

Persistent homology: a computational topology-based approach to study brain connectivity

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A mechanistic understanding of brain function and malfunction will necessary require to establish a causal theory of the brain. Candidates for global brain theories are not missing e.g. Friston's Free Energy minimization (Friston,2010), von Malsburg's correlation theory (Malsburg,1994), Abeles corticonomics (Abeles,1991), Llinás thalamo-cortical loop (Llinás,1993), Tononi's integrated information theory (Marshall, 2016) etc. but the jury is still out on a causal explanation of cognition. Neuroimaging reveals only correlations. Causality can only be investigated through intervention, that is, stimulation or lesion. This poses a tremendous challenge in a nonlinear highly coupled system like the brain. Intervention in one area of the brain can ripple to other parts in very complex and unpredictable ways. In this work we make the argument that network models fall short of producing mechanistic models of normal function and disease. Graphs are built by connecting one pair of elements at a time. The limitation of having exclusively dyadic (or bivariate in statistics jargon) relationships is a crucial limitation that is

often overlooked (Giusti,2016). Computational topology allows us to go beyond pairwise connections within an elegant mathematical framework. In particular, the connectomics of the mammalian brain can be studied with persistent homology. Persistent homology is a method of computational topology that studies the persistent structure in data sets. This framework provides a compact encoding of multi-scale relations and is agnostic to the way the coupling is computed (power-based, phase-based, Granger causality, dynamic time warping etc.) We will show using resting state fMRI connectivity data, how persistent homology provides new views to understand the interplay between strong and weak connections in the brain connectome.

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