MIOCARDIA: Integrating cardiac function and muscular architecture for a better diagnosis

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ABSTRACT

Deep understanding of myocardial structure of the heart would unravel crucial knowledge for clinical and medical procedures. The MIOCARDIA project is a multidisciplinary project in cooperation with l'Hospital de la Santa Creu i de Sant Pau, Clínica la Creu Blanca and Barcelona Supercomputing Center. The ultimate goal of this project is defining a computational model of the myocardium. The model takes into account the deep interrelation between the anatomy and the mechanics of the heart. The paper explains the workflow of the MIOCARDIA project. It also introduces a multiresolution reconstruction technique based on DT-MRI streamlining for simplified global myocardial model generation. Our reconstructions can restore the most complex myocardial structures and provides evidences of a global helical organization.

Categories and Subject Descriptors

I.4 [**Image Processing and Computer Vision**]: Miscellaneous; J.3 [**Life and Medical Sciences**]: Health

1. THE MIOCARDIA PROJECT

Myocardial fiber architecture plays a critical role in many functional aspects of the heart such as electrical propagation [3, 4] or force production [5]. However, there is a lack of consensus about the exact distribution of the myocardial fibers and their spatial arrangement that constitutes the gross (left and right ventricles) myocardial structure. We propose developing a 3D patient-sensitive model of the myocardium integrating, for the first time, the ventricular band anatomy (fibers orientation), the gross anatomy and its functionality. The complexity of the cardiac mechanisms requires the joint cooperation of groups from several disciplines. In our case, our integrative model requires complementary MR modalities, as well as, combining computational mechanics and image processing techniques. The MIOCARDIA project gathers researchers from the Computer Vision Center, l'Hospital de la Santa Creu i de Sant Pau, Clínica la Creu Blanca and Barcelona Supercomputing Center.

Regarding to the computer vision discipline, we have developed a set of image processing tools that take advantage of several modalities of medical imaging to obtain a complete model of the heart. The MIOCARDIA project involves the study of the functionality of the myocardium as well as its gross anatomy and the distribution of its fibers. The pipeline in figure 1 outlines the interaction between the modules that compose the computational simulation of the myocardium.

In order to study the motion of the heart we have developed a variational framework (Harmonic Phase Flow, HPF [7]) for tracking tissue motion in TMR sequences. Our variational approach tracks motion in a feature space best describing the image content and applies a regularization on the motion field only at image areas where the descriptors response is not reliable. The feature space is given by the response to a bank of Gabor filters in order to properly model tissue local deformation. By working in frequency (Gabor) domain HPF formulation is given by simple equations (opposite to registration algorithms working in intensity domain). The use of Gabor filters makes HPF able to properly model local tissue deformation at advance stages of the systolic cycle (in contrast to current techniques relying on Fourier). By applying the regularization term only at poorly tagged areas we do not overestimate motion at injured hypo kinetic territories.

Moreover, we have developed an normalized comparison domain to analyze the gross anatomy of the myocardium. We have designed a generic domain (the Normalized Parametric Domain, NPD [6]) mapping anatomic structures of medical images to a unitary cube. The NPD framework allows moving over the anatomic domain of the myocardium in (natural) radial and circumferential coordinates based on anatomical features at any time of the cardiac cycle. In this manner, the NPD allows the fusion of clinical parameters

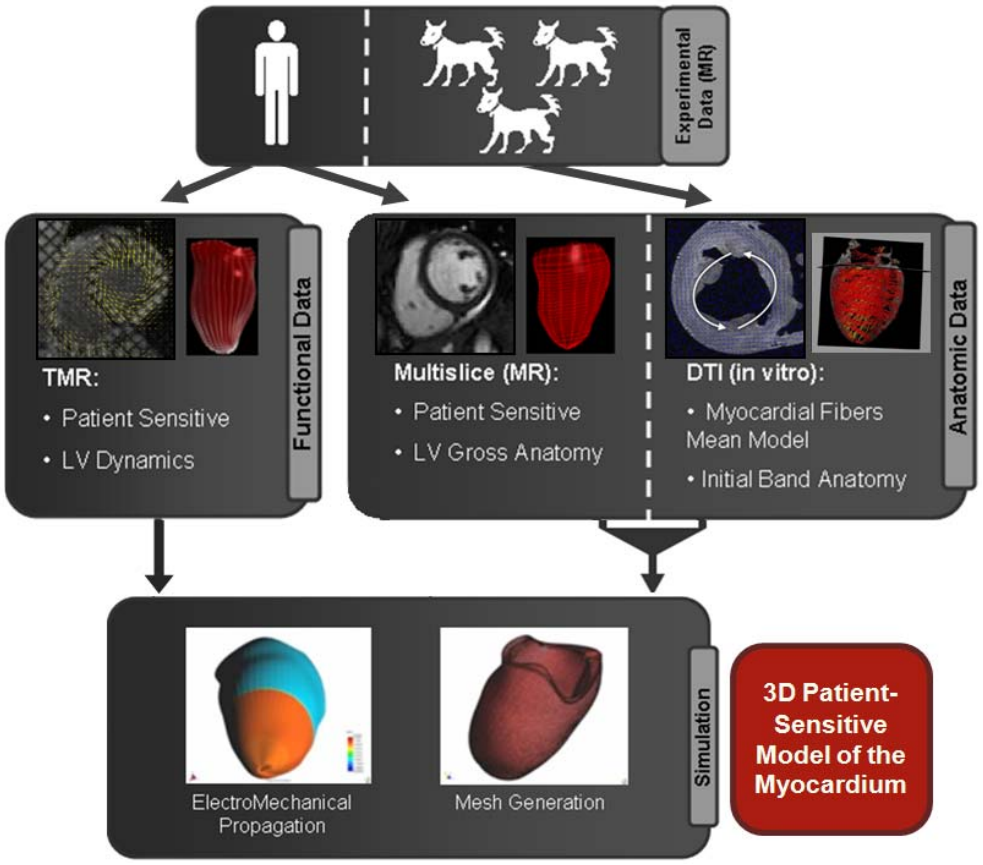


Figure 1: Scheme for the Computation of the Cardiac Model of the Myocardia Project.

of different natures (scalar and vectorial), their comparison across patients and, thus, definition of normality models.

Finally, our computational framework aims to model the fibers distribution from the information of the Diffusion Tensor Imaging (DTI). In this paper, we center our attention in this module of the MIOCARDIA project. This way, we follow exposing the computational strategy to develop it and our experimental results.

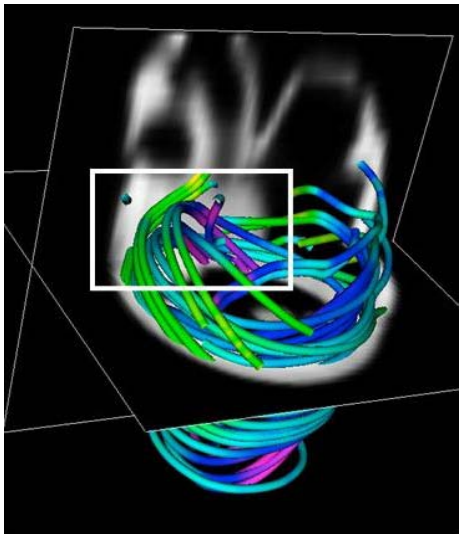
2. MULTI-RESOLUTION ANALYSIS OF THE FIBER DISTRIBUTION

During the last decade, a new modality of magnetic resonance imaging (Diffusion Tensor MRI, DT-MRI) has enabled computational validation of the muscular structure of the heart. This technique provides a discrete measurement of the 3D arrangement of myocytes [14] by the observation of local anisotropic diffusion of water molecules in biological tissues [9] [15]. Frequently, *heart tractography* is seen as a reconstruction composed by several *streamlines* [10] (also known as *fiber tracks* on this field). The main property that clearly defines a streamline is that it is a curve tangential to the vector field at any point of such curve. In this work, tractographies are composed by streamlines computed on the vectorial field of primary eigenvectors given by the diffusion tensor volumes. We computed those streamlines using a fifth order Runge-Kutta-Fehlbert [11] integration method that is able to provide successful results using variable integration steps based on error estimation.

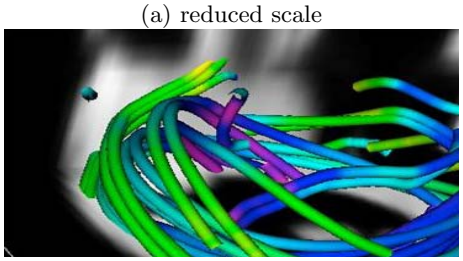
Fully detailed tractographic reconstructions fit perfectly to make low level descriptions, but might fail on a higher level of analysis as a result of their complexity. In order to obtain more comprehensive descriptions of global myocardial structure, we propose the use of a multiresolution approach applied to the standard tractographic algorithms. This may help us to generate simpler visualizations which in turn may help us to better understand the architecture of the heart.

Multiresolution models are usually applied to texture mapping and it is known as *mip mapping* [12] based on the well known *pyramid representation* [13]. This technique applies a gaussian filtering and later an exponential reduction via a subsampling of the full-scale texture. Reduced textures are somehow "summaries" of the original texture and would be used to represent this texture at different scales. These "summaries" are statistically complete in such a way the gaussian smoothing keeps the contextual information before applying downsampling. The use of these downscaled images is also common in other fields like in computer vision where this operation can be seen as a computation on the scalespace.

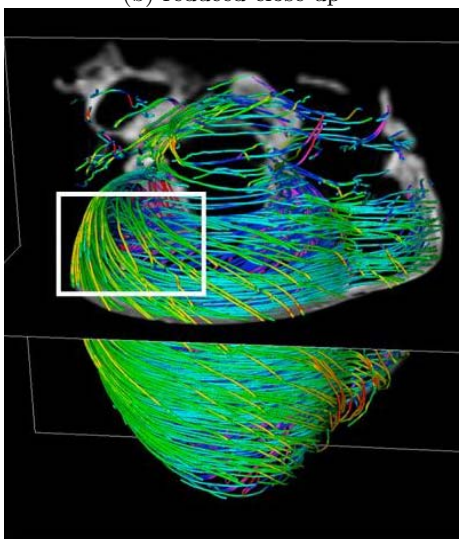
This technique can be applied to the DT-MRI dataset in order to simplify its complexity. By downscaling two orders of magnitude of the original sets and applying our stream-



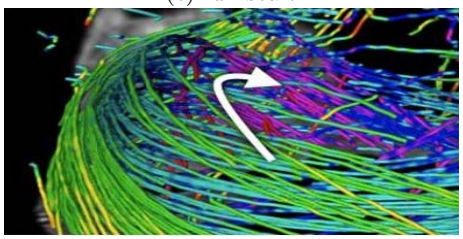
(a) reduced scale



(b) reduced close up



(c) full scale



(d) detailed close up

Figure 2: Reduced and full-scale tractographic reconstructions of the same heart sample, showing the complex structure of the Basal Ring.

lining, we get the simplified tractography. Analyzing the fullscale tractography is easy to notice that the simplified one keeps the main geometric features of fibers. Figure 2 illustrates this comparison. Therefore it allows an easier identification of global morphological tendencies. We have applied a comprehensive visualization of fiber tracts using a colormap that provides a proper assignment of colors according to the orientation of the myocardial fibers. Thus, in the simplified tractographic reconstruction it is easy to appreciate some details of the structure of the heart.

3. EXPERIMENTS: EVIDENCES OF AN HELICAL ARCHITECTURE

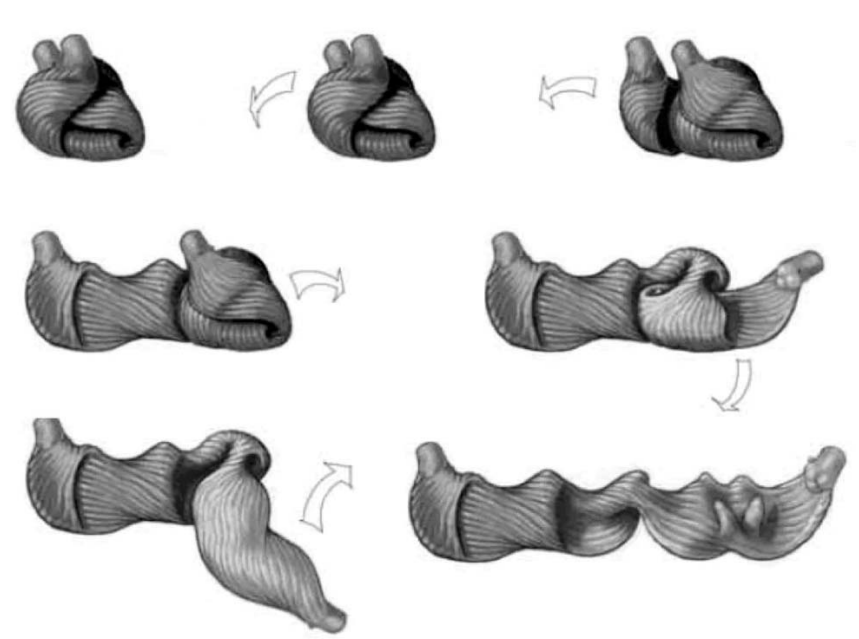
We have made a set of experiments to show the usefulness of our multiresolution tractography to identify myocardial muscular architecture. For this purpose, we have applied our methodology to the seven healthy canine studies of the Johns Hopkins University public database [16].

According to the results we have taken into consideration the validation of theory proposed by Dr. Torrent-Guasp called the Helical Ventricular Myocardial Band (HVMB). This theory presents the myocardium as a very interesting but architecturally complex structure and from this complexity has emerged a lot of controversy. The HVMB describes the heart as a unique muscular band (illustrated at Fig. 3 (a)) starting at the pulmonary artery (PA) and finishing at the Aorta (Ao). This muscle wraps the left ventricle and part of the right ventricle (right and left segments) connecting to an helicoidal structure starting at the basal ring going inside the left ventricle towards the apex and returning to connect with the Aorta (descendent and ascendent segments) wrapping with this turn the entire anatomy of the heart. As we decrease in the scale representation of the tractographic reconstruction we can observe the fiber distribution from the local details, to the global path arrangement. Thus, as we observe in the Fig. 3, dealing with the full scale representation we can compare some strategic points of the rubber silicone mould of the HVMB.

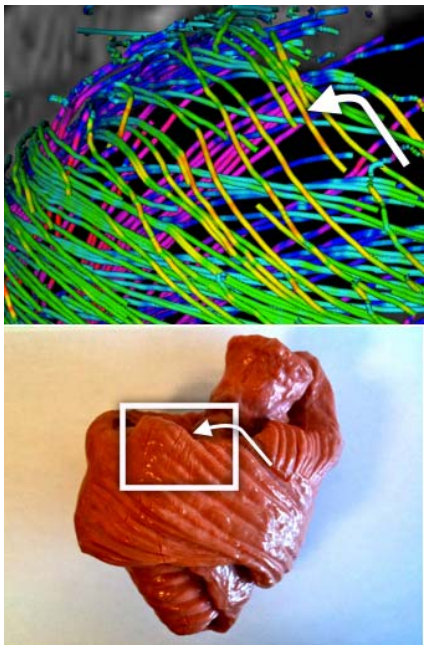
Moreover, dealing with the simplified tractography we evaluate the whole helicoidal schema proposed of the HVMB. In order to simplify the backbone myocardial fiber spatial orientation, we have explored the geometry of the heart by looking for long paths of the simplified model that can represent connected regions on the DT-MRI tractography. By manually picking seeds at the bassal level we have obtained continuous paths connecting both ventricles and wrapping the whole myocardium. Figure 4 shows four tracts of simplified models reconstructed from manually picked seeds located at basal level near the pulmonary artery. We have compared such tracts to the proposed HVMB (Fig. 5). There is a clear similarity between the theoretic model (Fig. 5, left) and reconstructed paths (Fig. 5, right). In both models the main segments (labeled from A to G) of the helical architecture are clearly identified.

4. CONCLUSION

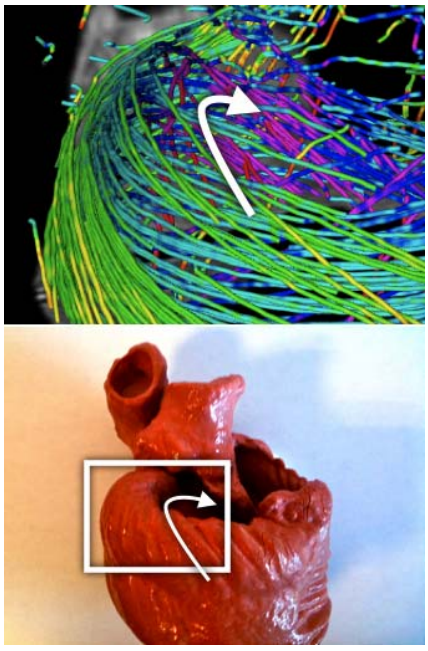
This project addresses the development of an integrative model of the functionality and muscular anatomy of the myocardium. The study merges the 3D motion (functionality) with the spatial disposition of the muscular band (anatomy)



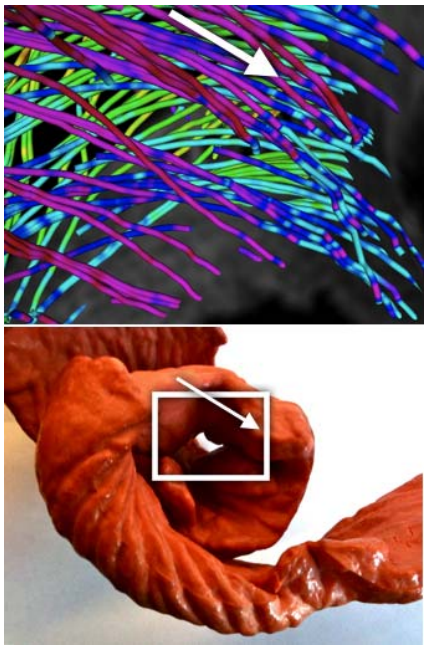
(a) Scheme of the wrapping on the HVMB theory



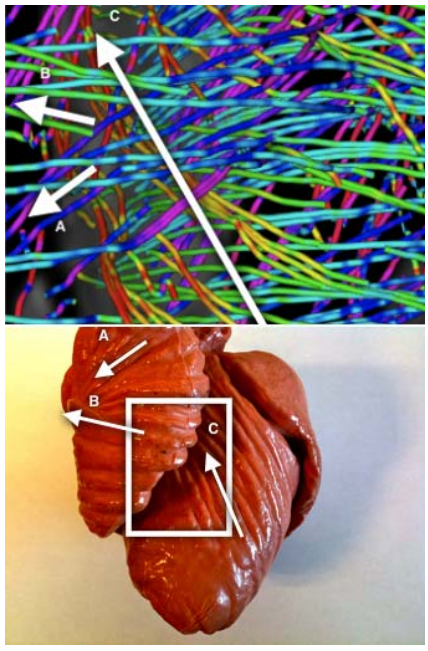
(b) Right Segment



(c) Left Segment



(d) Descendent Segment



(e) Ascendent Segment

Figure 3: Evidence of the HVMB according to fiber reconstruction

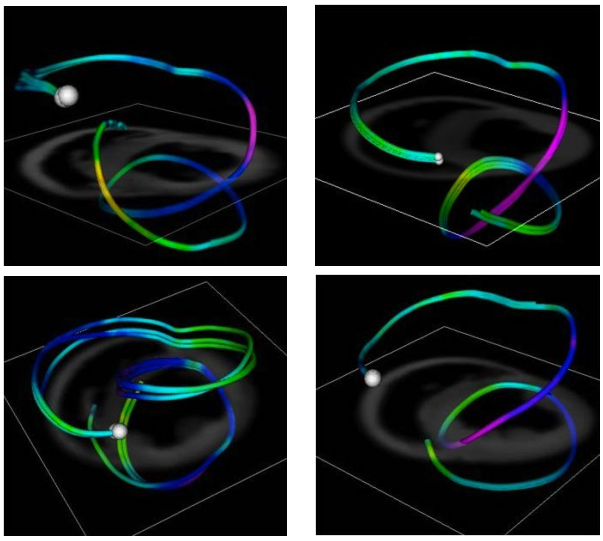


Figure 4: Example of tracts reconstructed with manually picked seeds (always chosen near the pulmonary artery) on simplified tractographies.

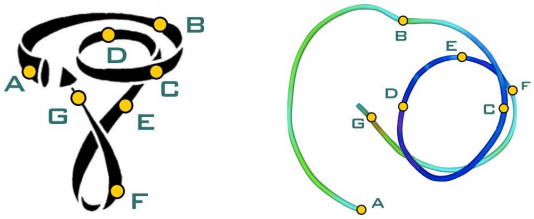


Figure 5: Torrent-Guasp's HVMB model compared to a tract reconstructed from a single manually picked seed on the DT-MRI volume with reference landmarks.

to allow the estimation of the electromechanical sequence of the heart. It is expected that information provided by the image analysis tools provides a computer model that fits the real mechanics of the myocardium. This challenging project seeks to create a high-end cardiac simulation tool with the potential to reproduce the heart behaviour with unprecedented accuracy and efficiency. This knowledge should become the seed of a new generation of medical supplementary tools for diagnosis of cardiac illnesses and a virtual scenario for developing surgical and resynchronization therapy techniques. Most of the existing models only consider the left ventricle (elliptic-like) external geometry. Our proposal takes into account the whole myocardium and presents a strategy to reconstruct the fiber architecture. We have used a multiscale analysis that shows evidences of the theory proposed by Dr. Torrent Guasp: the Helical Ventricular Myocardial Band.

5. ACKNOWLEDGMENT

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