Reconstruction of brainstem white-matter fiber systems with combinatorial tracking

S. Lifshits[1], A. Tamir[2], and Y. Assaf[1]

[1]Neurobiochemistry, Life Science Faculty, Tel-Aviv University, Tel-Aviv, Israel, [2]Statistics and Operations Reseach, Faculty of Exact Science, Tel-Aviv University

Introduction

DTI based Tractography is becoming increasingly popular for delineating white matter trajectories of the human brain [1,2]. Although DTI suffers from intrinsic limitations (e.g. partial volume effects) with recent probabilistic approaches, this methodology becomes a brain connectivity tool. Recently we suggested combinatorial tracking [8] in which the regular grid diffusion tensor data is mapped to a graph (as in graph theory), where the center of each voxel (graph node) is connected to its 26 neighbor voxel centers by graph edges. Each edge is assigned a transition probability, which is calculated by numeric integration of the Gaussian probability density function [7]. The model enables for fibers in 13 different directions to cross a voxel. Each two voxels can be connected by a path, but some paths have higher probability than others.

In this work we apply combinatorial fiber tracking[8] to the reconstruction of two fiber systems in the brainstem: the pyramidal decussation (PD) and the medial cerebellar peduncle (MCP). We compare the results of the two reconstruction algorithms, the most probable random walk path algorithm and the reaction path algorithm. Although both methods successfully reconstruct the PD, only the later reconstructs the MCP in an anatomically consistent manner.

Methods and Theory

MRI: The combinatorial tracking framework has been implemented on a conventional DTI data set of a single subject (healthy female 27 years) scanned on a 3T GE scanner. The DTI data set consisted of 27 axial slices with resolution of 3.4x3.4x4.0 mm^3. Scanning parameters were as follows: TE=88ms, b value of 1000 s/mm^2 (Δ/δ of 25/19ms) acquired over 19 gradient directions. The acquisition was gated to 30 R-R cardiac cycles.

Combinatorial tracking: The graph model of combinatorial tracking corresponds to a discrete time finite state irreducible Markov chain, where each voxel correspond to a state [6]. Under this framework we suggest two fiber reconstruction algorithms that work in the context of the Markov chain model.

The first algorithm, the most probable random walk path, finds a path form source to target which maximizes the product of transition probabilities along its edges. It is found by transformation of the transition probabilities (minus log) and by applying Dijkstra's shortest path[5] algorithm. The calculated path is given the following interpretation: given that a random walk started at the origin and ended at the target, most probably it followed the selected path. The mean first passage time (MFPT) is defined as the average time it takes of a random walk, which starts at the source voxel, to arrive at the target voxel for the first time. The MFPT between every pair of voxels in the network is calculated from the probability transition matrix using the fundamental matrix theorem[9] and is interpreted as a global connectivity matrix. The second algorithm, the reaction path algorithm, finds a path from the source to the target with minimum number of edges, among all paths, which decrease the mean first passage time to the target.

Combinatorial tracking was calculated by Matlab © (Mathworks, USA), BGL[10], Matlab BGL (David Gleich, Stanford University), Atlas[11] and visualized using VTK (Kitware Inc.).

Results and discussion

In order to compare the two algorithms we selected two fiber systems at the brainstem. At the first system, the pyramidal decussation, source voxels were selected at the medulla and target voxels above the pons (Figure 1). Fibers were reconstructed from each voxel of the source to every voxel of the target. At the second system, the medial cerebellar peduncle, source and target voxels were selected contra-laterly at the pons and fibers were reconstructed from each voxel of the source to every voxel of the target.

The result of the two algorithms is demonstrated in Figure 1. Both algorithms nicely demonstrate the decussation pattern. While only the reaction path algorithm is able to reconstruct the anterior connectivity pattern of the MCP. We suggest that the superiority of the reaction path algorithm is due to the fact that it is a global connectivity measure in the sense that the mean first passage time considers all paths to the target along with their probabilities. To that end this algorithm is a true connectivity measure as it can connect any source and target voxels.

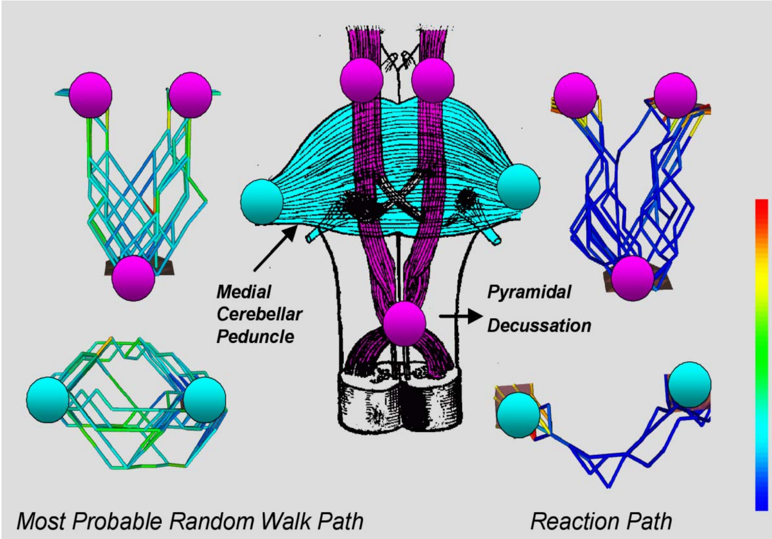

Figure 1: A comparison between two Combinatorial Fiber Tracking algorithms. Pyramidal Decussation source and target are colored in Magenta. Medial Cerebellar Peduncle source and target are colored in Cyan. On the left – edges are colored relative to transition probabilities. On the right – edges are colored relative to decrease in Mean First Passage Time to the target.

References: 1) Basser PJ, Pajevic S, Pierpaoli C et-al., Magn Reson Med 2000, 44:625-32; 2) Mori S, van Zijl PCM, NMR Biomed 2002, 15:468-480; 3) Behrens TEJ, Woolrich MW, Jenkinson M et-al., Magn Reson Med 2003, 50:1007-1088 ;4) Jones DK, Pierpaoli C, Magn Reson Med 2005, 53:1143-1149; 5) Ahuja RK, Magnanti TL, Orlin JB, “Netwrok Flows”, 1993, 1st Ed, Prentice Hall Publishers. 6) Papoulis A, Pillai SU, “Probability, Random Variables and Stochastic Processes", 2002, 4th Ed., McGraw Hill publishers; 7) Basser PJ, Mattiello J, LeBihan, D. Biophys J 1994, 66:259-267; 8) Lifshits S, Tamir A, Assaf Y, Proc. Intl Soc. Magn. Reson. Med. 2007, 234; 9) Grinstead CM, Snell JL, "Introduction to Probability", 1997, American Mathematical Society; 10) "The boost graph library: user guide and reference manual", 2002, Addison-Wesley Longman Publishing Co.; 11) Whaley RC , Dongarra JJ, Proc. SC: High Performance Networking and Computing Conference 1998, 1–27.