GPU-based Parallel Computing for Structural Network Analysis of Human Brain

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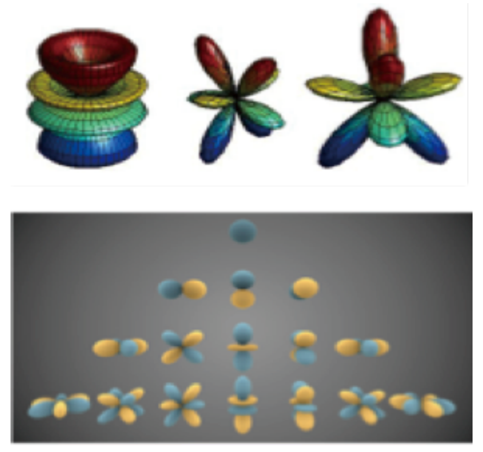
Abstract: In comparison with diffusion tensor imaging(DTI), high-angular resolution diffusion imaging (HARDI) can resolve the complex fiber crossing of each voxel in the brain. However, the image reconstruction time is longer than conventional technology. Therefore, we employed graphic processing unit (GPU) and CUDA to implement a GPU-based structural brain network analyses scheme including the high-speed QBI reconstruction using spherical harmonic functions, probabilistic tracography algorithm and brain network analyses based on graph theory. The results show that it could accelerate the processing of brain network analyses using GPU and CUDA for make lots of clinical applications workable and efficient.

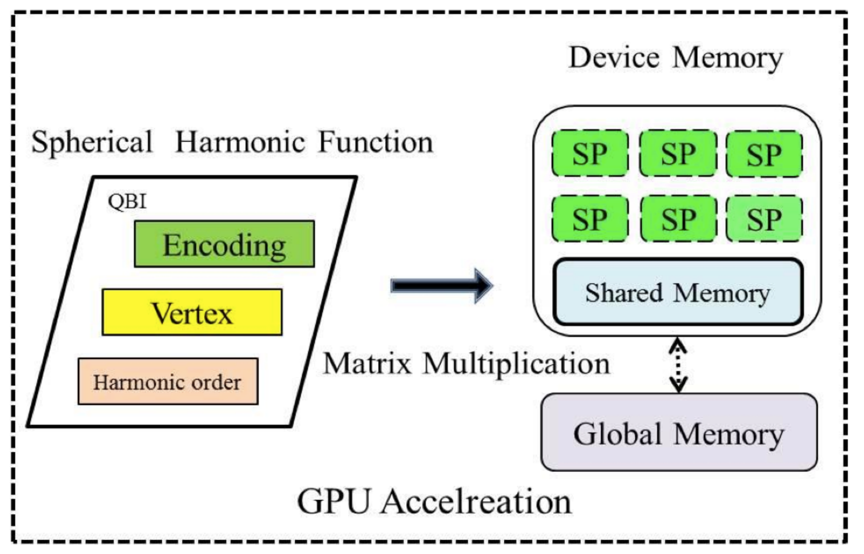
QBI Reconstruction → Probabilistic Tractography → Brain Network Analyses

QBI Reconstruction

All MRI data included QBI and T1-weighted images were acquired from National Yang Ming University 3T MRI. The QBI reconstruction could be applied using spherical harmonic functions for each voxel (image resolution= 96 x 96, slice number =60). We generate the spherical harmonic kernel once by CPU and then apply it for each voxel in the environment of GPU parallel processing .

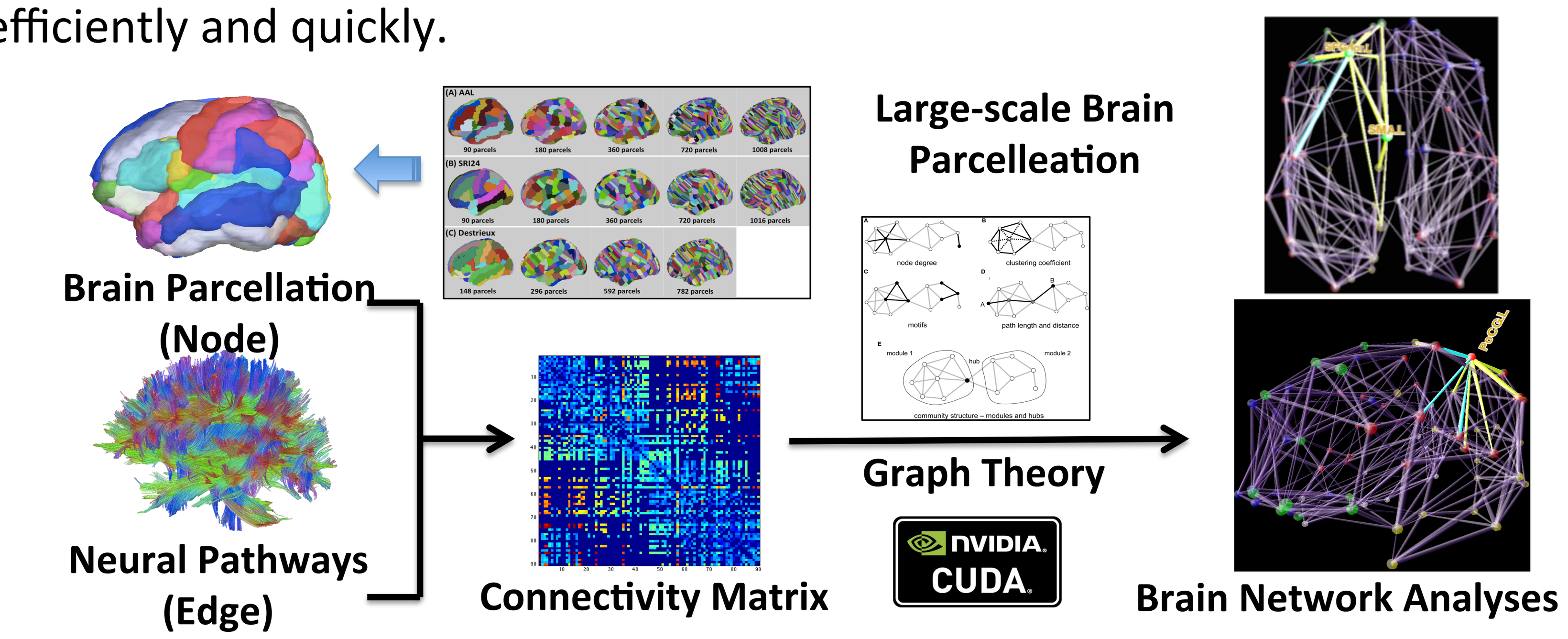


Spherical Harmonic Function



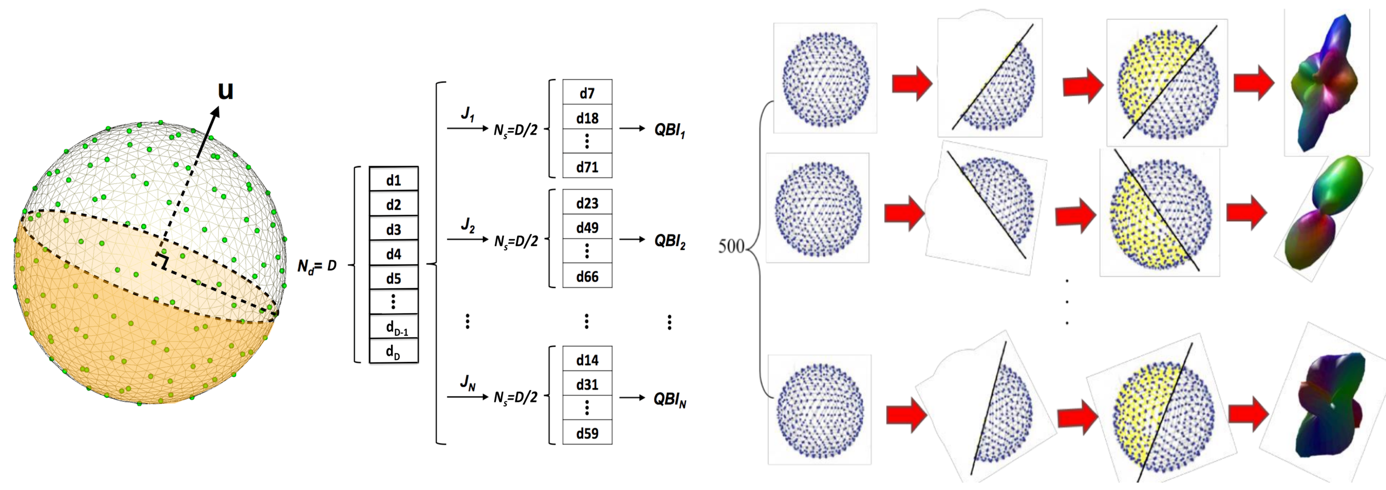
Brain Network Analyses

In comparison with multi-cores CPU or clusters, GPUs with CUDA is provided with the powerful of parallel computing and the benefit of low cost. By implementing the fundamental graph algorithm-all pair shortest path. Our GPU-based platform of human connectome will make the construction and analysis of large-scale brain network (number of nodes > 8000) more efficiently and quickly.

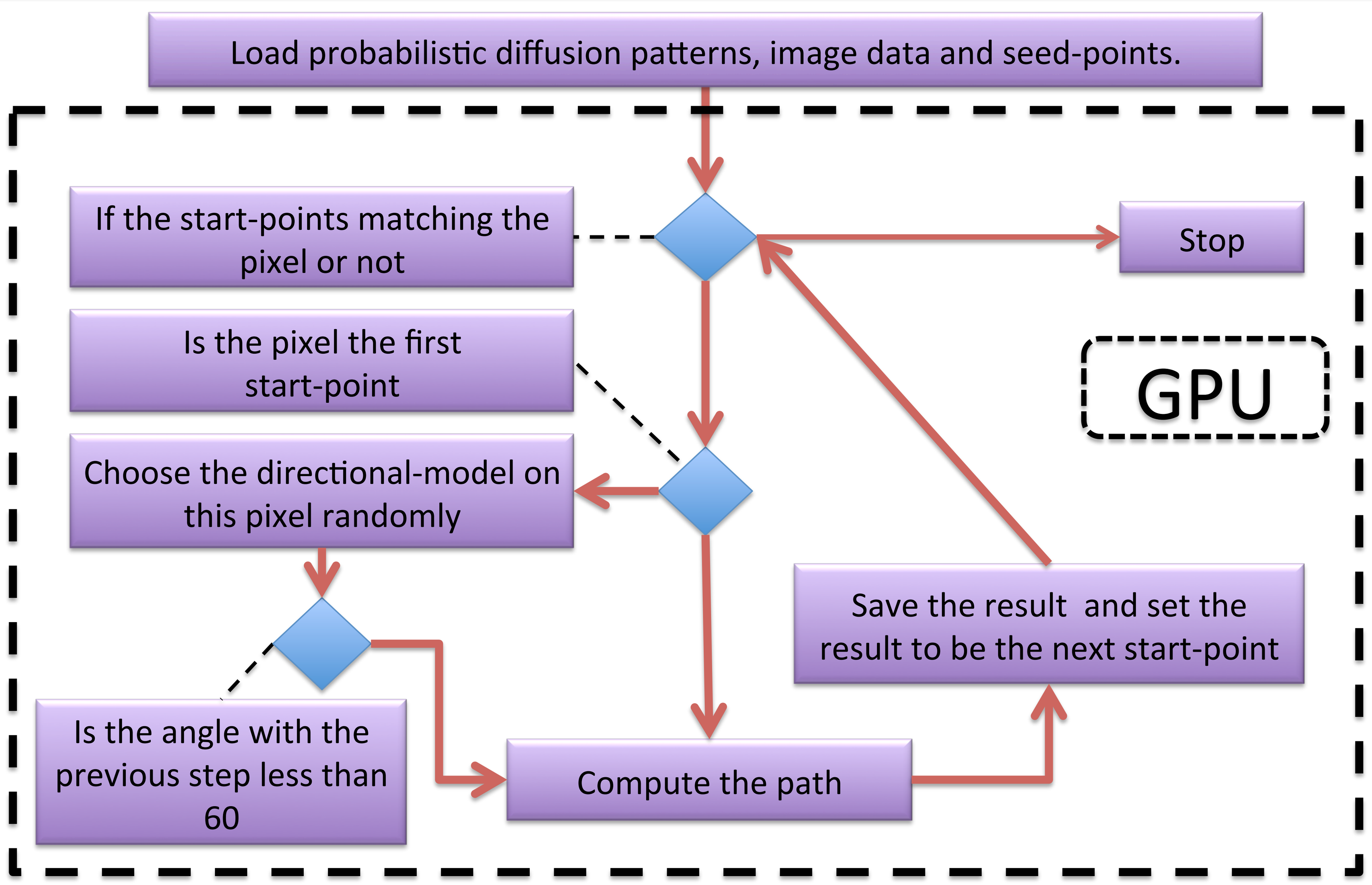


Probabilistic Tractography

Using this Jackknief-bootstrap resampling, we selected half sphere of Q-ball data randomly and copied data into the symmetrical sides for rebuild a new Q-ball dataset for 500 times repeatedly. Then the information of fiber orientations in all brain pixels would be reconstructed and estimated for 500 times. These fiber directions in each pixel could be integrated and regarded as a probabilistic diffusion pattern for further fiber tracking. The following flowchart shows the GPU-based probabilistic tractography algorithm.



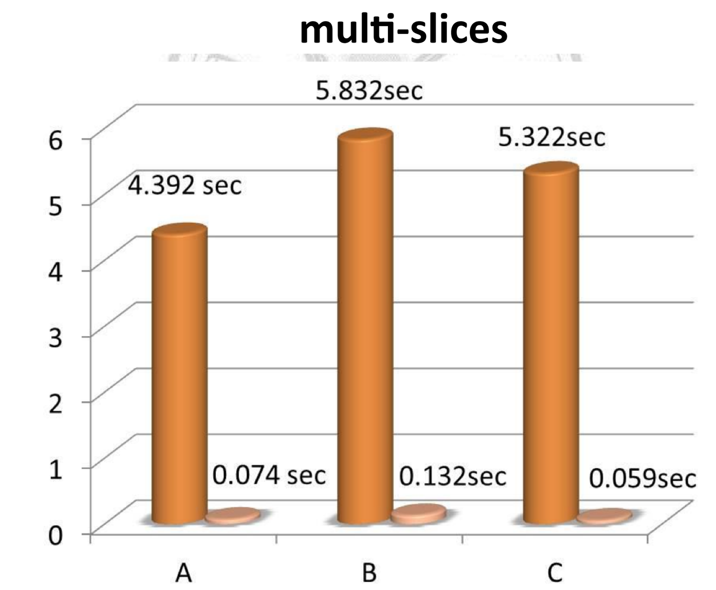
JackKnief Bootstrap QBI Resamping Scheme for Probabilistic Diffusion Pattern

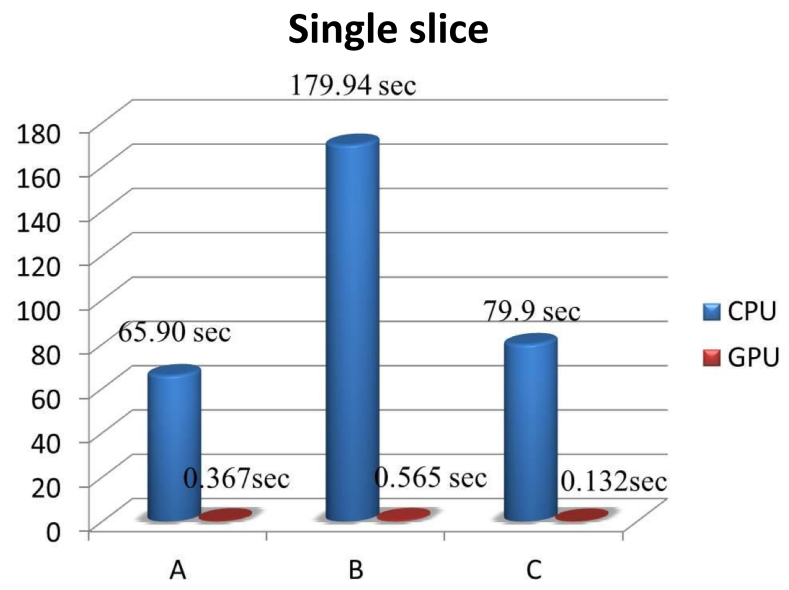


Results

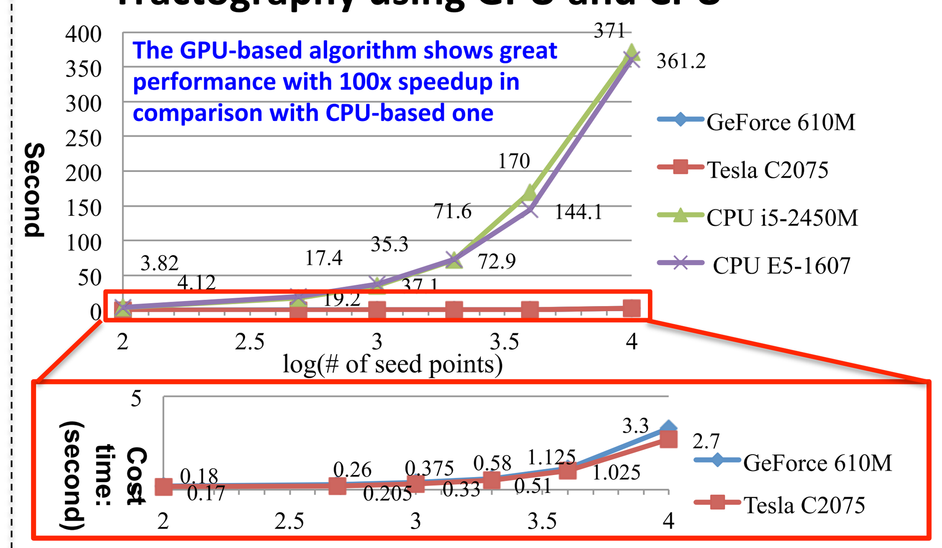
Time of CPU and GPU compute spherical harmonic function

hardware	CPU	GPU
A	Intel i7-3770	NVIDIA GTX560
B	Intel i5-s450M	NVIDIA Geforce 610M
C	Intel E5-1607	NVIDIA Tesla C2075

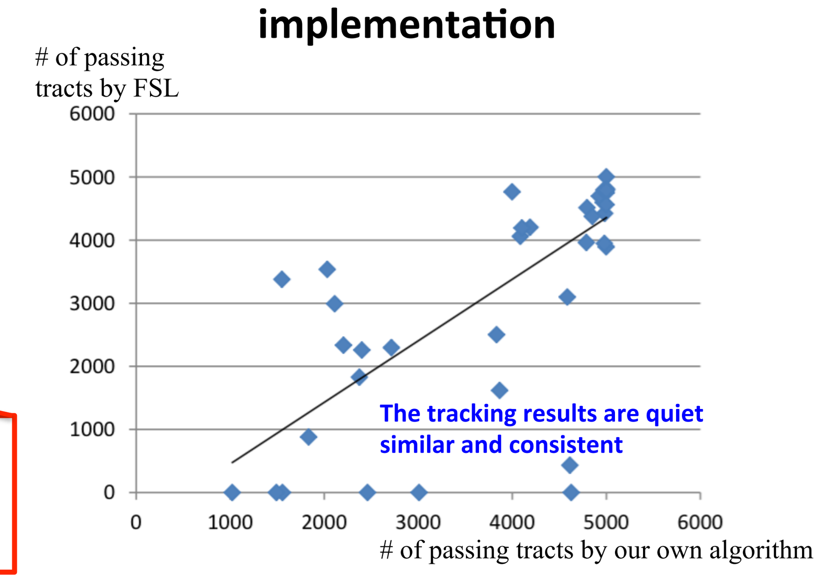


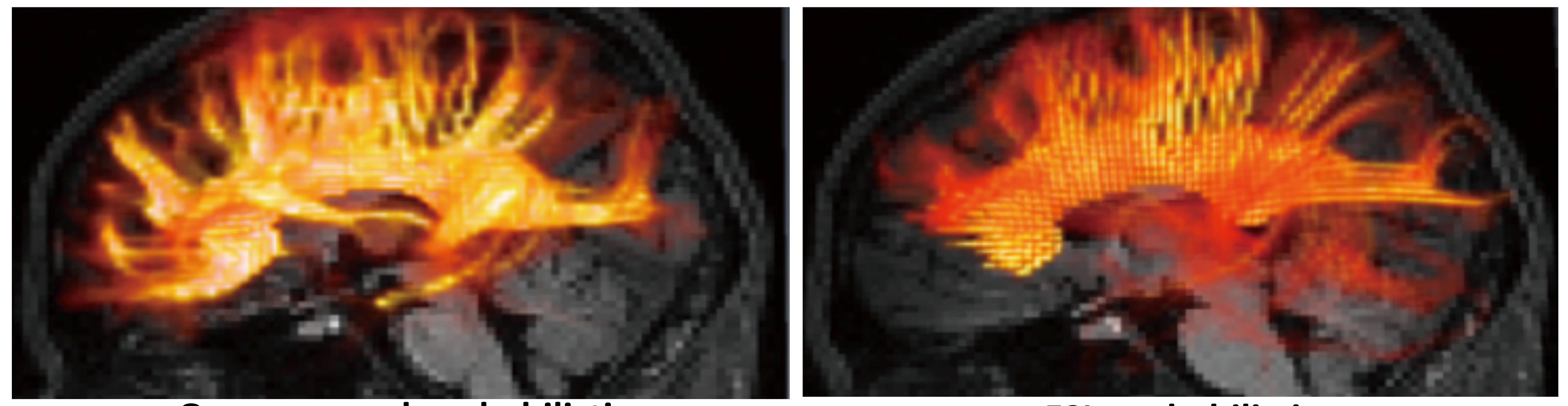


Performances of Probabilistic Tractography using GPU and CPU



Comparison of FSL probtractx and our implementation





Our proposed probabilistic Tratography algorithm

FSL probabilistic Tratography algorithm

The performance of all-pair shortest path in brain network using BCT/CPU/GPU

# of Brain Parcellations	Brain Connectivty Toolbox (sec)	Our-owned CPU (sec)	Our-owned GPU (sec)
90	0.33	0.010	0.0011
116	0.74	0.010	0.0013
180	1.32	0.014	0.002
360	4.97	0.070	0.01
490	11.16	0.17	0.035
720	27.02	0.49	0.10
1008	69.01	1.31	0.39

Our GPU-based APSP algorithm shows better performance than the existed software-BCT for brain network analysis with large number of brain parcellations

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