

Manual created by Alexander Leemans

Most recent version of *ExploreDTI* is: v4.8.6.

This manual is showcasing the very basic tools of *ExploreDTI*. It is far from complete, but it's a start! Any feedback is always welcome...

Q&A and discussion forum: <u>https://groups.google.com/group/e_dti</u>. Notifications and updates: <u>https://twitter.com/ExploreDTI</u>.

ExploreDTI was released at the ISMRM 2009 meeting. The abstract can be found here. The reference is:

Leemans A, Jeurissen B, Sijbers J, Jones DK. "ExploreDTI: A graphical toolbox for processing, analyzing, and visualizing diffusion MR data". Proceedings of the 17th Scientific Meeting, International Society for Magnetic Resonance in Medicine, Honolulu, USA, p. 3537, 2009.

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1. Installing / starting *ExploreDTI*

Standalone versions of *ExploreDTI* are available for Windows, Linux & Mac (only for 64 bit OS). With the standalone executable, there is no need have Matlab installed.

If you *do* have Matlab (R2010a or later) installed, there is also a P-code version of *ExploreDTI* that runs natively in Matlab and, therefore, in principal at least, can run on any platform (32 bit and 64 bit OS). At this stage, source code of *ExploreDTI* is not released.

It is recommended to install *ExploreDTI* on a computer with high-performance¹ specs: (i) multi-core CPU; (ii) RAM > 16 GB; and (iii) dedicated graphics cards / GPU's.

If you already tried to run the executable 'MainExploreDTI' before having read this part of the manual, you may have encountered the following error message (or something similar – MCR version may be different):

Error		×
4	Could not find version 8.3 of the MCR. Attempting to load mcImcrrt8_3.dll. Please install the correct version of the MCR. Contact your vendor if you do not have an installer for the MCR.	
	ОК	

Reading section **B**) below will clarify things...

A) Using ExploreDTI natively in Matlab

Put the 'Source' folder and the 'MainExploreDTI.p' file in your 'Matlab path' and type 'MainExploreDTI' in the command prompt (and press 'enter')... that should do it!

B) Installing & starting the standalone of ExploreDTI (no Matlab needed)...

Make sure your computer is up-to-date re java (e.g., <u>http://www.java.com</u>), graphics card drivers (e.g., for Intel graphics cards, <u>http://downloadcenter.intel.com</u>), OpenGL libs (e.g., <u>http://www.opengl.org/</u>), etc. Otherwise, you might get error messages or just weird bugs. *Perhaps only perform these updates, if need be*.

The standalone version of *ExploreDTI* is currently being developed in Matlab 8.3.0.532 (R2014a). The executable, "MainExploreDTI", only works AFTER you installed the (free!) Matlab-Common-Runtime (MCR) libs of that Matlab version – you can download the one for your OS of interest here (~ 600 MB): http://www.ExploreDTI.com/matlab/64/MCR_R2014a_win64_installer.zip (Windows – 64 bit) http://www.ExploreDTI.com/matlab/64/MCR_R2014a_glnxa64_installer.zip (Linux – 64 bit) http://www.ExploreDTI.com/matlab/64/MCR_R2014a_maci64_installer.zip (Mac – 64 bit)

To install the MCR libs file, simply follow the instructions. Note that MCR libraries from other Matlab versions are probably not compatible with these standalone versions of *ExploreDTI*. Again, note that you do NOT need a Matlab license to run *ExploreDTI*! For Linux/Mac, if you choose an installation directory for the MCR that is different from the default one, you need to use this path in the "run_MainExploreDTI.sh" as well.

¹ High-performance is defined here as: "Not getting annoyed by slow graphics rendering or insufficient RAM".

C) Running ExploreDTI ...

E.g. for Windows, after installing MCR libs – and perhaps the typically required Windows reboot – put the executable file 'MainExploreDTI.exe' in a folder, such as "C:\ExploreDTI". Then, double-click the executable 'MainExploreDTI.exe' (the actual *ExploreDTI* program!). This might take several seconds (or even a minute or two when executed for the first time), as it loads the required Matlab libs.

If things go well, for Windows, the screens below should appear – or at least something similar depending on the exact version of *ExploreDTI*:

1) The command prompt appears first (read only): it will provide information about the progress of certain calculations and reports 'errors/bugs/crashes' (btw, feedback of the latter is useful). If you get errors at this stage, you might need to look at the 'install' sections above (or just consult the forum...).



If you are running *ExploreDTI* in Matlab, it will appear in the Command Window:



2) Then, a 'splash-window' should appear. If so, things are looking good!



3) Finally, the actual *ExploreDTI* program should start up. If you see the window below, you are ready to go!

D Exp	ploreDTI v4.8.3	- © Alex	kander l	Leemans											
Data	Image map	Axis	Draw	Calculate	Color	Show	Hide	Delete	Settings	Palettes	Animations	Miscellanea	Help	Plugins	Calculate DTI *.mat file
			0	+					0	+			Ŀ	0	
]										

Most menu items are disabled at start-up to prevent you from accidentally crashing *ExploreDTI*. Exceptions are 'Data', 'Settings', 'Miscellanea', 'Plugins', 'Help', and 'Calculate DTI *.mat file' (if you run *ExploreDTI* in Matlab, the other menu items are not relevant, as they are built-in by Matlab itself). Note that menu item names may change in future releases. Also, the version number (here, v4.8.3) might be different.

If you are eager to try things out, download the example DTI *.mat file and load it via the 'Data' menu item: <u>http://www.exploredti.com/exampledataset.htm</u>. Tip: immediately after loading, the menu item 'Palettes' becomes available. Useful ones to start messing about are the 'Axis' and 'Draw' palettes.

If you want to use your own data, see the next section.

2. Converting your DWI's to an "ExploreDTI file" (*.mat)

This section describes how you can convert your raw diffusion data to the format of *ExploreDTI*. The endresult of this conversion step is a DTI *.mat file that contains pre-processed data, such as the diffusion tensor, eigenvalues, eigenvectors, mean diffusivity, fractional anisotropy, the DWIs, B-matrix, gradient directions, etc.

Background

Most likely, you conducted a diffusion MRI experiment (DTI, DKI, HARDI, DSI, ...), which has resulted in a folder (perhaps with sub-folders) of (un-)sorted dicom files. This type of format is not really practical (typically, each 2D image slice has its own file), so it usually converted to more manageable formats (where all slices/volumes are put in a single file), such as *.par/*.rec (Philips-specific), *.nii(.gz) (NIFTI), *.hdr/*.img (analyze), etc.

As an example, consider a typical diffusion MRI acquisition with 30 diffusion weighted images (DWI's) and 3 non-DWI's, i.e., the "b = 0 s/mm²" (or b0 in short) images, with each 3D image consisting of 60 slices. Compare the speed of loading 1980 (= $[30 + 3] \times 60$) separate dicom images vs. a single 4D *.nii file... it *does* make a difference! Mainly due to this efficiency issue, I opted for *.nii as the standard input file format to start processing with *ExploreDTI*.

All DWIs (including the b0 images) are assumed to be included in the 4D *.nii file with the b0 images at the beginning. If the b0 images are not at the beginning, there is a plugin 'Plugins' \rightarrow 'Shuffle/select 3D volume(s) in 4D *.nii file(s)' that you can use reorder the b0 images to the beginning. Alternatively, you can use the 'Sort DWI *.nii file(s) wrt b-values' plugin assuming you have a b-matrix *.txt file (see below).

Converting data (dicom/hdr-img/2dseq/par-rec) to NIFTI (*.nii)

In my opinion, a great tool to convert dicom files to NIFTI files is Chris Rorden's "dcm2nii" tool: <u>http://www.cabiatl.com/mricro/mricro/dcm2nii.html</u>. I have included this tool and MRIcron itself (allows one to view *.nii files), version 15 October 2008, as plugins into *ExploreDTI* (see menu item 'Plugins' \rightarrow 'Convert ...' \rightarrow 'Dicom folder(s) to *.nii files'). Similar for the other data formats (img/hdr, par/rec, '2dseq'), there are conversion tools to get the 4D *.nii data. In any case, the end result should be a 4D *.nii file. Important – as always – check the *.nii file for left/right flipping!

If you are familiar with Matlab, you may want to use the NIFTI tools developed by Jimmy Shen: <u>http://www.mathworks.nl/matlabcentral/fileexchange/8797</u>. This might be useful when you do not have dicom files, but some other format. Read the data into Matlab and then export them to a 4D *.nii file with these tools.

The B-matrix

To convert your *.nii data to an *ExploreDTI* 'DTI *.mat file', you also need the B-matrix (*or* the gradient directions and the b-value). I will spare you the details on how to derive the B-matrix – an example (B-matrix with 1 b0 and a b-value of 1000 s/mm²) is given below (left), derived from the 12 gradient directions, shown on the right.

Example B-matrix.txt - Notepad					Gradients.txt - Notepad	
File Edit Format View Help					File Edit Format View	Help
0.00000000 0.0000000 &14.40765652 65.18967083 0.00257270 -1.40905695 165.65429279 743.59254310 763.00556381 850.19364463 0.93302274 -54.35749941 216.12404514 11.53945569 781.83932364 77.30926760 1.44072689 -34.49089697 236.61207599 -849.95242726 833.86972410 -743.17633635 2.37890783 -87.53764712 183.64522152 23.57926143	0.000000 -774.87732493 2.88226527 0.43561773 23.88218985 27.83245736 -823.18086836 822.25278610 -67.56969386 16.86724813 40.12584058 -42.79343654 774.12862588	0.0000000 130453500 192.93393198 834.46353974 236.83616072 791.71107337 0.15403080 1.91110970 763.29486310 165.58673704 805.28967760 0.75686909	0.0000000 -31.01272277 -789.30347186 0.97770511 13.30559500 -810.75343524 -21.97594246 40.65270111 808.80677780 -30.29506933 -17.88083578 787.34381956 49.69740324	0.0000000 184.31643658 807.27112684 0.18687904 207.56345176 783.84006461 216.18880754 792.25000176 0.30060180 0.48271422 192.44947111 815.80550320	0.9024 0.026 -0.0016 0.439 0.4070 0.913 0.8735 0.486 -0.0305 0.889 0.4649 0.012 0.8842 0.043 0.0380 -0.454 -0.4864 0.857 0.9132 -0.406 -0.0488 0.897 -0.4285 -0.027	1 -0.4293 2 -0.8985 5 0.0005 7 0.0137 8 -0.4556 4 -0.8853 7 0.4650 3 -0.8901 9 0.0220 4 0.4387 5 -0.9032

The nice thing about "dcm2nii" (see previous section) is that it can produce "*.bval" and "*.bvec" files (see below).



From these "*.bval" and "*.bvec" files, the B-matrix *.txt file can be calculated (see menu item 'Plugins' \rightarrow 'Convert ...' \rightarrow '*.bval/*.bvec to B-matrix *.txt file(s)').

Making the *.mat file for ExploreDTI

OK – now the last step! By now, you should have a 4D *.nii file and its corresponding B-matrix (or gradient) *.txt file (as described/shown above). Now you can use the 'Convert raw data to DTI *.mat' tool (see below) to create the DTI *.mat file, which can then be loaded into *ExploreDTI*. You should *NOT* try to run the 'Custom-made data conversion tools' from this same menu item, as they are *custom-made* and, therefore, will *NOT* be suited for your data - crashes & incorrectly converted data are not excluded then!



The screen below pops up with detailed info given when you go 'mouse-over' on the yellow text:

ExploreDTI's data converter to create DTI *.mat files	
Format diffusion weighted data	4D Nifti (*.nii)
Permute spatial dimensions	AP RL IS
Flip spatial orientations	AP RL IS
Perform visual data check	No
Diffusion tensor estimation	Linear (high speed - low accu 🔽
Format diffusion information	Text file (*.txt)
Background masking approach	Automatic
Permute gradient components	x y z
The gradient components x, y, and z should correspond with the coordinate frame of the spatial dimensions	x y z 🗸
of the data. Here, you can swap the component. This will change the 'color-encoding'. The most widely	Single data set 🔽
b-value in units s/mm^2	1000
Voxel size [AP RL IS] (in mm)	222
Number of non-DW images	1
Number of DW images	45
Matrix size [AP RL IS]	128 128 60
Start converting to DT	l *.mat file(s)

One thing you should definitely check is: *MAKE SURE LEFT-RIGTH ORIENTATION IS NOT FLIPPED*! Btw, I use the radiological convention, i.e. left and right in the image represent right and left in the data set, respectively, that is, if you look at it in a 2D axial view with default settings. If you are not sure, just 'rotate' the image, so you can unambiguously 'see' the 3D nature of the data/object. My advice: always attach a marker on the right side of the subject (e.g., a vitamin pill) – you will never switch sides ever again ;-)! And secondly, use the plugin "Flip/permute dimensions in 3D/4D *.nii file(s)" to make all your nifti files – not just the DWIs, but also any other data such as T1, T2, etc. – "ExploreDTI compatible" to begin with... this will avoid unexpected axis flips (& permutations) in any following analyses.

After converting to *.mat, check whether you used the widely used color-convention for your data (left-right: red, top-bottom: blue, and front-back: green). So, if need be, change 'Permute gradient components' from 'x y z' to, for instance, 'y x z' to interchange red and green)!

Furthermore, you might need to change the sign of your gradient components, which is obviously very relevant for tractography (to do this, change 'Flip sign of gradient components'). For example, compare the images below ('Draw ROI' \rightarrow 'Draw Glyphs') – do you see the difference (the z-component was flipped: 'x y z' vs. 'x y -z')!?



Perform this check for the other views as well – there may be multiple components that need to be changed simultaneously (see below for another example: the x-component was flipped: 'x y z' vs. '-x y z')!



If you have problems converting your raw data, get help from the forum (upload your data). Otherwise, there are only a limited number of combinations possible... good luck!

3. Loading a DTI data set

Since *ExploreDTI* was developed originally only for DTI (hence the name – the other diffusion approaches came later), the only type of data you can load at start-up is a 'DTI *.mat file' (Matlab format). This *.mat file contains a set of variables with a fixed nomenclature (otherwise, *ExploreDTI* will not load the data). An example data set can be found on <u>www.ExploreDTI.com</u>.



If you have loaded a DTI *.mat file correctly, you should be able to see the following screen (with the menu items enabled now):



Notice that the figure name contains the full path (here: 'C:\ExploreDTI\DTI_Example.mat') of the DTI data set that is currently loaded (if you do not see anything, adjust masking or OpenGL setting: see Q&A forum).

Using the tools in *ExploreDTI* from the menu bar items can be a pain (e.g., when computationally expensive renderings are shown in the main axis object, the 'menu item refreshing' becomes extremely slow). To circumvent this issue, 'palettes' can be prompted containing a group of commands that can be accessed directly. When running *ExploreDTI* in Matlab (using the p-code version), these 'palettes' are 'docked' automatically in the figure window and can be placed in any way you want. The screenshots below will clarify this. I suggest to use these 'palettes' as much as possible – you will appreciate the benefits. As an example, if you are running *ExploreDTI* in Matlab, do the following (after loading a data set):





Then click 'Palettes' \rightarrow 'Axis' and 'Draw', and then delete (click the 'cross') the empty window, so three windows remain (see below).





You can continue to do this with other 'palettes' as well - they will appear in the menu bar at the bottom (or left/top/...) in a new 'tab' – click such a 'tab' to make it active and drag it to a field of your choice.

Right click on a window header if you want to further subdivide the windows (and incorporate other 'palettes'):

XPlane VYPlar Orthographic Zoom Orbit Orbit New Center Res	e VZPlane Perspective H/V Move F/B Light Set Toggle Light		
Draw Tools ROI: • Draw AND NC GLYPH: PDV (line) Draw glyphs	Maximize Draw Tools Undock Draw Tools Close Draw Tools Top/Bottom Tile Left/Right Tile Delete glyphs		
TRACT: Draw Color-encoding FE Render quality High Calculate tracts	Delete ☑ All Tract shape Lines Sub-sampling 1 Analyse tracts		R
Transparency Opaque Fancy tract stuff	Hyper width CU (Uncertainty) Hyper tube mode		

For the standalone versions, however, these 'docking' tools are not available anymore (it did work for releases R2009a and older – Matlab is going to look into it to see whether they will make it available again). As a result, all palettes are separate windows, which cannot be docked (see below)...



You will notice that the 'Main Window' (the one that contains the menu items) is 'set active' after any 'click' on any of the 'palettes' (is only useful when running it in Matlab using the docking tools). Just use a configuration like the one above where the windows do not overlap – otherwise, it can be confusing.

5. Data quality assessment

Quality assessment of DW images can be very labour-intensive. One approach to look at your 4D data is by 'looping' it. Do the following: 1) Load a DTI data set; 2) Set 'Image map' to DWIs. The resulting display might look weird, since the intensity range is by default set to [0 1000] – it represents the (first) non-DW image; 3) Now, 'Palettes' in the menu bar will allow you to open the 'QA DWIs' tools; 4) Click 'Set auto value' to set the intensity range for that image.



You can do several things now (see below): (1) use the image intensity sliders ('Min val' and 'Max val') to adjust the intensity range. (2) Activate 'loop'. Make sure there are multiple numbers indicated in the 'Volume range', for instance '23:50' (i.e., [23 24 25 ... 48 49 50]) or '23 50' (notice the difference!?). Note that during the looping, you cannot use the image intensity sliders ('Min val' and 'Max val'). (3) select the other 'Feature': 'Residuals' (i.e., the absolute residual values to the tensor fit).

Another quick semi-qualitative check is to look at the average residuals per DWI or across the DWIs for each voxel ('Show data quality summary' – see below):





A last quick way to check data quality is by inspecting the outlier profiles:



These tools are just useful from a qualitative point of view (e.g., to give feedback to the MR physicist in the event of artifacts). In practice, the robust diffusion (& kurtosis!) tensor estimation approach (i.e., '<u>REKINDLE</u>' – the default approach in *ExploreDTI* during correction for subject motion, eddy current distortions, ect.) will have taken this into account!

6. Drawing ROIs

Drawing an ROI requires you to 'uncheck' the 'image planes' on which you are *not* going to draw this ROI (it will give you an annoying warning pop-up, otherwise).

To actually draw an ROI (see below), first click the 'SEED' (or 'AND' / 'NOT') button and then 'left-click' each time to generate a point (notice that I have used the 'Zoom' and 'Move H/V' buttons to enlarge the slice to the region of interest). 'Right-click' to close the ROI (don't do anything else during this procedure or ExploreDTI will crash).



Note that you can save, load, hide, show, and delete single/multiple ROIs. See, for instance, below (menu item 'Data' \rightarrow 'Save single ROI (*.mat)'):

O D	(ploreDTI v4.8.1 - (© Alexand	ler Leem	ians C:	\Explore	DTT\DTI_	Example	e.mat			
Data	Image map	Axis Dra	aw Cal	lculate	Color	Show	Hide	Delete	Settings	Palettes	Animation
	Load DTI (*.mat)			Ctrl+	L						
	Load volume (*.m	nat,*.nii)							-	66	•
	Load fiber tracts (*.mat)									
	Load single ROI (*	'.mat)									
	Load multiple RO	I (*.mat)									
	Load CSD FOD (*.	mat,*.nii)			_						
	Save fiber tracts ('	*.mat,*.nii	,*.txt)								
	Save mask of ROI	s (*.mat,*.	nii)								
	Save single ROI (*	.mat)									
	Save multiple ROI	[(*.mat)									
	export current vol	lume as R(GB (*.ma	t)							

7. Quantitative ROI analysis

Once you have drawn one or more 2D ROIs (see example below), you can extract DTI related parameters, such as the FA, MD, and the eigenvalues, which may be useful for quantitative analyses.

	👂 Exp	loreDTI v4.8.1	© Ale	xander l	eemans C	\Explore	ΟΠ\ΟΠ_	Example	e.mat									
	Data	Image map	Axis	Draw	Calculate	Color	Show	Hide	Delete	Settings	Palettes	Animations	Miscellanea	Help	Plugins	Calculate	DTI *.ma	t file
			-	64	Tract Analy Analy	s ze Tracts ze Tracts	from R(DI's Ider of r	nasks	C	66	÷				Ŀ	30	Ŀ
					Analy	ze Tracts	from At	las labe	ls									
					Descr	iptive Sta	tistics		<u> </u>	ROI								
					Brain	context				Iracts								
L																		
L																		
I.																		

After you click 'Calculate' \rightarrow 'ROI' (see above), a popup appears (see below) asking you to export the statistics to a simple text file (so afterwards, you can import the numbers into SPSS, Excel, or any other program you want to use for further statistical analyses...).

Saving st	tats
?	Do you also want to save output to a txt-file?
	Yes No

Finally, a popup window appears with the relevant numbers in it (see below).

ExploreDTI statistics Date: 15/09/2010 Time: 15:45:23
ROI statistics
FA> average = 0.78487 ; SD = 0.14041 ; SE = 0.023084 ; N = 37 ; 95%CI = [0.7387, 0.83103] median = 0.83258 ; [25, 75]-percentiles = [0.76193, 0.86492]
MD (mm*2/s)> average = 0.00089634 ; SD = 0.00015742 ; SE = 2.588e-005 ; N = 37 ; 95%CI = [0.00084458, 0.0009481] median = 0.00087361 ; [25, 75]-percentiles = [0.00078093, 0.00097482]
L1 (mm*2/s)> average = 0.0019592 ; SD = 0.00017868 ; SE = 2.9374e-005 ; N = 37 ; 95%CI = (0.0019004, 0.0020179) median = 0.0019339 ; [25, 75]-percentiles = (0.0018448, 0.0020683]
L2 (mm*2/s)> average = 0.00041484 ; SD = 0.00024933 ; SE = 4.0989e-005 ; N = 37 ; 95%Cl = [0.00033287, 0.00049682] median = 0.00034819 ; [25, 75]-percentiles = [0.00028005, 0.00050469]
L3 (mm^2/s)> average = 0.000315 ; SD = 0.00019846 ; SE = 3.2626e-005 ; N = 37 ; 95%CI = [0.00024975, 0.00038026] median = 0.000253 ; [25, 75]-percentiles = [0.00020061, 0.00037583]

The corresponding text file output looks as follows (I hope you understand – from comparing with the image above – what each number represents ;-):

ExploreDTT_Stats.t	xt - Notepad						_	
File Edit Format	View Help							
0.78486554 0.00089634 0.00195916 0.00041484 0.00031500 37.0000000	0.14041212 0.00015742 0.00017868 0.00024933 0.00019846	0.02308361 0.00002588 0.00002937 0.00004099 0.00003263	0.73869831 0.00084458 0.00190042 0.00033287 0.00024975	0.83103276 0.00094810 0.00201791 0.00049682 0.00038026	0.83258456 0.00087361 0.00193389 0.00034819 0.00025300	0.76193139 0.00078093 0.00184477 0.00028005 0.00020061	0.86492459 0.00097482 0.00206831 0.00050469 0.00037583	E F

DTI (*Basser et al, MRM 44:625-632, 2000*) and CSD (*Jeurissen B. et al, HBM 32:461-479, 2011*) based tractography algorithms have been implemented. By default, the CSD approach implemented in *ExploreDTI* uses recursive calibration of the response function (*Tax C.M.W. et al, NeuroImage 86:67-80, 2014*).

Although one could draw a seed region and then perform tractography from that seed region, I would suggest to do 'whole brain tractography' instead and then use the 'analyze' functionality to extract fiber tract pathways from ROIs, as defined by 'SEEDs' (equivalent to 'OR' gate then), 'ANDs', and 'NOTs'. This reduces the user-bias of SEED ROI definition.

The best way to explain the above in detail is by giving an example: let us extract the 'arcuate fasciculus' (or at least, the reconstructed pathways that *may* represent that WM bundle) and calculate the average FA, MD, etc. along that pathway.

A) Perform 'whole brain tractography' (that is, using a deterministic streamline approach, based on the DTI model). No need to load a DTI *.mat-file yet – just start *ExploreDTI* and go to 'Plugins' (see below):



You can do this for multiple data sets as well (see below, by choosing a folder of DTI *.mat files), but for now, let us choose a single DTI data set.

	O Deterministic streamline tract 🗖 🔳 💌
	Seedpoint Resolution (in mm)
	Seed FA threshold
	0.2
	FA tracking threshold range (limits: [0 1])
	0.2 1
	MD tracking threshold range (limits: [0 realmax])
	Linear geometry tracking threshold range (limits: [0 1])
	Planar geometry tracking threshold range (limits: [0, 1])
	0 1
	Spherical Geometry tracking threshold range (limits: [0 1])
	0 1
	Fiber Length Range (in mm)
	50 500
	Angle threshold (in degree)
Whole brain tractography	
	Step size
For?	Interpolation method (NN: 0: Linear: 1: Cubic: 2)
	1
Single DTI data set (default) Multiple DTI data sets	OK Cancel

Select a DTI *.mat file and save the tracts to a *.mat file, as shown below:



Then the calculations start:

O not close waitbar: unexpected errors may occur!	
Performing whole brain tractography	
	J

Depending on your computer 'specs' it will take around 1 to 10 minutes (that is, for the default values above).

B) Load the tracts (after you have loaded the corresponding DTI *.mat file).



Notice that this eats away your memory (3 GB is no exception – depending mainly on step size and seed resolution)...

C) Placing ROIs to select a structure of interest. Draw 'AND' gates that define regions that would intersect the "arcuate fasciculus". You might need to draw 'NOT' gates to omit fiber tracts that are not of interest. Then, click 'Analyse tracts' and click 'Draw'. In this example, I used 'Tubes' as 'Tract representations' and clicked 'Toggle Light' to give a 3D feel to it. To increase render speed, I've set 'Sub-sampling' to '4'.







Similar to the ROI analysis, you can calculate the stats of fiber tract structures (note that you can also save, load, hide, etc. tracts). I *recommend* saving the end-result as a 'tracts *.mat file', as there is a plugin tool that can convert an entire set of such tract *.mat files to a *.txt file (see 'Plugins' \rightarrow 'Convert' \rightarrow 'Info of tract *.mat file(s) to *.txt'), which contains the corresponding summary statistics.

9. Tract segment analysis

Assume you want to analyse a particular segment of a fiber tract bundle, such as shown below. Here, for instance, we are only interested in a particular segment of these "corticospinal" tracts as outlined by the two AND ROIs. To extract this part of the tracts, go to settings first and check 'segment only' (see below). When checked, clicking 'analyse' will generate a pop-up to save the tract segment (uncheck it afterwards!).





The segmented tracts can then be loaded into ExploreDTI (see below):

Analyse tracts



From this segment, measures of interest (FA, MD, etc.) can be calculated as outlined before. A more general approach to select 'tract segments' of interest is the 'splitter' tool, which uses the SEED (= OR) gates to 'split' the tracts at those positions. The tracts that have been split are then saved. Once reloaded, use 'AND'/'SEED' gates to select the segments of interest:



Save in:	5_Example_	Tractography	•	+ 🗈 💣 💷	-
(Ang	Name		^		
Recent Places Desktop	🕌 Input 🔒 Output				
Computer Computer Network	4				
	File name:	Tracts_split.mat		•	Save
	Save as type:	MAT-files (*.mat)		-	Cancel



Select tract da	ta	3
Look in:] 5_Example_Tractography 💌 🗲 🗈 📸 🖬 🕇	
Recent Places	Name	
	Tracts_split.mat	
Network		
	<	F
	File name: Tracts_split.mat Open Cancel Cancel Cancel	

Draw an 'AND' (green ROI) to select the segment of interest:



Uncheck 'splitter tool', then click 'Analyse tracts' and delete the previous 'display':



Finally, click 'Draw' tracts – only the selected segment will remain:



10. Correcting for subject motion & eddy current induced geometric distortions

The relevant reference for this tool is "Leemans A. and Jones D.K., Magnetic Resonance in Medicine 61(6):1336-1349, 2009 (<u>http://www.ncbi.nlm.nih.gov/pubmed/19319973</u>). The tool to correct for subject motion & eddy current induced geometric distortions can be found in: 'Plugins' \rightarrow 'Correct for subject motion & EC/EPI distortions'. See the menu item 'Settings' \rightarrow 'SM/EC/EPI correction' for more details. I also recommend using multi-core support for this tool (that is, if you have this Matlab toolbox installed): see 'Use parallel computation' in the 'Settings'. By default, the EPI correction step is omitted (see Section 11).

The output is again a DTI *.mat file, but then with the (default) extension '_MD_C_native.mat'. See the before/after examples below:

Before correction

After correction



Before correction

After correction



11. Correcting for EPI/susceptibility distortions

There are several ways to (try to) correct for these deformations. The approach I implemented is based on the work of Irfanoglu et al (http://www.ncbi.nlm.nih.gov/pubmed/22401760) and is integrated with the "subject motion / eddy current distortions" correction tool. In this way, all corrections (SM/EC/EPI) can be performed in one interpolation step (to minimize blurring effects). In summary, if you have an 'undistorted' modality (T1,T2,...), you can use it to unwarp the deformations that are present in your diffusion data:



After 'checking' \rightarrow 'Yes, to do the EPI correction (non-rigid)', a popup will appear asking you to fill in the suffix of the file that will be used to do the correction. Example: if the DTI file is called "Data_set_M.mat" (below, left), then name the T1 file "Data_set_M_T1.nii" (below, right). For a T2, I suggest to use 'Non-DWI' as the choice for 'Define image type for registration', for a T1, you could also try 'Avg(DWIs)' or 'FA'. Masking the T1 (or T2 etc.) data ('zero' value as background) increases the performance (note: scalp may still be present as shown below).



"Data_set_M.mat" (uncorrected)



T1 data set: "Data_set_M_T1.nii"

Important to know: the diffusion data will be resampled to the space of the 'undistorted' modality... you may want to adjust the field-of-view and/or resolution to keep the size of the resulting 'corrected' diffusion data manageable. To actually 'see' how the tool performed, you may want to compare this corrected result with the 'non-corrected' data. You can do this, by checking one of the 'rigid' counterparts: e.g., 'yes, to a single data set (rigid)' instead – then the output will just resample the data to the undistorted (T1) data space:



Uncorrected (rigid) for EPI distortions

Corrected (non-rigid) for EPI distortions

By default, the non-linear deformations are allowed along any orientation. In practice, however, correction will likely improve if the registration is constrained to model deformations only along the phase encoding direction. To do this (assume: A-P orientation), change "Deformation axes" to [1 0 0].



And make sure you first use the plugin "Flip/permute dimensions in 3D/4D *.nii file(s)" to make your nifti files (T1, T2, etc.) "ExploreDTI compatible"... this will avoid unexpected axis flips (& permutations) in the resulting files.

12. Diffusion Kurtosis Imaging (DKI)

To calculate the kurtosis parameters, just set 'NaN' as the b-value when converting your *.nii DWIs and *.txt B-matrix to a *.mat file:

ExploreDTI's data converter to create DTI *.mat files	
Format diffusion weighted data	4D Nifti (*.nii)
Permute spatial dimensions	AP RL IS
Flip spatial orientations	AP RL IS
Perform visual data check	No
Diffusion tensor estimation	Linear 🔹
Format diffusion information	Text file (*.txt)
Background masking approach	Automatic
Permute gradient components	x y z 🔻
Flip sign of gradient components	x y z
Data processing mode	Single data set
b-value in units s/mm^2	NaN
Voxel size [AP RL IS] (in mm)	2.5 2.5 2.5
Number of non-DW images	1
Number of DW images	120
Matrix size [AP RL IS]	128 128 60
Start converting to D	۲۱ *.mat file(s)

You can do everything (correction steps, DTI based tractography, etc.) as before. The most common kurtosis metrics (MK, RK, AK, KA) can be exported from the 'Export stuff to *.nii files' tool in the menu item 'Plugins':

Apparent diffusion coefficients ('_ADCs.nii') ADCs - reconstructed with DT model ('_ADCs_DT.nii') DWIs - reconstructed with DT model ('_DWIs_DT.nii') DWI residuals from DT ('_res_DWI_DT.nii') ADC residuals from DT ('_res_ADC_DT.nii') Mask ('_mask.nii') Lattice Index ('_LI.nii') Mean of DWIs ('_mean_DVIs.nii') Mean of DWIs ('_mean_B0s.nii') HARDI (see settings) ('_HARDI_Lmax_8_CSD_RF_NSim_0.8_8.nii') Diffusion kurtosis tensor ('_KT.nii') Mean kurtosis ('_MK.nii') Axial kurtosis ('_AK.nii') Radial kurtosis ('_AK.nii') Mode of anisotropy ('_KA.nii') Mode of anisotropy ('_AM.nii') Diffusion tensor norm ('_DTN.nii') Skeletonized FA ('_FA_Skeleton.nii') Axonal Water Fraction (from DKI) ('_AWF.nii') Tortuosity (from DKI) ('_TORT.nii')	T
Select all	
OK Cancel	

The REKINDLE (Robust Extraction of Kurtosis INDices with Linear Estimation) approach (default setting while correcting for subject motion, eddy current induced distortions and/or EPI deformations) is preferred for computing these kurtosis metrics (Tax C.M.W. et al, Magnetic Resonance in Medicine 73:794-808, 2015).

13. Automated "atlas based" tractography

This tool is based on the work presented in Lebel et al. (http://www.ncbi.nlm.nih.gov/pubmed/18295509). In summary, it works as follows. First, define a set of ROIs (AND/NOT gates) that would extract your tract of interest (based on an atlas/template or on a representative single subject). Using this information (the 'template' and these regions-of-interest – ROIs), the tract of interest is automatically reconstructed for all your data sets. Below, an example is given on how to do this for pathways of the right uncinate fasciculus (R-UNC).

The input of this tool is a set of DTI *.mat files and their corresponding 'whole-brain' tract *.mat files. In this example, the data sets were all in native space and the tracts were reconstructed with DTI. As you can see below, there are just 3 subjects (FYI – the computation time is roughly 5 to 20 min per data set).



I could use a nice FA template (there are many!), but in this example, I will create a 'pseudo FA atlas template' myself from "Data_1". So simply export the FA from 'Data_1.mat' via 'Plugins' \rightarrow 'Export stuff to *.nii files': select 'Single data set', then select the 'FA', and save it somewhere (e.g., in the same folder that contains all the *.mat files):



Now, we are going to define the ROIs that will be used to reconstruct the pathways of the R-UNC. This is the step that requires our 'prior knowledge' (aka 'anatomical expertise'): "The uncinate fasciculus is a hook-shaped bundle that links the forward portions of the temporal lobe with the inferior frontal gyrus and the lower surfaces of the frontal lobe. It does this by arising lateral to the amygdala and hippocampus in the temporal lobe curving in an upward pathway behind the external capsule inward of the insular cortex and continuing up into the posterior part of the orbital gyrus." – that is, according to the Wiki page! The idea now is to define a configuration of AND/NOT ROIs that would select only these pathways and would leave out all other tract

pathways of the brain. So let us create such ROIs for our 'template', i.e., 'Data_1.mat'. First, load the DTI file: 'Data_1.mat' and then the tracts file: 'Data_1_Tracts_DTI.mat'. If you were to click 'Draw tracts', you would see all of them (see below – but just do NOT do this – rendering will take forever!). I only do this to show the location of the R-UNC pathways in the context of the rest of the brain. The R-UNC connects the temporal (yellow) with the 'inferior frontal' (white) region.





So if I draw two AND ROIs (as in the image above), the only tracts that would remain are these 'frontotemporal' connections. This is shown below (the yellow ROI above corresponds with the green 'temporal' AND ROI below on the left; the white ROI above corresponds with the green AND ROI below on the right):



If you click 'Analyse tracts' (in the 'Draw Tools' palette) or in the menu item 'Calculate' \rightarrow 'Analyze tracts from ROIs', and then (after deleting the previous 'whole-brain' tracts display), click 'Draw tracts', you should see the image below:



Ideally, only the tracts of interest (R-UNC) are left. In practice, however, there will probably be 'spurious' tract pathways that are not part of the structure of interest, but still connect both ROIs (as is the case in this example). These unwanted pathways can be removed by including NOT gates. Try to be as conservative as possible to minimize excluding the ones that are 'correct'. Below, two NOT ROIs are drawn: one covering the entire mid-sagittal slice, and a second one on a coronal slice posterior (with some margin) to the temporal ROI (after deleting the previous tract display, click 'Analyse' again and 'Draw tracts'):



If you are happy with the end result, save each of the ROIs as a separate 3D *.nii mask (using 'Data' \rightarrow 'Save mask of ROIs'). In this example, I did not save each ROI yet, so I will save all the ROIs in one go with 'Data' \rightarrow 'Save multiple ROIs'. In doing so, I created a folder 'ROIs_mat' (below on the left):



In this folder (above right), there are now 4 ROIs. The following step consists of creating 3D *.nii files from each of these ROIs. The resulting 3D *.nii masks have values '0' representing the background and non-zero values representing the actual ROI. First, delete all ROIs in the current display, and load "ROI_AND_1.mat" via 'Data' \rightarrow 'Load single ROI' (below left) and then save it via 'Data' \rightarrow 'Save mask of ROI(s)'. A popup will appear (below right). Here, you should choose 'Nifti' format.



Then, another popup appears, asking you:



The choice here is not too important to be honest, as you just want to create a mask with '0' values in the background and non-zero values in the ROI. So just select 'AND (1)'. The next step, however, which is giving a name to this *.nii file, is crucial as it is the name itself (or at least part of it) that will reflect what type of ROI mask it represents! So in this case, being an AND ROI, we name it: 'ROI_AND_temporal.nii' and put it in a new folder that I created called 'ROI_masks' (see below).

p. 31

Save mask of	ROIs as				×
Save in:	📔 ROI_masks		•	← 🗈 💣 📰▼	
Ca.	Name	*		Date modified	Туре
Recent Places		No items n	natch your s	earch.	
Desktop					
Libraries					
Computer					
Network					
	•				P.
	File name:	ROI_AND_temporal.nii		•	Save
	Save as type:	(*.nii)		•	Cancel

Again: there *should* be a part of the name that is called 'ROI_AND' – the rest (before or after 'ROI_AND') can be anything (in this case '_temporal'). Now, you can do the same for the other ROIs. Analogously, for the NOT ROIs, there should be a part of the file name that is 'ROI_NOT' (see below).

der	ः - □ 0	
der	Name Name ROI_masks ROIs_mat Data_1.mat Data_1_FA.nii Data_1_Tracts_DTI.mat Data_2.mat Data_2.mat Data_3.mat Data_3_Tracts_DTI.mat	 Name ROI_AND_frontal.nii ROI_AND_temporal.nii ROI_NOT_coronal.nii ROI_NOT_midsagittal.nii
	4	+ < III +

Finally – now we can actually use the tool! So go to 'Plugins' \rightarrow 'Atlas based tractography segmentation'! If you click it, there will be the request to select the 'atlas template'. Here, you will select the FA map of our 'representative' subject, i.e., 'Data_1_FA.nii' (see below).

Select atlas ter	emplate (3D *.nii)	
Look in:	🍒 Input 💽 🗢 🛅 🕶	
S	Name A ROI_masks	
	BOIs_mat Data_1_FA.nii	
Desktop		
Libraries		
Computer		
Network		
	<	<u>_</u>
	File name: Data_1_FA.nii _ Open	
	Files of type: (*.nii) Cancel	

In the next step, select the folder of 3D *.nii masks:

Browse For Folder
Select the folder of 3D 'ROI_AND', 'ROI_OR', and/or 'ROI_NOT' *.nii file(s)
▲]] 8_Example_atlas_based_tractography
4 🍌 Input
ROI_masks
📔 ROIs_mat
🍑 Output 🗸 🗸
Folder: ROI_masks
Make New Folder OK Cancel

The next popup states:



Quick intermezzo! By 'segment', I refer to the piece that is between the two outer ROIs. As an example, consider the two tract representations of (part of) the cingulum below. The right one is what I mean with 'segment' – so just a section, defined by the two ROIs.



Back to the R-UNC... So now, let us take the entire bundle of pathways (so click 'No' in the popup window). Then, we need to select the folder that contains the DTI (and tract) *.mat files (see below).

Browse For F	folder 📃 🔀
Select the	folder of DTI *.mat file(s)
	8_Example_atlas_based_tractography Input
	ROI_masks
	🐌 ROIs_mat 💷 📗
	🔒 Output 🗸 🗸
Eolder:	Input
Make Ne	w Folder OK Cancel

After you select this folder, you get yet another popup asking you to fill in the suffix part of the tract *.mat file and the suffix part for the name of the output tract *.mat name (see below – note: "it's case sensitive").

Atlas based tractography analysis	s
Extension name for whole brain tract *.n _Tracts_DTI.mat	nat file (e.g.: '_tracts.mat')
Extension name for the fiber bundle trac '_Left_Cingulum.mat')	t*.mat file (e.g.:
_R_UNC.mat	
	OK Cancel

The final popup appears asking to select a folder to put the output files:

Browse For Folder	x
Select the folder to save the output *.mat tract file(s)	
🖌 📕 📕 8_Example_atlas_based_tractography	۱ I
🖌 🌙 Input	
📕 ROI_masks	
📕 ROIs_mat	
J Output	-
Folder: Output	
Make New Folder OK Cancel]

And now ... have a cup of coffee (see below)!



When this "wait bar" disappears, the analysis has finished and you should see output files like the ones below:



I highlighted the tract *.mat files (above): these are the results! The other data sets are the warped templates and ROIs for each data set (just a post-hoc sanity check – or to see what went wrong if it did go wrong).

So let's just look at the R_UNC tract results for each data set below:



"Data_1_R_UNC.mat" (as expected – we used this one to define the R-UNC in the first place!)

"Data_2_R_UNC.mat"



"Data_3_R_UNC.mat"



Not bad ;-)! Finally, to get the statistics of these tracts, use the tool 'Plugins' \rightarrow 'Convert' \rightarrow 'Info of tract *.mat file(s) to *.txt'. One more thing: with 'Settings' \rightarrow 'Atlas based tractography' \rightarrow 'Tract length range', you can further constrain the output tracts to be within a specific length range (again – just an extra way of using prior knowledge in the analysis).

14. Network analysis tools...

If you think of the brain as a network of connections between brain regions, you may be interested in investigating the properties of this network. With *ExploreDTI*, you can obtain the so-called "connectivity matrices" (CMs), from which you can derive network properties, such as "efficiency", "small-worldness", etc. In addition, with *ExploreDTI* you can create the typical network visualizations.

For more background information and example studies in which the network analysis tools of *ExploreDTI* have been used, see the work of Reijmer YD et al (Neurology 2013, Diabetes 2013, Brain 2015) and Caeyenberghs K et al (Brain Struct Funct 2014, Hum Brain Mapp 2014, Neuroimage Clin 2012, Front Hum Neurosci 2013).

In the following, I will first explain how to compute the CMs. Note: there are two ways in *ExploreDTI* to obtain these CMs: "From atlas template/labels" and "From predefined ROI labels" (see below). After that, I will show you how to make network visualizations.



The difference, in a nutshell, is that with the "From atlas template/labels" tool, you will need an atlas template with associated labels (ROIs), which will be registered to each subject's data set. With the other tool ("From predefined ROI labels"), the ROIs are already derived with another approach (for instance, a T1-based cortical segmentation) and located in the same image space as the diffusion data (see example p. 44).
Let's have a look at the "From atlas template/labels" tool. For each subject, you will need the following data sets: a DTI *.mat file and its associated whole-brain tracts data set (see example below for 2 subjects):

Burn	New folder
	Name
	DTI_data_Subj_01_Tracts.mat DTI_data_Subj_02.mat DTI_data_Subj_02_Tracts.mat

The other files that you will need to run this tool are related to the atlas that you want to use. As an example, let's consider the AAL atlas (see: Tzourio-Mazoyer N et al, NeuroImage 2002). Converted for *ExploreDTI* purposes, the relevant AAL atlas information is now represented in three files:

Name
AAL_Label_Names.txt
🔺 AAL_Labels.nii
AAL_Template.nii

You can download these files from: <u>http://www.exploredti.com/templates/AAL_Template.zip</u>. This one and other examples of such atlas template/label files are provided in the folder "~/Source/Templates".

The *.txt file consists of two columns: the first column contains "0" or "1" values (meaning "0": do not use this ROI in the analysis; "1": do use it for analysis) and in the second column, the label name of the ROI is given. Each ROI is given on a separate row:

AAL_Label_Names.txt - Notepad	
<u>File Edit Format View H</u> elp	
1 Precentral L 1 Precentral R 1 Frontal Sup L 1 Frontal Sup R 1 Frontal Sup Orb L 1 Frontal Sup Orb R 1 Frontal Mid L 1 Frontal Mid Orb L 1 Frontal Mid Orb L 1 Frontal Mid Orb R 1 Frontal Inf Oper L 1 Frontal Inf Oper R 1 Frontal Inf Tri L 1 Frontal Inf Tri R 1 Frontal Inf Orb L 1 Frontal Inf Orb R 1 Frontal Inf Orb R	

The actual row number 'is' important as it represents the intensity value in the associated "Labels" file. So in this case, the 3D nifti file "AAL_Labels.nii" contains the ROIs described in the *.txt file above. More specifically, the region with "0" values is background, the region with intensity values of "1" represents "Precentral L", the region with intensity values of "2" represents "Precentral R", etc. The corresponding AAL atlas template (here, "AAL_Template.nii") is needed to perform the registration. Both files are shown below with MRIcron:





Let's actually run this tool now... Go to "Plugins" and then (see below) "From atlas template/labels" (btw, to speed up things, you may want to use the "Use parallel computing..." option in "Settings" – make sure you have enough memory... memory usage will be proportional with the number of cores that you define and can be roughly in the order of 2 GB per core).



The steps to follow are first:

Select atlas labels (3D *.nii)		
🕞 🗢 📕 « Local Disk (C:) 🕨 ExploreDTI		
Organize 🔻 New folder		
Name		
AAL_Labels.nii		
AAL_Template.nii		

Then:



Then:



Then:



Recall... this is the folder that also contains the *.mat tract files (see below - this is important for the next step).

uter 🕨 Local Disk (C:) 🕨 ExploreDTI 🕨 Data	
ls Help	
e in library 🔻 Share with 👻 Burn	N
Name	
🛅 DTI_data_Subj_01.mat	
🛅 DTI_data_Subj_01_Tracts.mat	
🛅 DTI_data_Subj_02.mat	
🛅 DTI_data_Subj_02_Tracts.mat	

Then you need to enter the end-part of the tract file name – simply to find the corresponding files (note: this is case-sensitive!):

Network analysis			
Extension name for tract *.mat file _Tracts.mat	(e.g.: '_tracts.mat')		
Extension name for 3D/4D *.nii volume file (e.g.: '_MTR.nii')			
	OK Cancel		

Keep the second line empty (unless you have a *.nii file that is registered to the diffusion data that you want to integrate in this pipeline... anyway, I'll explain this particular feature on another occasion).

The next step is then to select the folder to save all the output (here, I made a folder called "Output" – just because I can):

Select the folder to	save the outp	out	: *.mat	t networ
Q → ↓ «	ExploreDTI	Þ	Data	۲
Organize 🔻	New folder			
Name	<u>^</u>			
퉬 Output				

Then the next pop-up appears:



Well – as it says, you can choose to save tracts (if there are any) between the different combinations of the ROIs defined in the template. Let us proceed with yes, then the following pop-up shows all these potential ROI combinations (as an example, I'll choose the tracts that connect the left anterior and posterior cingulate cortices):

Select inter-label tract bundles	
-	
Cinquium Ant L. conn. Calcarine I	
Cingulum Ant L conn Calcarine R	
Cingulum Ant L conn Caudate L	
Cingulum Ant L conn Caudate R	
Cingulum Ant L	
Cingulum Ant L_conn_Cingulum Ant R	
Cingulum Ant L_conn_Cingulum Mid L	
Cingulum Ant L_conn_Cingulum Mid R	
Cingulum Ant L conn Cingulum Post L	
Cingulum Ant L_conn_Cingulum Post R	
Cingulum Ant L_conn_Cuneus L	
Cingulum Ant L_conn_Cuneus R	
Cingulum Ant L_conn_Frontal Inf Oper L	
Cingulum Ant L_conn_Frontal Inf Oper R	
Cingulum Ant L_conn_Frontal Inf Orb L	
Cingulum Ant L_conn_Frontal Inf Orb R	
Cingulum Ant L_conn_Frontal Inf Tri D	
Cingulum Ant L_conn_Frontal Med Orb L	
Cingulum Ant L conn Frontal Med Orb R	
Cingulum Ant L conn Frontal Mid I	
Cingulum Ant L conn Frontal Mid Orb L	
Cingulum Ant L conn Frontal Mid Orb R	
Cingulum Ant L conn Frontal Mid R	
Cingulum Ant L_conn_Frontal Sup L	
Cingulum Ant L_conn_Frontal Sup Medial L	
Cingulum Ant L_conn_Frontal Sup Medial R	
Cingulum Ant L_conn_Frontal Sup Orb L	
Cingulum Ant L_conn_Frontal Sup Orb R	
Cingulum Ant L_conn_Frontal Sup R	
Cingulum Ant L_conn_Fusiform L	
Cingulum Ant L_conn_Fusitorm R	
Cingulum Ant L_conn_Heschi L	
Cingulum Ant L_conn_Heschi R	
Cingulum Ant L_conn_Hippocampus L	
Cingulum Ant L_conn_Insula L	
Cingulum Ant L conn Insula R	
Cingulum Ant L conn Lingual L	
Cingulum Ant L conn Lingual R	
Cingulum Ant L conn Occipital Inf L	
Cingulum Ant L_conn_Occipital Inf R	
Cingulum Ant L_conn_Occipital Mid L	
Cingulum Ant L. conn. Occinital Mid P	Ť
Select all	
OK Cance	el

These files can be loaded into ExploreDTI afterwards (sanity checks!) or used for other analysis purposes...

The final pop-up before the processing actually starts is:



In short, with *ExploreDTI* you can differentiate between tract pathways "passing through" two ROIs and those that actually "end" in these ROIs (see sketch below). In current literature, this differentiation is generally not made – the "pass" definition is implicitly taken then. FYI – there is hardly any extra computational cost if you compute both ("pass" and "end"), hence the third option.



"PASS" definition: A is connected to B, B is connected to C, A is connected to C "END" definition: A is connected to C (the pathway terminates in regions A and C, but not in B)

Processing time per data set is approximately 10 min to 2 h depending on your hardware specs, data size, etc. The output files are (FYI, I chose the "PASS and END" option):

(1) "Temp_atlas_labels.nii": this is simply the "template labels" file of the atlas, but then only with the ROIs that you have selected for analysis (recall: the first column in the text file being "0" or "1"). In this example, notice that the cerebellar ROIs are not included. This data set will be useful for visualization purposes (see later).



(2) For each subject, there will be a "Template_X.nii" and a "Labels_X.nii" file with the "X" representing the tract file name (so in this example, the "X" is "DTI_data_Subj_01_Tracts" for subject 1 and "_DTI_data_Subj_02_Tracts" for subject 2):

Labels_DTI_data_Subj_01_Tracts.nii
Template_DTI_data_Subj_01_Tracts.nii
Labels_DTI_data_Subj_02_Tracts.nii
Template_DTI_data_Subj_02_Tracts.nii

The "Template_X.nii" and "Labels_X.nii" files are just the transformed "template" versions for each subject (this output serves for quality control).

(3) If you chose to export "inter-label" tract bundles, these will be located in "temp_X" folders with the X reflecting the subject tract file names (with "END" / "PASS" specification). In this example:

Name
퉬 temp_PASS_DTI_data_Subj_02_Tracts
퉬 temp_END_DTI_data_Subj_02_Tracts
temp_PASS_DTI_data_Subj_01_Tracts
퉬 temp_END_DTI_data_Subj_01_Tracts

(4) The actual "connectivity matrices" (CMs)! For each subject, the following *.mat files are generated (I highlighted the files for subject 1):

As you can see, there are CMs for "PASS" and "END" definitions. Each *.mat file contains one variable, called "CM" and is simply an N x N matrix with N the number of ROIs in the analysis.

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There are many ways to construct a CM. The value at position (i,j) of CM either represents the "number of tracts" (*_number_of_tracts_*), fractional anisotropy (*_FA_*), mean/axial/radial diffusivity (*_MD/AD/RD_*), second/third eigenvalue (*_L2/L3_*), the linear/planar/spherical ("Westin") anisotropy measures (*_CL/CP/CS_*), the average tract length (*_average_tract_length_*), the binary value: connection or not (*_binary_*), the density weight (see definition in P. Hagmann et al PLoS Biol 2008, *_density_weight_*), percentage of tracts (*_percentage_of_tracts_*), tract volume (*_tract_volume_*), the distance between the ROI centers of gravity (*_inter_label_distances_*), and in case of CSD: the amplitude of the fiber orientation distribution (*_FOD_*) of the fiber bundle connecting ROI "i" with ROI "j".

For the other option, "From predefined ROI labels" (see below), the only difference is that for each subject, you'll need a separate 3D *.nii file (same name, but with suffix added, such as "_labels.nii") with ROIs in a similar format to the "atlas labels" *.nii file from above. Note that these "label" files must be in the same space of the diffusion data (computation times are in the order of a few minutes to a few hours per data set, depending on size).

Gaussian smoothing (*.nii) TV for Gibbs ringing in non-DWI's (4D *.nii)		\backslash
Network analysis tools	Get 'connectivity' matrices	From atlas template/labels
Atlas based tractography segmentation	Get Label coordinates	From predefined ROI labels
Mask 3D *.nii file	Get Label volumes & surface areas	
	Create template labels from MNI coordinates	
	Calculate connectivity SNR	

I will explain the "From predefined ROI labels" plugin with an example. Assume you want to compute the ROIs with <u>FreeSurfer</u>.

After using FreeSurfer ("recon -all"), the result should be something like the folder structure shown on the left below:



The important folder for now is "mri" and looks something like the right above.

First, convert the FreeSurfer stuff to "ExploreDTI compatible *.nii files":



Select multiple:



Then select that "mri" folder:

Name	^
퉬 orig	

Just make a new folder "nii" and select it as the output folder

New folder			
*	Name	*	
	\mu nii		
-1	鷆 orig		
=	鷆 transforms		

Then wait a bit:



The result looks something like:

Name
🛎 aparc.a2009s+aseg.nii
🧉 aparc+aseg.nii
🧉 aseg.auto.nii
🥌 aseg.auto_noCCseg.nii
👛 aseg.nii
🧉 brain.finalsurfs.nii
🧉 brain.nii
🧉 brainmask.auto.nii
🧉 brainmask.nii
🛎 filled.nii
🛎 lh.ribbon.nii
🛎 norm.nii
🛎 nu.nii
🛎 nu_noneck.nii
🧃 orig.nii
🛎 orig_nu.nii
🛎 rawavg.nii
🛎 rh.ribbon.nii
🛎 ribbon.nii
🛎 T1.nii
🛎 wm.asegedit.nii
🛎 wm.nii
🛎 wm.seg.nii
🛎 wmparc.nii

The "brain.nii" file is now actually useful! If your DTI *.mat file (the "uncorrected data"!) is called: "Sub_01.mat", then rename this "brain.nii" file to "Sub_01_T1_brain.nii". Now you can use "Sub_01_T1_brain.nii" for doing the SM/EC/EPI distortion correction step (see p. 24/25). Make sure you change the deformation axes settings to [1 0 0] (assuming you have the PE along the AP axis). The result after applying the "Correct for subject..." plugin should be something like:

Name
🛅 Sub_01.mat
🛅 Sub_01_MD_C_native.mat
脑 Sub_01_MD_C_trafo.mat
🛎 Sub_01_T1_brain.nii

Quick intermezzo: You can check the result by overlaying the color-coded FA with the T1:





Figures - ExploreDTI v4.8.4 - © Alexander Leemans F:		
Data Image map Axis Draw	Calculate	Color
Load DTI (*.mat)	Ctrl+	L
Load volume (*.mat,*.nii)		
Load fiber tracts (*.mat)		
Load single ROI (*.mat)		
Load multiple ROIs (*.mat)		
Load CSD FOD (*.mat,*.nii)		
Save fiber tracts (* mat * nii * tv	H)	









"Miscellanea \rightarrow Fuse CV with FEFA"... Looks good!

Now do some fiber tractography: DTI or CSD based – whatever you like ;-)! FYI, I named the resulting tract file: "Sub_01_MD_C_trafo_Tracts.mat".

Name
🛅 Sub_01.mat
🛅 Sub_01_MD_C_native.mat
🛅 Sub_01_MD_C_trafo.mat
🛅 Sub_01_MD_C_trafo_Tracts.mat
🧉 Sub_01_T1_brain.nii

Now, we're going to convert the freesurfer *.nii parcellations to *ExploreDTI* compatible *.nii parcellations (this produces the label *.txt files as well):

Make a new folder "E_DTI" in the "nii" folder:

Name
\mu e_dti
🛎 aparc.a2009s+aseg.nii
🛎 aparc+aseg.nii
aseg.auto.nii 🗠
aseg.auto_noCCseg.nii
aseg.nii 🦉
brain.finalsurfs.nii
brain.nii
brainmask.auto.nii
brainmask.nii
filled.nii
Ih.ribbon.nii
anorm.nii
🕘 nu.nii
🛎 nu_noneck.nii
a orig.nii
a orig_nu.nii
🧉 rawavg.nii
🛎 rh.ribbon.nii
🧉 ribbon.nii
a T1.nii
🛎 wm.asegedit.nii
a wm.nii
🍯 wm.seg.nii
🛎 wmparc.nii

In Plugins, go to:

Automated FOV cropping of DTI *.mat files	Different B	
Convert	Info of tract *.mat file(s) to *.txt	
Get diffusion metrics from	*.bval/*.bvec to B-matrix *.txt file(s)	
Gaussian smoothing (*.nii)	B-matrix in DTI *.mat file(s) to *.bval/*.bvec file(s)	
TV for Gibbs ringing in non-DWI's (4D *.nii)	3D *.nii 'stack' to 4D *.nii	
Network analysis tools	Dicom folder(s) to *.nii files	
Atlas based tractography segmentation	Diffusion *.par/*.rec to *.nii/*.txt (version 1)	
Mask 3D *.nii file	Diffusion *.par/*.rec to *.nii/*.txt (version 2)	
	'2dseq' to *.nii	
	'method' to B-matrix *.txt	
	'*.img/*.hdr' to *.nii	
	Tract *.mat file(s) to *.vtk	
	Folder of images to movie (uncompressed *.avi)	
	*.nii to *.nii.gz (compress)	
	*.nii.gz to *.nii (decompress)	
	Freesurfer files to *.nii	
	Freesurfer parcellations (*.nii) to E_DTI format	
•		
outo processina		
Single or multiple data sets?		

And select the "nii" folder as input and the "E_DTI" folder as output. Then wait a few seconds... The output is now something like:

Single

Multiple

aparc.a2009s+aseg_E_DTI.nii 🖉	
aparc.a2009s+aseg_E_DTI_color.txt	
aparc.a2009s+aseg_E_DTI_labels.txt	
👛 aparc+aseg_E_DTI.nii	
aparc+aseg_E_DTI_color.txt	
aparc+aseg_E_DTI_labels.txt	
👛 aseg.auto_E_DTI.nii	Ih.ribbon_E_DTI.nii
aseg.auto_E_DTI_color.txt	lh.ribbon_E_DTI_color.txt
aseg.auto_E_DTI_labels.txt	lh.ribbon_E_DTI_labels.txt
🛎 aseg.auto_noCCseg_E_DTI.nii	🛥 rh.ribbon_E_DTI.nii
aseg.auto_noCCseg_E_DTI_color.txt	rh.ribbon_E_DTI_color.txt
aseg.auto_noCCseg_E_DTI_labels.txt	rh.ribbon_E_DTI_labels.txt
🛎 aseg_E_DTI.nii	🛥 ribbon_E_DTI.nii
aseg_E_DTI_color.txt	ribbon_E_DTI_color.txt
aseg_E_DTI_labels.txt	ribbon E DTI labels.txt
🥌 filled_E_DTI.nii	wmparc E DTI.nii
filled_E_DTI_color.txt	wmparc E DTI color.txt
filled_E_DTI_labels.txt	wmparc E DTI labels.txt
Ih.ribbon F DTI.nii	

Use for instance the "Desikan-Killiany" atlas ("aparc+aseg_E_DTI") and only the relevant labels (change "1" values to "0" if you do not want to use them):

aparc+aseg_E_DTI_labels.txt - Notepad	aparc+aseg_E_DTI_labels.txt - Notepad
File Edit Format View Help	File Edit Format View Help
<pre>D Left-Cerebral-White-Matter 0 Left-Cerebral-white-Matter 0 Left-Cerebellum-white-Matter 0 Left-Cerebellum-cortex 1 Left-Thalamus-Proper 1 Left-Putamen 1 Left-Putamen 1 Left-Putamen 1 Left-Putamen 1 Left-Putamen 1 Left-Aunygdala 0 CSF 1 Left-Accumbens-area 1 Left-VentralDC 0 Left-vessel 0 Left-vessel 0 Right-Cerebral-White-Matter 0 Right-Cerebral-White-Matter 0 Right-Cerebellum-White-Matter 0 Right-Cerebellum-Cortex 1 Right-Cerebellum-Cortex 1 Right-Caudate 1 Right-Caudate 1 Right-Pallidum 1 Right-Hippocampus 1 Right-Accumbens-area 1 Right-Pallidum 1 Right-Pallidum 1 Right-Pallidum 1 Right-Mutamen 1 Right-Accumbens-area 1 Right-Cortensities 0 Optic-Chiasm 0 CC_Posterior 0 CC_Central 0 CC_Mid_Anterior 0 CC_Central 0 CC_Mid_Anterior 0 CC_Chid_Anterior 0 CC_Chid_Anterior 0 CC_Chid_Anterior 0 CC_Anterior 0 CC_Anterior 1 ctx-lh-inferiorparietal 1 ctx-lh-inferiorparietal</pre>	<pre>1 ctx = h-middl etemporal 1 ctx = h-paracentral 1 ctx = h-parsopercularis 1 ctx = h-parsopottalis 1 ctx = h-parsorbitalis 1 ctx = h-parsorbitalis 1 ctx = h-parsorbitalis 1 ctx = h-percentral 1 ctx = h-precentral 1 ctx = h-superiorfontal 1 ctx = h-frontalpole 1 ctx = h-transversetemporal 1 ctx = h-transversetemporal 1 ctx = h-caudalanteriorcingulate 1 ctx = h-caudalanteriorcingulate 1 ctx = h-fusiform 1 ctx = h-fusifor = hore = hore</pre>

So, here, a total of 84 nodes... Just as an example.

But feel free to use another parcellation scheme!

Now rename the label file "aparc+aseg_E_DTI.nii" to "Sub_01_MD_C_trafo_labels.nii" and put it in the folder with the *.mat DTI file (move non-relevant files to another folder and make a folder "output"):

Name
鷆 output
Label_names.txt
🛅 Sub_01_MD_C_trafo.mat
Sub_01_MD_C_trafo_labels.nii
脑 Sub_01_MD_C_trafo_Tracts.mat

BTW – I just renamed "aparc+aseg_E_DTI_labels.txt" to "Label_names.txt", but not really necessary (and only one such *.txt file is needed for all subjects when using the network tool below).

Now - finally ready to use the network tool (make sure you have enough RAM on your PC!):



Select the folder with the DTI *.mat files (in this example only 1 subject is in it, but it works for multiple subjects too):

	New folder Name Doutput
Given this below:	
	Name uotput Label_names.txt Sub_01_MD_C_trafo.mat Sub_01_MD_C_trafo_labels.nii Sub_01_MD_C_trafo_Tracts.mat

It should be clear that (set the "volume *.nii file extension" to "empty"):

🌖 Network a	nalysis	
Extension nam	e for tract *.mat file	
_Tracts.mat		
Extension nam	e for 3D/4D *.nii volume file (set e	mpty if not relevant)
Extension nom	e for 3D *.nii ROI labels file	
_labels.nii		
		OK Cancel

Then, select the text file:

Then... similar as before... I say "No" here for sake of simplicity (see below):



Then, choose the "type of connection" (END/PASS) – see above for explanation... Just select both for now (not too much additional computational cost anyway):

Type of connection between label ROIs	
Choose 'PASS', 'END', or both 'PASS' and 'END' PASS END PASS and END	

And finally, select the output folder:

•	Name	
	퉬 output	
=		

And then wait...

Do not close waitbar: unexpected errors may occur!	
Waitbar	
(

Could be a few hours per subject... depending on PC specs! But it can be parallelized with the setting (again: check RAM!!!):



The output is as before (see p. 42-44):

Name 1 Sub_01_MD_C_trafo_Tracts_AD_END.mat 1 Sub_01_MD_C_trafo_Tracts_AD_PASS.mat Sub_01_MD_C_trafo_Tracts_average_tract_length_END.mat 1 Sub 01 MD C trafo Tracts average tract length PASS.mat 1 Sub 01 MD C trafo Tracts binary END.mat 🛅 Sub_01_MD_C_trafo_Tracts_binary_PASS.mat 1 Sub_01_MD_C_trafo_Tracts_CL_END.mat Sub_01_MD_C_trafo_Tracts_CL_PASS.mat Sub_01_MD_C_trafo_Tracts_CP_END.mat Sub_01_MD_C_trafo_Tracts_CP_PASS.mat Sub_01_MD_C_trafo_Tracts_CS_END.mat 1 Sub_01_MD_C_trafo_Tracts_CS_PASS.mat Sub_01_MD_C_trafo_Tracts_density_weight_END.mat Sub_01_MD_C_trafo_Tracts_density_weight_PASS.mat 1 Sub 01 MD C trafo Tracts FA END.mat Sub_01_MD_C_trafo_Tracts_FA_PASS.mat Sub_01_MD_C_trafo_Tracts_inter_label_distances.mat Sub_01_MD_C_trafo_Tracts_L2_END.mat Sub_01_MD_C_trafo_Tracts_L2_PASS.mat Sub_01_MD_C_trafo_Tracts_L3_END.mat Sub_01_MD_C_trafo_Tracts_L3_PASS.mat Sub_01_MD_C_trafo_Tracts_MD_END.mat 1 Sub_01_MD_C_trafo_Tracts_MD_PASS.mat Sub_01_MD_C_trafo_Tracts_number_of_tracts_END.mat 🚵 Sub 01_MD_C trafo Tracts number of tracts PΔSS mat

Note: to speed up calculations, you could resample the relevant files to a lower resolution (e.g., [2 2 2] mm instead of [1 1 1] mm results in a speed-up factor of 8!) – before starting the SM/EC/EPI correction step.

Hopefully, you can now manage to get these CMs... So what's next? Well, now you need another software tool that allows you to compute the "graph theory" measures and perform group analyses – no need for me to reinvent the wheel here ;-)! Based on a quick Google search, BCT (<u>http://www.brain-connectivity-toolbox.net</u>) and GAT (<u>http://ncnl.stanford.edu/tools.html</u>) seem to be good candidates – but don't quote me on it... I have not tried these tools myself.

And now... the visuals! Perhaps the most complicated part... and it takes a lot of work, but then again, it may be worth it (think: cover of journal)! There are many options and different ways to create these connectivity visualizations (aka: "connectography"), but for now, I will just provide a "quick" example.

Step 1: download the DTI 2mm template (see below) and wait a few seconds (or minutes):





Step 2: Load the resulting "ICBM_Mori_DTI_2mm.mat" file in ExploreDTI (see below):

Step 3: "Get label coordinates... \rightarrow MNI" (see below):



Select the "atlas labels" *.nii and the *.txt "label names" files... Here:

Select atlas labels (3D *.nii)	Select label names (two column *.txt)
Co V K Local Disk (C:) + ExploreDTI +	✓ 😺 « Local Disk (C:) → ExploreDTI →
Organize 🔻 New folder	Organize 🔻 New folder
Name	Name
AAL_Labels.nii	Data
AAL_Template.nii	AAL_Label_Names.txt
AAL_Template.nii	AAL_Label_Names.txt

And save the output as:

Save label coordinates as	x
Correction of the second seco	٩
Organize 🔻 New folder	0
Image: Contacts ^ Image: Desktop Image: Desktop Image: Downloads Image: Desk	ł
File name: Label_coordinates.txt Save as type: text files (*.txt)	•
Hide Folders	

In this step, the MNI coordinates of the center of gravity of the ROIs were computed:

🧾 La	bel_coordinates	.txt - No	otepad
File	Edit Format	View	Help
-40	-7	50	
40	-9	51	
-19	34	41	
21	30	43	
-18	46	-14	
17	47	-15	
-34	32	34	
37	32	33	
-32	49	-11	
32	52	-12	
-49	14	10	
49	20	12	
10	29	13	
-37	30	-13	
	20		

Step 4: Load these "node" coordinates (see below):

tions	Miscellanea	Debug	Desktop	Wir	ndow	Help	Plug	ins C	alculate D1	TI *.mat	file 계 전 >	<
	Make fig	gure								⊞ [188	
-	Change	working o	directory					40				
	Change	backgrou	nd color					46	+			
	Show da	ata quality	summary									
	Overlay	tract visita	ation map	•								
	Fuse CV	with FEF4	4									
	Fuse CV	with MNI	label									
	View CV	in multi-	slice									
	Surface	render ma	ask (3D *.ni	ii)								
	Downloa	ad		•								
	'Connec	tivity' net	work		-	Nodes	1	Size		-		
						Edges	1	Opaci	ty	•		
						Labels	<u>ا</u>	Color				
					1	Show	<u> </u>	Load o	oordinate	s I	MNI	
								Rende	er quality		ExploreDTI	11



Now, use the "Axis Palette" to uncheck the image planes and "hide the axis":

ori_DT	I_2mm.mat	/ inguies	Figures
ings	Palettes Animations Miscellanea De	Data Image map Axis Draw Calculate Color Show Hide	Data Imagemap Axis Draw Calculate Color Show
	Axis		
	Draw	Hide Reverse view Cross hairs	Show Reverse view Cross hairs
	PASTA		
	QA DWIs		
	QA Volume	XView XView ZView	XView XView ZView
	Multi-fiber visualization	Aview Then Lylew	
	1700	✓ XPlane ✓ YPlane ✓ ZPlane	XPlane YPlane ZPlane

Step 5: now, you will actually see nothing, but then click "Show \rightarrow Nodes" (see below):

Delete Settings Palettes Animation	Miscellanea De <u>b</u> ug <u>D</u> esktop	Window Help Plugins Calculate DTI*.mat file
	Make figure	8088
■ 55 ■	Change working directory Change background color Show data quality summary Overlay tract visitation map Fuse CV with FEFA Fuse CV with MNI label View CV in multi-slice Surface render mask (3D *.nii Download	▶ 46
	'Connectivity' network	Nodes 🕨
		Edges Labels Labels
		Edges Label Names

Also click "Toggle light" to get shading effects (see below):



You can right-click these "nodes" to change their properties:



Step 6: Now let's change the color, size, and opacity of these nodes (starting with "size"):

							-			
ons	Miscellanea	Debug	Desktop	Window	Help	Plugins	Calculate D1	'I *.mat f	ile 🛚	
	Make fig	jure					⊞		80	
	Change Change Show da Overlay 1 Fuse CV Fuse CV View CV Surface 1 Downloa	working o backgrou ita quality tract visita with FEFA with MNI 'in multi-: render ma ad	directory nd color summary ation map A label slice ask (3D *.nii)	•			46			
	'Connec	tivity' net	work	1	lodes	Size		I P	lot range	
	110			E	dges I	Opa	city	۱ v	alue range	
			5°0 20	L S	abels i	Colo Load Reno	r I coordinates der quality	P L	oad file (1 co	lumn *.txt file)

The idea is now to select a text file that contains "numbers" reflecting relative size differences. In this example, I just generated some numbers (N = 90 rows)...

🧾 So	ome_p	roperty.txt	- Note	pad
File	Edit	Format	View	Help
281	.74.0	00		
270)58.0	000		
289	015.0	00		
320	89.0	00		
76	54.0	000		
78	359.0	000		
387	22.0	000		
403	374.0	00		
71	12.0	00		
80	057.0	00		
82	271.0	000		
111	.74.0	000		
201	.04.0	000		
1/1	32.0	000		
135	90.0	000		

Now go to "Plot range" and adjust "5" to something like [1 6] (see below):



Now "right-click" a node and choose "Delete all nodes" (see below):



And then, draw the nodes again (see below) – with the new settings for size, you will see:





Similarly, you can adjust the node opacity and color... For opacity, use, for instance, a "plot range" of about [0.1 1] ("0" is invisible and "1" is fully opaque) with min-max color "Mapping" (see below):

									_ 0				
	itions	Miscellanea	Debug	Desktop	Window	Help	Plugins	Calculate DT	I *.mat	file 🔉			
		Make fi	gure					Ξ		80			
		Change Change	working di backgroun	irectory id color				46 보					
		Show da Overlay	ata quality s tract visitat	summary tion map	•								
		Fuse CV Fuse CV	with FEFA	label									
Network Analysis		Surface	render mas	sk (3D *.nii)									
Set node opacity (plot range)		'Connec	tivity' netw	/ork	E N	lodes I daes I	Size Opac	itv	* *				/
					L	abels I	Color			Approach		Single color	1
OK Cancel					s	how I	Load	coordinates	•	Value range	\checkmark	Mapping	
							Rend	er quality		Color map	1	True indexed colors	

You can increase the "Nodes" \rightarrow "Render quality" to get higher-resolution images (at the cost of slower interaction):

Set render directions	
Number of render directions (0 -> custom; 1 5 -> 512: 6 -> 1024: 7 -> 2048: 8 -> 4096)	-> 16; 2 -> 64; 3 ->128; 4 -> 256;
4	
	OK Cancel

The result (with "hsv" color map):



The "Value range" setting is useful for visualizing differences in node (and edge) properties, for instance, between populations. By defining such a fixed value range, the same "dynamic range" for display will be chosen. Otherwise, due to the min-max mapping, you accidently may be comparing apples with oranges. Note that with this setting, you can also perform "value clipping" to get a more "efficient" visualization (e.g., think of outliers). Anyway... moving on!

Step 7: Let's add some label names... this was a fun step to script (the nerdy stuff)! Simply "Load Label names..." and if need be change "Font size & color" (btw, I've quickly set the node opacity back to "1" for better visibility of *all* nodes):



Now, do the following (click "Two columns"):





Or if you take the more *artistic* "Ring" option (btw, use the "Miscellanea" \rightarrow "Make figure" tool to make high-res images):





Step 8: Now, let's remove the label names and add some brain context (e.g., left hemisphere - see below):

And adjust some settings - e.g. set opacity to 0.1 (right-click, see below):





p. 65

Step 9: finally, let's add some "edges"... First define which edges exist:

ins	Miscellanea	Debug	Deskton	Window	Help	Plugins	Calculate DTI *.mat file	
	Make fi	jure	Desktop		Theip	riagins		
	Change Change Show de Overlay Fuse CV Fuse CV View CV Surface	working of backgrou ata quality tract visita with FEFA with MNI i in multi- render ma	directory ind color r summary ation map A I label slice ask (3D *.nii)					
•	Connec	aa tivity' net	work	N	odes 🕨			
0	•	•		E C	dges abels now	Size Opac Color	ity	+ + +
•	•					Load Rend	binary 'CM' matrix (*.mat er quality	:file) 📥

As an example, I'm picking a result from subject 1 here (just for sake of simplicity):

Select binary edge matrix ('CM' matrix *.mat)
🚱 🔍 🛡 🕌 « ExploreDTI 🕨 Data 🕨 Outpu
Organize 🔻 New folder
Name
temp_PASS_DTI_data_Subj_01_Tracts
temp_PASS_DTI_data_Subj_02_Tracts
DTI_data_Subj_01_Tracts_AD_END.mat
DTI_data_Subj_01_Tracts_AD_PASS.mat
DTI_data_Subj_01_Tracts_average_tract_le
DTI_data_Subj_01_Tracts_average_tract_le
DTI_data_Subj_01_Tracts_binary_END.mat
DTI_data_Subj_01_Tracts_binary_PASS.mat
DTI_data_Subj_01_Tracts_CL_END.mat
DTI_data_Subj_01_Tracts_CL_PASS.mat
•

Now, you *could* already show the edges (see below):



But likely, it will not be very informative (with default settings - see below):



Right-click to delete all the edges and adjust settings of color/size/opacity – in a similar way as with the nodes to get something like this:



That's all for now ;-)!

The fun stuff ;-)! First, you need to define a set of "axis views", which will form the basis of the "path" of the animation. Let's start off with the first "axis view", which will then be the start of the animation (see below).



Do the following: "Settings \rightarrow Axis view \rightarrow Export settings".



Now save the *.txt file in an empty folder. Here, I've named it "View_1.txt" and I've put it in the folder "C:\ExploreDTI" (see below).

Export axis view settings as									
Coord and a state of the st	cal Disk (C:) 🕨	ExploreDTI	- - - + j	Search ExploreDTI	٩				
Organize 🔻 Ne	w folder				:= • 🕡				
Name 🔻 Date m	odified	Туре	Size						
		No items match	your search.						
File name:	View_1.txt								
Save as type:	text files (*.txt)			•				
🔺 Hide Folders				Save	Cancel				

Now, we need to define the next "axis view". So "manipulate" (e.g., zoom in, move, orbit, etc.) the figure (i.e., the camera axis settings) to another "axis view". I rotated and zoomed in to the "axis view" shown below:



Save this axis view (just like before: "Settings \rightarrow Axis view \rightarrow Export settings"), but now name it "View_2.txt". The numbering is important, as it will determine the order of the "axis views" in the animation. You can repeat these steps as many times as you want. As shown below, I saved nine "axis views".

		X
Good ▼ 4y Search ExploreDTI Y Search ExploreDTI ▼ 4y		٩
File Edit View Tools Help		
Organize Include in library Share with Burn New folder		?
Name		
View_1.txt		
View_2.txt		
View_3.txt		
View_4.txt		
View_5.txt		
View_6.txt		
View_7.txt		
View_8.txt		
View_9.txt		
<		- F
9 items		

In summary, these text files contain "camera settings" that form the "key frames" in the animation. Here's what such a file looks like:

Wiew_1.txt - Note	epad		
File Edit Format	t View Help		
124.02100000 0.00296055 86.91199453 30.00000000 30.66750000 387.76350000	79.31728000 -0.04302720 2.45334303 30.00000000	113.94820000 0.99906951	*
			Ŧ
		4	.đ

These numbers correspond with the axis properties as shown in "Settings \rightarrow Axis view \rightarrow Define settings" (see below). Btw, if you want, you can edit these values... think outside the box ;-)!

🜒 Axis view 🗖 🗖 💌
Camera target [x y z]
124.021 79.31728 113.9482
'Sky' vector [x y z]
0.0029606 -0.043027 0.99907
Axis [azimuth elevation] (deg)
86.912 2.45334
Light [azimuth elevation] (deg)
30 30
Camera 'perspective' angle (deg)
30.6675
Camera distance
387.7635
OK Cancel

If you want your animation to loop in a natural "cyclic" way, then copy the file "View_1.txt" to "View_9.txt" (that's what I did here... so the last frame of the animation is equal to the first frame).

The next step is to actually have a look at the animation. To do this, you need to "Load the folder of axis views" in the "Animations \rightarrow Axis view paths" menu item (see below).



Here, I have selected this folder: "C:\ExploreDTI". Then, just click "And... Action!" in the "Animations \rightarrow Axis view paths" menu item (see below):



Hopefully, you'll see something happening as shown below:



At this stage, you're simply "checking" your animation... If you are happy with the "path" of animation, then you can adjust the "number of frames" (the temporal resolution). Also the spatial resolution can be adjusted

(think "full HD" or even "4K" resolution of the frames). My suggestion, start with low values of "number of frames" (e.g., 100) and "print resolution" (e.g., 100) for sake of efficiency and then increase these values to whatever you want. The final step is to create all the frames (the "computational expensive" part). So define an output folder (click "Export frames"):

Palettes	Animations	Miscellanea	Debug	Desktop	Window	Help	F
	Show fra	ame					
	Make ro	tate movie					
163 主	Axis viev	v paths 🛛 🕨	Set n	umber of fi	rames		
			Set p	rint resoluti	ion	1	
			Expo	rt frames		J	
			Load	folder of a	xis views		
			And.	Action!		internation of the local division of the loc	
			1.00°	-		-	2

I created a new subfolder "Frames" (see below) and selected that one.

Select the folder to export the frames								
🚱 🔵 🗢 退 « Local Disk (1	C:) ▶ ExploreDTI ▶	✓ ⁴ → Sear	rch ExploreDTI	Q				
Organize 🔻 New folder			:==	• 🔞				
Name		<u>^</u>						
퉬 Frames								
)				
Folder:	Frames							
		Select	Folder	ancel				

Notice that "Export frames" is now "checked"...

alettes	Animations	Miscellanea	Debug	Desktop	Window	Help	Plugins
	Show fra	ame					
	Make ro	tate movie					
3 🔸	Axis viev	v paths 🛛 🕨	Set n	umber of fr	ames		
			Set p	rint resoluti	ion	1	
			✓ Ехро	rt frames			
			Load	folder of a	kis views		
			And.	Action!		and the second second	
				1.0	and the second second	-	State of the local division of the local div

If you click "And...Action!" now (while "Export frames" is "checked"), it will export the frames of your animation to that folder. Note that printing a single frame may take a few seconds (depending on the object rendering and the "print resolution").

If you made the animation with, for instance, 100 frames, the folder will contain 100 images ("png" format – see below).



The last step is now to create a movie from all these "frames". There are many (free) tools out there to do this... Here's one: "VirtualDub" (<u>http://www.virtualdub.org</u>).

As an example, I ran the animation with 1080 frames and 240 dpi resolution. I used 27 frames per second and cropped the size to 1920 by 1080 (HD) resolution...

The result can be seen here: http://youtu.be/X4HSHE4S6ng
16. Automated / atlas based ROI analysis

There are two ways to do this:

nations	Miscellanea	Debug	Desktop	Window	Help	Plugins	Calculate DTI *.mat file 🏻 🗶 🛪 🗙		
						Co	prrect for subject motion & EC/EPI distortion	ns	
						W	hole brain tractography	•	
0	+					3D) *.nii 2 3D *.nii		
						Exp	port stuff to *.nii files		
						Fli	p left-right orientation of DTI *.mat file		
						Ge	nerate synthetic diffusion MRI data	•	
						Re	sample 3D/4D *.nii file(s)		
						Fli	p/permute dimension(s) of 3D/4D *.nii file(s)	
						Sh	uffle/select 3D volume(s) in 4D *.nii file(s)		
						So	rt DWI *.nii file(s) wrt b-values		
						Ge	t precisions (wild bootstrap) of DTI *.mat		
						Ch	neck motion/distortion correction		
						Ch	neck outlier profiles		
						Op	oen 'MRIcroN' (© Chris Rorden)		
						Cr	op size of *.nii file		
						Co	oncatenate DTI *.mat files (to *.nii)		
						Co	oncatenate tract *.mat files (to *.mat)		
						Ge	enerate diffusion gradient directions		
						Re	gularize DWIs (4D *.nii)		
						Tra	act info from other modality		
						Clo	osing the Venetian blinds		
						Pe	rform uniform tract resampling		/
						Su	mmary uniformly resampled tract *.mat file	s	
						Au	tomated FOV cropping of DTI *.mat files		
						Co	nvert		
						Ge	t diffusion metrics from	1	Atlas labels
						Ga	ussian smoothing (*.nii)	1	ROIs in native space
						TV	for Gibbs ringing in non-DWI's (4D *.nii)		

The top one ('Atlas labels') has been used, for instance, in "Kersbergen KJ et al, NeuroImage, 2014" and uses an atlas template, its labels (i.e. the ROIs), the label names, and the DTI *.mat file(s) as input. In short, by warping the atlas template (and transforming the associated labels) to each individual data set, diffusion metrics are calculated in each ROI. Here's how it works:

Assume you have the following input data set ("Subject_1.mat" is the DTI file; the other three files are the template files... you can find them in folder ~\ExploreDTI\Source\Templates):

	III 🔹 🗍 🔞
•	Name
	🛎 SRI24_Template.nii
	SRI24_tzo116plus_Label_Names.txt
	SRI24_tzo116plus_Labels.nii
	🛅 Subject_1.mat

Then choose what applies for your data:

O Diffusion metrics fro
Single or multiple data sets?
Single Multiple

Here, I'll choose "Multiple"... I select my "Input" folder which has the DTI files in it:

-		
▼ ∢	m	۱.
Folder: Input		
	Select Folder Cancel	

Then, select the output folder:

Folder: Output Select Folder Cancel				4
Select Folder Cancel	Folder:	Output		
			Select Folder	Cancel

Then, select the atlas labels (screenshot below included simply for illustration purpose):





Then, select the atlas template:

Name SRI24_Template.nii SRI24_tzo116plus_Labels.nii	File Edit Overlay Draw Window Help X Image: Y 120 Image: Z 78 to fit Image: Amage: Amag
< III File name: SR124_Template.nii ▼ (*.nii) ▼ Open Cancel .i	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

And finally, the label names:

Name	
SRI24_tzo116plus_Label_Names.txt	
< III	
File name: SRI24_tzo116plus_Label_Names.txt 🔻	(*.bd) 🗸
	Open Cancel

Note that you can choose your labels by setting "1" in the first column... "0" values indicate that you will not include that ROI/label in the analysis (FYI, only a part of the file content is shown below):

And then wait a few minutes (up to a few hours depending on data size and number of atlas labels)



The output looks like this (the *.nii files are for quality control):



As an example, I'll open the "Average FA.txt" file in Excel:

	194	. (-	J**					
	А	В	С	D	E	F	G	
1		Thalamus_R	Thalamus_L	Corpus_Callosum_AP_0	Corpus_Callosum_AP_1	Corpus_Callosum_AP_2	Corpus_Callosum_AP_3	Cor
2	Subject_1	0.34982246	0.33281156	0.47112158	0.65627211	0.58885288	0.53871077	
3								
4								

Н	I	J	К	L
pus_Callosum_AP_4	Corpus_Callosum_AP_5	Corpus_Callosum_AP_6	Corpus_Callosum_AP_7	Corpus_Callosum_AP_8
0.60971981	0.58315009	0.61916775	0.68645954	0.81332505

If you had more subject data sets, then the file above would have had more rows... That's it!

Now let's look at the other option ('ROIs in native space'):

Perform uniform tract resampling		
Summary uniformly resampled tract *.mat files	;	
Automated FOV cropping of DTI *.mat files		
Convert	•	
Get diffusion metrics from	I.	Atlas labels
Gaussian smoothing (*.nii)		ROIs in native space
TV for Gibbs ringing in non-DWI's (4D *.nii)	T	
Network analysis tools	•	
Atlas based tractography segmentation		
Mask 3D *.nii file		

In this case, we assume that the ROIs are already in the same space of the diffusion data. The format of the ROIs is as usual: a 3D *.nii file with "0" values reflecting the background and values 1, 2, 3, etc. representing ROI 1, ROI 2, ROI 3, etc. The *.txt file with label names corresponds to the ROIs where the row number denotes the ROI number (see below).





As usual, "0" values in the *.txt file mean that these ROIs are not considered for analysis.

The input typically looks something like (here, folder name was "ROI_analysis" - see later):

*	Name
1	🚵 Sub_01_MD_C_trafo.mat
	Sub_01_MD_C_trafo_label_names.txt
	Sub_01_MD_C_trafo_labels.nii
	Sub_01_MD_C_trafo_T1.nii

"Sub_01_MD_C_trafo.mat" is the DTI file. Note that it was transformed to the T1-weighted image, i.e. "Sub_01_MD_C_trafo_T1.nii", during SM/EC/EPI distortion correction. "Sub_01_MD_C_trafo_labels.nii" has the labels and "Sub_01_MD_C_trafo_label_names.txt" the corresponding label names:



OK - let's run the 'ROIs in native space' tool ... First, select the input folder of DTI *.mat files:

•			
der:	ROI_analysis		
		Select Folder	Cance
_			

Then fill in the suffix parts corresponding to the labels/ROI *.nii file and label names *.txt file:

🕥 Diffusion metrics from ROIs in native space	×				
Extension name for ROIs *.nii files					
_labels.nii					
Extension name for label *.txt files					
_label_names.txt					
OK Cancel					

Finally, select an output folder:

•			
der:	Output_ROI_analysis		
		Select Folder	Cancel
_			

Typically, this only takes a few minutes... The output looks like:



If we open for instance "Average FA.txt" in Excel, we get:

	Clippoard Ia	FC	οητ	La la	Alighn	ient	la NI	umper is		
	Q38 👻	(f x								
	А	В	С	D	E	F	G	Н	1	J
1	File name	3rd-ventricle	4th-ventricle	brain-stem	cc_anterior	cc_central	cc_mid_anterior	cc_mid_posterior	cc_posterior	csf
2	Sub_01_MD_C_trafo	N/A	N/A	0.35902919	0.60191505	0.41827561	0.37418305	0.36821181	0.58660962	N/A
3										

Again, each row represents a subject's data set. The "N/A" indicates that for that ROI, there was a "0" value in the label names *.txt file.

That's it!

17. Along-tract analysis

For research papers where this kind of analysis has been used, see for instance <u>O'Hanlon E. et al, JAMA</u> <u>Psychiatry 2015</u>, <u>Szczepankiewicz F. et al, NeuroImage 2013</u>, and <u>Reijmer Y.D. et al, Stroke 2013</u>. The methodological details are based on <u>Colby J.B. et al, NeuroImage 2012</u>.

In summary, the idea is to investigate properties of a fiber bundle along its trajectory instead of averaging these properties across its entire path length. The following figure (adjusted from <u>Perrone D. et al,</u> <u>NeuroImage 2015</u>) should clarify this concept. As an example, 'K' points along a mid-sagittal segment of the forceps minor are compared (e.g., with a t-test) between 'M' healthy controls and 'N' patients.



Some considerations... First, for each subject a fiber bundle (segment) needs to be computed. This can, for instance, be achieved with the tool described in Section 13 (or simply manually on a subject-per-subject basis). My personal preference is to use a specific "segment" to make sure the "endings" of a fiber tract are defined in a better way (see below):



Entire fiber bundle





 \rightarrow



Segment only

 \rightarrow

Second, the fiber bundles need to be resampled with a predefined number of points (i.e., "K" – as in the figure above), which should be same for each subject (to ensure correspondence). A reasonable value for "K" is to divide the average (across subjects) tract length of the fiber bundle of interest by the length scale of the voxel size. For example, if the voxel size is $2 \times 2 \times 2 \text{ mm}^3$ and the average length of the reconstructed uncinate fasciculus segments approximately equal to 70 mm, then K = 70/2 = 35 points should be fine. Taking more points will not add any new information and by sampling fewer points, you may miss information.

The input for the ExploreDTI tool consists of the tract (segment) *.mat files – all together in a single folder:

^	1 Subj_01_UNC_L.mat	1 Subj_06_UNC_R.mat
	1 Subj_01_UNC_R.mat	1 Subj_07_UNC_L.mat
	1 Subj_02_UNC_L.mat	1 Subj_07_UNC_R.mat
	1 Subj_02_UNC_R.mat	1 Subj_08_UNC_L.mat
	1 Subj_03_UNC_L.mat	1 Subj_08_UNC_R.mat
-	1 Subj_03_UNC_R.mat	1 Subj_09_UNC_L.mat
-	1 Subj_04_UNC_L.mat	1 Subj_09_UNC_R.mat
	1 Subj_04_UNC_R.mat	1 Subj_10_UNC_L.mat
	1 Subj_05_UNC_L.mat	1 Subj_10_UNC_R.mat
	1 Subj_05_UNC_R.mat	
÷	1 Subj_06_UNC_L.mat	

For this toy example, the idea is now to compare diffusion properties between the left and the right uncinate fasciculi for 10 subjects.

Step 1: Resample all the tract files with "K = 35" points. Go to 'Plugins' \rightarrow 'Perform uniform...'

Tract info from other modality		
Closing the Venetian blinds		
Perform uniform tract resampling		
Summary uniformly resampled tract *.mat files		
A. to an to 1 COV		
Uniform tract resampling		
Number of tract samples (integer > 1)		
35		

Then choose multiple data and select the folder of the tract *.mat files:

Uniform tract resamp	▼
Single or multiple data sets?	Folder: Tracts
Single Multiple	

Save the uniformly resampled (UR) tracts in an output folder (here: "UR_tracts"):

∢ [III	,
der:	UR_tracts	
	Select Folde	der Cancel
		4

The output of this step is simply another set of tract *.mat files and can be used/visualized as any other tract *.mat file (notice the suffix "_ur" being added):

			0
Subj_01_UNC_L_ur.mat	🔚 Subj_06_UNC_L_ur.mat		
1 Subj_01_UNC_R_ur.mat	1 Subj_06_UNC_R_ur.mat		
1 Subj_02_UNC_L_ur.mat	🚵 Subj_07_UNC_L_ur.mat		
h Subj_02_UNC_R_ur.mat	1 Subj_07_UNC_R_ur.mat		
h Subj_03_UNC_L_ur.mat	1 Subj_08_UNC_L_ur.mat		
1 Subj_03_UNC_R_ur.mat	1 Subj_08_UNC_R_ur.mat		
h Subj_04_UNC_L_ur.mat	1 Subj_09_UNC_L_ur.mat		
1 Subj_04_UNC_R_ur.mat	1 Subj_09_UNC_R_ur.mat		
1 Subj_05_UNC_L_ur.mat	🚵 Subj_10_UNC_L_ur.mat		
1 Subj_05_UNC_R_ur.mat	1 Subj_10_UNC_R_ur.mat		

Step 2: for each tract *.mat file, the fiber bundle (set of trajectories) will be reduced to a single "averaged" pathway. This is achieved with the plugin:

	mace more norm other modulity	
	Closing the Venetian blinds	
	Perform uniform tract resampling	
	Summary uniformly resampled tract *.mat files	
	Automated FOV cropping of DTI *.mat files	
	Convert	F

Select that folder of UR tract *.mat files:

Folder: UR_tracts	
	Select Folder C

Save the summary of the UR tract *.mat files in some output folder (e.g., summary_tracts):

Folder:	summary_tracts	
		Colora Coldar
		Select Folder
-		

Then use "mean" or "median" to do the averaging of the diffusion metrics (I only included the option to check whether it would make a difference... well, it appears it doesn't – so simply take the mean):

Summarizing tract information
Choose type of tract information reduction
mean median

The end result looks like:

AD.txt	🛅 Subj_06_UNC_L_ur_ri.mat
FA.txt	🔠 Subj_06_UNC_R_ur_ri.mat
MD.txt	勧 Subj_07_UNC_L_ur_ri.mat
RD.txt	🔚 Subj_07_UNC_R_ur_ri.mat
🔚 Subj_01_UNC_L_ur_ri.mat	🔚 Subj_08_UNC_L_ur_ri.mat
🚹 Subj_01_UNC_R_ur_ri.mat	🔚 Subj_08_UNC_R_ur_ri.mat
🚹 Subj_02_UNC_L_ur_ri.mat	🛅 Subj_09_UNC_L_ur_ri.mat
Subj_02_UNC_R_ur_ri.mat	🔚 Subj_09_UNC_R_ur_ri.mat
Subj_03_UNC_L_ur_ri.mat	🔚 Subj_10_UNC_L_ur_ri.mat
Subj_03_UNC_R_ur_ri.mat	Subj_10_UNC_R_ur_ri.mat
Subj_04_UNC_L_ur_ri.mat	X.txt
Subj_04_UNC_R_ur_ri.mat	Y.txt
Subj_05_UNC_L_ur_ri.mat	Z.txt
Subj_05_UNC_R_ur_ri.mat	

Now, each tract *.mat file simply consists of a single trajectory. After making sure that the endings of the pathways correspond between the subjects (and left/right sides), the figure below shows the 10 left and 10 right tracts with color-encoding reflecting this correspondence across subjects/sides:



Top view

Frontal view

The *.txt files contain the diffusion measures (or world coordinates) along the pathways (columns) for each data set (rows). For instance, for the FA:

	А	В	С	D	E	F	G	Н	1	J	К	L	М
1	Subj_01_UNC_L_ur	0.1978476	0.22410513	0.2455098	0.27902072	0.30362992	0.29933797	0.30122764	0.30527867	0.31157305	0.34083669	0.3560173	0.3678282
2	Subj_01_UNC_R_ur	0.11055904	0.15978238	0.23502203	0.23698129	0.26954632	0.24962346	0.23676009	0.25822902	0.28972203	0.3209552	0.34120971	0.352996
3	Subj_02_UNC_L_ur	0.20158867	0.19965639	0.23552328	0.29726335	0.34429403	0.34226217	0.3506436	0.3589523	0.37879391	0.40932784	0.40323674	0.4032865
4	Subj_02_UNC_R_ur	0.1765241	0.19477864	0.22247859	0.26083997	0.30781773	0.33403664	0.33748694	0.33021006	0.35423194	0.37576671	0.36522666	0.3652608
5	Subj_03_UNC_L_ur	0.19127484	0.17575671	0.20828917	0.23658924	0.29802598	0.35943015	0.35779146	0.3439793	0.36541418	0.40783358	0.42191944	0.4155703
6	Subj_03_UNC_R_ur	0.19147925	0.17908318	0.23166281	0.27487564	0.25862883	0.24843832	0.26600498	0.29443066	0.33786838	0.37346705	0.38445964	0.4054504:
7	Subj_04_UNC_L_ur	0.1905824	0.17127414	0.1837973	0.20057766	0.24413764	0.28880355	0.30610703	0.30908539	0.31823764	0.33898552	0.36140458	0.3859752
8	Subj_04_UNC_R_ur	0.17405451	0.2097058	0.24863955	0.24997392	0.27101473	0.26741215	0.27704688	0.29827911	0.31022659	0.32790035	0.34713296	0.36669024
9	Subj_05_UNC_L_ur	0.13664559	0.15025762	0.21736874	0.24490603	0.27221143	0.26830379	0.28086123	0.28896291	0.30132772	0.33091689	0.37051946	0.383306
10	Subj_05_UNC_R_ur	0.11808045	0.15467317	0.18753063	0.20965887	0.23808695	0.25501636	0.26953916	0.26650675	0.2678526	0.30538511	0.35020485	0.3739258
11	Subj_06_UNC_L_ur	0.16642318	0.15367524	0.16371438	0.16622704	0.19131964	0.24309958	0.29620403	0.28209809	0.26062938	0.25497078	0.25091611	0.258653
12	Subj_06_UNC_R_ur	0.21171651	0.19861943	0.20237974	0.24363264	0.23383232	0.24241234	0.26169646	0.26316012	0.26830285	0.29336377	0.31923048	0.3291594
13	Subj_07_UNC_L_ur	0.15631274	0.18008358	0.21962814	0.25606323	0.2919215	0.30409192	0.3179618	0.33296327	0.35105555	0.37207939	0.37981124	0.374865
14	Subj_07_UNC_R_ur	0.13472333	0.14371899	0.17163569	0.21561202	0.24857433	0.27469067	0.28772675	0.2881444	0.28266783	0.29386919	0.30111358	0.2998688
15	Subj_08_UNC_L_ur	0.22718161	0.24060717	0.28001925	0.32101761	0.33841739	0.35196553	0.35207963	0.35601877	0.36165745	0.35485697	0.34946282	0.3566723
16	Subj_08_UNC_R_ur	0.21355266	0.22388502	0.25485338	0.28713744	0.32507106	0.35151734	0.36047656	0.35025877	0.35200782	0.3595545	0.35920834	0.3707059:
17	Subj_09_UNC_L_ur	0.23606914	0.23613196	0.24934666	0.27026541	0.31566818	0.35292476	0.36597455	0.38389892	0.41378311	0.4327728	0.44255176	0.4503983:
18	Subj_09_UNC_R_ur	0.16175105	0.1993354	0.23409755	0.26175589	0.25954058	0.23257936	0.23484776	0.27780853	0.29362327	0.30860555	0.32880112	0.3403587
19	Subj_10_UNC_L_ur	0.1628739	0.17451604	0.23039423	0.25174676	0.27804873	0.32202658	0.34790749	0.35836527	0.3746804	0.40557555	0.41904306	0.4035664
20	Subj_10_UNC_R_ur	0.21180424	0.2181099	0.24345584	0.29529049	0.33967236	0.35978288	0.34684397	0.33096345	0.34154448	0.35541155	0.36118051	0.391724
21													

Or when plotting the left (blue) versus the right (red) side FA values (error bars are simply the standard deviation across subjects):



While there are some significant (uncorrected p<0.05) differences (lowest p-value was roughly 0.003 - see below), one may argue that a correction factor of 35 (Bonferroni – number of t-tests) needs to be included... No significant difference then for any point along the tract.



Using the corresponding "X" (front-back), "Y" (left-right), and "Z" (bottom-top) coordinate *.txt files, it's trivial to understand what is the beginning/ending of the plot (for instance for the uncinate fasciculus, the temporal pole has typically lower values of the z-coordinates than the orbitofrontal part).

That's all for now!