WHITE MATTER FIBER TRACTOGRAPHY WITH GENETIC ALGORITHM

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Introduction
Diffusion tensor imaging (DTI) based fiber tractography has become a primary tool for non-invasive exploration of white matter structures in the human brain [1]. To date a variety of fiber tracking algorithms have been proposed [2, 3], the basic principle of which is integrating local fiber directions from pre-defined seed point(s) sequentially to generate fiber connection pathways. A common drawback of the streamline-like tracking methods, either deterministic or probabilistic, is the cumulative errors arising from random image noise and/or partial volume averaging along the tracking path [4], even with certain regularizations on the basis of geometric or other constraints. In this work, a novel fiber tracking technique based on well established genetic algorithms was proposed. It allows global constraints to be elegantly imposed on the fiber pathways, and hence possesses superb immunity to local imaging artifacts. Furthermore, it provides solutions for fiber connection pathways between two designated regions of interest; 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.

Method
Genetic algorithms (GAs) are search techniques for finding exact or approximate solutions to optimization problems [5]. They are a particular class of evolutionary computation that uses concepts from evolutionary biology such as inheritance/selection, recombination, and mutation. The proposed fiber tracking technique is based on an adaptation of the GAs. Briefly, for a pair of regions of interest (ROIs), a large number of random fiber pathways that connect both ROIs are generated initially. These pathways are evaluated for fitness to the diffusion tensor field and fiber geometric constraint. They are then selected according to the fitness function, which are subsequently recombined and mutated to yield new solutions of fiber pathways for the next generation. These processes are iterated until convergence. Below is the outline of the implementation procedure for one iteration of the algorithm:

1) Initialization: Fiber pathways are space curves \( f(t) \) that can be expressed in Cartesian system as Fourier series, i.e.:

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

where \( c \) denotes the \( x, y, \) or \( z \) direction in the Cartesian system, \( n \) is the order of Fourier series, \( a_n \) 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. In this work, a total number of 2000 random curves with a maximum order of 10 are generated initially by randomly assigning values to the coefficients \( a_n \) and \( b_n \).

2) Selection: Each curve is evaluated for fitness to the solution according the cost function below:

\[
C_f = a \sum_{i} \arccos(\hat{v} \cdot \hat{e}_i) + \beta \sum_{i} \arccos(\hat{e}_i \cdot \hat{e}_j),
\]

where \( \hat{V} \) is a unit vector that denotes the tangential direction at the \( i \)th point of the curve, and \( \hat{e}_i \) is the major eigenvector of the local diffusion tensor. The first term in the above cost function imposes a smoothness constraint on the fiber pathway, and the second term encourages consistency between the fiber and tensor dominant directions; the relative weights of these two terms are regulated by the parameter \( a \) and \( \beta \) . Using this cost function, a subset of fibers are selected as parents using an importance sampling scheme that gives preferences to fibers with lower values of the cost function.

3) Reproduction: Coefficients of the parent curves selected above are randomly recombined to produce a population of new curves as offspring, which are then mutated by perturbing the values of these coefficients.

To evaluate comprehensively the performance of the fiber tracking technique proposed, two synthetic datasets with increasing geometric complexity were designed. Diffusion weighting was simulated along 32 non-collinear directions with \( b \) value of 1000 \( s / \text{mm}^2 \). The diffusion parameters were similar to those in physiological conditions, and the diffusion weighted data were corrupted with zero mean Gaussian noise at a standard deviation of 0.05. In addition, three sets of in vivo DTI data were acquired from different healthy volunteers, with parameter settings the same as before [2]. Fibers were tracked between the left/right thalamus and left/right Brodmann’s area (BA) 17 in the occipital lobe, and between the left Broca’s area and the pre-motor region. These ROIs were defined using the WFU PickAtlas tool in SPM2 [6] or determined using functional MRI signals [7]. A total number of 50 iterations were performed for both the synthetic and in vivo DTI data.

Results
Figure 1a and 1b below show the tracking results for the two synthetic datasets respectively, and 1c and 1b are their corresponding cost functions. It can be seen that the curves converge to the true “fiber pathways” very well, and the cost functions decrease with the number of iterations. Figure 2a-c are tracking results for the in vivo data and 2d-f are their respective cost functions. These pathways are consistent across the three subjects, and exhibit good agreement with known neuroanatomy.

Discussion and Conclusion
The experiments demonstrate that the fiber tracking algorithm we proposed can reconstruct white matter fiber trajectories faithfully for both synthetic and in vivo DTI data, which offers a great promise for using it as a reliable tool for routine fiber tracking. Compared to existing methods, the new tracking algorithm incorporates a global constraint, thus making it insensitive to image noise and other local artifacts. In addition, it generates fiber pathways that are independent of the tracking direction – this greatly benefits subsequent quantitative characterization of structure connectivity between two regions.

References