

Michael Hucka<sup>1</sup> / Frank T. Bergmann<sup>1</sup> / Claudine Chaouiya<sup>2</sup> / Andreas Dräger<sup>3,4,5</sup> / Stefan Hoops<sup>6</sup> / Sarah M. Keating<sup>7</sup> / Matthias König<sup>8</sup> / Nicolas Le Novère<sup>9</sup> / Chris J. Myers<sup>10</sup> / Brett G. Olivier<sup>11</sup> / Sven Sahle<sup>12</sup> / James C. Schaff<sup>13</sup> / Rahuman Sheriff<sup>7</sup> / Lucian P. Smith<sup>14</sup> / Dagmar Waltemath<sup>15</sup> / Darren J. Wilkinson<sup>16</sup> / Fengkai Zhang<sup>17</sup>

# The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 2 Core Release 2

<sup>1</sup> California Institute of Technology, Pasadena, CA, USA. <https://orcid.org/0000-0001-9105-5960>,  
<https://orcid.org/0000-0001-5553-4702>.

<sup>2</sup> Aix-Marseille University, CNRS, I2M, Marseille, France. <https://orcid.org/0000-0003-2350-0756>.

<sup>3</sup> Department of Computer Science, University of Tübingen, Tübingen, Germany. <https://orcid.org/0000-0002-1240-5553>.

<sup>4</sup> Computational Systems Biology of Infection and Antimicrobial-Resistant Pathogens, Institute for Biomedical Informatics (IBMI), University of Tübingen, Tübingen, Germany. <https://orcid.org/0000-0002-1240-5553>.

<sup>5</sup> German Center for Infection Research (DZIF), Tübingen, Germany. <https://orcid.org/0000-0002-1240-5553>.

<sup>6</sup> Virginia Bioinformatics Institute, Blacksburg, VA, USA. <https://orcid.org/0000-0001-8503-8371>.

<sup>7</sup> European Bioinformatics Institute, Cambridge, UK. <https://orcid.org/0000-0002-3356-3542>,  
<https://orcid.org/0000-0003-0705-9809>.

<sup>8</sup> Humboldt University Berlin, Berlin, Germany. <https://orcid.org/0000-0003-1725-179X>.

<sup>9</sup> Babraham Institute, Cambridge, UK. <https://orcid.org/0000-0002-6309-7327>.

<sup>10</sup> University of Utah, Salt Lake City, UT, USA. <https://orcid.org/0000-0002-8762-8444>.

<sup>11</sup> VU University Amsterdam, Amsterdam, Netherlands. <https://orcid.org/0000-0002-5293-5321>.

<sup>12</sup> University of Heidelberg, Heidelberg, Germany

<sup>13</sup> University of Connecticut, Storrs, CT, USA. <https://orcid.org/0000-0003-3286-7736>.

<sup>14</sup> University of Washington, Seattle, WA, USA, E-mail: [lpsmith@uw.edu](mailto:lpsmith@uw.edu). <https://orcid.org/0000-0001-7002-6386>.

<sup>15</sup> University Medicine Greifswald, Greifswald, Germany. <https://orcid.org/0000-0002-5886-5563>.

<sup>16</sup> Newcastle University, Newcastle, Germany. <https://orcid.org/0000-0003-0736-802X>.

<sup>17</sup> NIAID/NIH, Bethesda, MD, USA. <https://orcid.org/0000-0001-7112-9328>.

## Abstract:


Computational models can help researchers to interpret data, understand biological functions, and make quantitative predictions. The Systems Biology Markup Language (SBML) is a file format for representing computational models in a declarative form that different software systems can exchange. SBML is oriented towards describing biological processes of the sort common in research on a number of topics, including metabolic pathways, cell signaling pathways, and many others. By supporting SBML as an input/output format, different tools can all operate on an identical representation of a model, removing opportunities for translation errors and assuring a common starting point for analyses and simulations. This document provides the specification for *Release 2* of *Version 2* of *SBML Level 3 Core*. The specification defines the data structures prescribed by SBML as well as their encoding in XML, the eXtensible Markup Language. *Release 2* corrects some errors and clarifies some ambiguities discovered in *Release 1*. This specification also defines validation rules that determine the validity of an SBML document, and provides many examples of models in SBML form. Other materials and software are available from the SBML project website at <http://sbml.org/>.

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Lucian P. Smith is the corresponding author.

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