

# JSBML Beginners Guide

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## *Authors:*

Thomas M. Hamm<sup>a</sup>  
Andreas Dräger<sup>a</sup>

Nicolas Rodriguez<sup>b</sup>  
Michael Hucka<sup>c</sup>

## *Institutional affiliations:*

<sup>a</sup> Computational Systems Biology of Infection and Antimicrobial-Resistance, University of Tübingen, Tübingen, Germany

<sup>b</sup> The Babraham Institute, Babraham Campus, Cambridge, UK

<sup>c</sup> Computing and Mathematical Sciences, California Institute of Technology, Pasadena, CA, USA

SBML (the Systems Biology Markup Language) is an XML-based model representation format for storing and exchanging computational descriptions of biological processes. To read, write, manipulate, and perform higher-level operations on SBML files and data streams, software applications need to map SBML entities to suitable software objects. JSBML provides a pure Java library for this purpose. It supports all Levels and Versions of SBML and provides many powerful features, including facilities to help migrate from the use of libSBML (a popular library for SBML that is not written in Java).

This document provides an introduction to JSBML and its use. It is aimed at both developers writing new Java-based applications as well as those who want to adapt libSBML-based applications to using JSBML. This user guide is a companion to the JSBML API documentation.

The JSBML home page is <http://sbml.org/Software/JSBML>.

The JSBML discussion group is <https://groups.google.com/forum/#!forum/jsbml-development>.



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# 1 Getting started with JSBML



Getting started with JSBML [\[1, 2\]](#)







- [1] Andreas Dräger. *Computational Modeling of Biochemical Networks*. PhD thesis, University of Tuebingen, Tübingen, Germany, January 2011.
- [2] Andreas Dräger, Nicolas Rodriguez, Marine Dumousseau, Alexander Dörr, Clemens Wrzodek, Nicolas Le Novère, Andreas Zell, and Michael Hucka. JSBML: a flexible Java library for working with SBML. *Bioinformatics*, 27(15):2167–2168, June 2011.