Helical Structure of Cardiac Ventricular Anatomy by Diffusion Tensor MRI Multi-resolution Tractograpy

Ferran Poveda[1], Enric Martí[1], Debora Gil[2,1], Francesc Carreras[3], and Manel Ballester[4]

[1] Department of Computer Science - Universitat Autònoma de Barcelona,

[2] Computer Vision Center - Universitat Autònoma de Barcelona,

[3] Cardiac Imaging Unit, Hospital de la Santa Creu i Sant Pau, Barcelona, and

[4] Department of Medicine, Universitat de Lleida, Spain

It is widely accepted that the myocardial fiber architecture plays a critical role in myocardial contractility and relaxation [1]. However, there is a lack of consensus about the distribution of the myocardial fibers and their spatial arrangement in the left and right ventricles. An understanding of the cardiac architecture should benefit the ventricular functional assessment, left ventricular reconstructive surgery planning, or resynchronization therapy in heart failure. Researchers have proposed several conceptual models to describe the architecture of the heart either from gross dissection to histological presentation. The cardiac mesh model [2] proposes that the myocytes are arranged from longitudinally and radially changing their angulation along the myocardial depth. On the other side, the helical ventricular myocardial band model states that the ventricular myocardium is a continuous anatomical helical layout of myocardial fibers [1].

Diffusion Tensor magnetic resonance imaging (DT-MRI), which provides a discrete measurement of the 3D arrangement of myocytes by the observation of local anisotropic diffusion of water molecules, h. This has enabled computational validation of the muscular structure of the heart. It has allowed the measurement of the whole cardiac architecture with acceptable resolution (300 µm × 300 µm × 1000 µm) compared to size of myocytes (50 – 100 µm long and 10 – 20 µm thick). In this correspondence we introduce a multi-scale tractographic visualization approach based on DT-MRI streamlining to decipher properties of the architectural organization of the heart.

Canine datasets used in this study come from the public library of the Johns Hopkins University [3]. Each heart was placed in an acrylic container filled with Fomblin, a perfluoropolyether (Ausimon, Thorofare, NJ), which has a low dielectric effect and minimal MR signal thereby increasing contrast and eliminating unwanted susceptibility artifacts near the boundary of the heart. The long axis of the hearts was aligned with the z-axis of the scanner and images 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 a 40 mT/m maximum gradient amplitude and a 150 T/m/s slew rate. Hearts were placed in the center of the coil and 3-D fast-spin echo sequence was used to acquire diffusion images. The datasets were arranged in 256x256x108 array, wherein each voxel

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consisted of 3 eigenvalues and 3 eigenvectors; size of each voxel was 312.5x312.5x800 µm. Tractography was performed as a reconstruction comprising several streamlines [4] (i.e. a curve tangential to the vectorial field of primary eigenvectors given at the diffusion tensor volumes) using a fifth order Runge-Kutta-Fehlbert integration method. Our fullscale reconstruction was built with near to 350 seeds; these seeds were randomly chosen over the entire anatomy only taking out a very small range of points related to the lowest eigenvalues that are likely to be bad starting points for the reconstruction. The basal ring and atrial cavities were always included for reconstruction. Tractography is a graphical representation inherited from fluid mechanics where both direction and orientation of the vector fields are a meaningful part of the represented information. We applied a geometrical reorganization of the vector field using local coordinate systems coherent to ventricular anatomy and fluid mechanics. Ventricular anatomy could be described by means of a longitudinal axis and angular coordinates with respect to this axis on axial cuts (Fig. 1). Coloring techniques were based on axial and longitudinal angulations of fibers to help in the interpretation of the tractography models, which highlighted different features of the fiber architecture adding valuable information of existent muscular layers. In order to further clarify the anatomic characterization we applied multiresolution models that build different models of the same data with different levels of detail and not loosing fidelity. This technique is based on the well known pyramid representation [5], which applies a Gaussian filtering and subsequent exponential reduction via a subsampling of the full-scale information. Reduced information is a summary of the original and would be used to represent it at different scales. This technique can be applied to the DT-MRI dataset in order to simplify its complexity. By downscaling two orders of magnitude of the original sets and applying our streamlining, we got the simplified tractography (Fig. 2). Comparing to the fullscale tractography shown in Fig. 1 it is easy to notice that the simplified one keeps the main geometric features of fibers.

The simplified tractographic reconstruction method (Fig. 1) showed a continuous helical structure of the ventricular myocardium, starting at the pulmonary artery (PA) and finishing at the aorta (Ao). The helical structure started at the basal ring going inside the left ventricle towards the apex and returning to connect with the aorta as descending and ascending segments wrapping the entire anatomy of the ventricles. In order to further simplify the backbone myocardial fiber spatial orientation we explored the geometry of the heart by looking for long paths that can represent connected regions on the DT-MRI tractography. The goal of this procedure was to provide a comprehensive reconstruction allowing interpretation at first sight by any possible observer. By manually picking seeds at the basal level we obtained continuous paths connecting both ventricles and wrapping the whole myocardium. Figure 2 shows four tracts of simplified models reconstructed from manually picked seeds located at basal level near the pulmonary artery. We observe that the tracts define a sample-wide coherent helical structure for all canine samples. The use of visualizations with single tracts changes the way in which this structure can be viewed.

Our reconstructions support a helical ventricular myocardial fiber array from a complete set of local evidences and also from a global automated reconstruction of the myocardial structure.

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Figure legends

Figure 1: A. Tractography reconstruction with near 350 seeds. Represented on a full-color scheme determining orientations of the fibers. **B.** Two-color scheme set raise the difference between ascending and descending fibers. **C.** Simplified tractography.

Figure 2: Example of tracts reconstructed with manually picked sedes, always chosen near the pulmonary artery, on simplified tractography.

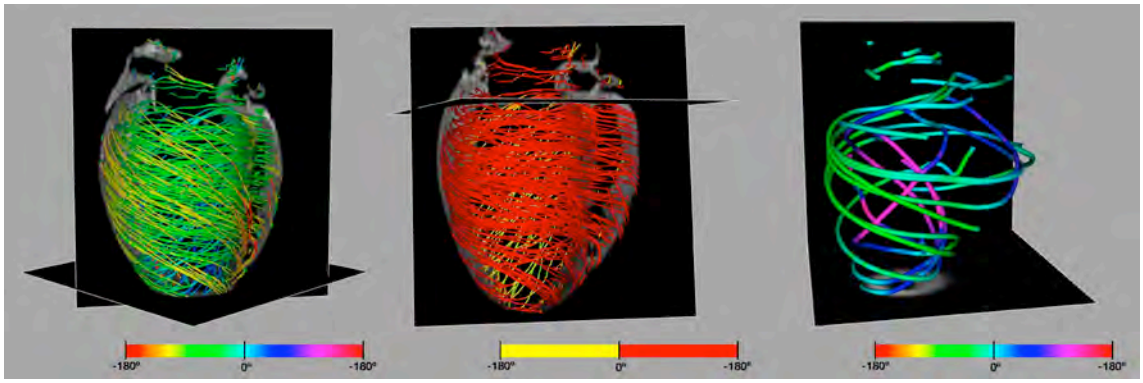

Figure 1

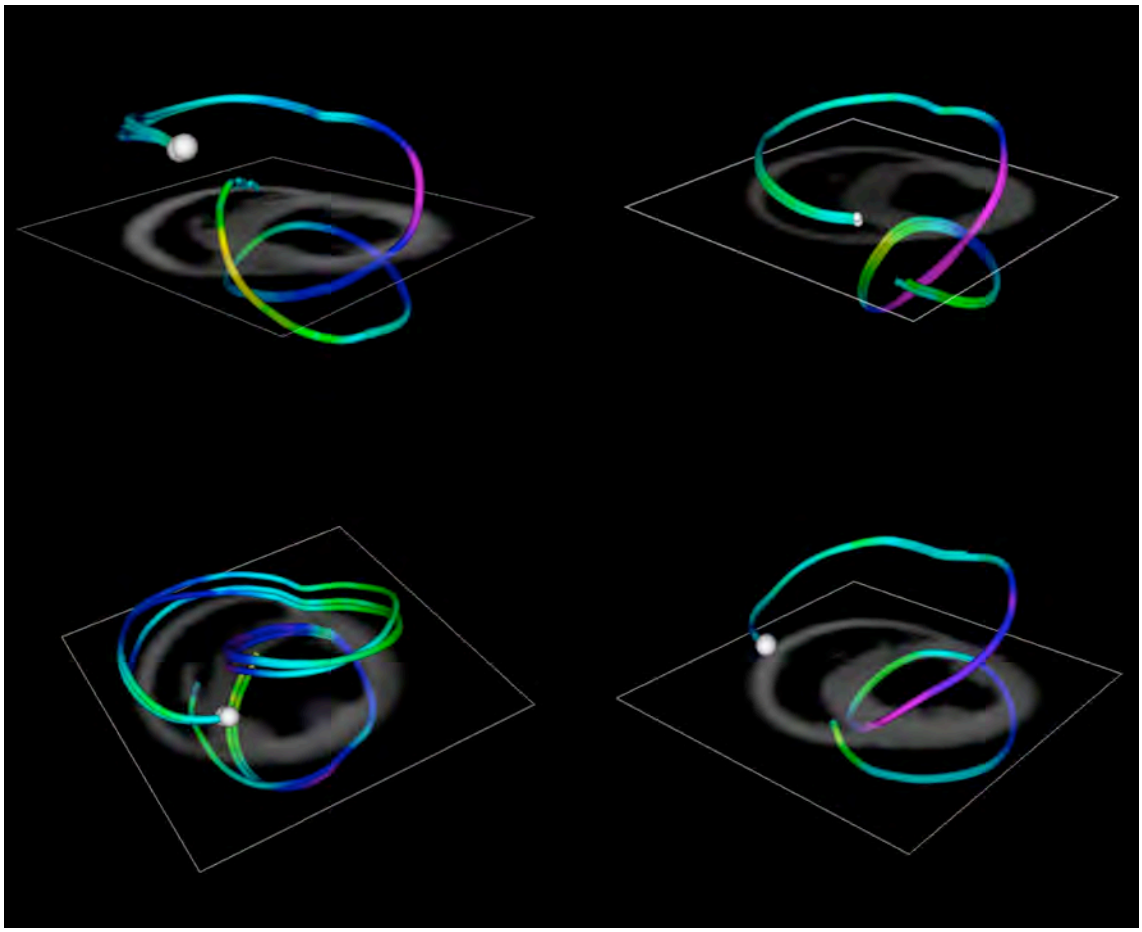

Figure 2