Preparation of Diffusion–Weighted MR Image Data for Cortical Parcellation

Z. Nagy[1], D. L. Thomas[2], N. Weiskopf[1], and M. Sereno[3,4]

[1]Wellcome Trust Centre for Neuroimaging, University College London, London, United Kingdom, [2]Institute of Neurology, Department of Brain Repair and Rehabilitation, University College London, London, United Kingdom, [3]Department of Psychology, University College London, London, United Kingdom, [4]Department of Psychology, Birkbeck College, London, United Kingdom

Introduction: The map produced by Korbinian Brodmann {1,2} parcellates the cortex into 43 distinct areas based on cell body stained histological investigations and provides cognitive and anatomical neuroscience with a commonly held reference system for spatial localization. However, the Brodmann map lacks objectivity, used a single contrast for parcellation and importantly ignores inter-individual variability. Consequently, much effort has been aimed at using magnetic resonance imaging (MRI) to map out the histology of the human cortex in-vivo at a much finer spatial resolution – though the choice of appropriate MRI contrast is not clear. While diffusion tensor imaging (DTI) {3} has primarily been used to scrutinize the microstructure of brain white matter (WM), some investigators have found uses of this modality in grey matter (GM) as well. Some followed the development of cortical GM in fetuses {4} while others parcellated the nuclei of the amygdala {5}. Deoni et al. used a "time-series"-like method to parcellate the nuclei of the thalamus where high level of correlation in the signal variability with respect to diffusion direction was taken to identify homologous tissue types {6}. Here we develop the image processing steps required to prepare DTI data for the use of pattern recognition analyses in order to thus parcellate the cortical mantle in-vivo using.

Methods: Ethics: Involvement of the human volunteer was permitted by the local ethics committee and a written informed consent was signed prior to examination.

MRI Data Acquisition: DTI data was collected on a 3 T scanner (Tim Trio, Siemens Healthcare, Erlangen, Germany) using a 32-channel receive only head coil. Two datasets were collected to examine test / re–test concordance. Each dataset consisted of 61 diffusion weighted images (DWIs) with a b–value = 1000 s/mm^2 and diffusion directions distributed evenly on the surface of a sphere {7} and 1 image with b = 100 s/mm^2 to aid alignment (See Table 1). The images had 2.3 mm^3 resolution and were collected with TE = 90 ms and TR = 7.3 s. Separately, four T1-weighted MP–RAGE images were collected on a 1.5 T scanner (Avanto, Siemens Healthcare) using a 32-channel receive-only head coil. The images had 1.0 mm^3 resolution and were collected with TE = 3.57 ms and TR = 2.75 s.

Cortical Signal Intensity Extraction: The MP–RAGE image was used to reconstruct the surface of the GM/WM boundary (FreeSurfer). The test–retest scans were first aligned on a DWI direction–by–direction basis (AFNI 3dvolreg, heptic interpolation). The b0 image sets of the DTI data were then aligned with the mean T1–weighted MP–RAGE image. The transformation matrix was then used to align remaining diffusion–weighted images. At every GM/WM boundary vertex we used the local normal to move 1 mm into the GM to sample the signal from each diffusion–weighted image. Therefore at each vertex point we had a vector of 61 signal intensity values. These values were mapped to the cortical surface and also read into Matlab 7.10 (MathWorks, Natick, USA) for further processing.

Results: Figure 1 displays two different diffusion–encoding directions, each acquired twice indicating that signal intensity in an image with a given diffusion weighting is highly reproducible. Pixel intensity corresponds to the raw the diffusion–weighted signal. Figure 2 (bottom) displays the mean signal intensity from 50 neighbouring surface vertex points in two different regions of interest (top) where Area 1 is green and Area 2 is blue. The x axis ranges for 61 different diffusion encoding direction while the y axis is signal intensity in arbitrary units. Note that the signal "time series" indicates that diffusion is anisotropic and is different for the two regions while highly reproducible within the region and on test–retest.

Figure 1 – Test Re–Test variability vs Diffusion Direction Contrast

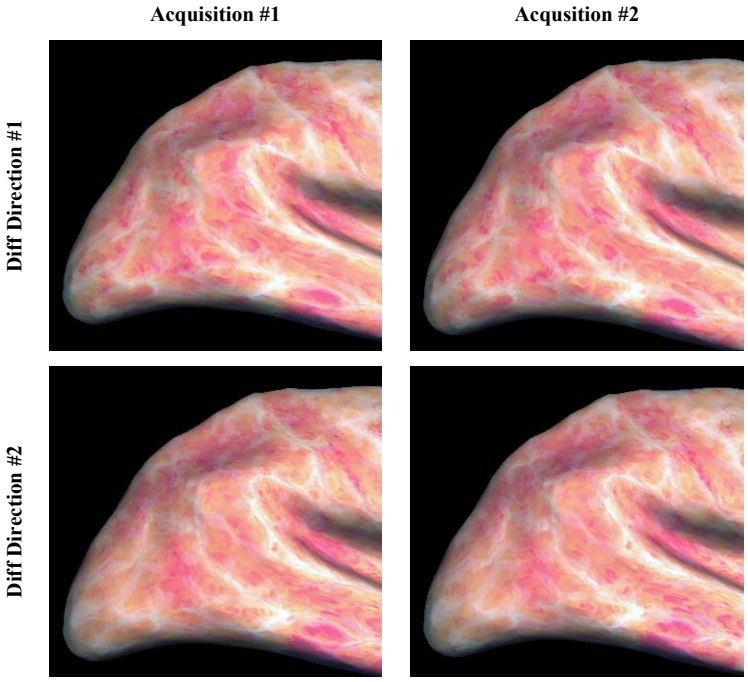
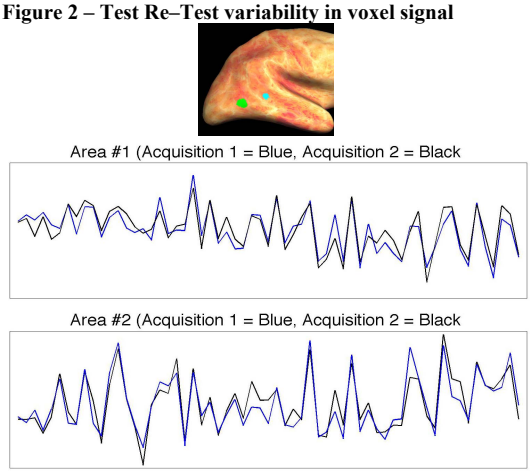


Figure 2 – Test Re–Test variability in voxel signal



Discussion: We demonstrated that there is available diffusion–weighted signal in voxels containing brain GM. This signal is larger than the inherent image noise and test–to–test variability. With a dataset that is prepared as presented here, one can begin to explore the tissue characteristics of cortical GM. We propose, it should be possible to identify homologous areas of tissue using pattern classification methods. We identified several limitations and ways to remedy them. The cortical layer is only 2–4 mm in thickness. Because of the relatively coarse spatial resolution of EPI data in this study it was only possibly to make a point estimate of the diffusion profile at each surface vertex. This biases the results because at different spatial locations it is not known which layer is sampled. Thus it is likely that when comparing regions to each other different layers are involved. To remedy this data with higher resolution is needed which will be possible with parallel imaging and higher field strengths. Another limitation of this study is the inherent difficulty to register the MP–RAGE images with the EPI data that suffers from susceptibility induced distortions, though these can be corrected in principle (8). However, our aim here was only to demonstrate the existence of a stable diffusion signal, which has a clear dependence on the direction of the applied diffusion/weighting, and to propose a potential approach for in–vivo parcellation of the individual cortex using patter recognition analyses.

References (1) Brodmann (1909) Barth, Leipzig, Germany (2) Zilles (2010) Nature Reviews Neurosci. Vol. 11: p139–145 (3) Basser (1996) J. Magnetic Resonance B, Vol. 111:p209–219 (4) McKinstry (2002) Cerebral Cortex, Vol. 12: p1237–1243 (5) Solano–Castiella (2010) Neuroimage, Vol. 49(4):p2958–2965 (6) Deoni (2006) ISMRM Converence Proceeding p2734 (7) Jansons (2003) Inf. Process Med. Imaging, Vol. 18:p672 (8) Andersson (2003) Neuroimage, Vol. 20(2):p870–888

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