SigNetSim : A web tool for modeling and analyzing quantitative biochemical networks

Vincent Noël [1], Marcelo S. Reis [1], Matheus H.S. Dias [1], Lulu Wu [1 2], Amanda S. Guimarães [1 2], Daniel F. Reverbel [2], Junior Barrera [1 2], and Hugo A. Armelin [1 3]

[1] LETA-CeTICS, Instituto Butantan, Brazil
[2] Instituto de Matemática e Estatística, Universidade de São Paulo, Brazil
[3] Instituto de Química, Universidade de São Paulo, Brazil

Molecular biology is experiencing a revolution, thanks to data acquisition becoming increasingly cheaper, and to the development of Systems Biology, an emergent research field that shows new ways to study such high-throughput data. However, biologists need a new generation of tools capable of handling large quantitative datasets, and also performing rigorous mathematical analysis of the kinetic models that may be derived from them. SigNetSim is a web tool coded in Python 2.7 using the Django framework, and Bootstrap as a graphical front-end. It is designed to perform most computer-intensive work server-side, which make it usable from most devices. It enables its user to easily create or edit quantitative models, using the latest standard to describe biological models (SBML L3V1). It is also compatible with the Hierarchical Model Composition package, which enable to describe models as a collection of modules, which are by themselves SBML models. SigNetSim can simulate models, both time series and steady states, and plot the results using interactive JavaScript libraries. It also includes some basic database to store experimental data, which associate a set of treatments to a set of observations. Database entries can later be used to simulate an experiment, using the list of treatments as initial conditions for the simulations. SigNetSim also enables the user to look for values of kinetic constants for the model which are able to reproduce the experimental data, using a parallel global optimisation method (simulated annealing). Finally, SigNetSim can perform dynamical analysis of the model, using exact methods thanks to a symbolic representation of the mathematical model, or other methods like numerical continuation techniques for bifurcation analysis. User can also use directly libSigNetSim, the core library of SigNetSim, from Jupyter notebooks in order to work directly on the models in Python, including the symbolic math version. Both the web interface and the library are available on GitHub, under free software license. It has already proved to be a very useful tool to work on quantitative models in our team. Thanks to its user-friendly web interface, even researchers and students that are inexperienced in programming can build, adjust and simulate models for both scientific and didactic purposes. We are currently adding support for model annotations, which allow to use standard formats to describe model components, and easily generate informative graphical diagrams.

This work was supported by grants #12/20186-9, #13/07467-1, and #13/24212-7 of the São Paulo Research Foundation (FAPESP) and fellowships from CNPq.