IMPROVED GLOBAL CARDIAC TRACTOGRAPHY WITH SIMULATED ANNEALING

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ABSTRACT

We propose a new fibre tracking algorithm for cardiac DT-MRI that parts with the locally "greedy" paradigm intrinsic to conventional tracking algorithms. We formulate the fibre tracking problem as the global problem of computing paths in a boolean-weighted undirected graph. Each voxel is a vertex and egdes connect every pair of neighboring voxels. We solve the underlying optimization task by Metropolis type annealing.

The key features of our approach are: global optimality (unlike conventional tracking algorithms) and optimal balance between the density of fibres and the amount of available data. Besides, seed points are no longer needed; fibres are predicted in one shot for the whole DT-MRI volume without initialization artifacts.

Index Terms— Graph modeling, diffusion tensor magnetic resonance imaging (DT-MRI), fibre tracking, tractography, human heart.

1. INTRODUCTION

Inferring on cardiac muscular organization from diffusion tensor magnetic resonance imaging (DT-MRI) relies on the properties of water diffusion in the tissues. Water molecules diffuse more easily along the fibre tracts than across them, and this anisotropy is captured by the diffusion-weighted MR signal. The tractography methods use the information of directionality contained in diffusion data to infer the fibre architecture of the human heart.

Streamlining tractography methods use simple line propagation techniques, in which a single trajectory is propagated bidirectionally from a manually defined seed point. Such local approaches estimate 3D curves by integrating the eigenvector with largest eigenvalue [1] or the direction maximizing an appropriately constructed Bayesian posterior distribution [2]. More recently, probabilistic tracking algorithms have been introduced [3], [4], whereby trajectories are constructed independently by repeatedly invoking a local tracking algorithm. The direction of the line segment at each increment is determined by Monte Carlo sampling from a Bayesian posterior distribution. In the resulting set of trajectories, some correspond to real fibre bundles and others are inevitably spurious.

Streamlining and probabilistic methods are local approaches subject to the specification of a starting point for the fibre tracts. In this paper, we present a global approach to tractography based on graph modeling, where vertices are voxels of the diffusion tensor (DT) volume and edges represent the possible connection of two neighbooring voxels by a fibre bundle. Once the graph is defined, the problem is to select the edges that best correspond to the available data and remove all others by minimizing a global cost functional. Optimization is performed by simulated annealing as ICM-like algorithms do not produce satisfactory enough results and graph-cut techniques do not apply.

The main merit of our approach is that specification of seeds for initializing the tractography process is not necessary anymore. It produces in one shot estimates of the principal fibre bundles which capture the global organization of the cardiac muscle.

The paper is organized as follows. Section 2 presents our data acquisition context and formulates the essential aspects of our graph modeling approach. The experimental results on real data are exposed in Section 3. Finally, conclusions and perspectives are given in Section 4.

2. MATERIALS AND METHODS

2.1. Data acquisition

We studied a set of sixteen *ex vivo* human hearts from healthy to severely diseased. Each heart was placed in a plastic container filled with hydrophilic gel to maintain a diastolic shape. The data were acquired with a Siemens Avanto 1.5T MR Scanner. Diffusion images were obtained using an echo planar imaging (EPI) pulse sequence with the following parameters : 128×128 matrix, $2 \times 2 \times 2\,\mathrm{mm}^3$ resolution and 52 axial contiguous slices. The DT-MRI acquisition protocol is generally defined by the number N_d of diffusion sensitizing directions and the number N_e of excitations used for signal averaging: (N_d,N_e). In this work, (N_d,N_e) = $(12, 4)$ was selected among other combinations in agreement with the comparison of the quality of acquisition protocols conducted in [5]. The acquisition time for a 3-D dataset was $7'37''$.

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2.2. Graph model

We represent a diffusion tensor volume as a boolean-weighted undirected graph. Vertices are voxels of the diffusion tensor volume and edges connect every pair of neighboring voxels (26 connectivity). Let V be the set of vertices of the graph and $E(v)$ be the set of edges adjacent to vertex v. As depicted in fig. 1, our method selects the edges that best fit the available data by minimizing a cost functional describing the tractography problem in a global way. The weight of an edge e is denoted by w_e and is either 0 or 1, $w_e = 1$ meaning that e is part of a fibre.

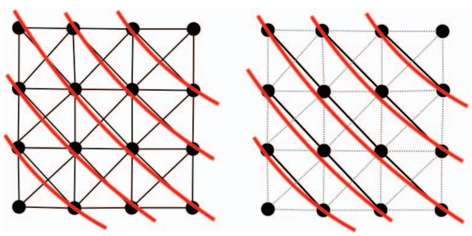

Fig. 1. **Left:** Representation of the DT volume as a boolean-weighted undirected graph. Fibers to be predicted are displayed in red. **Right:** Fiber approximation after minimization of the functional. Edges which are parts of fibres have a weight equal to 1 (plain edges) and the others have zero weight (dashed edges).

In order to select the best edges in the graph, we minimize a cost functional $J : \{0, 1\}^{|E|} \to \mathbb{R}$ whose argument is the set of weights $w = \{w_e; e \in E\}$ assigned to the edges. This functional is made of two terms: a data fidelity term and a topological criterion.

2.2.1. *Data fidelity term: Compatibility of edge and tensor*

The role of the data fidelity term is to favor edges connecting two voxels that are likely to be connected by a fibre bundle. There are two ways to define this term : edge-wise (an edge is compared to two tensors) or vertex-wise (a tensor is compared to two edges). The edge-wise model restricts fibre orientations to edges, which is unsatisfactory since fibre orientation can be arbitrary, while edge orientation possibilities are very limited. Therefore, we propose a data fidelity term based on the vertex-wise model.

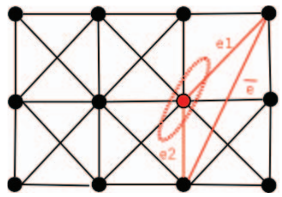

Fig. 2. Tangent-based data fidelity term

Orientation cost function. A set of two adjacent edges with common endvertex v define the tangent of a possible fibre bundle going through v. Given an edge with endvertices u and v, we denote the vectors $\overrightarrow{uv}$ and $\overrightarrow{vu}$ by $\varepsilon_u(e)$ and $\varepsilon_v(e)$, respectively. The tangent can be compared to the associated vertex tensor $\mathbf{T}_v$ using the following cost function, which favors the case where the mean orientation of the set of adjacent edges (the tangent of the fibre bundle) is aligned with the vertex tensor :

$$M(\mathbf{T}_v, e_1, e_2) = \left(1 - \frac{\|\mathbf{T}_v \bar{e}\|_2}{\|\bar{e}\|_2 \, \left\|\mathbf{T}_v\right\|_2}\right)^{\gamma} \tag{1}$$

where $\gamma > 0$, $\bar{e} = \varepsilon_v(e_1) - \varepsilon_v(e_2)$ represents the mean orientation defined by edges e_1, e_2 adjacent to vertex v (see fig. 2) and $|||.|||_2$ is the spectral norm induced by the Euclidean norm ($|||A|||_2 = \sup\limits_{x \neq 0} \frac{\|Ax\|_2}{\|x\|_2}$ which reduces to the largest eigenvalue in modulus when A is symmetric).

Data fidelity term. Using the orientation cost function, the data fidelity term F_{data} has the following form:

$$F_{\text{data}}(w) = \sum_{v \in V} F_v(w), \tag{2}$$

where $F_v(w) =$

$$\begin{cases} \dfrac{1}{\Gamma} \displaystyle\sum_{\substack{\{e_1,e_2\} \subset E(v) \,:\, e_1 \neq e_2 \\ \varepsilon_v(e_1) . \varepsilon_v(e_2) < 0}} w_{e_1} w_{e_2} M(\mathbf{T}_v, e_1, e_2) & \text{if } d(v) \geqslant 2 \\ 1 & \text{if } d(v) = 1 \\ 0.5 & \text{otherwise} \end{cases} \tag{3}$$

with $d(v) = \sum\limits_{e \in E(v)} w_e$. The normalization constant Γ corresponds to the set of true weighted edge-pairs at vertex v :

$$\Gamma = \sum_{\substack{\{e_1,e_2\} \subset E(v) \,:\, e_1 \neq e_2 \\ \varepsilon_v(e_1) . \varepsilon_v(e_2) < 0}} w_{e_1} w_{e_2}. \tag{4}$$

The constraint $\varepsilon_v(e_1) \,.\, \varepsilon_v(e_2) < 0$ in the summation is meant to enforce cardiac geometrical constraints. In the human heart, it is assumed that the centers of connected neighboring voxels are joined by fibre tracts forming circular arcs. Simple geometrical considerations can be used to discriminate arcs whose radius of curvature are not compatible with the human heart architecture. In particular, it is natural to ignore combinations of edges with an angle smaller to $\pi/2$.

2.2.2. Topological criterion

There exists many configurations in the graph that do not correspond to fibres, such as multiple branches at one vertex. Histological studies have shown that crossing does not occur in the human left ventricule [6]. It is thus necessary to add a criterion to specify that the graph is composed of lineic objects. Efficient way to introduce such prior information at a local level is to force each vertex to be connected to at most two neighbors.

We define the topological cost function to be:

$$F_{\text{topo}}(w) = \sum_{v \in V} \Phi_v(w), \tag{5}$$

where

$$\Phi_v(W) = \begin{cases} d(v) - 2 & \text{if } d(v) > 2 \\ 0 & \text{otherwise.} \end{cases} \tag{6}$$

2.2.3. Optimization by Metropolis-type annealing algorithm

The previous criteria can be gathered in a global cost functional characterizing our problem:

$$J : w \in \{0,1\}^{|E|} \mapsto F_{\text{data}}(w) + F_{\text{topo}}(w). \tag{7}$$

The minimization of (7) is a difficult optimization task we propose to solve by simulated annealing. Let C denote the configuration space $\{0,1\}^{|E|}$ and let $q = \{q(v,w) : v, w \in C\}$ be a symmetric and irreductible Markov kernel on C called the communication kernel. In most practical situations, q is defined by:

$$q(w,x) = \begin{cases} |\mathcal{N}_w(C)|^{-1} & \text{if } x \in \mathcal{N}_w(C), \\ 0 & \text{otherwise} \end{cases} \tag{8}$$

where $N_w(C)$ is the set of configurations $x \in C$ such that $|\{e \in E \,|\, x_e \neq w_e\}| = 1$ (i.e. $x = w$ except for one edge). For any $\beta \in \mathbb{R}_+^*$, define the transition probability matrix P_β on C by

$$P_\beta(w,x) =$$

$$\begin{cases} q(w,x)\exp(-\beta(J(x) - J(w))^+) & \text{if } x \neq w, \\ 1 - \sum_{z \in C \setminus \{w\}} P_\beta(w,z) & \text{otherwise,} \end{cases} \tag{9}$$

where $a^+ := \max\{a, 0\}$ and let $(\beta_n)_{n \in \mathbb{N}^*}$ be a nondecreasing positive real sequence called cooling schedule. A Metropolis-type annealing algorithm to minimize J is a discrete-time nonhomogeneous Markov chain $(X_n)_{n \in \mathbb{N}^*}$ with transitions $\mathrm{P}(X_n = x | X_{n-1} = w) = P_{\beta_n}(w,x)$, $w, x \in C$. Under our assumptions, P_β is irreductible and aperiodic. Its unique equilibrum probability measure is the Gibbs distribution π_β with the energy J at the temperature β^{-1} defined by : $\pi_\beta(w) = Z^{-1}\exp(-\beta J(w))$, $w \in C$, where Z is a normalizing constant. It is easy to check that π_β tends to the uniform distribution on the set $C_{\min}$ of global minima of J as β tends to infinity. Hence, the idea of annealing is that, for sufficiently slowly increasing cooling schedules, the law of X_n should be close to π_{β_n} and, consequently, one can expect that

$$\lim_{n \to \infty} \inf_{w \in C} \mathrm{P}(X_n \in C_{\min} | X_0 = w) = 1. \tag{10}$$

Early results (e.g. [7]) show that this desirable property holds for suitable adjusted logarithmic schedules. However, it is demonstrated in [8] that the exponential cooling schedules must be prefered as soon as one deals with a finite amount of computing time.

In our case, we use piecewise constant exponential cooling schedules of the form:

$$\beta_n = \beta_{\min} \left(\frac{\beta_{\max}}{\beta_{\min}} \right)^{\frac{1}{\nu - 1}(\lceil \frac{\nu}{N} n \rceil - 1)} \tag{11}$$

where $\beta_{\min}$ and $\beta_{\max}$ respectively denote the initial and final inverse temperature values, ν is the number of temperature steps, and N is the length of the annealing chain. The selection of $\beta_{\min}$ and $\beta_{\max}$ is performed according to the methods proposed in [9] in the context of image reconstruction. Finally, note that the optimization method is arbitrarily initialized with a fully connected graph.

3. EXPERIMENTAL RESULTS

Table 1. Mean energy per vertex (at convergence) and computation time associated with fibre tract estimations from real cardiac dataset.

method	comp. time	energy
ICM	58”	0.5952
Metropolis /10^3 iter.	1’55”	0.5114
Metropolis /10^4 iter.	19’23”	0.3960
Metropolis /10^5 iter.	194’48”	0.3662

Table 1 gives the energies associated with the ICM-like algorithm presented in [10] and the Metropolis-type annealing algorithm. Compared to ICM, the Metropolis-type annealing algorithm produces configurations with substantially lower energies and hence better approximations of the global cardiac structure according to our model. Increasing the number of iterations for the Metropolis-type annealing algorithm leads to better estimates but is more time consuming. The computation times for the different minimization methods are given in table 1 for the tractography of a whole heart ($128 \times 128 \times 52$ vertices), with an optimized implementation written in the C language, on a standard PC.

Fig. 3 displays results on human data using (A) ICM, and (B) Metropolis-type annealing (as described in section 2.1)

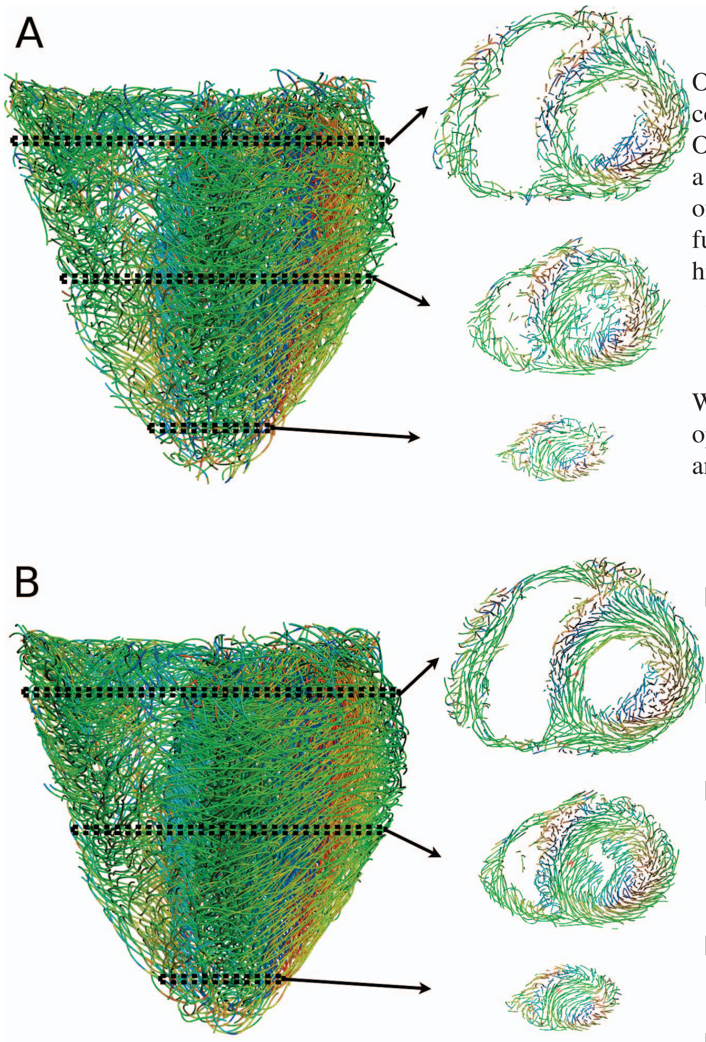

Fig. 3. Global fibre prediction detailled through the left ventricular wall (from top to bottom : top view of basal, equatorial and apical cuts), (**A**) using ICM, (**B**) using Metropolis-type annealing.

with 10^5 iterations which takes about 3 hours. They were obtained by extracting the connected components of the graph whose set of weights minimizes J. Each of these components approximates the geometry of a fibre bundle: we know the voxels through which a fibre runs, but we don't know exactly where in each voxel. Since cardiac fibres should be reasonably smooth, we constrained the geometry with smoothing B-Splines. Results associated with Metropolis-type annealing show better agreement between predicted fibres and histological knowledge about the structure of the human myocardium than ICM-like algorithm.

4. CONCLUSIONS AND PERSPECTIVES

Our graph model together with Metropolis-type relaxation constitutes a novel and effective approach to tractography. Our experiments show that it is particularly interesting for a better understanding of the architecture and organization of the cardiac muscle continuum. Future work will include further validation against other imaging techniques and/or histological cuts.

5. ACKNOWLEDGEMENTS

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