Tissue structure complexity maps from high angular resolution diffusion weighted magnetic resonance measurements.

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Abstract. We describe a method to classify the complexity of water diffusion in tissue, or tissue structure, from high angular resolution diffusion weighted (DW) MR measurements. We fit the series of even order spherical harmonics (SHs) to the measured data and use an ANOVA deletion of variables test to determine at what order the series can be truncated. The level of truncation indicates whether the diffusion at each voxel is isotropic, anisotropic Gaussian or non-Gaussian. Clusters of non-Gaussian voxels are observed consistently in data from various regions of the human brain with b-values typical of clinical scans.

Method. DW-MR data was acquired from four healthy volunteers using a protocol similar to that outlined by Jones [1]. All subjects gave informed consent. Three unweighted ($b = 0$ s/mm^2) images were acquired together with 60 DW images with different gradient directions spread evenly over the hemisphere, with diffusion time Δ=0.04s, gradient pulse width δ=0.032s and gradient strength G=0.022Tm^{-1}, which gives $b \approx 1000$ s/mm^2 in each case. The image array is acquired as 96x96 in plane, reconstructed as128x128, with a field of view of 220mm and a total of 42 slices evenly spaced at 2.5mm intervals were acquired. Each DW measurement gives rise to a measure of the diffusion coefficient in a particular direction. SHs up to order 8 were fit to the set of diffusion coefficient measurements at each voxel by computing the least squares fit of these models, [2].
The spherical harmonic series is analogous to the Fourier series. Any function of the sphere can be described by a linear combination of spherical harmonic functions:

$$f(\theta,\varphi) = \sum_{l=0}^{\infty} \sum_{m=-l}^{l} c_{l,m} Y_{l,m}(\theta,\varphi) . \qquad (1)$$

$l = 0, 1, 2, \ldots$ defines the *order* of the SH and $m \in \{-l, \ldots, 0, \ldots l\}$ indexes the $2l+1$ SH functions of order l; $\theta \in [0, \pi)$ and $\varphi \in [0, 2\pi)$ are the angles of colatitude and longitude, respectively. The profile of the diffusion coefficient over the sphere is real valued and exhibits antipodal symmetry, so that $f(\theta, \varphi) = f(-\theta, -\varphi)$, which allows us to reduce the number of parameters required to define this series. In particular, we can set the coefficients of all the odd order SHs to zero, since these functions represent components of functions that are not antipodally symmetric [2].
We can truncate this series at any order 0, 2, 4, 6 or 8 by setting the coefficients of the SHs above that order to zero. If we truncate the series at order 0, we obtain an isotropic model of the diffusion, since the single order 0 SH is constant over the sphere. If we truncate at order 2, we obtain a Gaussian model equivalent to the familiar diffusion tensor [3]. Truncation at higher orders allows a range of more complex shapes to be modeled. If we truncate the series too low, the model may not reflect the behaviour of the underlying diffusion process adequately. On the other hand, if we truncate too high, the model will incorporate unwanted noise effects. We use sequential ANOVA deletion of variables tests [4] to determine at what order the addition of new terms in the SH series ceases to improve the fit of the model to the data significantly and thus determine the order of the SH model required at each voxel. This process yields a map of truncation orders that show whether the diffusion at each location in the brain is isotropic, anisotropic Gaussian or non-Gaussian. These maps indicate the complexity of the tissue structure within each voxel and may thus be used as a '*stain*' to provide extra diagnostic information in pathologies involving neuronal loss, degeneration or demyelination, since higher order behaviour will tend to disappear in the affected areas.

Results. The procedure outlined above was applied to the four data sets. Three axial slices from one of these data sets are shown in figure 1. For each slice, the fractional anisotropy map is shown together with the corresponding SH truncation order map. Each slice contains distinct clusters of non-Gaussian (mostly order 4) profiles (highlighted) indicating significant non-Gaussian behaviour in the corresponding tissue regions. In the slice on the left, the region corresponding to the pons contains a dense cluster of non-Gaussian profiles in precisely the region where the inferior-superior pyramidal tracts cross the left-right transverse pontine fibres. In the center slice non-Gaussian clusters appear in the anterior-posterior optic radiation where it is crossed by left-right fibres of the corpus callosum. The right hand slice shows that a large proportion of voxels in the corona radiata exhibit non-Gaussian behaviour, most likely due to interactions between the diverging fibres of the corona radiata and the U-fibres. Results in our other data sets are consistent with these findings [2].

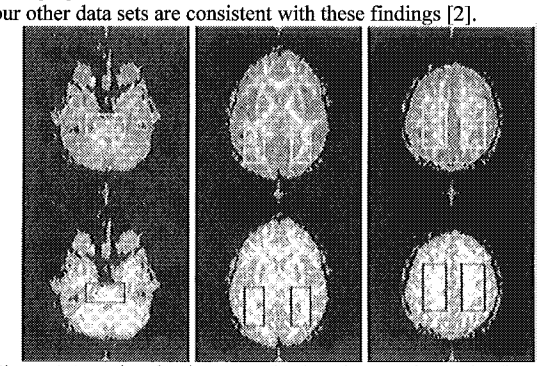

Figure 1. Fractional anistotropy (top) and truncation order (bottom - black is backgroud, dark grey order 0, light grey order 2, white order 4 or above) maps for 3 axial slices of human brain data.

Discussion. We have outlined a method for classifying the complexity of diffusive behaviour from sets of high-angular resolution DW-MR measurements. More details of the method can be found in [2], where a careful validation of the method using synthetic data is also described. Maps of this complexity provide valuable information for analyzing brain tissue structure. Moreover, they indicate where the familiar diffusion tensor model, which assumes diffusion is Gaussian, is likely to be unreliable. The method has been shown to be effective when applied to data acquired with easily achievable imaging parameters.

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