Large-Scale Anatomical Networks: Does node refining matter?

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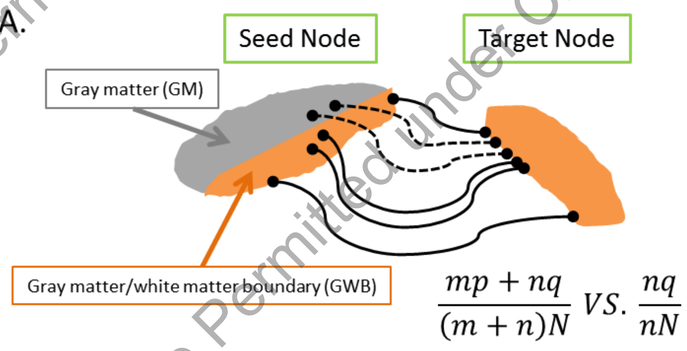
Motivation & Background

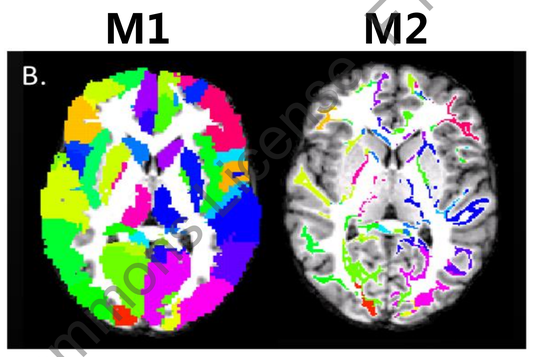
Construction anatomical connections of large-scale brain networks via diffusion magnetic resonance imaging (dMRI) plays an important role in modeling the human connectome [1]. Previous studies have demonstrated that significant effects exist on the topological properties if applying different prior atlas [2, 3]. **However, little is known whether the node refining in anatomical network construction matters.** Here, node refining refers to **whether to compute the gray matter/white matter boundary (GWB)** for each node in the raw prior atlas before being used to construct the whole-brain networks with tractography.



Dataset & Methods

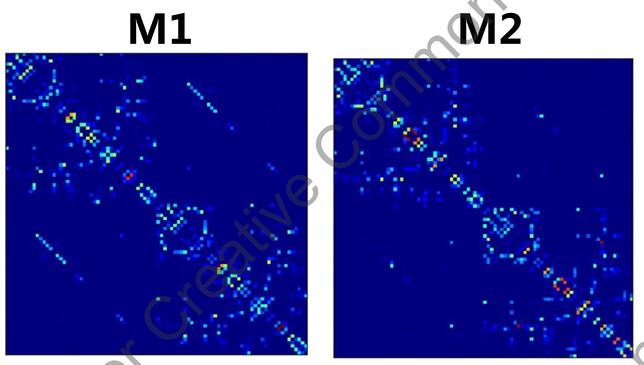
Fifty young healthy participants (25 female).

dMRI: 64 diffusion directions with b=1000s/mm2, and one b0 image;
MRI: 1.33 mm slice thickness and 128 sagittal slices;
Tools: FSL, AFNI, PANDA [4], and GRETNA [5].
Network Metrics: characteristic path length, clustering coefficient, Gamma, Lambda, Sigma, and local and global efficiency.
Two Methods: raw AAL atlas (**M1**), and refined AAL atlas (**M2**) by projecting raw nodes to the GWB.

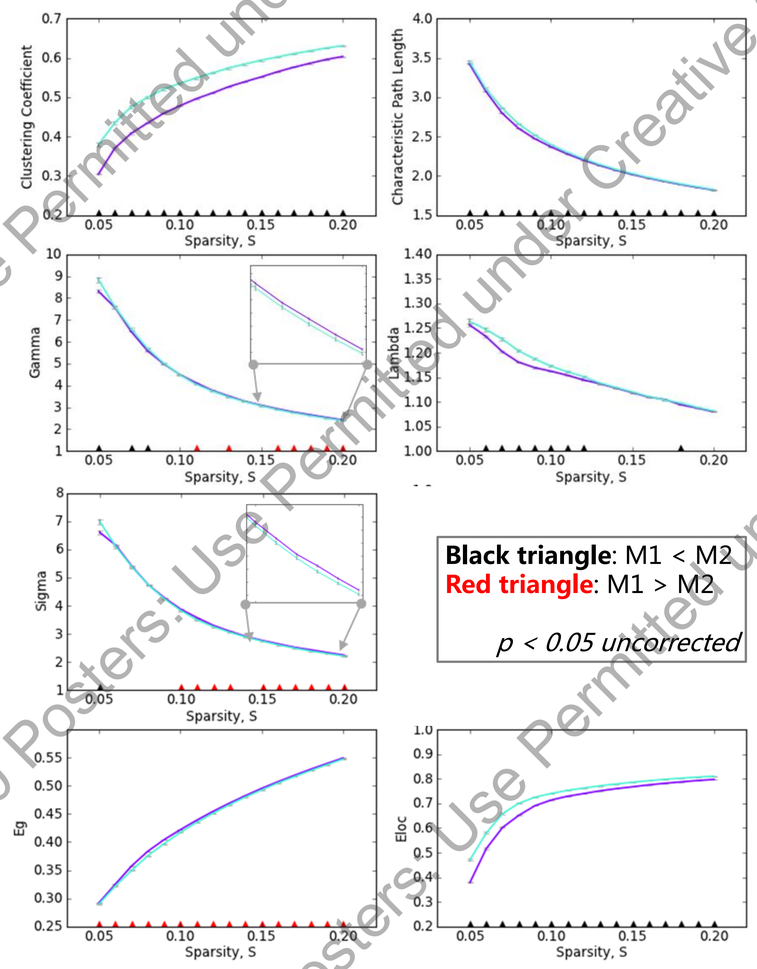


Results

1. Two example networks



2. Node refining effects



In sum, **significant node-refining effects** on topological metrics in large-scale anatomical network analysis, suggesting that **node-refining does matter in quantifying anatomical topological properties**.

References

[1] Sporns et al., 2005; [2] Wang et al., 2009; [3] Zalesky et al., 2010; [4] Cui et al., 2013; [5] http://www.nitrc.org/projects/gretna/