Multiscale Tractography for Representing Heart Muscular Architecture

Ferran Poveda[1], Debora Gil[2], Albert Andaluz[2], and Enric Marti[1]

[1] Computer Science Department - Autonomous University of Barcelona, Spain
{ferran.poveda,enric.marti}@uab.es
[2] Computer Vision Center,Autonomous University of Barcelona, Spain
{debora,aandaluz}@cvc.uab.es

Abstract. Deep understanding of myocardial structure of the heart would unravel crucial knowledge for clinical and medical procedures. Although the muscular architecture of the heart has been debated by countless researchers, the controversy is still alive. Diffusion Tensor MRI, DT-MRI, is a unique imaging technique for computational validation of the muscular structure of the heart. By the complex arrangement of myocites, existing techniques can not provide comprehensive descriptions of the global muscular architecture.
In this paper we introduce 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 indicate a global helical organization.

Keywords: Streamlining, multiscale tractography, cardiac fiber architecture, DT-MRI.

1 Introduction

Myocardial fiber architecture plays a critical role in many functional aspects of the heart such as electrical propagation [1,2] or force production [3]. However, the exact distribution of the myocardial fibers and their spatial arrangement that constitutes the gross (left and right ventricles) myocardial structure is nowadays still controversial.

Researchers have proposed several conceptual models for an accurate description of the heart's architecture, either from the dissection or the histology point of view. Opposition to these theories comes from the reproducibility of the dissection process required to deduce the models. Some studies [4,5] argue the surgeon performing the dissections would introduce a bias in the final geometric interpretation.

During the last decade, Diffusion Tensor MRI (DT-MRI) has been established as a reference imaging modality for the rapid measurement of the whole cardiac architecture at the cost of a relative small but acceptable resolution. This technique provides a discrete measurement of the 3D arrangement of myocites [6] by observing local anisotropic diffusion of water molecules [7]. Usually, DT-MRI data provides a volume of three-dimensional tensors. The most significant component of these tensors (*primary eigenvector*) represents the orientation of myocites on a given voxel. Despite having this detailed information, interpreting DT-MRI outcome for heart architecture validation is not direct. Most of the existing techniques are based on fiber *tractography*, which usually reconstructs fibers with streamlines [8]. Although *tractography* has been successfully used for fiber visualization [9,10,11,12,13], most of the existing approaches do not provide enough evidence for either supporting or invalidating any particular architectural model.

To achieve an objective and descriptive myocardial architecture, one must consider several issues. First, the tractography should include the whole myocardium anatomy. Defining the basal ring, for instance, is crucial for fully understanding heart anatomy. However, in many works [10,13,14] the myocardial volume is cut just below the mitral valve, to remove the auricular cavities, which thin structures might disturb the performance of tractography methods. Since such cut discards the basal ring, reconstructions might be incomplete for a global interpretation of the cardiac architecture. Second, tractography is a technique inherited from the study of fluids. In this field, orientation of vector fields stands for fluid stream directions and, thus, reconstructions present no ambiguity. However, in anatomical structures, DT-MRI vector fields have an orientation that does not correspond to any physiological property. For a successful tractography reconstruction, DTI vector fields should be reoriented. The few existing approaches are based on either local properties of the flux or parametric models of the heart. By their local nature, local approaches [13] might introduce suboptimal fibers not consistent with the global structure. Meanwhile, by their complexity, parametric models of the ventricles [11] are usually restricted to the left ventricle. Finally, fully detailed tractographic reconstructions are valid for low-level descriptions, but might fail on a higher level of analysis because of their complexity. In order to extract more comprehensive descriptions of global myocardial structure, algorithms should provide simplified representations.

In this work we introduce a tractography-based strategy for comprehensive description of the myocardial fiber architecture. In this way, we incorporate gross anatomical knowledge to streamline techniques as well as auricular noise reduction, based on numerical integration error estimation. Our study on healthy *ex-vivo* canine heart DT-MRI datasets shows evidence of a global helical structure which might conform to one of the existing conceptual models.

2 Multi-resolution Tractography Consistent with Heart Anatomy

Heart tractography [10] is a reconstruction of cardiac muscular fibers composed by several *streamlines* (or *fiber tracks*) associated to DTI primary eigenvector. A streamline is a curve tangential to the vector field at any point of such curve. Therefore, if we parametrize the initial 3D streamline trajectory in time t as

$$\gamma(t) = (x(t), y(t), z(t)) \tag{1}$$

and we define the the primary DTI eigenvector as:

$$\overrightarrow{\mathbf{V}} = (u(x, y, z), v(x, y, z), w(x, y, z)) \tag{2}$$

then, the streamline is given by the cross product of the curve's (1) first derivative and the primary eigenvector (2) :

$$\frac{d\overrightarrow{\gamma}(t)}{dt} \times \overrightarrow{\mathbf{V}}(\gamma(t)) = 0 \ . \tag{3}$$

However, it is not feasible to solve (3) analytically. For this reason, we have chosen to reconstruct fibers using a fifth order Runge-Kutta-Fehlbert [15] integration method with adaptive integration steps based on an estimation of the integration error.

This method solves the following differential equation:

$$\frac{d\gamma(t)}{dt} = \overrightarrow{\mathbf{V}}(\gamma(t)) \tag{4}$$

where the initial point (*seed*) of the streamline is defined by:

$$\gamma(0) = (x_0, y_0, z_0) \ . \tag{5}$$

Objective interpretations of the myocardial architecture from fiber tractography require addressing three main issues:

- **Data completeness:** noise on the streamline reconstruction is mainly caused by thin auricular tissue which introduces significant clutter on the visualization. To minimize such artefact, our streamlining method stops integration of streams with large Runge-Kutta estimated reconstruction error.
- **DT-MRI Vector field orientation:** we apply a geometric reorientation of the vector field using local coordinates coherent to heart anatomy and fluid mechanics. We describe heart anatomy by a longitudinal axis and angular coordinates with respect this axis on axial cuts. To properly reorient both ventricles, we set our longitudinal axis across the left ventricle, near the septum, ensuring that it never crosses any myocardial wall. Furthermore, to validate the vector field for streamlining, this axis should define for each axial cut a center of rotation. Therefore, at every axial cut of the DT-MRI

we reorganize vector orientations on a *stream-like* fashion around the point O, that is, the intersection between the axis and the current axial cut

$$O = (o_1, o_2, o_3) \ . \tag{6}$$

Finally, given a point in space:

$$P = (x, y, z) \tag{7}$$

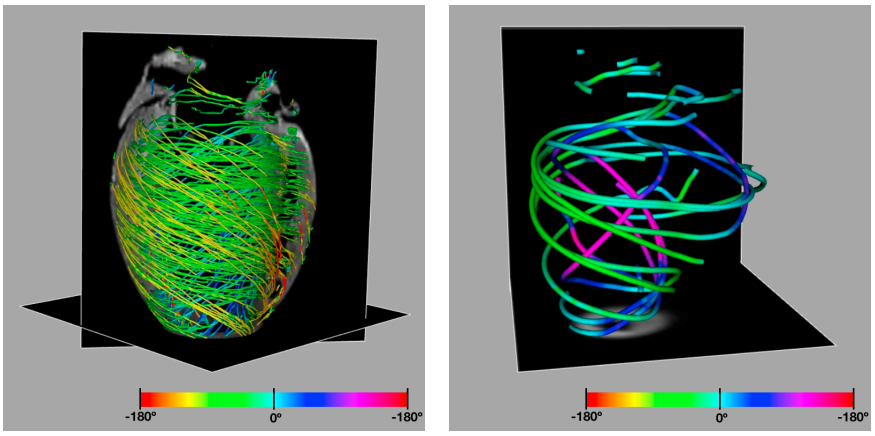
and the position vector defined by O and P :

$$\overrightarrow{OP} = P - O = (x - o_1, y - o_2, z - o_3) \tag{8}$$

every vector is reoriented according to the sign of the cross product between DT-MRI (2) and its position vector (8):

$$\overrightarrow{\mathbf{V}}(P) \rightarrow sign(\overrightarrow{\mathbf{V}}(P) \times \overrightarrow{OP})\overrightarrow{\mathbf{V}}(P) \ . \tag{9}$$

– **Visualization:** comprehensive visualization of fiber tracts should involve proper assignment of colors providing information about myocardial fiber orientation. Often, colormap definitions use global coordinates, which might mislead the global structure. To properly encode the anatomical structure, we should consider colormaps based on local information. We use the fiber angulation with respect the longitudinal axis, since the longitudinal angulation suggests more valuable information about muscular layers.



(a) full (b) simplified

Fig. 1. Multiresolution tractography: full scale tractography (a) and simplified tractography (b)

2.1 Multi-resolution Tractography

Fully detailed tractography representation has been the leading modality to comprehend the heart. On this task, tractographic models have achieved interesting results but have also shown weakness not helping to clarify a widely accepted unique theory describing the global architecture of the heart.

In real life, when an observer tries to make a gross analysis he can step away a few meters from the object of analysis and get a more contextual view. Computationally, this translates into a multiresolution approach. Multiresolution techniques build models of the same data at different levels of detail while remaining accurate to the source. A common approach for multiresolution decomposition is *mip mapping* [16] based on a *pyramid representation* [17]. This technique applies a gaussian filtering and later an exponential reduction via a subsampling of the full-scale data volume. Reduced data volumes summarize the original information and represent it at different levels of detail. The reductions are statistically complete in such a way the gaussian smoothing keeps the information before applying downsampling.

Figure 1(a) shows the longitudinal color map on a full-scale reconstruction of fibers. Longitudinal angles are encoded following the code of the bottom colorbar. By downscaling two orders of magnitude the original sets and applying our streamlining, we get the simplified tractography shown in Fig. 1(b).

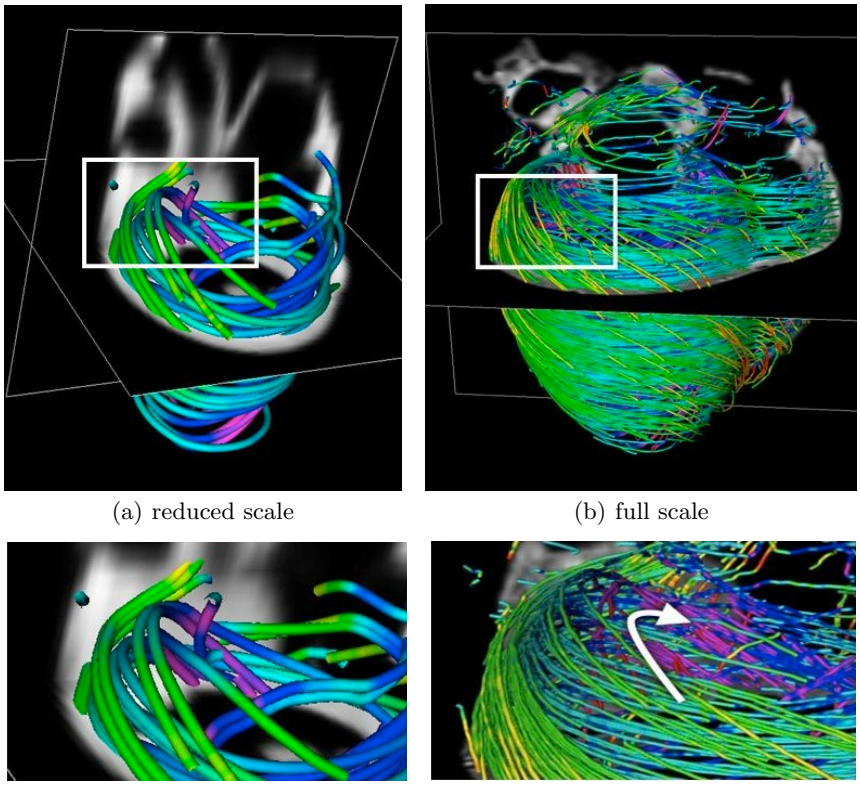
3 Results

The goal of our experiments is to show the usefulness of our multi-resolution tractography to identify myocardial muscular architecture. For this purpose, we have applied our methodology to seven *ex-vivo* healthy canine studies from the Johns Hopkins University (JHU) public database [18,19].

JHU acquired each canine heart with a 4-element knee phased array coil on a 1.5 T General Electrics MRI Scanner. An enhanced gradient system with 40 mT/m maximum gradient amplitude and a 150 T/m/s slew rate was used. Image sizes ranged between 256 x 256 x 108 and 256 x 256 x 130 voxels. Image resolution was fixed at 312.5 x 312.5 x 800 μm. Finally, 16 diffusion gradients were arranged in a non-collinear fashion, with a maximum b-value of 1,500 s/mm^2.

Full scale tractographies have been build with 250 seeds randomly chosen over the entire anatomy. This amount assure complete visual reconstructions of the heart anatomy. In order to get a coherent number of streams between resolution levels, seeds in lower levels have been selected by scaling the positions at full resolution to the downscaling magnitude.

Figure 2 shows our multiscale tractographic reconstruction of muscular fibers, full-scale in fig. 2 (a) and simplified model in fig. 2 (b). For each resolution we also show a close-up (indicated by white rectangles in full-size images) of the basal level in bottom images. The full-scale model restores the complete myocardium including tracts wrapping at the basal ring towards the endocardium and connecting the left and right ventricles at the basal level. The simplified model keeps



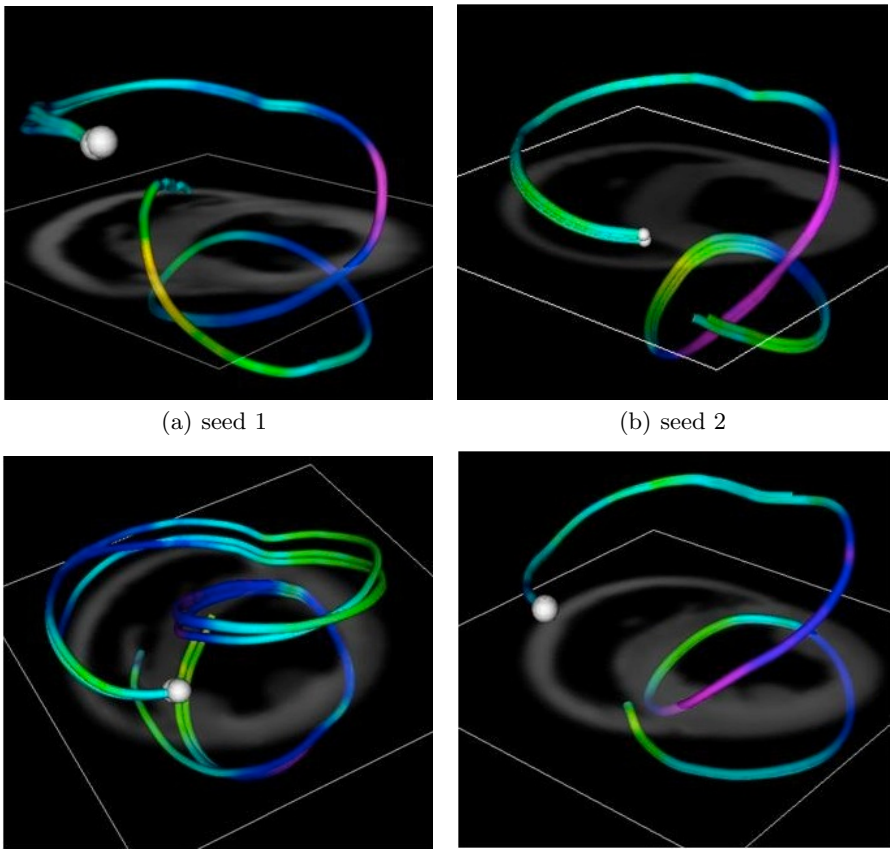
(a) reduced scale (b) full scale

(c) reduced close up (d) detailed close up

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

the main geometric features of fibers (see basal loop close-up) allowing an easier identification of global tendencies.

To obtain a representation of the heart principal architecture, we have considered the longest paths from our simplified models. Figure 3 shows four tracts of simplified models restored from manually picked seeds found at basal level near the pulmonary artery. We note that the tracts define a sample-wide coherent helical arrangement for all canine samples. Helical disposition has been reported in recent tractography studies [20] and reviews of several techniques [21,22]. Helical arrangement of myocites has also been historically reported by some medical studies [23,24] and might agree with the Torrent-Guasp's conceptual model of the existence of a unique muscular band wrapping the whole myocardium [25].



(a) seed 1 (b) seed 2

(c) seed 3 (d) seed 4

Fig. 3. Example of tracts reconstructed with manually picked seeds, always chosen near the pulmonary artery, on simplified tractographies.

4 Conclusions and Future Work

Heart tractography from DT-MRI studies is the preferred objective approach for exploring the cardiac muscular architecture. However, existing reconstructions yield incomplete models too complex for identifying any global architecture.

This work contributes to heart tractography in two key aspects. First, we have adapted streamlining techniques to the particularities of the DT-MRI vector fields in the specific context of cardiac imaging for robust reconstruction of complex structures such as the basal loop. Second, we have introduced a multiresolution tractography technique for achieving simplified DT-MRI representations consistent with global features of the heart structure.

The reconstructions on healthy hearts recovers the whole myocardial anatomy and points out a muscular tissue connectivity describing an helicoid. Such helical

structure has been described in several works and might support Torrent-Guasp's conceptual model.

In addition to this theoretical application, this multi resolution approach may allow future systematic clinical applications where other researchers are also working to obtain interactive performances [26].

Moreover, there is still room for improvements. Although the impact of auricular noise has been reduced, reconstructions still restore some disconnected tracts at the auricular level. We are currently developing a quality metric for discarding non robust tracts.

We are also aware that experts may demand further evidence of the repeatability of Dr. Torrent-Guasp conceptual model. For this purpose, we are focusing on obtaining statistical results about the variability of the helical structure. This way, we will work on the validation of variability of this apparent helical structure. As a proof of concept, we have already worked with isolated samples. In the next stage we plan to add existing cardiac atlases which give an statistical grounding [27,28] as well as applying these methods to other varied samples. Finally, we are also working on further study of the architecture which may hide some other interesting properties than the global coherence supporting Torrent-Guasp's theory.

Acknowledgments

This work was supported by the Spanish projects PI071188, TIN2009-13618 and CONSOLIDER-INGENIO 2010 (CSD2007-00018). The 2nd author has been supported by The Ramon y Cajal Program. We also want to thank Drs. Patrick A. Helm and Raimond L. Winslow at the Center for Cardiovascular Bioinformatics and Modeling and Dr. Elliot McVeigh at the National Institute of Health for provision of data.

References

1. Roberts, D., Hersh, L., Scher, A.: Influence of cardiac fiber orientation on wavefront voltage, conduction velocity, and tissue resistivity in the dog. Circ. Res. **44** (1979) 701–712
2. Taccardi, B., E. Macchi, R.L., Ershler, P.: Effect of myocardial fiber direction on epicardial potentials. Circulation **90** (1994) 3076–3090
3. LeGrice, I., Takayama, Y., Covell, J.: Transverse shear along myocardial cleavage planes provides a mechanism for normal systolic wall thickening. Circ. **77** (1995) 182–193
4. Lev, M., Simkins, C.: Architecture of the human ventricular myocardium; technic for study using a modification of the mall-maccallum method. Laboratory investigation **5**(5) (1956) 396–409
5. Grant, R.P.: Notes on the muscular architecture of the left ventricle. Circulation **32** (Aug 1965) 301–8
6. Scollan, D.F., Holmes, A., Winslow, R., Forder, J.: Histological validation of myocardial microstructure obtained from diffusion tensor magnetic resonance imaging. Am J Physiol **275**(6 Pt 2) (Dec 1998) H2308–18

7. Moseley, M.E., Cohen, Y., Kucharczyk, J., Mintorovitch, J., Asgari, H.S., Wendland, M.F., Tsuruda, J., Norman, D.: Diffusion-weighted mr imaging of anisotropic water diffusion in cat central nervous system. Radiology **176**(2) (Aug 1990) 439–45
8. Granger, R.A.: Fluid mechanics. Courier Dover Publications (Jan 1995)
9. Basser, P., Pajevic, S., Pierpaoli, C., Duda, J.: In vivo fiber tractography using dt-mri data. Magnetic Resonance in Medicine **44**(4) (Oct 2000) 625–632
10. Zhukov, L., Barr, A.: Heart-muscle fiber reconstruction from diffusion tensor mri. Visualization, 2003. VIS 2003. IEEE (2003) 597 – 602
11. Helm, P., Beg, M.F., Miller, M.I., Winslow, R.L.: Measuring and mapping cardiac fiber and laminar architecture using diffusion tensor mr imaging. Ann N Y Acad Sci **1047** (Jun 2005) 296–307
12. Peeters, T., Vilanova, A., Strijkerst, G., ter Haar Romeny, B.: Visualization of the fibrous structure of the heart. Vision, modelling and visualization (2006) 309–316
13. Rohmer, D., Sitek, A., Gullberg, G.: Reconstruction and visualization of fiber and laminar structure in the normal human heart from ex vivo diffusion tensor magnetic resonance imaging (dtmri) data. Investigative Radiology **42**(11) (Nov 2007) 777–789
14. Frindel, C., Schaerer, J., Gueth, P., Clarysse, P., Zhu, Y.M., Robini, M.: A global approach to cardiac tractography. Biomedical Imaging: From Nano to Macro, 2008. ISBI 2008. 5th IEEE International Symposium on (Apr 2008) 883 – 886
15. Fehlberg, E.: Klassische runge-kutta-formeln vierter und niedrigerer ordnung mit schrittweiten-kontrolle und ihre anwendung auf wärmeleitungsprobleme. Computing (Arch. Elektron. Rechnen) **6** (1970) 61–71
16. Williams, L.: Pyramidal parametrics. SIGGRAPH '83: Proceedings of the 10th annual conference on Computer graphics and interactive techniques **17**(3) (Jul 1983) 1–11
17. Burt, P.: Fast filter transform for image processing. Computer Graphics and Image Processing **16**(1) (May 1981) 20–51
18. Helm, P.A., Winslow, R.L.: Dtmri data archive. Available online at `http://gforge.icm.jhu.edu/gf/project/dtmri_data_sets/wiki/`.
19. Helm, P.A.: A novel technique for quantifying variability of cardiac anatomy: Application to the dyssynchronous failing heart. PhD thesis, Johns Hopkins University (2005)
20. Gao, C., Ye, W., Li, L., Zhang, T., Ren, C., Cheng, L., Yan, J.: Investigation on the structure of ventricular mass using magnetic resonance diffusion tensor imaging. The heart surgery forum **12**(2) (Apr 2009) E85–9
21. Kocica, M., Corno, A., Lackovic, V., Kanjuh, V.: The helical ventricular myocardial band of torrent-guasp. Seminars in Thoracic and Cardiovascular Surgery **10**(1) (Jan 2007) 52–60
22. Buckberg, G.D., Mahajan, A., Jung, B., Markl, M., Hennig, J., Ballester-Rodes, M.: Mri myocardial motion and fiber tracking: a confirmation of knowledge from different imaging modalities. European journal of cardio-thoracic surgery : official journal of the European Association for Cardio-thoracic Surgery **29**(1) (Apr 2006) S165–77
23. Lower, R.: Tractatus de Corde: Item de Motu Et Colore Sanguinis et chyli in eum transitu. apud Danielem Elzevirium (1669)
24. Mall, F.P.: On the muscular architecture of the ventricles of the human heart. American Journal of Anatomy **11**(3) (Jan 1911) 211–266
25. Torrent-Guasp, F.: El ciclo cardiaco: Consideraciones críticas sobre la interpretación clásica y nuevas ideas sobre el mismo. Diana, Madrid (1954)

26. Peeters, T., Vilanova, A., ter Haar Romeny, B.M.: Interactive fibre structure visualization of the heart. Computer Graphics Forum **28**(8) (2009) 2140–2150
27. Peyrat, J.M., Sermesant, M., Pennec, X., Delingette, H., Xu, C., McVeigh, E., Ayache, N.: Towards a statistical atlas of cardiac fiber structure. Medical Image Computing and Computer-Assisted Intervention **9**(1) (Jan 2006) 297–304
28. Peyrat, J.M., Sermesant, M., Pennec, X., Delingette, H., Xu, C., McVeigh, E., Ayache, N.: A computational framework for the statistical analysis of cardiac diffusion tensors: Application to a small database of canine hearts. IEEE Transactions on Medical Imaging **26**(11) (Nov 2007) 1500