Abstract Submitted
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Physical limits on computation by assemblies of allosteric proteins[1] JOHN ROBINSON, University of Alabama at Birmingham — Assemblies of allosteric proteins are the principle information processing devices in biology. Using the Ca^{2+}-sensitive cardiac regulatory assembly as a paradigm for Brownian computation, we examine how system complexity and system resetting impose physical limits on computation. Nearest-neighbor-limited interactions among assembly components constrains the topology of the system's macrostate free energy landscape and produces degenerate transition probabilities. As a result, signaling fidelity and deactivation kinetics can not be simultaneously optimized. This imposes an upper limit on the rate of information processing by assemblies of allosteric proteins that couple to a single ligand type.

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