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Author

David Fange

Title (English)

A comparison of stochastic and deterministic modelling using MesoRD on the Min-system in *E. coli*

Title (Swedish)

Abstract

A comparison of the mesoscopic and macroscopic reaction-diffusion modelling has been performed. The comparison has been done on a full 3D model using Monte Carlo simulation, solving the reaction-diffusion master equation, and deterministic simulation, solving partial differential equations. All simulations were done on the Min-system in *E. coli*. In many cases the stochastic and deterministic simulations has been observed to show similar results, in which the oscillations periods and spatial positioning of the involved proteins are equivalent in the two types of simulations. Differences between the stochastic and deterministic simulation has been observed for *E. coli* mutants with abnormal shape. In these cases the stochastic simulation will show a drift from the pattern observed from deterministic simulations. In the case of a mutant with spherical shape the stochastic simulation shows a behaviour that describes the experimental data better than the deterministic simulation.

Keywords

Min proteins, macroscopic, mesoscopic, reaction-diffusion simulation

Supervisors

Johan Elf

Department of Cell & Molecular Biology, Uppsala University

Scientific reviewer

Per Lötstedt

Department of Information Technology, Uppsala University

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Biology Education Centre Biomedical Center Husargatan 3 Uppsala

Box 592 S-75124 Uppsala Tel +46 (0)18 4710000 Fax +46 (0)18 555217