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Talk: Simulations of Bacteria with Morphogenetic Systems

Joint work with Martin Pavlíček

Abstract: Morphogenetic (M) systems is a computational model inspired by morphogenesis of living cells. Mathematically, it is based partly on the concept of P systems with proteins on membranes providing abstract metabolic processes, and partly on the algorithmic self-assembly of tiles. An M system, however, generalizes both concepts into a unique framework. It allows to self-assemble 1D or 2D primitives of arbitrary pre-defined shapes into 2D or 3D forms, while the process is controlled by flow of atomic objects due to P-system-like rules. It was shown that M systems are computationally universal, error-prone, with strong self-healing properties, and able to solve NP-hard problems in a polynomial time.

Here we show that M systems are also able to simulate key processes in bacteria on a high level of granularity, while following important qualitative and quantitative macro-properties of the simulated cells. Initial experiments simulating growth of cytoskeleton inside cells were extended to cell fission processes under changing environmental conditions and to resistance of cells (e.g., E.Coli) to antibiotic agents. We show that, in spite of relative simplicity of the designed models of both prokaryotic and eukaryotic cells, their results faithfully correspond to published biological observations.