Human brain tissue microstructure characterization using 3D-SHORE on the HCP data

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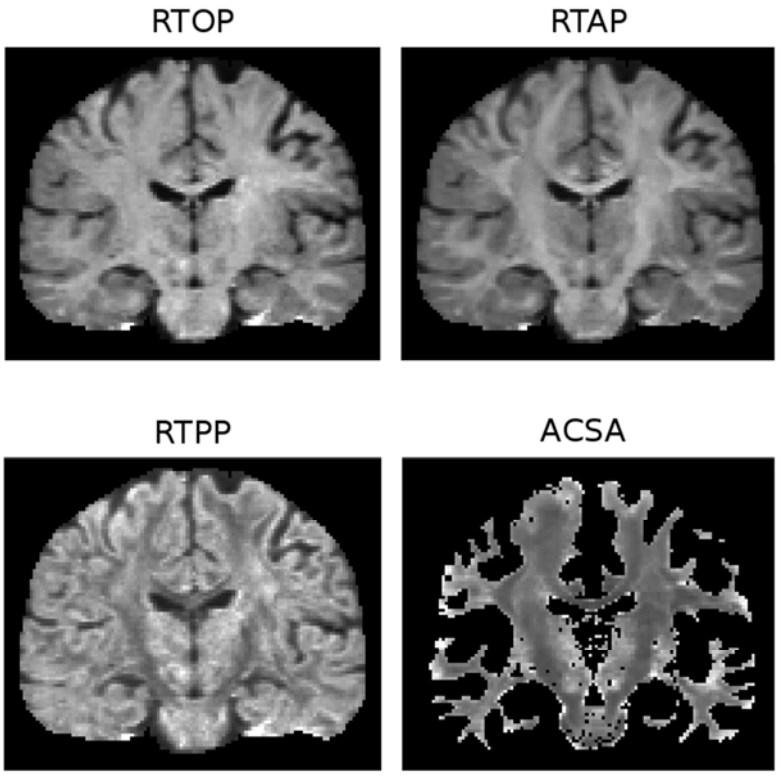
PURPOSE – The Human Connectome Project (HCP)[1] data is composed of high resolution multi-shell diffusion weighted imaging acquisitions. Continuous analytical reconstruction models, such as the 3D Simple Harmonic Oscillator based Reconstruction and Estimation[2] (3D-SHORE), are able to process multi-shell acquisition natively and give an analytical representation of the Ensemble Average Propagator (EAP). From the EAP, it is then possible to retrieve information about the water molecules displacement like the Orientation Distribution Function (ODF), necessary to perform brain tractography, but also other scalar indices that can provide accurate estimation of microstructural properties of the brain tissues. A large number of studies have been conducted on the HCP data targeting the extraction of fibers orientation information, while the assessment of tissue microstructural properties on this data is still unexplored. In this work, microstructural features are inferred from the reconstruction of the HCP data using the 3D-SHORE model. The related numerical measures[3] are: i) Return To the Origin Probability (RTOP), ii) Return To the Axis Probability (RTAP) and iii) Return To the Plane Probability (RTPP), which are calculated and used for assessing the potential of multi-shell acquisitions for characterizing human brain tissues.



MATERIALS AND METHODS – The HCP diffusion data has a high spatial resolution of 1.25 mm isotropic voxels. 288 DW measurements were acquired distributing q-space points on three shells, 90 gradients per shell, respectively with b-values 1000, 2000 and 3000 s/mm^2 and 18 b_0 images. TE/TR= 78 ms/2.6 s, 145x174x145 matrix, delta and Delta were 10.6 and 43.1 ms.

HCP data were fitted using the orthonormal version of the 3D-SHORE equipped with two additional features: a voxel adaptive scale parameter and a quadratic programming (QP) fitting procedure. The scale parameter was calculated based on the mean diffusivity as estimated by fitting a tensorial model and allows adapting the spread of the basis functions to the measured diffusivity in each voxel[3]. QP regularization enables to add positivity constraints to the EAP. RTOP, RTAP and RTPP were computed analytically from the basis and the maps were extracted from the fitted coefficients. A modified version of the Dipy[4] (Diffusion Imaging in Python) implementation of the 3D-SHORE was used for both signal fitting an the creation of the indices maps. A white matter (WM) mask was created on the T1 image using the FSL tool FAST[5]. The apparent cross-sectional area (ACSA) was also extracted as in Ozarslan et al.[3]

RESULTS – RTOP is hyperintense in white matter indicating the higher level of restriction to diffusion orthogonally to the main fiber direction. This effect is stressed in the RTAP where it is possible to distinguish the principal WM tracts of the brain. RTPP is inversely correlated to the diffusivity along the main axis of the pore and is lower in pure WM areas as the corpus callosum. As observed in Ozarslan et al.[3] on a marmoset brain, the RTPP is larger in areas of fibers crossing. Extracting the ACSA in the WM mask reveals the differences in the different fiber bundles.

DISCUSSION & CONCLUSION – These results show that the HCP dataset allows extracting meaningful information regarding tissue microstructure, and can provide an estimation of the fibre bundle's apparent cross-sectional area (ACSA). The variations of RTOP, RTAP and RTPP are representative of changes in tissue composition and, as such, hold a great potential for the detection and assessment of pathological conditions such as stroke and demyelinating diseases. Future works will include the characterization of these biomarkers on simulated dataset and the comparisons with others microstructural biomarkers as the ones obtained from the NODDI.

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