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Tract Dictionary Learning for Fast and Robust Recognition of Fiber Bundles

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Abstract

In this paper, we propose an efficient framework for parcellation of white matter tractograms using discriminative dictionary learning. Key to our framework is the learning of a compact dictionary for each fiber bundle so that the streamlines within the bundle can be sufficiently represented. Dictionaries for multiple bundles are combined for whole-brain tractogram representation. These dictionaries are learned jointly to encourage inter-bundle incoherence for discriminative power. The proposed method allows tractograms to be assigned to more than one bundle, catering to scenarios where tractograms cannot be clearly separated. Experiments on a bundle-labeled HCP dataset and an infant dataset highlight the ability of our framework in grouping streamlines into anatomically plausible bundles.

Keywords

Diffusion MRI; Tractography; Fiber bundle; Dictionary learning

1 Introduction

Diffusion magnetic resonance imaging (DMRI) [1] allows analysis of white matter (WM) axonal trajectories via streamlines (i.e., tractogram) generated by a process called tractography. Automatically grouping several millions of streamlines into anatomically meaningful bundles is an important yet challenging task [2–4], since streamlines within a bundle can have different shapes, lengths, and endpoints.

A fiber tract is a collection of axons having common origin and destination sites. Automatic tract identification strategies can be based on regions of interest (ROIs) [5], clustering [2,3], atlases [2,6], and segmentation [7,8]. Many existing methods rely on point correspondences between streamlines [9]. However, even within the same bundle, streamlines can have different lengths and endpoints. Therefore, standard geometric distance measures often lead to poor results. Moreover, the streamlines are often first aligned to a common space defined for example by a tract atlas and then resampled with the same number of points to facilitate computation of distances between streamlines [3,10]. If the underlying anatomy is altered

due to pathology or development, meaningful information might be lost in the process of resampling [11].

In this paper, we propose a method to efficiently parcellate the whole-brain tractogram, catering especially to scenarios where streamline separation is challenging. This is achieved via tract dictionary learning (TractDL) to learn tractogram exemplars for fast and automated analysis of large datasets. Unlike existing dictionary-based approaches [12,13], our method adopts a natural means of enforcing consistency across hemispheres and is unconfounded by the lengths of streamlines. Instead of learning the dictionary in the native point space, we map the tractograms to a Hilbert space via cosine series representation. Parcellation is performed in the cosine representation space via a sparse framework with a set of learned dictionaries, each for a bundle. We exploit structured incoherence and shared features across bundles so that within-bundle variability is small but between-bundle variability is large. Using the dictionaries, whole-brain bilateral clustering is applied for simultaneous bundle parcellation in both hemispheres. We evaluated TractDL based on HCP data and infant data in comparison with existing bundle parcellation methods.

2 Methods

2.1 Modeling Fiber Streamlines

We represent the streamlines in Hilbert space [11]. Let $\mathbf{l} \in \mathbb{R}^{n \times 3}$ denote a streamline of a fiber bundle, consisting of n points $\{\mathbf{p}^{(j)}\}_{j=1}^n$. Note that n can be different for each streamline. We consider a function f^{-1} that maps these points onto the unit interval $[0, 1]$ as

$$f^{-1}:\mathbf{p}^{(j)} \rightarrow \frac{\sum_{i=2}^j \|\mathbf{p}^{(i)} - \mathbf{p}^{(i-1)}\|}{\sum_{i=2}^n \|\mathbf{p}^{(i)} - \mathbf{p}^{(i-1)}\|} = \gamma^{(j)}, \quad f^{-1}(\mathbf{p}^{(1)}) = 0. \quad (1)$$

That is, $\gamma^{(j)}$ indicates the ratio between the arc-length from the point $\mathbf{p}^{(1)}$ to $\mathbf{p}^{(j)}$, and the total arc-length from $\mathbf{p}^{(1)}$ to $\mathbf{p}^{(n)}$. We can parameterize the smooth inverse map $f: [0, 1] \rightarrow \mathbf{l}$ as a linear combination of smooth basis function.

Let the coordinates of f be (f_1, f_2, f_3) . Then, each coordinate can be approximated using K degree cosine series expansion [11]:

$$f_i(t) \simeq \sum_{k=0}^K c_{ki} \psi_k(t), \quad (2)$$

where $\{\psi_k\}$ is a cosine basis. Then, for $\{\gamma^{(j)}\}_{j=1}^n$ corresponding to n sampling points $\{\mathbf{p}^{(j)}\}_{j=1}^n$, we have

$$f_i(\gamma^{(j)}) \simeq \sum_{k=0}^K c_{ki} \psi_k(\gamma^{(j)}). \quad (3)$$

The matrix of cosine coefficients $C = \{c_{ki}\} \in \mathbb{R}^{(K+1) \times 3}$ can be estimated from $\mathbf{f} = \{f_i(\gamma^{(j)})\} \in \mathbb{R}^{n \times 3}$ in the least-squares manner as

$$C = (\Psi_K^T \Psi_K)^{-1} \Psi_K^T \mathbf{f}, \quad (4)$$

where $\Psi_K = \{\psi_k(\gamma^{(j)})\} \in \mathbb{R}^{n \times (K+1)}$. We note that the dimension of the coefficients $C \in \mathbb{R}^{(K+1) \times 3}$ only depends on the degree K of cosine series ($K=19$ in this paper), but not on the number of sampling points along the streamline.

2.2 Tract Dictionary Learning

Let $\mathbf{X}_t$ represent the set of cosine coefficients of the streamlines of t -th bundle. We learn a dictionary $\mathbf{D}_t$ for the t -th bundle using sparse dictionary learning (DL) by minimizing the following objective function:

$$\min_{\mathbf{A}_t, \mathbf{D}_t} \frac{1}{2} \|\mathbf{X}_t - \mathbf{D}_t \mathbf{A}_t\|_F^2 + \lambda \|\mathbf{A}_t\|_1. \quad (5)$$

Each column of $\mathbf{X}_t$ can be represented as a linear combination of a set of vectors in an over-complete dictionary $\mathbf{D}_t$ with sparse coefficients in the corresponding column of $\mathbf{A}_t$. Based on the coefficients, the streamlines can be classified into different bundles.

We train the dictionaries of multiple fiber bundles jointly. Note that if the dictionaries of the individual bundles are trained separately, they are not necessarily discriminative enough to help distinguish the streamlines from the different bundles. To obtain incoherent discriminative dictionaries, we let $\mathbf{X} = [\mathbf{X}_1, \mathbf{X}_2, \dots]$, $\mathbf{D} = [\mathbf{D}_1, \mathbf{D}_2, \dots]$, and $\mathbf{A} = [\mathbf{A}_1^T, \mathbf{A}_2^T, \dots]^T$, and solve the following problem:

$$\min_{\mathbf{A}, \mathbf{D}} \frac{1}{2} \|\mathbf{X} - \mathbf{D}\mathbf{A}\|_F^2 + \lambda \|\mathbf{A}\|_1 + \eta \sum_{t_1 \neq t_2} \|\mathbf{D}_{t_1}^T \mathbf{D}_{t_2}\|_F^2, \quad \text{s.t. } \mathbf{A} \geq 0, \quad (6)$$

where $\sum_{t_1 \neq t_2} \|\mathbf{D}_{t_1}^T \mathbf{D}_{t_2}\|_F^2$ encourages orthogonality between each dictionary pair [14]. λ and η are scalar tuning parameters. The size of each bundle dictionary is fixed as m . Each row of $\mathbf{X}$ is normalized to have zero mean and unit variance to remove the effects of distribution location and scale. In this paper, we solved (6) using an open source dictionary learning toolbox (DICTOL)¹.

2.3 Streamline Classification

The sparse code $\mathbf{a}_t$ of the cosine representation $\mathbf{x}$ of a streamline with respect to the dictionary of bundle t can be used for streamline classification. This is achieved by solving

¹<https://github.com/tiepvupsu/DICTOL>.

$$t^* = \arg \min_t \frac{1}{2} \|\mathbf{x} - \mathbf{D}_t \mathbf{a}_t\|_2^2 + \lambda \|\mathbf{a}_t\|_1 + (1 - \lambda) \|\mathbf{a}_t\|_2, \quad \text{s.t. } \mathbf{a}_t \geq 0, \quad (7)$$

where t^* is the label of streamline $\mathbf{x}$, and λ is a regularization parameter.

To rapidly classify whole-brain streamlines into bundles, we first perform unsupervised clustering to cluster the streamlines into a number of clusters. We employ a fast k-medoids clustering algorithm on the cosine representation coefficients of the streamlines. To improve clustering robustness, bilateral clustering is applied for simultaneous bundle parcellation in both cerebral hemispheres. A total of 2000 of fiber clusters are generated for good anatomical separation of the streamlines while maintaining good clustering consistency across subjects [3]. Figure 1 shows the clustering results, color-coded by local streamline orientations. We then randomly select 50 streamlines from each cluster and label each streamline via solving (7). The final bundle label assigned to each cluster is the label with count fraction (out of 50) greater than a threshold ν .

3 Experimental Results

3.1 Dataset

The dataset used for evaluation consisted of 72 WM tract bundles for each of 105 young adults from the Human Connectome Project (HCP) [15]. The ground-truth tracts were extracted semi-automatically from whole-brain tractograms [16]. 70 subjects were used for training and the remaining 35 subjects were used for testing. The fiber streamlines of each subject were transformed to a common space via affine transformation determined by volumetric registration. For each subject, 1000 streamlines were randomly selected from each bundle for training. For bundles with less than 1000 streamlines, all streamlines were selected. The abbreviations of the fiber bundles are defined in [16].

3.2 Validation

To choose the optimal dictionary size per bundle, we evaluated the leave-one-out cross-validation identification accuracy (ACC) [16,17] of association and projection tracts of the training subjects as a function of the dictionary size m . Figure 2 indicates a clear convergence trend when m is greater than 2000. Therefore, we used $m = 2000$ in our experiments. We also repeated tract classification 100 times with different tract samples and Fig. 3 indicates that classification variability across repetitions is low.

We used RecoBundles [2], a state-of-the-art bundle parcellation method, as the comparison method. RecoBundles registers the tractograms to a reference subject and uses clustering to detect streamlines that are similar to reference tracts. We used the default parameters while running RecoBundles on the 35 test subjects. For evaluation, we combined the 72 fiber bundles for each test subject to form whole-brain tractograms. To compare the accuracy of the methods, we let $\mathcal{X}_{\text{GT}}$ and $\mathcal{X}_{\text{RES}}$ be the ground-truth streamlines and the identified streamlines, respectively, and define the ACC of the tract identification in two ways:

$$\text{ACC}(\mathcal{X}_{\text{GT}}, \mathcal{X}_{\text{RES}}) = \frac{|\mathcal{X}_{\text{GT}} \cap \mathcal{X}_{\text{RES}}|}{|\mathcal{X}_{\text{GT}}|}, \quad \text{ACC}(\mathcal{X}_{\text{RES}}, \mathcal{X}_{\text{GT}}) = \frac{|\mathcal{X}_{\text{GT}} \cap \mathcal{X}_{\text{RES}}|}{|\mathcal{X}_{\text{RES}}|}. \quad (8)$$

Figure 4 indicates that TractDL yields higher classification accuracy in general, especially in identifying association and projection tracts.

To evaluate the robustness of TractDL, we regenerated the whole-brain tractogram of one subject randomly chosen from the testing dataset. We used MRtrix to compute the fiber orientation distribution functions with multi-shell multi-tissue constrained spherical deconvolution and generated two million fibers with anatomically constrained probabilistic tractography. By employing TractDL, we were able to identify difficult bundles such as UF, OR, CST, FPT, and POPT (Fig. 5).

To study hemispheric asymmetry of the bundles, we computed the laterality index: $\text{LI} = (L - R)/(L + R)$, where R and L are the streamline counts in the right and left hemispheres, respectively. Table 1 shows the absolute values of LI [18,19], which ranges from 0 (not lateralized) to 1 (completely lateralized). This confirms that fiber bundles identified by TractDL are more symmetric for most of the bundles, which is in line with previous studies [19,20].

To evaluate the generalizability of TractDL, we applied it to a 54-days-old infant subject image acquired as part of Baby Connectome Project (BCP) [21], with a protocol that is different from the training subjects. Tractography was conducted with asymmetry spectrum imaging (ASI) as described in [22,23]. ASI fits a mixture of asymmetric fiber orientation distribution function (AFODF) to the diffusion signal. Fiber streamlines were then generated by successively following local directions determined from the AFODF [23]. Figure 6 indicates that the bundles are correctly identified by TractDL.

4 Conclusion

We presented a method for fast and robust identification of fiber bundles of interest from a large number of streamlines. The coordinates of each streamline were parameterized as coefficients of cosine series expansions. Based on this representation, we constructed dictionaries for multiple bundles of the whole-brain tractogram. The dictionaries were learned jointly to encourage incoherence for tractogram classifications. The effectiveness, robustness, generalizability, and bilaterality of our method were validated by the experimental results.

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Fig. 1.
Inter-hemispheric bilateral clustering of the whole-brain tractogram.

Fig. 2.
ACC as a function of the dictionary size m .

Fig. 3.
ACC variation over 100 classification repetitions.

Fig. 4.

The identification ACC of each tract across subjects measured in two ways; $ACC(\mathcal{X}_{GT}, \mathcal{X}_{RES})$ (top) and $ACC(\mathcal{X}_{RES}, \mathcal{X}_{GT})$ (bottom).

Fig. 5.
The reference bundles and the bundles identified by white matter query language (WMQL) [5], RecoBundles, and TractDL.

Fig. 6.
Fiber bundles identified by TractDL in an infant subject.

Table 1.

Laterality index.

Laterality	ATR	UF	ST_FO	ICP	OR	T_PREM	ST_PREM	CST	POPT	FPT
Reference	0.2640	0.5539	0.2796	0.3311	0.3339	0.1066	0.2019	0.3669	0.0058	0.0887
WMQL	0.5236	0.5870	0.0470	0.0877	0.4539	0.5322	0.1483	0.0178	0.0714	0.3850
RecoBundles	0.5459	0.9872	0.0292	0.0178	0.2288	0.1581	0.1044	0.1706	0.4079	0.4501
TractDL	0.3071	0.2172	0.0844	0.0494	0.1143	0.2206	0.2188	0.0023	0.0896	0.0905