

Comparison Study of Two DTI Tractography Methods for Quantifying Brain Structural Connectivity

Qing Ji¹, John O. Glass¹, and Wilburn E. Reddick¹

¹Radiological Science, St.Jude Children's Research Hospital, Memphis, TN, United States

INTRODUCTION: Diffusion tensor imaging (DTI) tractography provides a non-invasive way to access the connectivity between anatomic structures in the brain and builds the foundation for the study of brain networks. There are two primary categories DTI based tractography methods: deterministic and probabilistic. Each one can be used to compute the connectivity between any two neuroanatomical regions. However, quantitative comparisons between the two algorithms have rarely been reported and the advantages and disadvantages of the methods have not been fully explored. In this study, we will quantitatively compare the two techniques for assessing structural connectivity.

METHOD AND MATERIAL: Eight healthy subjects were imaged with high resolution 3D T1-weighted images and a DTI scan acquired on a Siemens 3T scanner. The DTI data were acquired with 1.5x1.5x3 mm resolution, 40 slices (12 directions, b=700) and 4 repetitions. Each DTI data set was corrected for motion and eddy current distortions and registered to the T1-weighted image. Fiber tracking was performed for each data set using publicly available software packages Trackvis [1] for deterministic and FSL [2] for probabilistic tracking. Eighty-two neuroanatomical regions (34 cortical and 7 sub-cortical on each hemisphere) were obtained using FreeSurfer [3] on the 3D T1-weighted image. The voxels of those anatomical structures then served as the seed points for fiber tracking. The number of fibers connecting any two anatomic regions was used as a quantitative measure to assess the connectivity between regions. In the deterministic algorithm, fibers throughout the whole brain were first obtained using every voxel in the brain volume as a tracking seed, and then the fibers connecting any two structures were evaluated to produce a metric representing the average number of connecting fibers. In the probabilistic algorithm, the connection between any two brain structures was calculated individually for 5000 permutations. The number of tracks that successfully reached the target region from all seed voxels within the source region were summed and then divided by 5000 to produce a similar metric. Connectivity metrics from each of the tracking algorithms were compared with a linear regression within each subject. Besides the connection calculation, the probabilistic method also provided a path probability map for the fibers that passed through each neuroanatomical structure.

RESULTS: Figure 1 showed the typical connection matrixes obtained by deterministic and probabilistic methods for one subject. It is evident that the connection matrix obtained by the deterministic method had fewer connections and was sparser than the one obtained by the probabilistic method. Figure 2 showed a typical scatter plot of the connections created by the two algorithms for a single examination. Each point represented connectivity between two specific regions. A linear regression of the data showed that the connections calculated by the two techniques were significantly correlated. Linear correlation coefficients across the subjects were consistently between 0.76 and 0.82. With the proper threshold, the binary connection matrixes calculated by the two algorithms can be 90% to 95% matched. Fibers that pass through a neuroanatomical structure determined by the deterministic algorithm can also be compared with the fiber probability map created by the probabilistic algorithm. Figure 3 showed a typical deterministic fiber set that pass through the left thalamus overlaid on regions of interest created by thresholding the corresponding probability distribution. There are some high probabilities regions where the deterministic fibers were not able to track that provide some insight into the sparser connection matrix created by the deterministic method. Overall, there was good correspondence between the two methods.

DISCUSSION / CONCLUSION: Neuroanatomical connectivity metrics between the two tractography methods were significantly correlated and fiber tracks from the deterministic algorithm were spatially similar to fiber probability distributions created using the probabilistic algorithm. While there was a high degree of correspondence between the approaches, the maps are not equivocal. The probabilistic algorithm provides more connections among brain structures and the additional information of uncertainty.

REFERENCES:

- [1] Wang RP, et al. *Proceedings of ISMRM*, 2007.
- [2] Brehrens TE, et al. *Neuroimage*, **34**(1):144-55, 2007.
- [3] Dale AM, et al. *Neuroimage*, **9**(2):179-94, 1999.

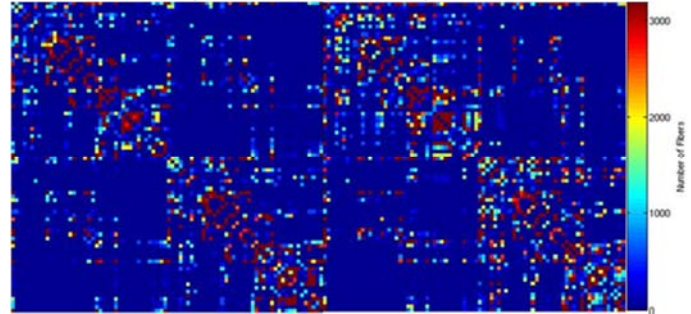


Figure 1: Connectivity matrixes calculated using deterministic (left) and probabilistic (right) algorithms.

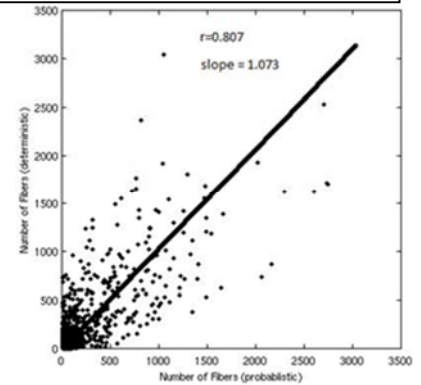


Figure 2: Relationship between connections calculated by two tractography algorithms.

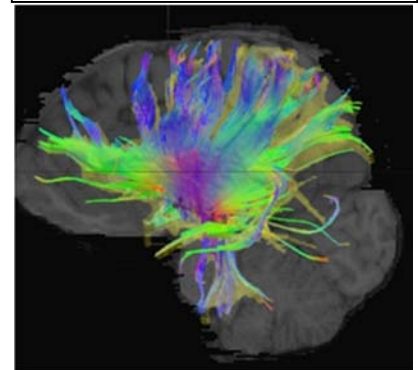


Figure 3: Deterministic tracked fibers that pass through the left thalamus overlaid on the yellow region of interest created by the path probability distribution around the same structure.