

Validation of the myocardial architecture in DT-MRI tractography

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Abstract—Deep understanding of myocardial structure may help to link form and function of the heart unraveling crucial knowledge for medical and surgical clinical procedures and studies. In this work we introduce two visualization techniques based on DT-MRI streamlining able to decipher interesting properties of the architectural organization of the heart.

I. INTRODUCTION

Almost three hundred and fifty years of a vivid scientific discussion precede us on the comprehension of the structure and function of the heart. Since the first observation of its muscular nature the many researchers in this area do not seem to have reached a clear consensus. However, many interesting theories have arisen from this discussion. Many works recognise complex structures around a helical basis as the refined concept of helicoidality of the famous work of F. Torrent-Guasp [1] which states that the heart might be constructed from a particular torsion of a unique muscular band (HVMB), giving to this structure the chance to define a logical correlation with its function. But other researchers do not even agree the helicoidality concept following L. Krehl's *triebwerkzeug* [2] which proposes that the myocytes are organised radially, changing its angulation along with myocardial depth also binding this architectural description to a functional one.

These few selected examples can draw the attention on the diversity of interpretations of all these studies. It is clear that the particular architecture of the heart, which is not well structured as the rest of the voluntary muscles, is an important problem to be able to come up with univocal evidences that can conclude complex theories as the HVMB or the *triebwerkzeug*.

II. DT-MRI AND TRACTOGRAPHY

On the last few years a new modality of magnetic resonance imaging made possible a computational validation of the muscular structure of the heart: the diffusion tensor MRI (DT-MRI). With this technique we can obtain discrete measurement of the 3D arrangement of myocytes by the observation of local anisotropic diffusion of water molecules caused by biological structures such as cell membranes. DT-MRI has also allowed to get rid of the drawbacks derived from histology and dissection in these studies being a non-destructive and repeatable procedure. Nonetheless, the interpretation of DT-MRI outcome for heart architecture validation is not direct. This is a problem inherited and shared with some neurological studies where DT-MRI is applied to comprehend the neuronal connectivity.

On both these fields computer graphics and fluid mechanics visualization techniques have helped to represent this data on a more complete way rather than the first crude data visualizations. This is the case of the *tractography* techniques used in white matter studies by Basser [3] that reconstruct 3D curves based on the integration of the vectorial field of the DT-MRI. Henceforth, tractography has become one of the key tools of the architectural study of the myocardium.

III. TOWARDS UNIVOCAL STRUCTURE COMPREHENSION

There are a lot of relevant works on the visualization of DT-MRI and heart structure study taking advantage of computational processing because this has been seen as a good proposal to build unique and questionless modelizations of the heart although this approach can also take to several sources of confusion. In order to achieve an objective and meaningful description of the myocardial structure, there are several issues that we consider that should be taken into account to improve our implementation of DT-MRI tractography reconstruction.

A. Completeness of the data

Myocardial DT-MRI volume is often cut just below the mitral valve to remove parts of the DT-MRI relative to the auricular cavities in order to reduce noise on tractography. However we include it in our work because this area is a special one to be reconstructed, looking to discard or accept some of the teoretical approaches to date as the HVMB. A wrong cut can compromise the correct representation.

B. Sense of DT-MRI Vector Fields

Tractography is a technique inherited from the study of fluids. In this field the sense of direction and orientation are both meaningful. However, DT-MRI data vectors in this particular case represent anatomical structure and the sense of direction does not correspond to an anatomical reality. Water diffusion can be found on both directions at the same time despite its directional representation on the DT-MRI volumes. In our work we handle this artifact with a simple geometric processing using a global coordinate system which can overcome the weakness of smoothing local changes on which previous works may fail [4].

C. Visualization

Comprehensive visualization of fiber tracts should improve a proper assignment of colors proving information about the

orientation of the myocardial fibers. The previous geometrical reorganization applied to the DT-MRI data also allows us to build local coordinate systems to build complete and meaningful colormaps better than those based on a global approach.

D. Multiscale analysis

To skip details and obtain a more comprehensive description of the global myocardial architecture, we have to see the big picture. To achieve this, we have implemented a multi-resolution model using *mip mapping* [5] which can provide us with simplified and more intuitive tractographies.

IV. EXPERIMENTAL SETTINGS AND RESULTS

Datasets used in this study are from the public database of the Johns Hopkins University from canine specimens. The dataset was arranged in about $256 \times 256 \times 108$ array where each voxel consisted of 3 eigenvalues and 3 eigenvectors. Each voxel was about $312.5 \mu\text{m} \times 312.5 \mu\text{m} \times 800 \mu\text{m}$. [6]

Tractographies presented in this paper have been computed using *streamlining* technique based on the resolution of parametrized curves using a fifth order Runge-Kutta-Fehlberg [7] integration method. Minimal integration steps have been chosen accordingly to the dataset spacing in order to avoid working with linearly interpolated data. Fullscale tractography presented in this study has been build with 200 seeds randomly chosen over the entire anatomy. The strategy for the seed selection in the reconstructions of lower resolution in the scale-space have been to vary proportionally these value.

We have already presented methodology and some results of an improved tractography procedure. However, one of the main focuses of our work has been obtaining robust but also easy to analyze tractographic models. Our multi-resolution models represent as much structural information on less streamlines, avoiding unnecessary details and clutter for its gross analysis. Fig. 1b and Fig. 1a represent the same heart with the complete and simplified reconstructions and it is easy to notice that the simplified one shows a more clear structure and also more smoothed due to the effects of downsampling.

But this work goes one step further to get an even more simple model. Thereby, we have explored the visualization volume looking for long paths that can represent connected regions on the DTI tractography and has been straightforward to find many tracts able to reconstruct a continuous path along the whole myocardium (Fig. 2). The use of this visualization changes the way in which this structure can be viewed. It enables to visually compare the theoretical schemes of the HVMB with the reconstruction showing a manifest similarity between them as pictured in Fig. 2.

V. CONCLUSION

Many results on the study of the heart muscular anatomy have been considered as an artefact leading to incomplete or even erroneous conclusions. For this reason we have taken into account several weaknesses on the most successful studies of this topic to present an approach to reach fully automated tractographic reconstructions of the heart from DT-MRI.

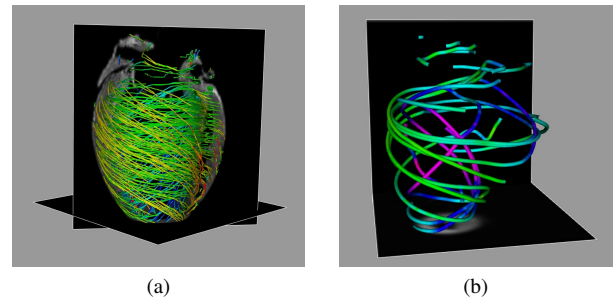


Fig. 1. (a) Full tractography reconstruction and (b) Simplified tractography represented on a full-color scheme determining orientations of the fibers

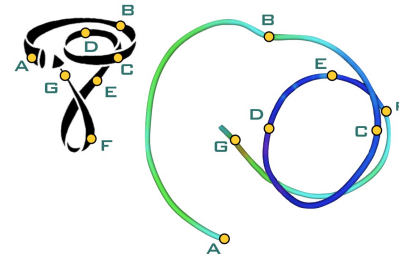


Fig. 2. Torrent-Guasp's HVMB theoretical model compared to a tract reconstructed from a single seed with landmarks for comparison

We have used all the data in DT-MRI without segmentation to avoid instrumentalization of the study, and we have demonstrated that it is possible to reconstruct some complex structures. Furthermore, we can show with our volume downsampling method unequivocal samples of the potential existence of a muscular band which forms the myocardium and supports Torrent-Guasp hypothesis. This results are shown by unique tracts that describe a clear muscular tissue connectivity along the whole myocardium.

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