

Polarization in Yeast Mating: Modeling and Simulation of Spatial Stochastic Phenomena

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We have developed a spatial stochastic model of polarisome formation in mating yeast, focusing on the tight localization of proteins on the membrane. This new model is built on simple mechanistic components, but is able to achieve a highly polarized phenotype with a relatively shallow input gradient. Preliminary results highlight the need for spatial stochastic modeling to reproduce experimental observations.

Spatial stochastic simulation is very computationally intensive. We have recently developed a new algorithm, the Diffusive Finite State Projection (DFSP) method for the efficient and accurate simulation of stochastic spatially inhomogeneous biochemical systems. DFSP makes use of a novel formulation of FSP to simulate diffusion, while reactions are handled by the Stochastic Simulation Algorithm (SSA). DFSP has already yielded substantial performance gains and is highly parallelizable.