A High-Dimensional Fiber Tract Atlas

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Abstract

We present a method for creation of an atlas of major white matter fiber tracts. Using spectral clustering, we automatically find many small fiber clusters in a population of subjects. The atlas thus takes the form of cluster centroids in the high-dimensional spectral embedding space. In this space, fiber tracts may be subdivided into multiple clusters, which then are manually labeled and grouped into anatomically meaningful entities, defining an atlas. In general, comparison of information across clusters from different brains is not straightforward, since the basis vectors defining the respective embedded spaces are *different.* Here we describe a way to transfer this embedded atlas information to a new subject via the Nystrom method [3], and we demonstrate the resulting tract labels on a new subject.

Introduction

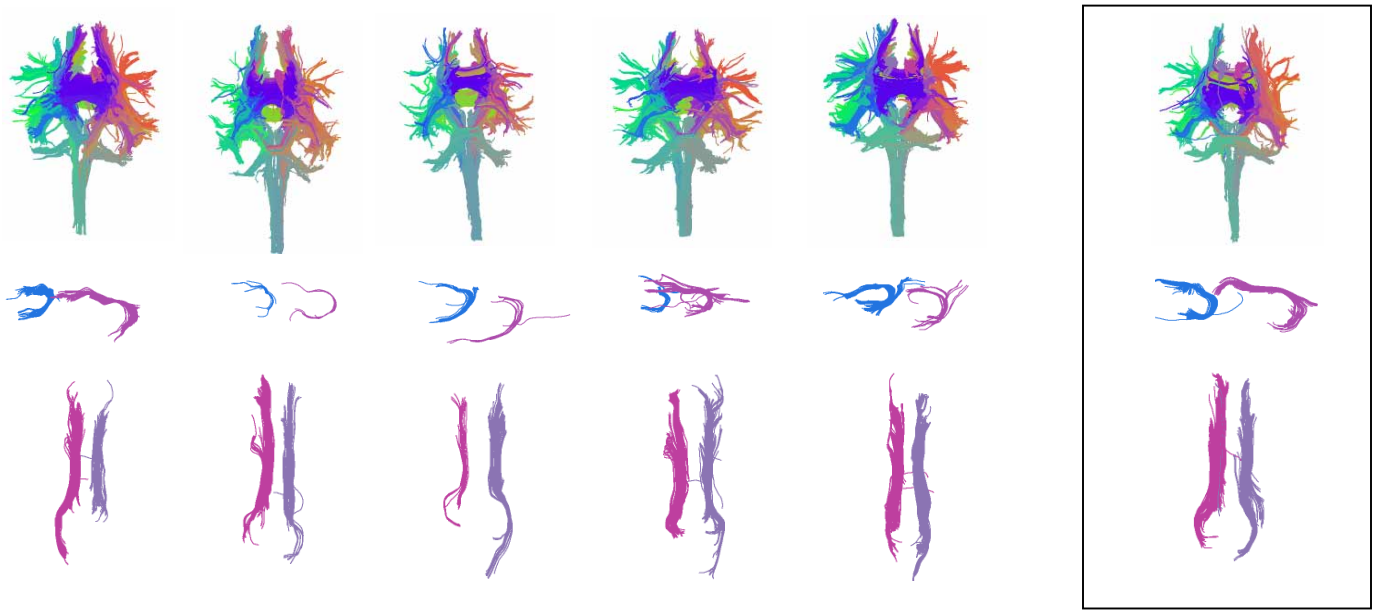
Our goal in generating a white matter atlas is to automate the process of defining regions of interest in the white matter for further analysis of diffusion tensor MRI (DTI) data. The atlas also has potential application in the area of DTI visualization via tractography. Prior work in white matter atlas building has employed tractography to define regions [5]; however these tractographic paths have been manually grouped using region of interest methods. Tractography-based white matter fiber clustering has been presented in several recent papers [1, 2, 4] but it has not yet been applied to the goal of atlas generation.

Methods

The atlas was created from 5 DTI datasets (LSDI scans with voxel size .86x.86x5mm and 6 gradient directions) and applied to a new dataset acquired with the same parameters. Tractography was performed in each dataset using 2nd-order Runge-Kutta integration. Paths were seeded where C_L (Westin's measure of linear tensor shape as described in [8]) was greater than 0.35, and paths terminated when C_L became less than 0.2. Only paths longer than 50mm were used in the clustering. Approximately 5,000 paths from each dataset were clustered simultaneously into 100 clusters using spectral clustering and the Nystrom method as presented in [4]. After clustering, the atlas consisted of a list of cluster centroids in the 20 dimensional spectral embedding space and information (eigenvector basis and normalization factors) for mapping a new subject's paths into that space. This is similar to the method of representing new data using a basis from kernel PCA, with the difference being that in spectral clustering the data affinity matrix is normalized. This normalization requires estimation of row and column sums of the full matrix (since we compute only a partial matrix using the Nystrom method). To extend this normalization to a row of new data from one new tractographic path, we estimated its row sum as described in [3], and we employed the column sums from the original (atlas) affinity matrix.

Results

Clusters from the five atlas brains are shown on the left followed by the new subject on the right. All 100 clusters are shown in the top row, followed by the uncinate fasciculi and cingulum bundles in the second and third rows. Note that the new subject has been automatically labeled with the atlas (colors indicate anatomical name).



Conclusion

We have presented a method for white matter atlas building and automatic tract labeling of new subjects which takes advantage of the power of high-dimensional atlas descriptors. Further experiments are needed to determine optimal parameter settings, and it will be of interest to build a more complete atlas using tractogaphy from higher resolution diffusion MRI data.

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