

Neuronal White Matter Atlas Creation using Diffusion Imaging

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Background and Objective: Diffusion MRI offers an *in vivo* contrast into local white matter (WM) architecture providing an invaluable tool for investigating pathologies which affect neuronal WM. Often diffusion based population studies make use of brain atlases to provide regions of interest (ROIs) from which local features are extracted. These atlases provide both a means of consolidating the vast quantities of imaging data to a more manageable level as well as a procedure to improve the quantification of anatomical changes. The majority of atlases make use of manual anatomical segmentations to determine regions corresponding to known named anatomical constructs that may be too large for statistical analysis or the atlas is not specific for a population (such as a pediatric population). The purpose of this paper is to generalize the HARDI atlas generation methods described in [1], to make use of DTI data, so that an atlas for each modality can be created for a population, facilitating a comparative analysis of both modalities when available. The goal of this framework is to create ROIs that are spatially uniform as measured by the Log-Euclidean DTI metric [2] making them ideal candidates for statistical analysis. We generate 2 atlases, one using DTI and the other HARDI datasets, on the same group of typically developing adolescents to demonstrate the comparison between the different diffusion models. This comparison reveals the relative benefit of using HARDI contrasts to identify complex WM regions.

Method: The atlas generation framework for DTI is analogous to that described for HARDI in [1]. First each subject's DTI datasets are registered to a common template, using the DTIDroid [3] registration algorithm. A population average DTI image is determined using log Euclidean averaging. An affinity matrix (K) is determined containing the pairwise similarities between all WM voxels. The similarity between the i^{th} and j^{th} voxel is

computed by $K_{ij} = e^{-\frac{\|p_i - p_j\|}{2\sigma_s}} e^{-\frac{d(t_i, t_j)}{2\sigma_f}}$, where the i^{th} voxel has a location of p_i and a diffusion tensor of t_i and $d(t_i, t_j)$ is the log Euclidean distance between the i^{th} and j^{th} tensor. This similarity is modulated by 2 smoothing terms one, σ_s , providing a means to smooth in the spatial domain while σ_f smoothes in the tensor domain. Once the affinity matrix is computed, a normalized cuts parcellation routine is used to divide the WM volume into spatial connected sub regions. The algorithm can be stopped once the log Euclidean variance is below a certain threshold or when a certain number of regions have been determined.

The dataset used in this report consists of DTI and HARDI datasets acquired from 27 healthy adolescent subjects (age 10.76 ± 2.35 years). DTI datasets were acquired on Siemens 3T Verio™ scanner using a single shot spin-echo, echo-planar sequence with the following parameters: TR/TE=16900/70 ms, b-value of 1000 s/mm² and 30 gradient directions. HARDI datasets were acquired using the same sequence but with the following parameters: TR/TE=14.7s/110ms, b-value of 3000 s/mm², 64 gradient directions and 2 b0 images. Preprocessing consisted of eddy current correction as well as the removal of Rician noise [4]. Diffusion tensors were then fit to the DTI datasets and the FOD model was fit to the HARDI data.

Results and Discussion: Using the above method a DTI atlas consisting of 150 regions was computed using $\sigma_s = 6mm$, and $\sigma_f = 0.3$. Similarly a HARDI atlas was computed using [1] and the same set of parameters. These parameters were chosen for illustrative purposes, in practice these would be fixed based on the specifics of the population under study as well as the granularity of the desired ROIs. Both the DTI and HARDI atlases can be seen in figure 1, displaying the general bilateral symmetry one would expect from anatomy. In addition, it can be seen that the HARDI atlas parcellates the anatomy better in the regions of complex WM (highlighted in yellow)

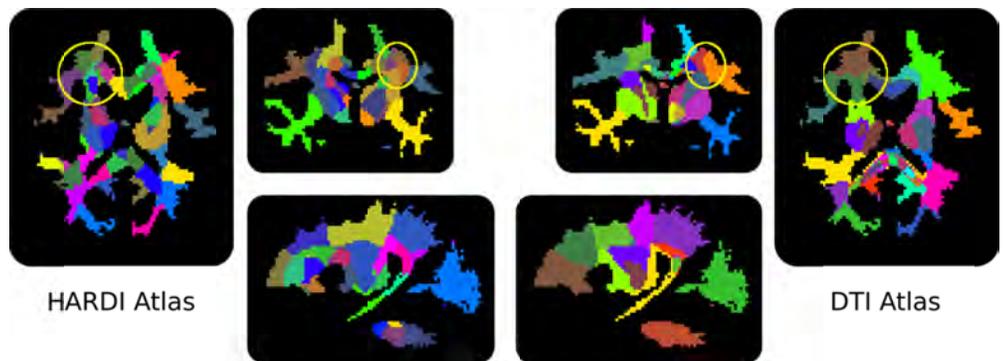


Figure 1: Representative slices of the HARDI (left) and DTI (right) atlases created on a set of 27 healthy subjects. Some areas of difference are highlighted in yellow wherein the complex WM regions are better segmented in the HARDI atlas.

Conclusion: The presented methodology is able to generate a WM population atlas using DTI datasets which allows researchers to generate study specific atlases suitable for subsequent ROI based statistical analysis. A comparison with the HARDI based atlas framework, is supplied, that illustrates the improved ability of HARDI to capture and delineate complex WM such as those involving fiber crossings. In studies focusing on the benefits of HARDI, these two atlases can be used in a single population for a comparative analysis between modalities.

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