Guided Diffusion Tensor Tractography with GTRACT: A Validation Study

Vincent A. Magnotta[1] and Peng Cheng[2]

[1] Department of Radiology, The University of Iowa, USA,
vincent-magnotta@uiowa.edu,
[2] Department of Radiology, Georgetown University, USA.

Abstract. A novel fiber tracking algorithm (GTRACT) was developed to enhance tracking through ambiguous regions where cross fibers, fiber merging or fanning may be occurring. The software was developed using several cross platform open-source toolkits (ITK, VTK, and FLTK). The algorithm was evaluated using a freely available digital phantom dataset provided by King's College London. The results show that the GTRACT algorithm performed significantly better than standard streamline approaches and is less affected by noise.

1 Introduction

Diffusion tensor imaging (DTI) is an emerging neuroimaging tool to study brain connectivity. Specifically, diffusion tensor imaging is the first noninvasive in vivo imaging tool that has the potential to generate brain connectivity trajectories by defining the course of white matter tracts. Diffusion is the result of water molecules' random thermal walk, also known as Brownian motion. In white matter fiber structures, the diffusion is restricted by the cell membrane and the axon myelin [1], thus the diffusivity of water molecules along the fiber direction is ten times larger than the perpendicular directions.

Current approaches for white matter fiber reconstruction can be divided into two types: streamline (SLT) and fast marching (FMT) algorithms. The streamline method assumes the orientation of the principal eigenvector, represents the orientation of the dominant axonal tracts. It has been verified that in regions where fiber bundle orientation is homogeneous and on the order of the voxel size or larger, the principal eigenvector direction accurately approximates the actual fiber orientation [2, 3]. A variation of SLT is the tensorline algorithm (TEND) was introduced by Lazar et al [3]. The algorithm uses the entire diffusion tensor to deflect the incoming vector. The fast marching method is a level set method where it is assumed that the front is propagating in one direction. Paker et al. proposed the Fast Marching Tractography [4]. FMT uses the orientation and shape of the diffusion tensor to define the speed of propagation. This front propagation speed is defined in such a way that the front propagates fastest when the propagating direction is co-linear with the eigenvector direction. The FMT can be used to estimate the likelihood of connectivity between any two voxels, and is capable of reconstructing branching pathways.

Currently, DTI scans are acquired at a resolution of approximately 2mm. Given that the size of neural axons is on the order of 10nm, DTI fiber tracking can only reflect the macroscopic structure of the fiber bundle, and can not be used to describe the white matter fiber at the cellular level. Due to partial volume effects, the diffusion tensor is a voxel-averaged signal. When there is non-uniform distribution of fiber structures within a voxel, such as fiber crossing, branching, and fanning, the directional information is averaged out [5]. SLT tracts tend to terminate when they encounter an ambiguous region. FMT is able to handle the fiber branching problem, but it can only find the minimal cost path between two points, which might be erroneous, especially at ambiguous regions, where the effects of noise are significant.

Noise in the acquired diffusion tensor images causes perturbations in the resulting diffusion tensor [6]. These perturbations affect both the geometry and orientation of the tensor causing the eigenvector to deviate from the true direction. This error accumulates as the tracking propagates [7–9] and is a function of the the signal-to-noise ratio (SNR), the shape of the trajectories, anisotropy, resolution and the particular interpolation method used.

Here we propose a new tracking algorithm: Guided Tensor Restored Anatomical Connectivity Tractography (GTRACT) that is aimed at solving the fiber crossing problem and quantifying connectivity between two regions with known anatomical connection.

2 Method

Based on previous work by this lab to study schizophrenia, we are interested in the connectivity between the cerebellum and thalamus. This fiber path starts from cerebellum, crosses from one hemisphere to another at the cerebellar peduncle, and tracks to the thalamus. SLT based methods we have tested have failed to track the fiber bundle connecting these two regions. This has lead to the development of a new iterative tracking algorithm, GTRACT. During the first pass of the algorithm, a graph search algorithm is used to facilitate tracking through ambiguous regions. A centerline fiber is computed from the first pass fibers and used to guide the tracking through ambiguous regions during a second pass of tracking.

2.1 GTRACT Algorithm

The GTRACT algorithm consists of four steps. The first step generates an initial guess for the fiber tracts. It includes a forward tracking and a backward tracking, using a partial and restricted 3D graph search algorithm. Partial means the 3D graph search is only performed in certain regions. Restricted means this algorithm uses a preset energy threshold and stopping criteria to reduce the search space, thus speeding up the algorithm tremendously. This step produces a group of energy minimized paths (3D optimal path with the maximum alignment to the tensor field) connecting two pre-defined regions, and these paths serve

as an approximation to the possible connections. This algorithm simulates the branching nature of the fiber paths and helps the fiber to propagate through ambiguous regions.

The second step of the algorithm is a merging operation that analyzes fiber bundles from forward tracking and backward tracking together, keeping only one copy of the fibers when duplicate copies exist, and discard fibers that lie far away from the main bundle. The third step creates the guide fiber. After the fibers are merged together, they are resampled into the same number of sub-divisions, and the mean position of the fiber bundle is calculated, which is similar to the center line of the fiber bundle.

The forth and final step is guided fiber tracking. This is an improved streamline tracking algorithm, which takes the mean fiber direction from step 3 as a guide to perform the fiber tracking. It incorporates the idea of the narrow band searching method, and produces smooth and accurate results.

The GTRACT software was written in C++ and was developed using several open-source cross platform toolkits: ITK, VTK and FLTK. The program has been tested under both Microsoft Windows and Linux based platforms. The software is freely available at the website http://mri.radiology.uiowa.edu.

2.2 Validation Data

Diffusion tensor phantom simulation data was obtained from the Centre for Neuroimaging Sciences, Institute of Psychiatry, King's College London (http://neurology.iop.kcl.ac.uk/dtidataset/Common_DTI_Dataset.htm). They have developed a database for simulated common fiber tract trajectories that can be used for testing, validation and comparison of various tractography algorithms. There are ten different trajectory structures in total. Datasets are provided over a range of SNR values (7, 15, and 31). The DTI data were simulated using a spin-echo sequence with the following parameters: number of encoding directions = 30 [10], b-value=1000 s/mm2, TE=90ms, NEX= 4, image resolution= 2x2x2mm.

For this study we focused on two of the datasets: linear tract and orthogonal crossing. The linear tract contains FA values along the tract that decreasing linearly from left to right, the FA value is between 0.7 and 0.15. This tract is overlaid on an isotropic, homogeneous background. T2 values for the tract and background were assumed to be the same as white matter (65 ms) and grey matter (95 ms) at 1.5T, respectively. The FA image shown here has a SNR of 31. For the crossing trajectories, two fiber bundles exist, one with a higher FA value (approximately 0.6), and one with a lower FA value (approximately 0.4). These tracts are overlaid in the same isotropic homogeneous background used for the linear trajectory.

Starting and ending regions were manually placed at the two ends of the fiber tract to be studied. The fiber structure was then extracted using a streamline algorithm [9, 11] with the following parameters: seed threshold = 0.3, tracking threshold = 0.25, step size = 1 voxel (2mm) and 0.1 voxel (0.2mm), curvature threshold = 45^o. The GTRACT algorithm was also applied, using the following

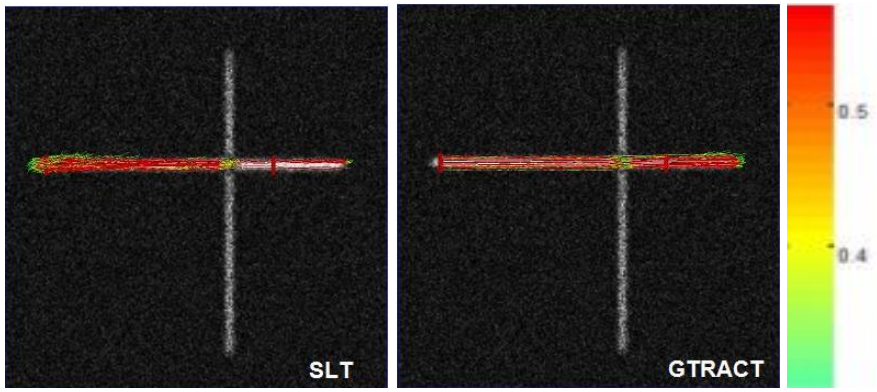

Fig. 1. Fiber tracking generated using the STL and GTRACT algorithms in the orthogonal crossing phantom.

parameters: seed threshold = 0.30, tracking threshold = 0.25, step size = 1 voxel (2mm), maximum branching points = 5, branching anisotropy threshold = 0.28, branching curvature threshold = 45^o, maximum length = various among different trajectories, guided tracking curvature threshold = 15^o. The tracking errors were accessed and compared between the methods.

3 Results

Both SLT and GTRACT methods are applied to the simulated phantom data. Compared to the SLT method, GTRACT was able to produce smoother fiber tracts and capable of handling the fiber crossing problem correctly (Figure 1).

The tracking error was accessed on two phantoms, the linear trajectory and the orthogonal crossing trajectory. The ideal tracks for these two phantoms are horizontal straight lines, one for every voxel at the far left where the FA value is greater than 0.3. The errors were averaged among the fibers. When calculating the error for the methods, only the fibers reaching the ending region were analyzed. Those terminating in the middle were not considered.

Figure 2 shows the error distance from the ideal track for both SLT and GTRACT methods for the linear trajectory under different signal-to-noise ratios (SNR = 7, 15, and 31). From the graphs, we can see that the tracking errors are nearly constant and cumulative. The slope for the error curves in the SNR=7 phantom are 0.0086 (SLT) and 0.0032 (GTRACT). In the SNR=15 phantom, the slopes were 0.0066 for SLT and 0.0046 for GTRACT. The SNR=31 phantom had equivalent slopes of 0.0046. While the tracking error for SLT is largely related to the SNR level, the GTRACT method has a smaller error and is less sensitive to the SNR. For the SNR=7 and SNR=15 phantoms, the error for the GTRACT algorithm is significantly smaller ($p < 0.01$) as compared to the both step sizes for the STL method. When the SNR=31, the error levels of two methods were not

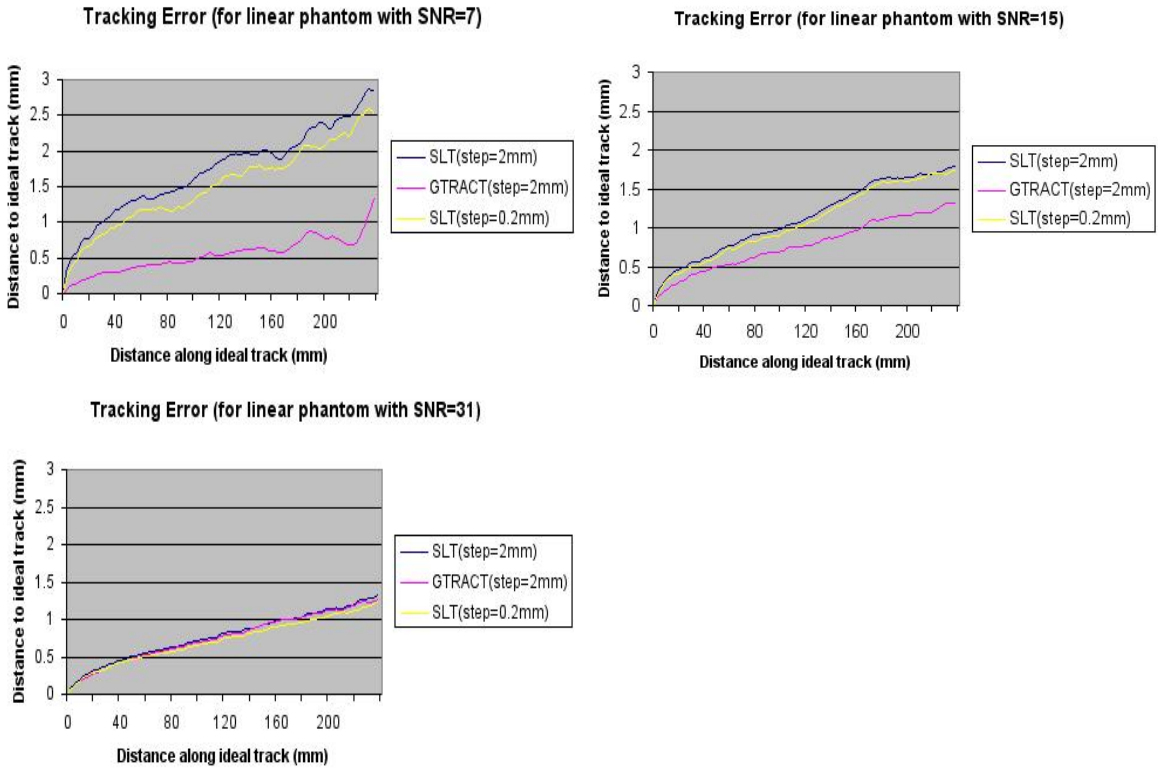

Fig. 2. Fiber tracking error for the STL and GTRACT algorithms in the linear phantom. Three different SNR values are shown: 7, 15, and 31.

different. Similar error measurements were obtained in the orthogonal crossing trajectory. The GTRACT showed significantly ($p < 0.01$) lower tracking error at SNR=7 and SNR=15. For the SNR=31, the error between the methods was similar.

4 Discussion

A novel fiber tracking algorithm GTRACT was developed and implemented using open-source tools for image processing and visualization. A validation study was conducted using freely available synthetic phantom data. Compared to the SLT method, GTRACT is able to produce smoother fiber tracts and tracking through the fiber crossing region. The tracking error was evaluated on the linear and orthogonal crossing trajectories with various SNR values, the results show that GTRACT has smaller tracking error and is insensitive to image noise.

References

1. Mori, S., van Zijl, P.: Fiber tracking: principles and strategies - a technical review. NMR Biomed **7-8** (2002) 468–480
2. Wedeen, V., Reese, T., Napadow, V., Gilbert, R.: Demonstration of primary and secondary muscle fiber architecture of the bovine tongue by diffusion tensor magnetic resonance imaging. Biophys J **80** (2001) 1024–1028
3. Lazar, M., Weinstein, D., Tsuruda, J., Hasan, K., Arfanakis, K., Meyerand, M., Badie, B., Rowley, H., Haughton, V., Field, A., Alexander, A.: White matter tractography using diffusion tensor deflection. Hum Brain Mapp **18** (2003) 306–321
4. Parker, G., Wheeler-Kingshott, C., Barker, G.: Estimating distributed anatomical connectivity using fast marching methods and diffusion tensor imaging. IEEE Trans Med Imaging **21** (2002) 505–512
5. Wiegell, M., Larsson, H., Wedeen, V.: Fiber crossing in human brain depicted with diffusion tensor mr imaging. Radiology **217** (2000) 897–903
6. Basser, P., Pajevic, S.: Statistical artifacts in diffusion tensor mri (dt-mri) caused by background noise. Magn Reson Med **44** (2000) 41–50
7. Lori, N., Akbudak, E., Shimony, J., Cull, T., Snyder, A., Guillory, R., Conturo, T.: Diffusion tensor fiber tracking of human brain connectivity: aquisition methods, reliability analysis and biological results. NMR Biomed **15** (2002) 494–515
8. Lazar, M., Alexander, A.: An error analysis of white matter tractography methods: synthetic diffusion tensor field simulations. Neuroimage **20** (2003) 1140–1153
9. Basser, P., Pajevic, S., Pierpaoli, C., Duda, J., Aldroubi, A.: In vivo fiber tractography using dt-mri data. Magn Reson Med **44** (2000) 625–632
10. Jones, D., Horsfield, M., Simmons, A.: Optimal strategies for measuring diffusion in anisotropic systems by magnetic resonance imaging. Magn Reson Med **42** (1999) 515–25
11. Parker, G., Haroon, H., Wheeler-Kingshott, C.: A framework for a streamline-based probabilistic index of connectivity (pico) using a structural interpretation of mri diffusion measurements. J Magn Reson Imaging **18** (2003) 242–254