Multiscale Organization of the Human Connectome via Laplacian Renormalization

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The human brain is a multiscale system that can be modeled as a hierarchical modular network of interacting regions. Understanding this architecture is essential to explaining emergent collective behaviors across spatial scales. Recent studies suggest that the connectome may display scale invariance, meaning that structural properties remain similar across resolutions. Establishing whether the brain exhibits such self-similar features would uncover fundamental wiring principles and constrain possible generative models of connectivity.

To investigate this, we employed the Laplacian Renormalization Group (LRG), a diffusion-based coarse-graining framework from statistical physics that generates a hierarchy of brain modules and produces downscaled networks through cluster contractions. This construction enables systematic multiscale analysis of the network structure. Applying the method, we found that classical descriptors such as degree distribution, clustering coefficient, and nearest-neighbor degree remain unchanged across coarse-grained levels, whereas the Fiedler eigenvalue scales with system size according to a power law consistent with a spectral dimension close to two, outlying the presence of scale invariance. We implemented the LRG method on a human connectome built from diffusion tractography data from 136 healthy subjects, integrating deterministic and probabilistic approaches into a weighted representation with a novel density-based scheme to correct for biases due to region size.

These findings support the view of the connectome as a self-similar multiscale system and point toward the broader notion of universality classes in networks, opening new avenues for probing the generative principles of structural connectivity.