

Processing steps dMRI data

Practical Project - PD and Freezing of Gait

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Overview

dMRI data processing

1. Preprocessing
2. Estimation of Fiber Orientation Distribution
3. Anatomically constrained Tractography (whole brain)
4. Tractography of connection of ROIs

1. Preprocessing

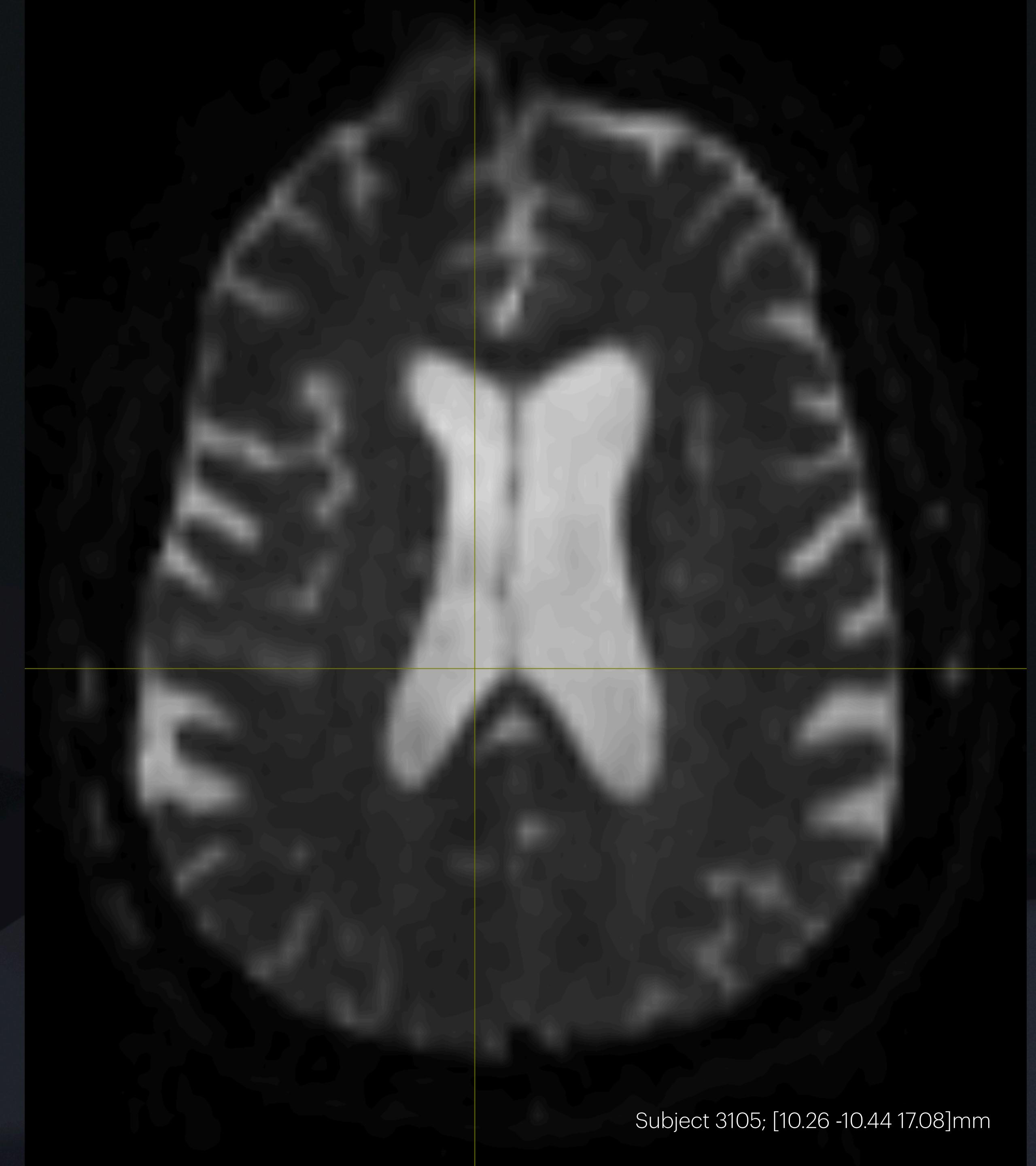
Denoise & Gibb's correction

dwidenoise input.mif output.mif

- Denoising raw dMRI data file

mrdegibbs input.mif output.mif -axes 0,1

- Correction for Gibb's rings



Subject 3105; [10.26 -10.44 17.08]mm

Creation of b0

- Use of containerised tool for synthetic b0 creation of reverse phase encoded data:
Synb0-DISCO
- Necessary input: b0 of phase encoded direction data, acqparams.txt & T1 scan

```
singularity run -e \  
-B $input_path/synb0_input/:/INPUTS \  
-B $output_path/synb0_output/:/OUTPUTS \  
-B /dss/work/laft0368/license_freesurfer/license.txt:/extra/freesurfer/license.txt \  
/dss/work/laft0368/toolbox/synb0-disco_v3.0.sif
```

Distortion & bias correction

```
dwifslpreproc input.mif output.mif  
-pe_dir AP  
-rpe_none  
-readout $readout  
-eddy_options "-topup=topup_files --repol  
--mporder=18"  
-eddyqc_all ./eddyqc_output
```

- Preprocessing of `input.mif` in AP direction, without reversed phase-encoding, with readout input, `eddy_options` and `eddy_output`.



Distortion & bias correction

dwibiascorrect ants input.mif output.mif

- Bias correction of input.mif
(→ preprocessed data)



Subject 3105; [10.26 -10.44 17.08]mm

2. Creation of Fiber Orientation Distribution

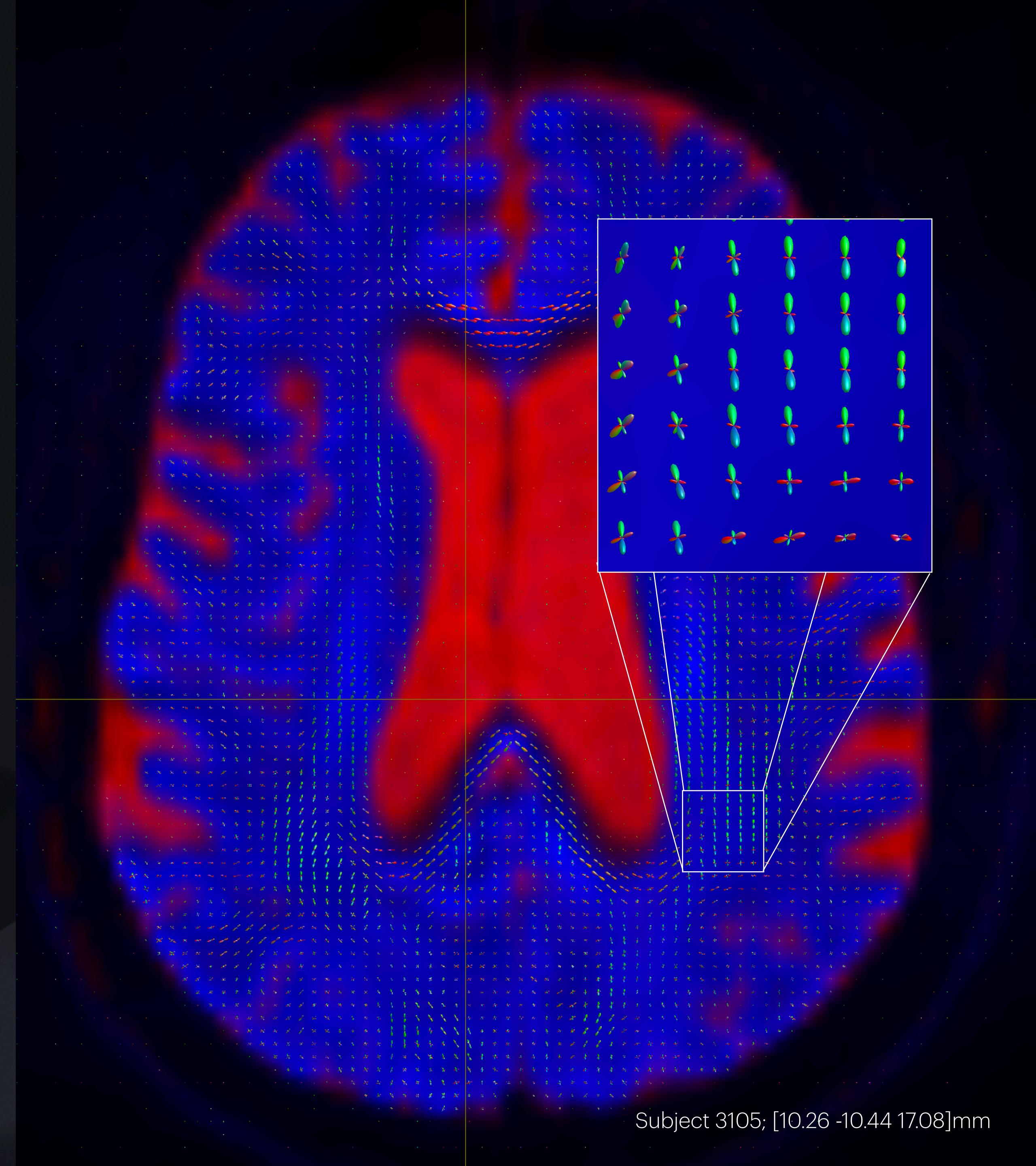
Estimation of FOD

```
dwiextract input.mif --bzero | mrmath -  
mean output.nii.gz -axis 3
```

- Extracting b0 from preprocessed data for mask creation

```
mri_synthstrip -i input.nii.gz -o  
output.nii.gz
```

- Creating brain tissue mask



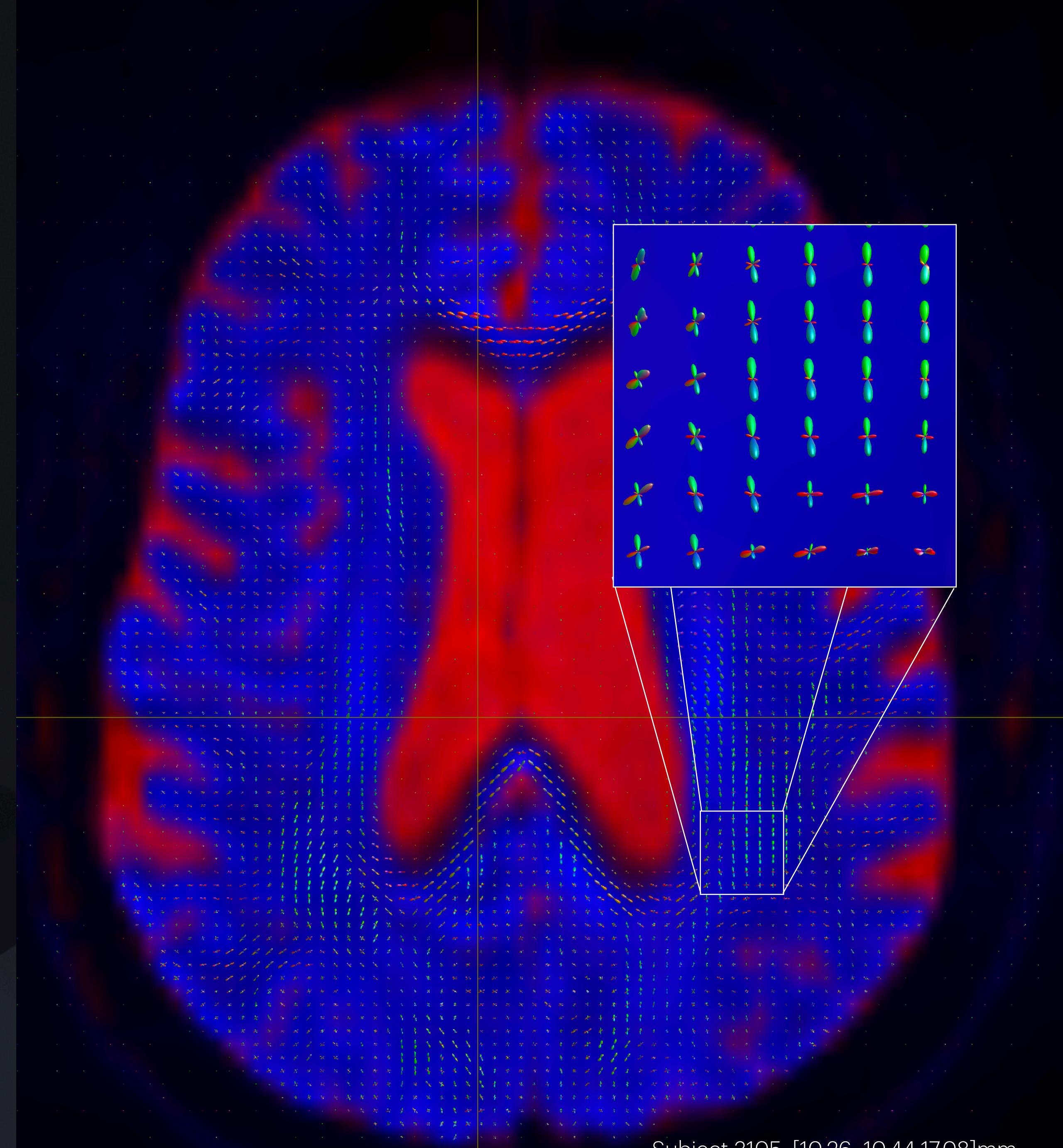
Estimation of FOD

```
dwi2response dhollander input.mif  
wm.txt gm.txt csf.txt -voxels voxels.mif
```

- Creation of voxel separation

```
dwi2fod msmt_csd input.mif -mask  
mask.nii.gz wm.txt wmfod.mif csf.txt  
csffod.mif -shells 0,1000
```

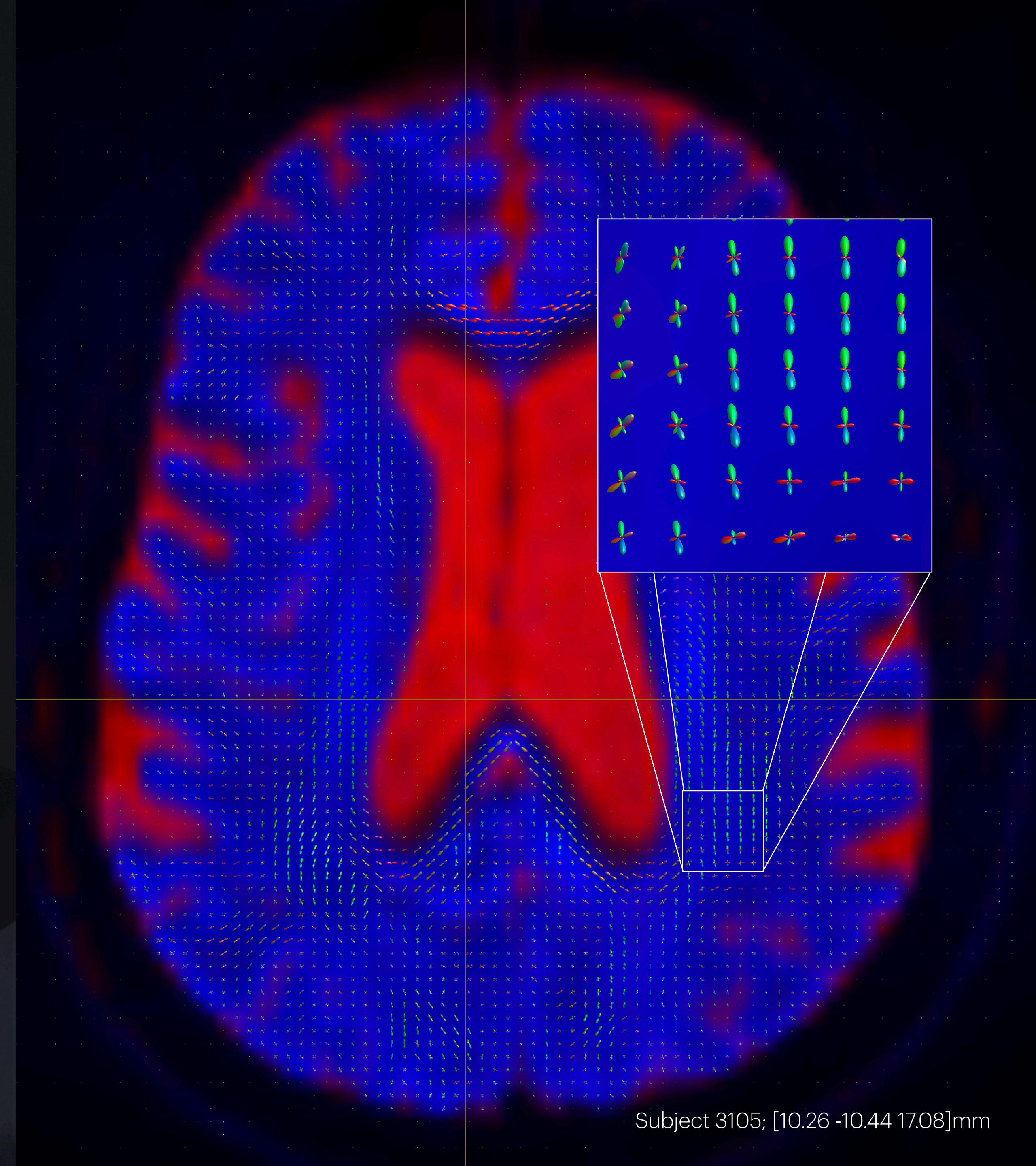
- Creation of FOD for each voxel (here only two shells!)



Estimation of FOD

```
mtnormalise wmfod.mif wmfod_norm.mif  
csffod.mif csffod_norm.mif -mask  
mask.nii.gz
```

- Normalisation of FOD for WM & CSF

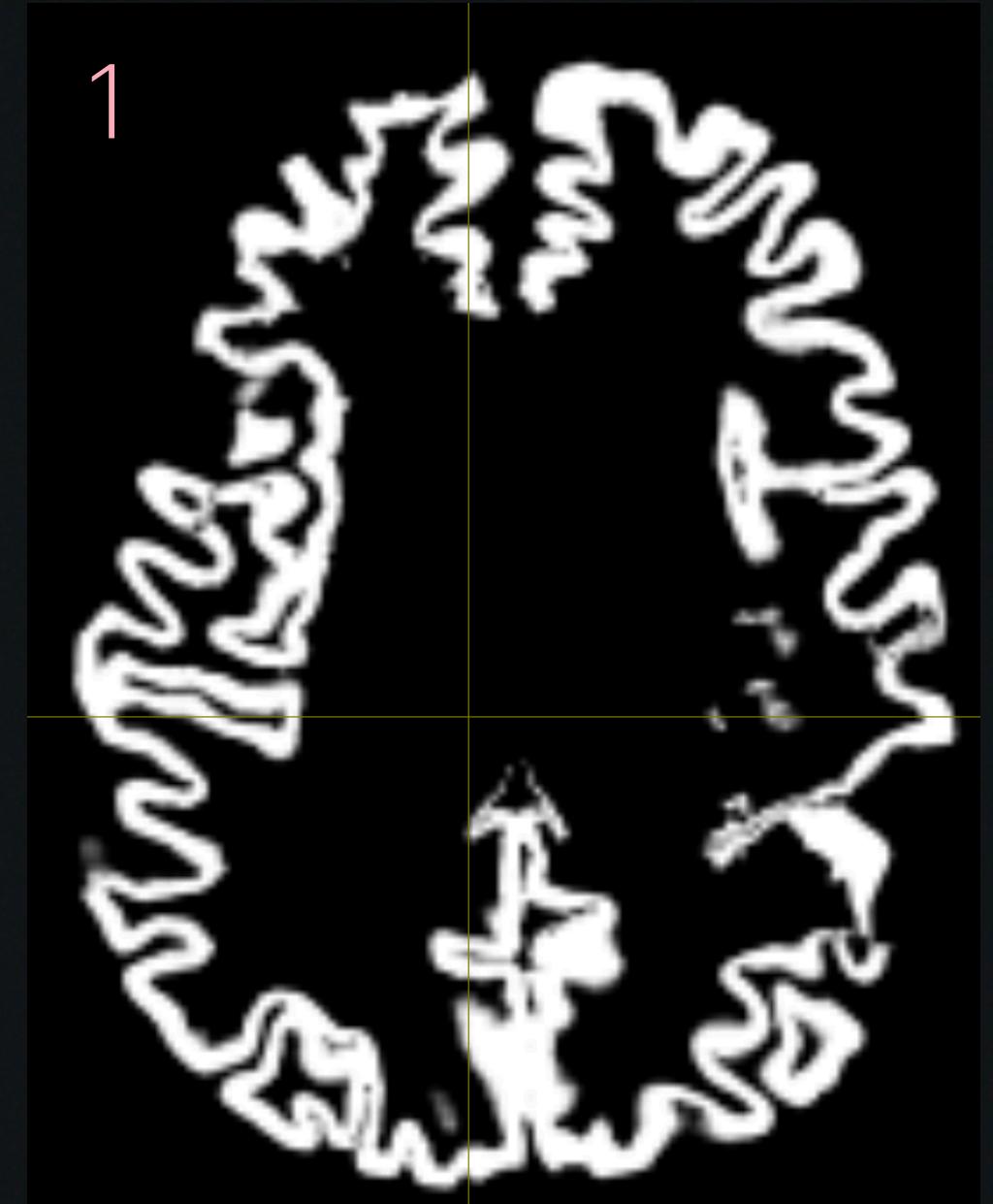


Subject 3105; [10.26 -10.44 17.08]mm

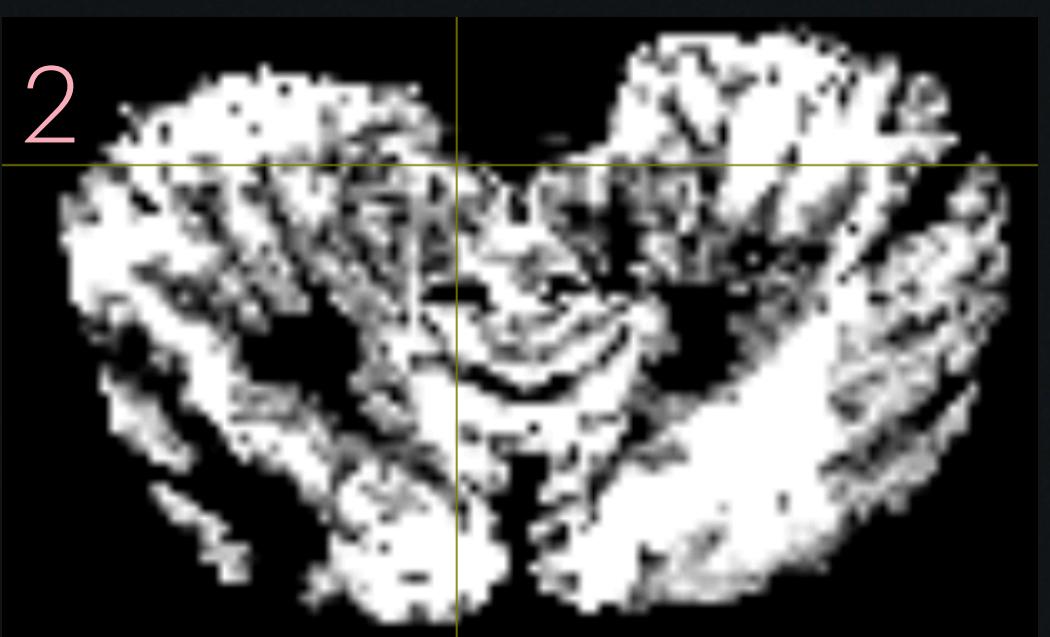
Dividing brain tissues

5ttgen hvs input.mif output.mif
-hippocampi subfields -thalam nuclei

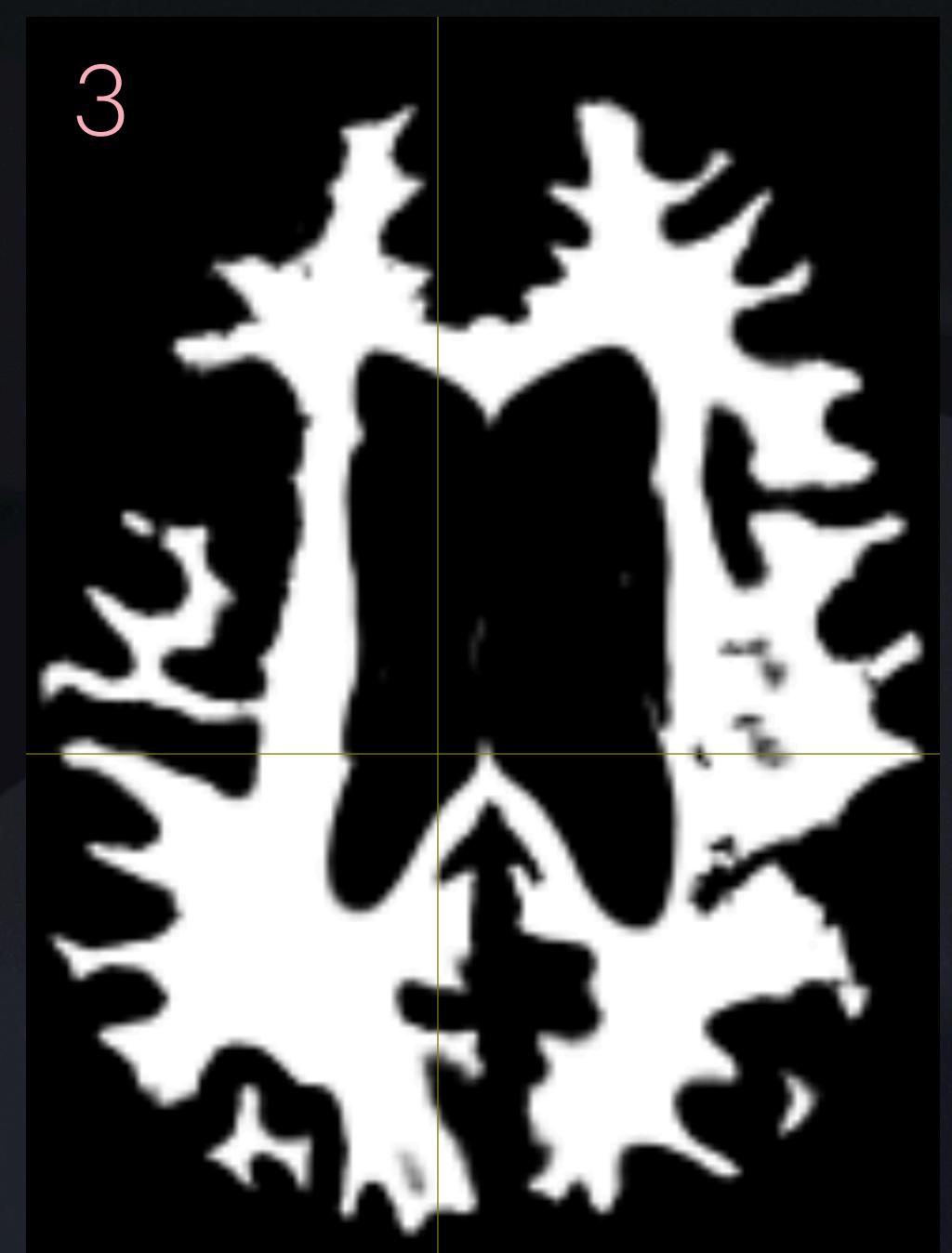
- 1: cortical grey matter
- 2: subcortical grey matter
- 3: white matter
- 4: cerebrospinal fluid
- 5: pathological tissue



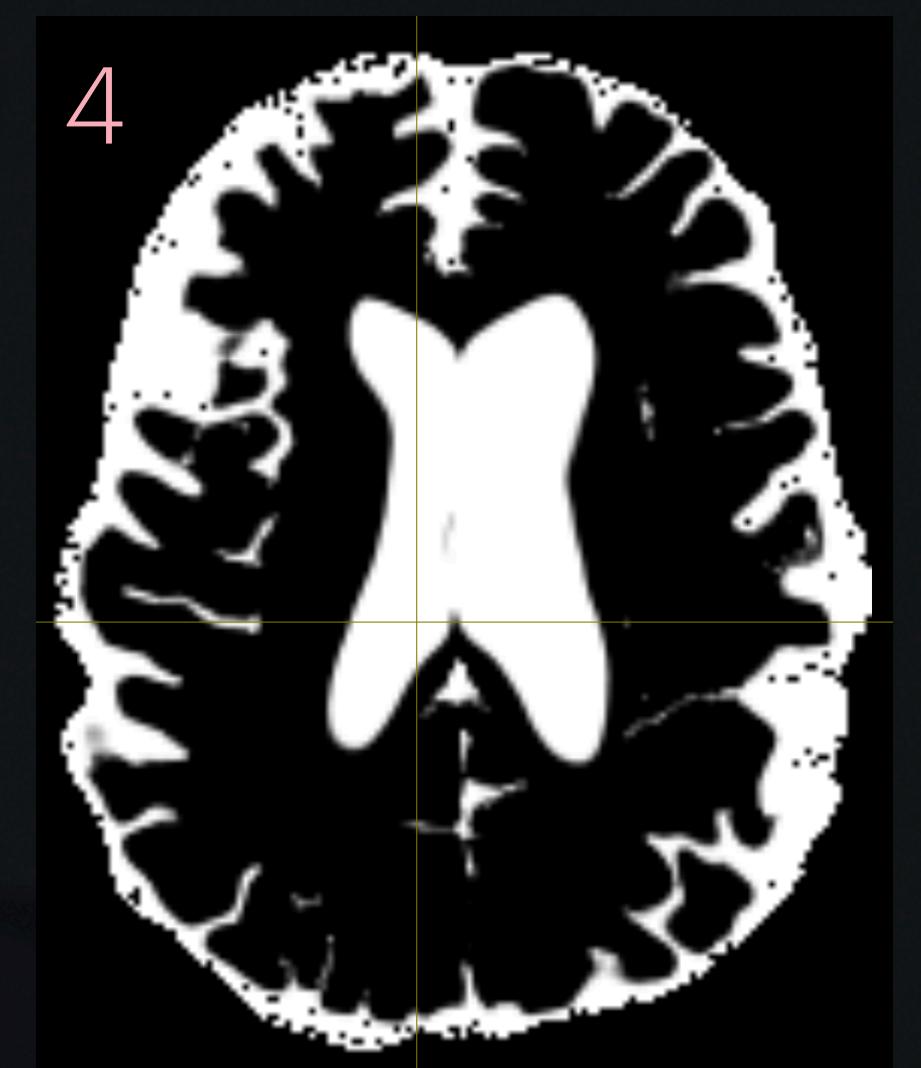
Subject 3105; [10.26 -10.44 17.08]mm



Subject 3105; [10.26 -10.44 -59.08]mm



Subject 3105; [10.26 -10.44 17.08]mm



Subject 3105; [10.26 -10.44 17.08]mm



Subject 3105; [10.26 -10.44 -11.08]mm

Surface creation

(All outputs will be saved in FSL directory, no need for definition in functions.)

```
recon-all -s subject -i input.nii.gz -all
```

- Reconstruction of cortical surface

```
segmentHA_T1.sh subject_ID
```

```
segmentThalamicNuclei.sh subject_ID
```

- Identification & segmentation of hippocampi and thalamus

3. Tractography of whole brain

Tractography preparation

```
dwiextract input_b0.mif --bzero | mrmath - mean output_mean_b0.mif -axis 3
```

```
mrconvert input_mean_b0.mif output_mean_b0.nii.gz
```

```
mrconvert brain.mgz braint1.nii.gz
```

```
epi_reg --epi=input_mean_b0.nii.gz --t1=t1.nii.gz --out=diff2struct_epi --t1brain=braint1.nii.gz
```

```
transformconvert diff2struct_epi.mat input_mean_b0.nii.gz t1.nii.gz flirt_import output_matrix.txt
```

- Creation of matrix to align dMRI and T1 data

Tractography preparation

```
mrtransform input_5tt.mif -linear input_matrix.txt -inverse output_coreg_5tt.mif
```

- Alignment of T1 to dMRI data & creation of co-registered brain tissues

Tractography

```
tckgen -select 20M -seed_dynamic  
wmfod_norm.mif -act input_coreg_5tt.mif  
-backtrack wmfod_norm.mif  
tracks_20m.tck
```

- Creation of whole brain tractogram

```
tcksift2 tracks_20m.tck wmfod_norm.mif  
weights_tracks -act 5tt_coreg.mif
```

- Reduction and correction of tractogram



4. Tractography of ROI connection

Mapping atlas to dMRI

```
mri_surf2surf --srcsubject fsaverage --trgsubject subject_ID --hemi lh --sval-annot lh.HCP-MMP1.annot --tval lh.hcpmmp1.annot
```

```
mri_surf2surf --srcsubject fsaverage --trgsubject subject_ID --hemi rh --sval-annot rh.HCP-MMP1.annot --tval rh.hcpmmp1.annot
```

- Mapping annotations of atlas to left & right hemispheres

```
mri_aparc2aseg --old-ribbon --s subject_ID --annot hcpmmp1 --o hcpmmp1.mgz
```

```
mrconvert hcpmmp1.mgz hcpmmp1.mif
```

- Mapping annotations of atlas to volumetric image, converting to .mif

Mapping atlas to dMRI

```
labelconvert hcpmmmp1.mif hcpmmmp1_original.txt hcpmmmp1_ordered.txt  
hcpmmmp1_parcels_nocoreg.mif
```

- Replacing random integers with rising numbers starting from 1

```
mrtransform hcpmmmp1_parcels_nocoreg.mif -linear input_matrix.txt -inverse  
hcpmmmp1_parcels_coreg.mif
```

- Registering ordered volumetric parcellation to dMRI

Connectome construction

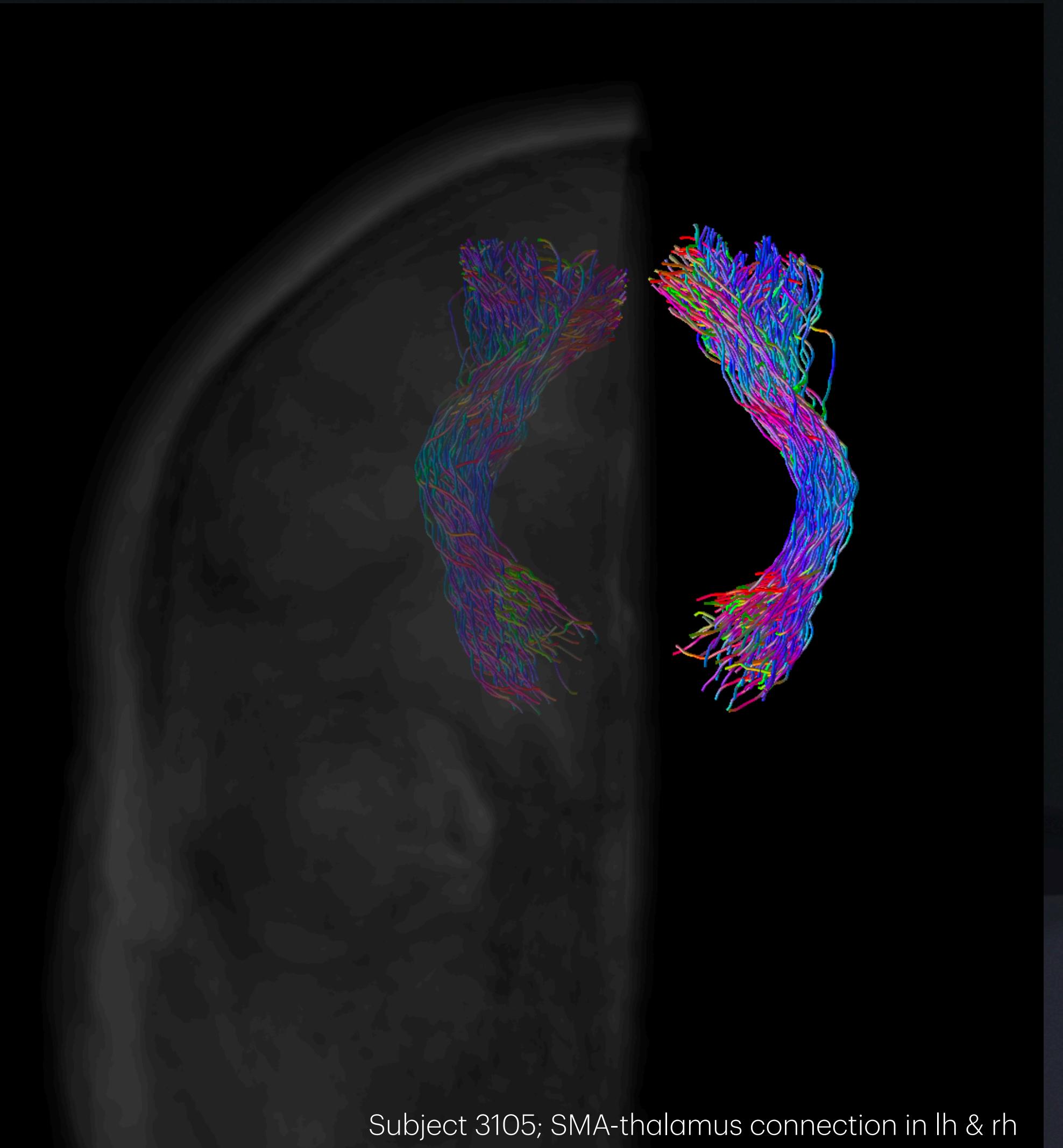
```
tck2connectome -symmetric -zero_diagonal -tck_weights_in weights_tracks tracks_20m.tck  
hcpmmp1 parcels_coreg.mif hcpmmp1.csv -out_assignment assignments_hcpmmp1.csv
```

- Creation of connectome for ROI connections

Visualisation of ROI connection

```
connectome2tck tracks_20m.tck  
assignments_hcpmmpl.csv  
lh_tracks_sma_thalamus.tck -nodes  
55,362 -exclusive -files single  
-tck_weights_in sift_coeffs.txt
```

- Extraction of connection from SMA (55) to thalamus (362) in **left hemisphere**



Subject 3105; SMA-thalamus connection in lh & rh

Annotation

These processing steps follow the B.A.T.M.A.N. tutorial (Tahedl, 2020) in great detail.

Tahedl, M. (2020). *B.A.T.M.A.N.: Basic and Advanced Tractography with MRtrix for All Neurophiles*.