

Answers to DTI Tutorial 2

The online tutorial can be found here:

<http://www.diffusion-imaging.com/2015/10/dti-tutorial-2-normalization-and.html>

Q1: Go through the DTI-TK preprocessing tutorial, indicate which lines of the above code correspond to which steps in the outline. What is the goal of each step? When you use this code make sure you use the right diffusivity units, the code above is just an example, find out how to convert your own here.

3-4: Make Sure DTI Volumes are Using the Correct Diffusivity Unit

5-13: Make Sure DTI Volumes Contain No Significant Outliers

14-16: Make Sure DTI Volumes are SPD

17-18: Check Whether DTI Volumes Share one Common Voxel Space

19-22: Clean up

Q2: Using TVtool investigate how and then write the code to produce the mean diffusivity (MD) map from the standardized tensor file (download 052212_s09_dti_eddy_fm_strip_sdt.nii.gz here). What other maps can that tool help produce?

```
TVtool -in 052212_s09_dti_eddy_fm_strip_sdt.nii.gz -ad
```

Q3: What are the 4 main diffusion measurements that are often used in DTI? Take a look at the explanation on this page, and describe which measure you would pick if you were selectively interested in white matter?

Mean diffusivity (MD), axial diffusivity (AD), radial diffusivity (RD), and fractional anisotropy (FA). I would probably pick FA, since it is most sensitive to white matter, but AD and RD could be helpful as well. MD would not be helpful when I am interested in white matter.

Q4: Which step do you think will take the most time to run? Note the step where you resample your image to have isotropic voxel size, which line is this? Read this post on the importance, explain why we need isotropic voxels for fiber tracking. Resampling also alters the image dimensions, when you change those, you can read here that DTI-TK needs your image dimensions to be powers of 2. What are most likely often used powers of 2 in neuroimaging volume dimensions?

The diffeomorphic warp would take the longest to run, since it has the most degrees of freedom. Line 6 converts the voxels to 1x1x1mm resolution, which is an isotropic resolution (equal in all directions). Using isotropic voxels makes sure that we get an unbiased estimate of the tracts, and that we don't miss out on smaller or bendier tracts. Regions with crossing fibers will underestimate FA when voxels are not isotropic.

Common powers of 2 in our imaging data would include 64, 128, 256 and 512.

Q5: Open fslview, click "File" -> "Open standard". In this directory and in the directory atlases you can browse all the different atlases that are automatically loaded with FSL. You can also find the atlas images in your installed FSL directory. Find the MNI template that you would like to use for registration. What is the name of that file? Give 1 reason why you would want to register your data to this template.

MNI152_T1_1mm_brain.nii.gz - This T1 anatomical image is an average of 152 individuals, and has a 1x1x1mm isotropic resolution. This image shows brain only, since the skull has been stripped away.

Putting your data in a commonly used atlas space will help streamline coordinates that are significant between studies. It will furthermore offer the opportunity to use tools that are produced in that space, like segmented white matter regions by JHU.

Q6: Some of the code in this tutorial uses a "for loop" for the first time. Take a look at a tutorial on loops [here](#). Try to figure out how "for loops" work, then describe what you would put in the subjects.txt file from line 2. HINT: Remember how variables work in bash. Another option is to run the below code, instead of line 2 and 3. Can you describe what this would do?

```
for i in `ls *_diffeo_fa.nii.gz`;
do
prefix=`echo $i | awk 'BEGIN{FS="_diffeo_fa.nii.gz"}{print $1}``
```

In the subjects.txt file I would put a list of subject numbers, or subject prefixes. E.g. 001_s08 002_s08 003_s08 004_s08 etc.

Instead of reading a text file, this code reads a list of file names, and then strips off the part of the file name that is “_diffeo_fa.nii.gz”, so you only keep the subject prefix.

Q7: Note that DTI-TK outputs the trace (TR) instead of the MD value. Look up how trace relates to MD [here](#), and write the fslmaths code to convert TR to MD. If you are unsure how to do this, type fslmaths in your command line to see all the help options.

```
fslmaths 052212_s09_dti_eddy_fm_strip_sdt_tr.nii.gz -div 3
052212_s09_dti_eddy_fm_strip_sdt_md.nii.gz
```

Q8: Next describe what lines 10-13 accomplish, if you are unsure read [this documentation](#) on spatial smoothing. Finally in line 16 we merge all the individual FA images, describe why you might want to do that.

In those lines we smooth the data with a 4x4x4mm full width at half maximum (FWHM) gaussian smoothing kernel. This is an important step in order to smooth out noise and compensate for imperfect normalization.

We merge the data in line 16 so that we can view a movie of each individual subject in fslview, in order to get an impression of the quality of the data and normalization for each subject.

Q9: Look at the user guide for randomise, and try to get an impression of what the .mat file and .con file contain. Produce an example of both for the imaginary case that you have a patient group (n=3) and healthy control group (n=3), and you want to test where FA is significantly lower in the patient group, and where FA is significantly lower in the control group. What do the options -x and -T stand for in randomise?

```
/NumWaves      2          /ContrastName1  Control>Patient
/NumPoints     6          /ContrastName2  Patient>Control
/PPheights    1          1  /NumWaves      2
/Matrix       0          /NumContrasts   2
1             0          /PPheights     1          1
1             0          /RequiredEffect 45.704 45.704
1             0
0             1          /Matrix
0             1          1 -1
0             1          -1 1
.mat file                .con file
```

-T carry out Threshold-Free Cluster Enhancement

“TFCE (Threshold-Free Cluster Enhancement) is a new method for finding “clusters” in your data without having to define clusters in a binary way. Cluster-like structures are enhanced but the image remains fundamentally voxelwise; you can use the `-tfce` option in `fslmaths` to test this on an existing stats image. See the TFCE research page for more information. The “E”, “H” and neighbourhood-connectivity parameters have been optimised and should be left unchanged. These optimisations are different for

different "dimensionality" of your data; for normal, 3D data (such as in an FSL-VBM analysis), you should just use the `-T` option, while for TBSS analyses (that is in effect on the mostly "2D" white matter skeleton), you should use the `--T2` option." - <http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/Randomise/UserGuide>

Q10: Open fslview and open a standard 1mm MNI T1 image. Download example t-stat map (test_tstat1.nii.gz here), and add it to the MNI image. What you see is not yet very informative, click on the information dialog button (in blue circle) and change the Lookup table options. Make the first Red-Yellow, and turn the second one on, and make it Blue-Lightblue. Close the dialog screen. Go to this p-value calculator, and input in the t-ratio boxes that you want a probability that is 0.05 and you have 5 degrees of freedom (number of subjects - 1). What is your 2-tailed significant t-statistic? Input that number in the fslview screen as a minimum brightness value, and make 5 your maximum brightness value. Although this is obviously just test data, you now see what a noisy (when you only test 6 subjects you will most likely only find noise) t-stat map can look like. It is now up to you to start using your own data and improve on this! Remember to correct for multiple comparison when running your data to avoid inflated false discovery rates. You are running a t-tests on each individual voxel, which combine to multiple thousands per brain, and you will have to correct for this. Read more about familywise error rates here. What does the `-T` option do to help with this issue? HINT: Read this .pdf on the background of threshold-free cluster enhancement (TFCE).

QuickCalcs

1. Select category 2. Choose calculator 3. Enter data 4. View results

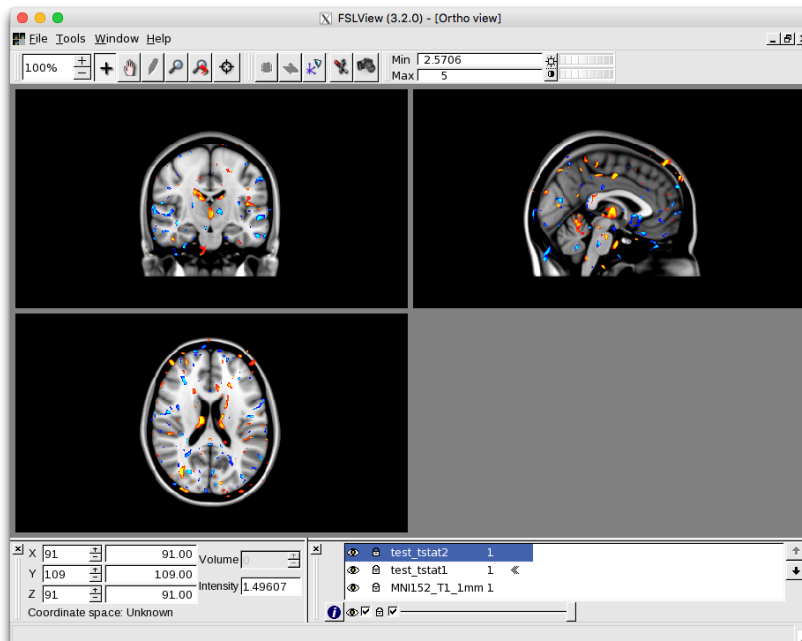
Statistical Ratio Results

Probability = 0.05 df=5
Two tailed: t= 2.5706
5.000% of a t distribution has values greater than 2.571 or less than -2.5706.

One tailed: t= 2.0150
5.000% of a t distribution has values greater than 2.015
5.000% of a t distribution has values less than - 2.015

Modified November 18, 2013 to fix the one-tailed P values for t distribution.

2-tailed significance is at: $t > 2.5706$.



The TFCE option will only report clusters that are of large enough size to be significant; this is a method based on the older cluster-based thresholding to correct for multiple comparisons.