

# Fiber Bundle Selection And Scalar Measurement

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# Learning Objectives

Following this tutorial, you'll be able to:

- 1) select fiber bundles passing through region(s) of interest, and
- 2) calculate scalar measurements (such as FA and trace) from fiber bundles.

# Tutorial Outline

- Editing multiple labels
- Whole braining tractography
- Fiber bundle selection
- Fiber bundle scalar measurements

# Pre-requisite

- This tutorial is a following-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

Welcome to Slicer

3D Slicer 4.5.0-1

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

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

Name	Size	Kind	Modified
diffussiontutorialdata.mrml		Subdocument	Today, 1:38 PM
Master Scene View.png	333 KB	PNG image	Today, 1:38 PM
corpusCallosum.vtk	4 MB	Document	Today, 1:38 PM
dwi.nrrd	85 MB	Document	Today, 1:38 PM
fa-label.nrrd	4 KB	Document	Today, 1:38 PM
fa.nrrd	1.7 MB	Document	Today, 1:38 PM
dti.nrrd	10.4 MB	Document	Today, 1:37 PM
dwi_mask.nrrd	28 KB	Document	Today, 1:37 PM
baseline.nrrd	1.4 MB	Document	Today, 1:37 PM

Add data into the scene

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

File	Description
...IData_TutorialContestWinter2016/diffussiontutorialdata.mrml	MRML Scene

Reset | OK | Cancel

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

# Load MRML data

3D Slicer 4.5.0-1

Modules: Welcome to Slicer

- 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

Click on the **Modules** menu and select the module **Data**

3D Slicer

Welcome

Load DICOM

Customize Slicer

Feedback

Share your stories enabled your research

We are always interested carefully read.

See more

About

The Main Window

Loading and Saving

Display

Mouse & Keyboard

Documentation & Tutorial

Acknowledgment

Data Probe

Show Zoomed Slice

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

R: 0.000mm

Y: R: 1.500mm

G: A: 1.500mm

5 cm

# 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:

- 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

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

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

5 cm

5 cm

5 cm

# Edit multiple labels

The screenshot displays the 3D Slicer 4.5.0-1 interface. The 'Editor' module is active, and a yellow box highlights the text 'Select the Yellow slice only layout' with a red arrow pointing to the 'Yellow slice only' option in the layout menu. The menu lists various layout options, including 'Conventional', 'Four-Up', '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', and 'Three by three slice'. The 'Yellow slice only' option is highlighted in blue. The main 3D view shows a brain slice with a green label. The bottom of the interface shows three zoomed-in slices: 'L: fa-label (100%)', 'F: fa (90%)', and 'B: fa'. The 'L' slice is a coronal view, the 'F' slice is a sagittal view, and the 'B' slice is an axial view. Each slice has a 5 cm scale bar.

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

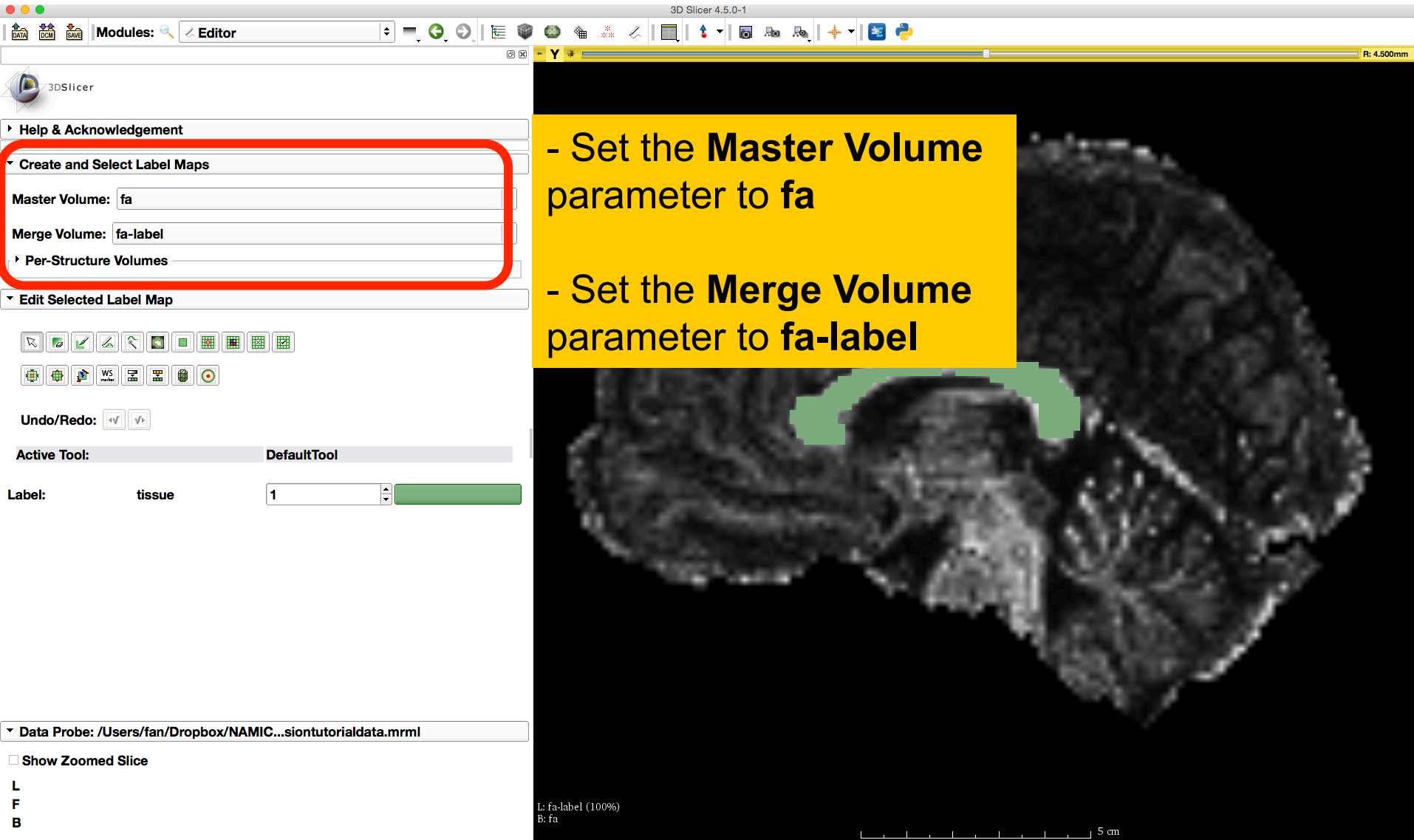
L: fa-label (100%)  
F: fa (90%)  
B: fa

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. 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).
  - Undo/Redo: [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**

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

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 in the 'Edit Selected Label Map' section.

# 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

R: 6.000mm

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

# Editing multiple labels

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

R: 7.500mm

Repeat the above step to draw the medial of Corpus Callosum with **label 3** on the next slice

# Editing multiple labels

3D Slicer 4.5.0-1

Modules: Editor

Help & Acknowledgement

Create and Select Label Maps

Repeat the above step 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

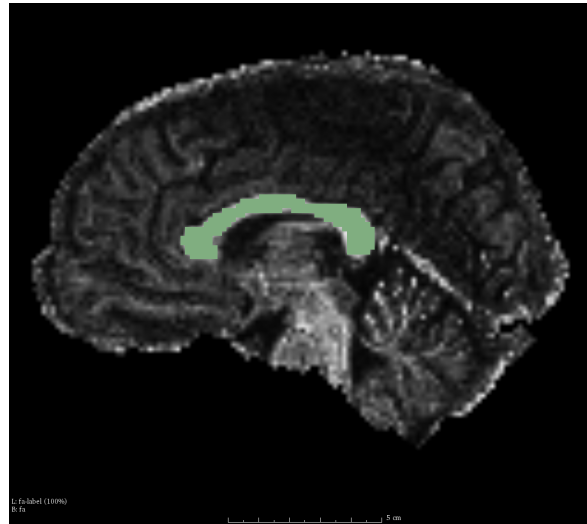
L: fa-label (100%)  
B: fa

5 cm

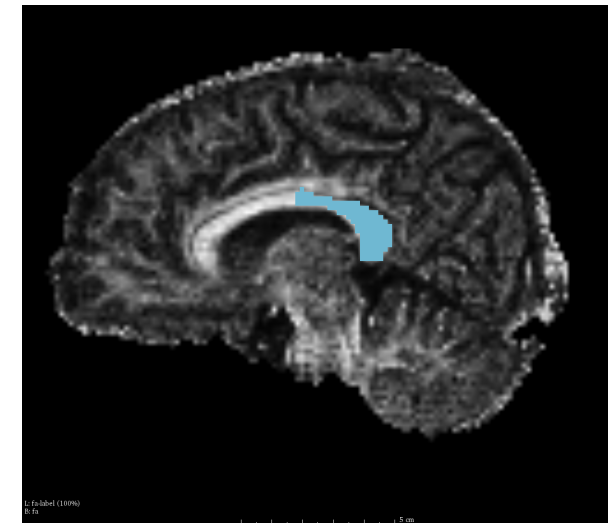
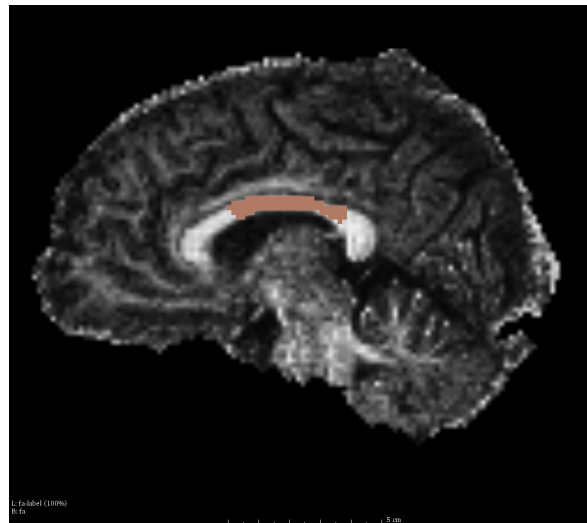
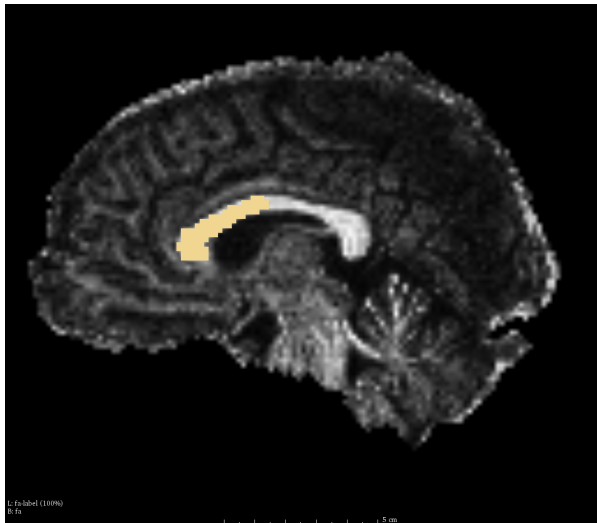
# Editing multiple labels

Label map with :

- **1 - entire CC**
- **2 - anterior CC**
- **3 - medial 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 chosen, which has opened a secondary menu where 'Tractography Label Map Seeding' is highlighted. A red arrow points from the 'Tractography Label Map Seeding' option to the 'Tractography' option in the main menu. Another red arrow points from the 'Tractography' option to the 'Diffusion' option. A yellow callout box with the text 'Go back to the Conventional layout' is positioned above the main menu, with a red arrow pointing to the 'Conventional' layout icon in the top toolbar. A second yellow callout box with the text 'Select the module Tractography Label Map Seeding' is positioned over the secondary menu, with a red arrow pointing to the 'Tractography Label Map Seeding' option. The main 3D view shows a brain slice with a green tractography line. Below the main view are three zoomed-in slices of the brain, each with a 5 cm scale bar. The interface includes a left sidebar with various tool icons and a top toolbar with icons for different views and actions.

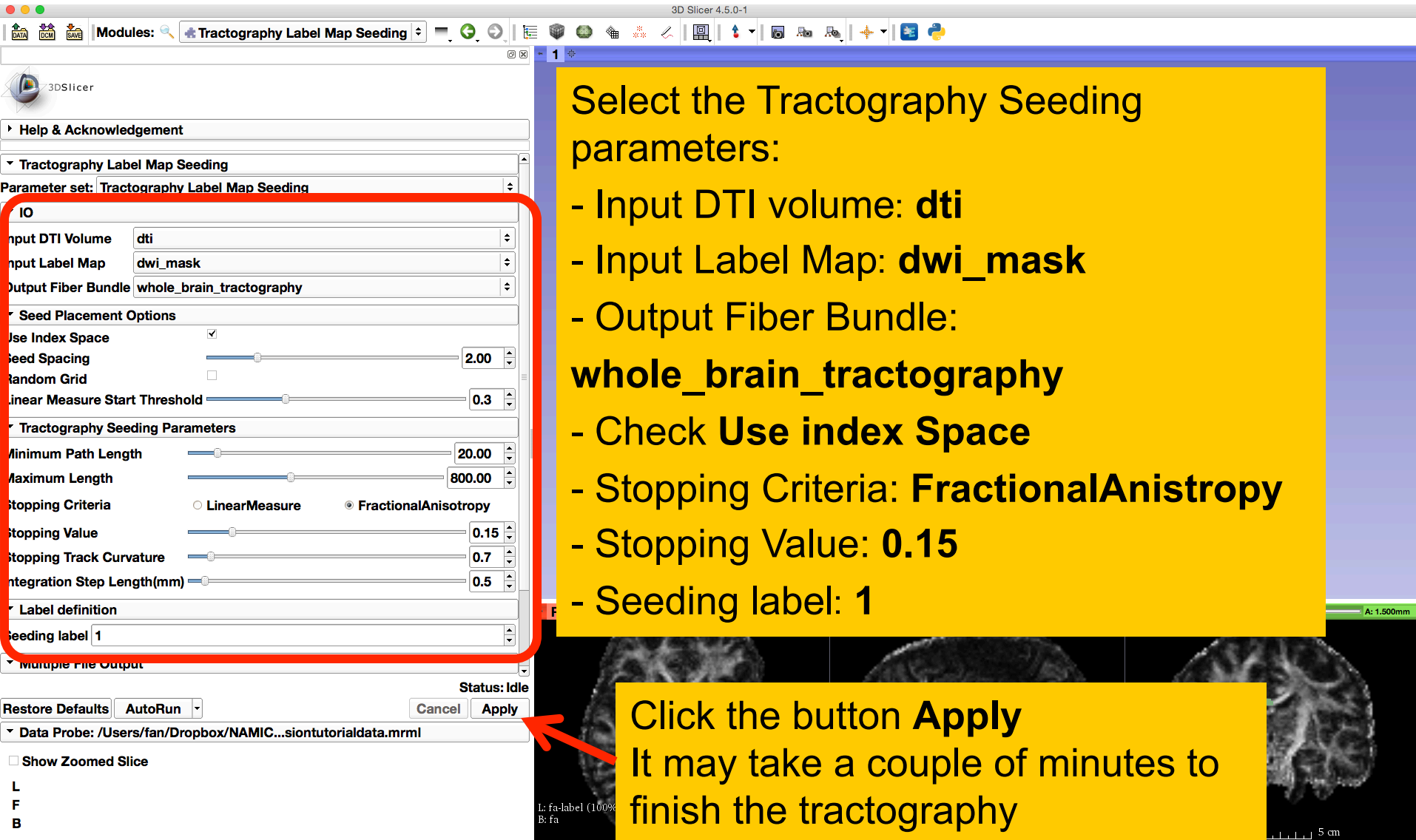
3D Slicer 4.5.0-1

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**

# 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

Help & Acknowledgement

Include Fibers  Line Tube GLV

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

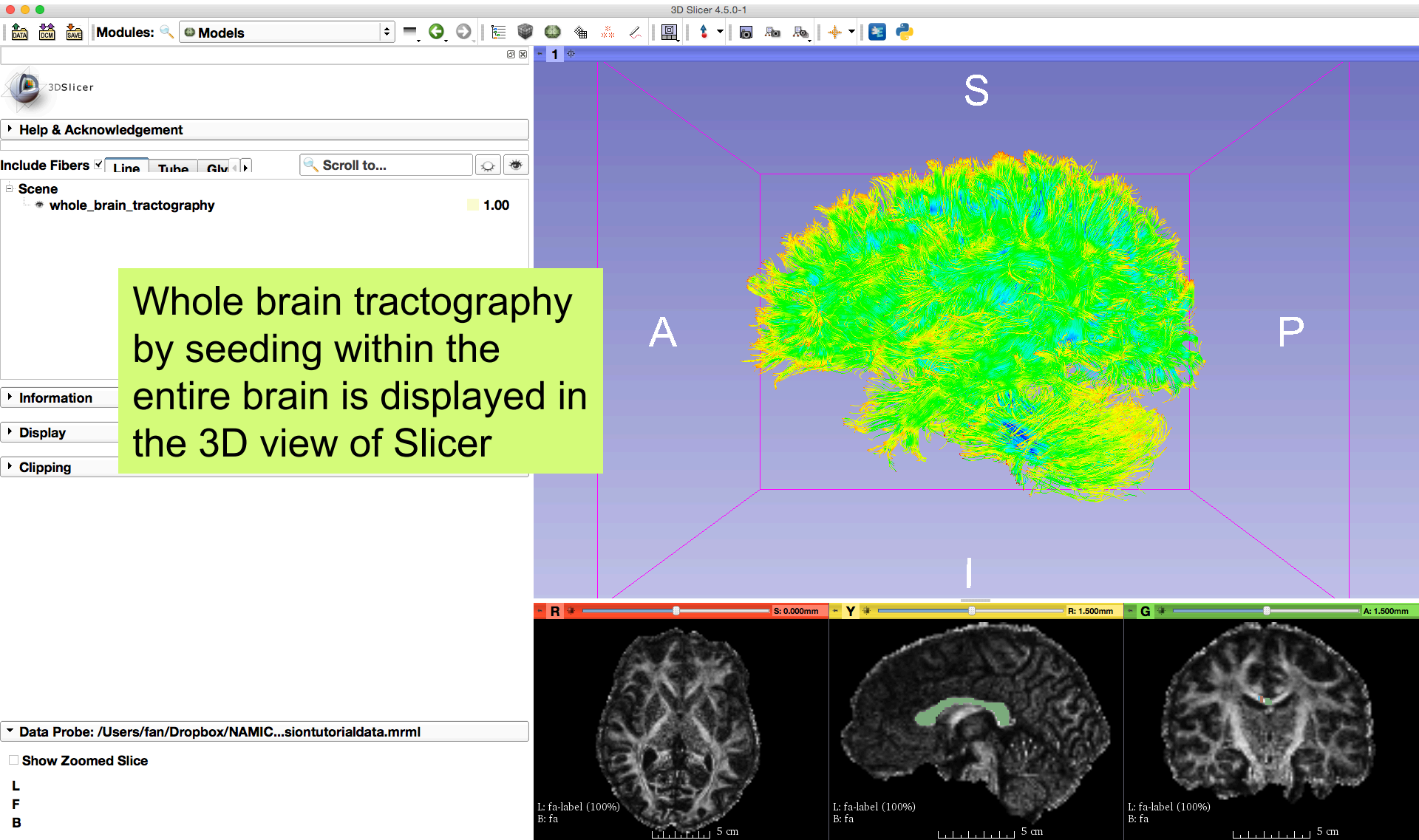
L: fa-label (100%)  
B: fa

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

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

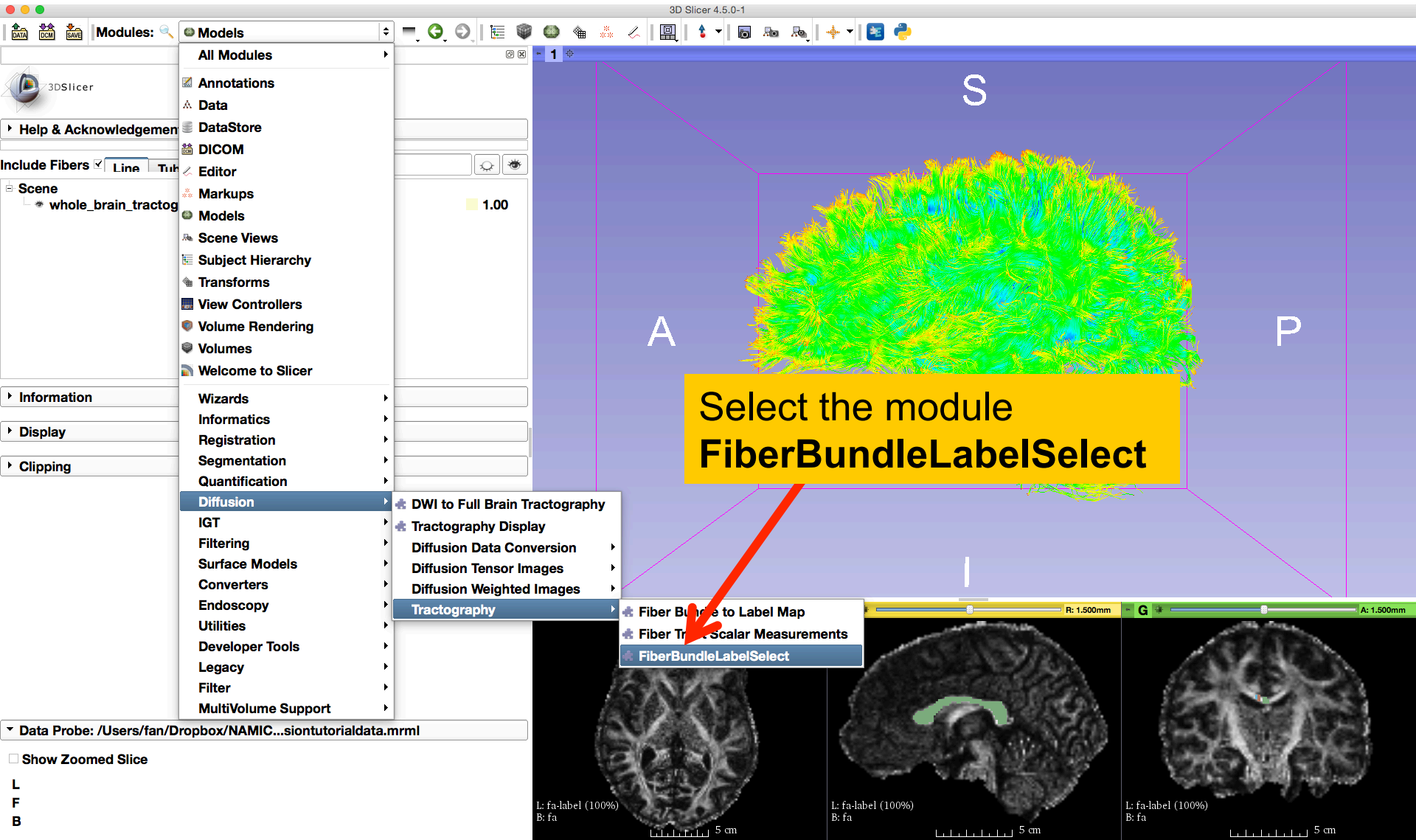
5 cm 5 cm 5 cm

# 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

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

Set the FiberBundleLabelSelection parameters:

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

Click the button **Apply**

# 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), R (Right), and P (Posterior). The left sidebar contains the 'Scene' panel with 'whole\_brain\_tractography' and 'bundle\_label1\_include' listed, both with a visibility of 1.00. A red arrow points to the 'Models' module icon in the top toolbar. Another red arrow points to the 'bundle\_label1\_include' entry in the Scene panel. At the bottom, three axial, sagittal, and coronal slices are shown, with the fiber bundle highlighted in green. The interface includes a top toolbar with various icons, a 'Modules' dropdown, and a 'Data Probe' section at the bottom left.

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

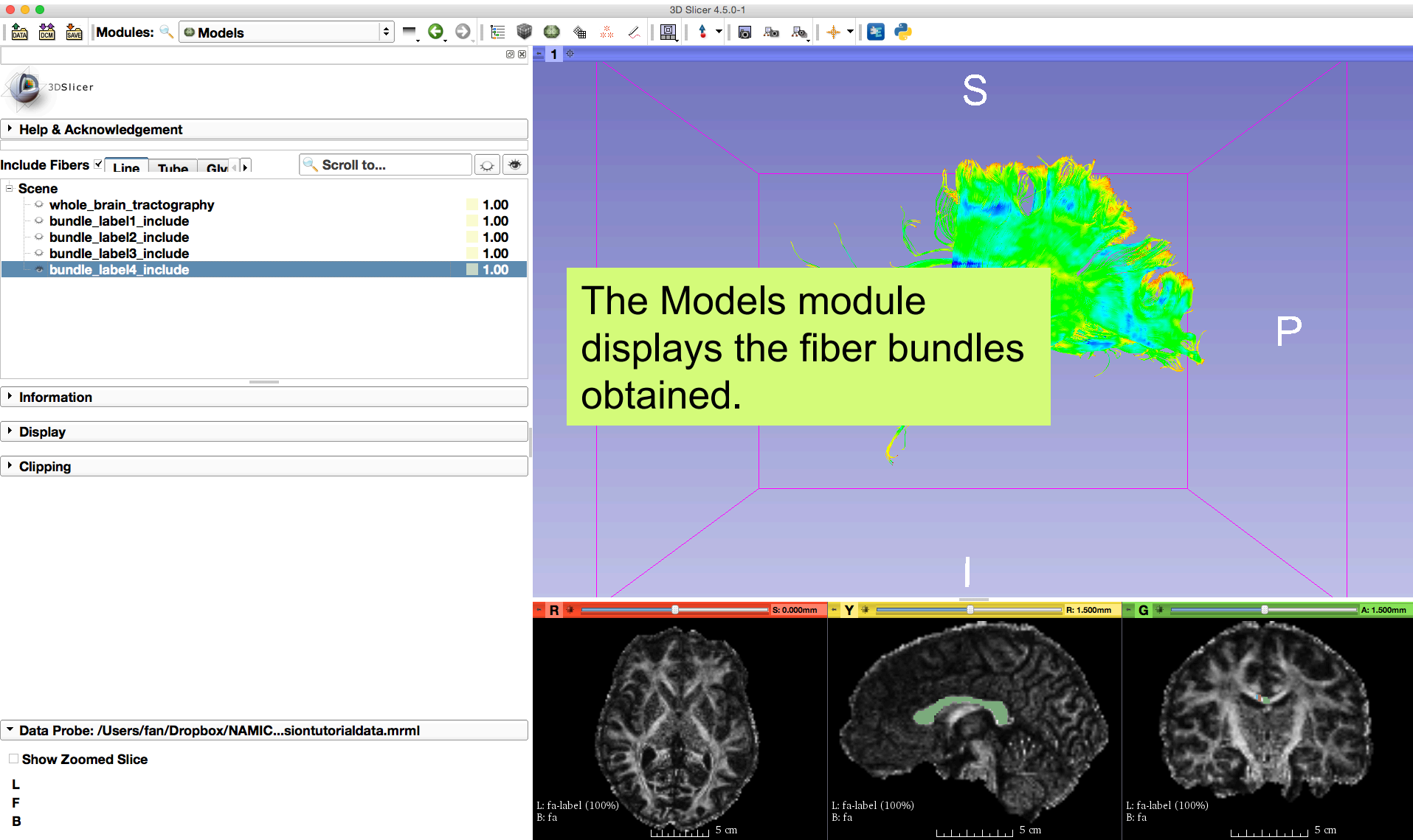
A yellow text box overlaid on the 3D view contains the following instructions:

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. A yellow box highlights a specific bundle. The axes are labeled S (Superior), I (Inferior), R (Right), and P (Posterior). The status bar at the bottom shows the process is **Completed** at **100%**. The bottom panel displays three axial slices of the brain with fiber bundles highlighted in green. The status bar at the bottom of the slices shows: L: fa-label (100%), B: fa.

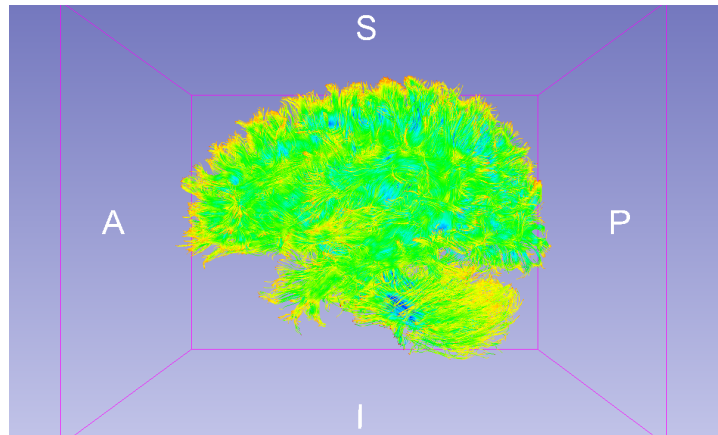


# Single Label Selection

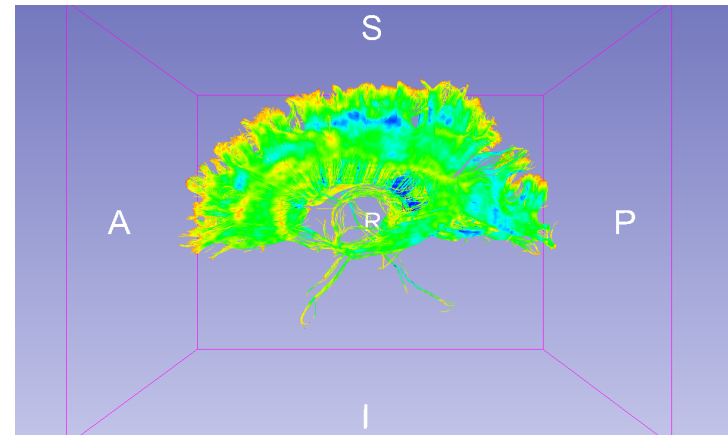


# Single Label Selection

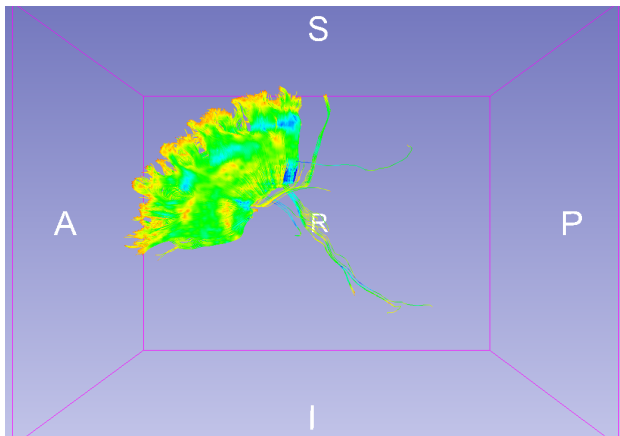
Whole Brain



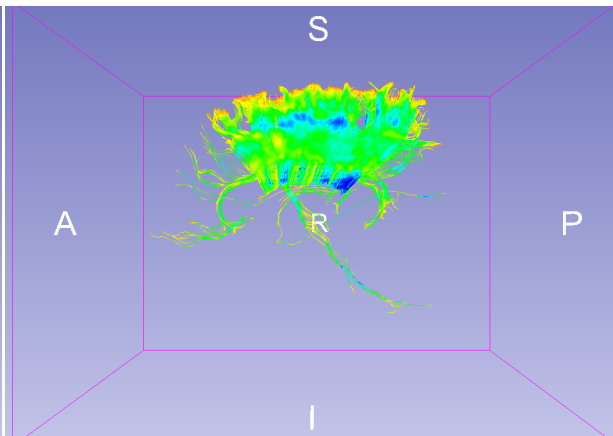
Label 1



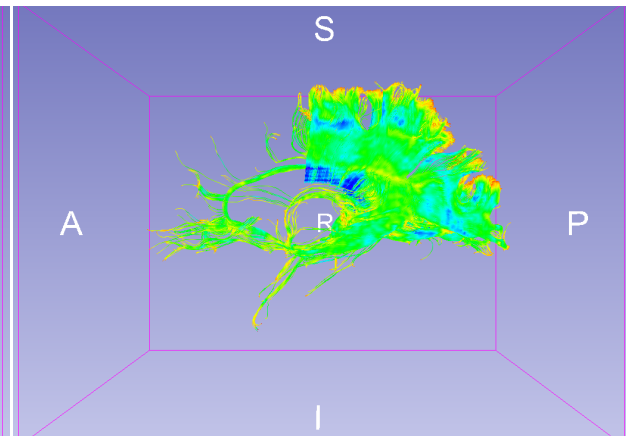
Label 2



Label 3

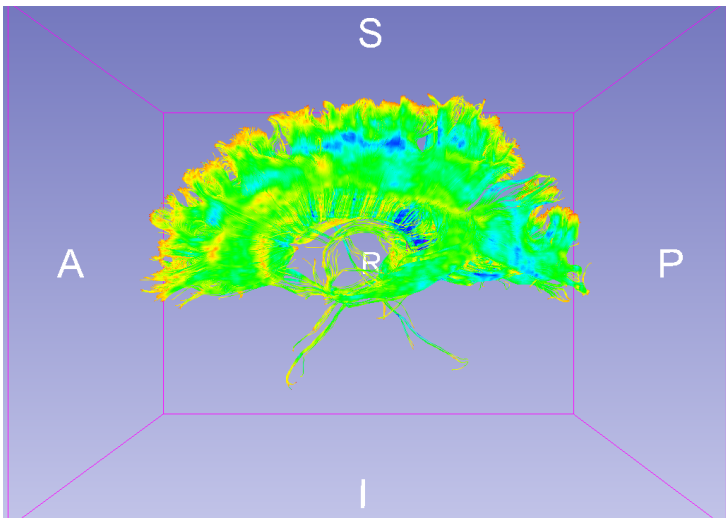


Label 4



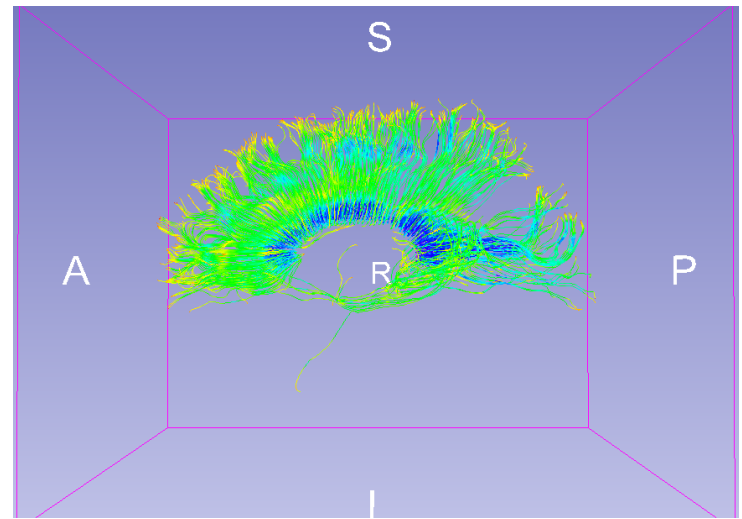
# Single Label Selection

Fiber Bundle Selection of Label 1  
from the Whole Brain Tractography



V.S.

Fiber Bundle Obtained by  
Seeding within Label 1



# Multiple Labels 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\_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/fan/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

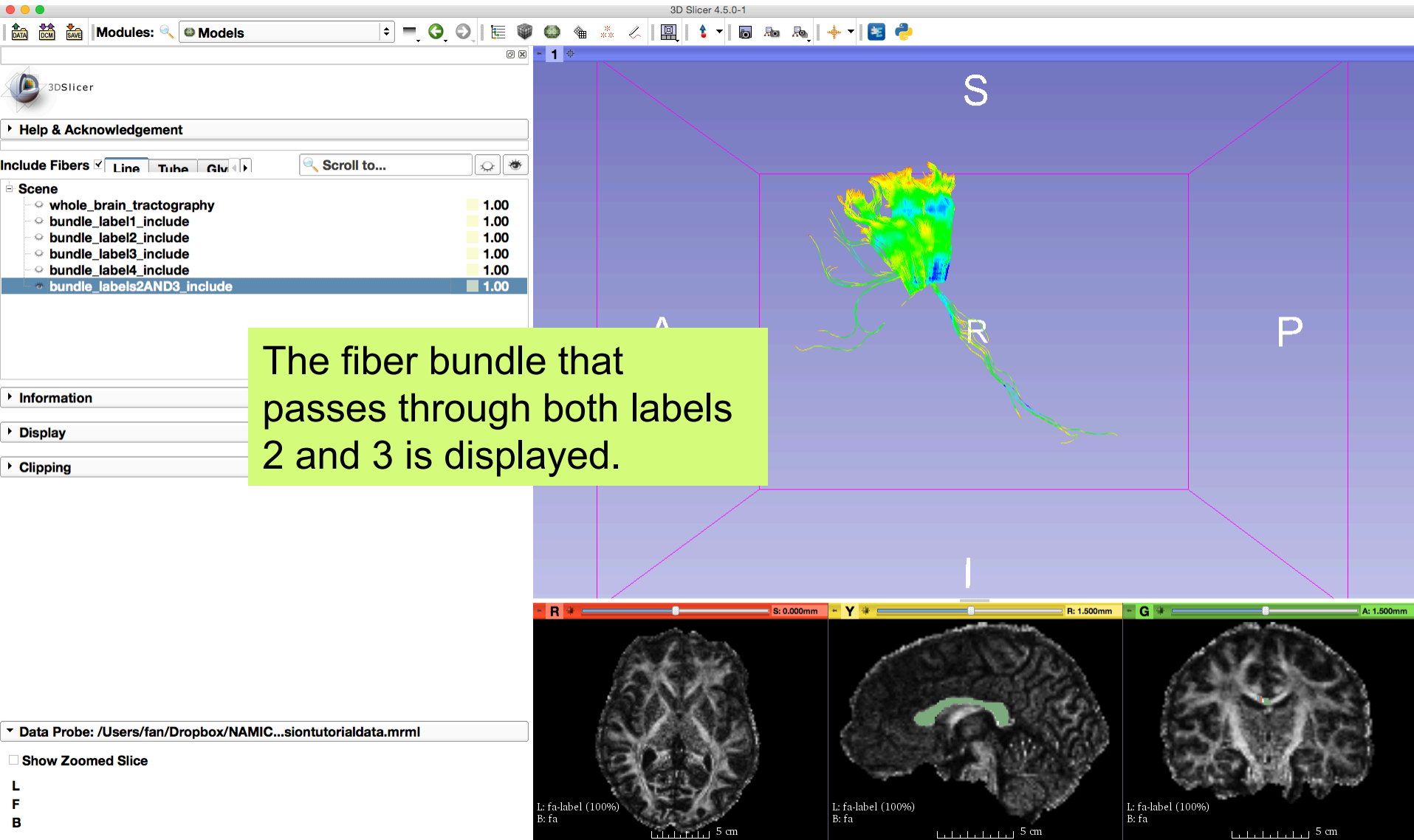
P

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

Click the button Apply

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

# Editing multiple labels



# Multiple Labels Selection

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

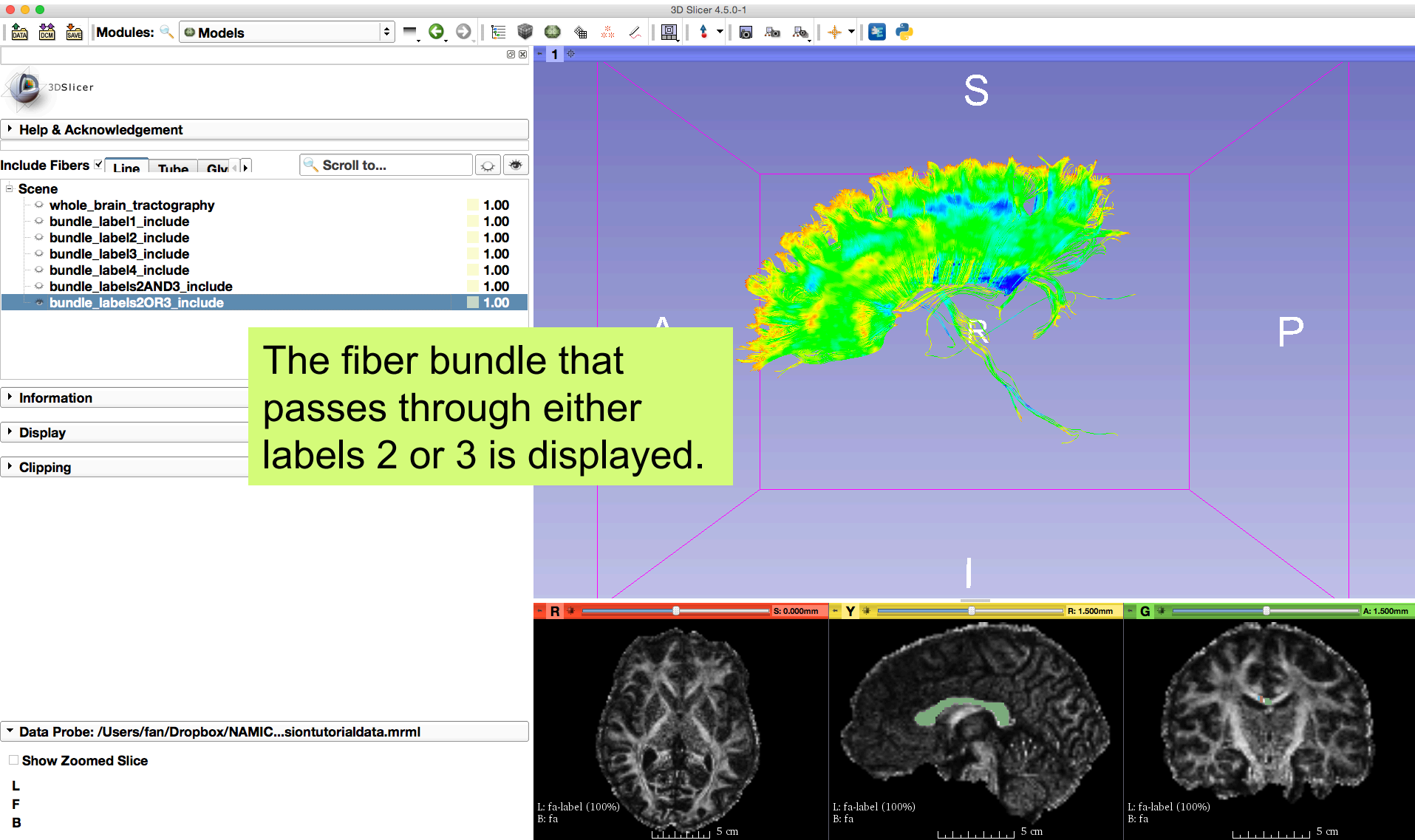
- Input Label Map: `fa-label`
- Input Fiber Bundle: `whole_brain_tractography`
- Output Fiber Bundle: `bundle_labels2OR3_include`
- Label regions definition:
  - Labels to include: `2,3`
  - Combine include labels:  OR  AND
  - Labels to exclude: (empty)
  - Combine exclude labels:  OR  AND

The 3D view shows a brain slice with fiber bundles. A yellow text box overlaid on the 3D view reads: "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`".

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

The bottom right corner shows three orthogonal views (L, F, B) 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



# Multiple Labels Selection

The image shows the 3D Slicer 4.5.0-1 interface. The main window displays a 3D view of fiber tractography in a brain, with a yellow text box overlaid that says "Try different combinations of labels." The 3D view is oriented with S (Superior), I (Inferior), and P (Posterior) axes. The left sidebar contains a "Scene" panel with a list of labels and their visibility status (1.00). The bottom of the interface shows three orthogonal slice views (R, Y, G) with a 5 cm scale bar. The R slice shows the fiber tractography in a coronal view, the Y slice shows it in a sagittal view, and the G slice shows it in an axial view. The Y slice has a green highlight on the fiber tractography. The R and G slices have a red highlight on the fiber tractography. The Y slice has a green highlight on the fiber tractography. The R and G slices have a red highlight on the fiber tractography.

3D Slicer 4.5.0-1

Modules: Models

3DSlicer

Help & Acknowledgement

Include Fibers Line Tube GLV Scroll to...

Scene

- whole\_brain\_tractography 1.00
- bundle\_label1\_include 1.00
- bundle\_label2\_include 1.00
- bundle\_label3\_include 1.00
- bundle\_label4\_include 1.00
- bundle\_labels2AND3\_include 1.00
- bundle\_labels2OR3\_include 1.00
- bundle\_labels3AND4\_include 1.00
- bundle\_labels3OR4\_include 1.00
- bundle\_labels2AND4\_include 1.00
- bundle\_labels2OR4\_include 1.00

Information

Display

Clipping

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

Show Zoomed Slice

L  
F  
B

S  
I  
P

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

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

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

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

5 cm

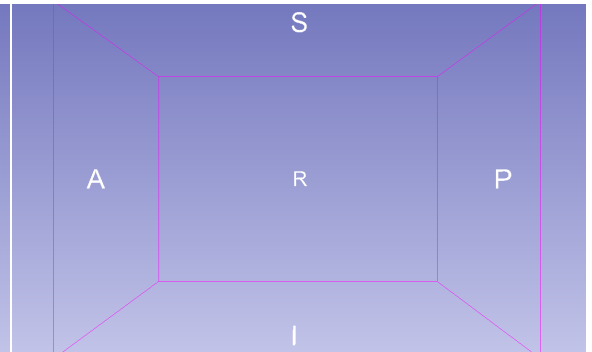
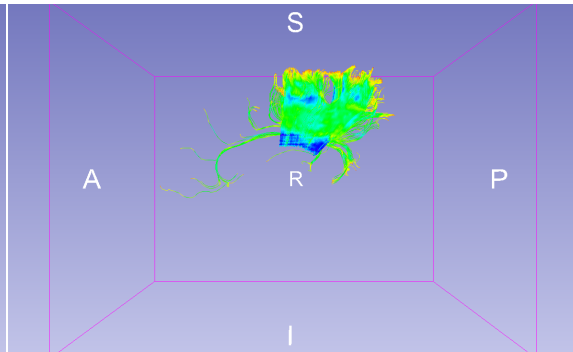
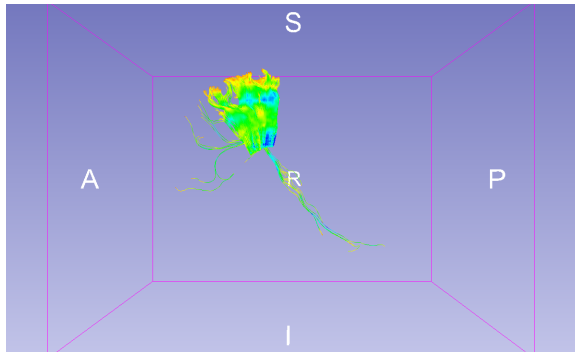


# Multiple Labels Selection

Labels 2 and 3

Labels 3 and 4

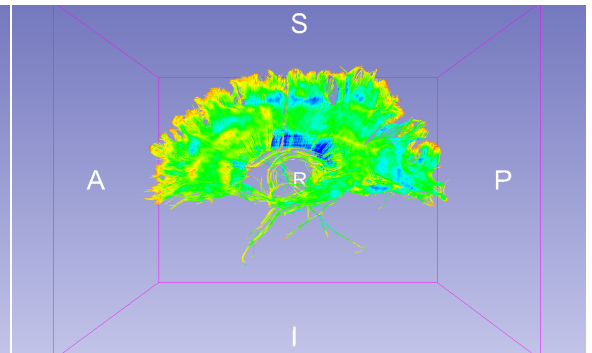
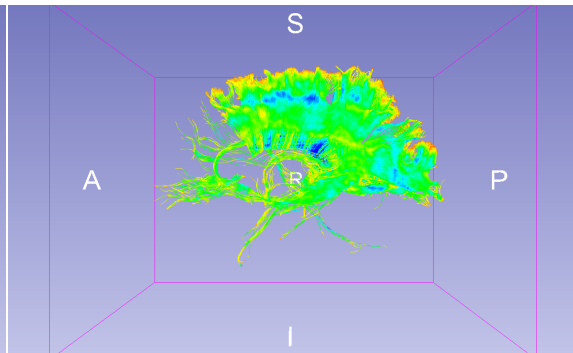
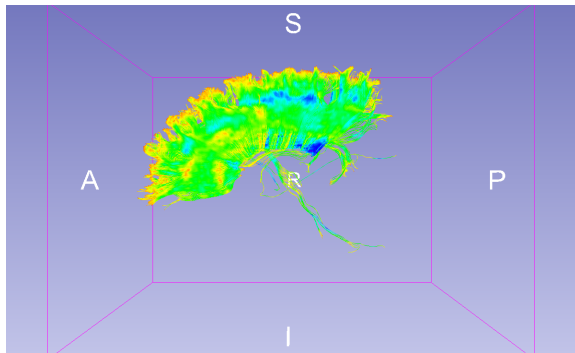
Labels 2 and 4 (empty)



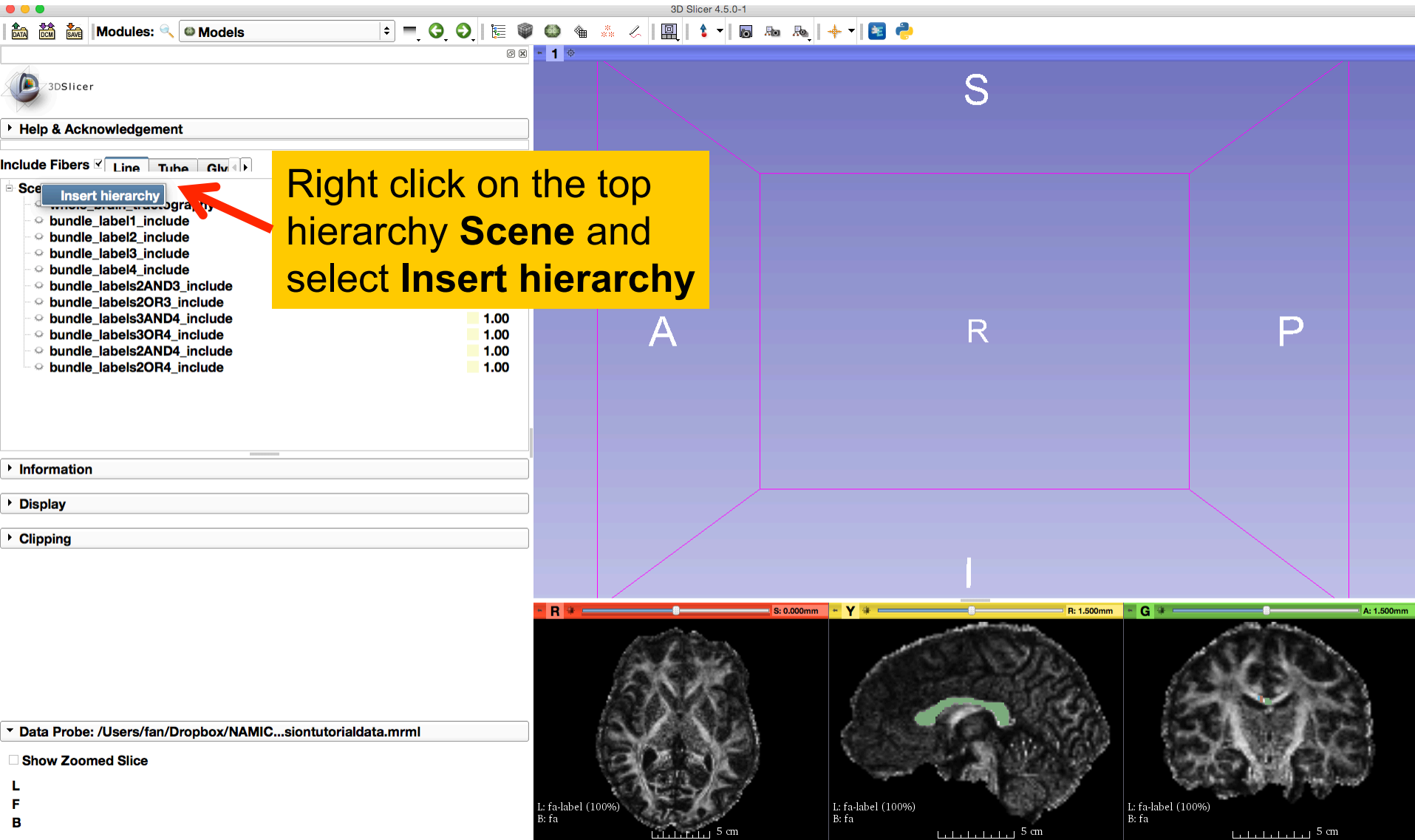
Labels 2 or 3

Labels 3 or 4

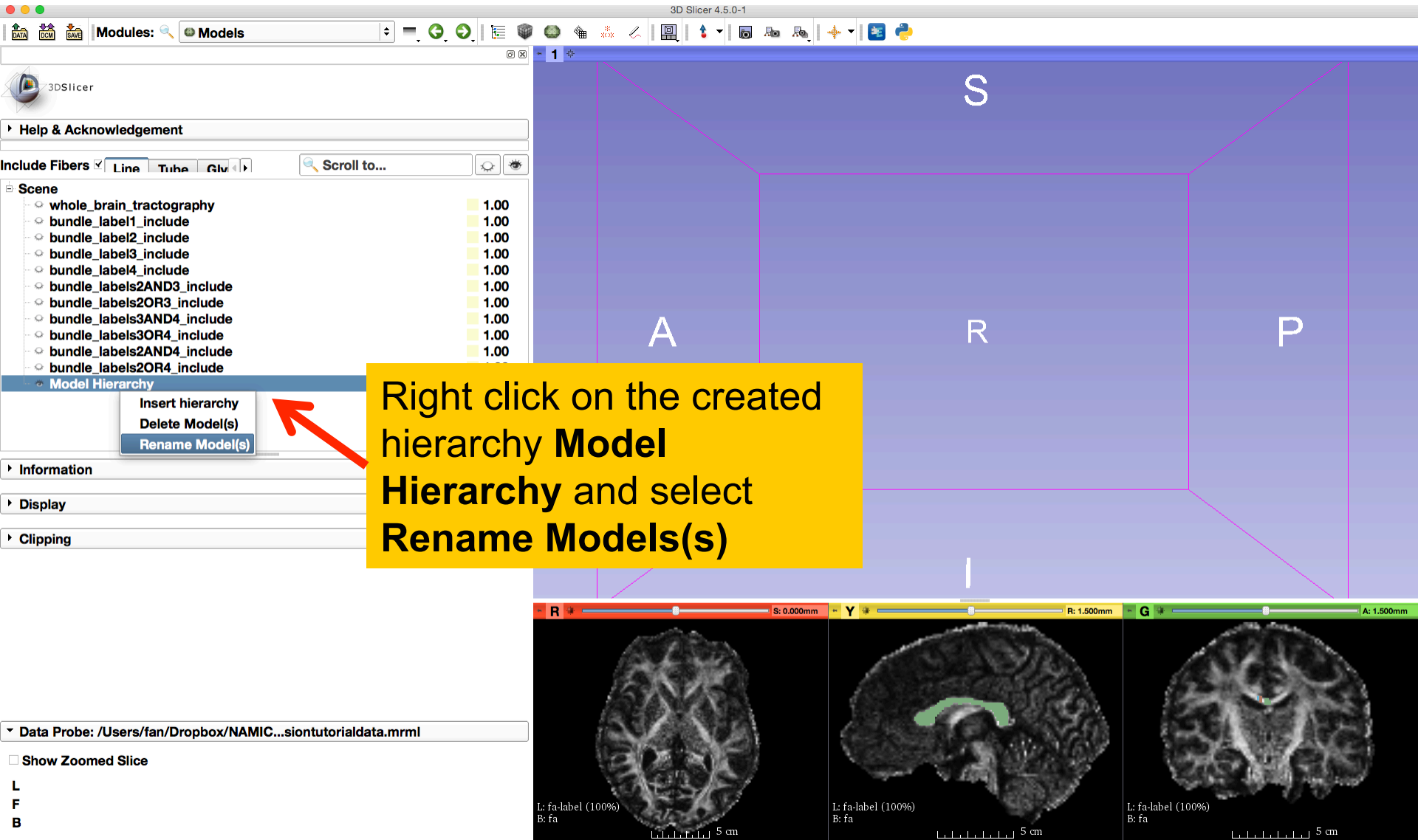
Labels 2 or 4



# Fiber Hierarchy



# Fiber Hierarchy



# Fiber Hierarchy

The screenshot shows the 3D Slicer 4.5.0-1 interface. On the left, the 'Scene' panel displays a hierarchy of fiber bundles. The 'single\_selection' folder is highlighted with a red box and contains four sub-items: 'bundle\_label1\_include', 'bundle\_label2\_include', 'bundle\_label3\_include', and 'bundle\_label4\_include', each with a value of 1.00. The main 3D view shows a brain model with a green fiber bundle highlighted. A yellow callout box with black text contains the following instructions:

**Rename the hierarchy to `single_selection`**

**Drag the fiber bundles from the single selection into this hierarchy.**

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

# Fiber Hierarchy

The image shows the 3D Slicer 4.5.0-1 interface. On the left, the 'Scene' panel displays a fiber hierarchy tree. The 'OR\_selection' node is highlighted with a red box. The 3D view shows a brain slice with a green fiber bundle. A yellow text box is overlaid on the 3D view, containing the text: 'Repeat the above steps to create ADD\_selection and OR\_selection'. The bottom of the interface shows three orthogonal views (axial, sagittal, and coronal) of the brain slice, with a 5 cm scale bar and a 1.500mm zoom level.

3D Slicer 4.5.0-1

Modules: Models

Scene

- whole\_brain\_fascography 1.00
  - single\_selection 1.00
    - bundle\_label1\_include 1.00
    - bundle\_label2\_include 1.00
    - bundle\_label3\_include 1.00
    - bundle\_label4\_include 1.00
  - ADD\_selection 1.00
    - bundle\_labels2AND3\_include 1.00
    - bundle\_labels2AND4\_include 1.00
    - bundle\_labels3AND4\_include 1.00
  - OR\_selection 1.00**
    - bundle\_labels2OR3\_include 1.00
    - bundle\_labels2OR4\_include 1.00
    - bundle\_labels3OR4\_include 1.00

Information

Display

Clipping

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

Show Zoomed Slice

L  
F  
B

S  
P  
I  
R  
Y  
G  
A: 1.500mm

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

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

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

5 cm

5 cm

5 cm

# Fiber Tract Scalar Measurements

The image shows the 3D Slicer 4.5.0-1 interface. The 'Modules' panel on the left is open, showing a tree view of modules. The 'Diffusion' module is selected, and its sub-menu is open, showing 'Fiber Tract Scalar Measurements' as the selected option. A yellow callout box with the text 'Select the module Fiber Tract Scalar Measurements' and a red arrow points to this option. The main 3D view shows a brain slice with a green fiber tract highlighted. The slice is labeled with 'S' (Superior), 'A' (Anterior), 'P' (Posterior), and 'I' (Inferior). The bottom of the interface shows three axial brain slices 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'. The bottom right corner has a red 'X' icon.

3D Slicer 4.5.0-1

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

- Data Probe: /Users/fan/Dropbox/NAMIC...siontutorialdata.mrml
- Show Zoomed Slice
- L
- F
- B

Select the module  
**Fiber Tract Scalar Measurements**

S  
A  
P  
I

R: 1.500mm G A: 1.500mm

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

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

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

5 cm

5 cm

5 cm

# Fiber Tract Scalar Measurements

3D Slicer 4.5.0-1

Modules: Fiber Tract Scalar Measurements

Help & Acknowledgement

Fiber Tract Scalar Measurements

Parameter set: Fiber Tract Scalar Measurements

IO

Select Input Type  Fibers\_Hierarchy  Fibers\_File\_Folder

Fibers Hierarchy: single\_selection

Fibers File Folder: /Volumes/Slicer-4.5.0-1-macosx-amd64

Output Text File: /Winter2016/single\_selection\_measurements.csv

Select Output Format  Row\_Hierarchy  Column\_Hierarchy

Output Field Separator  Comma  Space  Tab

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

Set the FiberTractScalarMeasurements parameters:

- Select Input Type: **Fibers\_Hierarchy**
- Fiber Hierarchy: **single\_selection**
- Output Text File: **XXX/single\_selection\_measurements.csv**
- Select Output Format: **Column\_Hierarchy**





# 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: ADD\_selection

Fibers File Folder: /Volumes/Slicer-4.5.0-1-macosx-amd64

Output Text File: stWinter2016/ADD\_selection\_measurements.csv

Select Output Format  Row\_Hierarchy  Column\_Hierarchy

Output Field Separator  Comma  Space  Tab

S

P

Change the input and output files to calculate the measurements from other hierarchies.

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

Click the button Apply

# Fiber Tract Scalar Measurements

single\_selection\_measurements.csv

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Name	Num_Points	Num_Fibers	Tensors_FractionalAnisotropy	Tensors_LinearMeasurement	Tensors_MaxEigenvalue	Tensors_MidEigenvalue	Tensors_MinEigenvalue	Tensors_PlanarMeasurement	Tensors_RelativeAnisotropy	Tensors_SphericalMeasurement	Tensors_Trace		
2	single_selection:bundle_label1_include	2127263	14306	0.525257	0.505662	0.001193	0.000558	0.000396	NAN	12022862.08	NAN	NAN		
3	single_selection:bundle_label2_include	708470	5564	0.484828	0.471678	0.001157	0.000579	0.000425	0.14296	0.321028	0.385363	NAN		
4	single_selection:bundle_label3_include	601023	4428	0.514121	0.490995	0.001166	0.000559	0.000393	0.154045	0.344331	0.35496	NAN		
5	single_selection:bundle_label4_include	1261823	7485	0.552797	0.528861	0.001211	0.00054	0.000373	NAN	77884731.35	NAN	NAN		
6	single_selection	4698579	31783	0.525133	0.504891	0.001189	0.000556	0.000394	0.041261	26359572.86	0.103511	0		

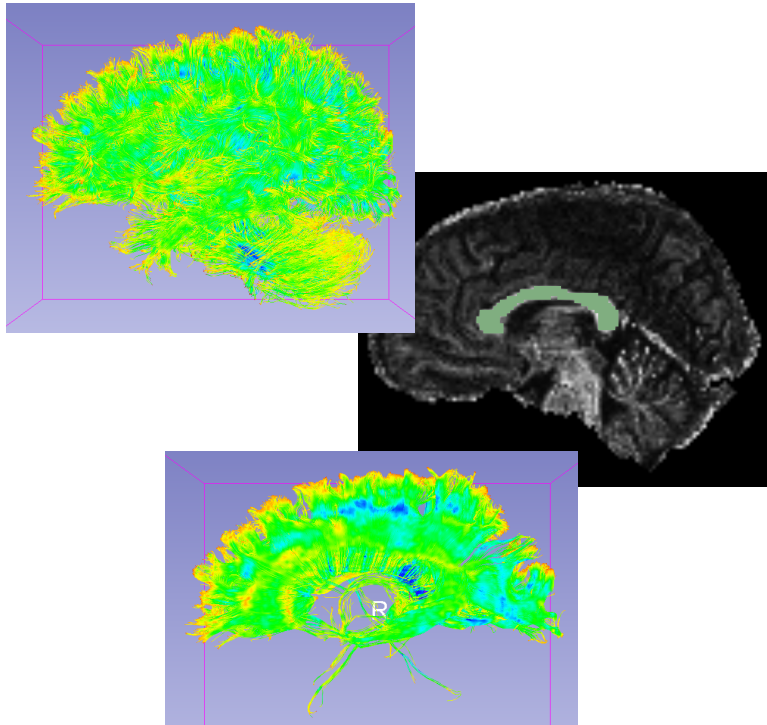
ADD\_selection\_measurements.csv

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	Name	Num_Points	Num_Fibers	Tensors_FractionalAnisotropy	Tensors_LinearMeasurement	Tensors_MaxEigenvalue	Tensors_MidEigenvalue	Tensors_MinEigenvalue	Tensors_PlanarMeasurement	Tensors_RelativeAnisotropy	Tensors_SphericalMeasurement	Tensors_Trace			
2	ADD_selection:bundle_labels2AND3_include	163814	1360	0.502443	0.490922	0.001174	0.000561	0.000414	0.135576	0.336349	0.373502	NAN			
3	ADD_selection:bundle_labels2AND4_include	0	0	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN	NAN			
4	ADD_selection:bundle_labels3AND4_include	310424	2131	0.518347	0.484738	0.001142	0.000556	0.000374	0.170168	0.347557	0.345094	NAN			
5	ADD_selection	474238	3491	0.512854	0.486874	0.001153	0.000558	0.000388	0.158219	0.343685	0.354907	0			

OR\_selection\_measurements.csv

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	Name	Num_Points	Num_Fibers	Tensors_FractionalAnisotropy	Tensors_LinearMeasurement	Tensors_MaxEigenvalue	Tensors_MidEigenvalue	Tensors_MinEigenvalue	Tensors_PlanarMeasurement	Tensors_RelativeAnisotropy	Tensors_SphericalMeasurement	Tensors_Trace			
2	OR_selection:bundle_labels2OR3_include	1145679	8632	0.497677	0.47906	0.001159	0.000571	0.00041	0.149831	0.331062	0.371109	NAN			
3	OR_selection:bundle_labels2OR4_include	1970293	13049	0.528357	0.508299	0.001191	0.000554	0.000392	NAN	49879254.3	NAN	NAN			
4	OR_selection:bundle_labels3OR4_include	1552422	9782	0.544712	0.523024	0.001207	0.000544	0.000381	NAN	63305432.07	NAN	NAN			
5	OR_selection	4668394	31463	0.526266	0.50602	0.001189	0.000555	0.000392	0.03677	42103021.18	0.091075	0			

# Conclusion



This tutorial guided you through the fiber bundle label selection and fiber tract scalar measurements for conducting further tractography processing.

single\_selection\_measurements.csv

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Name	Num_Points	Num_Fibers	Tensors_FractionalAnisotropy	Tensors_LinearMeasurement	Tensors_MaxEigenvalue	Tensors_MidEigenvalue	Tensors_MinEigenvalue	Tensors_PlanarMeasurement	Tensors_RelativeAnisotropy	Tensors_SphericalMeasurement	Tensors_Trace		
2	single_selection_bundle_label1_include	2127263	14306	0.525257	0.505662	0.001193	0.000558	0.000396	NAN	12022862.08	NAN	NAN		
3	single_selection_bundle_label2_include	708470	5564	0.484828	0.471678	0.001157	0.000579	0.000425	0.14296	0.321058	0.385363	NAN		
4	single_selection_bundle_label3_include	601023	4428	0.514121	0.480905	0.001166	0.000559	0.000393	0.154045	0.344311	0.35486	NAN		
5	single_selection_bundle_label4_include	1261823	7485	0.552797	0.528861	0.001211	0.00054	0.000373	NAN	77884731.35	NAN	NAN		
6	single_selection	4698579	31783	0.525133	0.504891	0.001189	0.000556	0.000394	0.041261	26359572.86	0.105911	0		

# Acknowledgments



**National Alliance for Medical Image Computing**

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