Slicer3 Training Tutorial Clustering of Fiber Tracts
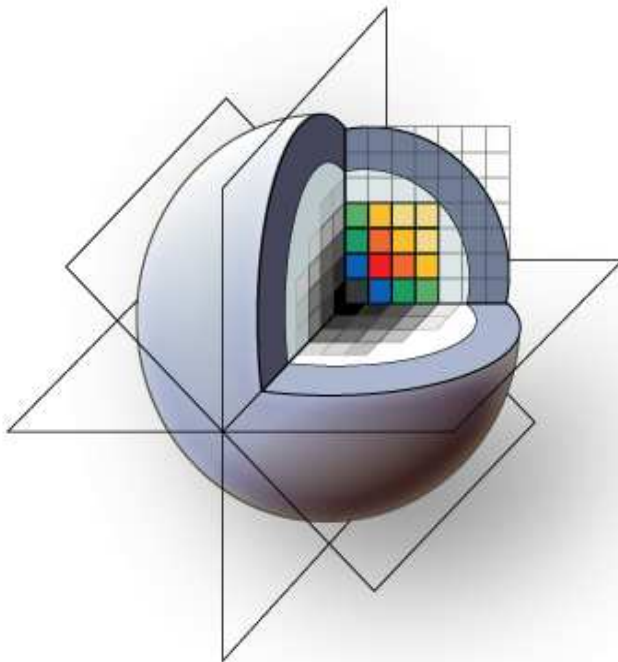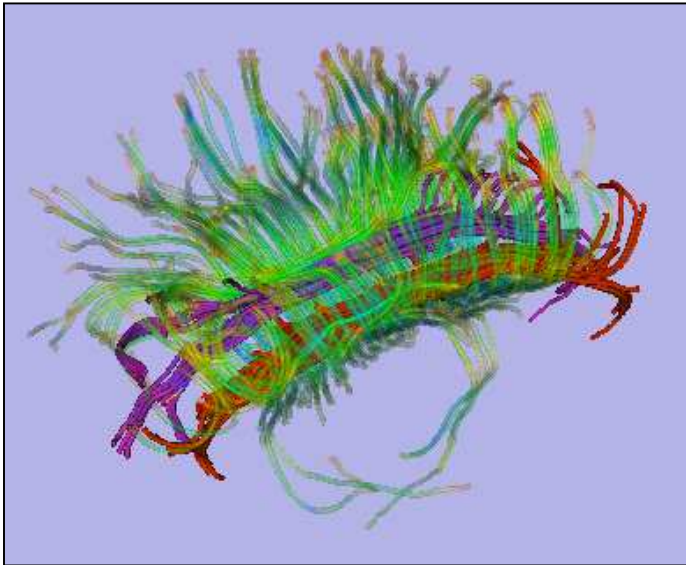
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GE Research

3DSlicer

Guiding you step by step through the process of clustering of fiber bundles from diffusion MRI.

Prerequisites

This tutorial assumes that you have already completed the tutorial **Data Loading and Visualization**. Also, the tutorial, **Processing of Diffusion Weighted Imaging and Diffusion Tensor Imaging data in Slicer3**, is highly recommended.

Tutorials for **Slicer3** are available at the following location:

- http://www.na-mic.org/Wiki/index.php/Slicer3.2:Training

Materials

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This tutorial requires the installation of the **Slicer3** software and the tutorial dataset. They are available at the following locations:

• **Slicer3** download page

http://www.slicer.org/pages/Downloads/

Note: download the latest file from Nightly Builds

• Tutorial dataset (tutorialData.zip)

http://www.nitrc.org/projects/quantitativedti/

Disclaimer: *It is the responsibility of the user of Slicer to comply with both the terms of the license and with the applicable laws, regulations, and rules.*

Overview

Introduction

- This module accepts as the input a set of fiber trajectories (3D curves) and a set of user specified initial centerlines. It groups the trajectories using an expectation-maximization algorithm and outputs the membership probabilities along with the updated cluster centers. It also outputs diffusion parameters along each trajectory with point correspondence to each cluster centerline to enable tract-oriented statistical analysis. Details of the algorithm are given in:

  M. Maddah, W. Eric L. Grimson, Simon K. Warfield, William M. Wells, "A unified framework for clustering and quantitative analysis of white matter fiber tracts," Medical Image Analysis, vol. 12, no. 2, pp. 191-202, 2008.
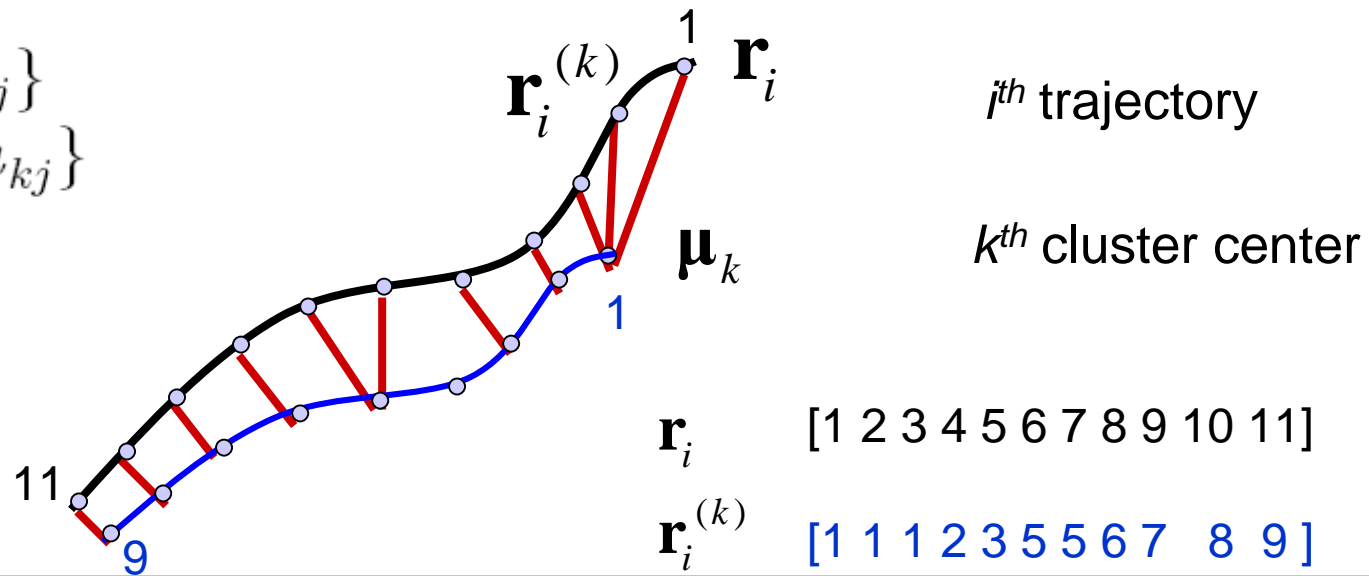
Technical Summary(1/4)

- Trajectories are sampled uniformly.
- A 3D curve is defined as the cluster center and is obtained by a weighted average of all of its corresponding points on the trajectories.
- A re-indexed version of each trajectory is built to reflect its point correspondence with each cluster center.

$$\mathbf{r}_i = \{\mathbf{r}_{ij}\}$$
$$\boldsymbol{\mu}_k = \{\boldsymbol{\mu}_{kj}\}$$

$\mathbf{r}_i^{(k)}$

$\mathbf{r}_i$

1

11

9

1

$\boldsymbol{\mu}_k$

i^{th} trajectory

k^{th} cluster center

$\mathbf{r}_i$ [1 2 3 4 5 6 7 8 9 10 11]

$\mathbf{r}_i^{(k)}$ [1 1 1 2 3 5 5 6 7   8 9]

Technical Summary (2/4)

- Trajectories are clustered based on their distance to each cluster center.

- Euclidean distance and point-correspondence are calculated efficiently by generating a distance map and a Voronoi diagram for each cluster center.

- A penalty term is added to the Euclidean distance to account for shape dissimilarity.

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- A Gamma mixture model is used to describe the clusters based on the distance between trajectories and cluster center ($\mathbf{d}_i = [d_{i1}...d_{iK}]$).

K: Number of clusters is defined by the user

$$p(\mathbf{d}_i|\Theta) = \sum_{k=1}^{K} w_k f_k(\mathbf{d}_i|\mathbf{g}_k)$$

Unknown mixing weights

Unknown parameters of Gamma distributions

$$f_k(\mathbf{d}_i|\mathbf{g}_k) = \text{Gamma}(d_{ik};\mathbf{g}_k) \prod_{j \neq k} \text{U}(d_{ij};0,d_0)$$

- The maximum likelihood estimation of unknown parameters are obtained through EM approach.

Technical Summary (4/4)

- In the expectation step, membership probability of each trajectory to each cluster is calculated; parameters are assumed to be known.

- In the maximization step the parameters of the mixture model are updated.

  Once the EM algorithm converges, cluster centers are updated. The procedure is repeated until convergence.

Module installation(1/5)

- **Select Extension Manager from View menu.**

Module installation(2/5)
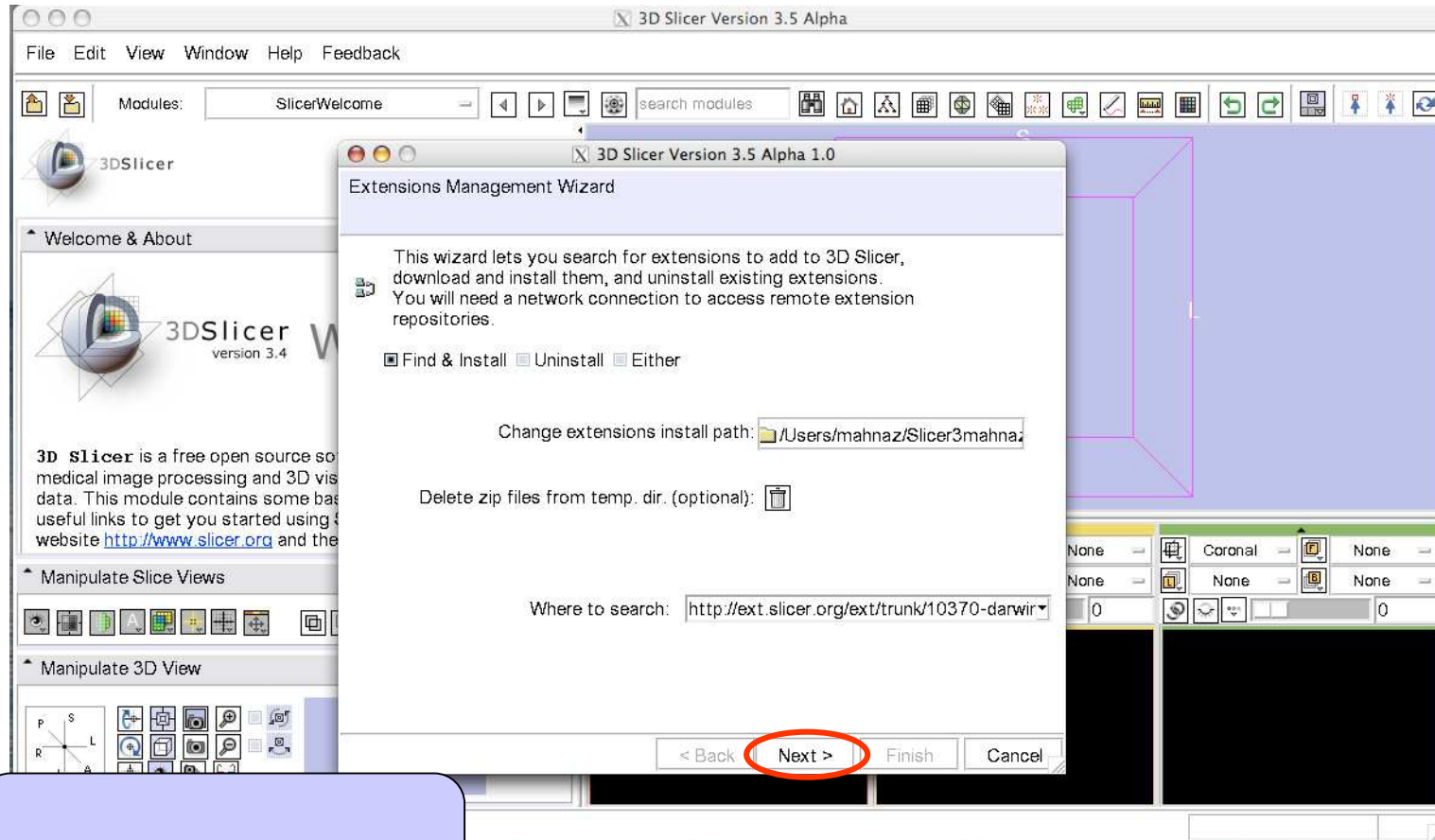
Select **Next**

Module installation(3/5)
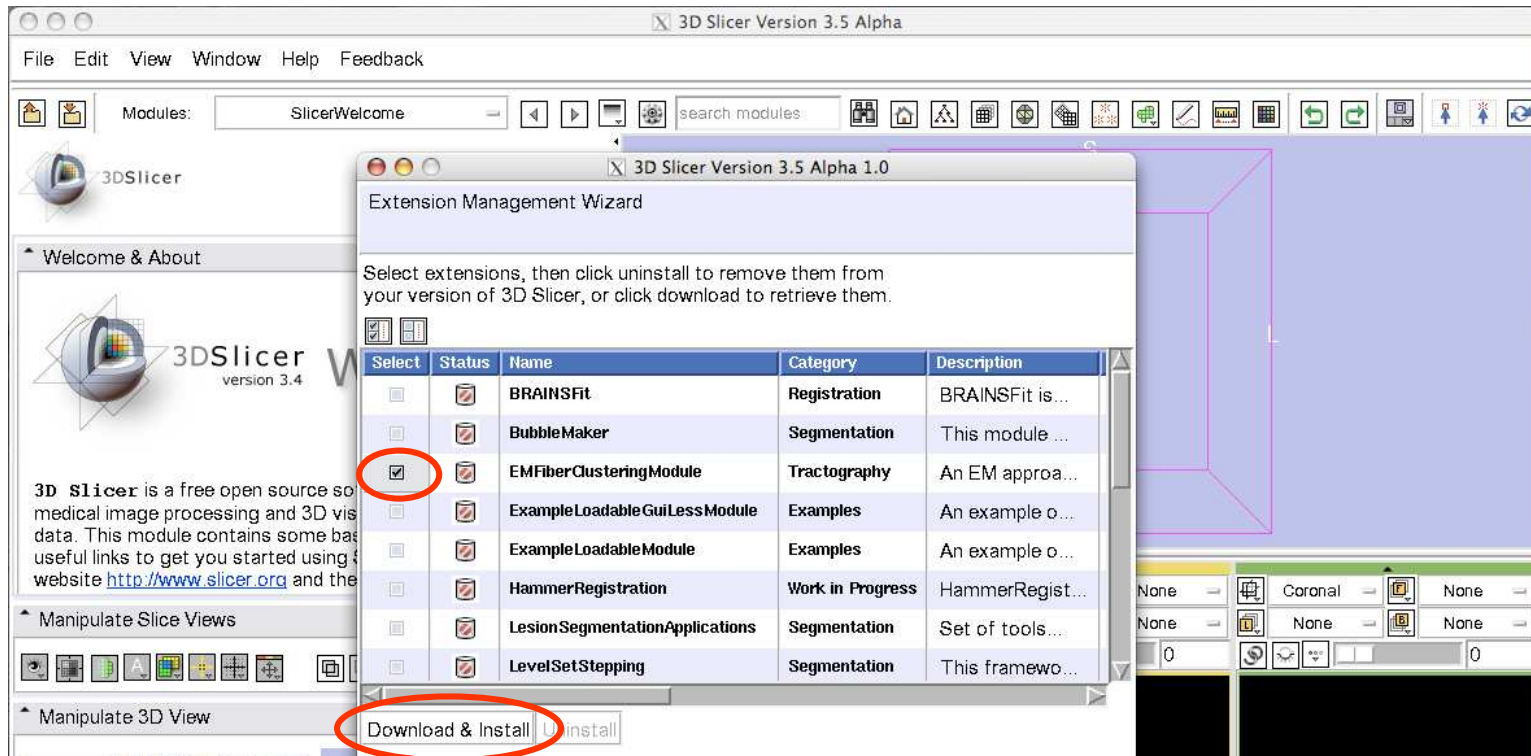
- **Select EMFiberClusteringModule** from the list.
- Apply **Download & Install.**

Module installation(4/5)

- **The module status turns green upon successful installation.**
- **Select Next.**

Module installation

- **You need to restart slicer to complete the installation**
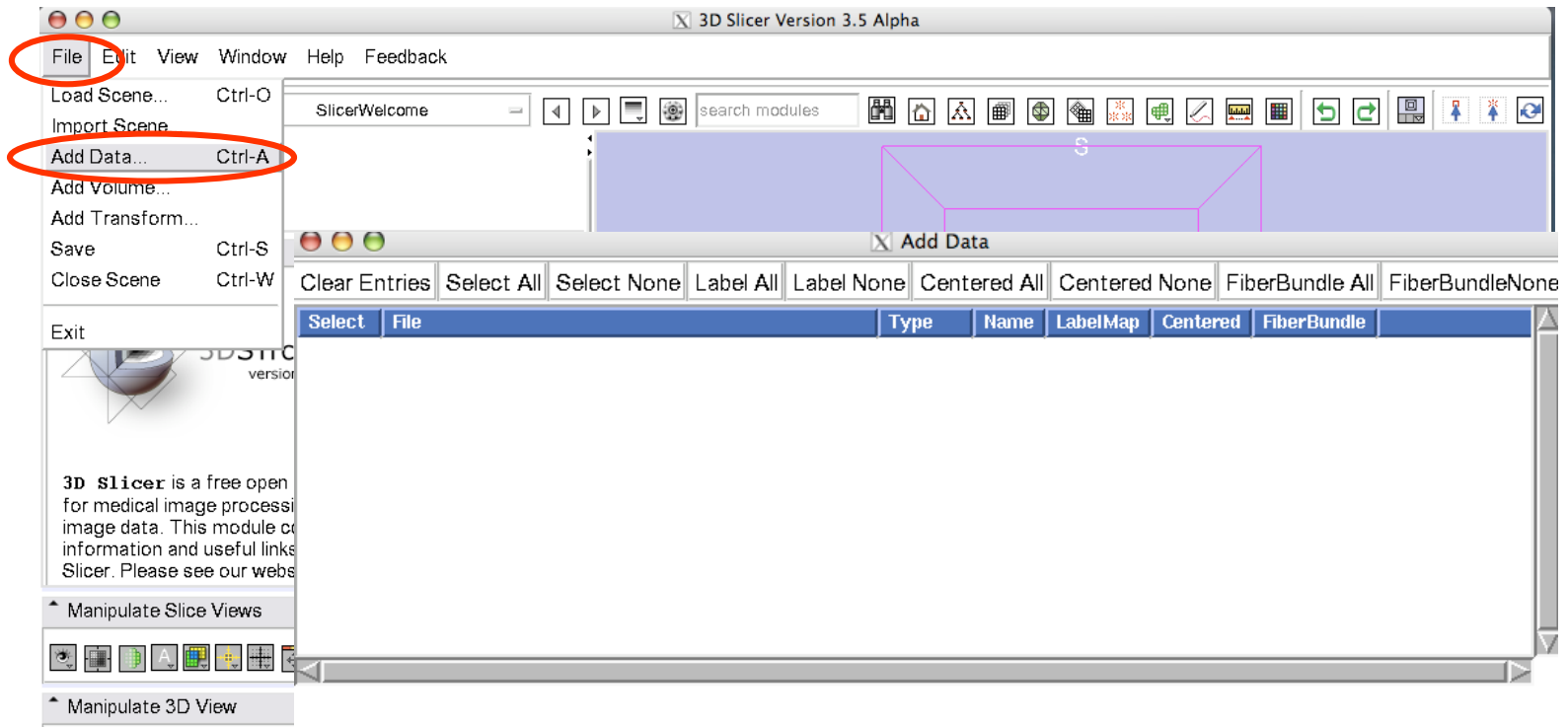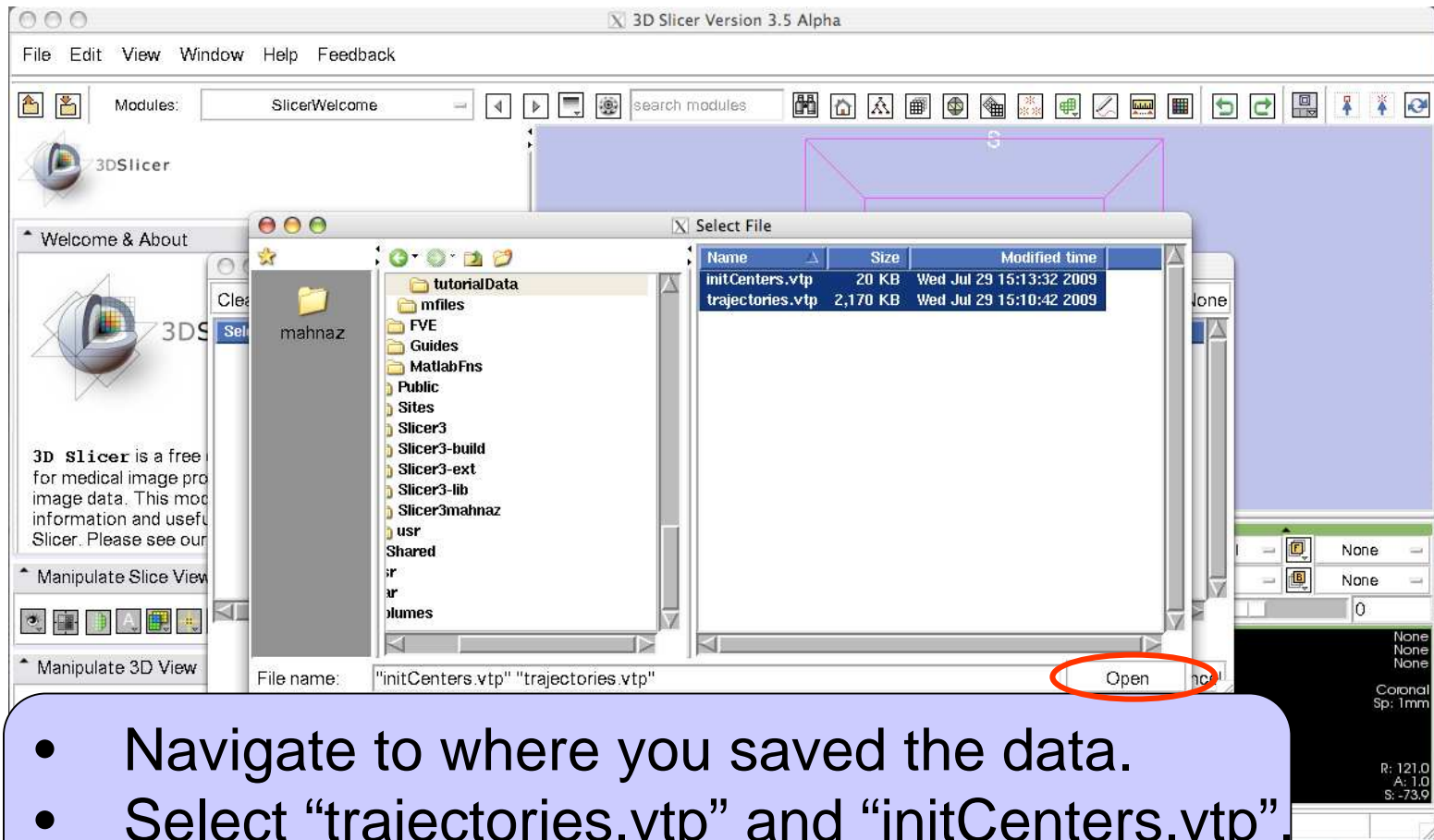
Loading data (1/3)

- Select **Add Data** from **File** menu.
- Select **AddFile(s).**
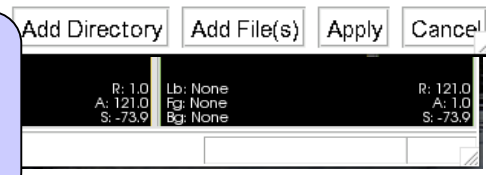
Loading data (2/3)

- Navigate to where you saved the data.
- Select "trajectories.vtp" and "initCenters.vtp".
- Select **Open.**

Loading data (3/3)

- Select **FiberBundle All.**
- Select **Apply.**
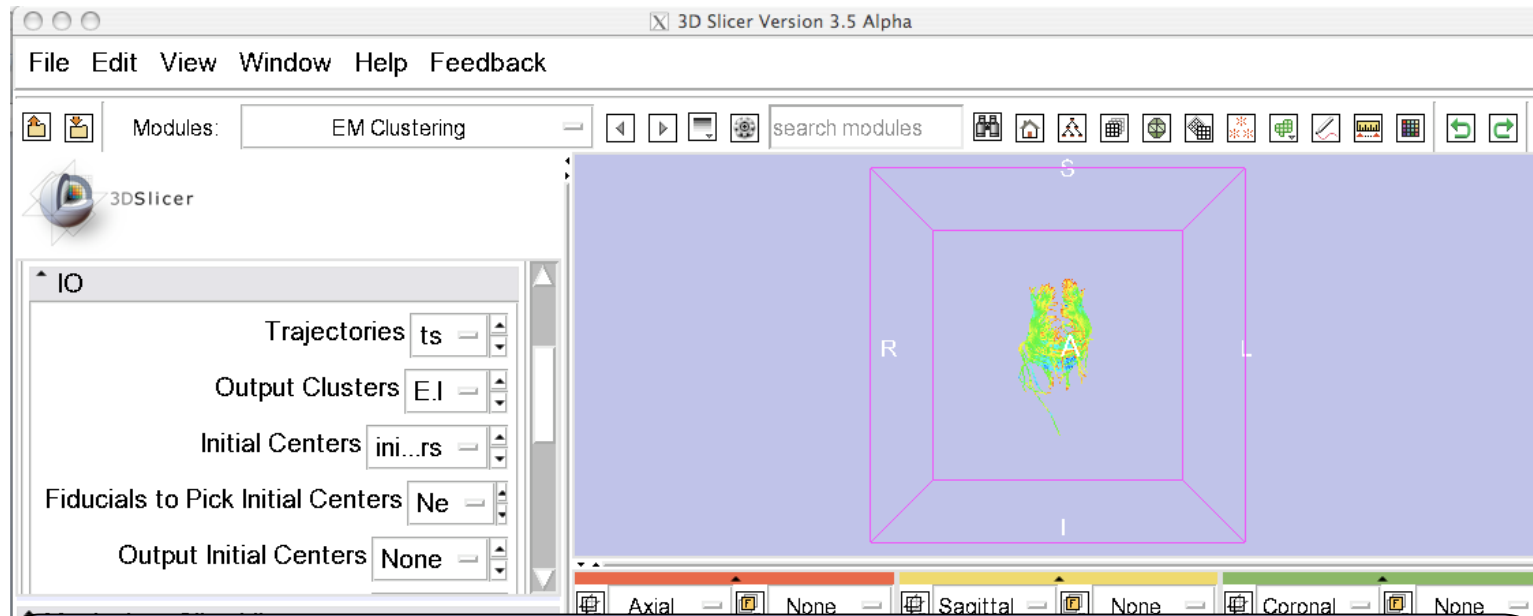
From the Modules, Select **Tractography** and then
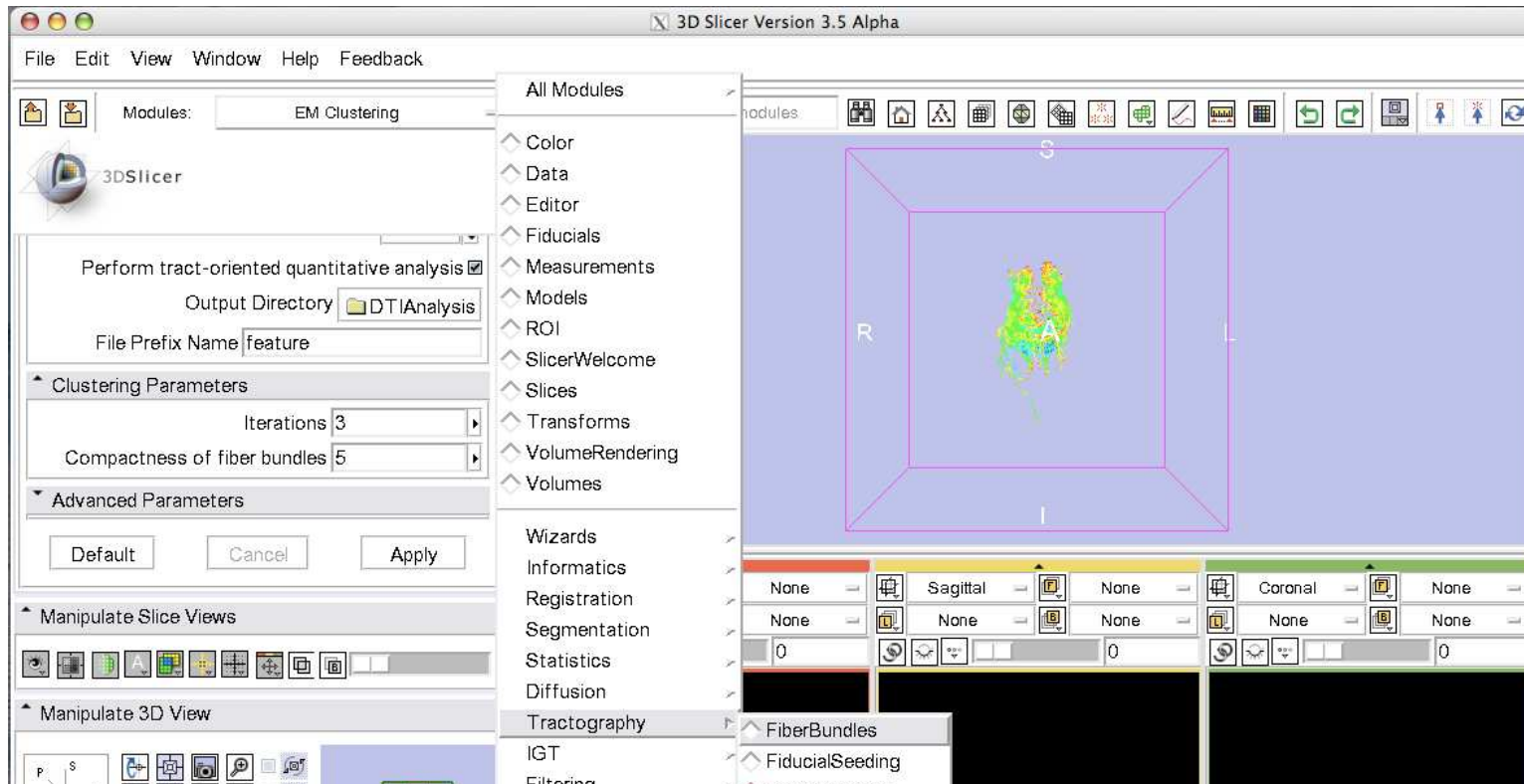**EM Clustering**.

EM Clustering (2/5)

- **Set the IO parameters:** Set the **Trajectories** to "trajectories.vtp", **Out Clusters** to "Create New Fiber Bundle", **Initial Centers** to "initialCenters.vtp", **Final Centers** to "Create New Fiber Bundle" and **Output Directory** to desired directory.

- Keep the default values for the rest of Parameters.
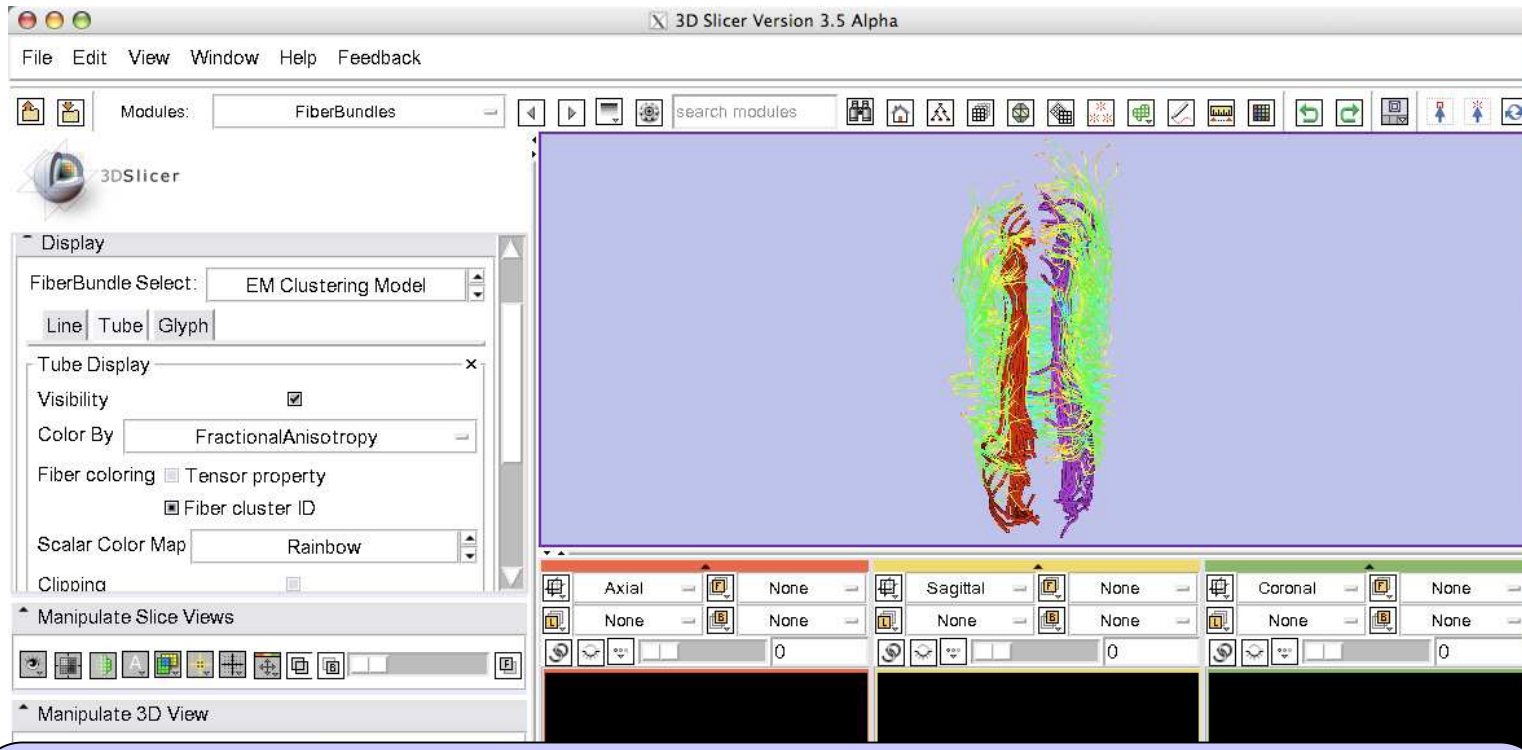
- Select **Apply**.

EM Clustering (3/5)

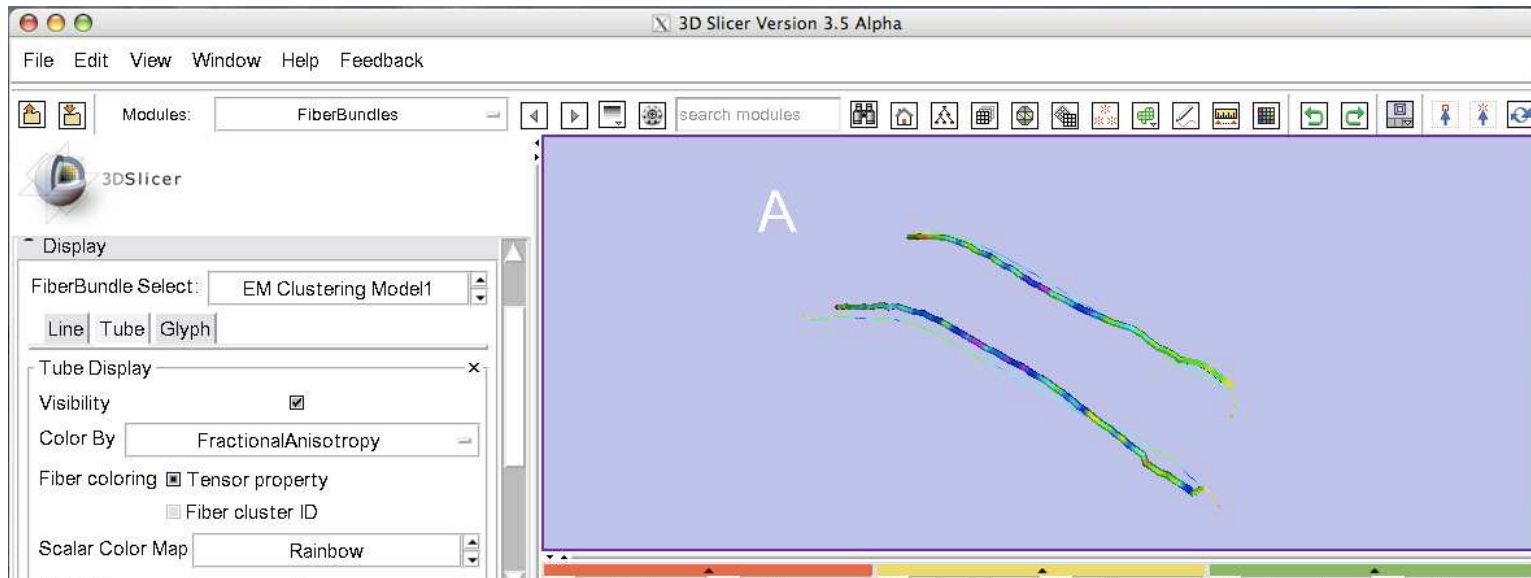- **When Clustering completed, go to FiberBundles module.**

EM Clustering (4/5)

- Select **EM Clustering Model** on **Display**
- Go to the **Tube** tab.
- Select **Fiber Cluster ID** for **Fiber coloring**.

- **Select EM Clustering Model1 on Display**
- Go to the **Tube** tab.
- Set the **Visibility** on.
  Make everything else invisible to see the final centers, colored by the mean FA.

Quantitative Analysis(1/2)

If you check marked

Perform tract-oriented quantitative analysis, in your specified **Output Directory**
you should have these files for each cluster X:
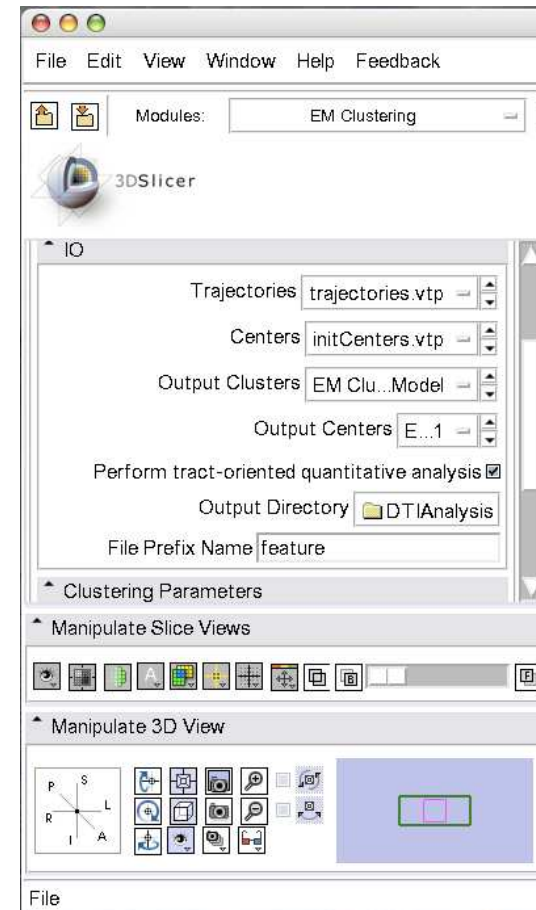
Cluster$X$.vtp

Center$X$.vtp

[**File Prefix**]_FA_cluster$X$.csv

[**File Prefix**]_MD_cluster$X$.csv

[**File Prefix**]_ParDiff_cluster$X$.csv

[**File Prefix**]_PerDiff_cluster$X$.csv
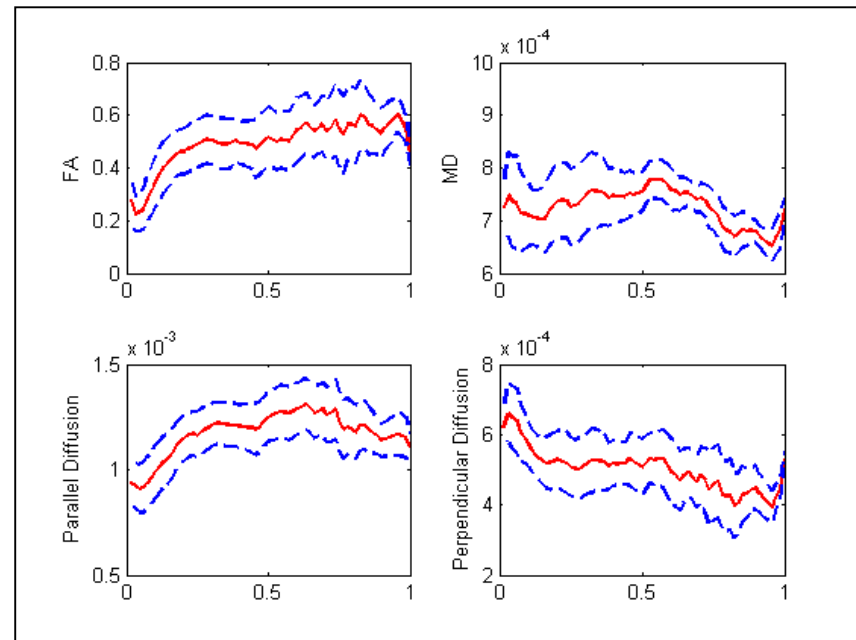
[**File Prefix**]_posterior$X$.csv

Quantitative Analysis(2/2)

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- On each CSV file, rows correspond to trajectories and columns correspond to a location along the bundle.
- -1 represents missing data.

You may use matlab scripts [here](#) to generate plots of diffusion parameters vs. normalized arg length for each cluster.
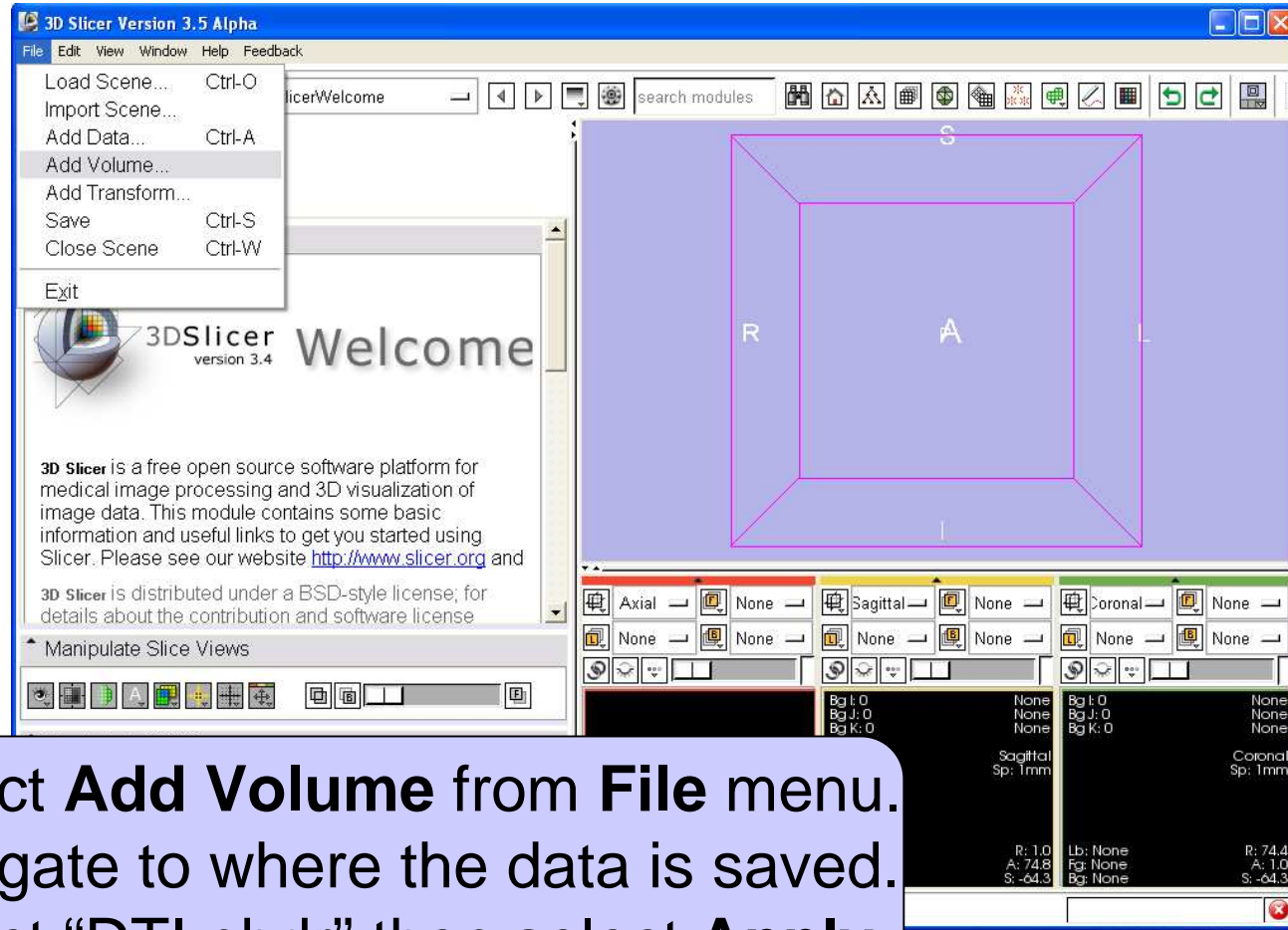
To work on your DTI data:

- Load your DT volume.
- Load/make your label image (ROI).
- Follow the next slides to do tractography and to create initial centers. Here, we use DTI.nhdr and FA-label.nhdr as our DTI and ROI volumes respectively.
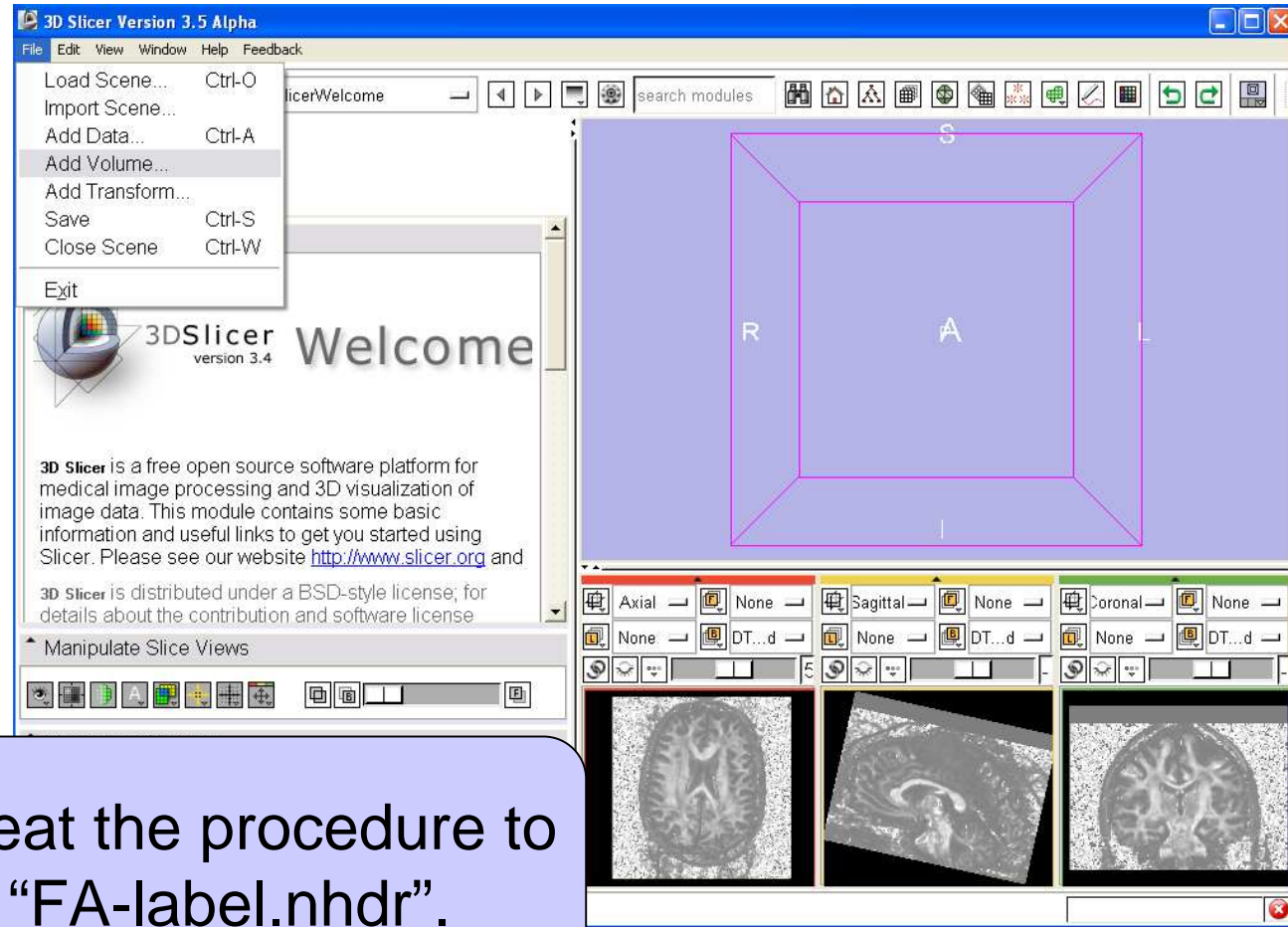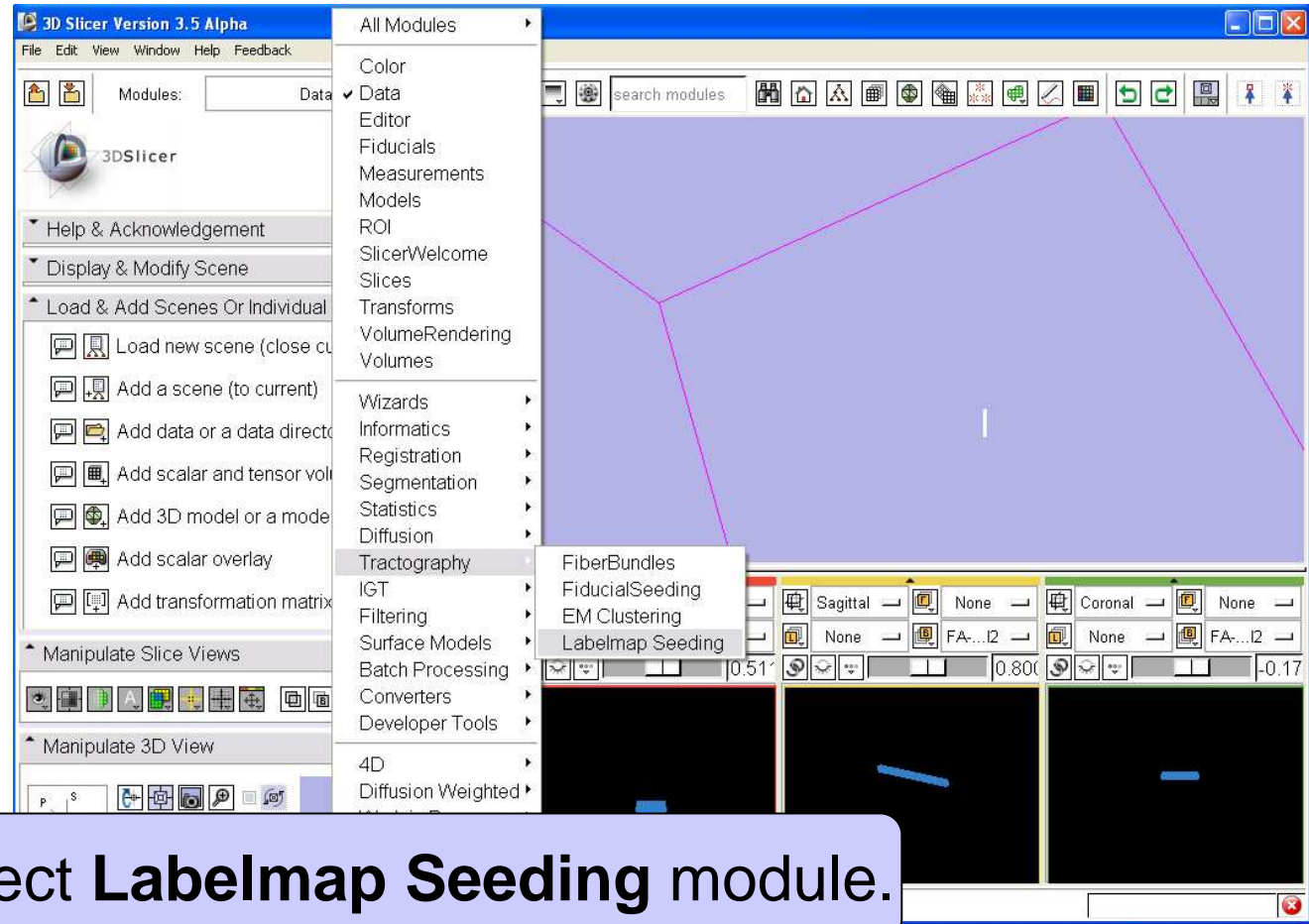
Loading DTI volume

- Select **Add Volume** from **File** menu.
- Navigate to where the data is saved.
- Select "DTI.nhdr" then select **Apply.**

Loading label map

- Repeat the procedure to load "FA-label.nhdr".
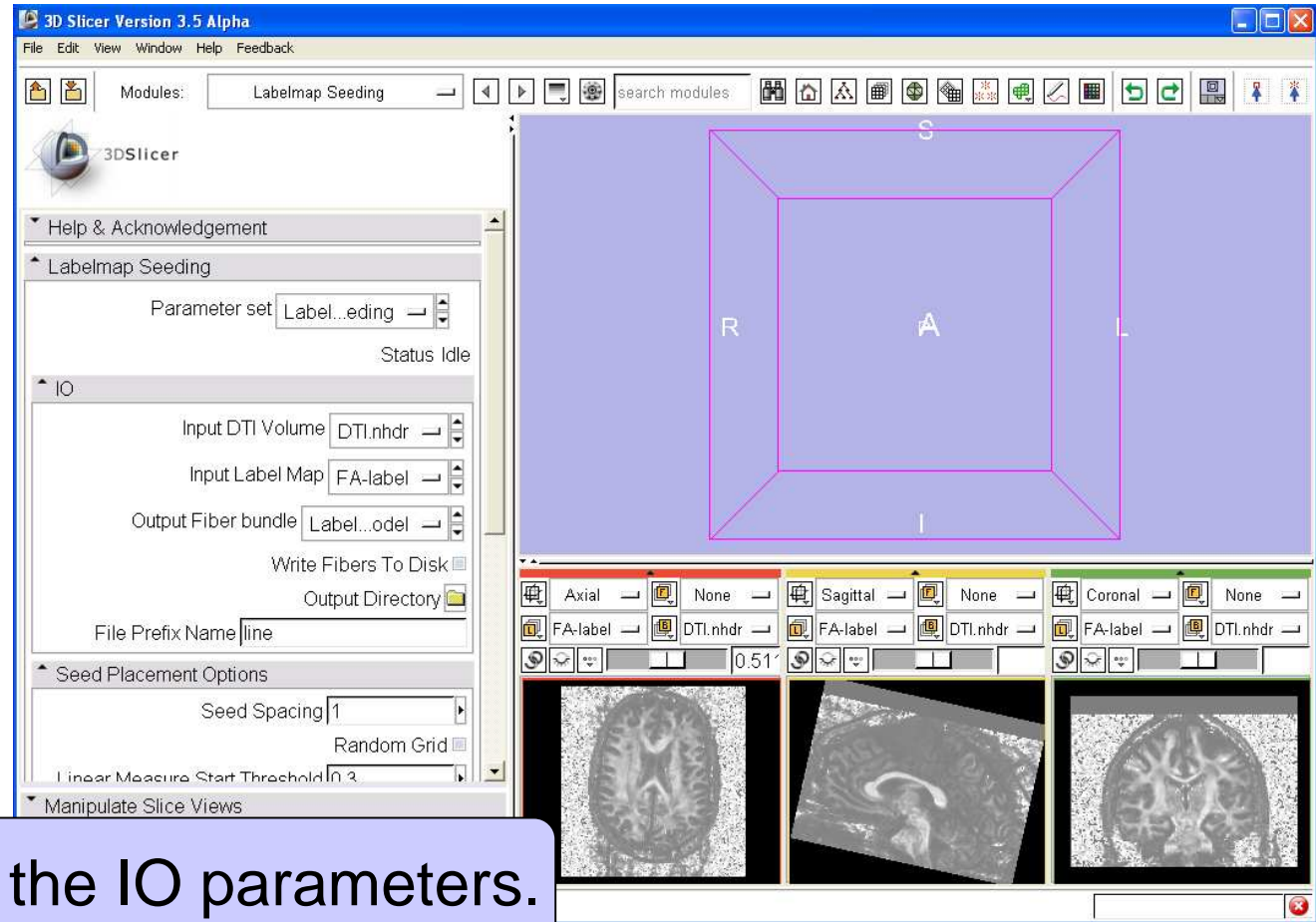
Tractography (1/4)
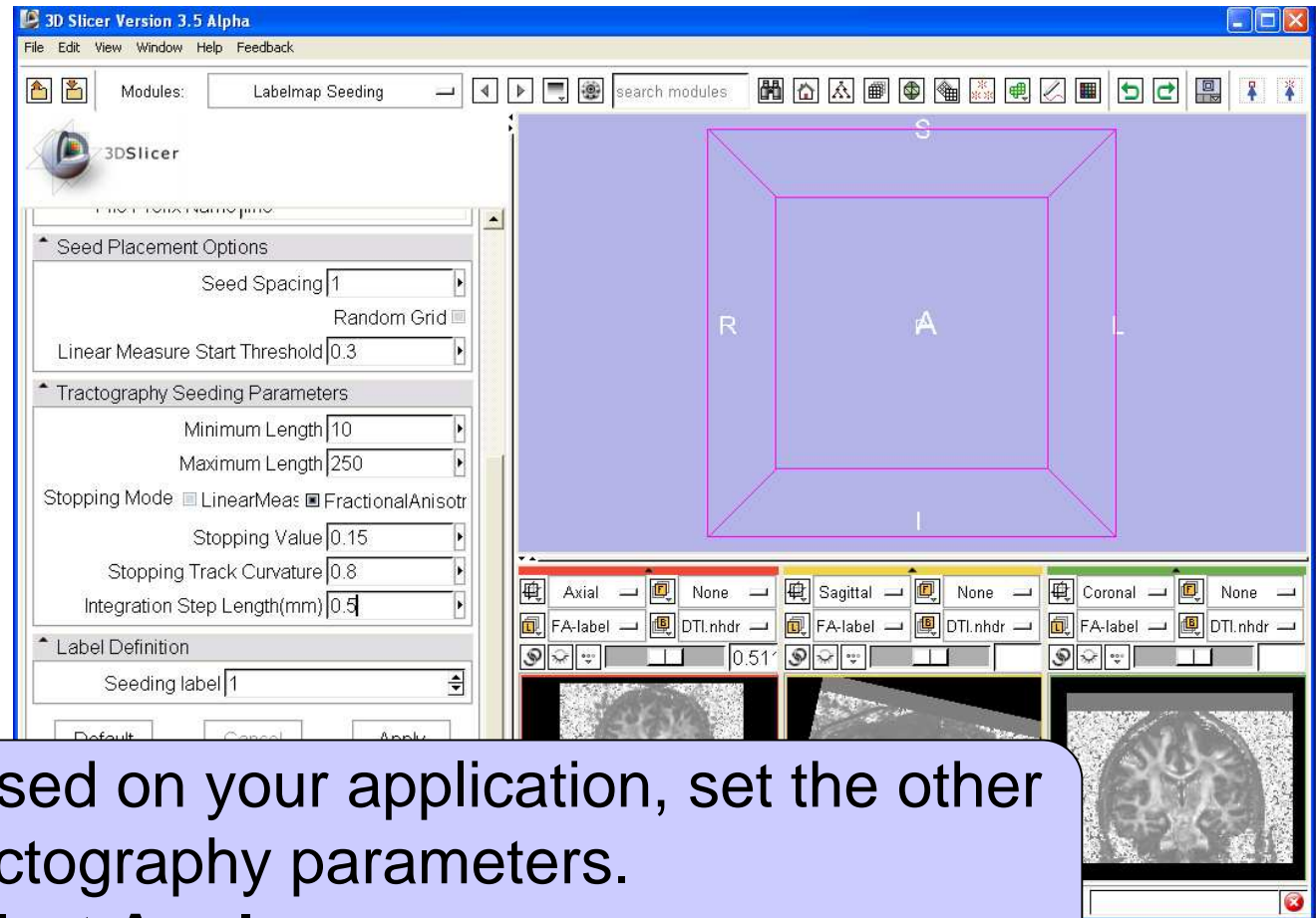

- **Select LabelMap Seeding module.**

Tractography (2/4)
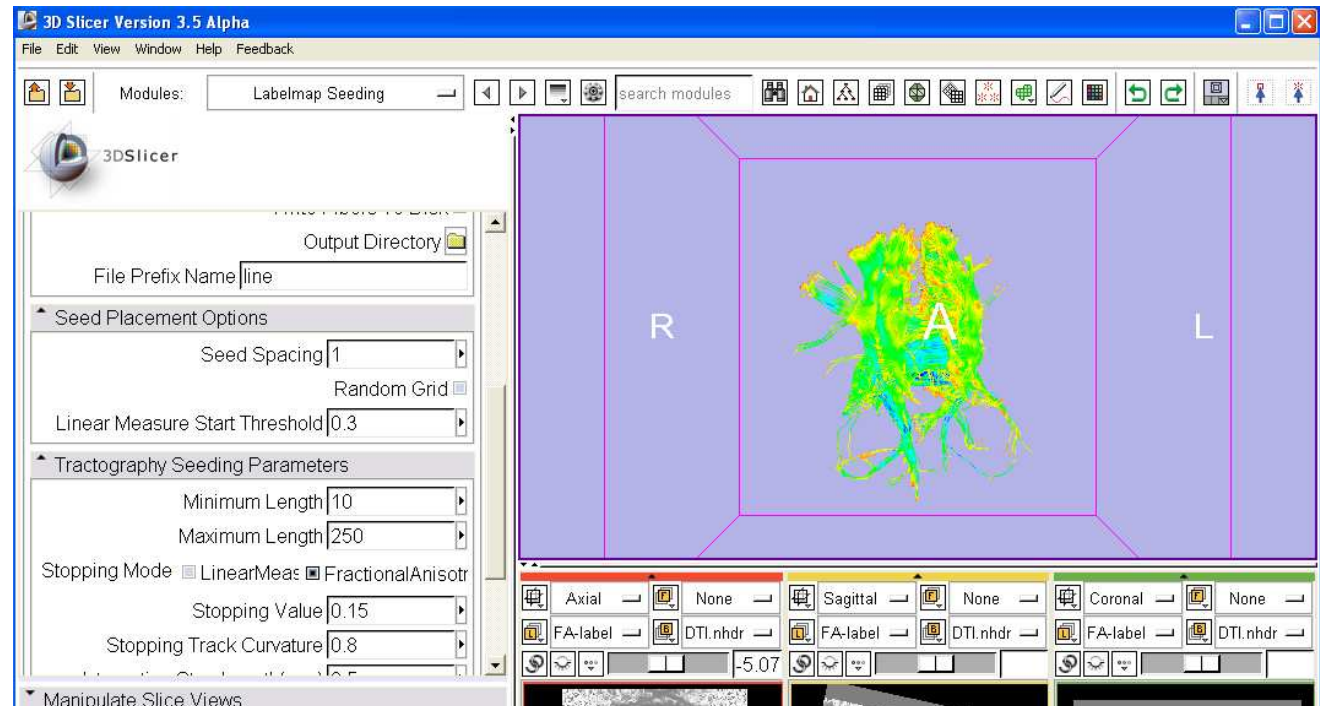

- **Set the IO parameters.**

Tractography (3/4)

- **Based on your application, set the other tractography parameters.**
- **Select Apply.**

Tractography (4/4)

- The output of tractography appears on the viewer.
- Fibers are colored based on their Fractional Anisotropy values.
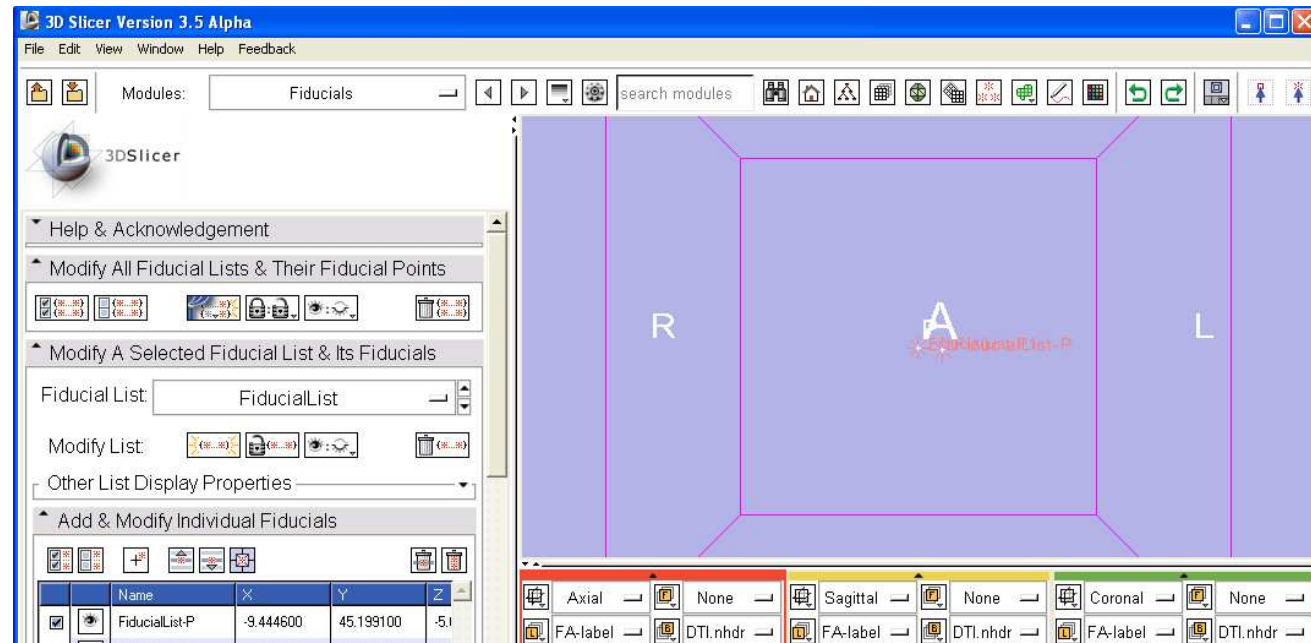
Creating initial centers (1/6)

- If you do not have initial centers (from an Atlas), there are two ways to create and pass them to the clustering module:

1. Extract trajectories by doing tractography on diffusion tensor data from a set of carefully selected seed points (Steps are explained in the next slides) .

2. Pass a fiducial list to the clustering module (**Fiducials to Pick Initial Centers**). In this case the module internally picks the closest trajectories to every fiducial in the list and will use them as the initial centers. Set the **Output Initial Centers** to "Create New Fiber Bundle" to examine the selected initial centers after the run is complete.

- **Set Fiducial List to Create New FiducialList.**
- Select one of the slice viewers by clicking inside the viewer.
- Add fiducials at desired places by entering **p.**
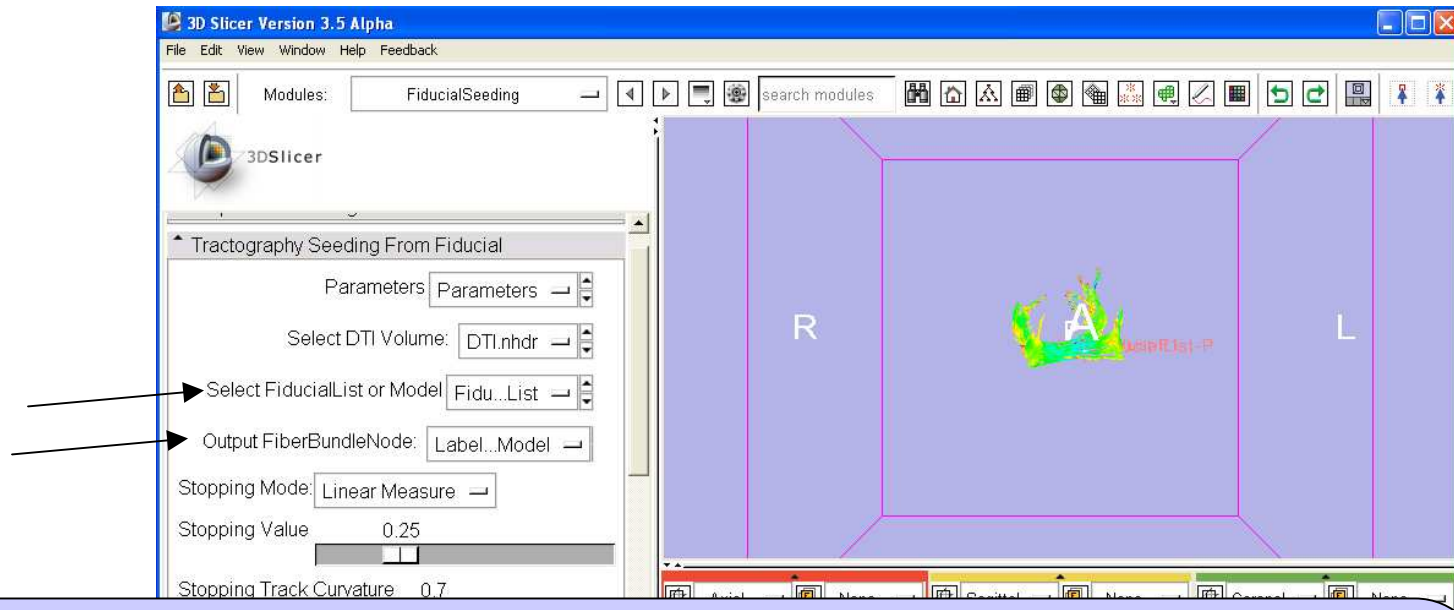
Creating initial centers (3/6)

Select **FiducialSeeding** module.
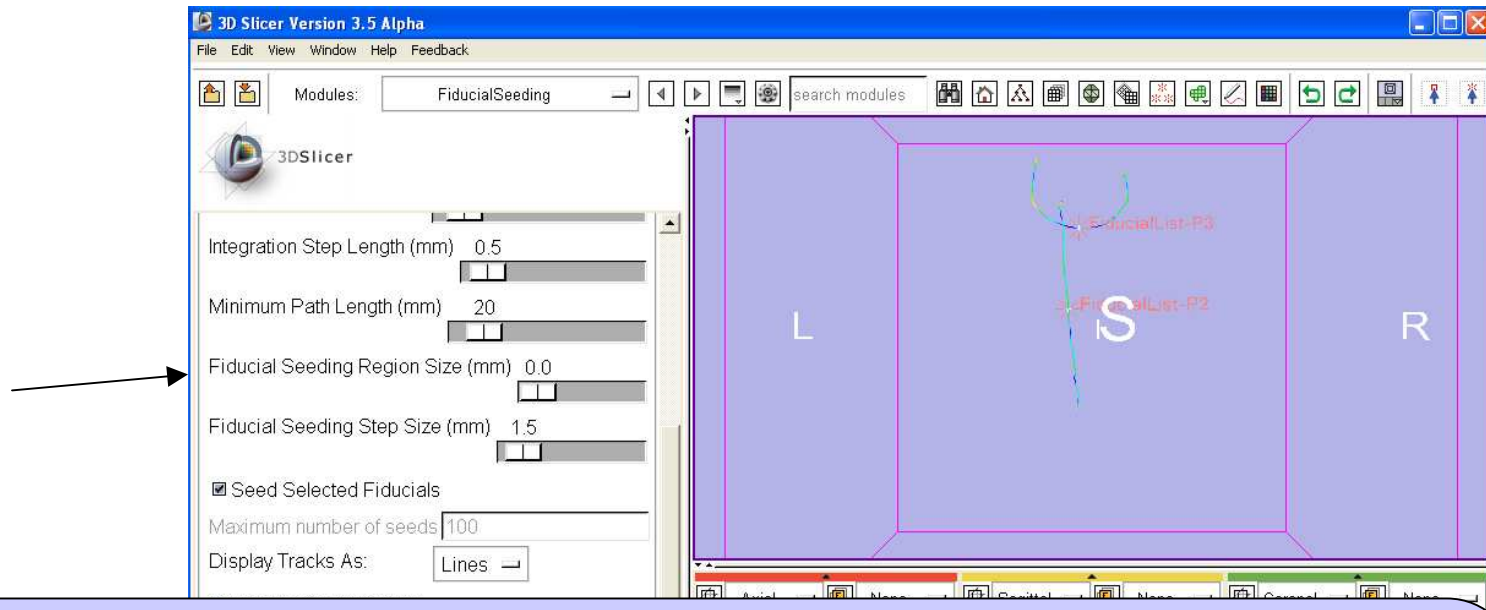
- **Set Output FiberBundleNode to Create New FiberBundle.**
- As soon as you set your Fiducial List as an input in **Select FiducialList or Model,** tractography is being done with the default parameters.
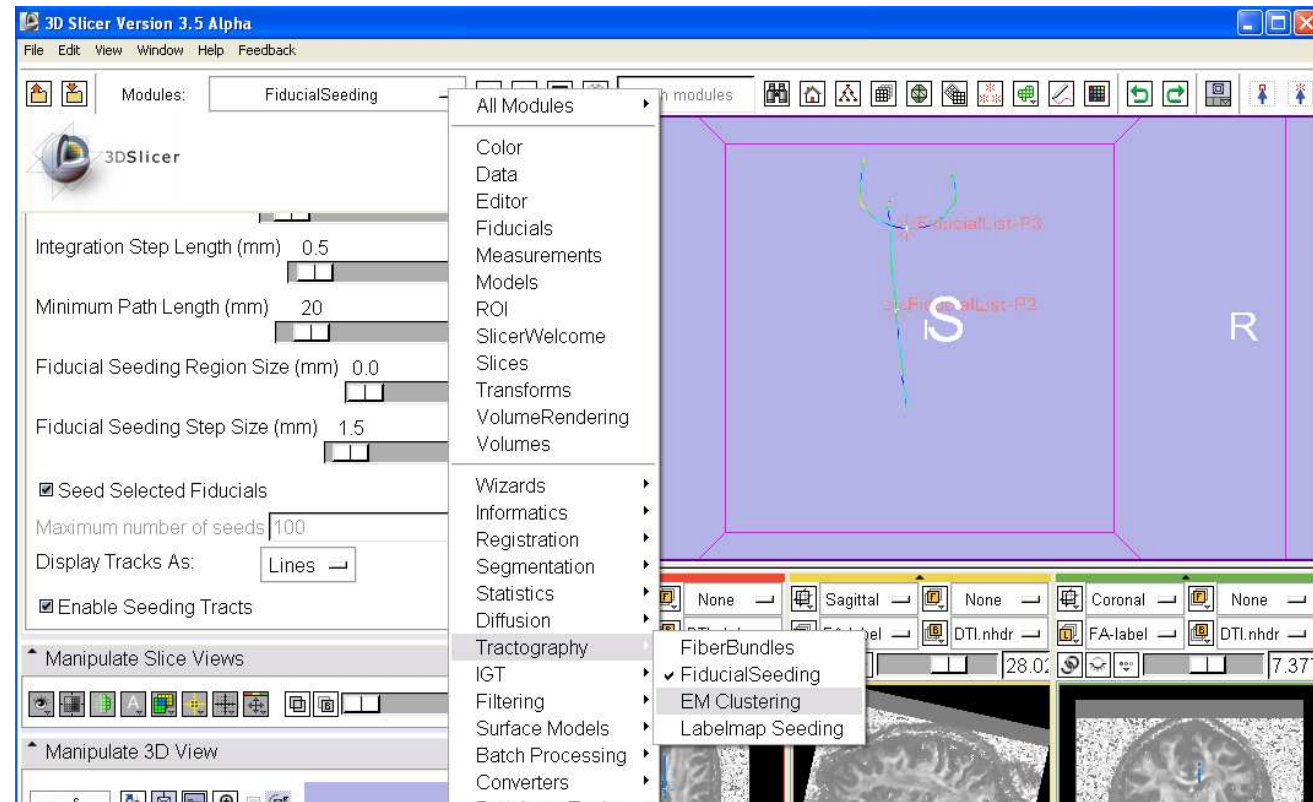
- Set the **Fiducial Seeding Region Size** to 0.0 to get only one fiber per seed.
- On the viewer you may move around every seed to get a trajectory that represents the shape of your desired cluster.

To cluster your trajectories go to **EM Clustering** module.

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