Human Atlas of Cardiac Architecture from DT-MRI

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1. ABSTRACT

A human statistical atlas of the cardiac fiber architecture is constructed from *ex-vivo* diffusion tensor images and is based on a set of 10 normal human hearts. To the best of our knowledge, this is the first time that such study has been conducted with human data. We have developed a semi-automated method where only minimal interactions are required for the segmentation of the myocardium, and where the registrations are fully automated via symmetric log domain diffeomorphic demons. The results on the variability of human cardiac fibers concur with studies on other mammals. The cardiac fiber orientation is indeed much more consistent across our population than the orientation of the cardiac laminar sheets.

2. INTRODUCTION

As technology evolves, the cardiac fibers can now be imaged via diffusion tensor magnetic resonance imaging (DT-MRI). Various acquisition schemes have been proposed toward *in-vivo* diffusion weighted imaging (DWI) [1] but its feasibility remains very challenging due to physiological motion and will still require the use of an extrapolation model in the future. The availability of a full 3D atlas of the cardiac fibers opens the door to not only the construction of more accurate extrapolation models for *in-vivo* acquisitions, but also to a better understanding of various cardiac mechanical functions, cardiac electrophysiology patterns and remodeling processes. So far only canine studies [2,3] have been considered and only single *ex-vivo* human 3D dataset [4] has been studied. They revealed that the fiber orientation is consistent across a population while the laminar sheet orientations (the fibers are structured as piled up sheets) are more variable. Thanks to a unique access to a human dataset [5], previous studies are extended to humans.

We intended to build a human atlas using a semi-automated method where the only required interactions are for the segmentation of the myocardium. Registration among all hearts is fully automated via symmetric log domain diffeomorphic demons [6]. Once a morphological atlas of the heart is obtained, all tensor fields are transformed to the reference heart using a reorientation strategy preserving the fiber structure [7]. The study on human fiber variability concurs with the canine results.

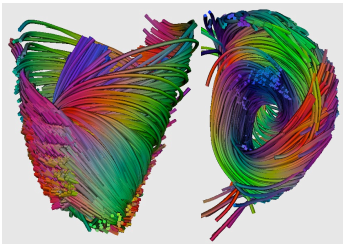

Figure 1: Average tensor field showing the left ventricle (left, view from front to back, right, from head to feet)

3. MATERIALS AND METHOD

From a database of post-mortem hearts (all extra-cardiac sudden deaths), 10 samples were classified as healthy after controlling their weight, wall thickness and subsequent pathology examination. Hearts were placed in a plastic container and filled with hydrophilic gel to maintain a diastolic shape. All images were acquired within 24 hours after death [5,8] on a 1.5T MR scanner (Avanto Siemens) with a bipolar echo planar imaging using 12 gradient directions. B_0 images were used for the construction of the morphological atlas. The registration is therefore free from any information on the fiber orientation (i.e., the variability study uses unbiased tensor fields). Our method is achieved in three steps. 1) Myocardial segmentation: the user provides two points (one on each in ventricle) and the optimal epicardium and endocardium are found via graph cut optimization [9]. The resulting myocardium mask is guaranteed to be topologically consistent (i.e., having two connected ventricle walls with no segmentation-related defects). 2) Registration of all hearts to a reference template. As inverse transformations are required for the construction of our atlas, our registration method is based on symmetric log domain diffeomorphic demons [6]. The myocardium masks, initially aligned rigidly [10], feed the symmetric demons method. The registration is ultimately refined with masked images (with original B_0 image intensities). 3) Atlas construction: the reference template is iteratively refined toward an average shape of the heart using Guimond *et al*. method [11]. The tensor fields are at last transformed using the finite strain reorientation strategy [7] (preserving the tensor field structure).

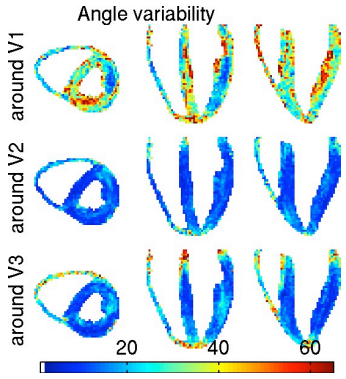

Figure 2: Variability of the fiber architecture (top, laminar sheet variability, middle and bottom, dispersion of the fiber orientation)

4. RESULTS

We study the variability of the cardiac fiber orientations. For each voxel, an average tensor D (3x3 matrix) and a covariance matrix Σ (6x6 matrix) are computed with the Log-Euclidean metric [12]. The principal components analysis of the average tensor D reveals the fiber orientation (with the first eigenvector v_1) and the normal of the laminar sheet (with the third eigenvector v_3). The figure 1 illustrates the average fiber structure in our human atlas. Peyrat *et al.* [2] show that the fiber structure variability can be studied by projecting the covariance matrix onto orthonormal bases formed by a combination of different eigenvectors v_1, v_2, v_3. The projection of the covariance matrix Σ onto the basis $W_4 = 1/\sqrt{2}\ (v_3v_2^t + v_2v_3^t)$ reveals the angular variability of the plane (v_2,v_3) around the principal axis v_1. That is the orientation of the laminar sheet around the fiber (see [2] for more details). We found a variability of 31.10º (top row of Fig. 2 and blue line in Fig. 3). The projection of the covariance matrix onto the basis $W_5 = 1/\sqrt{2}\ (v_3v_1^t + v_1v_3^t)$ and $W_6 = 1/\sqrt{2}\ (v_2v_1^t + v_1v_2^t)$ reveals the angular variability of the planes (v_1,v_3) and (v_1,v_2) around the axis v_2 and v_3. They describe the dispersion of the fiber orientation. With a variability of 11.53º and 13.04º (middle and bottom rows of Fig. 2 and green, red lines in Fig. 3), The orientation of fibers appears thus much more consistent within the population than the orientation of the laminar sheets.

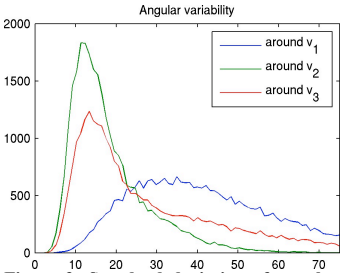

Figure 3: Standard deviation of angular variability, in blue, the laminar sheet orientation around the fiber (peak at 31.10º), in green and red, the dispersion of the fiber orientation (peaks at 11.53º and 13.04º)

5. CONCLUSION

We have developed a semi-automated method for the construction of the first statistical atlas of the cardiac fiber architecture from DT-MRI. The fiber structure variability has been studied on an initial dataset of 10 normal *ex-vivo* human hearts, showing that fiber orientation is more consistent than the laminar sheet orientation. This conclusion agrees with previous studies on canine datasets [2,3]. This cardiac fiber atlas is a first in humans and is an important advance in the knowledge of the human cardiac fiber architecture (so far mostly extrapolated from canine studies or destructive and sparse anatomic studies). This should improve the development of more accurate human cardiac modeling and should lead to a better understanding of human cardiac mechanical functions and electrophysiology.

6. REFERENCES: **[1]** Toussaint *et al.*, ISMRM, 2010. **[2]** Peyrat *et al.*, TMI, 26:1500-1514, 2007. **[3]** Helm *et al.*, Mag. Res. In Med., 54(4):850-859, 2005. **[4]** Rohmer *et al.*, Invest Radiol, 42:777-789, 2007. **[5]** Frindel *et al.*, Med. Im. An. 13(3):405-418, 2009. **[6]** Vercauteren *et al.*, MICCAI, 754-761, 2008. **[7]** Alexander *et al.*, TMI, 20:1131-1139, 2001. **[8]** Rapacchi *et al.*, ISMRM, 2010. **[9]** Boykov, Jolly, MICCAI, 276-286, 2000. **[10]** Ourselin *et al.*, MICCAI, 557-566, 2000. **[11]** Guimond *et al.*, C. Vis. and Im. Understanding, 192-210, 2000. **[12]** Arsigny *et al.*, Mag. Res. in Med., 56(2):411-421, 2006.