

Parallel Global Tractography

Haiyong Wu¹, Dinggang Shen¹, and Pew-Thian Yap¹

¹Department of Radiology, University of North Carolina, Chapel Hill, North Carolina, United States

Target Audience: Diffusion MRI researchers who are interested in speeding up global tractography.

Introduction: Diffusion magnetic resonance imaging (DMRI) is a key imaging technique for in vivo investigation of white matter pathways in the brain. To trace white matter connections, local or global or tractography algorithms can be utilized. Local algorithms take a greedy approach and trace the connections path-by-point using small successive steps by following local voxel-wise distributions of axonal directions. They are hence susceptible to error accumulation. On the other hand, global algorithms reconstruct the connections simultaneously by determining the configuration of signal-generating fiber segments that best describes the measured data [1], hence promising better stability with respect to noise and imaging artifacts. However, global algorithms require long computation times that are often prohibitive in the clinical setting. We present here a reformulation of the global tractography algorithm described in [1] for a fast parallel implementation that can harness the power of multiple CPUs or GPUs.

Methods: Our method is motivated by this key observation - each fiber segment is affected by a limited sphere of influence. A fiber segment is influenced only by the fiber segments that are (or can potentially be) connected to its both ends and also by the diffusion-weighted signal in its proximity. This fact can be used to gain parallelism for significantly improving the speed of global tractography. To achieve this, we partition the image data into K regions that are mutually non-influential and statistically independent. Then the Metropolis-Hastings (MH) algorithm is applied in parallel by proposing changes to the fiber segments in these regions using the corresponding transition probabilities. The proposals in these regions are accepted/rejected based on their acceptance ratios. The independence condition ensures that the proposals for each of the K regions can be accepted and rejected separately but in parallel. We denote the configuration of the fiber segments by M and the measured diffusion-weighted signal by D . The goal of global tractography is to maximize the posterior probability $P(M|D)$ with respect to M [1]. For parallel implementation, we partition the posterior density into subposterior densities [2], i.e., $P(M|D) = P(M_0|D) \prod_{i=1}^K P(M_i|D)$, where M_i denotes the configuration of fiber segments in the i -th region and M_0 denotes the region that separates the K regions and keep them independent. Sampling and updating are then performed independently and in parallel in these K regions for a number of rounds. We then repeat the process again by a different random partition of the data. The parallel global tractography (PGT) algorithm is summarized as follows:

1. **Data Partitioning:** Partition the image data into K partitions that are mutually independent.
2. **Parallel Proposals:** In parallel propose changes for the fiber segments in these regions according to the corresponding transition probabilities and accept/reject the proposals based on their acceptance ratios. Repeat this step for sufficient number of times.
3. **Concurrent Updates:** Update M with all accepted proposals and repeat from Step 1 until convergence.

Results: The datasets and the parameters in [3] are used for evaluation using an iMac with a 3.4GHz Intel Core i7 and 8GB of RAM. Using hyper-threading, PGT was performed using 8 parallel threads. Fig. 1(a) shows that the PGT performs as well as the original single thread version in terms of the number of fiber segments and fiber tracts. However, Fig. 1(b) shows that PGT requires significantly less time for generating the proposals required to arrive at similar tractography results.

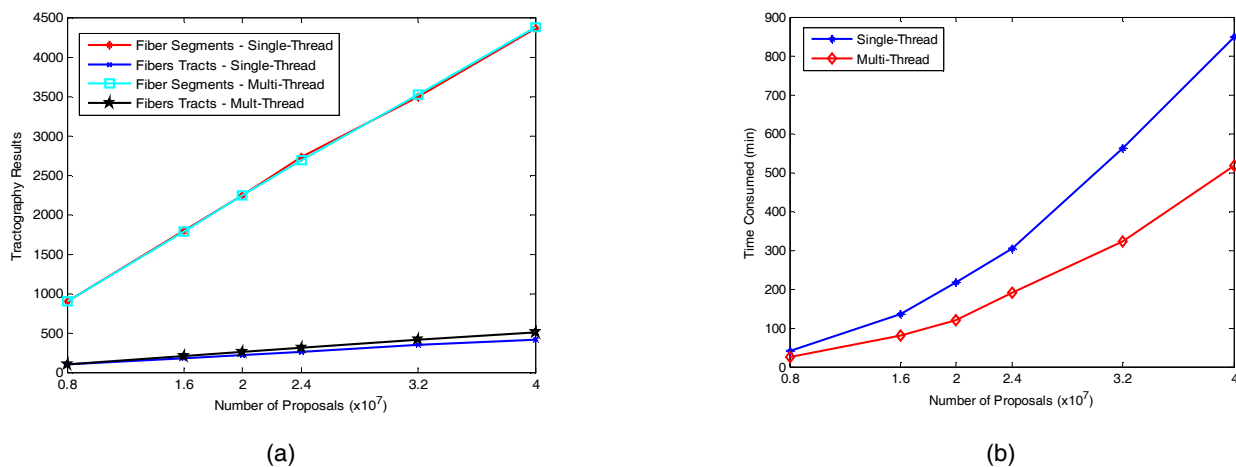


Fig. 1. Comparison between single- and multi-thread global tractography.

Conclusion: The proposed algorithm helps reduce the time cost associated with the global optimization process required in global tractography. Future implementation involving GPUs will further increase the speed and make the algorithm more feasible for large-scale studies.

References: [1] Reisert et al., "Global fiber reconstruction becomes practical," *Neuroimage*, 54(2), 955-962, 2011. [2] Neiswanger et al., "Asymptotically Exact, Embarrassingly Parallel MCMC," arXiv, 2014. [3] Yap et al., "A generative model for resolution enhancement of diffusion MRI data," *MICCAI*, 16, 527-534, 2013.