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"Information Flow Limits in Connectomes"

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Abstract:

With the growing amount of connectome data being gathered, it behooves us to develop systems-theoretic methods to analyze this data so as to provide insights into the function of neuronal circuits. I start by describing some linear systems methods for predicting functional neuronal subcircuits from connectome data. Next I develop models and compute capacities for gap junction synapses. Then I develop information-theoretic lower bounds on computation speed arising from limitations of anatomical connectivity and physical noise. For the nematode Caenorhabditis elegans, these bounds are predictive of biological timescales. Moreover, the hub-and-spoke architecture of C. elegans functional subcircuits are optimal under constraint on number of synapses. In closing, I will discuss state-of-the-art methods for connectome data acquisition using compressed sensing-inspired multineuron excitation and a message-passing reconstruction algorithm.