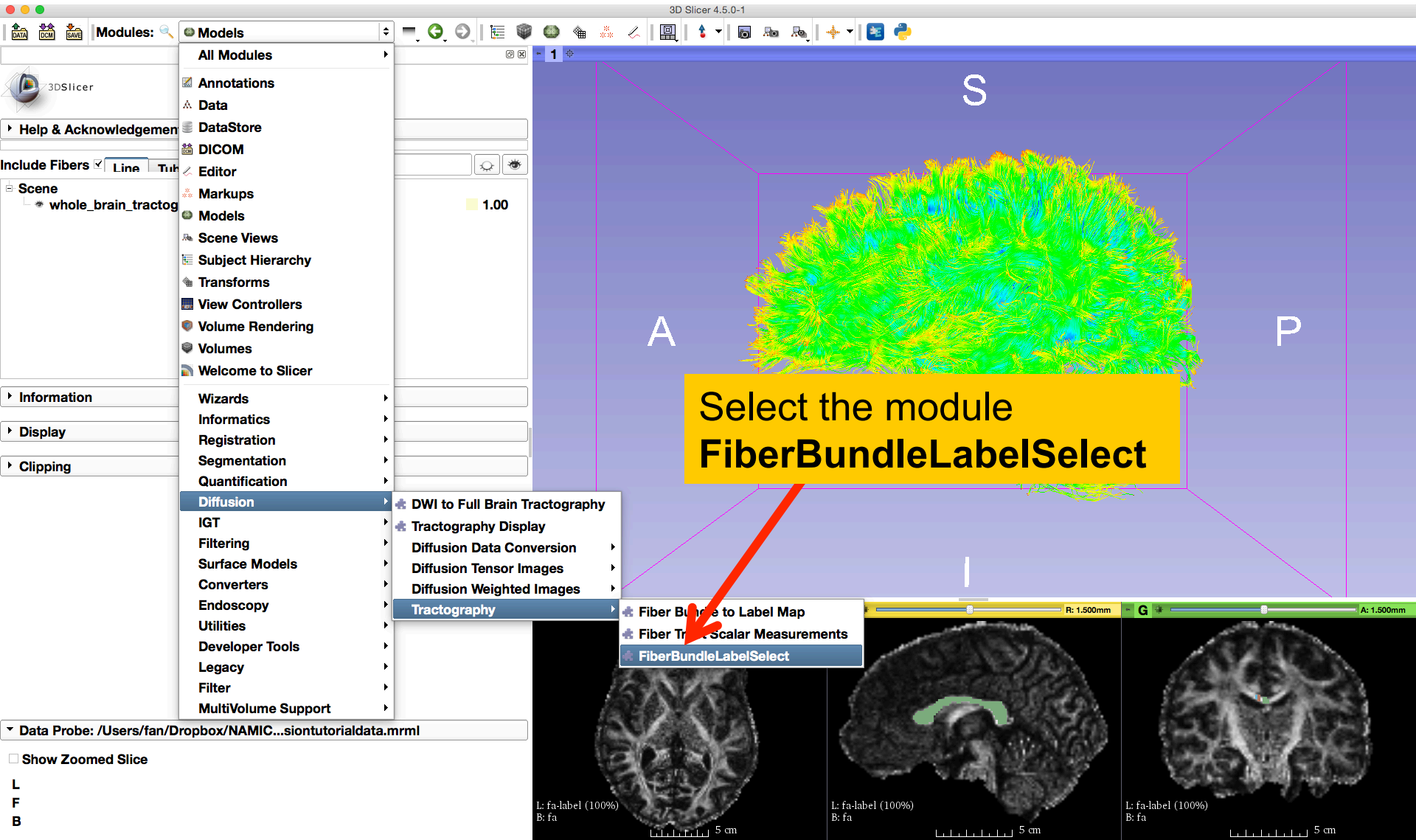
L: fa-label (100%)  
B: fa

5 cm 5 cm 5 cm

# Whole Brain Tractography



# Fiber Bundle Label Selection



# Single Label Selection

The screenshot displays the 3D Slicer 4.5.0-1 interface. The 'FiberBundleLabelSelect' module is active, and its parameters are shown in the left sidebar. A red box highlights the 'Input Label Map', 'Input Fiber Bundle', and 'Output Fiber Bundle' fields. The 'Labels to include' field is set to '1'. The 'Combine include labels' and 'Combine exclude labels' options are set to 'OR'. The 'Status: Idle' indicator is visible above the 'Apply' button. A yellow callout box points to the 'Apply' button with the text 'Click the button Apply'. The 3D view at the bottom shows three brain slices in axial, sagittal, and coronal views, with a 5 cm scale bar and labels 'L: fa-label (100%)' and 'B: fa'.

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 main 3D view shows a brain with a fiber bundle highlighted in green and yellow, set against a blue background with anatomical planes labeled 'S' (Superior), 'A' (Anterior), and 'P' (Posterior). The bundle is labeled 'R' (Right). The left sidebar contains the 'Scene' panel with a tree view showing 'whole\_brain\_tractography' and 'bundle\_label1\_include', both with a visibility of 1.00. A red arrow points to the 'bundle\_label1\_include' entry. The top toolbar has a red arrow pointing to the 'Models' module icon. The bottom panel shows three axial slices of the brain with a green fiber bundle overlaid. 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'. A scale bar of 5 cm is visible at the bottom of each slice.

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



# Single Label Selection

The screenshot displays the 3D Slicer 4.5.0-1 interface. The **FiberBundleLabelSelect** module is active, with the following configuration:

- 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: (empty)
  - Combine exclude labels:  OR  AND

A yellow text box overlaid on the 3D view contains the following instructions:

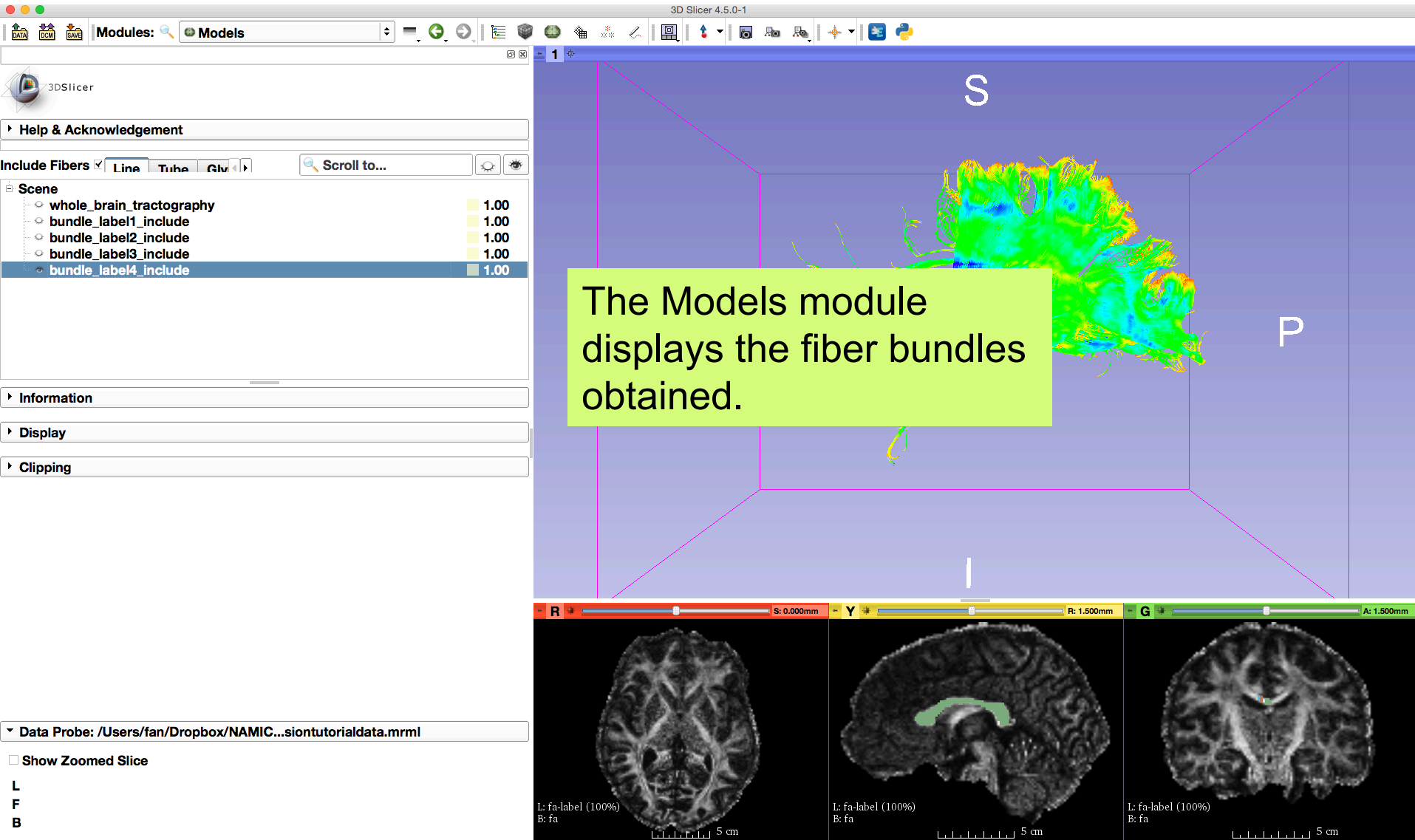
Repeat the above steps to perform fiber bundle selections of labels **2**, **3** and **4** individually and obtain the selected bundles of **bundle\_label2\_include**, **bundle\_label3\_include** and **bundle\_label4\_include** respectively

The 3D view shows a brain model with fiber bundles. The selected bundle (label 2) is highlighted in green. The axes are labeled S (Superior), I (Inferior), R (Right), and P (Posterior). The status bar at the bottom indicates the process is completed (100%).

At the bottom, three axial slices are shown 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".

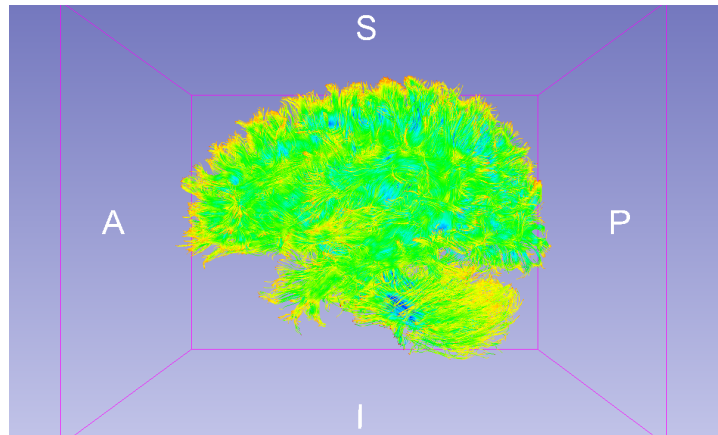


# Single Label Selection

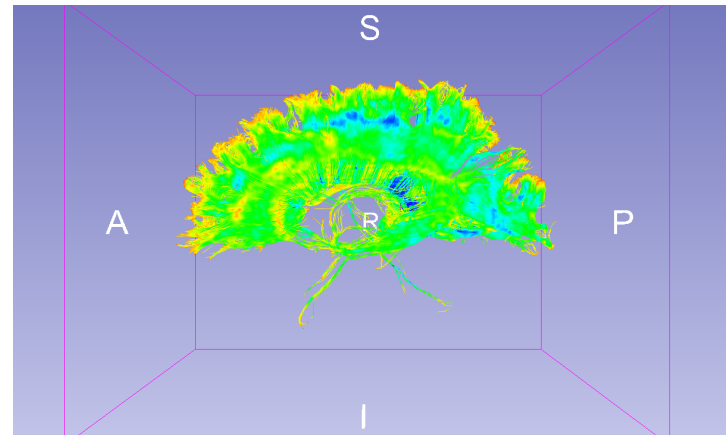


# Single Label Selection

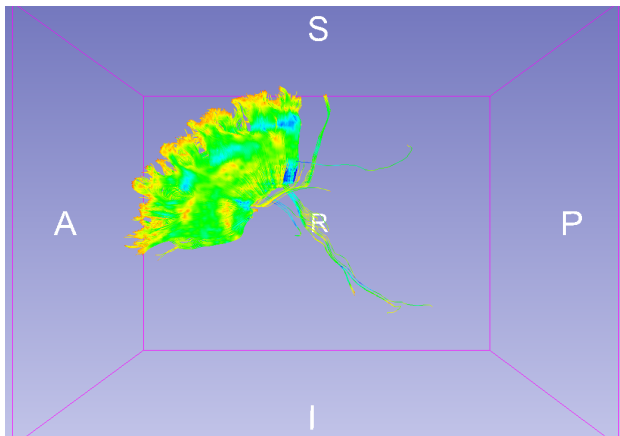
Whole Brain



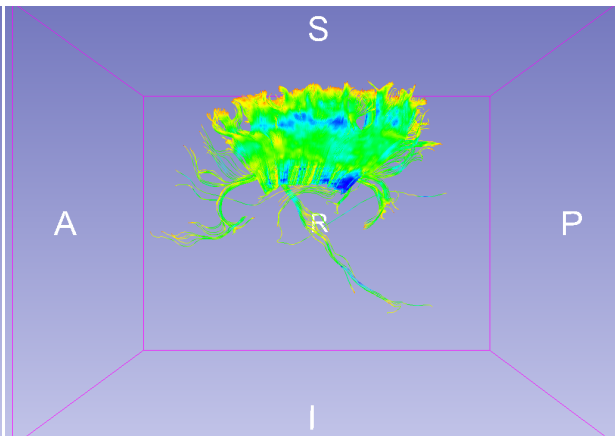
Label 1



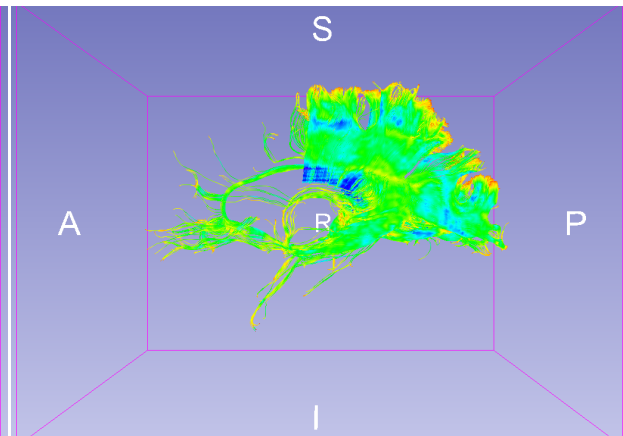
Label 2



Label 3



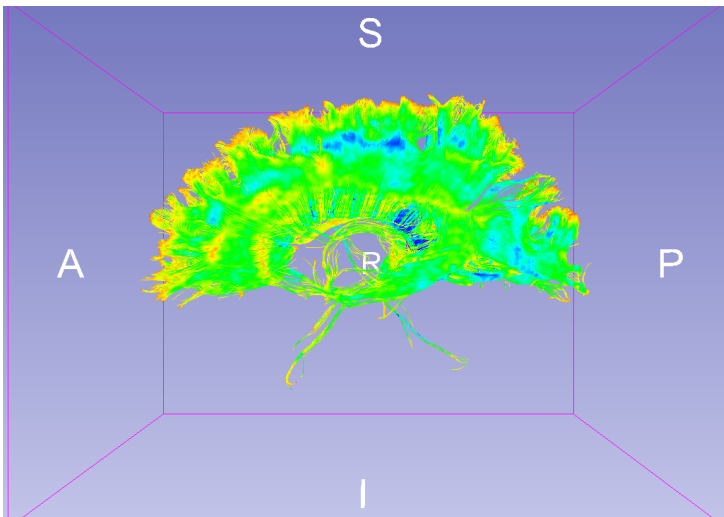
Label 4



# Single Label Selection

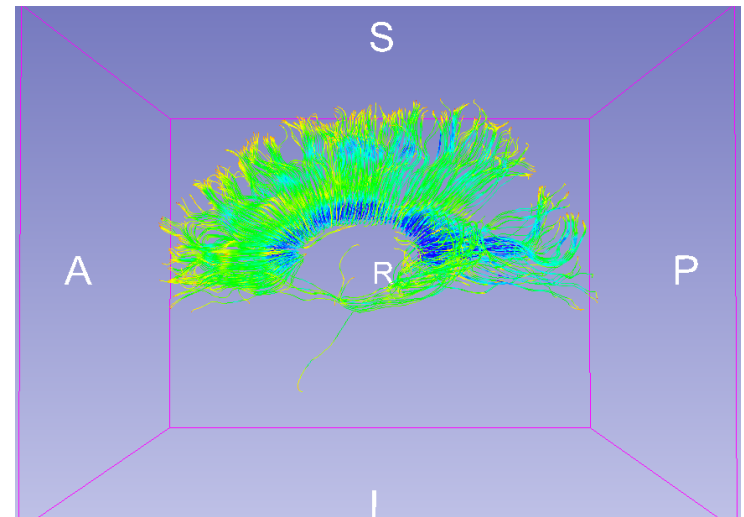
Notice that whole brain seeding creates a denser fiber bundle than seeding from the label 1.

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

S

P

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

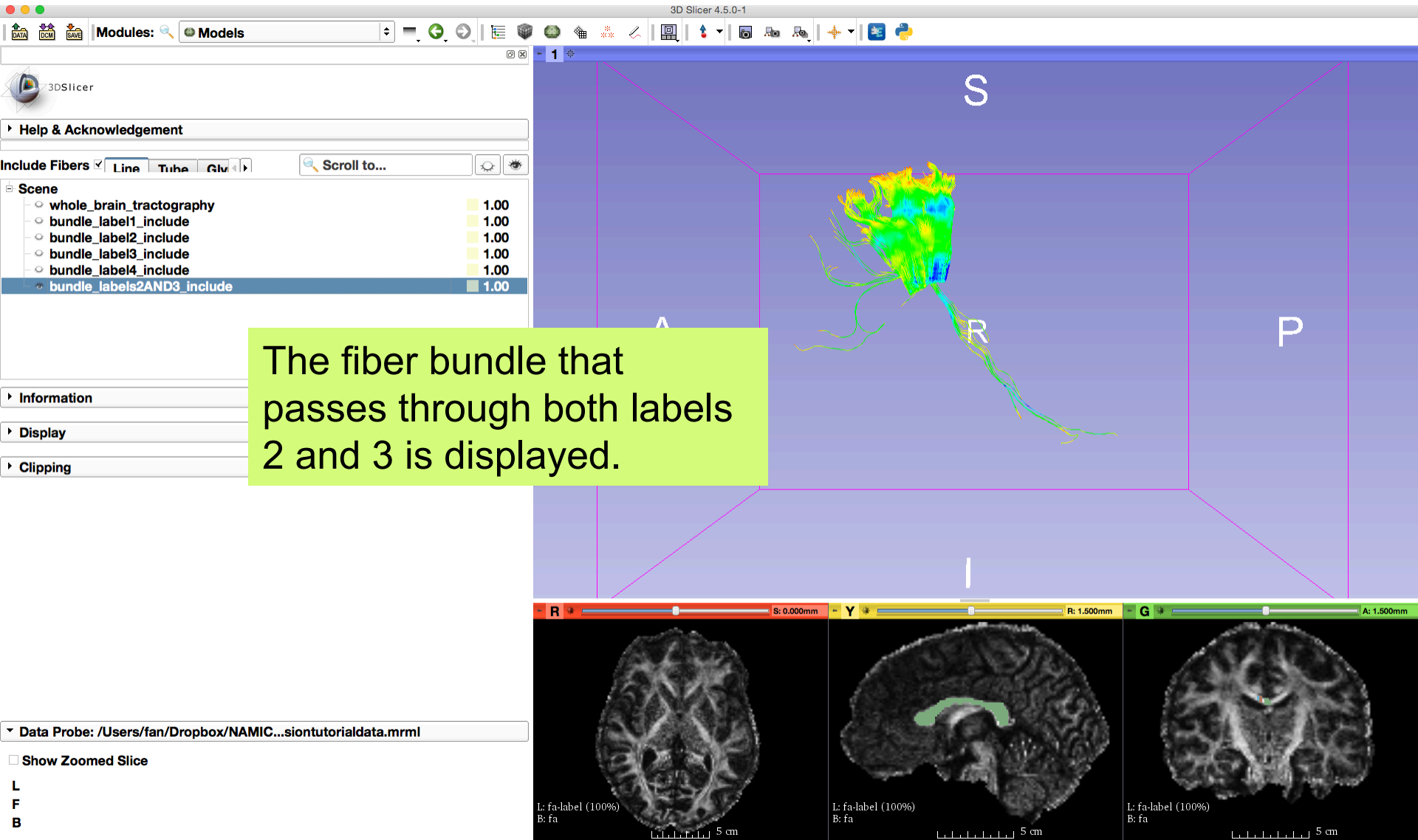
Set the FiberBundleLabelSelection parameters:

- 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** (selected)
  - Labels to exclude: (empty)
  - Combine exclude labels: **OR** (selected)

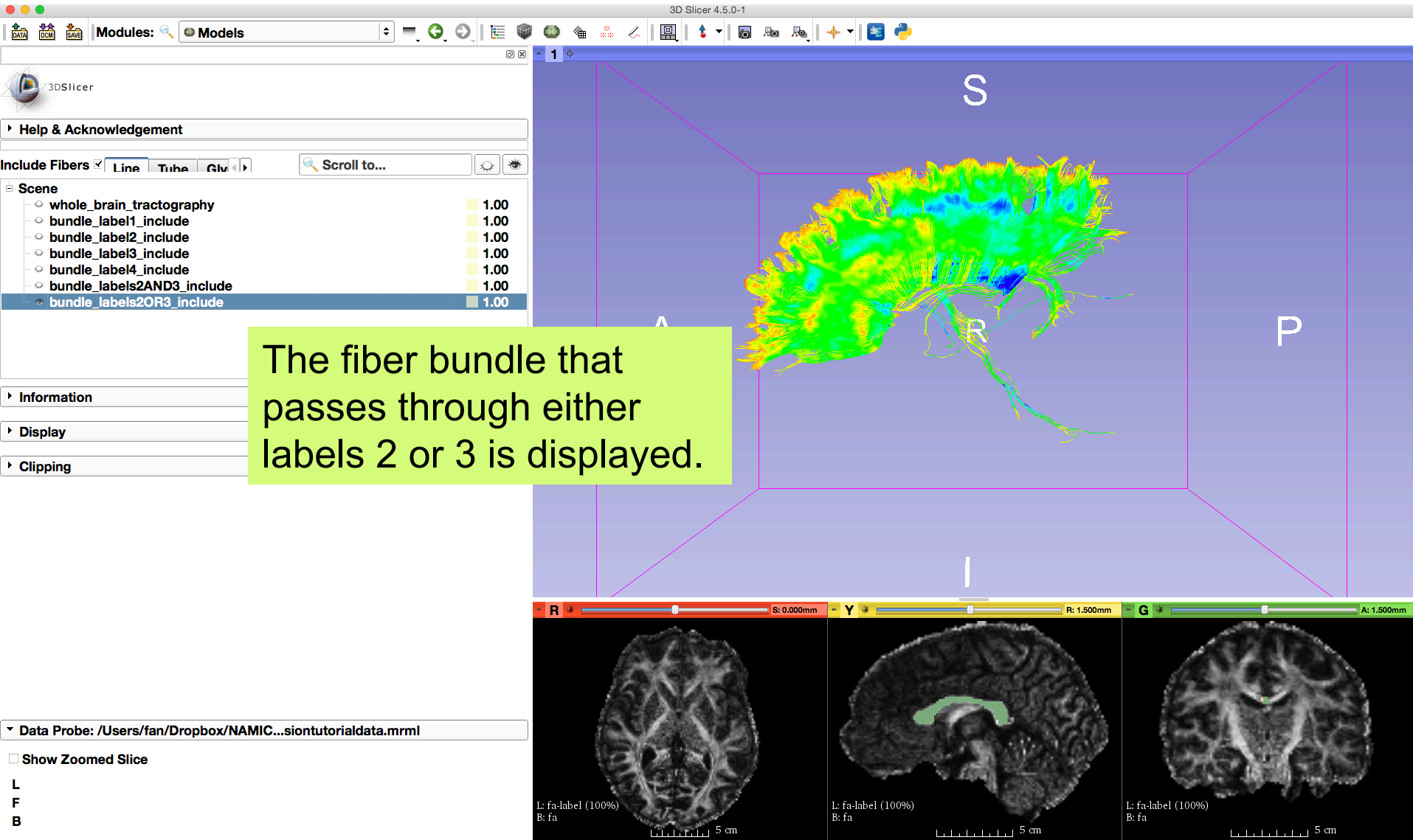
The 3D view shows a brain slice with fiber bundles. A yellow box highlights the text: "Repeat the above steps to select the fiber bundle that passes through labels 2 or 3 and obtain the selection result of **bundle\_labels2OR3\_include**".

A red box highlights the "Combine include labels" section, with a red arrow pointing to a yellow box that says: "Set **Combine include labels** to **OR**".

At the bottom, the status bar shows "Status: Completed 100%". A red arrow points to the "Apply" button, with a yellow box that says: "Click the button **Apply**".

The bottom right shows three orthogonal views (axial, sagittal, coronal) of the brain slice, each with a 5 cm scale bar. The labels for these views are: L: fa-label (100%), B: fa.

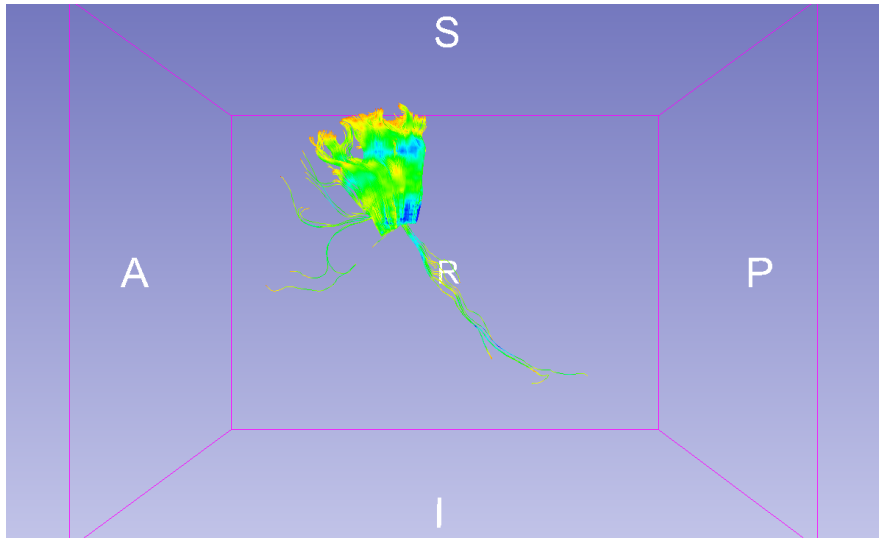
# Multiple Labels Selection (OR)



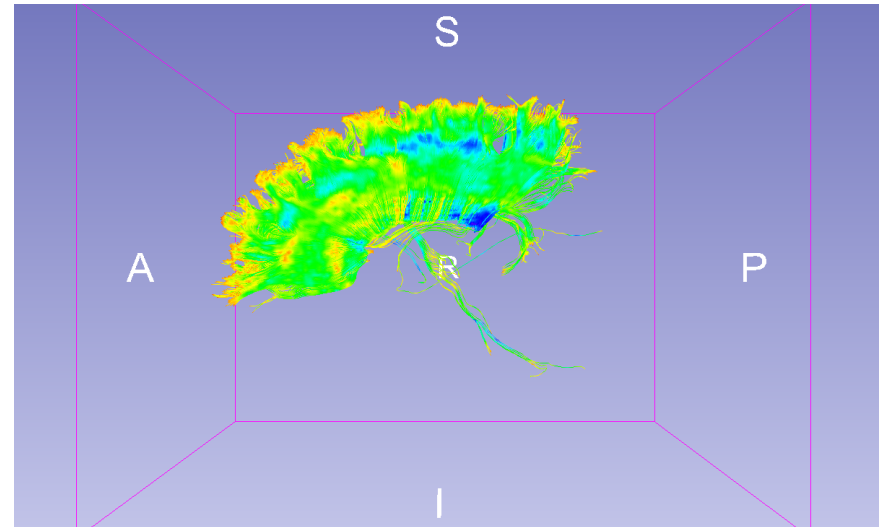


# Multiple Labels Selection

Labels 2 and 3



Labels 2 or 3



# Save Fiber Bundles

3D Slicer 4.5.0-1

Modules: Models

Click the button **SAVE**

Save Scene and Unsaved Data

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** 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
    - 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

Scene

- corpusCallosum
- whole\_brain\_tractogr
- bundle\_label1\_includ
- bundle\_label2\_includ
- bundle\_label3\_includ
- bundle\_label4\_includ
- bundle\_labels2AND3
- bundle\_labels2OR3**

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**

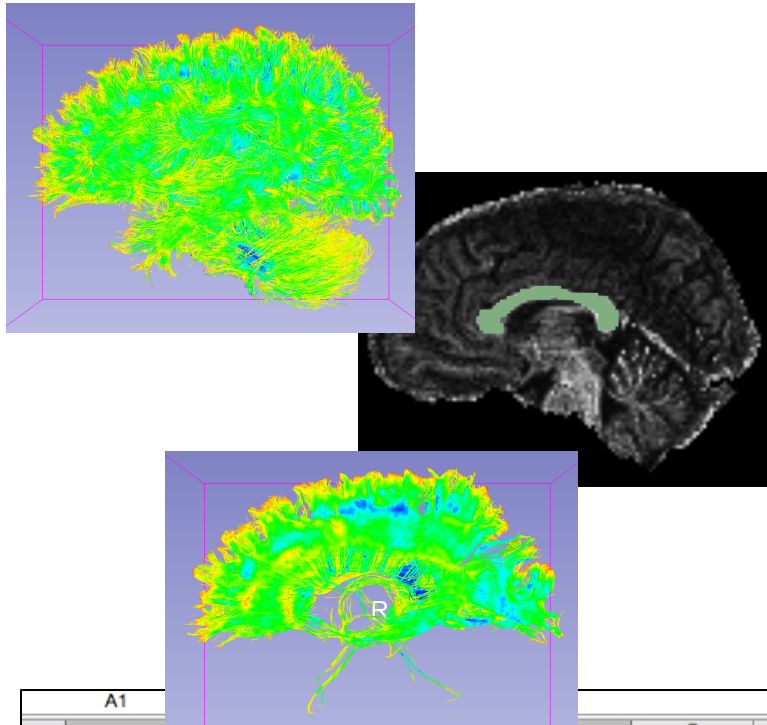
Click the button **Apply**

# 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	E	F
1	Name	Num_Points	Num_Fibers	Tensors_FractionalAnisotropy	Tensors_LinearMeasurement	Tensors
2	/Users/fan/Desktop/fiberbundles/bundle_label1_include.vtk	2127263	14306	0.525257	0.505662	
3	/Users/fan/Desktop/fiberbundles/bundle_label2_include.vtk	708470	5564	0.484828	0.471678	
4	/Users/fan/Desktop/fiberbundles/bundle_label3_include.vtk	601023	4428	0.514121	0.490995	
5	/Users/fan/Desktop/fiberbundles/bundle_label4_include.vtk	1261823	7485	0.552797	0.528861	
6	/Users/fan/Desktop/fiberbundles/bundle_labels2AND3_include.vtk	163814	1360	0.502443	0.490922	
7	/Users/fan/Desktop/fiberbundles/bundle_labels2OR3_include.vtk	1145679	8632	0.497677	0.47906	
8						

# 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



**National Alliance for Medical Image Computing**  
NIH U54EB005149