

Supplementary Software:

The resource presented here includes code and analysis routines for each dataset. These are available for downloading under the corresponding “Detailed Info” section in our website: <https://marmosetbrainmapping.org/data.html>, and are also listed below. Please refer to the website for additional details.

A. 150 μm dMRI Dataset (<https://marmosetbrainmapping.org/150um.html>)

Required software: Mrtrix3, FSL 5.0.1

A.1. Denoising DWI (by Mrtrix3)

Note: The 150 μm dMRI data set consists of diffusion data acquired with b values of 0, 2400, 4800 and 7200 s/mm^2 . To improve the sensitivity at high b values, the images with $b = 7200$ s/mm^2 were acquired with 2 averages, while the images with other b values only had one single average. Because of this, the images with $b = 7200$ have a different scaling factor that affects both the signal and noise values. To correct this, we performed the following steps for denoising of the data. More discussion details can be found in [this link](#).

```
$ mrconvert raw_noscale.nii.gz raw_noscale.mif -fslgrad raw.bvecs raw.bvals
$ dwiextract raw_noscale.mif -shell 7200 b7200.mif
$ dwiextract raw_noscale.mif -shell 0,2400,4800 raw_other_shells.mif
$ mrcalc b7200.mif 2 -sqrt -div b7200_sqrt2.mif
$ mrcat raw_other_shells.mif b7200_sqrt2.mif -axis 3 dwi_constant_noise.mif
$ dwidenoise dwi_constant_noise.mif dwi_denoised.mif -noise dwi_noise.nii.gz -mask
raw_mask.nii.gz -extent 9,9,9 -force
$ dwiextract dwi_denoised.mif -shell 7200 b7200_denoised.mif
$ mrcalc b7200_denoised.mif 2 -sqrt -div b7200_denoised_sqrt2.mif
$ dwiextract dwi_denoised.mif -shell 0,2400,4800 other_shells.mif
$ mrcat other_shells.mif b7200_denoised_sqrt2.mif -axis 3 dwi_final.mif
$ mrconvert dwi_final.mif dwi_final.nii.gz -export_grad_fsl dwi_final.bvecs dwi_final.bvals
```

A.2. Eddy current correction and DTI-fitting (by FSL)

```
$ eddy_correct dwi_final.nii.gz data.nii.gz 0 spline
$ fdt_rotate_bvecs dwi_final.bvecs bvecs data.ecclog
$ dtifit -k data.nii.gz -o DTIFIT -m mask.nii.gz -r bvecs -b bvals
```

A.3. MRtrix3-based pipeline for dMRI tractography (by MRtrx3)

The Mrtrix3-based pipeline for dMRI tractography, including multi-tissue constrained spherical deconvolution, is identical to the pipeline for the 80 μm data (section B.3 below), except that we used "-lmax 0,6,10,14" for the white matter response function estimation.

B. 80 μm dMRI dataset (<https://marmosetbrainmapping.org/80um.html>)

Required software: Mrtrix3.0, FSL 5.0.1, Tortoise 3.1.4

B.1. DWI Data Preprocessing by Mrtrix3 and FSL

Note: We used b0, b2400, and b4800 for the preprocessing. b30 was excluded in this preprocessing pipeline. In Mrtrix3, you can specify how many threads (\$NumofThreads) in the "-nthread" option for multi-threaded processing.

B.1.1. Denoising DWI (by Mrtrix3)

```
$ dwidenoise raw.nii.gz dwi_denoised.nii.gz -noise noise.nii.gz -extent 7,7,7 -force -nthread $NumofThreads
```

B.1.2. Eddy current correction and DTI-fitting (by FSL)

```
$ eddy_correct dwi_denoised.nii.gz data.nii.gz 0 spline
$ fdt_rotate_bvecs raw.bvecs bvecs data.ecclog
$ dtifit -k data.nii.gz -o DTIFIT -m mask.nii.gz -r bvecs -b bvals
```

B.2. DWI Data Preprocessing By Tortoise

Software: Tortoise 3.1.4 and FSL (optional)

Note: We used all DWIs for the preprocessing, including b30, in this preprocessing pipeline. DWI are co-registered to structural images during the preprocessing stage.

B.2.1. Preprocessing by Tortoise

```
$ ImportNIFTI -i raw.nii -p horizontal --bvals raw.bvals --bvecs raw.bvecs
$ DIFFPREP -i ./raw_proc/raw.list --will_be_drugged 0 --do_QC 0 --is_human_brain 0 -s T2.nii
-d for_final --high_b 0 --res 0.08 0.08 0.08
$ TORTOISEBmatrixToFSLBVecs ./raw_proc/raw_DMC.bmtxt
```

B.2.2. DTIFIT by FSL (optional)

```
$ cp ./raw_proc/raw_DMC.nii data.nii
$ cp ./raw_proc/raw_DMC.bvecs bvecs
$ dtifit -k data.nii -r bvecs -b bvals -m mask.nii.gz -o DTIFIT
```

B.3. MRtrix3-based pipeline for dMRI tractography (by MRtrix3)

Note: Our 80 μm dMRI data used b = 0, b = 2400, and b = 4800 s/mm²

B.3.1. Multi-tissue constrained spherical deconvolution

```
$ mrconvert data.nii.gz data.mif -fslgrad bvecs bvals -force -nthread $NumofThreads
$ dwi2response manual data.mif WM_manual_selected_voxels.nii.gz WM.res -mask mask.nii.gz
-lmax 0,6,10 -force -nthread $NumofThreads
$ dwi2response manual data.mif GM_manual_selected_voxels.nii.gz GM.res -mask mask.nii.gz -
lmax 0,0,0 -force -nthread $NumofThreads
```

```
$ dwi2fod msmt_csd data.mif WM.res fod_WM.mif GM.res fod_GM.mif -mask mask.nii.gz -force -nthread $NumofThreads
```

```
$ mrcalc fod_WM.mi mask_righthalf.nii.gz -mult fod_masked.mif -force -nthread $NumofThreads
```

Note1: WM_manual_selected_voxels and GM_manual_selected_voxels are manually defined. You may also use other automatic methods in dwi2response.

Note2: To reduce RAM and CPU requirements in dwi2fod, we removed many gray matter voxels using a conservative threshold (FOD < 0.05) and the left hemisphere. If you have time, or a very powerful computer, you can ignore this step.

B.3.2.a. Tractography for reconstructing white matter tracts of interest (e.g., see Fig. 7)

Note: We combined the tracking results with different angles (30,45,60). In addition, the tracking results are affected by which ROI is used as the seed. Thus, we used different inclusion masks as seeds and combined all those results as well. As different trackings may use different number of inclusion masks, we used ROI# to reset this variable here.

```
$ tckgen -stop -select 5k -angle 30 -maxlength 75 -seed_image seed_ROI1.nii.gz -include include_ROI1.nii.gz -include include_ROI#.nii.gz -exclude exclude_ROI1.nii.gz -exclude exclude_ROI#.nii.gz -mask mask.nii.gz fod_masked.mif tracks_5K_ROI_a30_p1.tck -force -nthreads $NumofThreads
```

```
$ tckgen -stop -select 5k -angle 45 -maxlength 75 -seed_image seed_ROI1.nii.gz -include include_ROI1.nii.gz -include include_ROI#.nii.gz -exclude exclude_ROI1.nii.gz -exclude exclude_ROI#.nii.gz -mask mask.nii.gz fod_masked.mif tracks_5K_ROI_a45_p1.tck -force -nthreads $NumofThreads
```

```
$ tckgen -stop -select 5k -angle 60 -maxlength 75 -seed_image seed_ROI1.nii.gz -include include_ROI1.nii.gz -include include_ROI#.nii.gz -exclude exclude_ROI1.nii.gz -exclude exclude_ROI#.nii.gz -mask mask.nii.gz fod_masked.mif tracks_5K_ROI_a60_p1.tck -force -nthreads $NumofThreads
```

```
$ tckgen -stop -select 5k -angle 30 -maxlength 75 -seed_image seed_ROI#.nii.gz -include include_ROI1.nii.gz -include include_ROI#.nii.gz -exclude exclude_ROI1.nii.gz -exclude exclude_ROI#.nii.gz -mask mask.nii.gz fod_masked.mif tracks_5K_ROI_a30_p#.tck -force -nthreads $NumofThreads
```

```
$ tckgen -stop -select 5k -angle 45 -maxlength 75 -seed_image seed_ROI#.nii.gz -include include_ROI1.nii.gz -include include_ROI#.nii.gz -exclude exclude_ROI1.nii.gz -exclude exclude_ROI#.nii.gz -mask mask.nii.gz fod_masked.mif tracks_5K_ROI_a45_p#.tck -force -nthreads $NumofThreads
```

```
$ tckgen -stop -select 5k -angle 60 -maxlength 75 -seed_image seed_ROI#.nii.gz -include include_ROI1.nii.gz -include include_ROI#.nii.gz -exclude exclude_ROI1.nii.gz -exclude exclude_ROI#.nii.gz -mask mask.nii.gz fod_masked.mif tracks_5K_ROI_a60_p#.tck -force -nthreads $NumofThreads
```

```
$ tckedit tracks_5K_ROI_a30_p1.tck tracks_5K_ROI_a45_p1.tck tracks_5K_ROI_a60_p1.tck tracks_5K_ROI_a30_p#.tck tracks_5K_ROI_a45_p#.tck tracks_5K_ROI_a60_p#.tck tracks_all_ROI.tck -force -nthread $NumofThreads
```

```
$ tckmap tracks_all_ROI.tck tracks_all_ROI.nii.gz -template fod_masked.mif -force -nthread $NumofThreads
```

B.3.2.b. Tractography for reconstructing white matter tracts of interest (e.g., see Fig. 8)

Note: ROI $\{i\}$ and ROI $\{j\}$ were two connected cortical regions in the [neuronal-tracing database](#)

```
$ tckgen -stop -select 1k -angle 30 -maxlength 75 -seed_image ROI $\{i\}$ .nii.gz -include ROI $\{j\}$ .nii.gz -mask mask.nii.gz fod_masked.mif ROI $\{i\}$ toROI $\{j\}$ _a30.tck -force -nthreads $NumofThreads
```

```
$ tckgen -stop -select 1k -angle 45 -maxlength 75 -seed_image ROI $\{i\}$ .nii.gz -include ROI $\{j\}$ .nii.gz -mask mask.nii.gz fod_masked.mif ROI $\{i\}$ toROI $\{j\}$ _a45.tck -force -nthreads $NumofThreads
```

```
$ tckgen -stop -select 1k -angle 60 -maxlength 75 -seed_image ROI $\{i\}$ .nii.gz -include ROI $\{j\}$ .nii.gz -mask mask.nii.gz fod_masked.mif ROI $\{i\}$ toROI $\{j\}$ _a60.tck -force -nthreads $NumofThreads
```

```
$ tckedit ROI $\{i\}$ toROI $\{j\}$ _a30.tck ROI $\{i\}$ toROI $\{j\}$ _a45.tck ROI $\{i\}$ toROI $\{j\}$ _a60.tck ROI $\{i\}$ toROI $\{j\}$ .tck
```

```
$ tckmap ROI $\{i\}$ toROI $\{j\}$ .tck ROI $\{i\}$ toROI $\{j\}$ .nii.gz -template fod_masked.mif -force -nthread $NumofThreads
```

C. 64 μ m dMRI Dataset (<https://marmosetbrainmapping.org/64um.html>)

Required software: **Mrtrix3, FSL 5.0.1**

Note: We used $b = 0$, $b = 2400$, and $b = 4800$ s/mm² for the preprocessing. The images acquired with $b = 30$ s/mm² were excluded from the preprocessing pipeline.

C.1. Denoising DWI (by Mrtrix3)

```
$ dwidenoise raw.nii.gz dwi_denoised.nii.gz -noise noise.nii.gz -extent 7,7,7 -force
```

C.2. Eddy current correction and DTI-fitting (by FSL)

```
$ eddy_correct dwi_denoised.nii.gz data.nii.gz 0 spline
```

```
$ fdt_rotate_bvecs raw.bvecs bvecs data.ecclog
```

```
$ dtifit -k data.nii.gz -o DTIFIT -m mask.nii.gz -r bvecs -b bvals
```

C.3. MRtrix3-based pipeline for dMRI tractography (by MRtr3)

The Mrtrix3-based pipeline for dMRI tractography, including multi-tissue constrained spherical deconvolution, is identical to the pipeline for the 80 μ m data (section B.3 above).

For the track map shown in Figure 4, we used the following command:

```
$ tckgen -select 10000000 -angle 60 -minlength 3 -maxlength 75 -seed_dynamic
```

```
fod_masked.mif -seed_cutoff 0.1 -mask mask.nii.gz fod_masked.mif tracks_10_million.tck -force -nthread $NumofThreads
```

```
$ tckmap tracks_10_million.tck tckmap_fod.mif -vox 0.05 -dec -force -nthreads $NumofThreads
```