PAGANI Toolkit: Parallel Software Package for Fast Mapping of High-Resolution Human Brain Connectome (Poster #1878)

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Source Code Released On
https://www.nitrc.org
/projects/pagani_toolkit

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

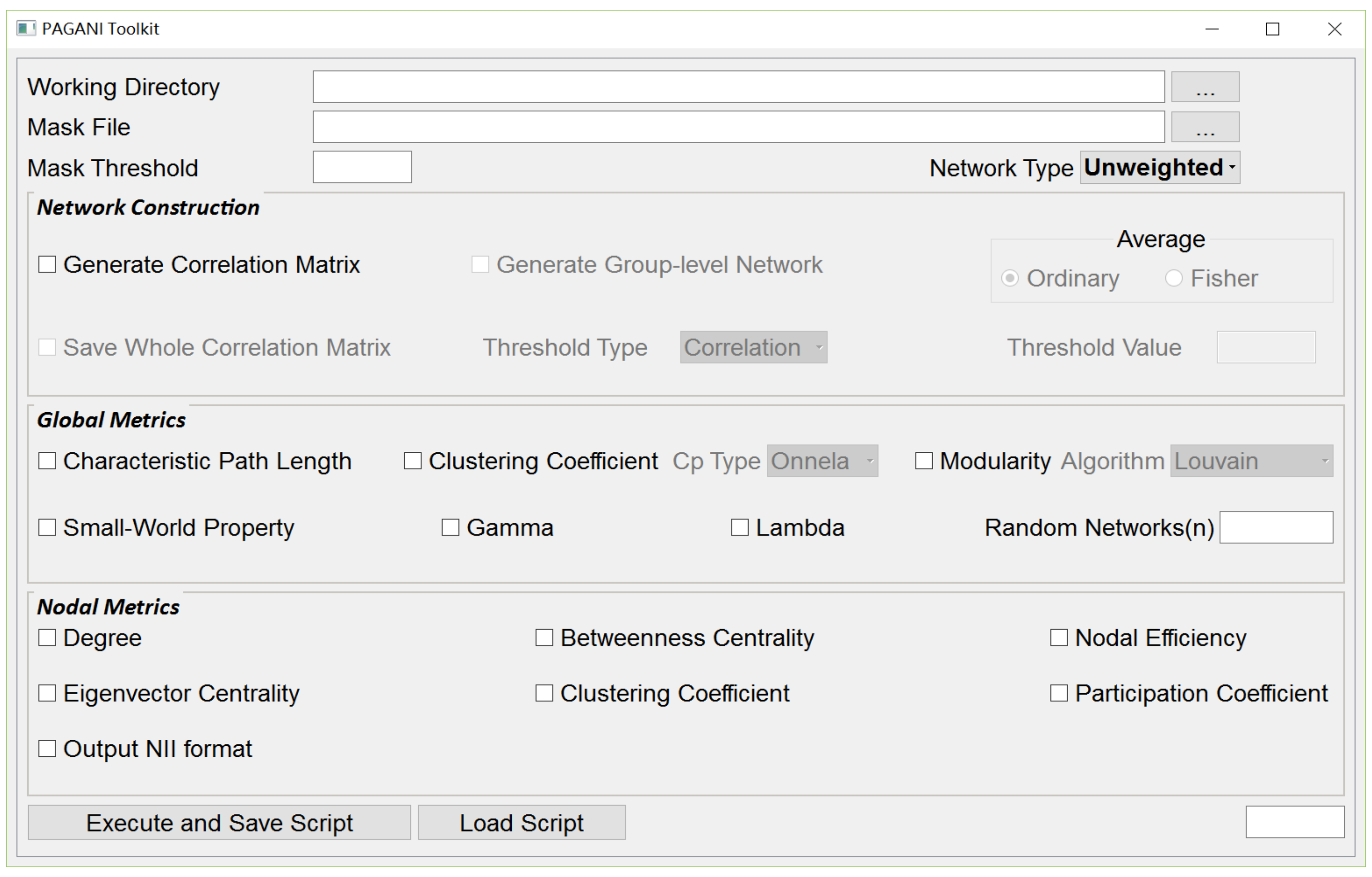
Toolkits overview.

- 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.
- Consists of **the background computation part** and **the GUI**. 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.

Toolkits workflow.

- Two main steps: **network construction** and **network analysis** (Fig 2).
- **Network construction**. The input should be preprocessed fMRI data. GPU-based acceleration algorithm calculates Pearson's correlations between every pair of voxels within an customized mask, resulting the voxel-level functional networks. Either binary or weighted network type can be selected for further analysis.
- **Network analysis**. A set of graph-theoretical functions quantify both global and local topological properties of brain connectomes. GPUs accelerate the computations of eigenvector-based modularity [5], characteristic length path, nodal efficiency, betweenness and eigenvector centrality. 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].
- **Advantages**.
  - ✓ **High Speed.** Faster than other widely used graph theory tools.
  - ✓ **Scalability.** Blocked design and using Compressed Sparse Row format ensure the scalability.
  - ✓ **Low cost and easy setup.** Only a PC with an NVIDIA GPU is required.

Fig1. The graphical user interface of PAGANI Toolkit



PAGANI Toolkit

Working Directory ...
Mask File ...
Mask Threshold
Network Type **Unweighted**

Network Construction

□ Generate Correlation Matrix
□ Generate Group-level Network
Average: ● Ordinary ○ Fisher
□ Save Whole Correlation Matrix
Threshold Type: Correlation
Threshold Value

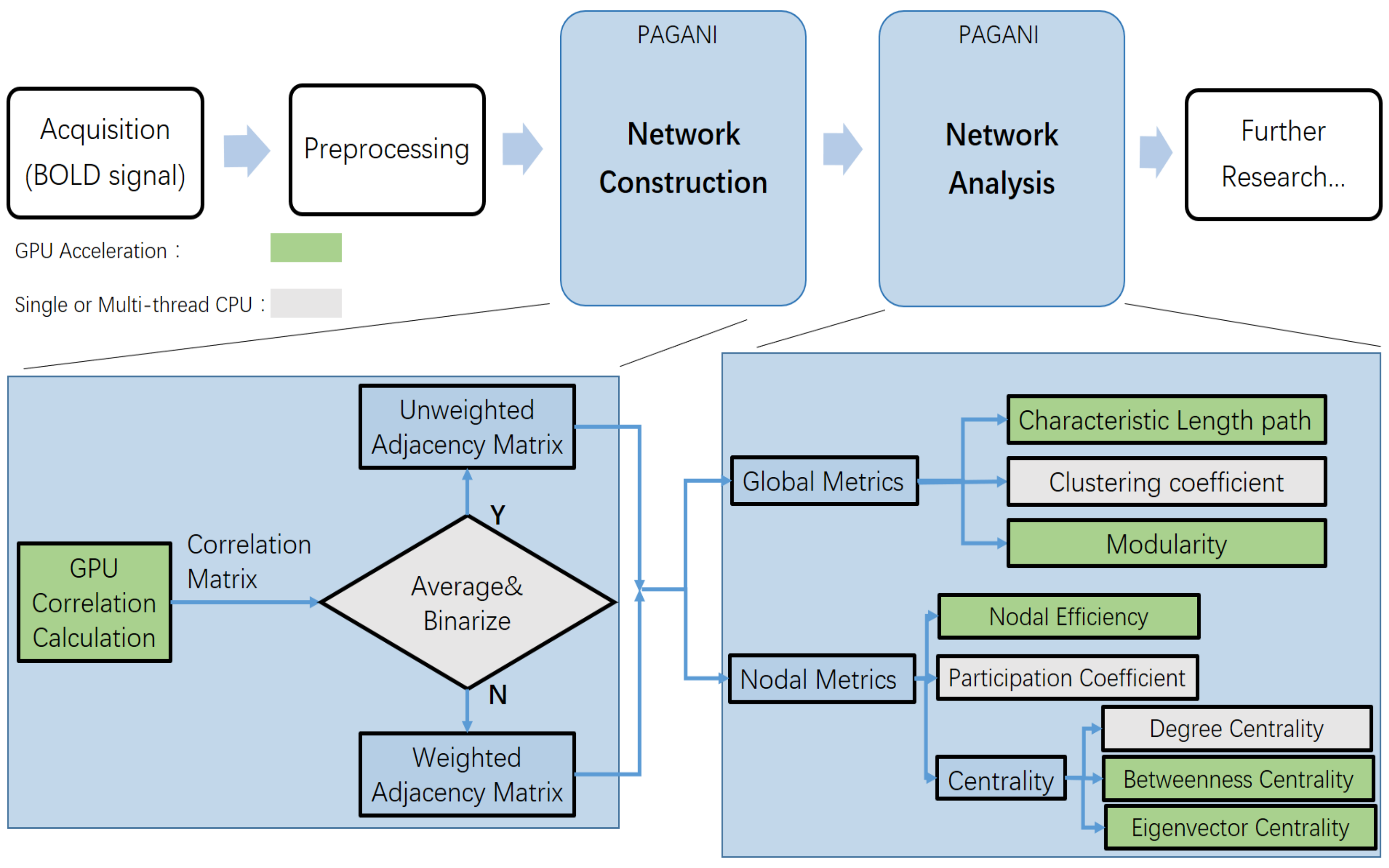
Global Metrics

□ Characteristic Path Length
□ Clustering Coefficient — Cp Type: Onnela
□ Modularity — Algorithm: Louvain
□ Small-World Property
□ Gamma
□ Lambda
Random Networks(n)

Nodal Metrics

□ Degree
□ Betweenness Centrality
□ Nodal Efficiency
□ Eigenvector Centrality
□ Clustering Coefficient
□ Participation Coefficient
□ Output NII format

Fig2. The work flow of PAGANI Toolkit



Results

Output file format. Network construction process outputs sparse correlation matrix in CSR format. Global metrics including LP, global clustering coefficient, modularity (Newman and Louvain), and small-worldness are exported in text files. Nodal metrics (e.g., nodal efficiency, degree, local clustering coefficient, participation coefficient, BC and EC) are stored in customized .nm format and can be converted to 3D nifti files by our software.

Performance and Speedup. We compared the running time of PAGANI Toolkit calculating some network metrics on GPUs with a single-core CPU implementation (Table 1). The test subject data were randomly selected from a public dataset (http://fcon_1000.projects.nitrc.org /indi/CoRR/html/bnu_1.html) and normalized to a 4mm isotropic voxel size. The constructed network contains ~30000 nodes within a gray matter mask. As seen in Table 1, Algorithms accelerated by GPUs in PAGANI Toolkit have a better performance than traditional CPU implementation in network construction and all kinds of networks metrics estimations, especially in the computation of all-pairs shortest paths by BFW algorithm[6], more than 100 times faster.

Table1. Comparisons of the time consumed between the hybrid framework and a single-thread CPU implementation.

	Unweighted Network			Weighted Network		
Sparsity	1%	2%	3%	1%	2%	3%
Correlation Matrix						
GPU	1.70			1.82		
1-thread CPU	73.88			73.43		
Speedup	43.46			40.35		
All-Pairs-Shortest-Path						
GPU BFW	79.09	79.69	75.84	76.28	76.31	76.23
1-thread CPU BFW	$>2.6\text{x}10^4$			$>2.6\text{x}10^4$		
Speedup	>100			>100		
Newman Modular Detection						
GPU	117.94	309.33	507.44	61.78	65.21	97.92
1-thread CPU	454.24	1098.31	1992.72			
Speedup	3.85	3.55	3.93			
Betweenness Centrality						
GPU	224.93	414.37	614.30	Not applied in weighted network for current version		
1-thread CPU	953.26	1681.67	2597.23			
Speedup	4.24	4.06	4.23			

Conclusions

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

References

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