

## LibSBML 3.0: An API library for SBML

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Systems Biology has stimulated the formalization of an increasing number of biological/biochemical models. The Systems Biology Markup Language (SBML), an XML-based format for encoding computational models of biochemical networks, is becoming accepted as a de facto standard for representing such models [1], facilitating their systematic exchange and storage. Although software developers can add support for SBML to their software applications using a generic XML parser library, it is more convenient and efficient to use a higher-level, SBML-specific interface library that provides features for parsing and manipulating SBML objects directly. To this end, we have developed libSBML, an application programming interface (API) for reading, writing, manipulating, and validating data in SBML format.

LibSBML 3.0 was released in August 2007 and includes many additional features compared to previous versions of libSBML. Among the new features are the following: (1) an XML parser abstraction layer provides uniform functionality regardless of the underlying XML parser used (Expat, Xerces-C, or libxml2); (2) unification of the internal object models between levels and versions of SBML enables support for all SBML levels and versions to be achieved using a single library; (3) consistency-checking and validation of models is now independent of the XML schema for SBML and can be customized to check any combination of the available sets of validation rules, for example, to include or exclude checking units of quantities in mathematical formulas, overdetermined models, etc.; (4) annotations and notes can be manipulated as either strings or new *XMLNode* objects; and (5) there is a specialized interface supporting reading/writing annotations compliant with MIRIAM [2].

In this poster, we describe the major changes introduced in libSBML 3.0 and detail some of the additional features of the library.

LibSBML 3.0 is written in ISO C and C++ and provides language bindings for C, C++, Java, Python, Perl, Lisp, MATLAB, and Octave and is known to run on Linux, Windows and MacOS X. The package is distributed in both source-code form and as precompiled dynamic libraries for the Microsoft Windows. Extensive documentation for several of the language bindings is also available both online and as part of the source distribution.

LibSBML is distributed under the terms of the LGPL open-source license.

## References

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- [2] Le Novère, N., Finney, A., Hucka, M., Bhalla, U. S., Campagne, F., Collado-Vides, J., Crampin, E. J., Halstead, M., Klipp, E., Mendes, P., Nielsen, P., Sauro, H., Shapiro, B., Snoep, J. L., Spence, H. D. & Wanner, B. L. Minimum Information Requested in the Annotation of biochemical Models (MIRIAM). *Nature Biotechnology*, 23:1509–1515, 2005.