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Systems Biology

▶ Metabotropic Receptors (G Protein Coupled Receptors)

Systems Biology Markup Language (SBML)

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Synonyms

SBML

Definition

SBML (the Systems Biology Markup Language, http://sbml.org) is a representation format designed to enable software systems to communicate and store computational models of biological processes. It is not intended as a universal language for quantitative models; rather, SBML's purpose is to serve as a *lingua franca* for exchanging the essential aspects of a computational model between widely different software systems and databases.

Detailed Description

A vast number of modeling and simulation software tools are available today for research in biological domains such as computational neuroscience. This wealth of resources is a boon to researchers, but it also presents interoperability problems. Different software tools for systems biology are implemented in different programming languages, run on

different operating systems, express models using different mathematical frameworks, provide different analysis methods, present different user interfaces, and support different data formats. Despite working with different tools, researchers want to disseminate their work widely, as well as reuse and extend the models of other researchers. They do not want to hardcode their models as software programs nor assume everyone uses the same computing environment; they need common exchange formats for representing their models in such a way that a variety of software systems can read and write them.

SBML (the Systems Biology Markup Language) is such an exchange format for communicating and storing computational models of biological processes (Hucka et al. 2003). It is not a universal language for representing all possible models; rather, it enables communication of the essential aspects of a model, together with annotations that permit any aspect of the model to be elaborated and linked to external data resources. An important principle in SBML is that models are decomposed into explicitly labeled constituent elements (e.g., substances involved in processes, compartments where they are located, etc.); models are *not* cast directly into a specific form such as differential equations. This abstract approach makes it possible for a software tool to translate the SBML form of a model into whatever internal form the tool actually uses – whether that be differential equations, stochastic systems, or some other framework. Although SBML has its roots in general simulations of biochemical reaction networks, it can be used more generally to express other types of models where biological entities are involved in, and modified by, processes that occur over time. It is used today in research on a number of topics, including cell signaling pathways, metabolic pathways, biochemical reactions, gene regulation, and many others.

The latest generation of SBML, which is called SBML Level 3, is modular in the sense of having a defined core set of features and optional *packages* that add features on top of the core. This modular approach means that models can declare which feature-sets they use, and likewise, software tools can declare which packages they support. It also means that the development of SBML Level 3 can proceed in a modular fashion. SBML Level 3 package development is today an ongoing activity, with packages being created to extend SBML in many areas that its core functionality does not directly support. Examples include models whose species have structure and/or state variables, models with spatially nonhomogeneous compartments and spatially dependent processes, and models in which species and processes refer to qualitative entities and processes rather than quantitative ones.

Cross-References

- ▶ Bimolecular Reactions, Modeling of
- ▶ CellML
- ▶ Dynamical Systems: Overview
- ▶ Enzyme Kinetics, Modeling of
- ▶ Gillespie Algorithm for Biochemical Reaction Simulation
- ▶ Model Reproducibility: Overview
- ▶ Numerical Integration Methods
- ▶ Signaling Pathways, Modeling of
- ▶ Software Tools for Modeling in Computational Neuroscience: Overview

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Systems with Two or More Phase-Spaces

- ▶ Multistability: Stopping Events with Single Pulses