Journal of Neuroscience Methods 184 (2009) 375–379

Contents lists available at ScienceDirect

Journal of Neuroscience Methods

journal homepage: www.elsevier.com/locate/jneumeth

Short communication

Genetic white matter fiber tractography with global optimization

Xi Wu[a,b,c], Qing Xu[c,d], Lei Xu[c,e], Jiliu Zhou[a], Adam W. Anderson[c,f], Zhaohua Ding[c,d,f,g,*]

[a] College of Electronics and Information Engineering, Sichuan University, PR China
[b] Department of Electronic Engineering, Chengdu University of Information Technology, PR China
[c] Vanderbilt University Institute of Imaging Science, Vanderbilt University, USA
[d] Department of Electrical Engineering and Computer Science, Vanderbilt University, USA
[e] Department of Biostatistics, Vanderbilt University, USA
[f] Department of Biomedical Engineering, Vanderbilt University, USA
[g] Chemical and Physical Biology Program, Vanderbilt University, USA

ARTICLE INFO

Article history:
Received 27 May 2009
Received in revised form 30 July 2009
Accepted 30 July 2009

Keywords:
Diffusion tensor imaging
Fiber tracking
Genetic algorithm
Global optimization

ABSTRACT

Diffusion tensor imaging (DTI) tractography is a novel technique that can delineate the trajectories between cortical region of the human brain non-invasively. In this paper, a novel DTI based white matter fiber tractography using genetic algorithm is presented. Adapting the concepts from evolutionary biology which include selection, recombination and mutation, globally optimized fiber pathways are generated iteratively. Global optimality of the fiber tracts is evaluated using Bayes decision rule, which simultaneously considers both the fiber geometric smoothness and consistency with the tensor field. This global optimality assigns the tracking fibers great immunity to random image noise and other local image artifacts, thus avoiding the detrimental effects of cumulative noise on fiber tracking. Experiments with synthetic and in vivo human DTI data have demonstrated the feasibility and robustness of this new fiber tracking technique, and an improved performance over commonly used probabilistic fiber tracking.

1. Introduction

Diffusion tensor imaging (DTI) has become a primary tool for non-invasive exploration of the structure of living tissue in vivo (Basser et al., 1994). Since its first introduction a decade ago, this new imaging modality has been widely used to reconstruct neuronal fiber pathways in the human brain (Mori and van Zijl, 2002). To date a variety of tracking algorithms have been proposed to infer fiber connections in the human brain (Lu et al., 2006; Friman et al., 2006; Zhang et al., 2009), the basic principle of which is sequentially integrating local fiber directions from pre-defined seed point(s) to generate fiber connection pathways. Typically, these tracking algorithms "grow" fiber pathways by piecing a line segment to the end of the preceding segment. These methods can be broadly divided into two categories: deterministic fiber tractography (Lu et al., 2006) and probabilistic fiber tractography (Friman et al., 2006).

A common drawback of the above streamline-like tracking methods, either deterministic or probabilistic, is cumulative errors arising from random image noise and/or partial volume averaging (PVA) along the tracking path (Alexander et al., 2001; Anderson, 2001), even with certain regularizations on the basis of geometric or other constraints. Furthermore, as the direction information that stream-like tracking methods rely on is only derived locally, the tracking results from these methods are not a globally optimized solution.

In this work, a novel fiber tracking technique based on well established genetic algorithms was proposed. The proposed technique allows globally optimized solutions to the fiber pathways to be obtained, and hence possesses superb immunity to local imaging artifacts. Additionally, the proposed technique provides optimal solutions for fiber connection pathways between two designated ROIs; this offers a great potential of applying it to studies of structure–function relations in the human brain, in which the structural connectivity between two functionally related regions is often sought.

2. Method

A common practice of fiber tracking is to track fiber pathways that connect to certain ROIs, among which a most useful application is to find connecting pathways between an ROI pair. Fiber tracking between a pair of ROIs can be cast as a path finding problem to which an optimal solution is found by genetic algorithm (GA). In this context, the goal is to evolve from initial solutions to produce a set of fibers with best fitness to the given data, which is presumably an optimal solution to the fiber path. Details of the implementation

* Corresponding author at: Vanderbilt University Institute of Imaging Science, 1161 21st Avenue South, MCN AA-1105, Nashville, TN 37232-2310, USA. Tel.: +1 615 322 7889; fax: +1 615 322 0734.
E-mail address: zhaohua.ding@vanderbilt.edu (Z. Ding).

0165-0270/$ – see front matter © 2009 Elsevier B.V. All rights reserved.
doi:10.1016/j.jneumeth.2009.07.032

procedure for one iteration of the genetic tracking algorithm, called GeneTrack henceforth, are given below.

2.1. Initialization

In a typical GA, solutions are encoded as strings of binary bits, which are analogous to chromosomes in biology. Binary strings can be extended to continuous strings, which are chosen as initial solutions in our design. More specifically, we represent an arbitrary fiber pathway between a pair of ROIs with a space curve (f), and express the curve f as Fourier series (of continuous values) in Cartesian system, i.e.

$$f^d(t) = \sum_{n=1}^{N} \left[a_n^d \cos(nt) + b_n^d \sin(nt) \right], \quad (1)$$

where superscript d denotes the x, y, or z direction in the Cartesian system, n is the order of Fourier series, t is the number of points in curve f, the a_n and b_n are coefficients of the cosine and sine components respectively, and N is the maximum order of Fourier series for approximation with reasonable accuracy ($t = 50$ and $N = 10$ in this work). According to the equation above, every fiber curve can be represented by $2N$ Fourier coefficients in each direction, which consists of N coefficients for both a_n and b_n. The $6N$ coefficients in all three directions, which correspond to the genes of the chromosomes, encode the solutions for the fiber pathways between an ROI pair and will be used for recombination and mutation to produce offspring in later steps.

2.2. Selection

In designing objective functions for selecting best fit solutions among the candidates, two primary considerations are taken into account. First, the solutions should possess best geometric smoothness along the entire fiber path. Second, the solutions should be those best fit the diffusion tensor field among all candidates. Simultaneously considerations of these (with certain trade-off) may yield solutions that are globally optimal in the sense that the curves are both smooth and reasonably fit the data.

Globally optimal solutions may be obtained by using the classical Bayesian theory (Duda and Hart, 1973). Let $\mathbf{T}$ denote the diffusion tensor field and C denote spatial curves that cover all possible fiber pathways connecting the designated ROI pair. According to the Bayes decision rule, the optimal solution C_{opt} is the one with maximum *a posteriori* (MAP) probability $p(C|\mathbf{T})$:

$$p(C|\mathbf{T}) = \frac{p(C)p(\mathbf{T}|C)}{p(\mathbf{T})}. \quad (2)$$

Since $p(\mathbf{T})$ is independent of C, maximizing $p(C|\mathbf{T})$ reduces to maximizing the product of $p(C)$ and $p(\mathbf{T}|C)$. The term $p(C)$ is a prior probability of curve C, which is the probability of the existence of curve C without any measurement data; the term $p(\mathbf{T}|C)$ is a conditional probability, which defines the probability of the existence of tensor field $\mathbf{T}$ given curve C.

To find the MAP solution, $p(C)$ and $p(\mathbf{T}|C)$ need to be modeled. In our design, these probabilities are modeled so that constraints on curve smoothness and consistency with tensor field are imposed. First, let us assume the tensor field to be a Markovian random field (MRF), and v_t be a unit vector representing the local tangential direction at the tth point of the curve. According to the MRF theory, v_t is a random realization of the vector field in the neighborhood of t, which observes a Gibbs distribution (Geman and Geman, 1984):

$$p(C) = \frac{1}{Z_1} \prod_t e^{-p(v_t)} = \frac{1}{Z_1} e^{-\sum_t p(v_t)} \quad (3)$$

where Z_1 is a normalization constant. When only the preceding point along the curve is considered, a simple definition of $P(v_t)$ is

$$p(v_t) = \arccos(v_t \cdot v_{t-1}) \quad (4)$$

This definition of the prior probability gives preference to the curves with low curvature, thus imposing a smoothness constraint to the fiber.

Second, assuming that the tensor measurement in voxel t depends only on the local fascicle direction v_t, the conditional probability $p(\mathbf{T}|C)$ can be rewritten as a second Gibbs distribution below:

$$p(\mathbf{T}|C) = \frac{1}{Z_2} \prod_t e^{-p(T_t|v_t)} = \frac{1}{Z_2} e^{-\sum_t p(T_t|v_t)}, \quad (5)$$

where Z_2 is a normalizing constant.

In order for the probability $p(\mathbf{T}_t|v_t)$ to decrease with the discrepancy between the local fiber direction v_t and the major eigenvector of the local diffusion tensor e_t, we propose the following conditional probability model:

$$p(\mathbf{T}_t|v_t) = \arccos(v_t \cdot e_t) \quad (6)$$

Combining all the previous models (Eqs. (3) and (5)) leads to an expression for $p(C|\mathbf{T})$ which turns out to be a new Gibbs distribution:

$$p(C|T) = \frac{1}{Z_3} e^{-\sum_t p(v_t) + \alpha p(T_t|v_t)} \quad (7)$$

where $Z_3 = Z_1 \times Z_2$.

With this new Gibbs distribution, an optimal solution can be reached by minimizing the following cost function:

$$f_{\text{cost}} = \sum_t p(v_t) + \alpha \sum_t p(\mathbf{T}_t|v_t). \quad (8)$$

The first term in the above cost function imposes a smoothness constraint on the fiber pathway, and the second term encourages a consistency between the fiber and tensor dominant directions. The relative weights of these two terms are determined by the parameter α, which regulates the trade-off between the smoothness of the fiber and consistency with the data. In this work, the range of α is chosen to be between 0 and 10.

2.3. Recombination

The subset of optimal fibers selected above is recombined to form a new set of fibers. This is implemented by randomly selecting a value for each of the $6N$ coefficients in Eq. (1) from the parent fibers, so that the coefficients for each new fiber come from different parents. This new set of fibers, along with a small number of best fit parents, constitute the offspring for the next generation.

2.4. Mutation

The mutation process perturbs the coefficients of the above fibers so that each solution contains a new set of values for the coefficients. To maintain the stability of this algorithm, the amount of perturbation for each coefficient is at the order of one standard deviation of the coefficients in the existing fibers. This provides stability to the solution, and in the meantime offers an opportunity to generate new solutions that better fit the cost function.

3. Tracking experiments and results

To evaluate comprehensively the performance of the GeneTrack algorithm proposed, we have carried out a series of fiber tracking experiments on synthetic and in vivo human DTI datasets. Fiber