The ERATO Systems Biology Workbench

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Introduction

The ERATO Systems Biology Workbench (SBW) is an extensible software framework enabling the creation of an integrated, easy-to-use software environment that allows the sharing of models and resources between simulation and analysis tools for systems biology. In this poster we summarize the project goals and current status.

Goals of the SBW Project

Integrate a variety of software tools that implement different approaches to modeling, parameter analysis, and other related tasks
Enable the construction of complex hierarchical multicellular models from arrays of model components
Enable the interaction with biologically-oriented databases containing data, models and other relevant information

Principles of the SBW project

Be open source: use a variant of the GNU library license
Be portable to Windows and Linux
Use current and emerging standards such as Python 2 and the Systems Biology Markup Language (SBML)
Ensure tools are easy to use
Reduce the time spent by developers both creating software infrastructure and creating tools that exist in a similar form in other packages, allowing developers to concentrate on the development of new algorithms and models
Use the workbench as a vehicle for collaboration between developers of bioinformatics technology

Architecture

To facilitate modularization and extensibility, SBW is a software framework that enables separate compiled modules or plug-ins to be combined to form a functioning application. Currently the plug-ins can either be applications, dynamic libraries or Java JAR files. Plug-ins can be created in several programming languages. SBW currently employs components written in Delphi and Java, and we have written plugins in C++. We plan to create bridges to other languages including Python.

Intercommunication between plug-ins is performed by a simple message passing mechanism. Plugins are registered with a directory. This directory indexes plug-ins by category. A category groups together plugins with a common interface.

Phase 1

Designer

This plugin provides a GUI for drawing biochemical pathways. The Designer exports the model in SBML format. The SBW integration allows the user to select an analysis to be invoked on the model.

Jarnac

This plugin provides the following ODE-based analyses: Time-Based simulation, Steady state analysis and Metabolic Control Analysis.

Optimization

This allows the fitting of model parameters to experimental data.

Phase 2

Bifurcation

We will integrate a standard bifurcation tool.

3D Plotting

We will integrate 3D plotting functionality to support time based simulation and bifurcation analyses.

Phase 3

Multi-mode simulation

We will develop a new time-based simulation component that will enable very fast yet accurate simulation of biochemical networks. This simulator will combine Stochastic and ODE techniques using novel algorithms developed in collaboration with leading researchers in the field.

Transparent database access

We will develop a several plugins to enable the user to download models from bioinformatics databases.

Modular and Multi-cellular models

As part of phase 3 we will enable SBML Level 2 support by:

Extending and developing model capture tools to support hierarchical models
Developing a tool that translates SBML Level 1 from Level 2 to enable existing analyses to be applied to Level 2 models.

Packaging

We plan to create a Windows installation as part of phase 1 and a Linux installation as part of phase 2. These packages will include plug-ins as they become available and tutorials with working models supplemented later by online documentation. We plan to set up web resources appropriate to open source development, including a public bug database.

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The System Biology Workbench - http://www.cds.caltech.edu/erato/
ERATO Kitano Project - http://www.sysbio.jst.go.jp/
Jarnac - http://members.tripod.co.uk/sauro/biotech.htm