Mapping Out the Average Fiber Architecture from Diffusion Tensor MR Images Of *Ex-Vivo* Porcine Hearts

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Introduction: Myocardial fiber directions play an important role in the electro-mechanical function of the heart, which is often impared in cardiovascular disease (CVD). Fiber directions in healthy state can be determined via diffusion tensor DT MRI and then integrated into predictive image-based heart models and statistical atlases to help in diagnosis and therapy planning of CVD. However, such information is difficult to obtain *in-vivo*; thus, here, we present a pipeline for constructing a statistical fiber atlas from *ex-vivo* DT images of porcine hearts (with size similar to human hearts). We hypothesize that normalizing the cardiac geometries and reorienting local directional information on diffusion would yield an average DT field that preserves diffusion tensor and fiber orientations.

Methods: The diffusion-weighted (DW) MRI studies were performed on a dedicated 1.5T GE Signa Excite scanner using a small database of N=8 explanted healthy pig hearts, with approval from our institute. In the current study, we used the following MR parameters: TE=35 ms, TR=700 ms, ETL=2, b=0 for the unweighted MR images, and b=500 s/mm^2 when the seven diffusion gradients were applied, respectively [2]. Image resolution was ~0.5x0.5x1.6 mm. Notably, the total MR imaging time is ~10 hours/heart, which is not feasible for *in-vivo* patient studies.

A mean cardiac volume was generated by normalizing the anatomical structures of the eight subjects. This was done through an iterative groupwise registration scheme that converges to a stable average cardiac geometry. Every groupwise step was initialized by registering each subject to a current reference volume. The transformations from the pairwise alignments were used to compute updates to the reference geometries at each iteration.

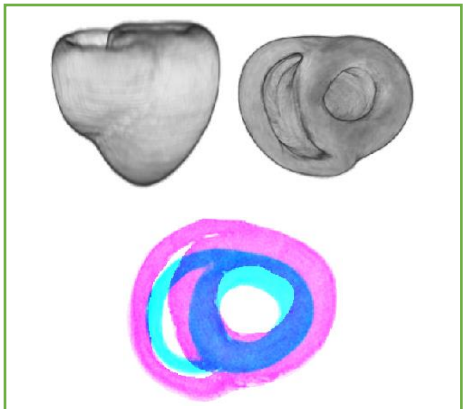

Fig. 1. The average geometry and the evolution of the reference geometries (the first reference image overlaid onto the final average).

We then projected the diffusion tensor (DT) field of each subject to a common reference frame using the final set of transformations from the groupwise step. This allowed us to compute the average DT field and visualize the preferential direction of diffusion at every voxel in the mean cardiac volume. Finally, the end-to-end pathway of diffusion given by the primary eigenvectors of the transformed diffusion tensors was tracked using MedInria (http://med.inria.fr).

Results and Conclusions: Pairwise alignments of the subjects to the reference geometries were performed via multilevel elastic registration. The groupwise scheme converged (after 7 iterations) to the mean volume shown in Fig. 1, along with the evolution of the reference geometries. The reoriented diffusion tensors were calculated using the Finite Strain method, and we found that the local orientation of the tensors were indeed preserved, as shown in the comparison between the magnified areas selected from the septum of the original and transformed tensors of one of the hearts (Fig. 2). In Fig. 3, we present the associated average cardiac fiber architecture obtained from the reoriented DT fields. Future work will focus on assessing the accuracy of fiber atlas using a leave-one-out validation method. Prior to clinical translation, we will also validate the output of 3D MR-based computer heart models that will integrate DTI fibers (as in [3]) vs. atlas fibers.

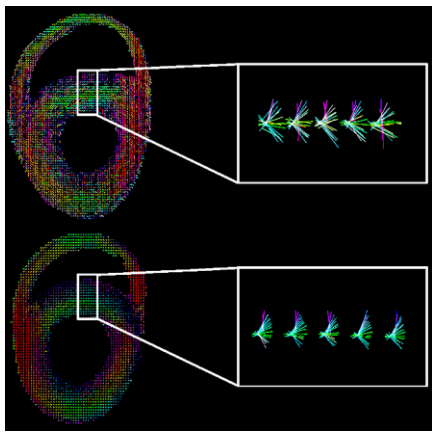

Fig. 2. Original and transformed tensors of one of the subjects.

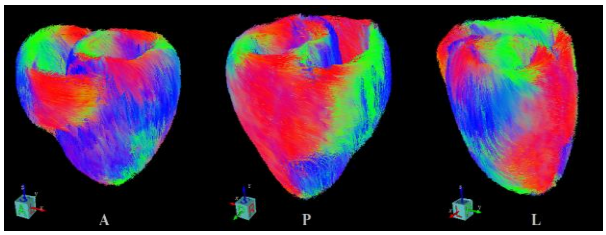

Fig. 3. Fiber Tractography. Cardiac fiber atlas obtained by tracking the end-to-end pathway of the principal direction of diffusion at every voxel.

References: [1] Peyrat, J.M., Sermesant, M., et al., IEEE Trans. Med. Imag. 26, 1500-14 (2007), [2] Pop, M., et al., Physics in Medicine and Biology. 58 (15), 5009-28 (2013), [3] Pop, M., et al., IEEE TBME 58(12) 3483 (2011)