Towards Constructing a Fiber Bundle Atlas
on Porcine Hearts with Diffusion Tensor Imaging

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ABSTRACT

We work on the first step towards building a fiber bundle atlas on porcine hearts with diffusion tensor imaging (DTI) by (1) generating porcine heart fiber models from DTI data, (2) clustering the DTI fibers, and (3) matching cross-subject DTI fiber bundles. We also explore the effects of different distance thresholds on the DTI fiber bundle clustering and matching. Our results show that (1) complete-linkage leads to greater number of matches than single-linkage; (2) the smaller the minimum distance threshold is, the more matched bundles are obtained; (3) several fiber bundles are consistently matched across subjects with different sets of parameters.

Keywords: Diffusion Tensor Imaging, fiber model, heart atlas, fiber clustering, distance.

Index Terms: I.3.8 [COMPUTER GRAPHICS]: Applications

1 INTRODUCTION

Diffusion tensor imaging (DTI) is one of the recently developed magnetic resonance imaging (MRI) techniques [2]. It opens up a unique approach to studying the heart, at both the microstructural level and the architectural level of the organization of myocardial fibers [6]. DTI tractography methods track a set of fibers that follow the principal direction of diffusion within the image volume [2]. The DTI datasets thus can be visualized as a dense set of 3D pathways [1] [2]. Study on white-matter fiber bundle template construction based on DTI tractography and fiber model clustering [3] encourages and inspires research on heart fiber bundle atlas construction. In this work, we use the single-linkage and complete-linkage of the agglomerative hierarchical clustering algorithms [4] to segment the fiber models. Then, we place all the clustered models into the same space by manual registration, and employ cross-subject bundle matching to identify the similarities in the fiber bundles among all the porcine heart subjects.

Improper set of parameters in either generating DTI fiber models or clustering would compromise the accuracy of the fiber bundle atlas, especially as the clustering process is sensitive to the change of distance threshold between fiber tracks. We therefore compare single-linkage and complete-linkage with (1) different distance parameters, and (2) their cross-subject matching results. This work would potentially enlighten choices of clustering method and distance parameters in generating fiber models and clustering in the heart fiber bundle atlas construction.

2 METHOD

In this section, we describe how we construct a porcine heart fiber bundle atlas and the parameters we use.

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2.1 Generating Fiber Track Models

GE 3T MRI scanner was used to collect diffusion-weighted images of five pig hearts at the College of Veterinary Medicine, Mississippi State University. Data volume of $256 \times 256 \times 158$ was acquired with a voxel size of $0.5859 \times 0.5859 \times 2.8$ mm for heart #1 - #3. Data volume of $256 \times 256 \times 139$ was acquired with a voxel size of $0.586 \times 0.586 \times 2.4$ mm for heart #4 and heart #5. The GE diffusion tensor imaging protocol was used, with two b values (0, 1000) and 55 gradient directions. DTI was then calculated from the diffusion-weighted images.

Five 3D fiber track models were generated for each of the heart subject to model the myocardial fibers based on the method in [5]. We set constraints such as minimum anisotropy, minimum length, or maximum curvature on the fiber tracks to exclude possible spurious fiber tracks from noise, partial-volume effects, or other imaging artifacts. The fiber tracks were integrated in major eigenvector field. The integration stopped when the linear anisotropy was too low, the signal-to-noise ratio was too low, or the change of direction was too great.

We use the mean of closest distances defined by Zhang et al. [5] to calculate the distance between the fibers. To avoid duplicated fibers, we set a minimum distance threshold between the fibers so that if a new fiber track is too close to an existing fiber track it would not be generated. The value of the minimum distance threshold is critical. On one hand, too large minimum distance would result in relatively small number of fiber tracks in the final model, potentially missing meaningful fibers. On the other hand, too low minimum distance threshold would lead to redundant fiber tracks, bringing about a larger number of fiber tracks in the model. Furthermore, generating fiber models is the first step of the whole fiber bundle atlas construction process. Improper minimum distance threshold would result in inaccuracy in atlas construction. In our work, we set the minimum distance threshold as 0.75 mm, 1.00 mm, 1.25 mm, and 1.50 mm, respectively.

2.2 Clustering

We use the single-link and complete-link of the agglomerative hierarchical clustering algorithm [4] to obtain anatomically meaningful fiber bundles from the fiber models. We design our algorithm to cluster the set of curves within a certain distance threshold. Both the single-linkage and complete-linkage clustering process stop when the distance between the clusters reaches the specified distance threshold. Therefore, the greater distance threshold is set to identifying the fiber bundles, the fewer numbers of clusters would be generated. An ideal distance threshold would prevent anatomically different fiber bundles from being merged into the same group, or fiber tracks that belong to the same anatomical bundle from being separated into different groups. We experiment and compare different distance thresholds. In single-linkage, the distance threshold is set to 2.0 mm, 2.25 mm, 2.5 mm, 2.75 mm, and 3.0 mm, respectively. In complete-linkage, the distance threshold is set to 14 mm, 17 mm, 20 mm, 23 mm, and 26 mm, respectively. In order to focus on large bundles, we remove those bundles with less than 20 fiber tracks after clustering.

2.3 Cross-subject Fiber Bundle Matching

We manually register all the five clustered fiber models to one particular model chosen at random. The registration was constrained to translation, rotation, and scaling operations only. Fiber clusters from two hearts are then aligned and compared according to the distance defined as follows:

$$D(X, Y) = \frac{\sum_{i=1}^{m} \sum_{j=1}^{n} (\, d(X_i, Y_j) + d(Y_j, X_i)\,)}{2mn},$$

where X and Y are the clusters of fiber tracks from two hearts. X_i and Y_j are fiber tracks belonging to X and Y, respectively. *m* and *n* are the number of fiber tracks in X and Y, respectively. d(a,b) is the mean of closest distances from fiber track *a* to fiber track *b* defined by Zhang et al. [5]. In order to be matched, cluster X and Y from two different hearts are compared to all the clusters from the other heart, and they must be mutually closest to each other. We relax the matching rule to mitigate the inaccuracy from manual registration by the following:

(a) If fiber bundles A, B and C are matched and fiber bundles A, B and D are matched, then we consider fiber bundles A, B, C and D to be matched.

(b) If fiber bundles A, B, C and D are matched, and fiber bundles A, B, C and E are matched, then we consider fiber bundles A, B, C, D and E are matched.

3 RESULTS

Complete-linkage results in greater number of match than single-linkage, as shown in Figure 1(left). The minimum distance threshold in generating fiber tracks in Figure 1 is 0.75 mm. Figure 1(right) demonstrates the effect of different minimum distance threshold in generating fiber tracks on matching. Smaller minimum distance leads to greater number of match. Note that for both figures in Figure 1, the y axes are scaled by the log of the number of matches.

From our observation, for different minimum distance thresholds in generating fiber models, a correspondent distance threshold in clustering can be found to obtain at least three similarly matched bundles using complete-linkage. As shown in Figure 2, five different colors are used to differentiate clusters from five different hearts. The white fiber tracks indicate a sparse heart fiber model as background. The matches on the left and in the middle are results from minimum distance of 1.0 mm in generating fiber tracks and distance threshold of 14 mm in clustering. The match on the right is from minimum distance of 1.5 mm in generating fiber tracks and distance threshold of 26 mm in clustering.

4 CONCLUSION

In conclusion, we completed the first step towards building a porcine heart fiber bundle atlas by generating fiber tracks from DTI, clustering these fiber tracks and matching the fiber bundles across five porcine hearts. We compare effects of different clustering and different parameters in generating fiber tracks and clustering on the matching. The experiment results suggest that (1) complete-linkage leads to greater number of matches than single-linkage, (2) smaller minimum distance threshold in generating fiber tracks result in greater number of matches, and (3) despite different minimum distance threshold in generating fiber tracks, a correspondent distance threshold in clustering can be found to obtain at least three similarly matched bundles. In future work, we will try to identify anatomically plausible fiber bundles based on input on our matching results from cardiologists. Our work has the potential to provide an automatic and robust way to find and study heart fiber bundles in DTI.
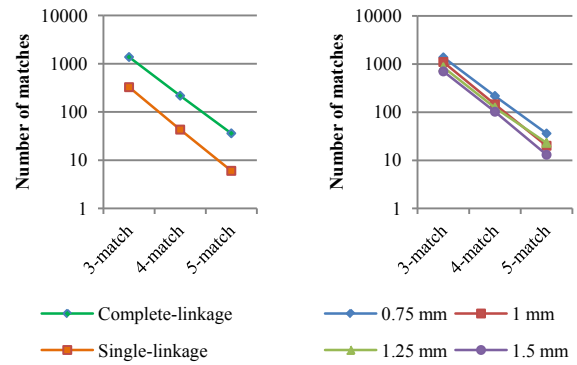

Figure 1: Left: Complete-linkage results in greater number of matches than single-linkage. The minimum distance threshold in generating fiber tracks is 0.75 mm. Right: The matching result of complete-linkage with different minimum distance thresholds in generating fiber tracks. Smaller minimum distance leads to greater number of matches. Note that for both figures the y axes are scaled by the log of the number of matches.
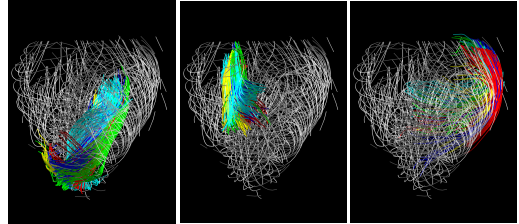

Figure 2: Three DTI fiber bundles are consistently matched across five subjects using complete-linkage clustering with different minimum distance thresholds. Five different colors are used to differentiate clusters from five different hearts. The white fiber tracks indicate a sparse heart fiber model as background. Left and middle: minimum distance threshold in generating fiber tracks is1.0 mm, distance threshold in clustering is 14 mm. Right: minimum distance threshold in generating fiber tracks is1.5 mm, distance threshold in clustering is 26 mm.

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