Evaluation of Diffusion MRI Based Feature Sets for the Classification of Primary Motor and Somatosensory Cortical Areas.

Tara Ganepola[1,2], Jiaying Zhang[2], Hui Zhang[2], Martin I Sereno[3], and Daniel C Alexander[2]

[1]Department of Cognitive, Perceptual and Brain Sciences, University College London, London, United Kingdom, [2]Centre for Medical Image Computing, University College London, London, United Kingdom, [3]Birkbeck-UCL Centre for Neuroimaging, University College London, London, United Kingdom

Synopsis

In the following work several diffusion based feature vectors (DTI, NODDI, spherical harmonic (SH) invariants and fourth order tensor invariants (T4)) are compared in order to validate their usability in grey matter investigations. It was found that using multi-shell data and non-biophysical models such as SH and T4 achieves the highest classification accuracy between the primary motor and somatosensory cortical areas, and thus is likely to characterise grey matter tissues domains more effectively.

Introduction

Diffusion MRI is predominantly used in white matter (WM) studies, however recent findings have highlighted that it can display sensitivity to the cyto/myeloarchitecture which defines cortical areas[1,2]. In the following, we aimed to assess the efficacy of several diffusion-based feature sets via a binary classification task using random forest classification (RFC) between the primary motor (M1) and somatosensory (S1) areas. Four tissue representations were selected: WM biophysical models, DTI[5] and NODDI[3] and non-parametric tissue representations, spherical harmonic based features[1](SH), and fourth order tensor invariants[4](T4). We posit that the more generalised features sets (T4, SH) will more effectively capture the higher complexity of micro-environments across grey matter(GM) regions, and thus provide more discriminative feature vectors. In addition, single and multiple b-shell datasets were tested to investigate the value of including several shells when examining GM[6].

Methods

Data/Pre-processing: Data for six subjects was obtained from the minimally preprocessed, 500-subjects release of the Human Connectome Project(HCP). Following surface reconstruction and registration of the B0s to the T1w image, the DWIs were sampled to each individual's cortical surface at the midpoint between the WM and pial surfaces.

Feature sets: **1.** The DT model was fit using both the 3-shell and single shell (b=1000s/mm2) data using FSL. The following metrics were used in the feature vector: fractional anisotropy (FA), mean diffusivity (MD), radiality index[2](RI).

2. The NODDI-Watson model was fit to the 3-shell diffusion data, taking orientation dispersion index (ODI), neurite density index (NDI) and extracellular volume fraction(V_iso) to create a [1x3] feature vector for each surface vertex, as above.

3. A 6th order spherical harmonic series was fit to the signal of each b-shell separately and a subset of the features presented in[1] were computed to obtain a [1x9] feature vector per vertex, per b-shell. At classification single b-shells were tested along with a [1x27] concatenation of all three b-shells.

4. 4th order tensors were fit to the signal of each b-shell and the 12 rotation invariants of [4] were calculated. As above, features vectors from each shell and the combined [1x36] were tested.

Classification: Two non-overlapping ROIs were selected using Freesurfer Brodmann Atlas labels BA3b (within S1) and BA4a (within M1) such that the regions are spatially separated by the fundus of the central sulcus, as seen in Figure 1A. These regions were selected as they exhibit distinct laminar appearances and are located consistently across subjects.

To generate training and test sets for each subject, 10%-subsets of the vertex points were randomly selected and excluded from the training phase. Ten pairs of exhaustive and unique training and test pairs were generated and used independently to ensure all data from within the ROIs was tested.

The sk-learn implementation of RFC was run on all feature sets for all subjects. The default parameter values were used for all variables except n_estimators which was increased to 15.

Results

Table1: Displays the percentage of correctly classified vertices across the test sets for each subject, for each feature set; in addition the average accuracy across all the subjects for each feature set is available in the bottom row. The multi-shell feature vectors consistently outperform the single shells; of these the non-parametric features surpass the biophysical features, with the SH achieving the highest accuracy.

Figure1: Shows the ground truth classification and the RFC results for the multi-shell feature vectors displayed on the cortical surface of subject 1.

Discussion

To evaluate their utility in GM applications several diffusion-based features sets were tested via M1/S1 classification. Results reveal that multi-shell data is preferable over single-shell data for this task. As no single b-shell outperforms another, it is likely that a range of b-values better delineate the smaller micro-environments and complex tissue configurations present within GM. Given multi-shell datasets, the SH and T4 representations supersede the familiar metrics utilised in WM studies. This may be due, in part, to tissue assumptions inherent to biophysical models, causing a loss of detail compared to non-biophysical counterparts. NODDI performed similarly to DTI despite disentangling FA into more informative parameters (ODI,NDI), conceivably because RI is highly sensitive to dissimilarities regarding tissue orientation between M1 and S1[2]. SH achieved a marginal improvement over T4, possibly because they were based on a higher order signal representation.

In conclusion, it may be beneficial to use more generalised, multi-shell, features for applications, such as parcellation. However, it is worth noting that biophysical models provide anatomically meaningful metrics, and may be preferable in applications which assess structure directly, for example, investigation of pathologies. Further testing on a larger cohort and alternative regions will be used to corroborate these findings.

Acknowledgements

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References

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Figures

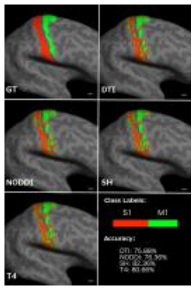

Figure 1: The ground truth (GT) regions of interest and the 3-shell classification results for subject 1 are shown on the lateral surface of the subject's cortical surface reconstruction. The percentage accuracy for the DTI, NODDI, SH and T4 feature vectors are given in the bottom right.

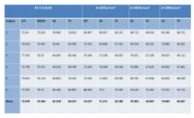

Table 1: Classification accuracy across all subjects and all multi-shell and single-shell feature vectors. The average accuracy for each feature set is highlighted in bold on the bottom row. Multi-shell feature vectors perform better than single shells. Non-biophysical models (SH and T4) provide the highest classification accuracy, of these the SH features slightly exceed T4. The NODDI and DTI feature vectors achieve similar results on average.

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