

# DTI Tutorial 3 - Fiber Tractography

Do Tromp<sup>1</sup>

<sup>1</sup>Affiliation not available

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DO TROMP

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CORRESPONDENCE:  
[do.tromp@gmail.com](mailto:do.tromp@gmail.com)

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Fiber tractography is a very elegant method that can be used to delineate individual fiber tracts from diffusion images. This tutorial will help you in a step-by-step way through the process.

In the first place you will need to produce both a tract-file and scalar-maps like fractional anisotropy (FA) maps and mean diffusivity (MD) maps. You can either simply download the [diffusion toolkit](#) which is highly compatible with the visualization program [TrackVis](#). Or you can use other tools like the ones from [Camino](#) (you will need this [camino to trackvis tool](#)) or [FSL Diffusion Toolbox](#). You can find more information on distortion correction and preprocessing [here](#) and [here](#), or you can go through the tutorials on analysis steps [here](#) and [here](#).

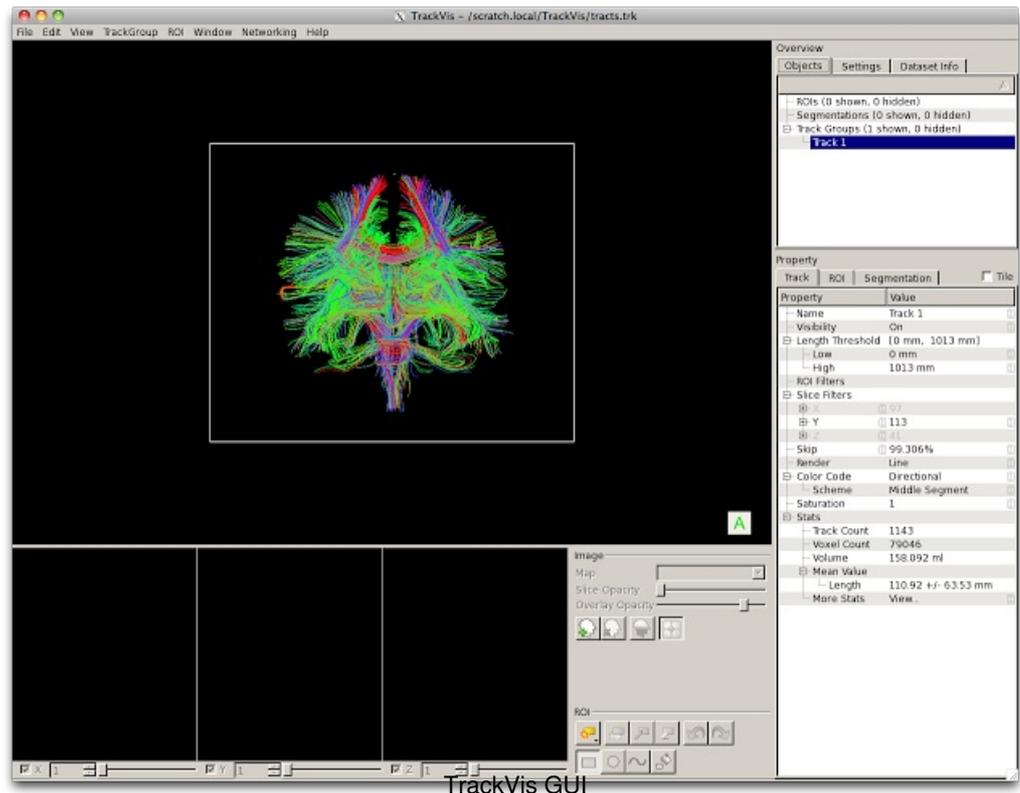
Once you have done that, the hardest part is pretty much over. Download the tract visualization program [TrackVis](#) [here](#). The software is free but you will have to register. TrackVis is compatible with windows, linux and mac. Both the diffusion toolkit and TrackVis are developed by some of the core scientists in diffusion imaging; [Van Wedeen](#) and [Ruopeng Wang](#). The support for the software is great, questions are readily answered through their [forum](#) (although currently offline due to spamming, for questions you can email them) and the software is still improving with updates. You will have to keep in mind that this is a three dimensional visualization program so it will demand a fairly decent memory performance of your computer, depending on the size of your files (voxel size, number of tracts). One hint when running whole brain tractography is to limit the number of tracts traced by applying a white matter mask (simply cutting off any voxels that have FA values below .15 or .2). Another tip is to use the MD map to get rid of much of the noise rim around the brain - by thresholding out the lowest 10%. If you do not have your own data you can download practice data from my [website](#) (look for the .trk file [although note that it is about 1GB to download], and the FA, MD, AD and RD files).

### LOAD TRACTS IN TRACKVIS

Open TrackVis by clicking the program icon in windows or mac, or through the terminal in linux:

Example code:

```
trackvis -new tracts.trk &
```



TrackVis GUI

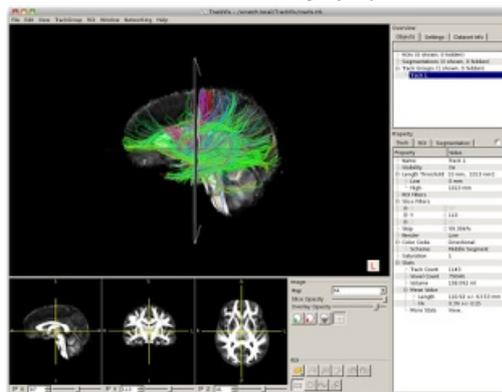
The panel on the right of the screen is called the **control panel**, which includes the overview and property section. The lower panel is called the **image panel**, which includes three orthogonal brain views, an image section and a ROI section. The main image with the 3D rendering is called the **render window**.

To load overlay scalar image click this button:



Then choose your scalar file e.g.: FA.nii.gz

If you load the scalar but can not see it on the main image play around with Slice Opacity.



Start to draw ROI's: click:



Choose Hand Draw - click on:



and:

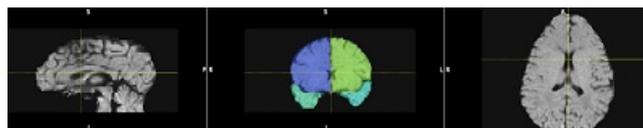


### PLAY AROUND WITH THE TOOLS:

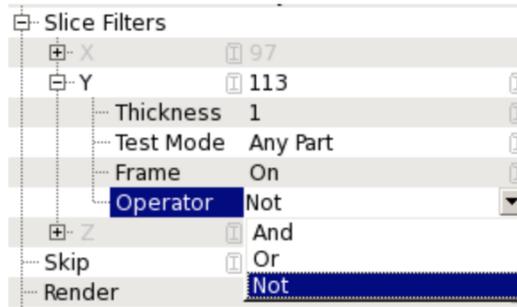
- - **What do the other ROI tools do?** More on this on the [TrackVis website](#)
- - You can only draw ROI's in the image panel and not on the 3D render window. To increase the size of the image panel you can slide it up to make it larger. Double click the render window to hide or show the image panel.
- - You can move the main image in both the render window and image panel by clicking and dragging - you can play around with this
- - Right click the main image to Reset or Straighten
- - Zoom in/out on the orthographic FA images and main image by scrolling - beware this is a slow and sensitive tool.
- - You can move the orthographic FA images with shift and click
- - You can adjust the orthographic FA images brightness with control and click
- - To start selecting specific white matter tracks you can use methods used by:
  - \* Mori et al: [Imaging Cortical Association Tracts in the Human Brain Using Diffusion-Tensor-Based Axonal Tracking, 2002](#)
  - \* Catani and de Schotten: [A diffusion tensor imaging tractography atlas for virtual in vivo dissections, 2008](#)

### HOW TO DELINEATE THE UNCINATE FASCICULUS (UNC)

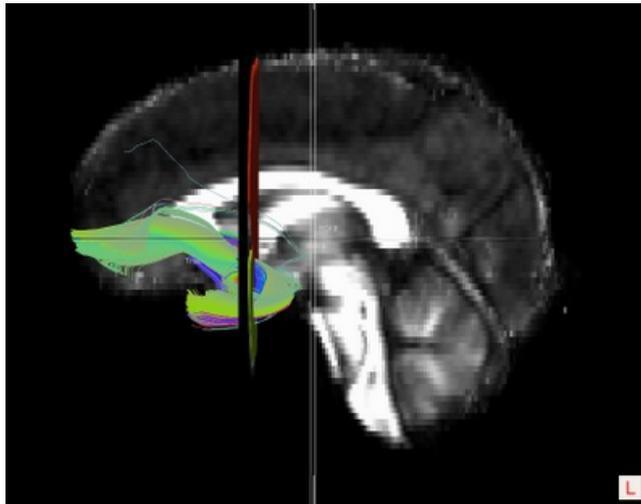
- - The delineation of the UNC is contingent on finding the correct coronal slice, specifically the most posterior coronal slice that shows clear separation of the frontal and temporal lobes bilaterally. An example is shown in the image below where each of the four UNC ROI's are shown from the image panel:



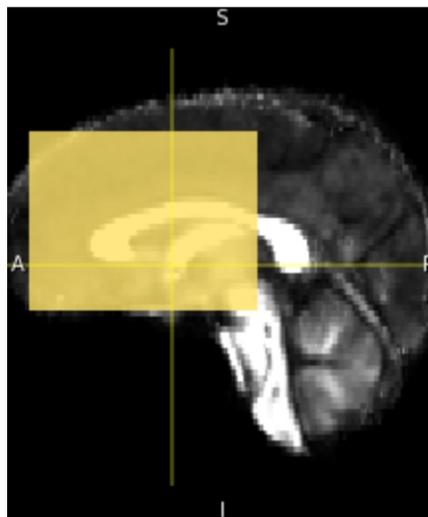
- - In the right Overview pane in the Objects tab right click Track 1 and select Toggle Existing ROI, choose both left ROI's
- - Then right click Track Groups and click New Track Group From Slice, once that is done toggle the two right ROI's for Track 2
- - In the Property pane expand the options for Slice Filters - Y, for Operator choose Not. Do this for Track 1 and 2.



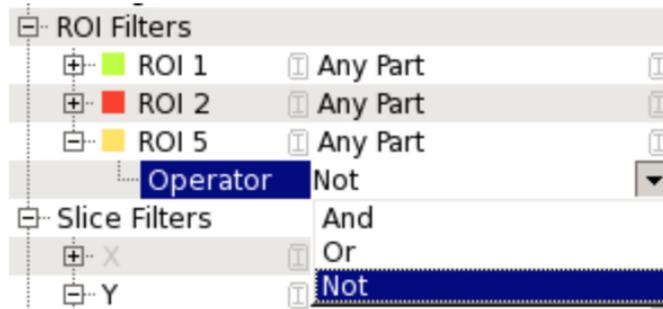
- - Next you double click Skip and deselect it, do this for both sides.
- - What you see now is roughly all the tracks for the Left and Right Uncinate Fasciculus.



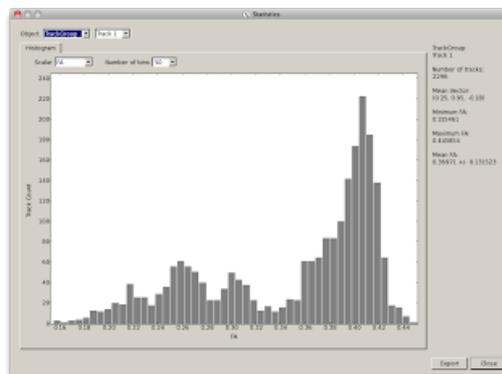
- - The tracks are not perfect yet, we want to get rid of some of the fibers that belong to other pathways or are just wrong
- - Create a new Hand Drawn ROI, choose the rectangle and draw a big rectangle in the middle of the sagittal plane:



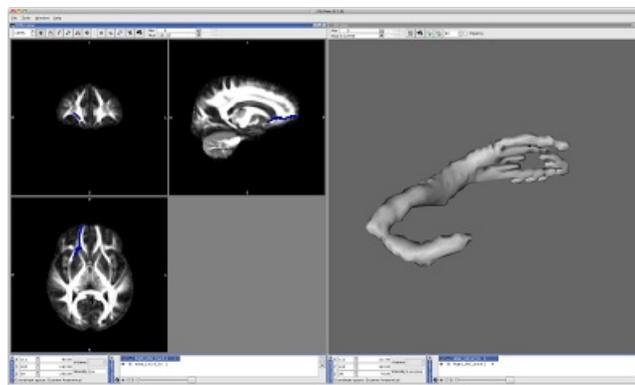
- - Toggle this fifth ROI to both Track 1 and 2, and in ROI Filters option for ROI 5 choose Operator - Not.



- - Play around with ROI 5 by adding area's in different planes until you achieve an Uncinate Fasciculus as in the movie below:
- - Now that your Right and Left Uncinate Fasciculi are perfect you can look at the stats, you can find those in the Overview pane underneath the Dataset Info tab. Click on More Stats - View



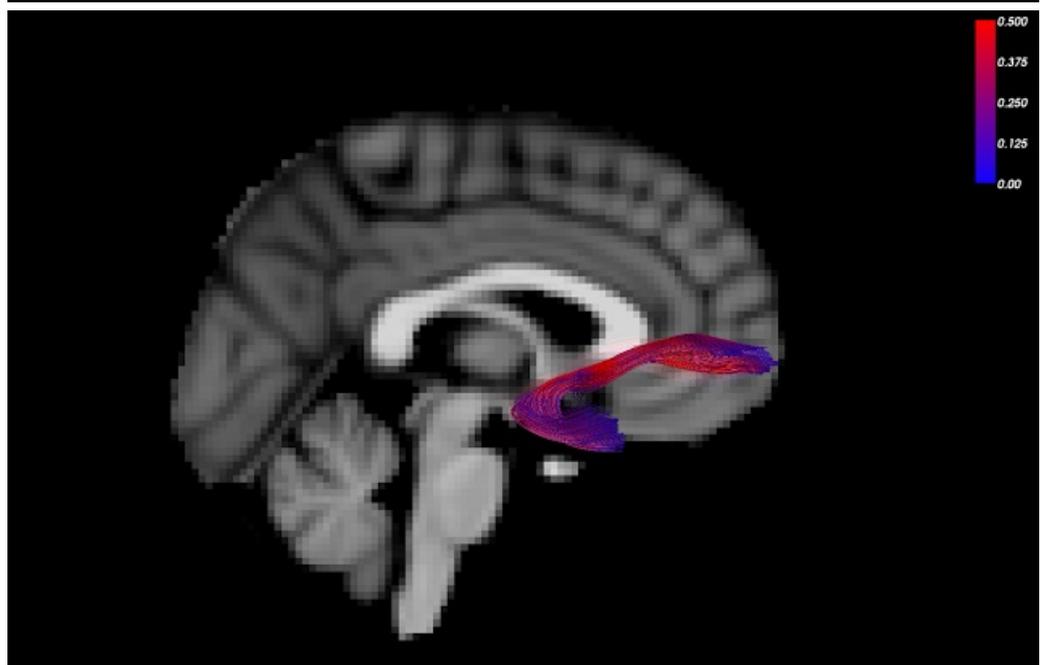
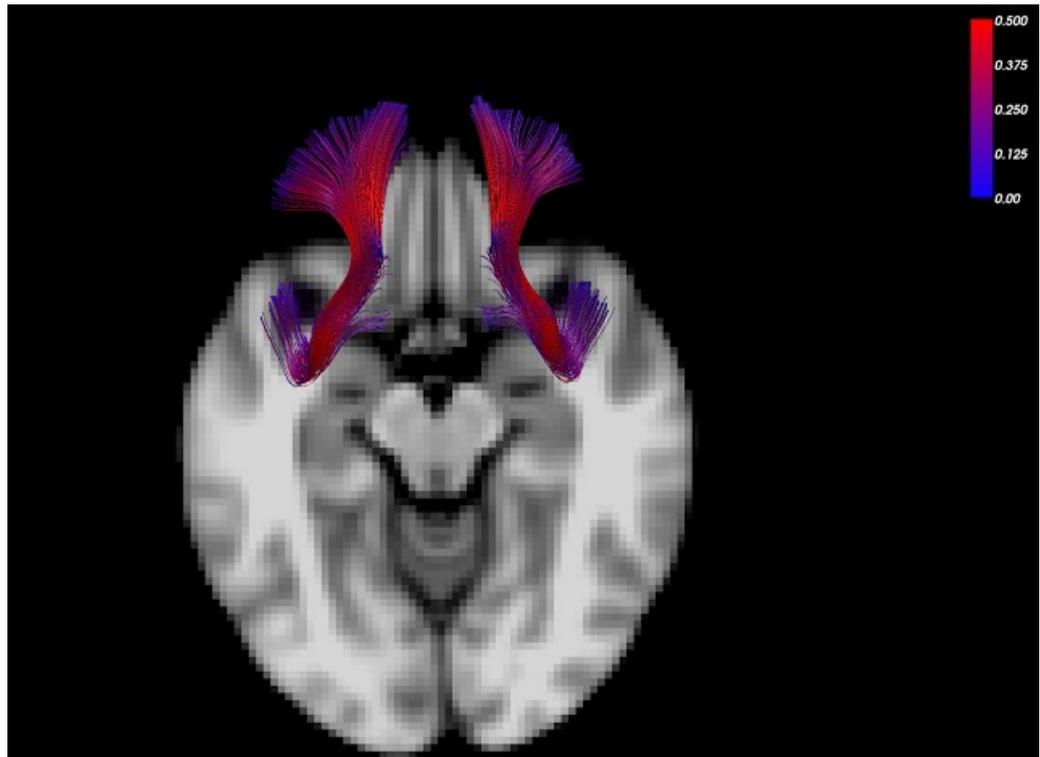
- -What is for example the Mean FA of your left Uncinate? And your right? And the whole brain?
- - You can export these stats with Export, do this for each side and the whole brain separately.
- - As a next step it is smart to start saving everything. Start with saving all the ROI's by right clicking them in the Overview pane, then click on Save, try to think of a good naming convention that can include the UNC and the ROI number.
- - Next click File and Save Scene. The newer versions of trackvis seem to deal with this better but if you run into issues with re-opening your scene file try to save the ROI's before you save the scene or it will not load them correctly once you want to re-open the scene.
- - Now click Track 1 and 2 and save those as NIfTI files, this gives you the option of opening these files in FSLVIEW and see them in 3D:



#### IMPROVE THE AESTHETICS

- - Hide all ROI's

- - Hide the Z-plane by unselecting Z in the orthographic view
- - In the Property pane find Color Code and click on Directional - choose Scalar. By default the FA map will now be used to color code the track, do this for both sides.
- - Adjust the Low and High Threshold for the color coding to be between 0 and 0.5
- - You can also adjust the color spectrum, BUT on certain occasions this will crash the program, so use with care.
- - Also you can choose to Render a tube instead of a line, try this but keep in mind that rendering this will take a moment.
- - The output can then look like this (the overlay in the below images is a T1 image registered to FA):



In the image below you can find some of the fiber tracts that are important in autism spectrum disorder

(ASD). In green the cingulum, in purple the uncinate fasciculus and in red and blue the arcuate fasciculus and superior longitudinal fasciculus respectively, image from [Travers et al. 2012](#).

