

Parcellation of the cortex using restricted diffusion properties

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Introduction: Traditionally parcellation of the cortex is achieved by visualization of the cortical cellular architecture (cortical layers). Although extreme image resolution at high magnetic fields (7T) allows visualization of the cortical layers with conventional T1 or T2 contrasts (1, 2), the applicability of such approach is limited. Diffusion MRI is a powerful tool for white matter characterization providing a multitude of micro-structural parameters such as axonal density and axon diameter distribution via advanced models as CHARMED (3) and AxCaliber (4). The volume fraction of the restricted component (Fr) extracted from CHARMED, is theoretically related to white matter structures. However, significant fraction of restricted volume can also be found in the cortical gray matter. This work aims to segment the cortex into neuro-anatomical regions based on variations in restricted diffusion properties along the cortex.

Methods: Scanning protocol: Subjects (n=15) underwent MRI scan consisting of DTI (19 direction, $b=0, 1000 \text{ s/mm}^2$, resolution of $1.58 \times 1.58 \times 2.1 \text{ mm}^3$), CHARMED (34 directions, $b=0, 1000, 2500, 4000 \text{ s/mm}^2$, resolution of $1.5 \times 1.5 \times 3 \text{ mm}^3$) and SPGR T1 (resolution of $1 \times 1 \times 1 \text{ mm}^3$) protocols.

Image Analysis: We used FREESURFER (5) to parcellate the cortex into 28 neuro-anatomical regions in each hemisphere using the SPGR images. The DTI and CHARMED maps (FA, MD and Fr) for each subject were randomly sampled in each region. The sample size was set to fifth of the voxels in the region. Mean Fr, FA and MD for each subject in each cortical region was computed, resulting in a matrix of 15-subjects by 56-cortical regions for each index (Fr, FA or MD). Each 15X56 matrix underwent hierarchical cluster analysis (HCA) to produce a dendrogram tree (Fig. 1). The dendrogram was cut according to the inconsistency, evaluated by the height of the dendrogram links, establishing clusters that include cortical regions that share similar Fr, FA or MD values. In addition we computed five intermediate surfaces (between the outer (pial) and the inner (gray matter-white matter boundary) surfaces) (6). These surfaces were used to calculate mean Fr/FA/MD along the cortex.

Results & Discussion: The HCA clustering (dendrogram) results (Fig. 1) indicate that homologous regions of the right and left hemispheres were unified into the same cluster in 21 out of 28 regions, while other regions show lateralization. The results of Fr, FA and MD based clustering were plotted on the outer surface of the cortex (Fig. 2). Both FA and MD exhibit less significant homologous characteristics (16 out of 28 and 13 out of 28 regions respectively).

Figure 3 shows mean Fr plotted from the outer to the inner surface of four representative regions. In general, mean Fr increases from the outer to the inner surface in all regions. However the mean Fr and its variance along the cortex differ among cortical regions as indicated in the HCA analysis. Moreover, in good agreement with the clustering results, homologous regions share similar mean Fr values throughout the depth of the cortex.

Conclusions: These results suggest that diffusion imaging bears significant information that reflects the amount of myelinated fibers in the cortex and the myelo-architecture in the restricted diffusion properties along the cortex (Fig. 3). This property can be the basis for cortical parcellation. Among the different diffusion properties CHARMED seems to be superior over DTI parameters for cortical characterization.

References: 1.N. B. Walters *et al.*, *Proc Natl Acad Sci U S A* **100**, 2981, 2003. 2.D. Barazany, Y. Assaf, *Cereb Cortex*, 2011. 3.Y. Assaf, P. J. Basser, *Neuroimage* **27**, 48, 2005. 4.D. Barazany, P. J. Basser, Y. Assaf, *Proc Intl Soc Magn Reson Med* **16**, 2008. 5.A. M. Dale, B. Fischl, M. I. Sereno, *Neuroimage* **9**, 179, 1999. 6.B. Fischl, A. M. Dale, *Proc Natl Acad Sci U S A* **97**, 11050, 2000.

