Logical Foundations and Fast Implementation of Probabilistic Tractography

Myron Zhang[1,2], Ken E. Sakaie[1], and Jones Stephen[1]
[1]*Imaging Institute, The Cleveland Clinic, Cleveland, OH, United States,* [2]*Physics, Cornell University, Ithaca, NY, United States*

Introduction Maps of whole-brain anatomical connections generated by tractography prove valuable for identifying targets for resection in the treatment of phamacoresistant epilepsy. Unfortunately, current implementations have difficulty identifying a number of important connections while relying on intuitively appealing but ad-hoc logic. In this contribution, we present a logical formulation of probabilistic tractography that lends itself to fast implementation. The method identifies connections throughout the entire brain and may prove important for presurgical planning and other medical applications.

Theory The objective is to derive the *number* of tracks in a voxel given *local probabilities* and *global conditions* on the tracks. We therefore define $\varphi(j)$ as the number of tracks in a voxel, j, subject to the *conditions* that the tracks reach a target voxel before returning to the seed or striking the boundary. Assuming that the number of tracks is conserved locally, $\varphi(j)$ is equal to the number of tracks flowing in from neighboring voxels i, which can be calculated from $\varphi(i)$ and the conditional probabilities, $p(i,j)$, that a track moves from i to j, subject to the conditions (eqn. 1). This conditional probability is related to a local probability, $\lambda(i,j)$, that a track moves from i to j without conditions, and the probability, $r(i)$, that a track in i satisfies the conditions (eqn. 2). Although $r(i)$ is a probability while $\varphi(i)$ is a track count, a similar local conservation argument using basic properties of probabilities holds (eqn. 3). As equations 1 and 3 are in the form of finite difference equations, for which a number of fast numerical solutions exist, the logic readily translates into a fast implementation. The only input from the imaging data is the local probability, $\lambda(i,j)$, which can be derived from a fiber orientation distribution (FOD) (1).

$$\varphi(j) = \sum_i p(i,j)\varphi(i) \quad \textbf{(1)} \qquad p(i,j) = \lambda(i,j)r(j)/r(i) \quad \textbf{(2)} \qquad r(i) = \sum_j \lambda(i,j)r(j) \quad \textbf{(3)}$$

Methods Anatomical images and high angular resolution diffusion imaging (HARDI) (2) were acquired on a Siemens TIM Trio (Siemens Medical Solutions, Erlangen) in 14 epilepsy patients under an internal review board-approved protocol. A white matter mask was generated from the anatomical images and coregistered to the HARDI data with FSL (3). The FOD was calculated in each voxel with user-independent optimized regularization (4) and integrated over sub-regions to determine local probabilities, $\lambda(i,j)$. The probability, $r(j)$ is then calculated (eqn. 3) using the conjugate gradient algorithm as implemented in MATLAB (the Mathworks, Natick) and used to find the conditional probability, $p(i,j)$ (eqn. 2). The conjugate gradient algorithm was then applied again to determine $\varphi(j)$ (eqn. 1). Track counts were calculated between a seed and target voxel placed in bilateral hand motor cortex. For comparison, tracks were also generated using a more standard FOD-based Monte Carlo probabilistic algorithm (4). Track counts were used as a proxy for anatomical connectivity.

Results Figure 1 shows anatomical connectivity to hand motor cortex. The proposed method finds connectivity to all regions of the white matter mask (fig. 1a) albeit at a low level in most regions. A slight threshold (1% of maximum) yielded a connectivity map (fig. 1b) similar to that generated by more the Monte Carlo method (fig. 1c, thresholds at 0 and maximum). The proposed method required 3 cpu-*seconds* to generate connectivity values to all regions of tissue. The Monte Carlo method required 78 cpu-*hours*, failed to assess connectivity to some regions, and demonstrated patchy connectivity with shorter run times.

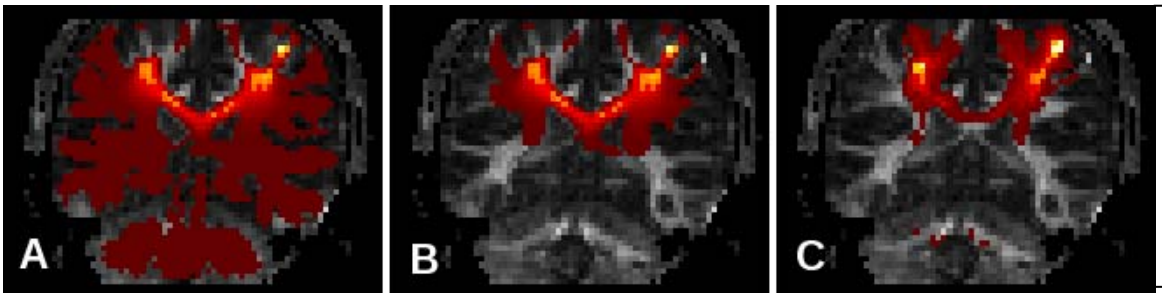

Figure 1. A) Anatomical connectivity to bilateral hand motor cortices with proposed method, minimum threshold 0, B) with 1% threshold, C) with standard Monte Carlo probabilistic tractography.

Discussion

The logical development provides new insight into probabilistic tractography in general. Termination criteria are built into the logical framework itself. Finding low but nonzero values of connectivity in all regions of tissue may be useful for statistical corrections for probabilistic tractography in general (5). The implementation is fast and shows promise for making whole-brain anatomical connectivity maps on a clinically relevant time scale.

References

1. Tournier J.D. et al. Neuroimage 23, 1176-1185 (2004).
2. Tuch, D.S. et al. Magn Reson Med 48, 577-582 (2002).
3. Smith, S.M. et al. Neuroimage 23 Suppl 1, S208-219 (2004),
4. Sakaie, K.E. & Lowe, M.J. Neuroimage 34, 169-176 (2007).
5. Morris, D.M. et al. Neuroimage 42, 1329-1339 (2008).

Acknowledgements: We gratefully acknowledge support from DOD grant PR100438.