

# PAGANI Toolkit: Parallel Computing Package for Fast Network Analyses of Brain Connectomes

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E-Poster

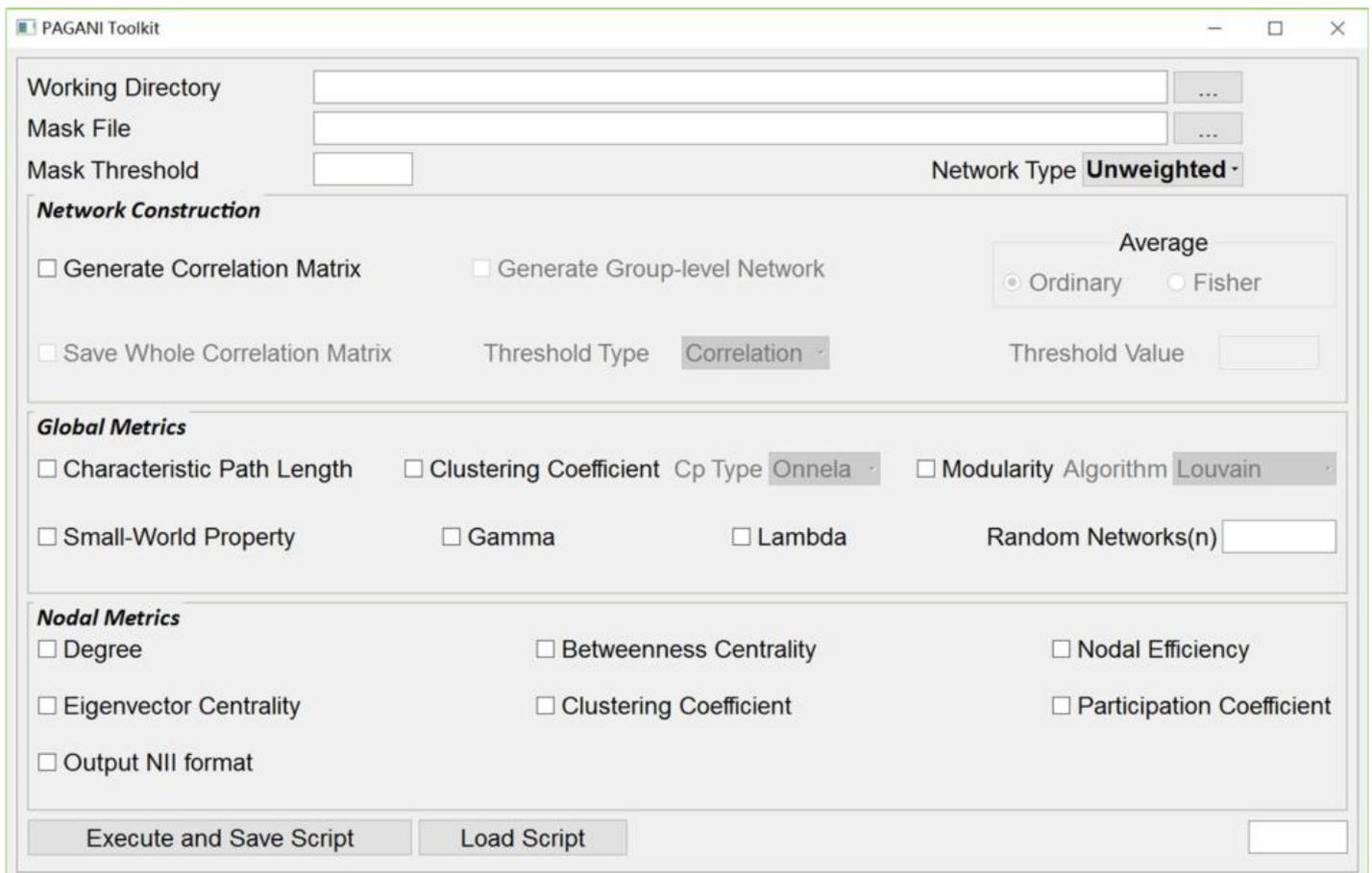
Introduction:

Recently, the combination of non-invasive magnetic resonance imaging technologies and graph theoretical approaches has emerged as a promising tool for mapping the topological properties of complex human brain networks (i.e., connectomes [1, 2]). The construction and analysis of high-resolution brain connectomes at a voxel scale are of great importance because they provide finer spatial information without prior parcellations [3]. However, the increasing amount of datasets and the growing network size bring forward high requirements for the computational capabilities. Here, we developed a parallel graph-theoretical analysis toolkit (PAGANI Toolkit) by extending our former developed hybrid CPU-GPU accelerated framework [4], aiming at fast mapping of voxel-level human brain connectomes.

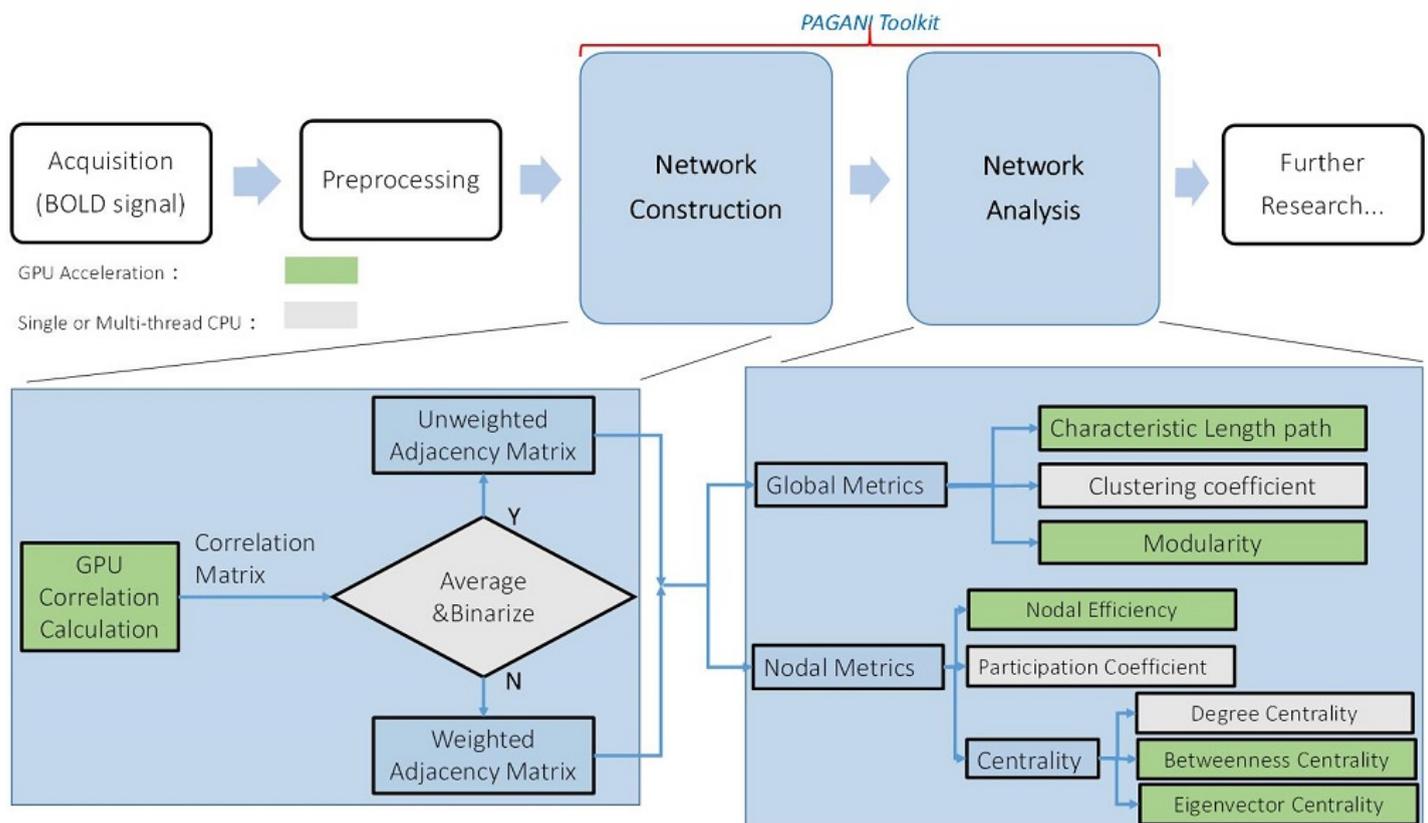
Methods:

PAGANI Toolkit was developed in a hybrid CPU-GPU framework, with C/C++ and CUDA (Computing Unified Device Architecture) as programming languages and QT as GUI (Graphical User Interface) designing software, under 64-bit Microsoft Windows environment. The computation part was packaged into independent executable files for different functions while the GUI (Fig. 1) was meticulously designed to flexibly generate scripts for performing the computations in batch.

The workflow of PAGANI Toolkit can be summarized into two main steps: network construction and network analysis (Fig 2). Briefly, the input for the network construction should be preprocessed fMRI data. GPU-based acceleration algorithm is applied to calculate Pearson's correlations between every pair of voxels within an input mask, resulting the voxel-level functional networks. Users can select either binary or weighted network type for further analysis according to whether they take connectivity strength into account. The network analysis part provides a set of functions to quantify both global and local topological properties of brain connectomes, using graph-theoretical approaches. GPUs are utilized to accelerate the computations of several network metrics that are extremely time-consuming but with high parallelism including eigenvector-based modularity [5], characteristic length path, nodal efficiency, betweenness and eigenvector centrality. GPU-based algorithms are further optimized to reduce the restriction of GPU memory and ensure the scalability. Other algorithms - unfit to be accelerated on GPUs including Louvain modularity [6], small-worldness, degree, clustering coefficient, and participation coefficient - are implemented on single or multi-core CPUs. For the details, see [4].



• Fig1. The graphical user interface of PAGANI Toolkit.



• Fig2. The work flow of PAGANI Toolkit

#### Results:

The software release with source codes of PAGANI Toolkit is uploaded on GitHub and can be downloaded freely on the NITRC website ([https://www.nitrc.org/projects/pagani\\_toolkit/](https://www.nitrc.org/projects/pagani_toolkit/)).

Network construction process can output a sparse correlation matrix in CSR format. Global metrics are exported in text files. Nodal metrics are stored in customized .nm format and can be converted to 3D nifti files with this software. As a test, resting-state fMRI data of a subject were preprocessed in a routine process and were normalized to a 4mm isotropic voxel size. We constructed the voxel-wise brain network with ~30000 nodes within a gray matter mask. As a comparison, we also implemented all the algorithms on single-core CPU. PAGANI toolkit finished network construction in 3

seconds and cost about 2 hours to calculate all network metrics at three sparsities (2%, 4%, and 6%) in both binary and weighted type. The time consumption was much lower than the single-core CPU implementation which cost tens of hours. Especially in the computation of characteristic path length by blocked FW algorithm [7], GPU-based algorithm was more than 100 times faster.

Conclusions:

PAGANI Toolkit exhibited enhanced applicability and efficacy of high-resolution brain network analysis, and thus could facilitate computations in connectome studies.

Informatics:

Workflows <sup>1</sup>

Modeling and Analysis Methods:

fMRI Connectivity and Network Modeling <sup>2</sup>

Poster Session:

Poster Session - Monday

Keywords:

Workflows

<sup>1|2</sup>Indicates the priority used for review

Sparsity	Unweighted Network			Weighted Network		
	2%	4%	6%	2%	4%	6%
<b>Correlation Matrix</b>						
GPU	1.70			1.82		
1-thread CPU	73.88			73.43		
Speedup	43.46			40.35		
<b>All-Pairs-Shortest-Path</b>						
GPU BFW	79.09	79.69	75.84	76.28	76.31	76.23
1-thread CPU BFW	>2.6x10 <sup>4</sup>			>2.6x10 <sup>4</sup>		
Speedup	>100			>100		
<b>Eigenvector-based Modular Detection</b>						
GPU	308.10	361.28	541.591	N/A		
1-thread CPU	1098.31	1342.52	2114.54			
Speedup	3.56	3.72	3.90			
<b>Betweenness Centrality</b>						
GPU	388.46	853.37	1863.24	N/A		
1-thread CPU	1681.67	3625.38	7342.68			
Speedup	4.33	4.25	3.94			

**Note:** GPU, Graphics Processing Units (NVIDIA GTX Geforce 680); CPU, Central Processing Unit (Intel i5-2300 @ 2.8GHz); BFW, blocked Floyd-Warshall; Eigenvector-based modular detection and betweenness centrality are not applied to the weighted network in the current version.

• Fig3. Comparisons of the time consumption between GPU-accelerated algorithms in PAGANI Toolkit and single-core CPU implementations.

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Please indicate which methods were used in your research:

Functional MRI

For human MRI, what field strength scanner do you use?

3.0T

Which processing packages did you use for your study?

SPM

Provide references in author date format

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