StochSS: Stochastic Simulation Service
An Integrated Development Environment for Simulation and Analysis of Discrete Stochastic Biochemical Models

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Abstract
We present StochSS: Stochastic Simulation as-a-Service, an integrated development environment for modeling and simulation of discrete stochastic biochemical systems. An easy to use GUI enables researchers to quickly develop and simulate biological models on a desktop or laptop, which can then be expanded or combined to incorporate increasing levels of complexity. As the demand for computational power increases, StochSS is able to seamlessly scale up by deploying cloud computing resources. The software currently supports simulation of ODE and well-mixed discrete stochastic models, parameter estimation of discrete stochastic models, and simulation of spatial stochastic models. StochSS is available for download at www.StochSS.org.

Our Vision
- Build your Model
  - StochSS provides an easy-to-use User Interface to quickly specify your model.
  - Species, Parameters, Reactions, and Geometry.
- Scale up the Complexity
  - In StochSS the same model can be used for multiple different types of simulation.
  - Deterministic (ODE) Simulation.
  - Stochastic Simulation.
  - Spatial Stochastic Simulation.
  - Parameter Sensitivity.
  - Estimation of Parameters from Data.
- Clusters On-Demand
  - Create a cluster with as much or as little computing power as you need, only when you need it.
- Insight from Modeling
  - The purpose of all modeling is to gain insight into the systems under study.
  - Insight requires visualization and analysis of simulation data.
  - StochSS provides state-of-the-art visualization of simulation results and easy methods to access and process data sets.

Roadmap
StochSS v1.4 released Sep 2014
Integration of PyURDME:
Spatial stochastic simulation on complex geometries using tetrahedral meshes.
Advanced visualization of mesh geometries and spatial simulation results via WebGL.

StochSS v1.3 released Jun 2014
Integration of StochOptim:
Parameter estimation tool for stochastic models via the MCEM method.
Advanced cloud computing cluster management and real-time visualization of parameter value convergence.

StochSS v1.2 released Mar 2014
Authentication / User system
Model sharing and collaborative workflow
Sensitivity analysis for ODE simulation
Computation of rare-event probabilities

StochSS v1.1 released Jan 2014
Windows support
Concentration models
ODE simulation
Model conversion: population to concentration
Enhanced management of cloud computing resources

StochSS v1.0 released Jun 2013
Mac & Linux support
Model development IDE
Simulation models locally
Launch cloud computing resources in EC2
Stochastic simulation of well-mixed systems (StochKit2)
Plotting time-series data, mean/stddev, histogram

Future Development
Advanced tools for data exploration and analysis
Global and local parameter sweeps
Spatial model: 3D domain specification
Spatial simulation methods: deterministic (PDE)
Hybrid stochastic mesoscopic/microscopic solvers

A wide range of powerful computational tools, all in one place!

- CVODE - ODE simulation
  - CVODE is a solver for stiff and nonstiff ordinary differential equation (ODE) systems with sensitivity analysis capabilities.
  - http://computation.llnl.gov/casc/ CVODE/

- StochKit - Stochastic Simulation
  - StochKit is an efficient, extensible stochastic simulation framework developed in the C++ language that aims to make stochastic simulation accessible to practicing biologists and chemists, while remaining open to extension via new stochastic and multiscale algorithms.
  - The current version of StochKit includes the popular Gillespie Stochastic Simulation Algorithm (SSA) Direct Method, our new Logarithmic Direct Method which is considerably faster than the original Direct Method, slow-scale SSA for multiscale problems, adaptive non-negativity preserving explicit tau-leaping, and core modules for explicit, implicit and impulsive tau-leaping methods.

- StochOptim - Parameter Estimation
  - StochSS implements parameter estimation for stochastic biochemical systems (StochOptim) via the Monte Carlo expectation-maximization with Modified Cross-Entropy method (MCEM). MCEM computes maximum likelihood parameter estimates (MLEs) and associated uncertainties in three consecutive phases: cross-entropy, Monte Carlo expectation-maximization (MCEM), and uncertainty quantification.
  - B.J. Daigle et al. BMC Bioinformatics (2011)

- PyURDME - Spatial Stochastic
  - PyURDME is a general software framework for modeling and simulation of stochastic reaction-diffusion processes on unstructured, tetrahedral (3D) and triangular (2D) meshes. Unstructured meshes allow for a more flexible handling of complex geometries compared to structured, Cartesian meshes. The current core simulation algorithm is based on the mesoscopic reaction-diffusion master equation (RDME) model.
  - PyURDME was originally based on the URDME software package, but has now been completely rewritten in Python and updated. It depends on the FEniCS libraries for mesh generation and assembly (see http://fenicsproject.org/).
  - The core simulation routines are implemented in C, and require GCC for compilation. The default solver is an efficient implementation of the Next Subvolume Method (NSM).