

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 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

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
diffusiontutorialdata.mrml	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

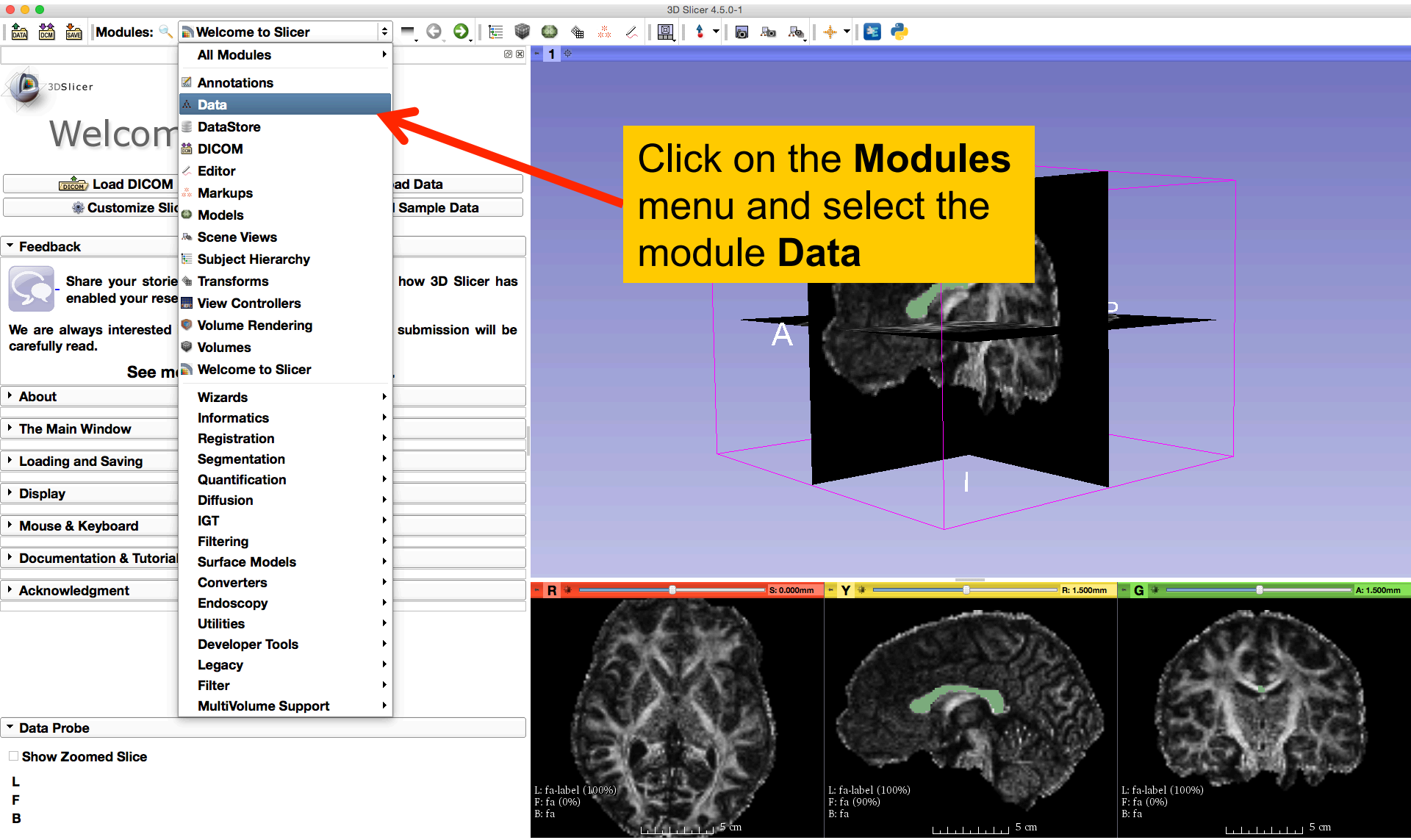
Click **OK** to load the dataset to Slicer

Show Zoom

L
F
B

5 cm 5 cm 5 cm

Load MRML Data



Load MRML Data

The screenshot shows the 3D Slicer 4.5.0-1 interface. The left sidebar contains a 'Nodes' panel with a tree view. The 'Default Scene Camera' node is highlighted with a red circle. The main 3D view shows a brain scan with a green label on the corpus callosum. The bottom of the interface shows three 2D slices (axial, sagittal, and coronal) with a 5 cm scale bar. The sagittal slice shows the green label on the corpus callosum. The bottom status bar shows the slice positions: S: 0.000mm, Y: 1.500mm, G: 1.500mm, A: 1.500mm.

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

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

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

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

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:

- 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

Display & Modify Scene

Nodes

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

Scene Model: Transform

Display MRI

Show Hidden

Filter:

MRML Node Inspector

Data Probe

Show Zoomed Slice

L

F

B

Select the module Editor

R 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

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

Create and Select Label Maps

Edit Selected Label Map

Undo/Redo:

Active Tool: DefaultTool

Label: tissue 1

1

R 1.500mm G 1.500mm A: 1.500mm

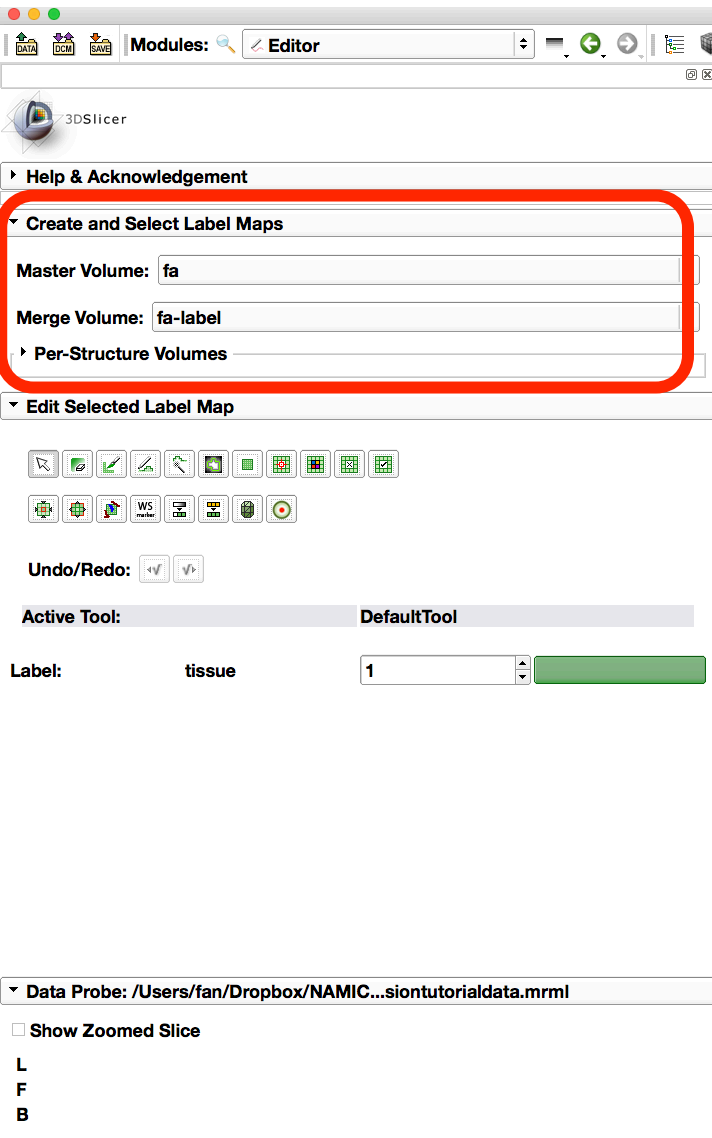
L: fa-label (100%)
F: fa (0%)
B: fa

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

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

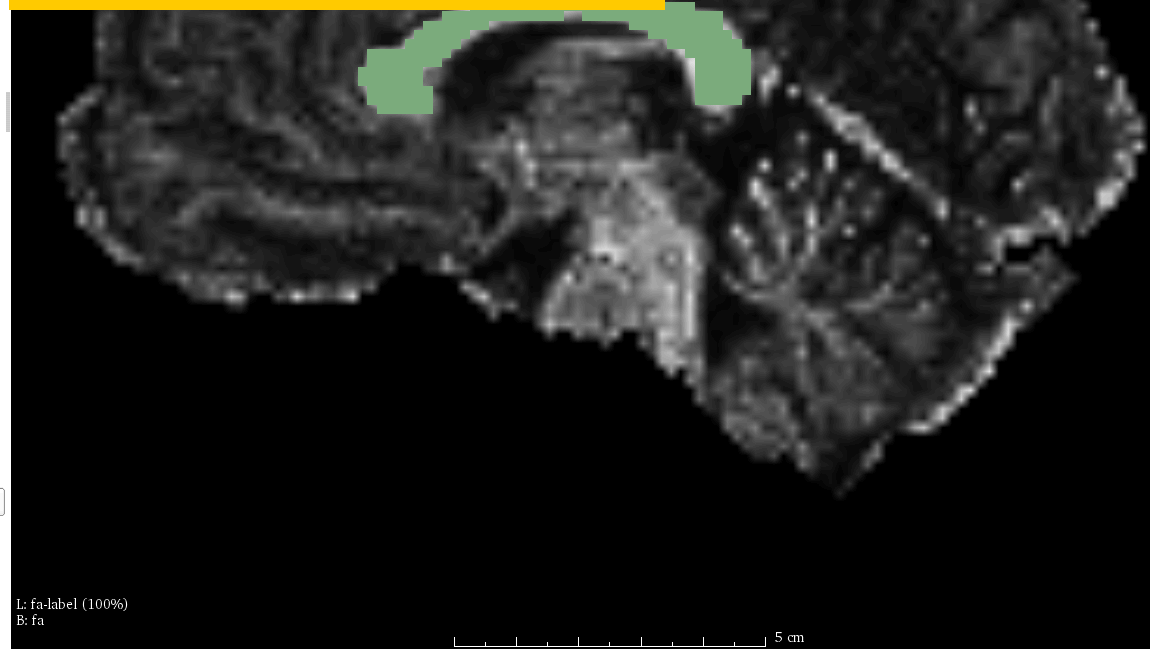
5 cm 5 cm 5 cm

Edit Multiple Labels



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

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



Edit Multiple Labels

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

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

Annotations on the image:

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

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

Edit Multiple Labels

3D Slicer 4.5.0-1

Modules: Editor

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

R: 6.000mm

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

Edit Multiple Labels

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

3D Slicer 4.5.0-1

Modules: Editor

3DSlicer

Help & Acknowledgement

Create and Select Label Maps

Master Volume

Merge Volume

Per-Structure

Edit Selection

Undo/Redo: [Undo] [Redo]

Active Tool: DrawEff

Label: skin 3

Paint Over

Threshold Paint

Apply

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

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

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

F None

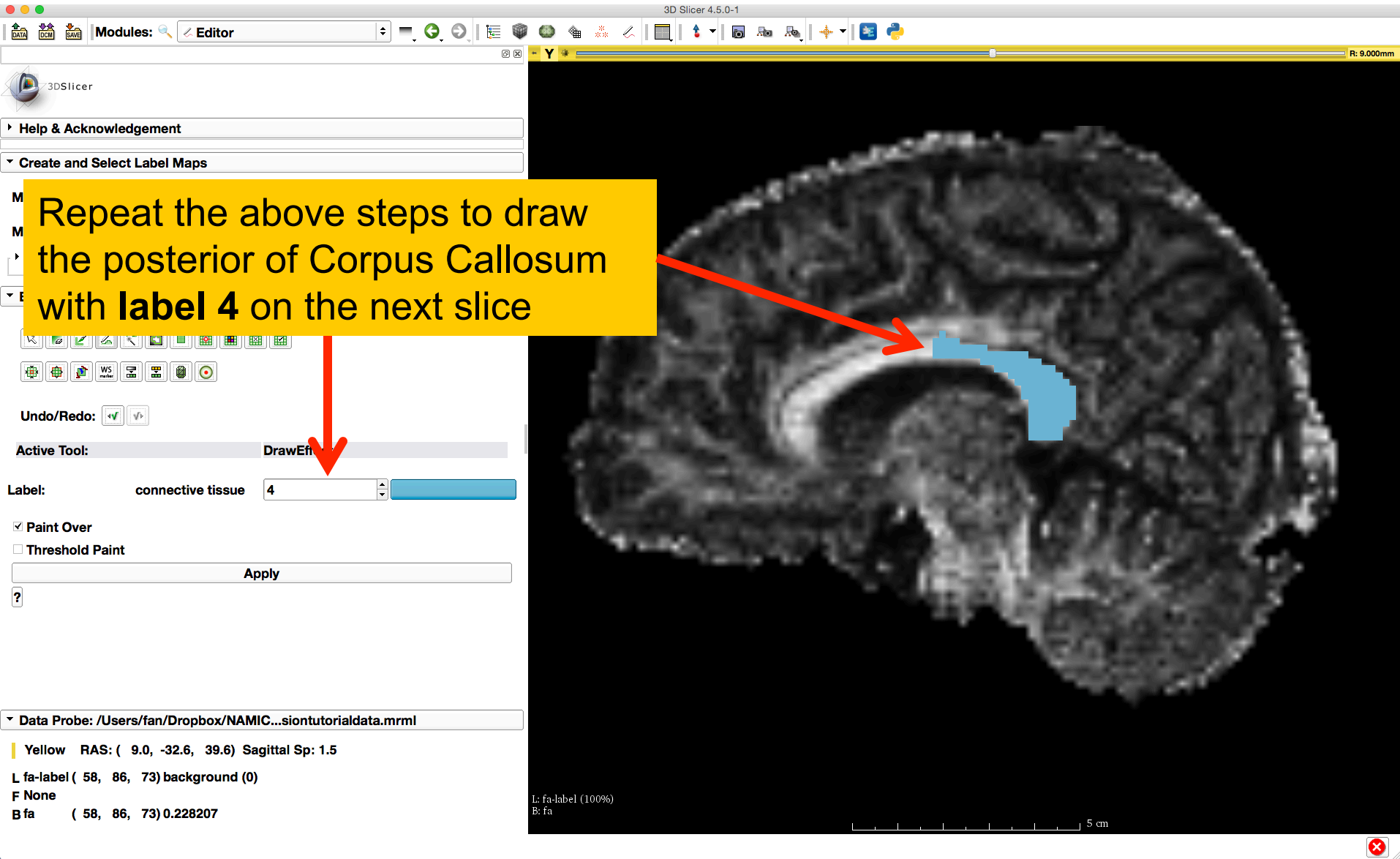
B fa (59, 61, 78) 0.308757

L: fa-label (100%)

B: fa

5 cm

Edit Multiple Labels



3D Slicer 4.5.0-1

Modules: Editor

Help & Acknowledgement

Create and Select Label Maps

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

Active Tool: DrawEff

Label: connective tissue 4

Paint Over

Threshold Paint

Apply

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

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

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

F None

B fa (58, 86, 73) 0.228207

L: fa-label (100%)

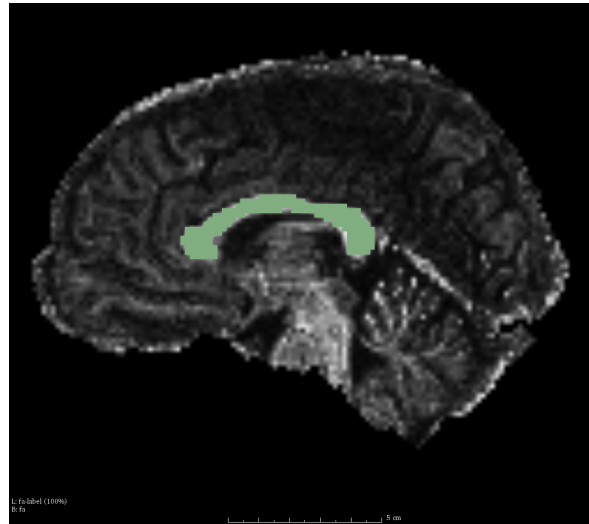
B: fa

5 cm

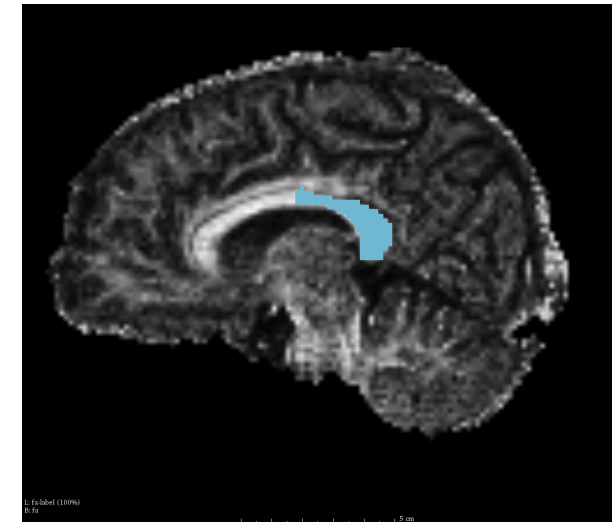
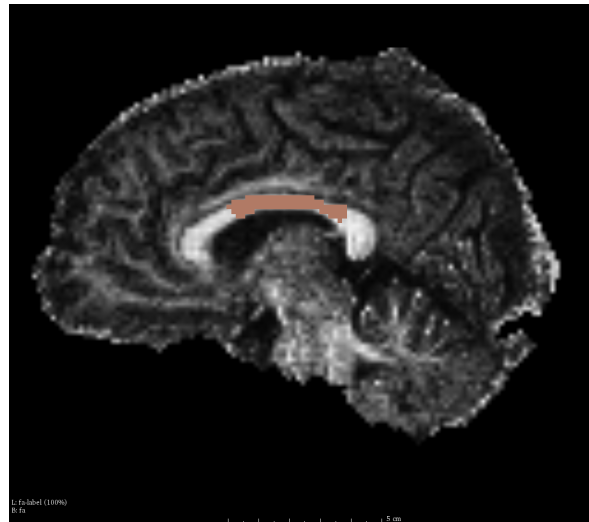
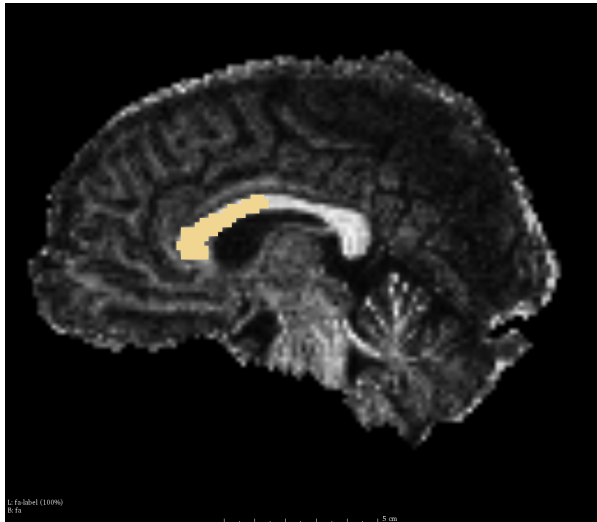
Edit Multiple Labels

Label map on individual slice, with :

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



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



Whole Brain Tractography

The image shows the 3D Slicer 4.5.0-1 interface. The left sidebar contains the 'Modules' list, with 'Diffusion' selected and its sub-menu open. The sub-menu includes 'DWI to Full Brain Tractography', 'Tractography Display', 'Diffusion Data Conversion', 'Diffusion Tensor Images', 'Diffusion Weighted Images', and 'Tractography'. The 'Diffusion Tensor Images' sub-menu is also open, showing 'Diffusion Tensor Scalar Measurements', 'Resample DTI Volume', 'Tractography Interactive Seeding', and 'Tractography Label Map Seeding'. A red arrow points from the 'Tractography Label Map Seeding' option to a yellow callout box. Another red arrow points from the 'Tractography Label Map Seeding' option to a yellow callout box. A third red arrow points from the 'Tractography Label Map Seeding' option to the 'Tractography Label Map Seeding' option in the sub-menu. The main 3D view shows a brain slice with a green tract. The bottom of the interface shows three panels of brain slices with a 5 cm scale bar.

3D Slicer 4.5.0-1

Go back to the **Conventional** layout

Select the module **Tractography Label Map Seeding**

- Diffusion
 - DWI to Full Brain Tractography
 - Tractography Display
 - Diffusion Data Conversion
 - Diffusion Tensor Images
 - Diffusion Tensor Scalar Measurements
 - Resample DTI Volume
 - Tractography Interactive Seeding
 - Tractography Label Map Seeding
 - Diffusion Weighted Images
 - Tractography
 - IGT
 - Filtering
 - Surface Models
 - Converters
 - Endoscopy
 - Utilities
 - Developer Tools
 - Legacy
 - Filter
 - MultiVolume Support

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

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

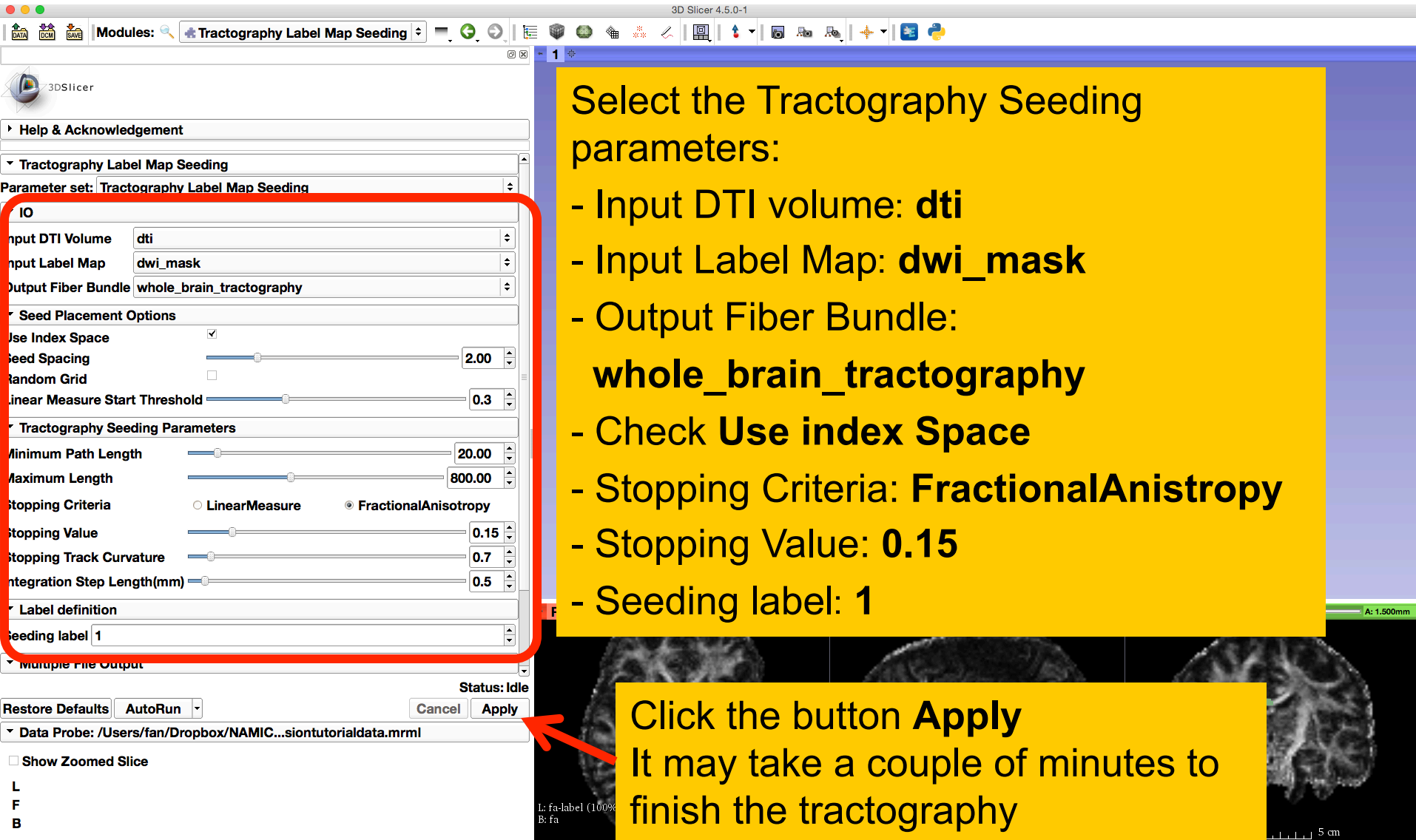
L: fa-label (100%)
B: fa

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 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

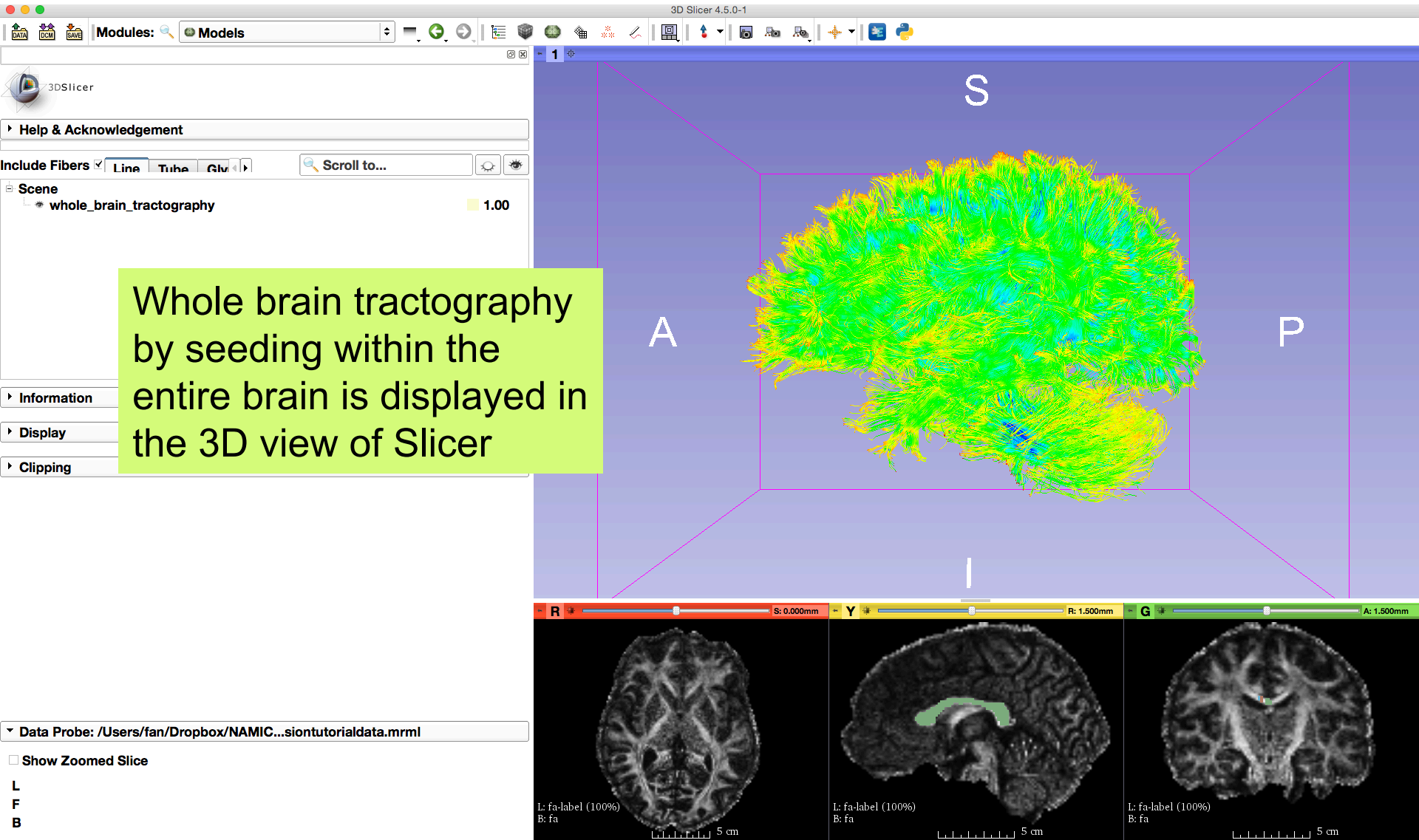
L: fa-label (100%)
B: fa

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

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

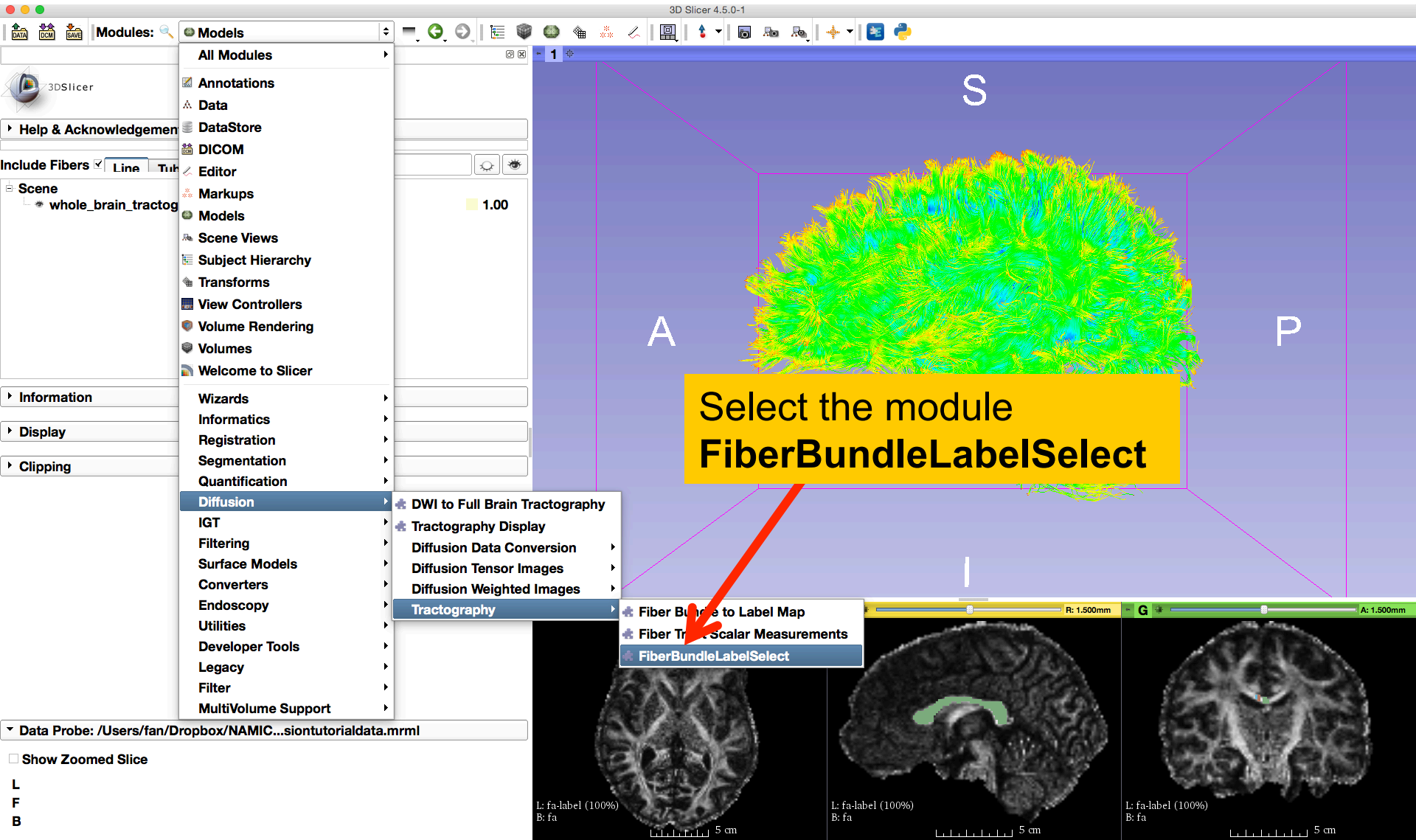
5 cm 5 cm 5 cm

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

The screenshot shows the 3D Slicer 4.5.0-1 interface. The 'FiberBundleLabelSelect' module is active, and its parameters are displayed in the left sidebar. A red box highlights the 'Input Label Map', 'Input Fiber Bundle', 'Output Fiber Bundle', and 'Labels to include' fields. The 'Labels to include' field contains the value '1'. The 'Apply' button is highlighted with a yellow box and an arrow pointing to it from 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), R (Right), and P (Posterior). The left sidebar contains the 'Scene' panel with a tree view showing 'whole_brain_tractography' and 'bundle_label1_include'. The 'Clipping' panel is visible below. 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 menu, 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

R S A R P

R S: 0.000mm A: 1.500mm

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

Single Label Selection

3D Slicer 4.5.0-1

Modules: FiberBundleLabelSelect

3DSlicer

Help & Acknowledgement

FiberBundleLabelSelect

Parameter set: FiberBundleLabelSelect

Input Label Map: fa-label

Input Fiber Bundle: whole_brain_tractography

Output Fiber Bundle: bundle_label2_include

Label regions definition

Labels to include: 2

Combine include labels: OR AND

Labels to exclude:

Combine exclude labels: OR AND

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

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

Show Zoomed Slice

L
F
B

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

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

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

5 cm

5 cm

5 cm

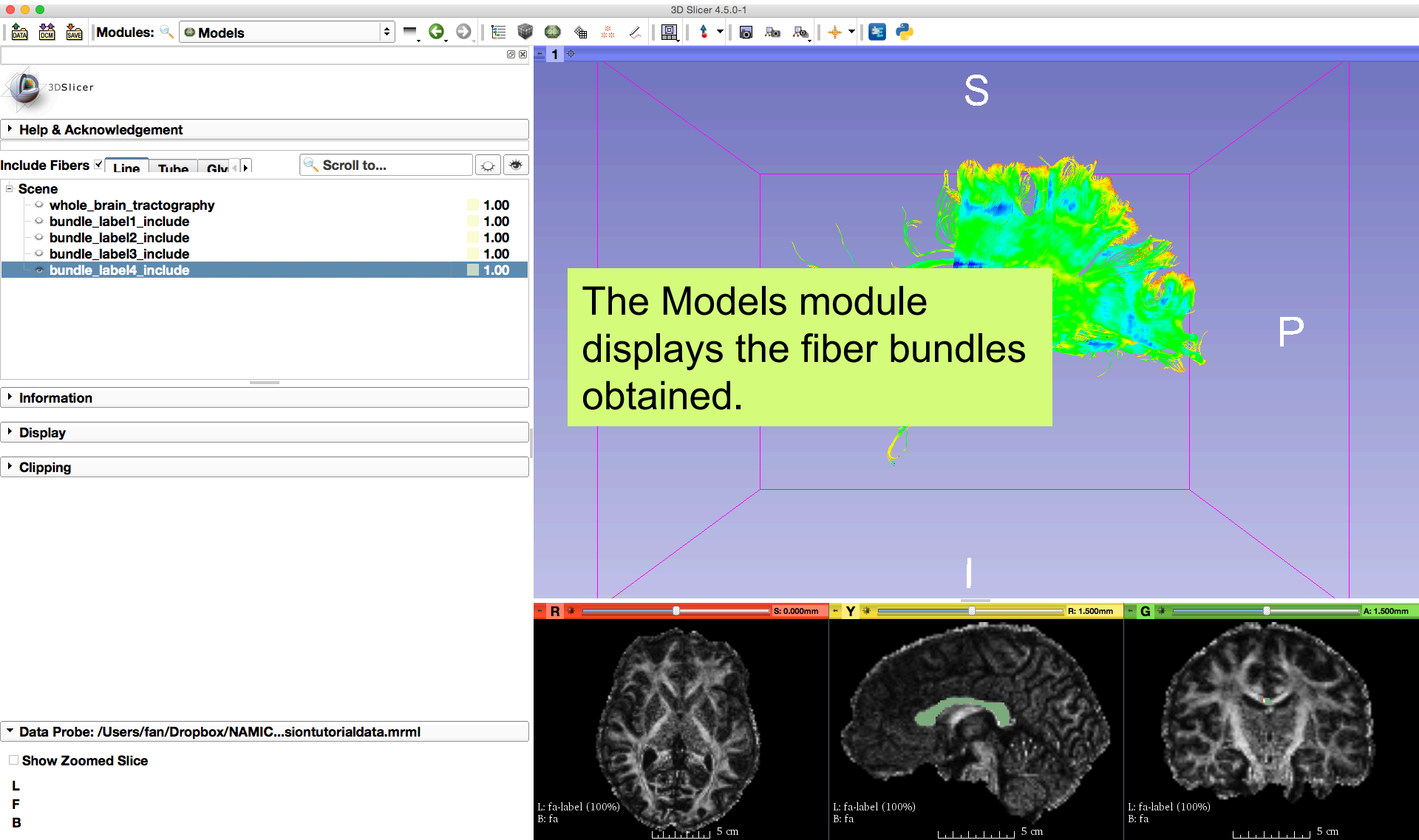
S

P

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

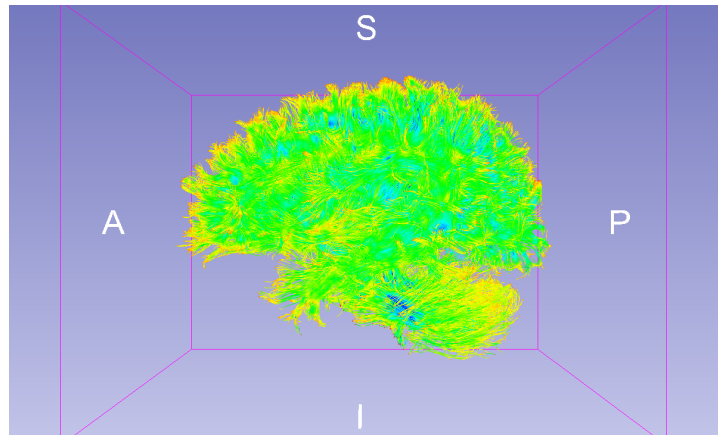
Repeat the above steps to perform fiber bundle selections of labels 2, 3 and 4 individually and obtain the selected bundles of **bundle_label2_include**, **bundle_label3_include** and **bundle_label4_include** respectively

Single Label Selection

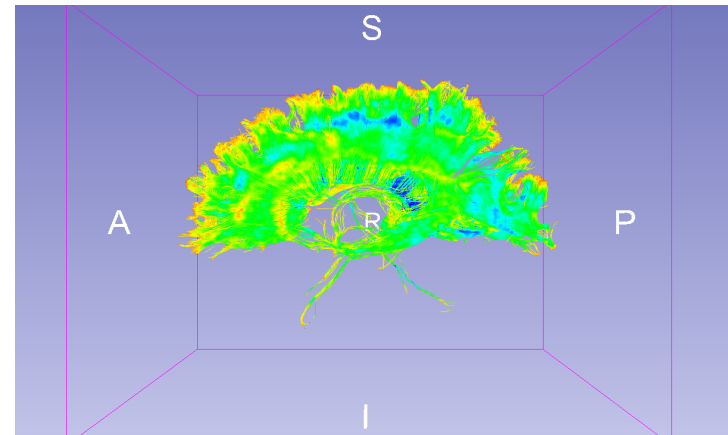


Single Label Selection

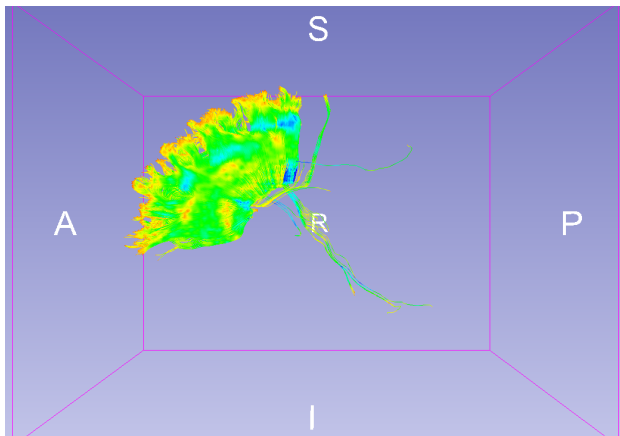
Whole Brain



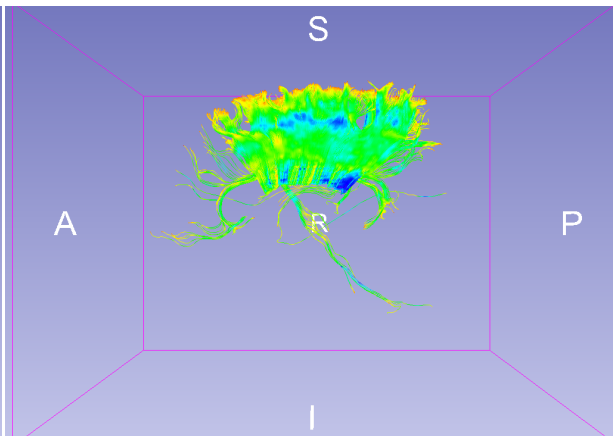
Label 1



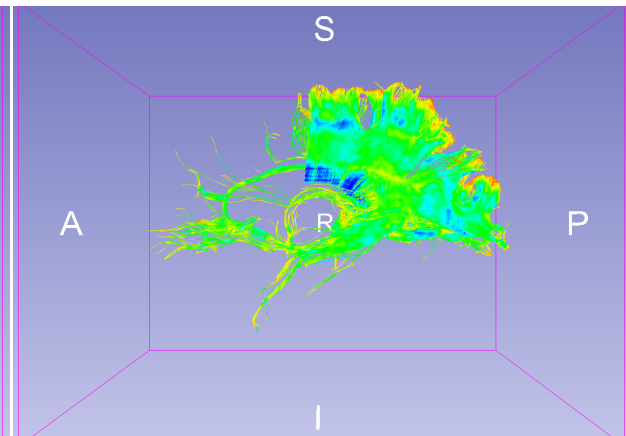
Label 2



Label 3



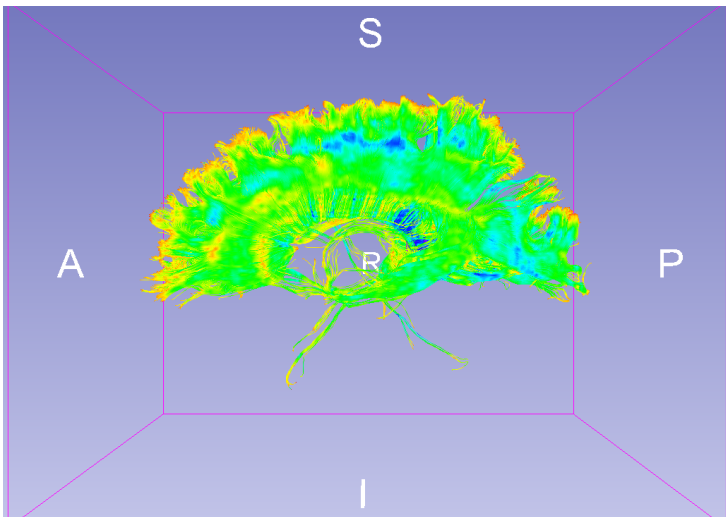
Label 4



Single Label Selection

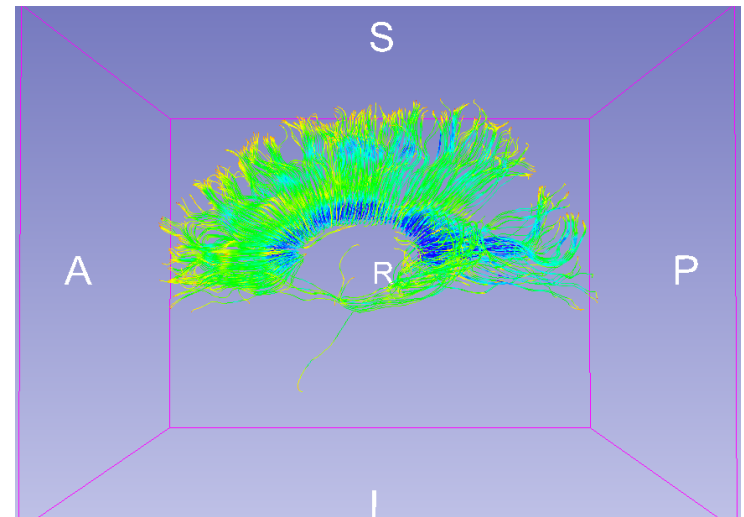
Notice that whole brain seeding creates a denser fiber bundle than seeding from the label 1.

Fiber Bundle Selection of Label 1
from the Whole Brain Tractography



V.S.

Fiber Bundle Obtained by
Seeding within Label 1



By viewing **corpusCallosum**
loaded in the MRML file

Multiple Labels Selection

FiberBundleLabelSelect allows users to perform multiple labels selection by providing a list of labels and selecting one logical operation:

- **OR**: fiber bundles that pass through **any label** in the list
- **AND**: fiber bundles that pass through **all labels** in the list

▼ Label regions definition

Labels to include

Combine include labels OR AND

Labels to exclude

Combine exclude labels AND

And or Or logical operation used to combine include labels

Multiple Labels Selection (AND)

3D Slicer 4.5.0-1

Modules: FiberBundleLabelSelect

Parameter set: FiberBundleLabelSelect

Input Label Map: fa-label

Input Fiber Bundle: whole_brain_tractography

Output Fiber Bundle: bundle_labels2AND3_include

Label regions definition

Labels to include: 2,3

Combine include labels: OR AND

Labels to exclude:

Combine exclude labels: OR AND

Status: Completed 100%

Restore Defaults AutoRun Cancel Apply

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

Show Zoomed Slice

L F B

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

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

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

5 cm 5 cm 5 cm

S

P

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

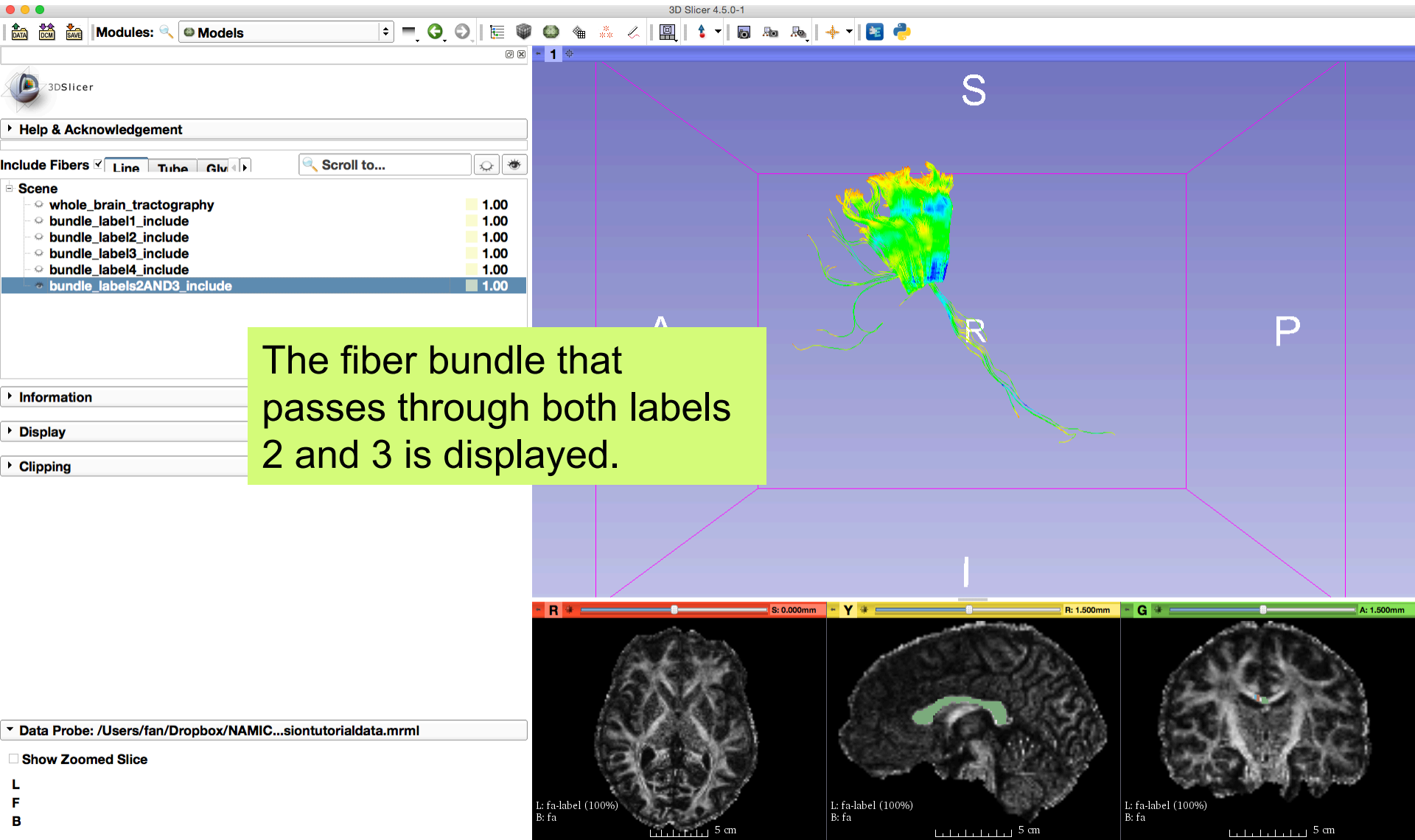
Set the FiberBundleLabelSelection parameters:

- 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:

- 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

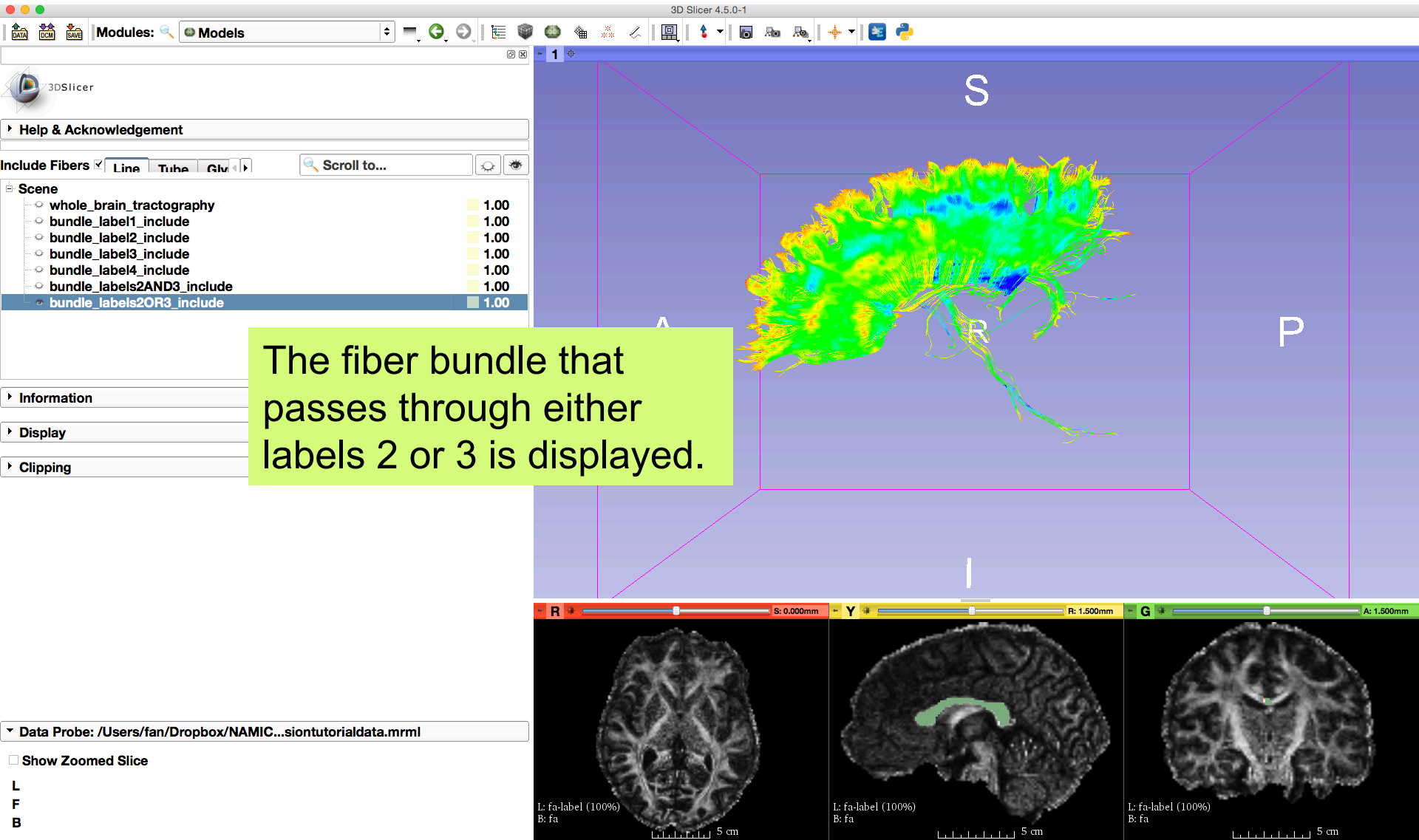
The 3D view shows a brain model with fiber bundles. A yellow box highlights the text: "Repeat the above steps to select the fiber bundle that passes through labels 2 or 3 and obtain the selection result of `bundle_labels2OR3_include`".

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".

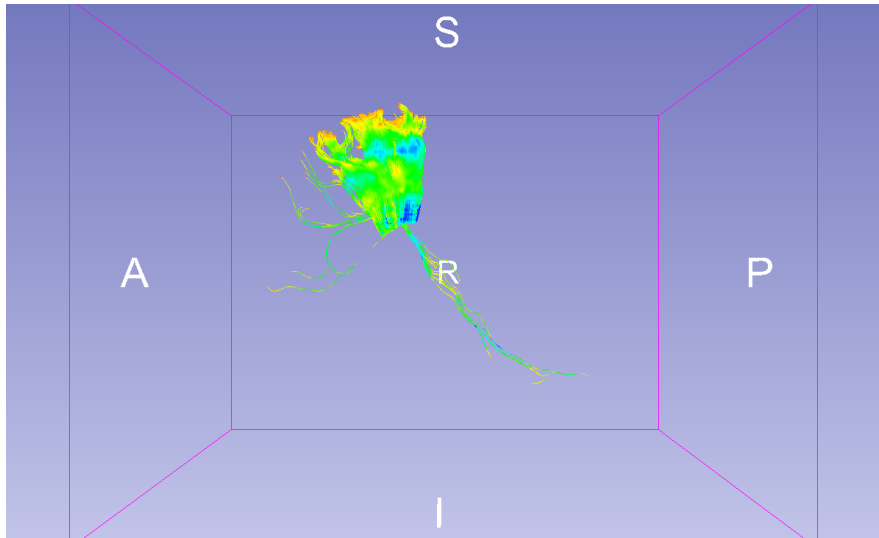
The bottom right shows three axial slices of the brain with fiber bundles. The left slice is labeled "L: fa-label (100%) B: fa". The middle slice is labeled "L: fa-label (100%) B: fa". The right slice is labeled "L: fa-label (100%) B: fa".

Multiple Labels Selection (OR)

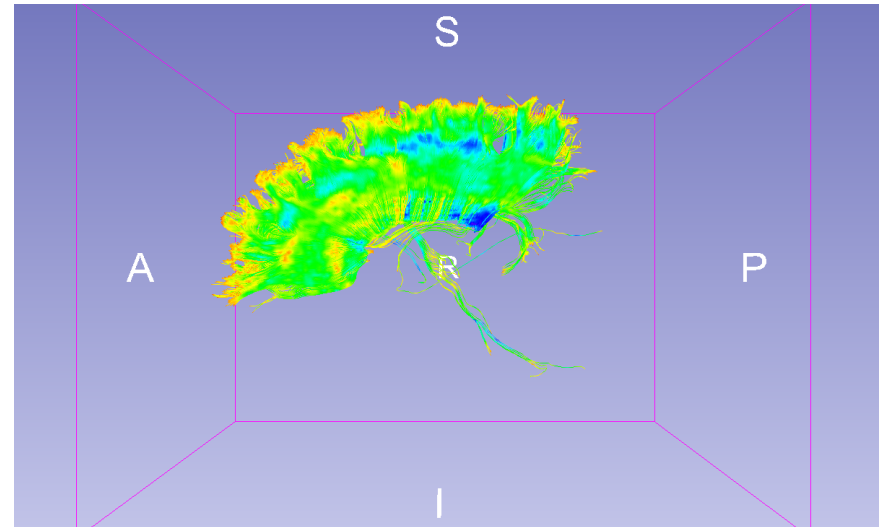


Multiple Labels Selection

Labels 2 and 3



Labels 2 or 3



Save Fiber Bundles

3D Slicer 4.5.0-1

Modules: Models

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**

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

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

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

5 cm 10 mm 10 mm

Fiber Tract Scalar Measurements

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

Select the module Fiber Tract Scalar Measurements

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

Information

Display

Clipping

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

Show Zoomed Slice

L
F
B

5 cm
10 mm
10 mm

Fiber Tract Scalar Measurements

3D Slicer 4.5.0-1

Modules: Fiber Tract Scalar Measurements

3DSlicer

Help & Acknowledgement

Fiber Tract Scalar Measurements

Parameter set: Fiber Tract Scalar Measurements

IO

Select Input Type Fibers_Hierarchy Fibers_File_Folder

Fibers Hierarchy Select a ModelHierarchy

Fibers File Folder /Users/fan/Desktop/fiberbundles

Output Text File esktop/fiberbundles/measurements.csv

Select Output Format Row_Hierarchy Column_Hierarchy

Output Field Separator Comma Space Tab

Status: Idle

Restore Defaults AutoRun

Cancel Apply

Data Probe

Show Zoomed Slice

L
F
B

5 cm 5 cm 5 cm

Set the FiberTractScalarMeasurements parameters:

- Select Input Type: **Fibers_File_Folder**
- Fibers File Folder: **XXX/fiberbundles**
- Output Text File: **XXX/fiberbundles/measurements.csv**
- Select Output Format: **Column_Hierarchy**
- Output Field Separator: **Tab**

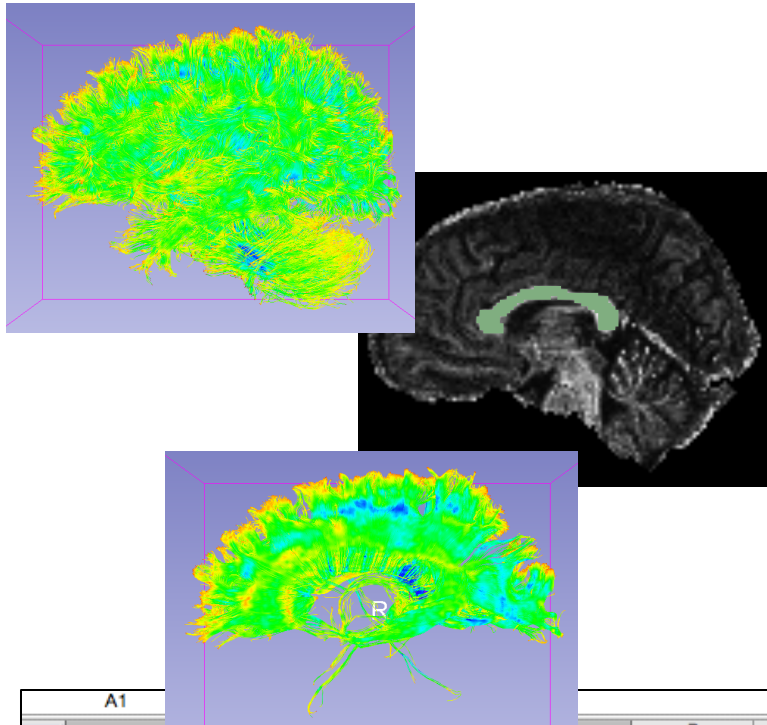
Click the button **Apply**

Fiber Tract Scalar Measurements

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

	A	B	C	D	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



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Cancer Research**

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