

SBML Level 2 Version 3

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Background

Researchers in systems biology today have access to a wide variety of software tools for computational modeling. Until the widespread adoption of the Systems Biology Markup Language (SBML) [1], users could not effectively transfer their models from one computational tool to another or share their models with fellow researchers. This has changed significantly in the last few years, with over 100 software projects (including several commercial developers) having adopted SBML as a common model definition language [2].

SBML is an XML-based exchange format for computational models of biochemical networks. It is being developed by an international community of interested developers and users. Development is proceeding in stages; each new Level of SBML extend the language's features compared to lower-numbered levels, and versions within Levels allows for corrections and changes to features [3].

New Developments

SBML Level 2 Version 3 is the latest definition of SBML, and was released in May, 2007 [4]. It represents substantial improvements to SBML Level 2. Among the changes compared to Version 1 are simplifications to the unit system, removal of language features that risked allowing the creation of inconsistent model definitions, introduction of support for the Systems Biology Ontology (SBO), introduction of an RDF-based annotation scheme for referring to external resources, various corrections to minor inconsistencies in the SBML language, and addition of validation rules defining what constitutes a syntactically and structurally correct SBML model definition.

In this poster, we describe the major changes introduced in SBML Level 2 Version 3. We also discuss libSBML 3.0, a portable software library for reading, writing and editing SBML.

References

- [1] Hucka, M., Finney, A., Sauro, H. M., Bolouri, H., Doyle, J. C., Kitano, H., Arkin, A. P., Bornstein, B. J., Bray, D., Cornish-Bowden, A., Cuellar, A. A., Dronov, S., Gilles, E. D., Ginkel, M., Gor, V., Goryanin, I. I., Hedley, W. J., Hodgman, T. C., Hofmeyr, J.-H., Hunter, P. J., Juty, N. S., Kasberger, J. L., Kremling, A., Kummer, U., Le Novère, N., Loew, L. M., Lucio, D., Mendes, P., Minch, E., Mjolsness, E. D., Nakayama, Y.,

- Nelson, M. R., Nielsen, P. F., Sakurada, T., Schaff, J. C., Shapiro, B. E., Shimizu, T. S., Spence, H. D., Stelling, J., Takahashi, K., Tomita, M., Wagner, J., and Wang, J. The Systems Biology Markup Language (SBML): A Medium for Representation and Exchange of Biochemical Network Models, *Bioinformatics*, 9(4):524–531, 2003.
- [2] SBML Project Home Page. Available via the World Wide Web at <http://sbml.org>, 2007.
- [3] Hucka, M., Finney, A., Bornstein, B. J., Keating, S. M., Shapiro, B. E., Matthews, J., Kovitz, B. L., Schilstra, M. J., Funahashi, A., Doyle, J. C., and Kitano, H. Evolving a Lingua Franca and Associated Software Infrastructure for Computational Systems Biology: The Systems Biology Markup Language (SBML) Project. *Systems Biology*, 1(1):41–53, 2004.
- [4] Hucka, M., Finney, A., Hoops, S., Keating, S., and Le Novère, N. Systems Biology Markup Language (SBML) Level 2: Structures and Facilities for Model Definitions. *Nature Precedings*, hdl:10101/npre.2007.58.1, 2007.