



MGH Adult Diffusion Data Acquisition Details

Introduction

The MGH-USC HCP team has acquired and shared diffusion imaging data from 35 healthy adults scanned on the customized Siemens 3T Connectom scanner. The imaging data is available to those who [register](#) and agree to the [Open Access Data Use Terms](#).

The hardware

The data were collected on the customized Siemens 3T Connectom scanner, which is a modified 3T Skyra system (MAGNETOM Skyra Siemens Healthcare), housed at the MGH/HST Athinoula A. Martinos Center for Biomedical Imaging (see Setsompop et al., 2013 for details of the scanner design and implementation). A 64-channel, tight-fitting brain array coil (Keil et al., 2013) was used for data acquisition.

Subjects

Data was acquired from healthy adults between the ages of 20 and 59. [Demographic information](#) available in ConnectomeDB includes gender and age range. The participants gave written consent, and the procedures were carried out in accordance with the institutional review board approval and procedures.

Summary of imaging protocols

Each dataset (in nifti format) consists of an MPRAGE scan, a high resolution T2-SPACE scan and diffusion scans with 4 different b-values.

Structural scans

Type	Description	TR/TE (ms)	TI (ms)	Flip Angle	FOV (mm)	Voxel Size	BW (Hz/Px)	iPAT	Acquisition Time (min:sec)
T1w	3D MPRAGE	2530/1.15	1100	7.0deg	256x256	1mm isotropic	651	2	6:02
T2w	3D T2-SPACE	3200/561			224x224	0.7mm isotropic	744	2	6:48

Diffusion scans

Parameter	Value
Sequence	Spin-echo EPI
TR/TE (ms)	8800/57
δ/Δ (ms)	12.9/21.8
FOV (mm)	210x210
Matrix	140x140
Slices	96 slices, 1.5mm thick, 1.5mm isotropic voxel size
iPAT	3
Multiband factor	1



Parameter	Value
Echo spacing (ms)	0.63
BW	1984 Hz/Px
Phase Partial Fourier	6/8
b-values	1000, 3000, 5000, 10,000 s/mm ²
Total acquisition time	89 mins

Other details: Structural scans were reviewed by a radiologist to assure absence of brain abnormalities. Diffusion data were acquired in oblique axial slices. Diffusion gradients are mono-polar. The echo time and diffusion times (δ/Δ) were optimized for the b-value=10,000 (s/mm²) shell, and fixed for all the lower b-value shells. The diffusion scans are comprised of 5 runs:

Run No.	b-value (s/mm ²)	diffusion directions	Acquisition Time (min:sec)
1	1,000	64	11:44
2	3,000	64	11:44
3	5,000	128 (set1)	21:51
4	10,000	128 (set1)	21:51
5	10,000	128 (set2)	21:51

One non-diffusion weighted (b=0) image was collected every 14 image volumes, yielding 552 volumes in total. Phase encoding direction was anterior to posterior. MultiBand acquisition was not used in this dataset.

Full scanning protocols (PDF)

Complete scanning protocols can be found in [Appendix I](#) (updated).

Minimum data preprocessing

The imaging data was processed with software tools in Freesurfer V5.3.0 (<http://freesurfer.net/fswiki/FreeSurferWiki/>) and FSL V5.0 (<http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/>).

Structural scans

1. Gradient nonlinearity correction. The distortion caused by the gradient nonlinearity was corrected based on the spherical harmonic coefficients. See (Glasser et al., 2013; Jovicich et al., 2006) for the method details, and the [WU-Minn HCP Data Release Reference Manual](#) for details of the need for gradient nonlinearity correction.

2. De-face and De-ear. A face mask was generated using the Freesurfer tool. The ear masks were drawn manually. These masks were then used to mask off the facial and ear regions on the MPRAGE and T2-SPACE images.

Diffusion scans

1. Gradient nonlinearity correction.

2. Motion correction. The $b=0$ images interspersed throughout the diffusion scans were used to estimate the bulk head motions with respect to the initial time point (first $b=0$ image), where the rigid transformation were calculated with the boundary based registration tool in the FreeSurfer package V5.3.0 (Greve and Fischl, 2009). For each $b=0$ image, this transformation was then applied to itself and the following 13 diffusion weighted images to correct for head motions. After motion correction, the b-vectors were adjusted according to the rigid rotation estimated.

3. Eddy current correction. The FSL's 'EDDY' tool (Andersson et al., 2012) was to correct for eddy current distortion. All 4 shells ($bvals = 1k, 3k, 5k, 10k \text{ s/mm}^2$) were concatenated (552 volumes in total), and passed into the EDDY tool.

4. b-vectors. After eddy current correction, the rigid rotational motion estimates obtained from both the motion correction step and the eddy current correction step were concatenated and applied to the original b-vectors for correction.

Other details: Both diffusion and structural data are provided in native space. Since the gradient field nonlinearity coefficients were protected by Siemens as proprietary information, the data provided as 'raw' for diffusion and T1w/T2w were already corrected for gradient nonlinearity.

Reference

1. Andersson, J.L., Xu, J., Yacoub, E., Auerbach, E., Moeller, S., Ugurbil, K., 2012. A comprehensive Gaussian Process framework for correcting distortions and movements in diffusion images. *Proc Intl Soc Mag Reson Med*, p. 2426.
2. Greve, D.N., Fischl, B., 2009. Accurate and robust brain image alignment using boundary-based registration. *Neuroimage* 48, 63-72.
3. Keil, B., Blau, J.N., Biber, S., Hoecht, P., Tountcheva, V., Setsompop, K., Triantafyllou, C., Wald, L.L., 2013. A 64-channel 3T array coil for accelerated brain MRI. *Magn Reson Med* 70, 248-258.
4. Setsompop, K., Kimmlingen, R., Eberlein, E., Witzel, T., Cohen-Adad, J., McNab, J.A., Keil, B., Tisdall, M.D., Hoecht, P., Dietz, P., Cauley, S.F., Tountcheva, V., Matschl, V., Lenz, V.H., Heberlein, K., Potthast, A., Thein, H., Van Horn, J., Toga, A., Schmitt, F., Lehne, D., Rosen, B.R., Wedeen, V., Wald, L.L., 2013. Pushing the limits of in vivo diffusion MRI for the Human Connectome Project. *Neuroimage* 80, 220-233.



Filenames in ConnectomeDB:

This section lists the filenames and directory structure provided in ConnectomeDB.

mgh_1001.zip (in /data/intradb/ftp/MGH/NIFTI/zips/bvec_fixed/) unzips to:

```
mgh_1001/  
  file_description.txt  
mgh_1001/anat/T1/  
T1.nii.gz  
mgh_1001/anat/T2/  
T2.nii.gz  
  mgh_1001/diff/preproc/  
  bvals.txt  
  bvecs_fsl_moco_norm.txt  
  bvecs_moco_norm.txt  
mgh_1001/diff/preproc/mri/  
diff_preproc.nii.gz  
mgh_1001/diff/raw/mri/  
  diff.nii.gz  
  bvecs.txt  
  bvecs_fsl.txt  
  bvals.txt  
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7322043912          13 files
```