Research Project in Bioinformatics

Graphical Editor for Systems Biology Models

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1 Background

In diverse applications, computational modeling has demonstrated to be useful for a variety of areas, ranging from fundamental research over biotechnology to applications within the health sector. As in other sciences, reproducible findings are of the highest importance. Over the past two decades, the format SBML [2] has advanced to the de facto standard for encoding systems biology models that satisfies this need [6]. However, this XML-based format has never been intended to be written or read by human users directly. Instead, dedicated software libraries should take care of importing and exporting models in SBML format.

Particularly in the life sciences, spreadsheet-based representations of information are prevalent. According to a recent questionnaire, many researchers desire to develop their models in user interfaces that present the information in table form. The format SBTab [4] has been developed to be compatible with SBML.

2 Aim

In this project, a graphical user interface should be developed that presents systems biology models in a form similar to SBTab, and that allows the user to edit the information. The software should cover the core of SBML as well as the so-called FBC extension (Flux Balance Constraints) for representing constraint-based models [5]. It should be programmed in a way to also enable the addition of further extension packages or additional levels and versions of SBML.
3 Approach

In a preceding bachelor’s thesis and as part of a students’ team project, two different versions of such a user interface have been developed. The SBMLSheets project is based on the InSilico framework that is based on OSGi technology and FXclipse. As such, SBMLSheets can be used in combination with further plugins for the InSilico framework, such as the simulation core. It is, therefore, most standardized and well suited for further extension. For this reason, it is intended to finalize an initial version of SBMLSheets as the result of this project. Recon 3D is a useful example model for testing the software.

4 Requirements

1. Experience in Java programming and JavaFX
2. Fundamental understanding of biochemistry
3. Interest in systems biology modeling
4. Enthusiasm and a sense for detail

References


