

Beyond thresholding: fully-weighted graph representations of brain functional connectivity

A. J. Schwarz¹, and J. McGonigle²

¹Psychological and Brain Sciences, Indiana University, Bloomington, IN, United States, ²Computer Science, University of Bristol, Bristol, United Kingdom

Introduction: Functional connectivity analyses of fMRI data have leveraged recent advances in complex network theory to derive fundamental properties of brain networks, including scale-free-like and “small world” properties [1]. However, these approaches have conventionally used a cut-off inter-node connection strength to threshold (or binarize) the network, retaining only the supra-threshold edges. This results in a sparse (and often binary) adjacency matrix amenable to conventional graph theoretic treatment, but requires the choice of a hard threshold (and verification of results over a range of such thresholds). The objective of the current study was to characterize the properties of *fully-weighted* human brain networks obtained by retaining all edges along with connection strength information, including the parametric dependence of a power law *adjacency function* (replacing the hard thresholding operation).

Methods: 3T resting fMRI time series data from NITRC were used in this study (N=25) [2]. Preprocessing included motion correction, brain extraction, spatial normalization, confound signal removal (white matter, CSF, head motion) and band-pass filtering (0.01<f<0.1Hz). Fully-weighted networks were created by applying an adjacency function (rather than a hard threshold) to Pearson correlations r_{ij} between all pairs of time courses from a 90-node brain parcellation [3]. We employed an adjacency function of a power law form [4,5] $w_{ij} = ((r_{ij} + 1)/2)^\beta$ to map each r_{ij} to a continuous edge weight w_{ij} in the range [0,1] (Fig.1).

Results: Fully-weighted networks became increasingly scale-free-like (dominated by low strength nodes, with comparatively few high-strength ‘hubs’) at values of $\beta \geq 12$ (Fig. 2(a)). Similarly, “small-world” properties, indicated by a clustering (cliquishness of connections) above that found in random comparator networks, also became apparent at larger values of β (Fig. 2(b)). Modular structure was apparent for networks created with $\beta \gg 1$ (Fig. 2(c)) as well as linearly mapped networks ($\beta=1$, Fig. 2(d)), albeit with a reduced dynamic range in the latter case. Node-wise values of node strength (summed connection weights) and clustering coefficient correlated strongly with corresponding parameters from hard-thresholded networks and were most reproducible (ICC(1,1)≥0.6) for $\beta \leq 12$.

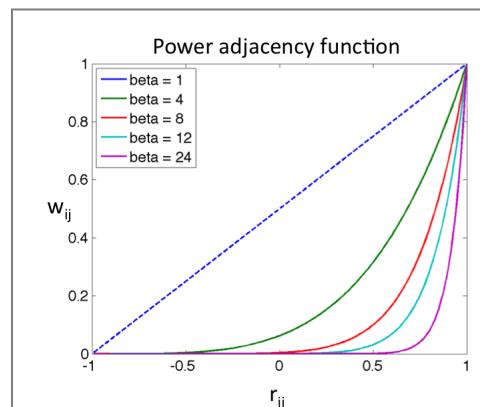


Fig. 1: Power law adjacency function for various values of β .

Conclusions:

- Fully-weighted networks provide a means to replace hard thresholding with a continuous mapping of correlation values into edge weights.
- A power law mapping with $\beta \gg 1$ allows weaker connections to be suppressed rather than removed, avoiding issues related to network fragmentation.
- $\beta \sim 12$ provided reproducible properties with scale-free-like and small world behavior similar to that found in binary networks.
- The linear mapping ($\beta=1$) retained modular structure only.

References:

- [1] Bullmore & Sporns (2009) *Nat Rev Neurosci* **10**(3) 186.
- [2] Shehzad *et al.* (2009) *Cereb Cortex* **19**(10) 2209; www.nitrc.org.
- [3] Tzourio-Mazoyer *et al.* (2002) *NeuroImage* **15**(1) 273.
- [4] Zhang & Horvath (2005) *Stat App Genetics Mol Biol* **4**(1) 1128.
- [5] Mumford *et al.* (2010) *NeuroImage* **52**(4) 1426.

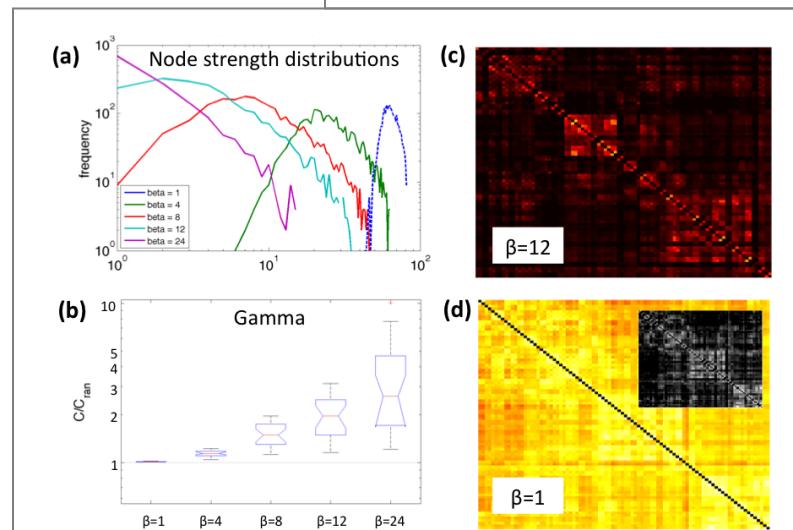


Fig. 2: (a) Node strength distribution and (b) relative clustering (γ) as a function of power law parameter β . Modular structure is retained for fully-weighted networks with $\beta=12$ (c) and $\beta=1$ (d), although with less dynamic range in the latter [inset: heaviest