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Multiscale Organization of the Human Connectome via Laplacian Renormalization

Keywords: Laplacian, Connectome, Scale invariance, Diffusion, Multiscale

Extended Abstract

The human brain is a complex multiscale system that can be modeled as a hierarchical modular network of interacting regions. In such a structure, modules contain smaller submodules in a nested organization, supporting the many-to-one relationship between brain function and structure. Investigating this multilevel architecture is essential to understanding emergent phenomena across spatial scales. Recent studies suggest that the connectome may show scale invariance [1, 2], meaning that its structural properties remain similar across resolutions. Establishing whether the human connectome possesses such self-similar features is crucial, as it would uncover fundamental wiring principles and constrain possible generative models of brain organization. To address this challenge, we adopt the Laplacian Renormalization Group (LRG), a diffusion-based coarse-graining framework from statistical physics specifically designed to probe cross-scale relations in complex systems [3].

We apply the LRG to a human connectome built from diffusion tractography imaging (DTI) data from 136 healthy subjects. Deterministic and probabilistic tractography were integrated into a weighted network that balances structural reliability with rich connectivity. To correct for biases due to region size, we introduce a density-based edge weighting scheme. The LRG generates a hierarchy of brain modules, from which partitions are extracted using a stability index defined in [4]. Cluster contraction then produces successive coarse-grained networks that preserve essential connectivity features across scales.

On these networks, we systematically examined topological descriptors to probe the presence of scale invariance. Classical measures such as degree distribution, clustering coefficient, and nearest-neighbor degree remain invariant across coarse-grained levels, suggesting self-similar wiring principles [1]. To provide stronger evidence, we turned to the spectral domain, based on theoretical results linking Laplacian eigenvalue distributions to scale-invariant network architectures [5]. Specifically, we analyzed the scaling of the Fiedler eigenvalue with respect to the system size, a quantity directly connected to the spectral dimension. Our findings reveal a clear power-law relation with an exponent consistent with a spectral dimension found also in [2]. This result provides independent evidence that the human connectome exhibits a self-similar organization across scales, reinforcing the view of the brain as a multiscale system with self-similar wiring principles.

Beyond evidence for self-similarity, these findings naturally point to the broader question of universality classes in networks. Identifying such classes could shed light on the generative principles underlying the human connectome. In particular, synthetic networks that share the same class as the connectome can reveal plausible wiring mechanisms driving brain organization, offering new perspectives on one of the most fundamental open problems in neuroscience: the origin of the structural connectivity of the brain.

References

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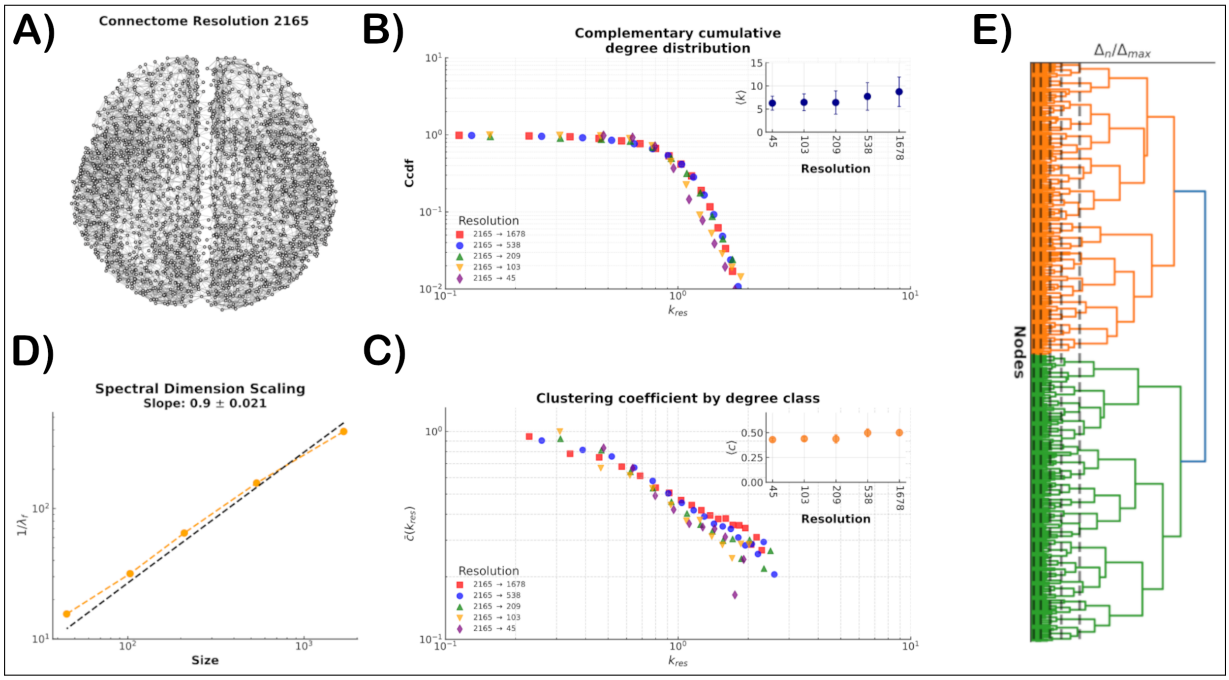

Figure 1: Panels illustrate multiscale features of the human connectome. **A)** Cross-subject connectome with 2165 brain regions as nodes linked by axonal bundles. **B)** Complementary cumulative degree distributions across renormalized scales, showing overlapping curves indicative of scale invariance (inset: average degree remains nearly constant across scales). **C)** Average clustering coefficient by degree class, with consistent trends across scales (inset: mean clustering across scales remains constant). **D)** Scaling of the Fiedler eigenvalue with system size, revealing a power-law relation. **E)** Hierarchical tree of the connectome, with dashed lines marking cuts used for coarse-graining.