




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DTI preprocessing, statistical and cluster analysis

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1 Works for me

 Sharedx.doi.org/10.17504/protocols.io.6qpvrldjozgm/v1

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ABSTRACT

This protocol outlines preprocessing, statistical and cluster analyses that were applied in 'Using whole-brain diffusion tensor analysis to evaluate white matter structural correlates of delayed visuospatial memory and one-week motor skill retention in nondemented older adults: A preliminary study' (<https://doi.org/10.1371/journal.pone.0274955>).

The following software packages are required to follow this protocol: FSL, MRtrix, Advanced Normalization Tools (Github: <https://github.com/ANTsX/ANTs>). Figures were created via AFNI.

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KEYWORDS

diffusion tensor imaging

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GUIDELINES

Double-check your images after each step!

Preprocessing data

- 1 Double-check if your native and original images are in FLOAT32 and oriented with the MNI.
-Convert to float-
fslmaths dwidata.nii.gz dwi.nii.gz -odt float
- 2 DWI Denoising:
dwidenoise -datatype float32 -noise level_noise.nii.gz [IN] [OUT_denoised]
dwidenoise -datatype float32 -noise level_noise.nii.gz dwi.nii.gz dwi_denoised.nii.gz
- 3 mrdegibbs [OUT_denoised] [OUT_Gibbs]
mrdegibbs dwi_denoised.nii.gz dwi_Gibbs.nii.gz
- 4 need brain – bet doesn't work as well as dwi2mask
dwi2mask -fslgrad bvecs.txt bvals.txt dwi_Gibbs.nii.gz temp_brain_mask.nii.gz
- 5 Run 'nodif_brain_mask.sh' script [e.g., **bash nodif_brain_mask.sh dwi_Gibbs.nii.gz 4214_52 temp_brain_mask.nii.gz**] to get temporary nodif brain masks for eddy.
Rename both of these nodif files with the prefix 'dwi_Gibbs_' e.g., 'dwi_Gibbs_brain_mask' for eddy. Delete the 'temp_brain' file.
- 6 Run eddy correction and get rotated vector file
eddy --imain=dwi_Gibbs.nii.gz --mask=dwi_Gibbs_brain_mask.nii.gz --index=index.txt --acqp=acqparams.txt --bvecs=bvecs.txt --bvals=bvals.txt --fwhm=0 --flm=quadratic --slm=linear --out=eddy_unwarped_images --data_is_shelled
- 7 Nodif and Brain extraction on the data.nii.gz
fslroi data.nii.gz nodif_data0 1

```
dwi2mask -fslgrad eddy_unwarped_images.eddy_rotated_bvecs.txt bvals.txt  
data.nii.gz temp_brain_mask.nii.gz
```

- 8 Run 'nodif_brain_mask.sh' script [e.g., **bash nodif_brain_mask.sh data.nii.gz 4214_52 temp_brain_mask.nii.gz**] output is 'nodif_brain_mask.nii.gz' and 'nodif_brain.nii.gz' rename and add 'data' in front, so 'data_nodif_brain'. Delete 'temp_brain' file.
- 9 Bias Field correction (via ANTs):
**dwibiascorrect ants data.nii.gz data_bias.nii.gz -fslgrad
eddy_unwarped_images.eddy_rotated_bvecs.txt bvals.txt -mask
data_nodif_brain_mask.nii.gz -bias bias_image.nii.gz -ants.b [100,3]**
- 10 Upsample DWI images for better coregistration with MNI template
mrgrid -vox 1.25 data_bias.nii.gz regrid data_bias_HR.nii.gz
- 11 Fit tensor model
**dtifit -k data_bias_HR.nii.gz -o DTI_map_w-linear_ -m nodif_brain_mask.nii.gz -r
eddy_unwarped_images.eddy_rotated_bvecs.txt -b bvals.txt -w**
- 12 Optional: create bash script to generate group template
Copy all the nodif_brain.nii.gz images into one folder and change directory to it. Then run:
bash buildtemplateparallel.sh -d 3 -o template -c 0 -r 1 -n 0 -i 3 *.nii.gz

***WarpImageMultiTransform 3 [in: FA map in native space] [out: FA map in template
space] -R templatetemplate.nii.gz [warp file] [affine file]***
- 13 At this point all participant FA maps should be in template space. Create a 4D (x,y,z + time) file with all your maps:
Insert all your FA in template space in one folder and run:
fslmerge -t [output] *.nii.gz
- 14 Create then apply mask from all subjects
**fslmaths all_FA.nii.gz -max 0 -Tmin -bin mean_mask -odt char
fslmaths all_FA.nii.gz -mas mean_mask all_FA.nii.gz**
- 15 Create a mean of the FA over-time and create white matter mask (thresholded at FA>0.20):
**fslmaths all_FA -Tmean mean_FA
fslmaths mean_FA -thr 0.20 -bin WM_mask**
- 16 Apply your mask to your smoothed maps:
fslmaths all_FA_smooth -mas mean_mask all_FA_smooth

- 17 At this point you should have a FA map 'all_FA.nii.gz' for all subjects.

Linear regression

- 18 Create linear regression script (that applies model voxel-by-voxel) using the LM.m function in MATLAB by using:
LM (file_ID1, raw_image_subject, mask)

e.g., **LM (covariates.txt, all_FA_smooth.nii, WM_mask.nii)**
- 19 Resulting files will be the FDR-corrected p-value and tstat maps for each variable.

Clusterize and apply white matter atlas to identify clusters

- 20 Example is for first behavioral variable 'score_1'
3dcalc -ascore_1_FDR.nii-expr 'a*1' -prefixscore_1_FDR_corrected.nii.gz
3dcalc -a score_1_tStat.nii -expr 'a*1' -prefix score_1_tStat_corrected.nii.gz
- 21 Split scores tStat into positive and negative (this provides you with positive and negative correlations):

Fslmathsscore_1_tStat_corrected.nii.gz -thr 0 positive_score1.nii.gz
Fslmathsscore_1_tStat_corrected.nii.gz -uthr 0 negative_score1.nii.gz
*For negative images, need to multiply by -1
Fslmaths negative_score1.nii.gz -mul -1 negative_score1.nii.gz
- 22 Get FDR-corrected p-value clusters that are less than 0.01 and that are at least 100 voxels in size
3dClusterize -nosum -1Dformat -inset score_1_FDR_corrected.nii.gz -idat 0 -ithr 0 -NN 2 -clust_nvox 100 -1sided RIGHT_TAIL 0.99 -pref_map Clust_mask_motor.nii.gz

fslmaths Clust_mask_motor.nii.gz -bin Clust_mask_motor.nii.gz
- 23 Coregister the template to MNI:

antsRegistrationSyN.sh -d 3 -m
/Users/syschaef/Desktop/4214_DTI/MRtrix_preproc/group_template/templatetemplate.nii.gz -f /usr/local/fsl/data/standard/MNI152_T1_1mm_brain.nii.gz -o
/Users/syschaef/Desktop/4214_DTI/MRtrix_preproc/template_to_MNI/templatetemplate_to_MNI -t s

- 24 Check that ROIs are Binarized (use nearest neighbor command when the images are binarized). Behavioral variables are 'score_1' and 'motor'

Transform clusters to MNI:

```
antsApplyTransforms -d 3 -i Clust_mask_motor.nii.gz -o
Clust_mask_motor_MNI.nii.gz -
r/usr/local/fsl/data/standard/MNI152_T1_1mm_brain.nii.gz -t
[/Users/syschaef/Desktop/4214_DTI/MRtrix_preproc/template_to_MNI/templatete
mplate_to_MNI1Warp.nii.gz,0] -t
[/Users/syschaef/Desktop/4214_DTI/MRtrix_preproc/template_to_MNI/templatete
mplate_to_MNI0GenericAffine.mat,0] -n NearestNeighbor
```

- 25 Transform scores tstat (positive and negative) to MNI space:

```
antsApplyTransforms -d 3 -ipositive_score1.nii.gz-opositive_score1_MNI.nii.gz -
r/usr/local/fsl/data/standard/MNI152_T1_1mm_brain.nii.gz -t
[/Users/syschaef/Desktop/4214_DTI/MRtrix_preproc/template_to_MNI/templatete
mplate_to_MNI1Warp.nii.gz,0] -t
[/Users/syschaef/Desktop/4214_DTI/MRtrix_preproc/template_to_MNI/templatete
mplate_to_MNI0GenericAffine.mat,0]
```

```
antsApplyTransforms -d 3 -inegative_score1.nii.gz-onegative_score1_MNI.nii.gz -
r/usr/local/fsl/data/standard/MNI152_T1_1mm_brain.nii.gz -t
[/Users/syschaef/Desktop/4214_DTI/MRtrix_preproc/template_to_MNI/templatete
mplate_to_MNI1Warp.nii.gz,0] -t
[/Users/syschaef/Desktop/4214_DTI/MRtrix_preproc/template_to_MNI/templatete
mplate_to_MNI0GenericAffine.mat,0]
```

- 26 Mask the tstat scores with significant cluster files:

Positive:

```
fslmathspositive_score1_MNI.nii.gz -mas
Clust_mask_motor_MNI.nii.gzpositive_score1masked_MNI.nii.gz
fslmathspositive_score1masked_MNI.nii.gz -bin
Clust_mask_motor_positive_MNI.nii.gz
```

Negative:

```
fslmathsnegative_score1_MNI.nii.gz -mas
Clust_mask_motor_MNI.nii.gznegative_score1masked_MNI.nii.gz
fslmathsnegative_score1masked_MNI.nii.gz -bin
Clust_mask_motor_negative_MNI.nii.gz
```

- 27 Custom code extracted significant cluster locations from the JHU white matter atlas, but use



the atlas of your choice and identify clusters by using '**fslmaths**' (see fslwiki for tutorial)