SBRML – A Markup Language for Encoding Systems Biology Results

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• Introduction

The wide acceptance of Systems Biology Markup Language (SBML) as standard format for models of biochemical systems makes it possible to build, share, evaluate and develop biochemical models cooperatively. However, it is currently no standard format for encoding the results of computational analyses of systems biology models. To address this issue, we present here the Systems Biology Results Markup Language (SBRML) level 1, an XML-based format for representing systems biology results. SBRML is a software-neutral language intended to allow any type of systems biology results to be represented. It associates a model with several data sets. Each data set consists of a series of values associated with model variables, and their corresponding parameter values. SBRML provides a flexible way of indexing both simulation results and experimental data to model parameter values which supports both spreadsheet-like data or multidimensional data cubes.

• SBRML Structure & Components

The initial state of a biochemical reaction network is defined in the SBML model. To simulate and analyse the network reaction, a software package takes the SBML model as input and transforms that initial state through a specific operation. The outcome of an operation is a new state of the system. Often an operation produces a sequence of new states, e.g. a time course. The result of an operation therefore consists of one or more result components. SBRML describes the model that is used to generate the results, ontology terms that link all the terms/vocabularies used to external ontologies, the operation that is performed on the model and a flexible means for encoding the results of the operation. Below is the basic structure of SBRML and a brief description of its main components.

• SBRML Document Examples

• Discussion

- SBRML provides a simple but powerful structure for encoding simulation and experimental results.
- Standardization of systems biology results format will bring obvious benefits in terms of storage and retrieval, but will also benefit any program that needs to read data in the context of a biochemical model.
- Comments and feedback received during and after the presentation of SBRML specification at the 2008 SBML Forum in Sweden show that SBRML is a suitable solution to address the lack of standard format for encoding systems biology results.
- Very simple, flexible and powerful means of encoding systems biology results.
- Enables easy storage, retrieval and exchange of systems biology results.
- Simplifies the reading of systems biology data in the context of a biochemical model.
- Permits easy integration of simulation and experimental data from disparate and heterogeneous sources.
- The library (libSBML with API for C, C++, Java etc.) for reading and writing SBRML documents is currently being developed and will be released soon.

• References


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Online Example: http://www.comp-sys-bio.org/CopasiWeb/CopasiWebUI
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