[CL3-3]

Cliques and cavities in the human connectome

Ann Sizemore^{1,2}, Chad Giusti¹, Ari Kahn¹, Jean M. Vettel^{3,1,4}, Richard Betzel¹, Danielle S. Bassett^{1,5}

¹Department of Bioengineering, University of Pennsylvania ²Broad Institute, Harvard University and the Massachusetts Institute of Technology ³Human Research & Engineering Directorate, U.S. Army Research Laboratory ⁴Department of Psychological and Brain Sciences, University of California, Santa Barbara ⁵Department of Electrical & Systems Engineering, University of Pennsylvania

The complex tangles of neural wiring cooperate to support a diverse range of cognitive function. Efforts to understand neural architecture and its relation to function often study the connectome by translating this complex system into a network, with brain regions as nodes and white matter streamlines as edges. However, commonly applied graph theoretical tools are unable to capture mesoscale patterns of connections between brain regions which may be essential to cognition. Here we move to the language of algebraic topology in which we encode groups of all-to-all connected brain regions as cliques, which are both biologically relevant and allow us to see novel features such as topological cavities. While cliques of brain regions allow for rapid communication, topological cavities may promote parallel processing of information. Using an averaged connectome from eight healthy adults scanned in triplicate, we find a gradient of clique size along the anterior-posterior axis, consistent with previous studies of these areas. To find essential cavities we compute the persistent homology of the connectome and find topological cavities of different dimensions. We further investigate four long-lived persistent cavities and consistently detect these features across individual scans. We compare the persistent homology results to those obtained from a null model created by wiring minimization and find fewer and shorter-lived cavities arise in the averaged connectome. Yet we observe removing subcortical regions from the network yields similar persistence diagrams between the averaged connectome and null model, suggesting subcortical regions act as cone points within an efficiently wired cortical shell. We see most recovered minimal generators of persistent cavities link brain regions of early and late evolutionary origin, suggesting the importance of non-trivial loops in controlling higher brain function. Finally we speculate on the role of topological cycles in cognitive function and discuss the promise of applied topology in biological applications.