iBioSim: A Tool for the Analysis and Design of Genetic Circuits

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`iBioSim` supports learning of genetic circuit models, efficient abstraction-based analysis of these models, and the design of synthetic genetic circuits. `iBioSim` includes project management features and a graphical user interface that facilitates the development and maintenance of genetic circuit models as well as both experimental and simulation data. Models in `iBioSim` can be created using either an SBML editor or a *Genetic Circuit Model* (GCM) editor. The SBML editor and the `iBioSim` simulation engine support virtually all of SBML Level 2 Version 3 including reactions, rules, events, constraints, etc. The GCM editor improves the efficiency of model development by supporting modeling at a higher level of abstraction than the molecular level supported by SBML. Namely, a GCM includes only important species and their influences upon each other. `iBioSim` can automatically translate from GCM to SBML models for analysis. A GCM can be either manually created or automatically learned from time-series data. `iBioSim` also includes an efficient simulation engine that supports ODE, stochastic, and Markov chain analysis of these models. This engine utilizes automatic abstraction to improve analysis time, often by one to two orders of magnitude. Finally, `iBioSim` has a graphical editor for visualizing both time series and event probability analysis results.

`iBioSim` has been applied successfully to numerous projects including an analysis of the phage λ decision circuit and the *E.* coli Fim switch. It has also been applied to the design of a synthetic genetic Muller C-element, an asynchronous state-holding gate. In these and other efforts, the `iBioSim` tool with its support for automatic abstraction has been shown to greatly improve the productivity of researchers who are analyzing and designing genetic circuits.

This tutorial will cover the following topics:

1. Modeling genetic circuits using SBML and GCM.
2. Analysis of genetic circuits using ODEs and stochastic methods.
3. Circuit abstraction methods and Markov chain analysis.
4. Genetic circuit design.

The concepts will be motivated and illustrated using examples from the phage λ and Fim switch models as well as from synthetic genetic circuits such as the genetic Muller C-element. While the `iBioSim` tool will be utilized to present these concepts, the material will be generally applicable to other similar tools.

This tutorial will present in a condensed fashion that which is covered in our biological modeling courses at the University of Utah. For more information on these courses, please see:
`http://www.async.ece.utah.edu/~myers/ece6760/` and
`http://www.async.ece.utah.edu/~myers/math6790/`.
Materials for the tutorial will be drawn from a textbook that we prepared for these courses which has been accepted for publication by Taylor and Francis Publishing Group.

We are also interested in having an arena available for further demonstrations and discussions after the tutorial.