

# After 5 years, free systems biology markup language has proven popular

March 2 2010

---

A scientific paper that describes a file format used by scientists to represent models of biological processes has exceeded 500 citations in the ISI Web of Knowledge, an online academic database that documents the impact of scientific publications. The Systems Biology Markup Language (SBML) is designed to enable the exchange of quantitative models of biochemical networks between different computer software packages, allowing the models to be shared and published in a form other researchers can use in various software environments.

Information standards are needed by the systems biology community to help share, evaluate, and develop models of biological processes. Over the years, many scientists and computer specialists have contributed their time and expertise to the development of SBML as part of the international consortium known as the SBML Forum. The paper that first described the SBML information standard and which has exceeded the 500-citation milestone appeared in the journal *Bioinformatics* in 2003 and is entitled "The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models."

Michael Hucka, a Senior Research Fellow at the California Institute of Technology (Caltech) in Pasadena, and first author of the paper, has chaired the SBML Editors and SBML Team by community consensus since 2003. Today he works on all aspects of SBML and is involved with BioModels.net consortium efforts such as the BioModels Database (<http://www.ebi.ac.uk/biomodels>). Said Hucka, "We're all really pleased

by this outcome. The number of citations for our original paper is a validation of the usefulness of the SBML language to the scientific community. The development of SBML continues at pace thanks to the efforts of both a team of dedicated developers and an international community of volunteers and researchers, who act as SBML users and fellow developers. SBML is a free and open community resource that extends beyond the interests of any single group of researchers."

Back in 1999, when the SBML team was coming together, some of the early members of the group included Hamid Bolouri, John Doyle, Andrew Finney, Hiroaki Kitano, Herbert Sauro, and Hucka.\* Hiroaki Kitano, the principal investigator who started the SBML project, is director of Sony Computer Science Laboratories, Inc., and director of the Systems Biology Institute in Tokyo, Japan. Commented Kitano, "Systems biology has triggered a revolution in biology that in time will hugely impact scientific and medical practice. The idea of SBML came from the vision that compatibility and interoperability were going to be the issue once systems biology took-off. In 1999, the group that eventually became the SBML Team at Caltech and I organized a workshop to discuss issues in software platforms and how to solve them. This is when we decided to initiate the project. Since then, many people have found value in the project and the community has grown beyond critical mass. At the time, I was fortunate to be the recipient of Japanese Exploratory Research for Advanced Technology (ERATO) funding. ERATO funding is a large-scale, extremely flexible funding that helped me to support the initiative at an early stage, make the initiative happen, and assist in making the project self-sustainable. Breaking 500 in the citation index is a sure sign that SBML is coming of age."

SBML is a computer-readable format for describing qualitative and quantitative models of biochemical reaction networks. It can also be used to express gene regulatory networks and other phenomena of interest in systems biology. Stefan Hoops, computational systems

biologist at the Virginia Bioinformatics Institute (VBI) at Virginia Tech, served as an SBML Editor for three years. He helped to develop the latest edition of SBML, which is called Level 3, from 2007 until the end of 2009. Said Hoops, "SBML continues to develop in new directions. For example, the new Level 3 specification will allow a much more detailed description of biological models. As a modular solution, it is also becoming very easy to incorporate SBML into a wide range of software packages."

Pedro Mendes, associate professor at VBI and professor in the School of Computer Science, University of Manchester, England, commented, "The community-led and community-maintained initiative described in this paper set out to address a fundamental need in the systems biology community, namely to develop a computer language that facilitates communication and research for scientists interested in studying biochemical pathways and networks. SBML has been a focal point for the computational systems biology community and a catalyst for new developments in this area of research. This citation milestone affirms that SBML is the main standard in the growing field of systems biology."

**More information:**

Original paper: Hucka M, Finney A, Sauro HM, Bolouri H, Doyle JC, Kitano H, Arkin AP, Bornstein BJ, Bray D, Cornish-Bowden A, Cuellar AA, Dronov S, Gilles ED, Ginkel M, Gor V, Goryanin II, Hedley WJ, Hodgman TC, Hofmeyr JH, Hunter PJ, Juty NS, Kasberger JL, Kremling A, Kummer U, Le Novere N, Loew LM, Lucio D, Mendes P, Minch E, Mjolsness ED, Nakayama Y, Nelson MR, Nielsen PF, Sakurada T, Schaff JC, Shapiro BE, Shimizu TS, Spence HD, Stelling J, Takahashi K, Tomita M, Wagner J, Wang J (2003) The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models. *Bioinformatics* 19(4): 524-531. [PMID: 12611808]

The new SBML Level 3 Core specification is described in the following publication: Hucka, Michael, Bergmann, Frank, Hoops, Stefan, Keating, Sarah, Sahle, Sven, and Wilkinson, Darren. The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core (Release 1 Candidate). Available from Nature Precedings [\(2010\)](#)

Provided by Virginia Tech

Citation: After 5 years, free systems biology markup language has proven popular (2010, March 2) retrieved 26 April 2024 from <https://phys.org/news/2010-03-years-free-biology-markup-language.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.