Efficiently Solving the Stochastic Reaction-Diffusion Master Equation in C++ with a COMSOL Interface

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Abstract

Introduction: We are interested in quantitatively analyzing the interplay between biological cell architecture, such as microtubules, and cellular signaling processes in space and time. Specifically, we construct stochastic reaction-diffusion models of the budding yeast cell in 2D and 3D with embedded microtubules to investigate the interactions of bud-directed astral microtubules with their environment during mitosis in Saccharomyces cerevisiae. The models are based on the reaction-diffusion master equation (RDME), which is a coarse-grained approximation of microscopic Smoluchowski dynamics.

Use of COMSOL Multiphysics®: To efficiently simulate this type of model, we implemented a cross-platform, modular and high-performance C++ RDME solver framework that uses COMSOL Multiphysics for mesh generation and matrix assembly similar to [1]. Initial state and parameters are specified in MATLAB® (Mathworks, Nantucket / MA), and the complete initial state specification of the model is saved in HDF5 format. Reactions are directly compiled into the C++ solver executable, contributing to superior performance compared to published next sub-volume method solvers. Furthermore, we are currently working on enabling hybrid deterministic/stochastic simulation, such that computational effort for stochastic simulation can be focused on chemical species of interest. The output is written to an HDF5 file again, which can be re-used as a simulation input, thereby enforcing reproducibility. Simulation results can be analyzed in MATLAB by drag-and-dropping the HDF5 results file and re-imported into COMSOL Multiphysics for visualization and further analysis.

Results: Numerical performance of the solver was tested with the MinD/MinE example from [1], showing on average a two-fold speed up compared to a state of the art solver [1]. High-performance simulations allow us to link simulation results to experimental observations made with fluorescence microscopy, for which we developed an interface to our previously-presented virtual microscope [2]. This enables physically accurate in silico simulations of fluorescence microscopy experiments, given a particular model geometry and photometry as well as the microscopy setup. Applications include parameter estimation and experimental design.

Conclusion: We developed an RDME solver with a COMSOL Multiphysics interface with state-of-the-art performance, and made it easily interoperable with MATLAB and our virtual microscope. This will enable accurate system identification for stochastic spatio-

temporal models based on fluorescence microscopy data.

Reference

[1] B. Drawert et al., URDME: A Modular Framework for Stochastic Simulation of Reaction-Transport Processes in Complex Geometries., BMC Syst. Biol., Vol. 6, p. 76 (2012)
[2] D. K. Samuylov et al., Mapping Complex Spatio-Temporal Models to Image Space: The Virtual Microscope, ISBI 2015 (2015)