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Combining HARDI Datasets With More Than One b–Value Improves Diffusion MRI-Based Cortical Parcellation

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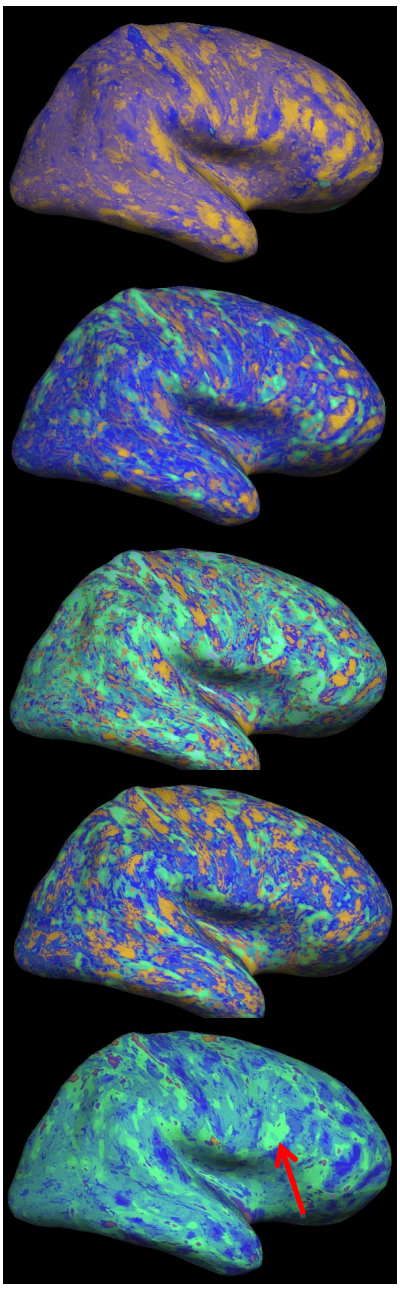
Target Audience: These methods are of interest for neuroscientists and neuroimaging experts interested in in–vivo, MRI–based parcellation of the cortex.

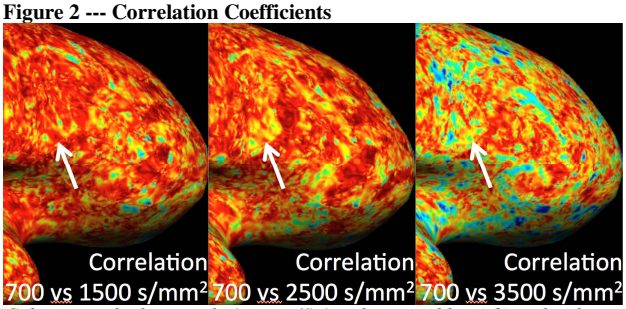
Purpose: In–vivo parcellation of the human cerebral cortex has received much interest[1,2,3]. Previous investigators used or T1/T2–weighted images[4] or maps of T1 relaxation times to estimate the extent of cortical myelination[5]. Others explored the utility high angular resolution diffusion–weighted imaging (HARDI)[6,7], fit the data to specific models and reported layer–specific heterogeneity in the cortex, which may be used to identify cortical areas. Others have used the HARDI data in a model–free fashion by spherical harmonic decomposition to characterise the underlying tissue[7]. In a similar fashion, we used a vector of 27 orientationally invariant HARDI features as a tissue fingerprint[8]. In the present study we investigate whether the discriminative power of such a fingerprint could be increased. Rather than using a 1D vector we propose to construct a 2D fingerprint matrix, where the 2nd dimension encodes b–value. Given that varying b–values probe different aspects of tissue microstructure, the expectation is that data from differing b–values will parcellate differently. The aim of this study is to investigate whether combining data from different b–values improves the parcellation.

Figure 1 --- K–means Clustering Results .



Methods: An adult human male was scanned, with written informed consent in accordance with local ethics guidelines on a 3T Trio scanner (Siemens, Erlangen, Germany), using body transmit and a 32–channel receive–only head coil. Four HARDI datasets had 2.3 mm isotropic resolution, 61 diffusion directions and b–values of 750, 1500, 2500 & 3500 s/mm^2. Minimum echo time, 84, 98, 109 & 118 ms was used for each with ~32 mT/m gradient amplitude for diffusion encoding. The MDEFT[9] structural image had 1 mm isotropic resolution and inversion/echo/repetition times of 910/2.5/7.9 ms respectively. The grey/white matter (GM/WM) and pial/GM boundaries were estimated from MDEFT image using FreeSurfer. The b0 image of each HARDI data set was aligned with the MDEFT image. The gradual, apparent shift in the phase–encoding direction was corrected in the diffusion–weighted images (DWIs). After the alignment of the HARDI and MDEFT images, the signal intensity of the HARDI datasets was sampled at each vertex point on GM/WM boundary surface, along the local surface normal, half way between the GM/WM boundary & the pial/GM boundary. This resulted in a 4x62 matrix of signal intensities. Spherical harmonic coefficients up to order 6 were estimated from each of the 4 data sets providing the 27–vector of orientationally invariant features[8]. This procedure provided 4x27 feature matrix at each WM surface vertex. Standard k–means clustering was employed to parcellate the cortical surface into 40 clusters, either separately for the 1x27 feature vector of each b–value or for the 4x27 feature matrix of all b–values together. For **Fig.1** the colors are arbitrary but clusters with similar feature vectors are painted in similar colors within a given b–value. There is an inherent inverse relationship between the signal–to–noise ratio (SNR) and b–value. To estimate the voxel–wise signal, the mean intensity was calculated across time (i.e. along the DWIs). The standard deviation (STD) of voxel intensities was calculated from a region at the edge of the corresponding b0 image outside of the brain. The ratio of the mean and STD was taken as the SNR for each HARDI data set.

Figure 2 --- Correlation Coefficients



Colors encode the correlation coefficient between blue (-1) and red (+1). White arrows point to the same area.

Results: **Fig.1** shows the results of k–mean clustering. From top to bottom the first 4 rows are based on b = 700, 1500, 2500 & 3500 s/mm^2 respectively. The image on the bottom is the k–mean clustering result when considering the 4x27 features simultaneously. The color scale in these images is identical but the k–means cluster group numbering is arbitrary. Note that the four b–values lead to dissimilar parcellations. This was expected as varying b–values probe different aspects of the microstructure. Using a 4x27 feature matrix rather resulted in a smoother, more continuous parcellation of cortical areas than was possible with any single 1x27 feature vector. See, for example, areas 3 and 4 (posterior and anterior banks of the central sulcus), an inferior frontal area (Broca's area – red arrow), and primary and secondary auditory areas on the superior temporal gyrus and posterior planum temporale. In **Fig.2** the correlation coefficients of the 1x27 vectors are indicated between the 1st and the other 3 HARDI data sets. Clearly the correlation is high between data from similar b–values (700 vs 1500 s/mm^2) but as the difference in b–values grows the correlation diminishes, indicating additional information harvested by collecting the extra data. Spatial heterogeneity in this respect is also evident in that other areas show high correlation for all 3 pairs of data. The SNR of the HARDI dataset with b = 700 s/mm^2 was about 4 times that of the one with b = 3500 s/mm^2 but the latter was still above the noise floor.

Discussion: These results strongly suggest that data from more than a single b–value shell contain information that improves the discriminative power of the k–mean clustering used to parcellate cortical gray matter. Dissimilar parcellation among different b–values may result from a) probing different aspect of the underlying microstructure, b) the different SNR or c) scan–rescan variability. We previously showed that the scan–rescan reproducibility is excellent[8] and here we found the SNR adequate for all 4 datasets. Future work will validate the histological specificity of this parcellating pipeline and optimise b–value selection.

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