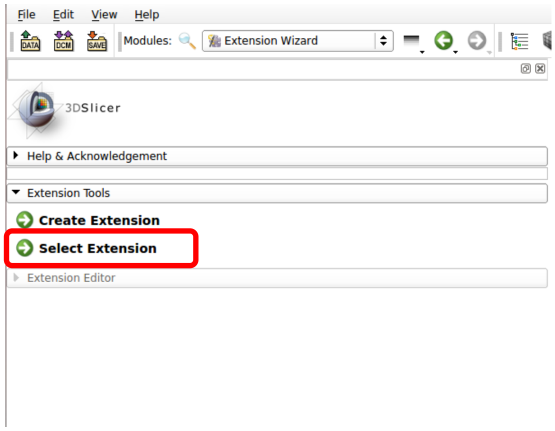
Introduction

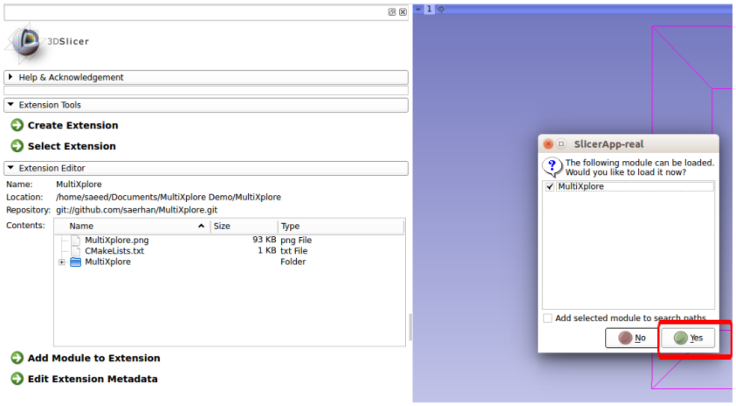
This document provides a step by step guide on how to properly load and run MultiXplore. Please refer to the journal paper for more conceptual discussions. If this package is used in part of your research projects with tangible results, please cite the journal paper.

Installation

In order to add the module, download the source code from NITRC and unzip it on your computer. Then, on the 3D Slicer, browse to the “Extension Wizard” module:



After clicking on “Select Extension” browse to the unzipped MultiXplore folder and select it. Upon feeding the right folder (MultiXplore_X.X/MultiXplore) this screen will appear:



Name: MultiXplore
Location: /home/saeed/Documents/MultiXplore Demo/MultiXplore
Repository: git://github.com/saerhan/MultiXplore.git
Contents:

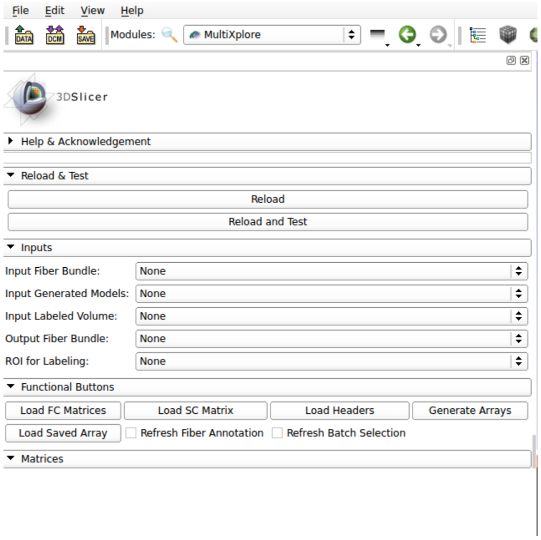
Name	Size	Type
MultiXplore.png	93 KB	png File
CMakeLists.txt	1 KB	txt File
MultiXplore		Folder

The following module can be loaded.
Would you like to load it now?

☑ MultiXplore

☐ Add selected module to search paths

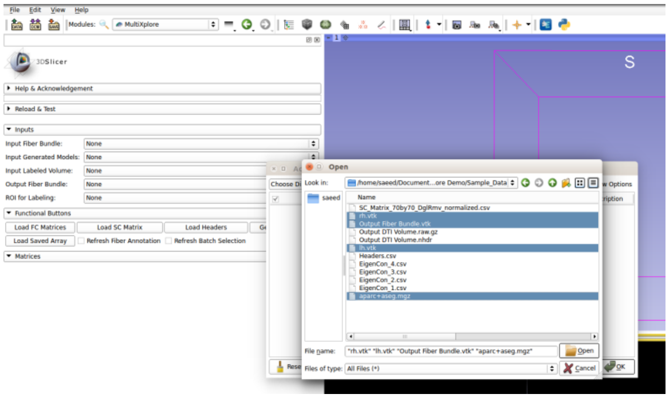
If you select “Yes” MultiXplore will be loaded to the 3D Slicer and can be found in module’s panel by browsing through (Example\MultiXplore):



Input Fiber Bundle: None
Input Generated Models: None
Input Labeled Volume: None
Output Fiber Bundle: None
ROI for Labeling: None

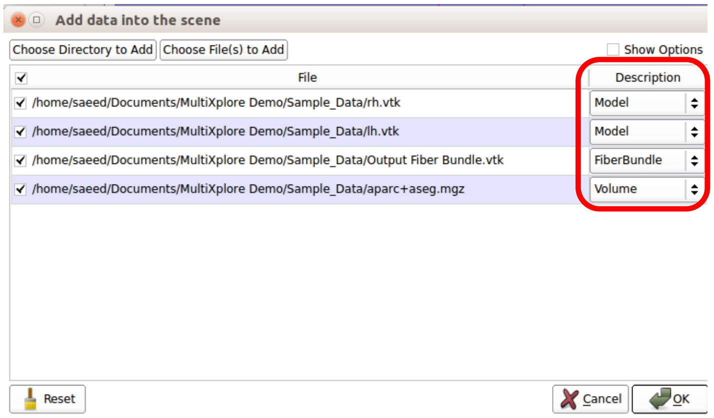
Loading Data

Next step would be loading ordinary imaging data into 3D Slicer. If you download Sample Data from the NITRC, you can follow the next steps easily using that. First, load fiber bundle, surface models and atlas parcellated brain volume using “Data” icon in 3D Slicer:



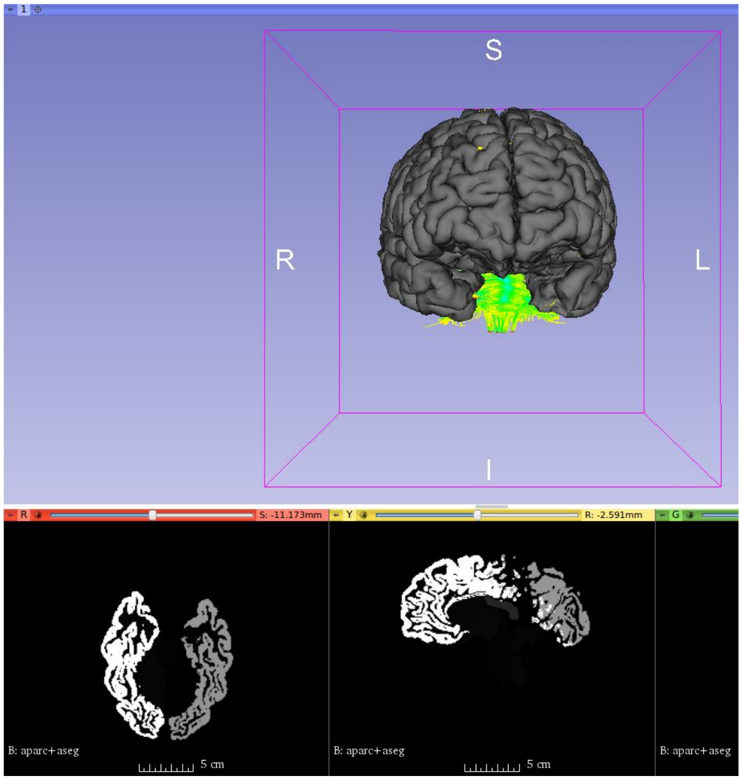
File name: "rh.vtk" "lh.vtk" "Output Fiber Bundle.vtk" "aparc+aseg.mgz"
Files of type: All Files (*)

And set “Description” as follows:

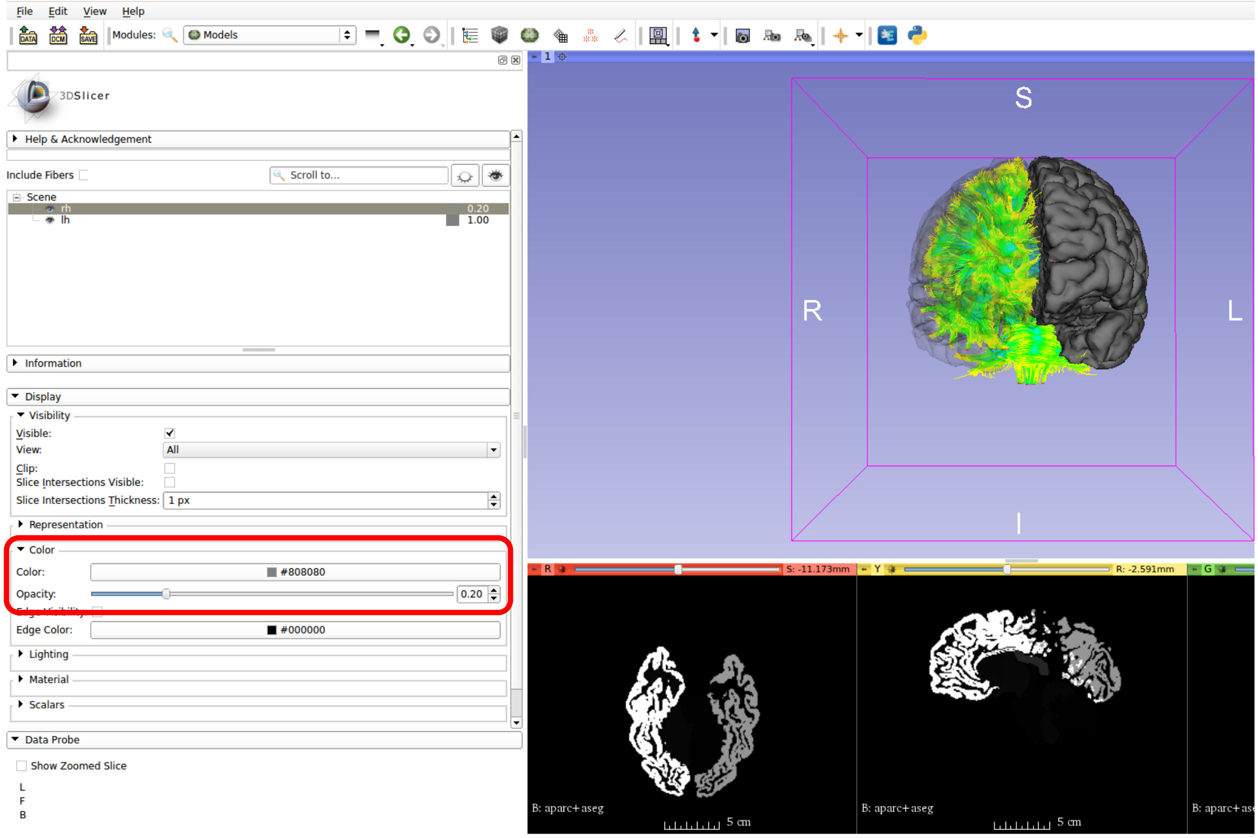


☑ File	Description
☑ /home/saeed/Documents/MultiXplore Demo/Sample_Data/rh.vtk	Model
☑ /home/saeed/Documents/MultiXplore Demo/Sample_Data/lh.vtk	Model
☑ /home/saeed/Documents/MultiXplore Demo/Sample_Data/Output Fiber Bundle.vtk	FiberBundle
☑ /home/saeed/Documents/MultiXplore Demo/Sample_Data/aparc+aseg.mgz	Volume

Normally, loaded data will immediately show up on the 2D or 3D view:



Opacity of the surface models can be lowered to see-through them:



Visible: ☑

View: All

Clip: ☐

Slice Intersections Visible: ☐

Slice Intersections Thickness: 1 px

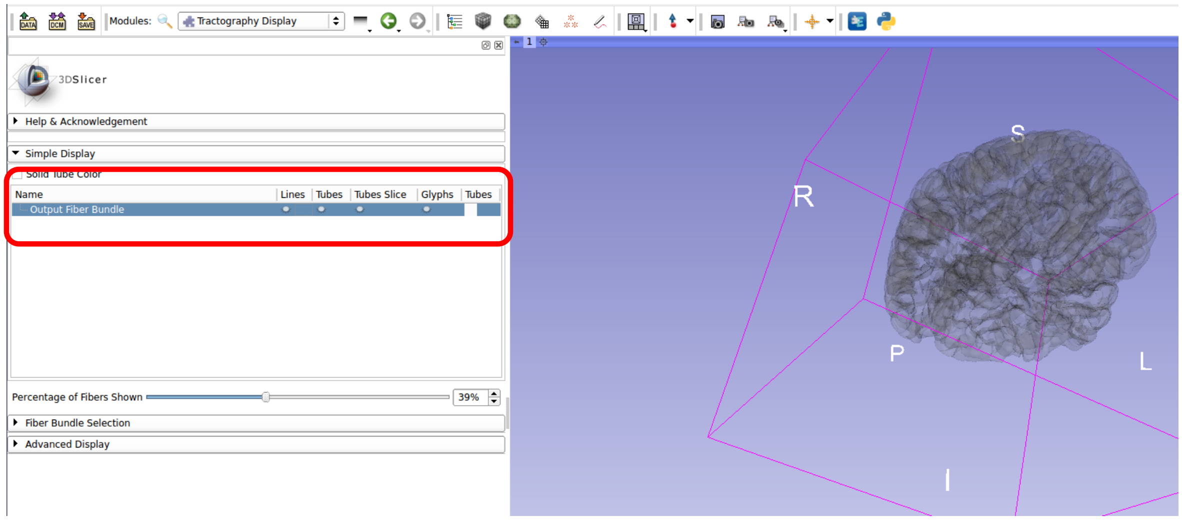
Color: #808080

Opacity: 0.20

Edge Visibility: ☐

Edge Color: #000000

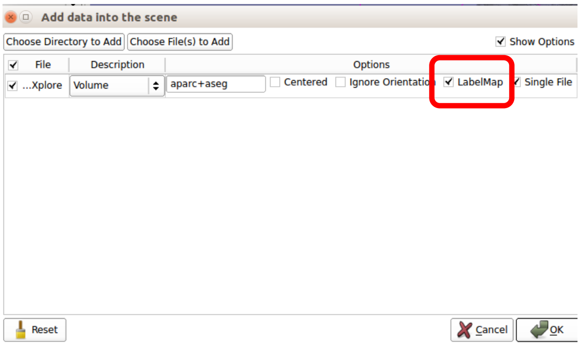
Hereafter, main fiber bundle can be hidden:



Percentage of Fibers Shown 39%

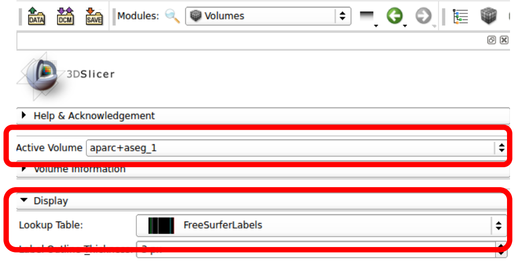
Creating Regional Models

For the purpose of the purpose of the making regional models, we have to load volumetric brain atlas one more time with a different import option (LabelMap activated):



☑ File	Description	Options				
☑ ...Xplore	Volume	aparc+aseg	☐ Centered	☐ Ignore Orientatio	☑ LabelMap	☑ Single File

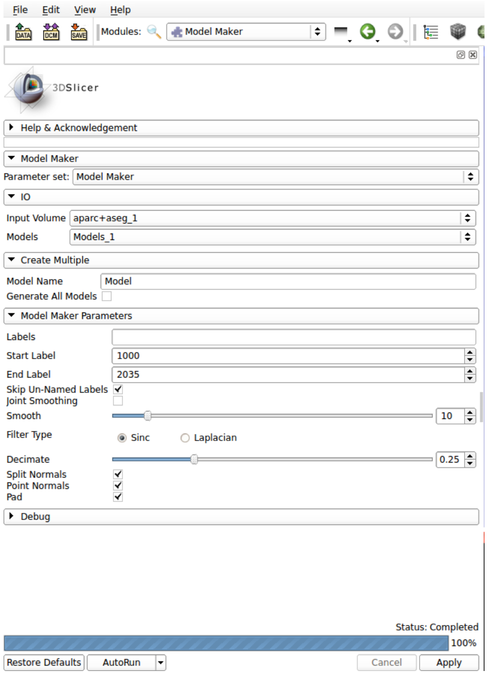
This option enables to assign a discrete "Lookup Table" to the labeled volume:



Active Volume: aparc+aseg_1

Lookup Table: FreeSurferLabels

And create separate surface models for the atlas ROIs:



Parameter set: Model Maker

Input Volume: aparc+aseg_1

Models: Models_1

Model Name: Model

Generate All Models ☐

Labels:

Start Label: 1000

End Label: 2035

Skip Un-Named Labels ☑

Joint Smoothing ☐

Smooth: 10

Filter Type: ● Sinc ○ Laplacian

Decimate: 0.25

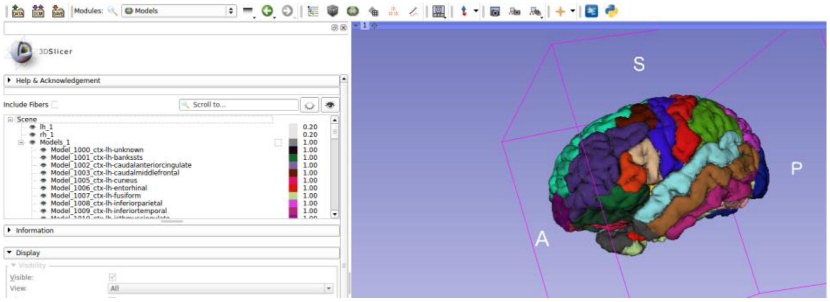
Split Normals ☑

Point Normals ☑

Pad ☑

Status: Completed

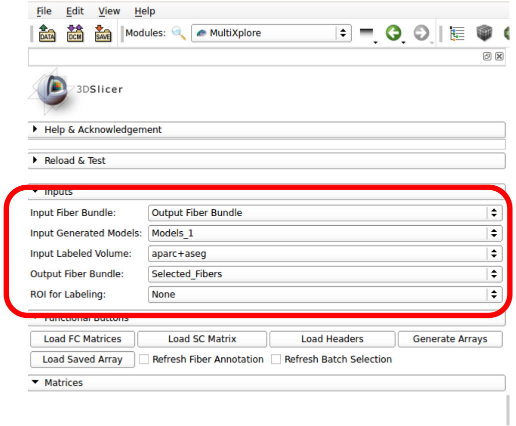
100%



Scene
lh_1 0.20
rh_1 0.20
Models_1 1.00
Model_1000_ctx-lh-unknown 1.00
Model_1001_ctx-lh-bankssts 1.00
Model_1002_ctx-lh-caudalanteriorcingulate 1.00
Model_1003_ctx-lh-caudalmiddlefrontal 1.00
Model_1005_ctx-lh-cuneus 1.00
Model_1006_ctx-lh-entorhinal 1.00
Model_1007_ctx-lh-fusiform 1.00
Model_1008_ctx-lh-inferiorparietal 1.00
Model_1009_ctx-lh-inferiortemporal 1.00

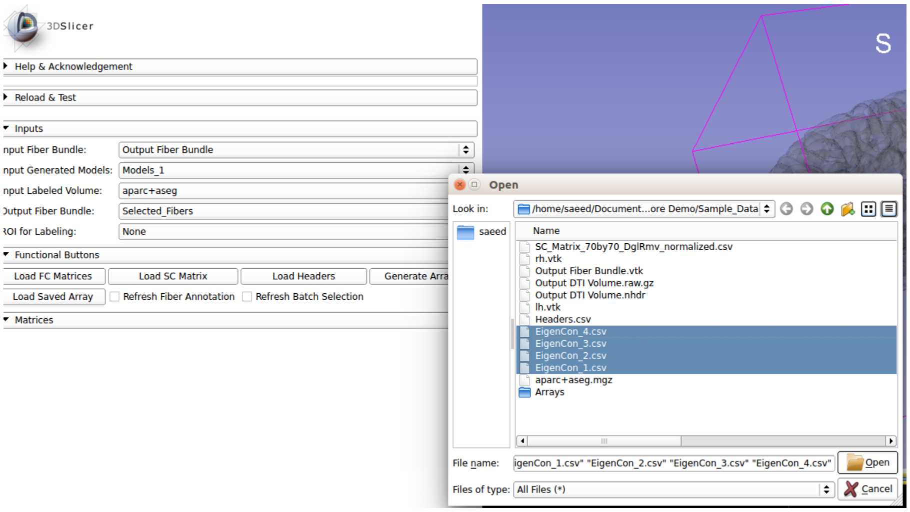
Input Specification

Once all of the necessary images are loaded to the 3D slicer, we can assign them to MultiXplore. “Output Fiber Bundle” needs to be created by using drop down box:



Input Fiber Bundle: Output Fiber Bundle
Input Generated Models: Models_1
Input Labeled Volume: aparc+aseg
Output Fiber Bundle: Selected_Fibers
ROI for Labeling: None

Connectivity matrices and Headers are next to be loaded into MultiXplore. Please note that all of the desired functional connectivity matrices should be loaded at once:



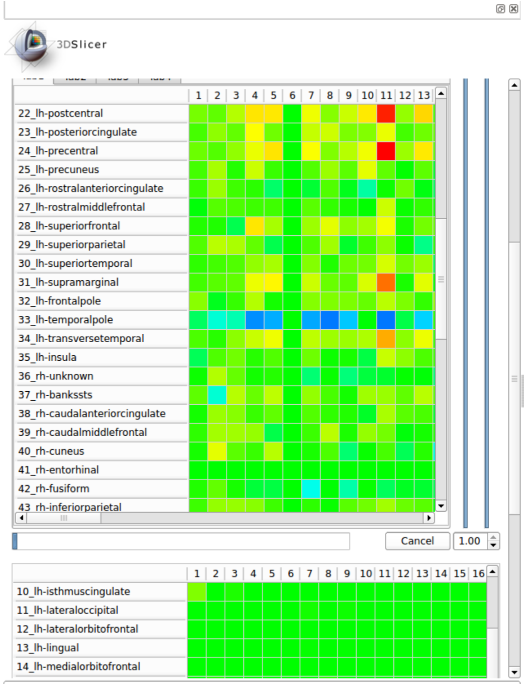
nput Fiber Bundle: Output Fiber Bundle
nput Generated Models: Models_1
nput Labeled Volume: aparc+aseg
Dutput Fiber Bundle: Selected_Fibers
ROI for Labeling: None

Look in: /home/saeed/Document...ore Demo/Sample_Data

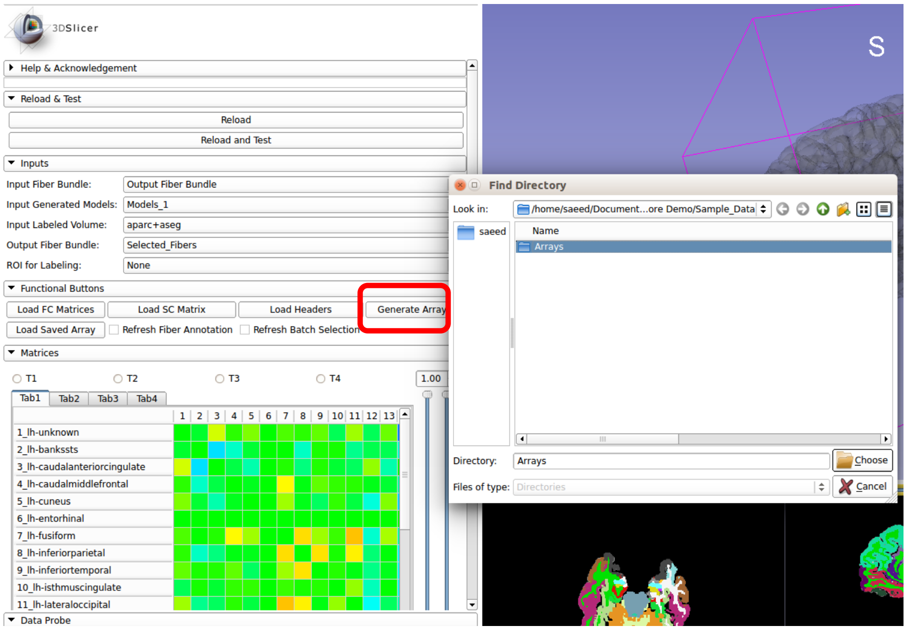
SC_Matrix_70by70_DglRmv_normalized.csv
rh.vtk
Output Fiber Bundle.vtk
Output DTI Volume.raw.gz
Output DTI Volume.nhdr
lh.vtk
Headers.csv
EigenCon_4.csv
EigenCon_3.csv
EigenCon_2.csv
EigenCon_1.csv
aparc+aseg.mgz
Arrays

File name: igenCon_1.csv" "EigenCon_2.csv" "EigenCon_3.csv" "EigenCon_4.csv"
Files of type: All Files (*)

And after loading matrices and header file, matrix panel looks like below:

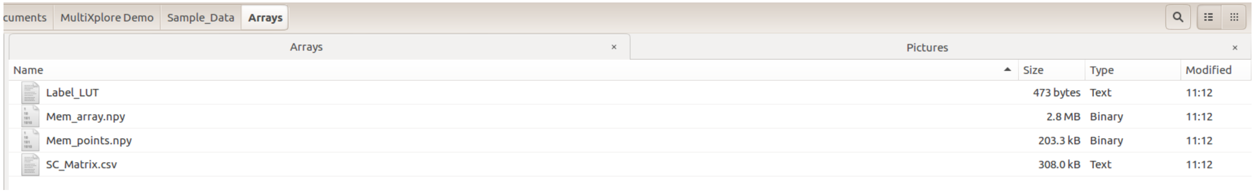


Also, after loading this, memory arrays can be generated (using “Generate Arrays”) and saved to the hard drive (Arrays). Please don’t try to do this before matrices; otherwise an error message will be issued in Slicer CLI.


Input Fiber Bundle: Output Fiber Bundle
Input Generated Models: Models_1
Input Labeled Volume: aparc+aseg
Output Fiber Bundle: Selected_Fibers
ROI for Labeling: None

Look in: /home/saeed/Document...ore Demo/Sample_Data
Directory: Arrays
Files of type: Directories

And after a bit of waiting, designated folder will look like this:

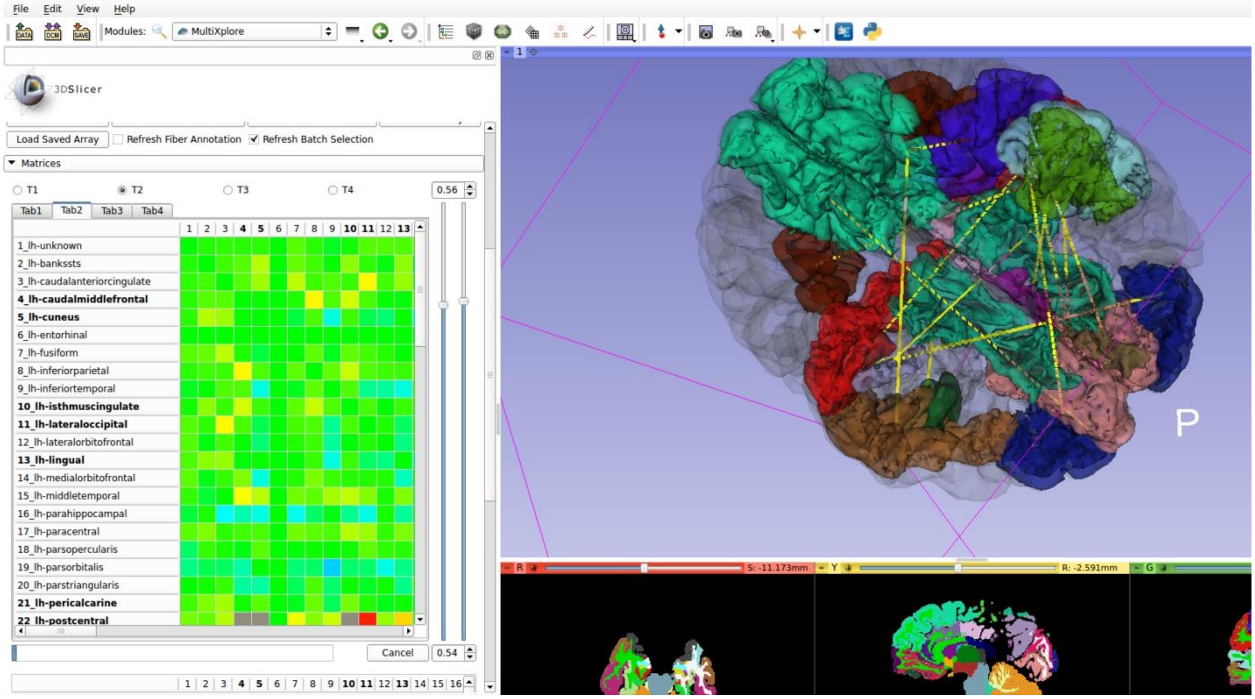


Name	Size	Type	Modified
Label_LUT	473 bytes	Text	11:12
Mem_array.npy	2.8 MB	Binary	11:12
Mem_points.npy	203.3 kB	Binary	11:12
SC_Matrix.csv	308.0 kB	Text	11:12

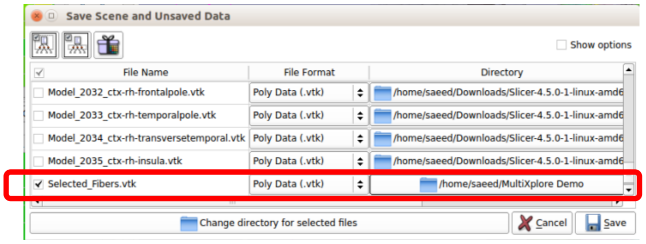
If user decides to load memory arrays from the hard drive, that also is doable using “Load Saved Array” and specifying the directory which arrays are saved to.

Selections and Fiber Annotation

In order to do batch selection, adjust the boundaries using slicer bars or spin boxes, hit the “Refresh Batch Selection” button and wait. You can monitor the changes through Slicer CLI.

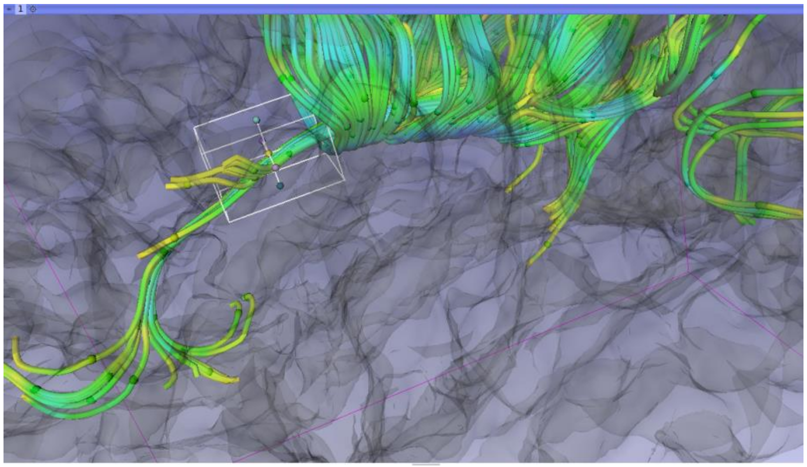


If you decide to save the generated fiber bundle you can easily do it through “Save” button in Slicer and choosing to save the “Selected_Fibers.vtk”:

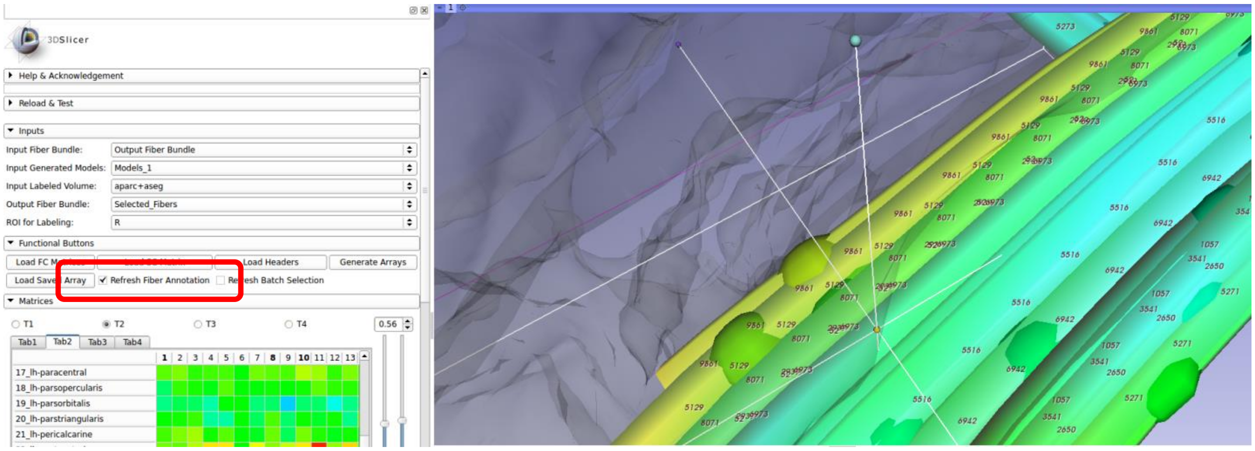


File Name	File Format	Directory
☐ Model_2032_ctx-rh-frontalpole.vtk	Poly Data (.vtk)	/home/saeed/Downloads/Slicer-4.5.0-1-linux-amd6
☐ Model_2033_ctx-rh-temporalpole.vtk	Poly Data (.vtk)	/home/saeed/Downloads/Slicer-4.5.0-1-linux-amd6
☐ Model_2034_ctx-rh-transversetemporal.vtk	Poly Data (.vtk)	/home/saeed/Downloads/Slicer-4.5.0-1-linux-amd6
☐ Model_2035_ctx-rh-insula.vtk	Poly Data (.vtk)	/home/saeed/Downloads/Slicer-4.5.0-1-linux-amd6
☑ Selected_Fibers.vtk	Poly Data (.vtk)	/home/saeed/MultiXplore Demo

Procedure for labeling the fibers is very straightforward. An ROI marker should be added to the 3D scene from Fiducial dialog of the 3D Slicer and adjusted properly to encapsulate desired portion of fibers:



After this, by clicking “Refresh Fiber Annotation”, fiber labels get updated:

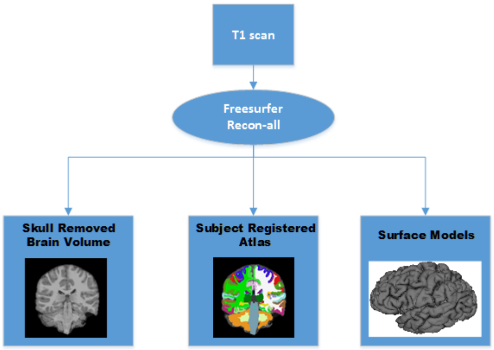


Input Fiber Bundle: Output Fiber Bundle
Input Generated Models: Models_1
Input Labeled Volume: aparc+aseg
Output Fiber Bundle: Selected_Fibers
ROI for Labeling: R

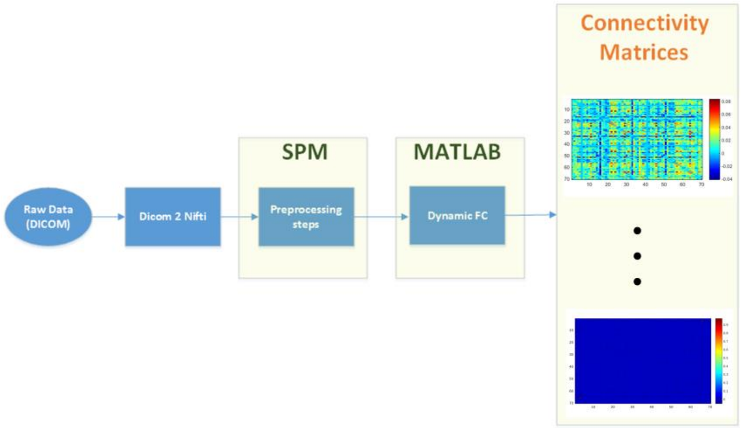
Raw Data Preparation Pipelines

Below are software pipelines that are used to prepare the sample data:

For T1 anatomical scan:



For fMRI:



For DWI: