169. PyBioS — object-oriented simulation tool for biological processes with application to the analysis of gene regulatory networks

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1 PyBioS — object-oriented tool for modeling and simulation of biological processes

Modeling and simulation systems are a valuable tool for the understanding of complex biological systems. We present an object-oriented, web-based environment that supports the modeling, simulation and storage of large models. The platform is implemented as a Python-product for the Zope web application server environment [4, 5]. The population of hierarchically ordered biological models according to cytological and molecular biological structures is done by the use of a web interface. It supports the generation of large models based on knowledge from high-troughput experiments, like expression profiles or protein/protein interaction data, or publicly available information like the metabolic data of the KEGG database or the Genome-Matrix [6]. Based on predefined kinetic laws automatic generation of ODE-systems and following simulation of time courses is supported through the web-interface. The models can be used for hypotheses generation by forward-modeling, e.g. for *in silico* knock-out experiments. Through automated import and population of systems via interaction networks, elements of array analysis such as clustering and reverse engineering can be incorporated. Visualization of the interaction networks is enabled by automatically generated graphs that include information about the objects, the reactions and the mass- and information-flow. SBML-export/import enables compatibility to other simulation tools.

2 Simulation of gene regulatory networks and clustering of gene expression profiles

We set up a framework in order to identify and validate parameters that are useful to describe gene regulatory systems [1]. The input is a network containing N nodes (genes) and K edges that describe the character of the interaction (activation, inhibition). Relevant parameters are for instance the connectivity of the nodes (regulatory input from other genes), the number of connected components (separate pathways in the system), or the number of regulating nodes (transcription factors). The regulatory network is automatically converted into a PyBioS-model that includes transcription, mRNA export into the cytosol, translation, protein-import into the nucleus and mRNA and protein degradation. Resulting concentration series at given time points with varying initial concentrations are clustered by the gene expression analysis tool J-Express [2] in order to judge the relevance of the input parameters. In the poster we present results according to various artificial networks and published gene regulatory data from yeast [3].

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