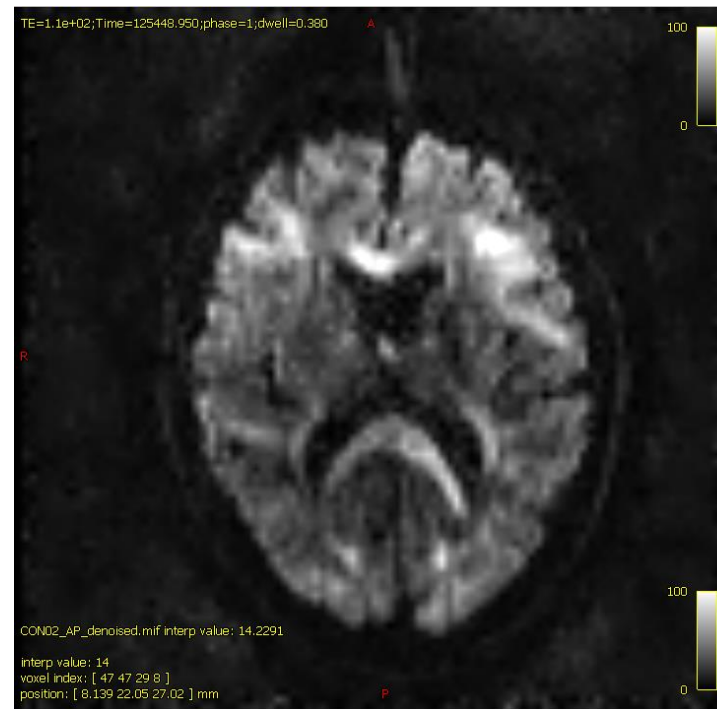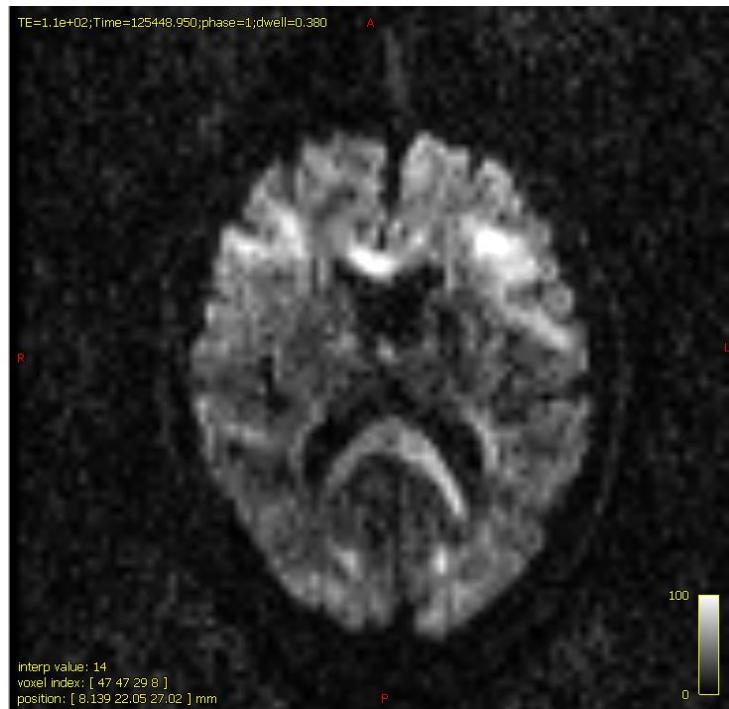# Diffusion Tractography and Connectivity Analysis in MRTrix

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DWI denoising

- Denoising must be performed as the first step of the pipeline

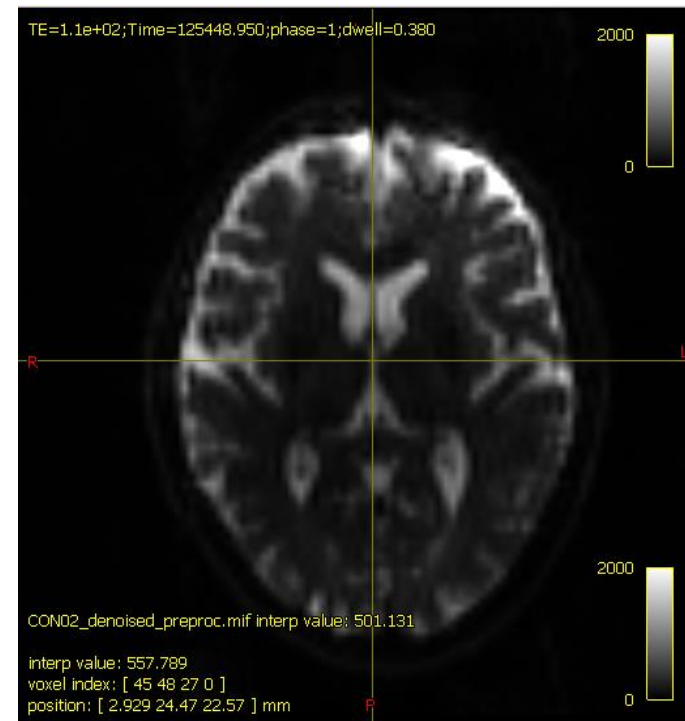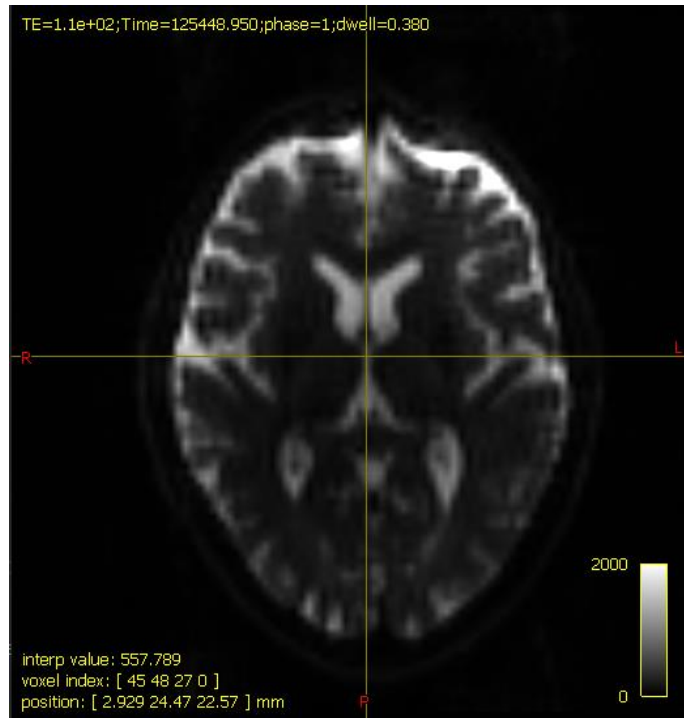- Exploits data redundancy in the patch-level PCA domain

Removal of Gibbs artefacts (optional)

- Removes Gibbs ringing artefacts from DWI images

- Designed for data acquired with full k-space

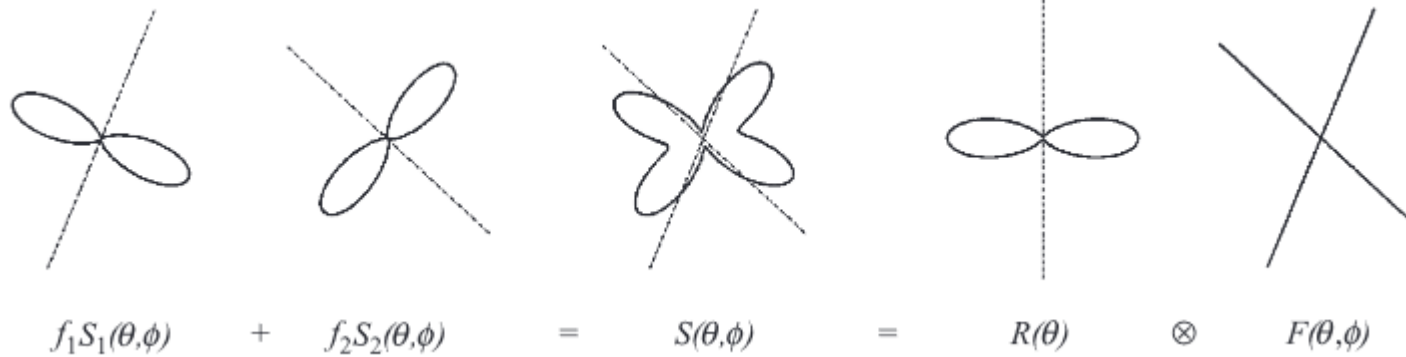- May fail for data acquired with Partial Fourier – always inspect the output
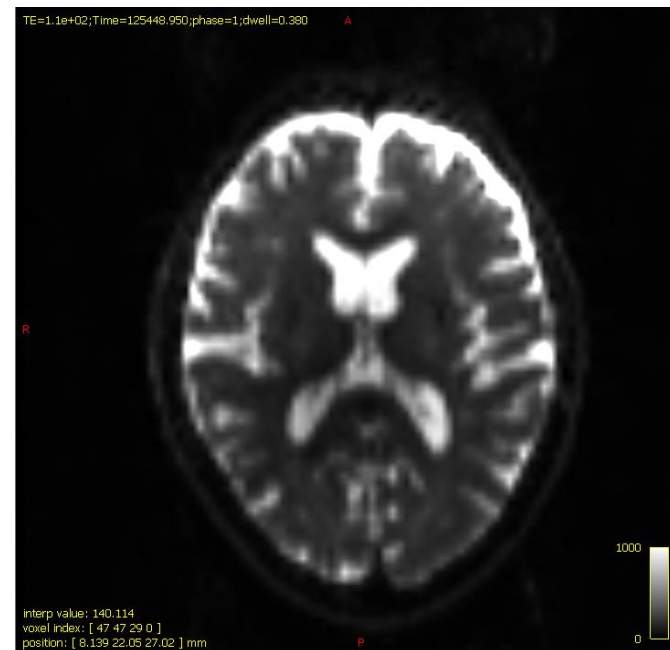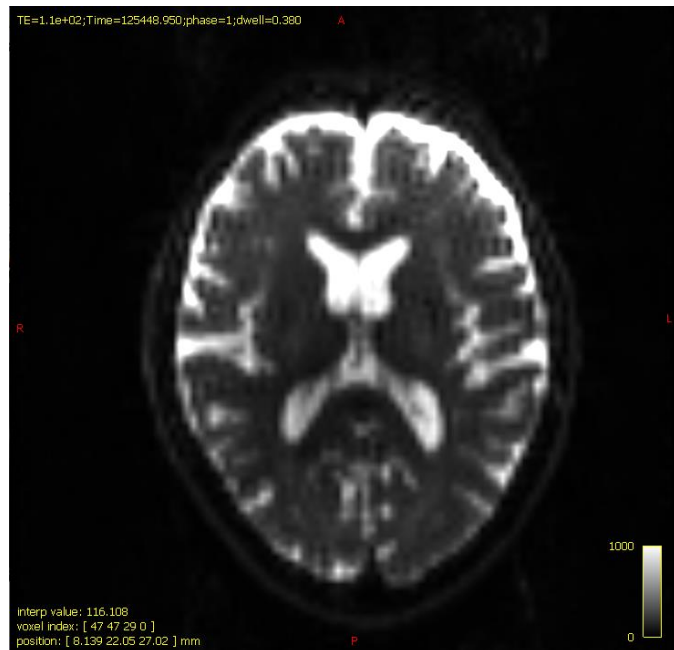
DWI distortion correction

- Pre-processing of DWI images using TOPUP and EDDY

Constrained Spherical Deconvolution (CSD)

Tournier et al. 2007

$$f_1 S_1(\theta,\phi) \quad + \quad f_2 S_2(\theta,\phi) \quad = \quad S(\theta,\phi) \quad = \quad R(\theta) \quad \otimes \quad F(\theta,\phi)$$

- Overall diffusion weighted signal attenuation

- Fibre orientation density function describing the fibre orientations present in the voxel

- Two distinct fibre orientations

- $S_1(\theta,\phi)$, $S_2(\theta,\phi)$ – diffusion weighted signal attenuation
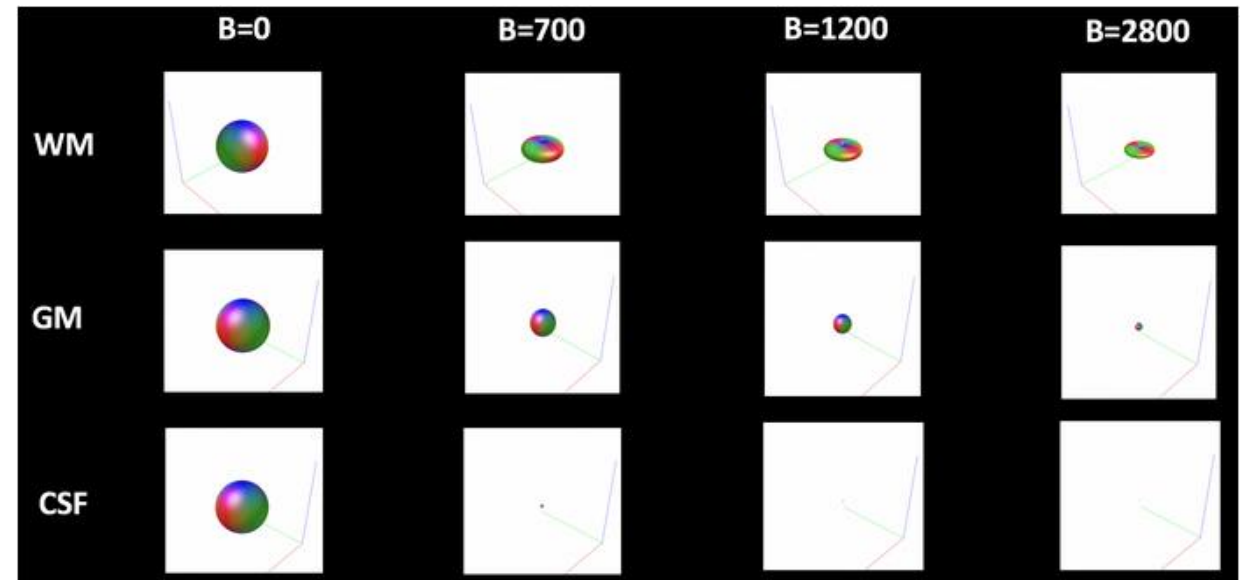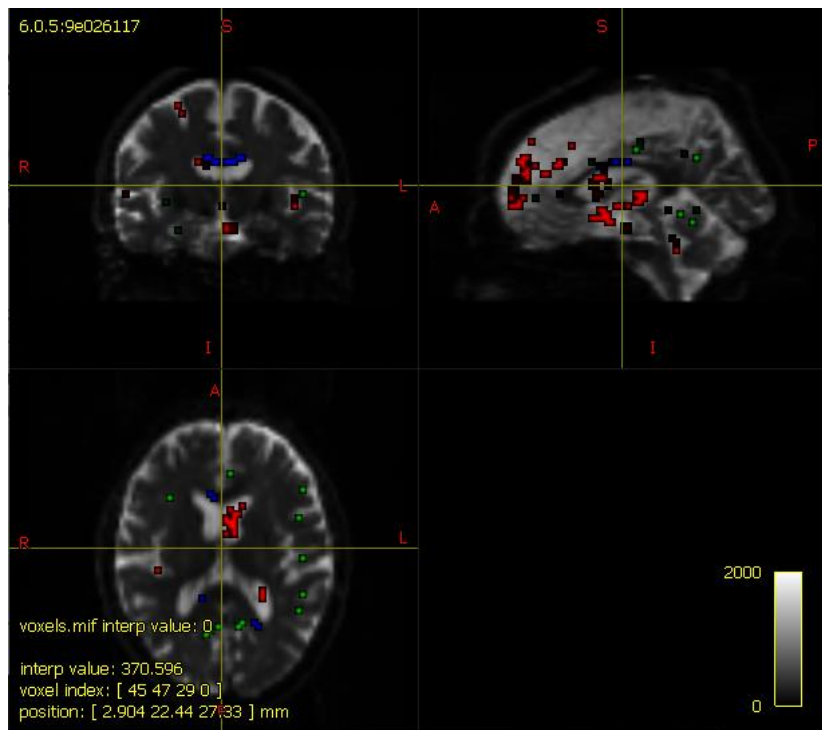
- f_1, f_2 – volume fractions

- Axially symmetric response function describing the signal attenuation measured for a single fibre population.

Constrained Spherical Deconvolution (CSD)
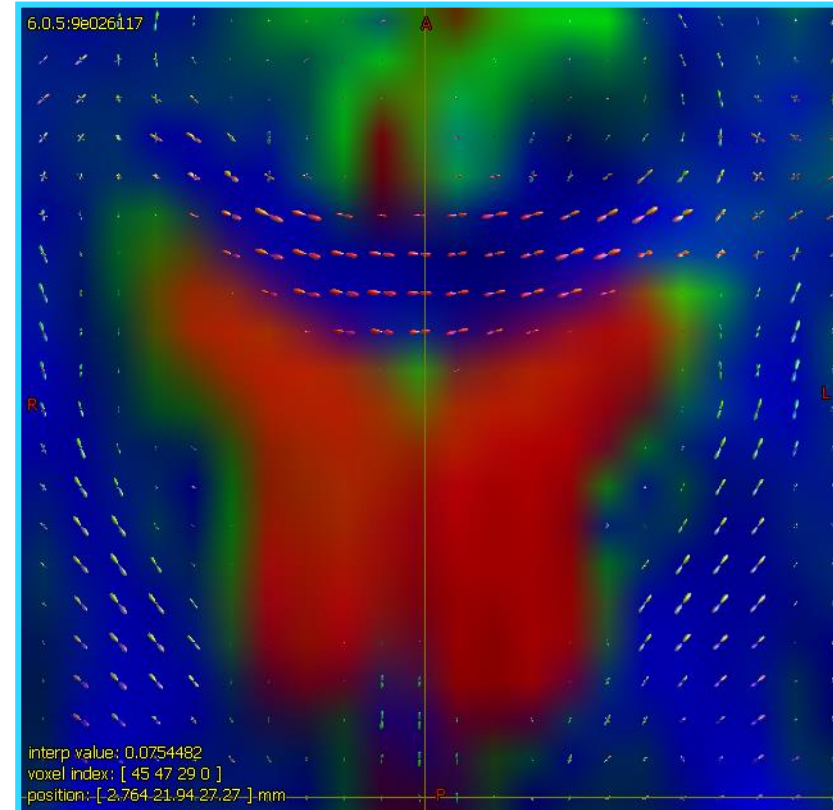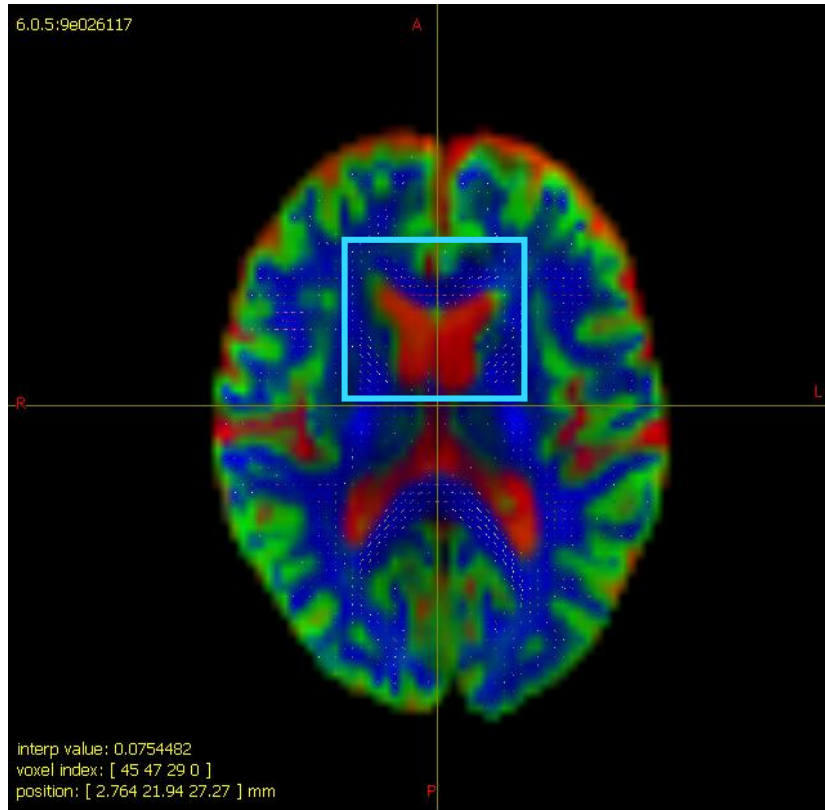
- Estimate the response function per tissue type

https://andysbrainbook.readthedocs.io/en/latest/MRtrix/MRtrix_Course/MRtrix_05_BasisFunctions.html

Constrained Spherical Deconvolution (CSD)

- Estimate the fiber orientation distribution function (ODF) per tissue per voxel
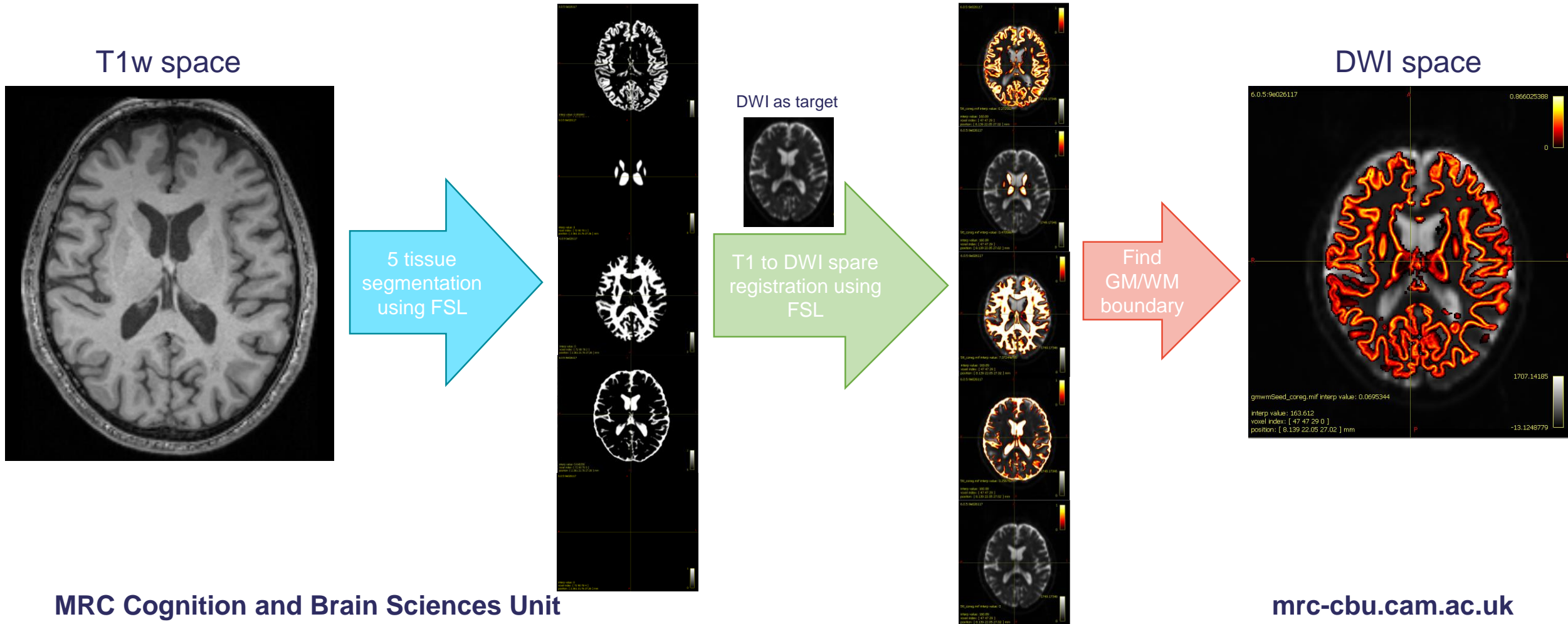
Anatomically Constrained Tractography (ACT)

- Find the GM/WM boundary to seed the streamlines

  - Tissue segmentation of T1w data using FSL tools

  - Image registration using FSL

 - Generate boundary mask in DWI space

Anatomically Constrained Tractography (ACT)

- Find the GM/WM boundary to seed the streamlines

T1w space

5 tissue segmentation using FSL

DWI as target

T1 to DWI spare registration using FSL

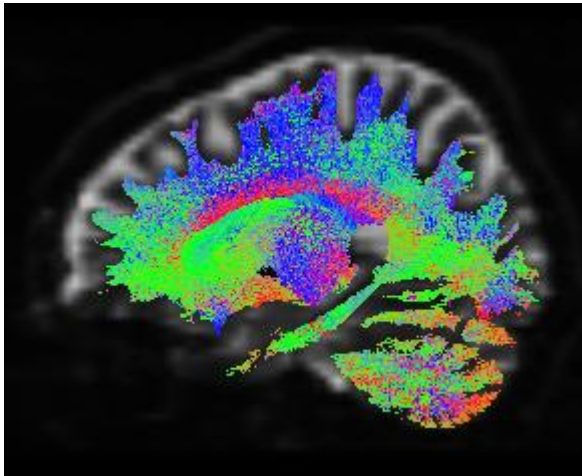Find GM/WM boundary

DWI space

Anatomically Constrained Tractography (ACT)

- Find the GM/WM boundary to seed the streamlines
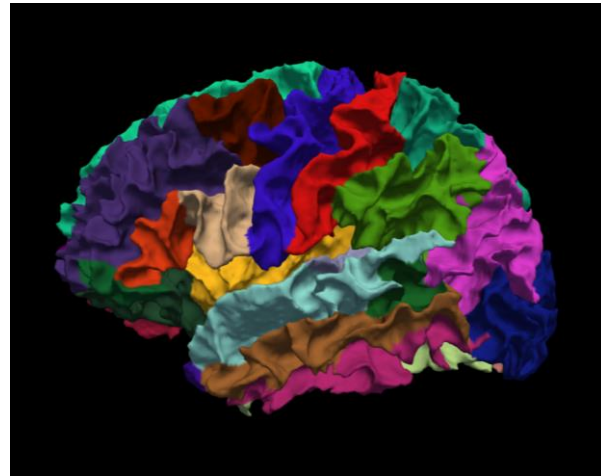
- Generate streamlines
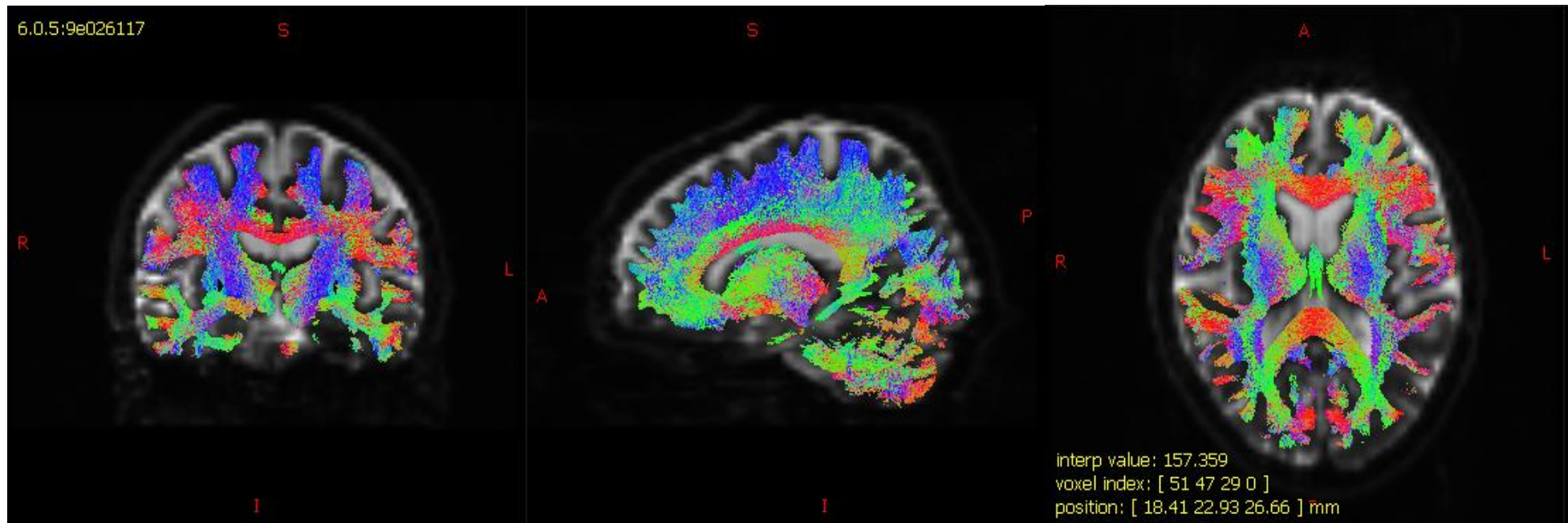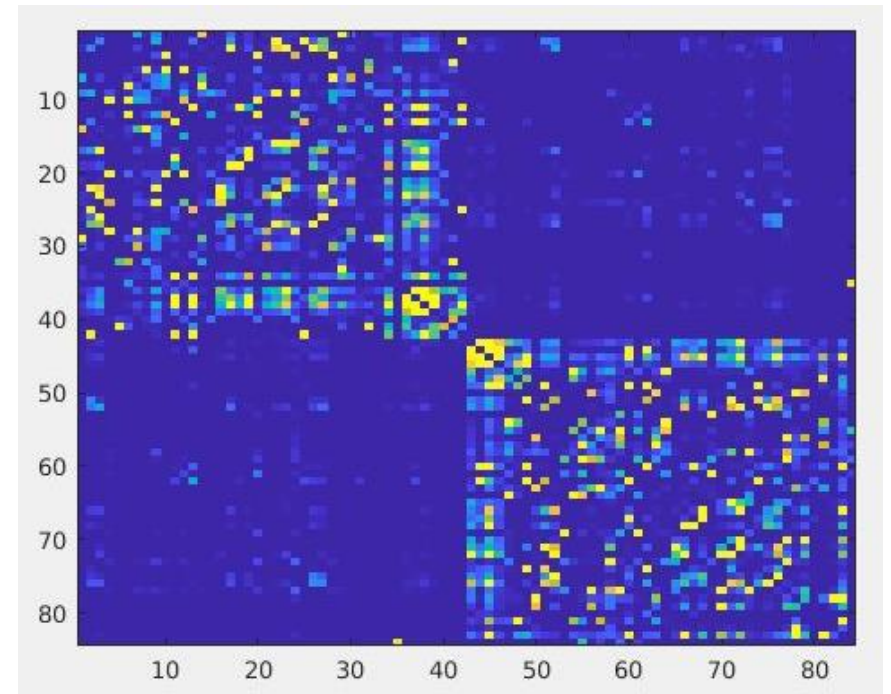
Creating the Connectome

- Parcellate the brain using Freesurfer

- Apply parcellation to the tractogram to generate a connectivity matrix, representing the number of streamlines connecting each pair of ROIs
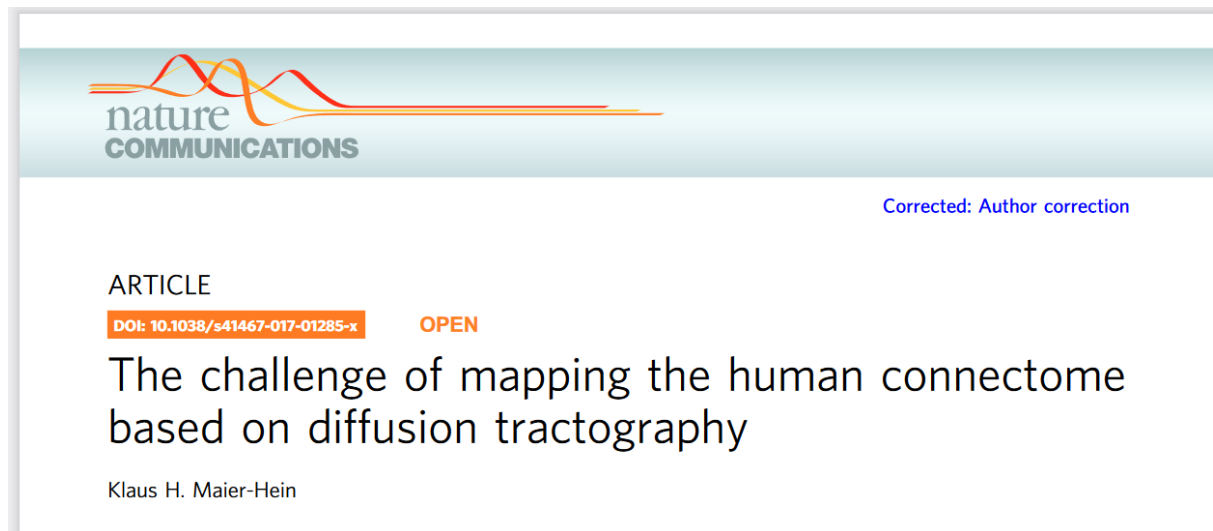
Interpretation of results

- Streamlines generated with diffusion MRI tractography lack polarity

- Even the best fiber orientation reconstruction algorithm cannot resolve all crossing fibers

- Structural connectomes are dominated by false positives

- Choice of fitting model, tracking algorithm, stopping criteria, etc, can also influence the connectome

Thank you