

ESTIMATING MYOCARDIAL FIBER ORIENTATIONS BY TEMPLATE WARPING

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ABSTRACT

Myocardial fiber orientations are an important element for accurate modeling of cardiac electromechanics. However it is extremely difficult to estimate these directly *in vivo* with current imaging techniques. Most current methods for cardiac modeling use synthetic models of fiber orientation which may fail to capture subtle variations of fiber orientations in different hearts. We present a method to map the fiber orientations obtained from diffusion tensors from a template onto patient-specific cardiac geometry, using elastic registration followed by a reorientation of the diffusion tensors based on the local rotation component of the transformation. The effectiveness of the diffusion tensor mapping is validated on a set of diffusion tensor imaging datasets obtained from 19 canine subjects. The algorithm was able to map the diffusion tensors effectively for both healthy and failing hearts.

1. INTRODUCTION

Modeling of cardiac structure and mechanical and electrophysiologic function, is an important method for understanding the complicated interactions that take place in the heart. Knowledge gained from cardiac modeling helps us to understand the mechanisms of heart failure, and may help point to ways to prevent and cure such pathologies. A large number of cardiac pathologies occur because of problems with the electro-mechanical coupling system within the heart. Consequently, this has been an area of active research inquiry. A comprehensive review of the field can be found in [1].

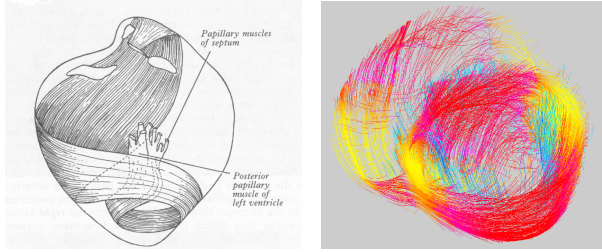
Since a muscle fiber can contract only along one direction, the heart has a complex structure of fiber orientations, allowing effective circumferential and longitudinal contraction. To achieve this anatomically, the muscle walls of the ventricles and the atria are composed of a single helically folded muscular structure [2] as can be seen in Figure 1(a). As a result of this complicated geometry, muscle fiber orientations need to be considered while modeling cardiac electro-mechanics. At present the prevailing hypothesis is that the diffusion properties of the muscle fibers play an important role in the propagation speed of cardiac activation current as the diffusion tensor

is proportional to the local conductivity, and also in the estimation of the orientation of forces generated by the muscles which are along the fiber direction. Therefore, knowledge of the diffusion tensor or at least the fiber orientations is very important for modeling purposes, especially if patient specific models are desired. However, *in-vivo* diffusion tensor imaging of the heart is not a practically realizable application at present, and as a result most modeling approaches use synthetic data for the fiber orientations. A common approach is to vary the elevation angle between the fiber and the short axis plane between $+90^\circ$ and -90° from the endocardium to the epicardium [1, 3]. These models of fiber orientations capture only the overall trends in orientation, and thus are not sufficient for patient specific modeling.

Better estimates of patient specific fiber orientation may be obtained by mapping diffusion tensors from a template onto patient imaging data. In this paper, we use a template derived from *in-vitro* diffusion tensor imaging of a harvested heart. These tensors are mapped onto individual patient's imaging data by performing an elastic registration between the patient and the template. Validation of the method was performed by evaluating the agreement between the mapped fibers and the true fibers measured from a set of 19 canine subjects, both healthy and failing, for which we have *ex-vivo* diffusion tensor data.

1.1. Diffusion Tensor Imaging

Diffusion Tensor Imaging (DTI) is an MR imaging technique to measure the anisotropic diffusion properties of biological tissues. This allows us to noninvasively infer the structure of the underlying tissue. Diffusion properties allow the classification of different types of tissues and can be used for tissue segmentation and tissue orientation detection. For the specific case of elongated cells like cardiomyocytes, the diffusion tends to be maximum along the primary axis of the muscle, which also happens to be the direction along which maximum strain is developed. The principal eigenvector of the diffusion tensor is known to align with fiber tracts in the brain [4] and also in the heart [5, 6]. Myocardial fiber orientations obtained from cardiac DTI are shown in Figure 1(b).



(a) Helicly folded muscular tissue in the heart, from [2] (b) Heart fiber orientations obtained from diffusion tensor imaging

Fig. 1. Heart fiber orientation in the human heart.

Diffusion is measured through a diffusion coefficient, which is represented with a symmetric second order tensor:

$$\mathbf{D} = \begin{pmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{pmatrix} \quad (1)$$

The 6 independent values of the tensor elements vary continuously with the spatial location in the tissue.

Eigenvalues λ_i and eigenvectors \mathbf{e}_i of the diffusion tensor (1) can be found as a solution to the eigenvalue problem:

$$\mathbf{D}\mathbf{e}_i = \lambda_i\mathbf{e}_i$$

Since the tensor is symmetric, its eigenvalues are always real numbers, and the eigenvectors are orthogonal and form a basis.

2. WARPING DIFFUSION TENSORS FROM TEMPLATE TO SUBJECTS

We select the diffusion tensor data of a patient, acquired in vitro, as the template and then use a very high-dimensional elastic registration technique [7] to estimate the deformation field that warps the template to the subject space, by using anatomical information in the form of MR images. This deformation field is used to map the fibers from the template to the subject. Note that it is more complicated to warp tensor fields than it is to warp scalar images. This is because the tensor must be reoriented on each image voxel, in addition to a voxel displacement that is implied by the deformation field. This is achieved by rotating the tensor by the local rotational component of the deformation field. We test the effectiveness of this tensor remapping algorithm by comparing the mapped tensors with the ground truth diffusion tensors for 19 canine datasets. The method of computing the transformation between the two anatomical images and the tensor reorientation algorithm are now described.

2.1. Deformable Image Registration

Image warping for deformable registration has received a great deal of attention during the past decade [8]. In the present work, we use a very high-dimensional elastic registration procedure, referred to as the hierarchical attribute matching mechanism for elastic registration (HAMMER) method [7], to determine the transformation between T1-weighted images of template and subject, and then apply it to the coregistered DT image of the template for obtaining patient-specific fibers. This registration approach uses image attributes to determine point correspondences between the subject image and a template, which resides in the stereotaxic space. The template is the patient for whom we have the diffusion tensors. A hierarchical sequence of piece-wise smooth transformations is then determined, so that the attributes of the warped images are as similar as possible to the attributes of the subject. Relatively fewer, more stable attributes are used in the initial stages of this procedure, which helps avoid local minima, a known problem in high-dimensional transformations. The details of this algorithm can be found in [7].

2.2. Tensor Reorientation

It is relatively simple to warp a scalar image by a known spatial transformation, i.e., transferring the image value from a particular voxel to a voxel in the subject image via an interpolation scheme. However, a more complex procedure is required to warp tensor fields. We use an approach similar to that proposed by Xu et al [9].

If we know the direction, \mathbf{v} , of the fiber on voxel with coordinates \mathbf{x} , we can readily find the rotated version, \mathbf{v}' , of \mathbf{v} , according to the warping transformation. If \mathbf{R} is the matrix that rotates \mathbf{v} to \mathbf{v}' , then \mathbf{R} should be applied to the respective tensor measurement. However, in practice we do not know \mathbf{v} and it is precisely what we would like to estimate. We only have a noisy orientation of \mathbf{v} , which is the principal direction (PD) of the corresponding tensor measurement. One could use the PD in place of \mathbf{v} as the fiber orientation, as proposed in [10]. However, that makes the approach vulnerable to noise, since the PD is only a noisy observation, and could be quite different from the true underlying fiber orientation.

Assuming that we know the probability density function (PDF), $f(\mathbf{v})$, of the fiber orientation \mathbf{v} , we can find the rotation matrix, $\tilde{\mathbf{R}}$, which minimizes the expected value of $\|\mathbf{v}' - \mathbf{R}\mathbf{v}\|^2$ over all orthonormal matrices \mathbf{R} :

$$\begin{aligned} \tilde{\mathbf{R}} &= \arg \min_{\mathbf{R}} E\{\|\mathbf{v}' - \mathbf{R}\mathbf{v}\|^2\} \\ &= \arg \min_{\mathbf{R}} \int_{\mathbf{v}} f(\mathbf{v})\|\mathbf{v}' - \mathbf{R}\mathbf{v}\|^2 d\mathbf{v} \end{aligned}$$

This problem can be solved by the Procrustean estimation [11], if a number of random samples, \mathbf{v} , are drawn from the PDF, and their respective rotated versions, \mathbf{v}' , are found by

the rotation that the warping field applies to \mathbf{v} . If we arrange these vectors \mathbf{v}' and \mathbf{v} to form the columns of the matrices \mathbf{A} and \mathbf{B} , respectively, then $\hat{\mathbf{R}}$ is found by minimizing:

$$\|\mathbf{A} - \mathbf{R}\mathbf{B}\|_2^2 = \|\mathbf{A}\|_2^2 + \|\mathbf{B}\|_2^2 + 2 \sum_i \omega_i (\mathbf{A}\mathbf{B}^T)$$

The PDF of the fiber orientations is estimated by taking random samples in a small neighborhood around voxel \mathbf{x} . More details on the algorithm can be found in [9].

3. VALIDATION

We used canine DTI datasets obtained from Center for Cardiovascular Bioinformatics and Modeling, Johns Hopkins University and acquired at the National Institutes of Health, to validate the effectiveness of our diffusion tensor remapping algorithm. A total of 19 canine subjects were scanned, of which 12 subjects were normal, and 7 had cardiac failure. The scans were performed *in vitro* after the hearts were harvested. Each heart was placed in an acrylic container filled with Fomblin, a perfluoropolyether (Ausimom, Thorofare, NJ). Fomblin has a low dielectric effect and minimal MR signal, thereby increasing contrast and eliminating unwanted susceptibility artifacts near the boundaries of the heart. The long axis of the heart was aligned with the z axis of the scanner. Images were acquired with a 4-element knee phased array coil on a 1.5 T GE CV/I MRI Scanner (GE, Medical System, Wausheka, WI) using an enhanced gradient system with 40 mT/m maximum gradient amplitude and a 150 T/m/s slew rate.

Since only the long axis of the heart was aligned with the z axis of the scanner, we first need to correct for rotation about the z axis. We picked one of the normal canine hearts as the template, and performed affine registration to warp the remaining subjects onto the template space. The diffusion tensors for these subjects were also rotated by the rotational component of the affine transform. We then perform the elastic registration using HAMMER to estimate the transformation that maps the template to the subject space. This transformation is then used to warp and reorient the diffusion tensors of template onto the subject. The quality of the mapping is measured by computing the angle between the principal direction of the mapped tensor and the principal direction of the ground truth obtained from the subject's DTI. This is shown in Figure 2.

The error in the fiber orientations is further demonstrated on one slice in Figure 3, by comparing the original fibers (in red) and the mapped fibers (in blue). Our method was able to successfully map the fibers for healthy as well as for failing canine hearts. The percentage of voxels where the error in the principal directions is less than 10° is shown in Figure 4. We evaluated for an error of less than 10° since it is close to the average error obtained from DTI imaging [5] and histological measurements [12]. We also compare this with

the error by using a synthetic model to estimate fiber orientations. The synthetic fiber orientations were produced by varying the elevation angle between the short axis plane and the fiber between $+90^\circ$ and -90° from the endocardium to the epicardium. Similar synthetic models have been used in [1, 3].

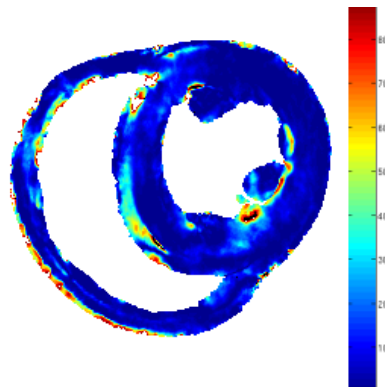


Fig. 2. The dot product of the mapped principal direction with the actual principal direction. The colormap is mapped to the angle between the mapped and the fiber orientations obtained from DTI. The image is overlaid on a segmentation of the heart based on the fractional anisotropy.

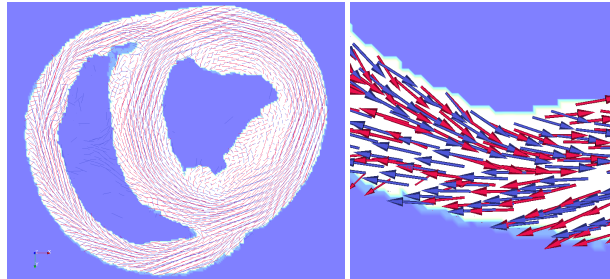


Fig. 3. Visual comparison between the principal directions of the original DT (blue) and the mapped DT (red). The glyphs are overlaid on a segmentation of the heart based on the fractional anisotropy of the mapped DT.

The method was able to map the fibers accurately for both healthy as well as for failing hearts that had left bundle branch blocks. Although, the percentage of voxels having an error of less than 10° was lower in the failing hearts as compared to the healthy ones, we observe that most of these errors are in the vicinity of the block as expected, and the fiber orientations away from the bundle branch block were similar to that observed in healthy patients. Therefore, our method should perform better for other pathologies like ventricular hypertrophy and infarction, since it has been shown that the muscle fiber orientations are not affected significantly by hypertrophy and

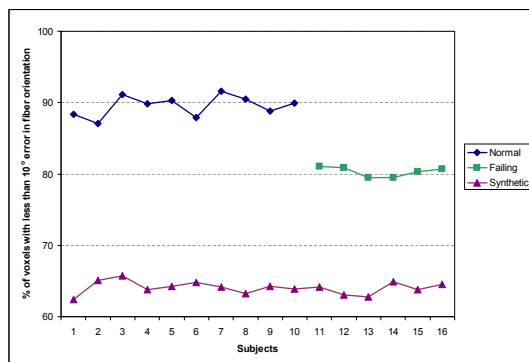


Fig. 4. The percentage of voxels having less than 10° error in the principal directions after mapping.

myocardial infarction[13].

4. CONCLUSIONS AND FUTURE WORK

Having good estimates of myocardial fiber orientations allows us to build more accurate electro-mechanical models of the heart. The validation experiments conducted on the canine hearts confirm that patient specific fiber orientations can be obtained using the proposed method. The results also confirm that the mapped fiber orientations are in better agreement with the actual fiber orientations compared to those obtained using synthetic models. Of course, we do need to validate the accuracy of the mapped fibers in being able to model accurately the electro-mechanical properties of the heart. For this we intend to use the mapped fibers to generate patient specific electro-mechanical models of the heart. While modeling cardiac electrophysiology, the diffusion tensor intervenes in the propagation speed as the diffusion tensor, D , is proportional to the local conductivity. We shall test the accuracy of the model against data obtained from electro-physiological tests. Similarly, we will extend this work to use it for modeling the motion of the heart. The motion predicted from the model shall be compared with cardiac motion estimates obtained from other techniques like tagged MR images. We also expect to develop better cardiac motion estimation from MR Cine images by using the mechanical model as a prior.

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