

# **Recent Developments in SBML**

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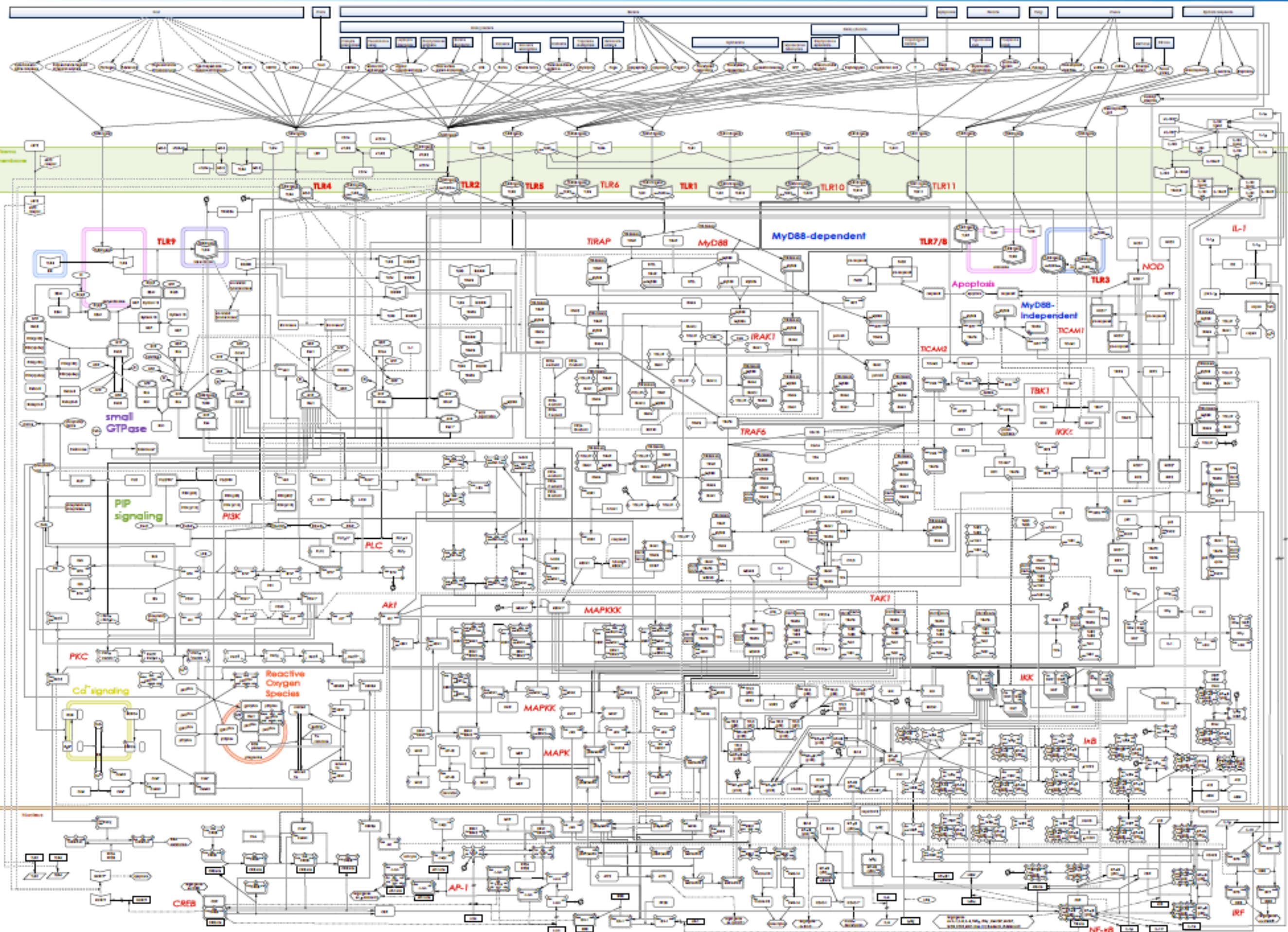
*COMBINE 2014, Los Angeles, August 2014*

**What is SBML for, and why would anyone care?**

**FILED**

[1] Ima Systems Biology Institute, Tokyo, Japan, [2] Department of Fundamental Science and Technology, Kaiti University, Tokyo, Japan, [3] Sony Computer Science Laboratories, Inc., Tokyo, Japan.

<http://www.systems-biology.org>

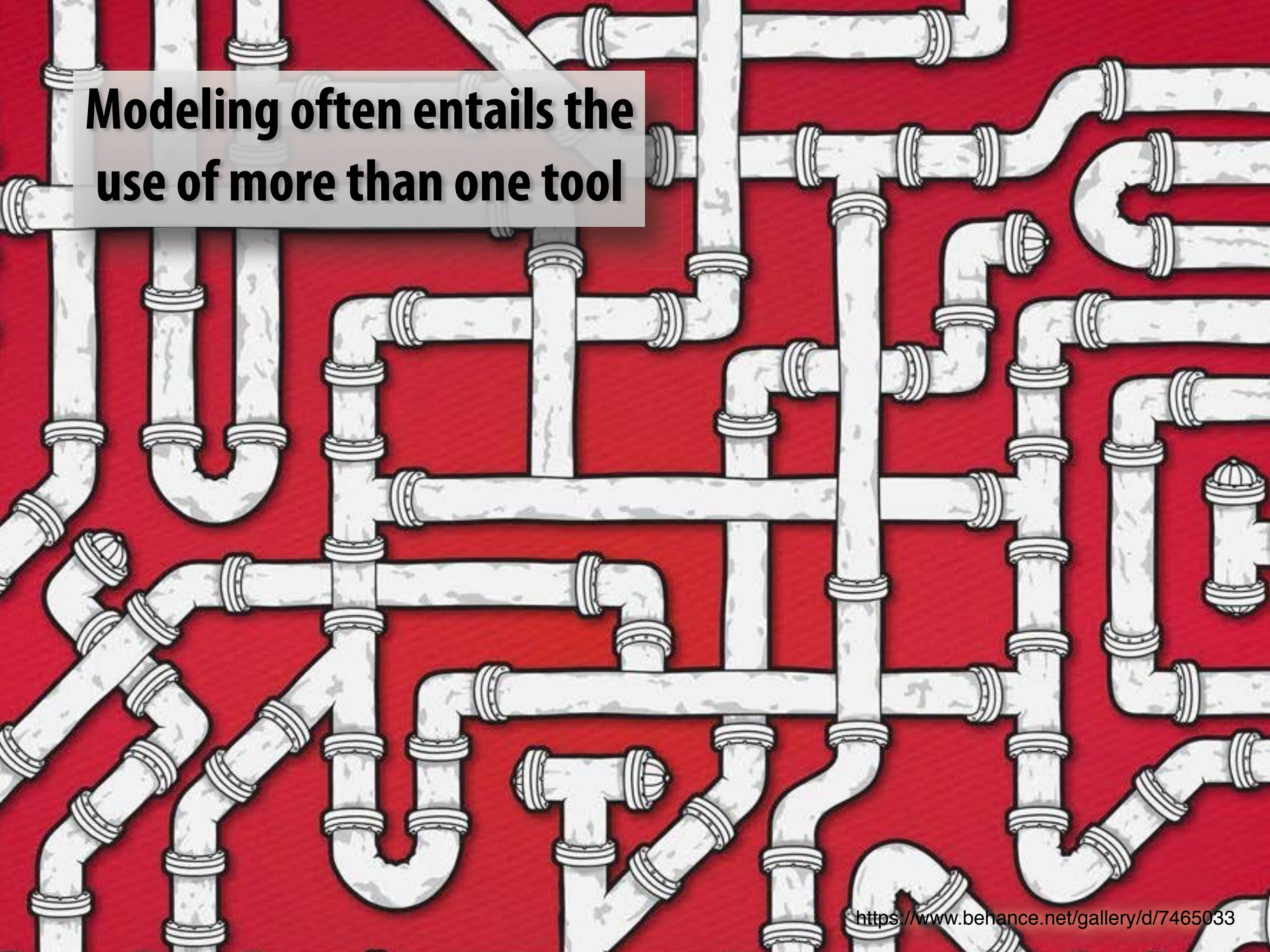




ABC-SysBio	CellNetAnalyzer	Karyote*	PaVESy	SBW: Auto Layout
acslXtreme	CellNOpt	KEGGconverter	PAYAO	sbw: javasim
ALC	Cellware	KEGGtranslator	PET	sbw: stochastic simulator
AMIGO	CLEML	Kineticon	PhysioLab Modeler	SCIpath
Antimony	CL-SBML	Kinsolver	PINT	SED-ML Web Tools
APMonitor	COBRA	libAnnotationSBML	PK-Sim / MoBi	semanticSBML
Arcadia	CompuCell3D	libRoadRunner	PNK	SensSB
Asmparts	ConsensusPathDB	libSBML	PottersWheel	SGMP
Athena	COPASI	libSBMLSim	PRISM	Sigmoid*
AutoSBW	CRdata	libStruct	ProcessDB	SIGNALIGN
AVIS	CycSim	MASS Toolbox	ProMoT	Signalink
BALSA	CySBML	MatCont	PROTON	SigPath
BASIS	Cytoscape	MathSBML	pybrn	SigTran
BetaWB	Cyto-Sim	Medicel	PyDSTool	SIMBA
Bifurcation Discovery Tool	DBSolve	MEMOSys	PySB	SimBiology
BiGG	DEDiscover	MesoRD	PySCeS	Simpathica
BiNoM	Dizzy	Meta-All	RANGE	SimPheny*
BiNoM Cytoscape Plugin	DOTcvpSB	Metaboflux	RAVEN	Simulate3D
Bio Sketch Pad	E-CELL	MetaCrop	Reactome	Simulation Core Library
BioBayes	ecellJ	MetaFluxNet	ReMatch	Simulation Tool
BIOCHAM	EPE	Metannogen	RMBNToolbox	SimWiz
BioCharon	ESS	Metatool	roadRunner	SloppyCell
BioCyc	Facile	MetExplore	RSBML	SmartCell
BioGRID	FAME	MetNetMaker	SABIO-RK	Snoopy
Biological Networks	FASIMU	MIRIAM Resources	Saint	SOSlib
BioMet Toolbox	FBASBW	MMT2	SBFC	SPDBS
BioModels Database	FERN	modelMaGe	SBML Harvester	SRS
BioModels Importer	FluxBalance	ModeRator	SBML Layout	STEPS
BioNessie	Fluxor	Modesto	SBML Reaction Finder	StochKit
BioNetGen	Genetdes	Moleculizer	SBML Translators	StochPy
BioPARKIN	Genetic Network Analyzer	MonaLisa	SBML2APM	StochSim
BioPathwise	Gepasi	Monod	SBML2BioPax	STOCKS
BioPAX2SBML	Gillespie2	MOOSE	SBML2LaTeX	SurreyFBA
BioRica	GINsim	MuVal (Multi-valued logic)	SBML2NEURON	SyBiL
BioSens	GNAT	Narrator	SBML2Octave	SYCAMORE
BioSPICE Dashboard	GNU MCSim	nemo	SBML2SMW	SynBioSS
BioSpreadsheet	GRENDEL	NetBuilder'	SBML2TikZ	Systrip
BioSyS	HSMB	NetPath	SBML2XPP	TERANODE Suite
BioTapestry	HybridSBML	NetPro	SBMLEditor	The Cell Collective
BioUML	iBioSim	Odefy	SBML-PET-MPI	Tide
BoolNet	IBRENA	Omix	SBMLR	TinkerCell
braincirc	Insilico Discovery	ONDEX	SBML-SAT	Trelis
BRENDA	insilicoIDE	optflux	SBML-shorthand	UTKornTools
BSTLab	iPathways	Oscill8	SBMLSim	VANTED
ByoDyn	JACOBIAN	PANTHER Pathway	SBMLSqueezer	Vcell
CADLIVE	Jacobian Viewer	PathArt	sbmltidy	WebCell
Cain	Jarnac	Pathway Access	SBMLToolbox	WinSCAMP
CARMEN	JarnacLite	Pathway Analyser	SBMM assistant	Wolfram SystemModeler
Cell Illustrator	JDesigner	Pathway Builder	SBO	xCellerator
CellDesigner	JigCell	Pathway Solver	SBSI	Xholon
Cellerator	JSBML	Pathway Visualizer	SBSIM	XPPAUT
CellMC	JSim	PATIKAWeb	SBW	
CellML2SBML	JWS Online			

Many software tools for modeling available today





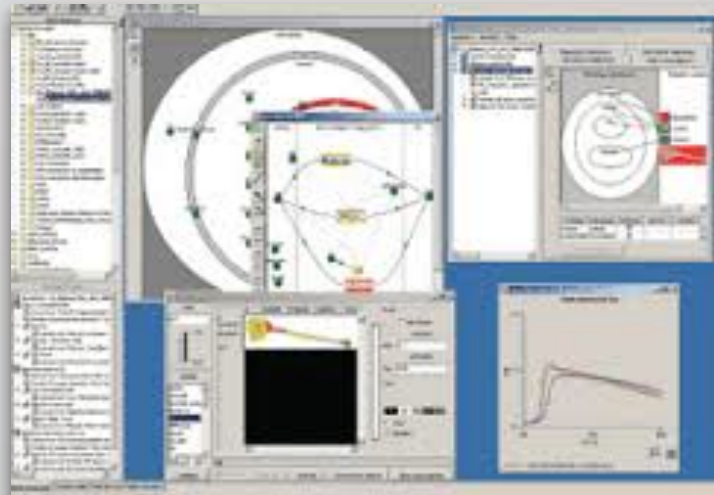
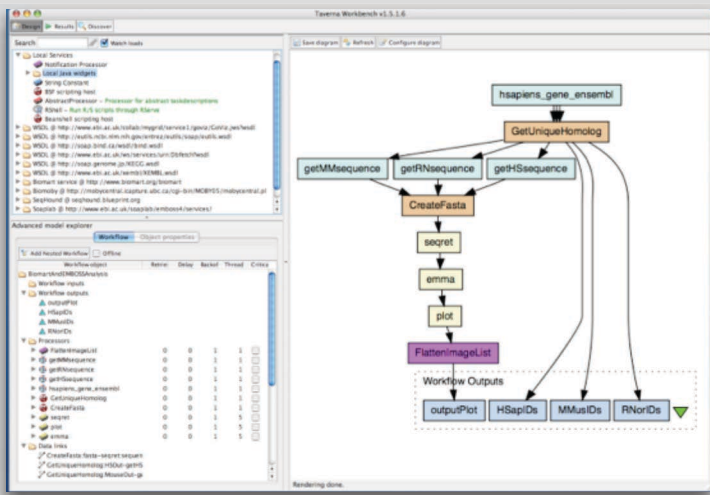
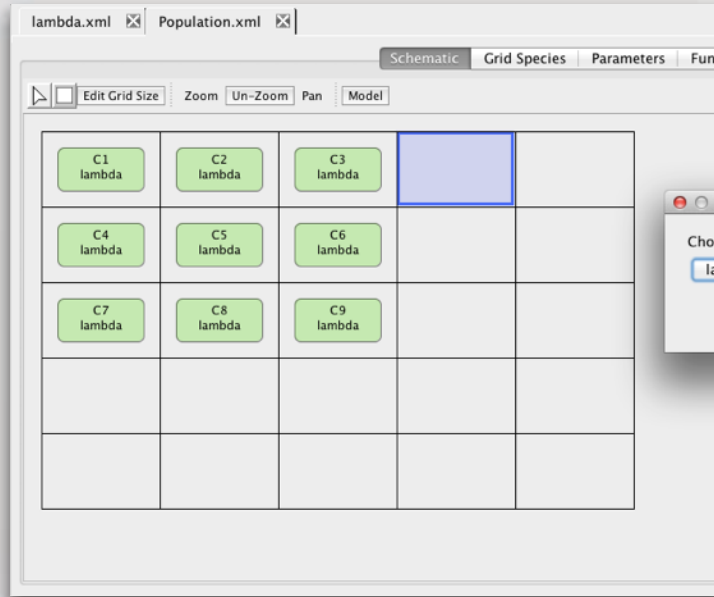
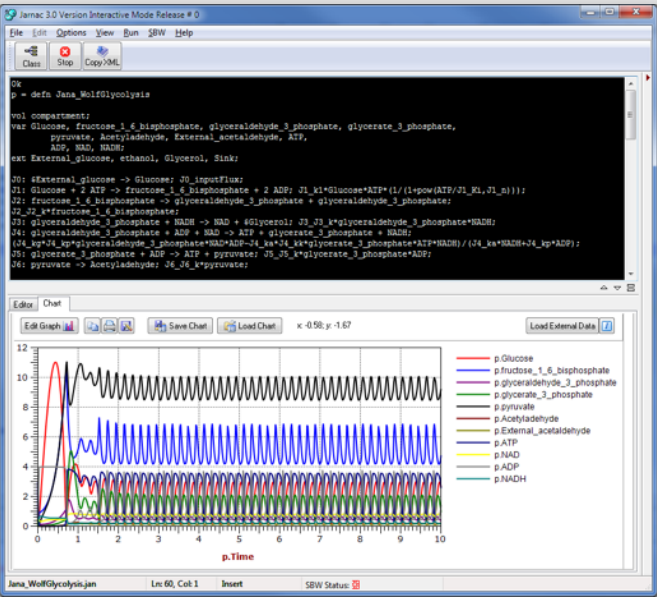
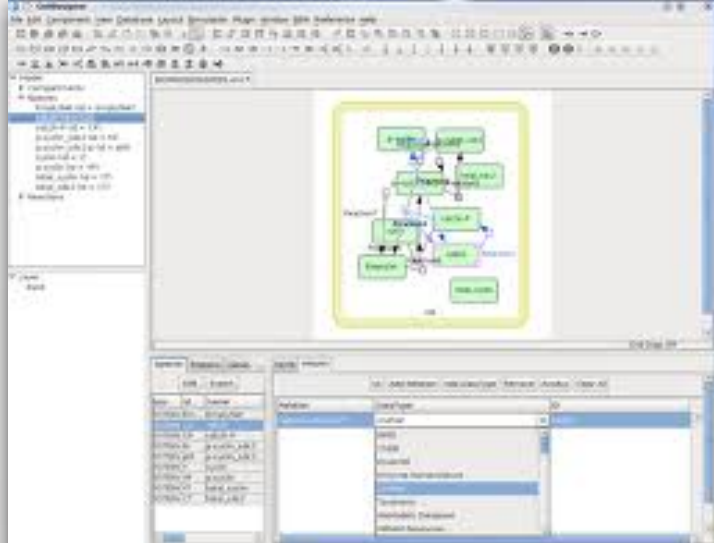
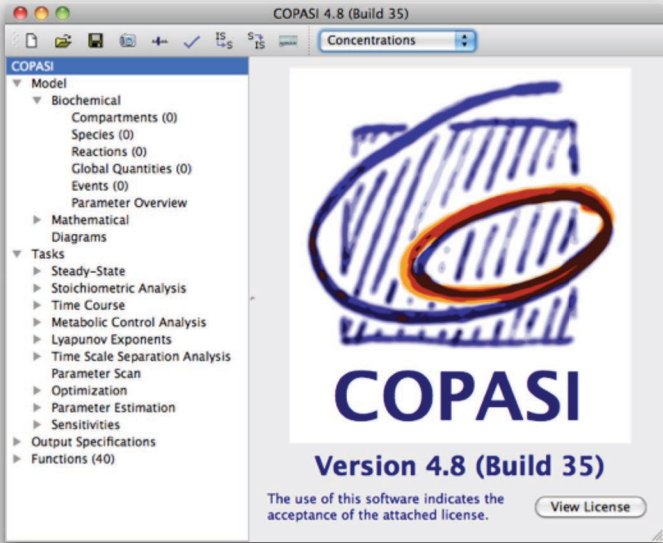
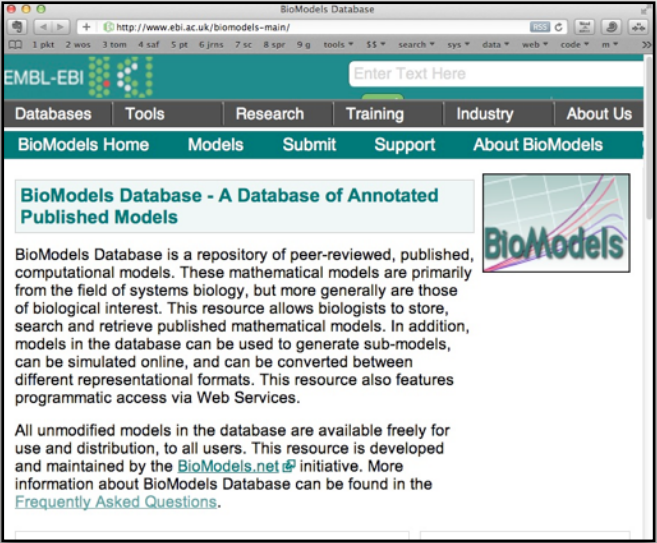
**Modeling often entails the  
use of more than one tool**





**Often need flexible,  
intermediate connections**







**Why not simply distribute a model in the original format?**

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Yes, do that – vital for good science

- Others can try to run model, understand it, verify it, reuse it, etc.
- Opinion: should **always do this**

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But it's still **not ideal** for communication of scientific results

- **Biological semantics** usually **not encoded**
- **Not everyone can run** the same software
- **Not everyone wants** to use the same software
- What if they want to use a **different conceptual framework**?
- How will people **relate the model to other work**?



**What *is* SBML?**

# The raw SBML (as XML)

```
<listOfSpecies>
  <species compartment="cytosol" id="ES" initialAmount="0" name="ES"/>
  <species compartment="cytosol" id="P" initialAmount="0" name="P"/>
  <species compartment="cytosol" id="S" initialAmount="1e-20" name="S"/>
  <species compartment="cytosol" id="E" initialAmount="5e-21" name="E"/>
</listOfSpecies>
<listOfReactions>
  <reaction id="veq">
    <listOfReactants>
      <speciesReference species="E"/>
      <speciesReference species="S"/>
    </listOfReactants>
    <listOfProducts>
      <speciesReference species="ES"/>
    </listOfProducts>
    <kineticLaw>
      <math xmlns="http://www.w3.org/1998/Math/MathML">
        <apply>
          <times/>
          <ci>cytosol</ci>
          <apply>
            <minus/>
            <apply>
              <times/>
              <ci>kon</ci>
              <ci>E</ci>
              <ci>S</ci>
            </apply>
            <apply>
              <times/>
              <ci>koff</ci>
              <ci>ES</ci>
            </apply>
          </apply>
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    </reaction>
  </listOfReactions>
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      <speciesReference species="S"/>
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    <listOfProducts>
      <speciesReference species="ES"/>
    </listOfProducts>
```

Don't work with it directly! Let software do it.

```
<kineticLaw>
  <math xmlns="http://www.w3.org/1998/Math/ML">
    <apply>
      <times/>
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      <apply>
        <minus/>
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        </apply>
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          <times/>
          <ci>koff</ci>
          <ci>ES</ci>
        </apply>
      </apply>
    </math>
  </kineticLaw>
```



# SBML = Systems Biology Markup Language

**Format** for **representing** models of biological processes

- Data structures + principles + serialization to XML
- (Mostly) Declarative, not procedural—not a scripting language

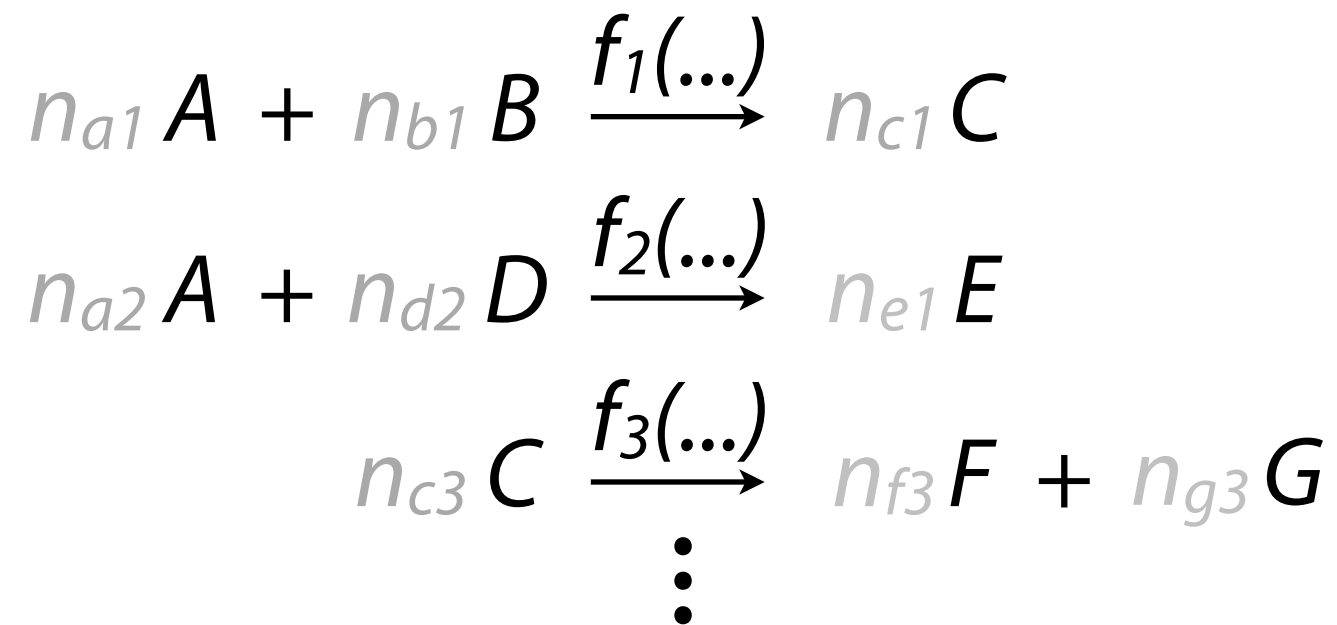
(Mostly) **neutral** with respect to modeling framework

- E.g., ODE, stochastic systems, etc.

For **software** to read/write, **not humans**

The *process* is central

- Literally called “**reaction**” (not necessarily biochemical)
- Participants are pools of entities of the same kind (“**species**”)



- Species are located in containers (“**compartments**”)

Models can further include:

- Other constants & variables
- Discontinuous **events**
- Unit definitions
- **Annotations**
- Other, explicit math

**Core SBML concepts are fairly simple**

## Example of model type

Typical ODE models (e.g., cell differentiation)

Conductance-based models (e.g., Hodgkin-Huxley)

*Typically do not use SBML “reaction” construct, but instead use “rate rules” construct*

Neural models (e.g., spiking neurons)

*Typically use “events” for discontinuous changes*

Pharmacokinetic/dynamics models

*“Species” are not required to be biochemical entities*

Infectious diseases

## Example model

BioModels Database model  
#BIOMD0000000451

BioModels Database model  
#BIOMD0000000020

BioModels Database model  
#BIOMD0000000127

BioModels Database model  
#BIOMD0000000234

BioModels Database model  
#MODEL1008060001

*List originally by Nicolas Le Novère*

**Core SBML constructs support many types of models**



Accepted by dozens of journals \*

**100's of software tools** available today

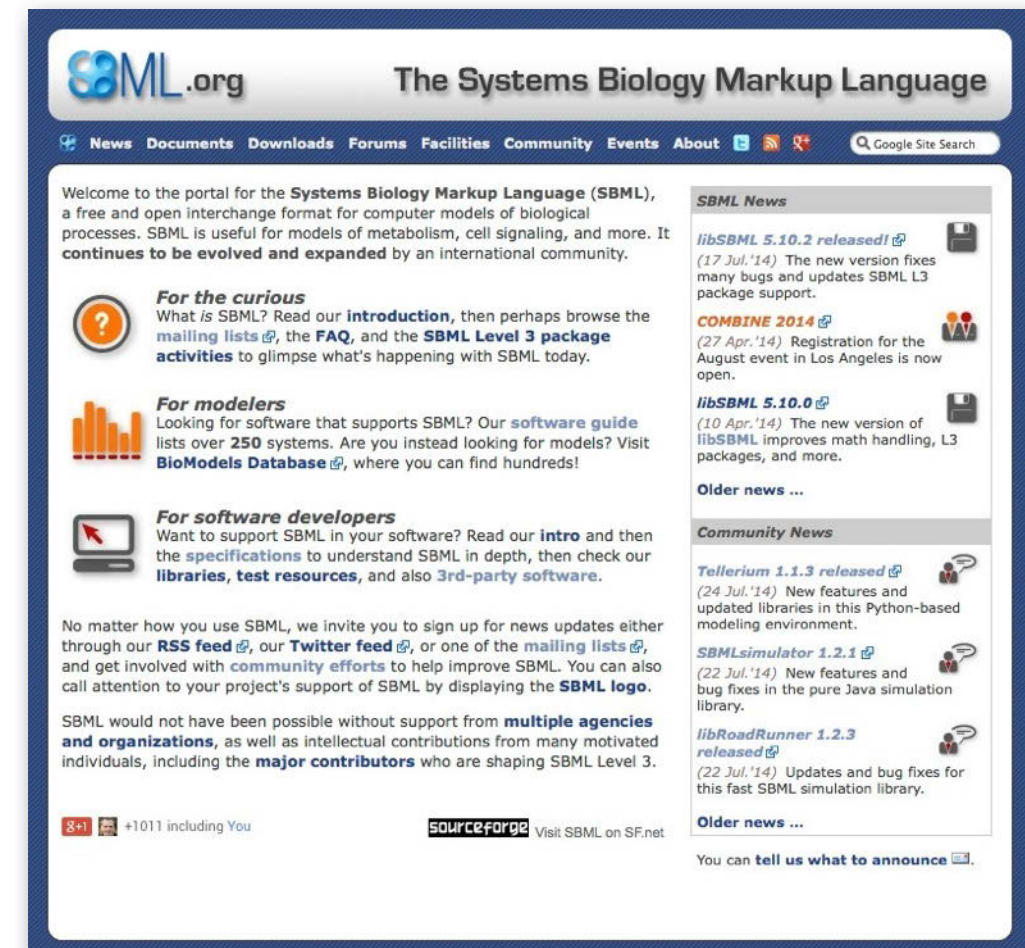
- Libraries: **libSBML, JSBML**
- 260+ listed in SBML Software Guide †

**1000's of models** available

- ... in public databases, e.g., BioModels Database, Reactome
- ... as supplementary data to papers
- ... in private repositories

\* [http://sbml.org/Documents/Publications\\_known\\_to\\_accept\\_submissions\\_in\\_SBML\\_format](http://sbml.org/Documents/Publications_known_to_accept_submissions_in_SBML_format)

† [http://sbml.org/SBML\\_Software\\_Guide](http://sbml.org/SBML_Software_Guide)



**<http://sbml.org>**

**Many examples of SBML and software resources are available**

**What resources are available for software developers?**



# SBML specification documents

Documents/Specifications – SBML.caltech.edu

sbml.org/Documents/Specifications

Reader

## SBML Level 3

At this time, only *Version 1 Core* of SBML Level 3 has been released. Definitions of packages to go with Version 1 Core are expected in the very near future. When the specifications become available, they will be listed below. For now, you can find information about the ongoing activities in the [community wiki](#).


### SBML Level 3 Version 1 Core


The most recent release of SBML Level 3 Version 1 Core is **Release 1**.


#### The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core


Authors: Michael Hucka, Frank Bergmann, Stefan Hoops, Sarah Keating, Sven Sahle, James Schaff, Lucian Smith, and Darren Wilkinson


*This is the final **Release 1** specification of 6 Oct. 2010.*

*The document link refers to the file on SourceForge.net. If you have any problems accessing the PDF file from there, a backup copy of the document is also available **locally from this server** .*

Specification → 

Errata → 

Submit issue → 

Schemas → 

Issues with the specification are tracked on the *issue tracker* whose link is indicated above. Accepted issues are periodically collected and listed on the *Errata* page indicated above. Once a general consensus emerges that the known errata warrant a new release of the SBML specification, a new *Release* is made.

### SBML Level 3 Packages

Each individual SBML Level 3 package effort has its own separate status page. Please follow the relevant links in the table below to find out more about a given package, including any draft specifications that may be available. This list is in



# API libraries

Downloads – SBML.org

sbml.org/Downloads

Reader

SBML.org

The Systems Biology Markup Language

News Documents Downloads Forums Facilities Community Events About


Google Site Search

Parent pages: [SBML.org](#)

## Downloads


### Software by the SBML Team and the BioModels.net Team

The SBML Project helps develop a variety of software packages for working with SBML. (Many more third-party packages also support SBML—visit the [SBML Software Guide](#) to find out more about them!)




#### LibSBML

A free, open-source [API](#) library for working with SBML content. It supports many programming languages and operating systems.




#### JSBML

A free, open-source, pure-Java library for working with SBML. It emulates libSBML's API, with more Java idioms and without native object code.




#### SBMLToolbox

A free, open-source package for working with SBML in [MATLAB](#). It provides functions for reading, writing, manipulating, and simulating SBML models.




#### SBML Converters

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#### SBMLeditor

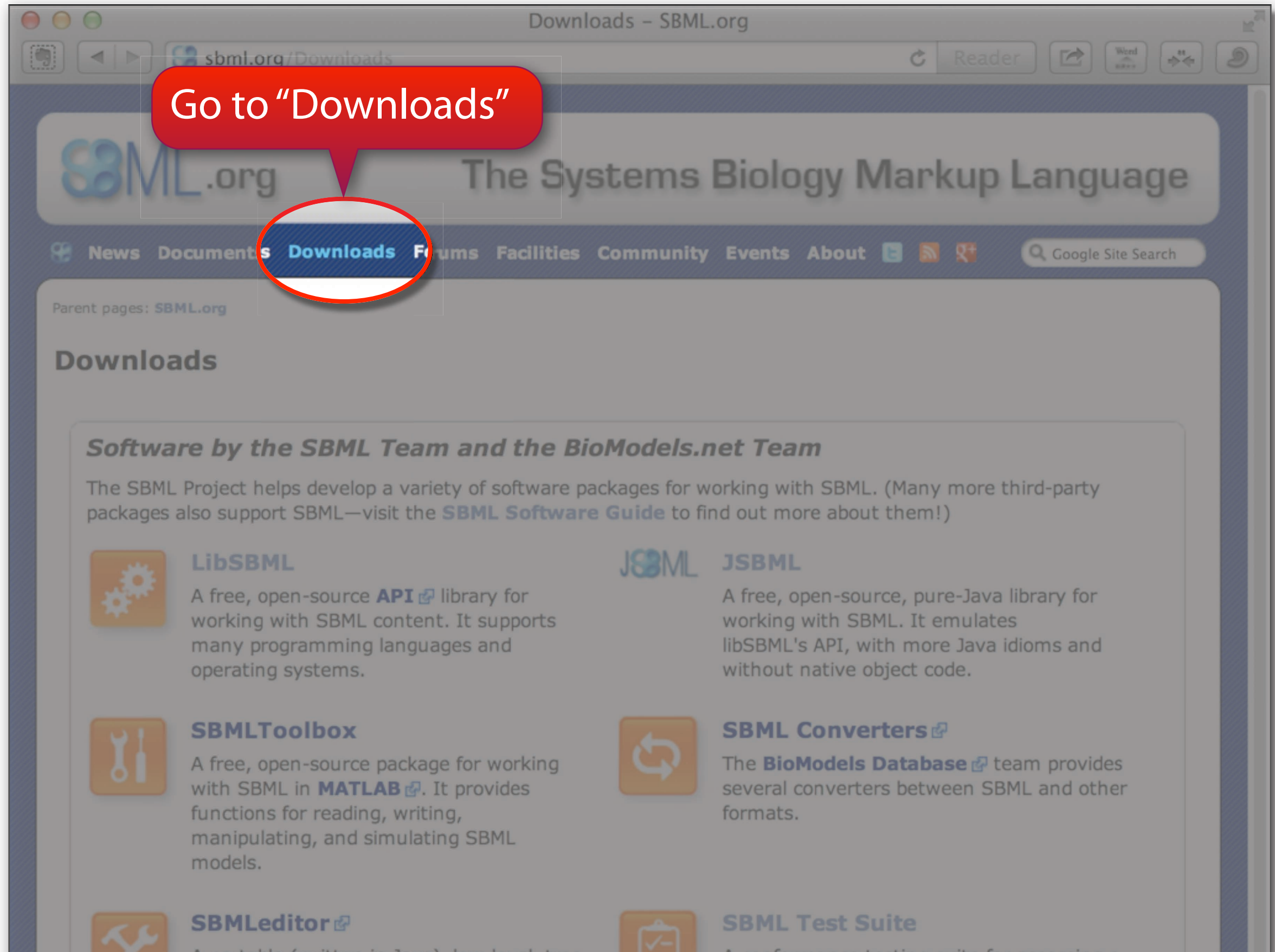
A graphical user interface for editing SBML models.



#### SBML Test Suite

A set of test cases for verifying the correctness of SBML implementations.

# API libraries



The screenshot shows a web browser window titled "Downloads - SBML.org". The address bar shows "sbml.org/Downloads". A red callout bubble with the text "Go to 'Downloads'" points to the "Downloads" link in the navigation bar. The navigation bar also includes links for "News", "Documents", "Forums", "Facilities", "Community", "Events", and "About". A search bar with the text "Google Site Search" is located on the right. The main content area is titled "Downloads" and features a section "Software by the SBML Team and the BioModels.net Team". This section lists several software packages: LibSBML, JSBML, SBMLToolbox, SBML Converters, SBMLEditor, and SBML Test Suite. Each package has an icon and a brief description.

Downloads - SBML.org

sbml.org/Downloads

Go to "Downloads"

SBML.org The Systems Biology Markup Language


News Documents **Downloads** Forums Facilities Community Events About

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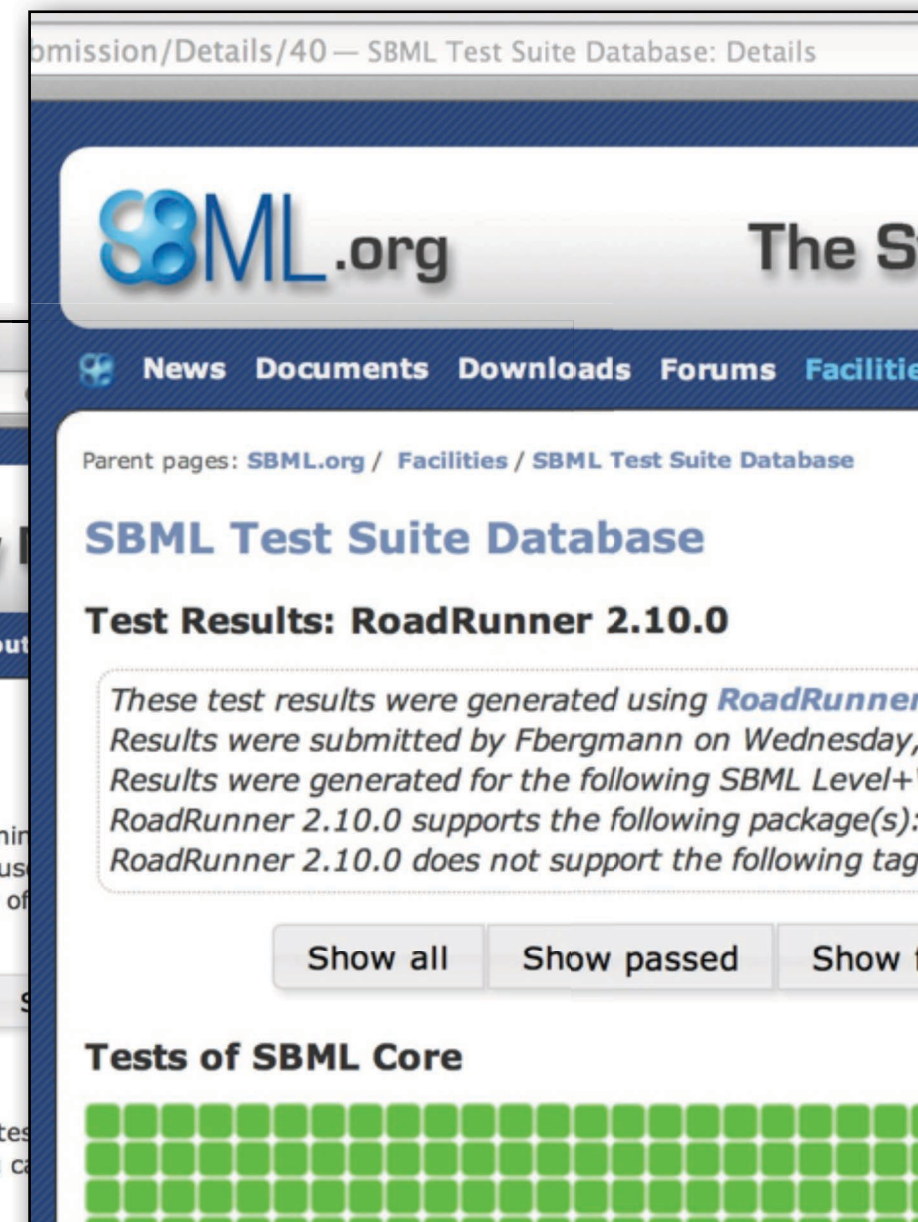
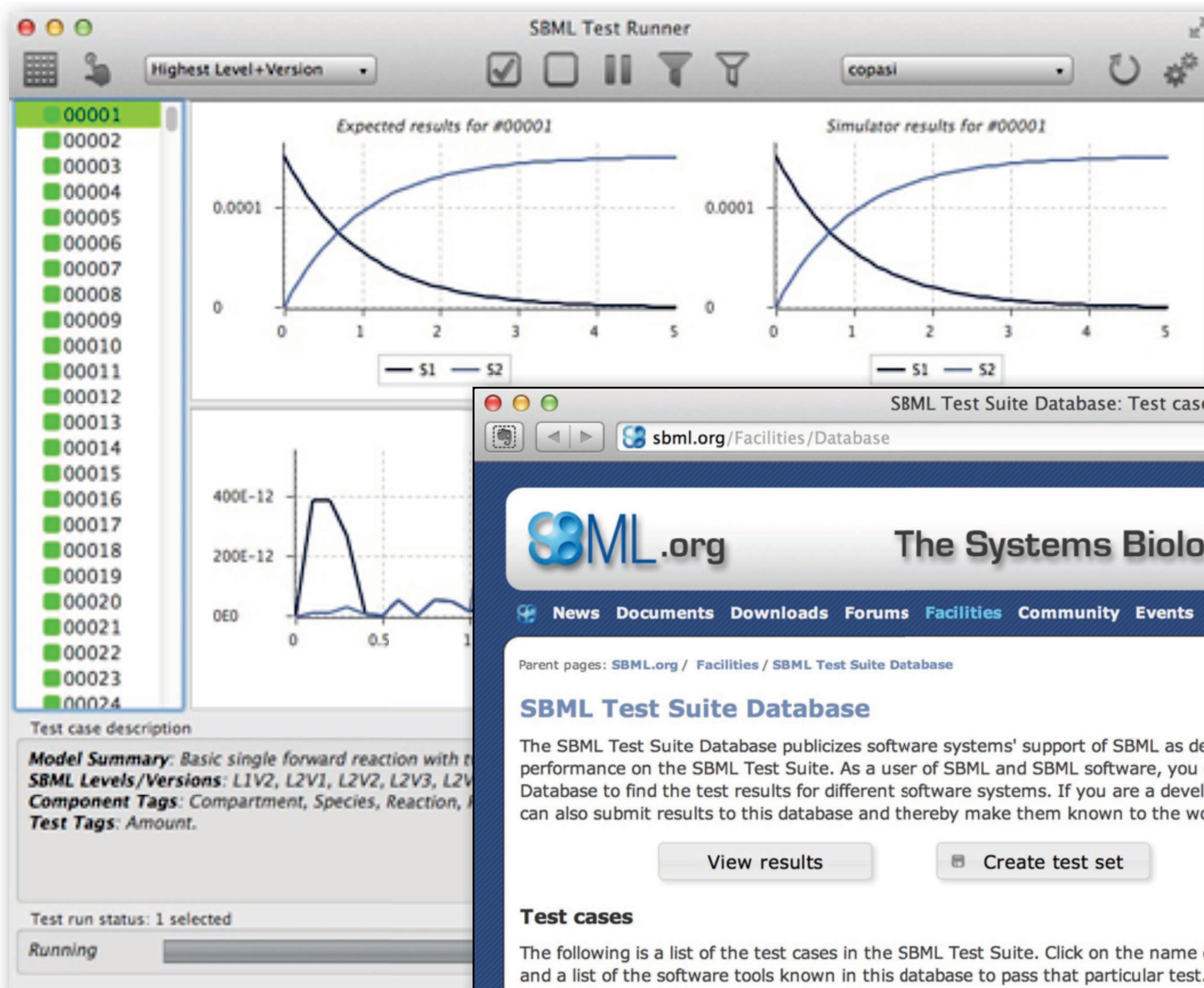
A set of test cases for verifying the correctness of SBML software.



# SBML Test Suite – [http://sbml.org/Facilities/SBML\\_Test\\_Suite](http://sbml.org/Facilities/SBML_Test_Suite)

Suite of **test cases** (1200) + **test runners** (both standalone app & online)

**Database of test results** on sbml.org





# Online SBML Validator – <http://sbml.org/Facilities/Validator>

The screenshot shows a web browser window with the title "Online SBML Validator" and the address bar displaying "sbml.org/Facilities/Validator/". The website has a blue header with the SBML.org logo and the text "The Systems Biology Markup Language". A navigation menu includes links for News, Documents, Downloads, Forums, Facilities (highlighted), Community, Events, and About. A Google Site Search bar is also present. The main content area explains the validator's purpose: testing the syntax and internal consistency of SBML files. It includes a "Sign in or Register" link and a section for retrieving previous validation results using a key. Below this, there are three tabs: "Upload File", "Submit URL", and "Paste SBML". The "Upload File" tab is active, showing a "Browse" button and a "Clear Queue" button. A "Validate now" button and a "Schedule for Validation" button are also visible. At the bottom, there are "Validation options" with several checkboxes, most of which are checked.

Online SBML Validator

sbml.org/Facilities/Validator/

**SBML.org** The Systems Biology Markup Language

News Documents Downloads Forums **Facilities** Community Events About

Google Site Search

Parent pages: [SBML.org](#) / [Facilities](#) / [Online SBML Validator](#)

This system can test the syntax and internal consistency of an SBML file. Passing this validator doesn't *guarantee* a file is 100% correct SBML, but it's the best automated assessment available.

Use the form below to upload your SBML content. You can also access this service via a [network API](#). By using any part of this service or website, you agree to be bound by the terms of the [privacy notice](#).

**Sign in** or **Register** with this service.

You can retrieve the result of a previously-scheduled validation run by entering its key here:

**Submit**

(E.g., 7bf66904-7d67-49bb-9127-bee77a8f96ba)

**Upload File** **Submit URL** **Paste SBML**

**Browse** **Clear Queue** **Validate now** **Schedule for Validation**

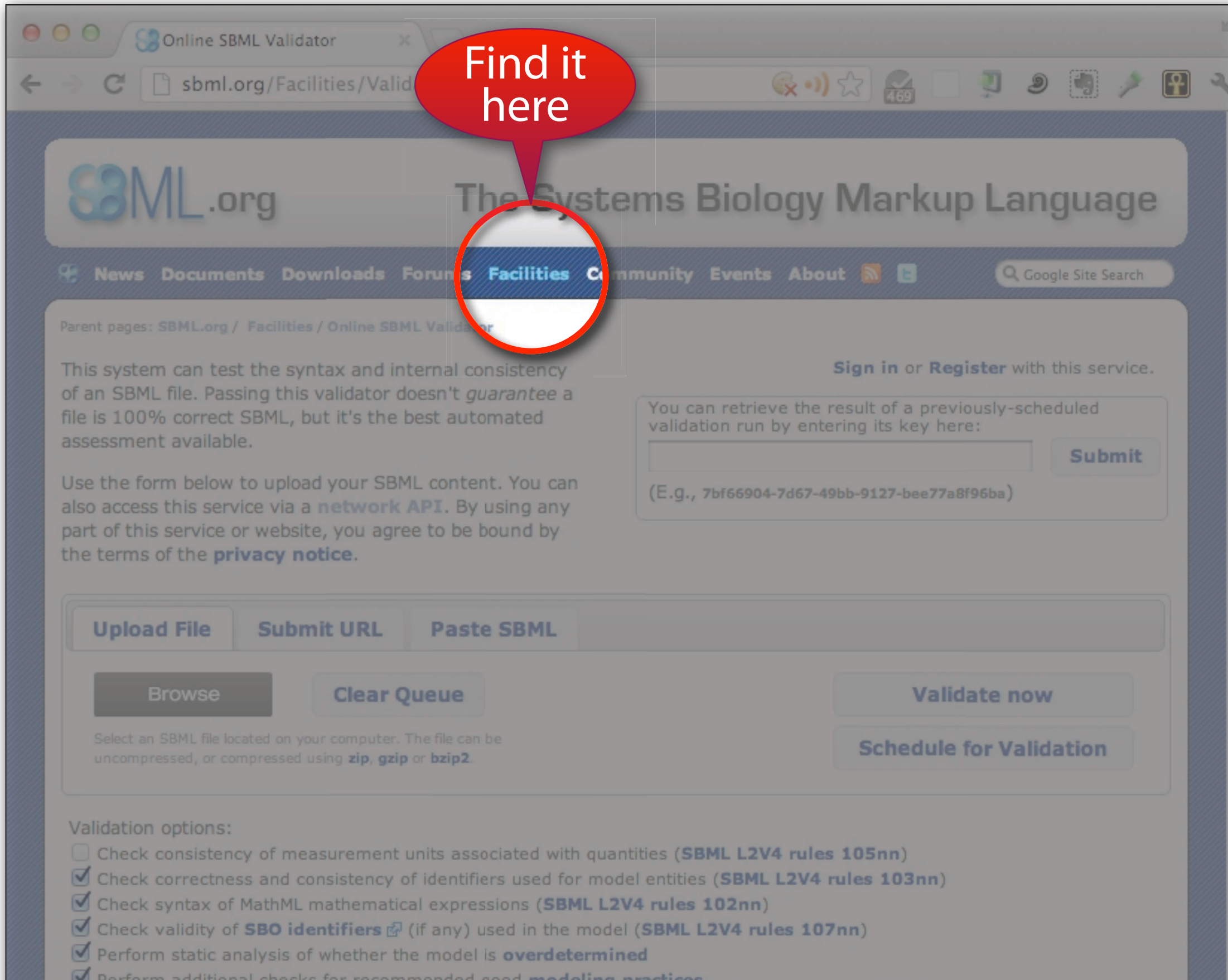
Select an SBML file located on your computer. The file can be uncompressed, or compressed using **zip**, **gzip** or **bzip2**.

**Validation options:**

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- ☒ Check correctness and consistency of identifiers used for model entities (**SBML L2V4 rules 103nn**)
- ☒ Check syntax of MathML mathematical expressions (**SBML L2V4 rules 102nn**)
- ☒ Check validity of **SBO identifiers** (if any) used in the model (**SBML L2V4 rules 107nn**)
- ☒ Perform static analysis of whether the model is **overdetermined**
- ☒ Perform additional checks for recommended good **modeling practices**



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Online SBML Validator

sbml.org/Facilities/Valid

Find it here

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The Systems Biology Markup Language

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# SBML Software Guide – [http://sbml.org/SBML\\_Software\\_Guide](http://sbml.org/SBML_Software_Guide)

Information about known  
SBML compatible software

**New questionnaire – please  
fill it out if you're a developer!**

**New version of the guide is  
coming!**

SBML Software Guide – SBML.caltech.edu

sbml.org/SBML\_Software\_Guide

SBML.org The Systems Biology Markup Language

News Documents Downloads Forums Facilities Community Events About


Parent pages: [SBML.org](#)

## SBML Software Guide


The following pages describe SBML-compatible software packages known to us. We offer different ways of viewing the information, all drawn from the same underlying data collected from the systems' developers via our [software survey](#). The *Matrix* provides a table listing all known software and a variety of their features; the *Summary* provides general descriptions of most of the software; and the *Showcase* provides a sequential slideshow of a subset of the software.

Number of software packages listed in the matrix today: **263**.


[Go to the SBML Software Matrix](#)



[Go to the SBML Software Summary](#)



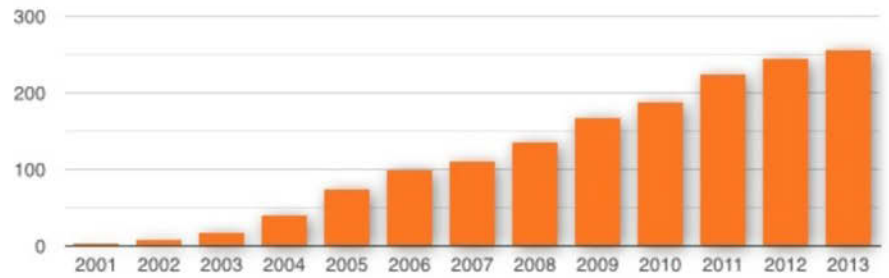
[Go to the SBML Software Showcase](#)



Please [tell us about additions and updates](#).

### Historical trend

The following graph shows the total number of known SBML-compatible software packages each year, as counted by the SBML Team. The counts shown are for approximately the middle of each year.



Year	Number of packages
2001	0
2002	10
2003	20
2004	40
2005	70
2006	100
2007	120
2008	150
2009	180
2010	200
2011	230
2012	250
2013	263

### SBML conformance testing

The [SBML Test Suite](#) provides an operational means of testing SBML support in software simulation and analysis systems. Software authors can choose to make the test results for their software public in the [SBML Test Suite Database](#), where you can inspect them.

[Go to the SBML Test Suite Database](#)

# SBML Software Guide – [http://sbml.org/SBML\\_Software\\_Guide](http://sbml.org/SBML_Software_Guide)

SBML.org

News Documents Downloads Forums


Parent pages: SBML.org

## SBML Software Guide

The following pages describe SBML-compatible software, all drawn from the same underlying information. The *Matrix* provides a table listing all known software; and the *Software Guide* provides descriptions of most of the software; and the *Software Survey* provides information about known software.

Number of software

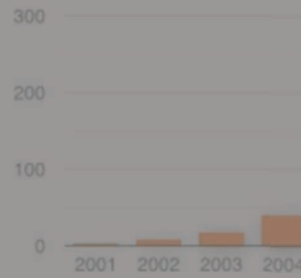
Go to the SBML Software Matrix



Please tell us about your software

### Historical trend

The following graph shows the total number of known SBML software tools over time. The counts shown are for approximate years.



Year	Number of software
2001	10
2002	20
2003	30
2004	40

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The **SBML Test Suite** provides an operational mechanism for testing SBML software systems. Software authors can choose to make their software conformant with the **SBML Test Suite Database**, where you can inspect them.

SBML Software Survey

<https://docs.google.com/forms/d/16FIRYvsG8FDOFxNmmuqLRk0yvwkYYVMxE...>

## SBML Software Survey

**What is your email address?**  
Providing an email address will enable us to send you the URL for updating your software entry in the future, and it will also enable us to contact you if we have any questions. Your email address will not be put in the SBML Software Guide.

**What is the software's short title, without version number?**  
Examples from existing software: "COPASI", "Virtual Cell", "JDesigner", "BioModels Database", "SBML2LaTeX".

**Does your software have alternative names?**  
If you renamed your software and it used to be called something else, please let us know the previous name(s). Also, if the software has both a standalone form and a plug-in for another system, the variants are probably not sufficiently distinct from the main or core system to be considered separate software tools in their own right. In that case, we would want to have a single entry for the software, but we need to know how to recognize the different forms. Please list the alternative names here, separated by commas. Examples: "CopasiWeb", "CopasiWS".

**What is the URL for the home page for your software?**  
This should be to a page that describes the software. (Note: this should NOT be a link to download the software; it should be the address of a human-readable, general page of information.)

**What is the version number your software at this time?**  
This is often a series of numbers, such as "1.1", "3.1.1", or similar.

**What was the date of your release of that version of your software?**  
Since you may not be filling out this form at the time the release was actually made, it is necessary to ask for this information separately.

**Please give a concise summary of your software.**  
What is its main purpose? What does it do? What kind of problems is it designed to address? Why might other users be interested in it? Please make sure to mention if it's an add-on package to another system (e.g., a plug-in for MATLAB). Please keep the length under 1024 characters.

about known  
software  
naire – please  
re a developer!  
of the guide is



# SBML Software Guide – [http://sbml.org/SBML\\_Software\\_Guide](http://sbml.org/SBML_Software_Guide)

Information about known  
SBML compatible software

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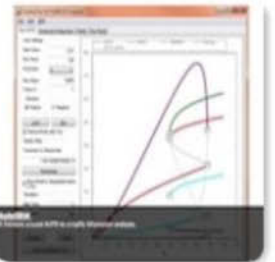
**Go to the SBML Software Matrix**



**Go to the SBML Software Summary**



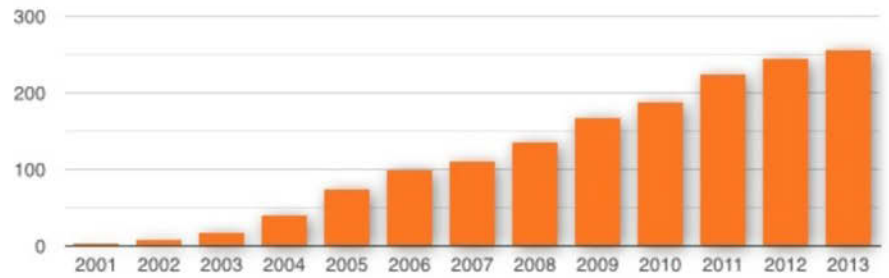
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[Go to the SBML Test Suite Database](#)

# SBML Software Guide – [http://sbml.org/SBML\\_Software\\_Guide](http://sbml.org/SBML_Software_Guide)

The screenshot shows the SBML Software Guide website. A red callout bubble with the text "Click here" points to a link that says "Please tell us about additions and updates." which is circled in red. The website header includes the SBML.org logo and the title "The Systems Biology Markup Language". The main content area has a section titled "SBML Software Guide" with a paragraph describing the software packages. Below this, there are three thumbnails: "Go to the SBML Software Matrix", "Go to the SBML Software Showcase", and "Please tell us about additions and updates." (circled in red). At the bottom, there is a bar chart titled "Historical trend" showing the number of software packages from 2001 to 2013, and a section titled "SBML conformance testing" with a link to the "SBML Test Suite Database".

SBML Software Guide – SBML.caltech.edu

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Number of software packages in the matrix today: **263**.

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[Click here](#)

Please [tell us about additions and updates](#).

#### Historical trend

The following graph shows the total number of known SBML-compatible software packages each year, as counted by the SBML Team. The counts shown are for approximately the middle of each year.

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2003	20
2004	30
2005	45
2006	60
2007	75
2008	90
2009	110
2010	130
2011	150
2012	170
2013	190

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[Go to the SBML Test Suite Database](#)

Information about known SBML compatible software

**New questionnaire – please fill it out if you're a developer!**

**New version of the guide is coming!**

**What has been happening with SBML lately?**



**Level 3 packages add constructs  
on top of SBML Level 3 Core**



Level 3 package	What it enables	Status
Hierarchical model composition	Models containing submodels	✓
Flux balance constraints	Constraint-based models	✓
Qualitative models	Petri net models, Boolean models	✓
Graph layout	Diagrams of models	✓
Multicomponent/state species	Entities w/ structure; also rule-based models	draft
Spatial	Nonhomogeneous spatial models	draft
Graph rendering	Diagrams of models	draft
Groups	Arbitrary grouping of components	draft
Arrays & sets	Arrays or sets of entities	draft
Dynamic structures	Creation & destruction of components	<b>draft</b>
Distributions	Numerical values as statistical distributions	in dev
Annotations	Richer annotation syntax	



Level 3 package	What it enables	Status
Hierarchical model composition	Models containing submodels	✓
Flux balance constraints	Constraint-based models	✓
Qualitative models	Petri net models, Boolean models	✓
Graph layout	Diagrams of models	✓
Multicomponent/state species	Entities w/ structure; also rule-	Updated draft
Spatial	Nonhomogeneous spatial mo	Updated draft
Graph rendering	Diagrams of models	draft
Groups	Arbitrary grouping of components	draft
Arrays & sets	Arrays or sets of entities	Updated draft
Dynamic structures	Creation & destruction of com	New draft
Distributions	Numerical values as statistical distributions	in dev
Annotations	Richer annotation syntax	

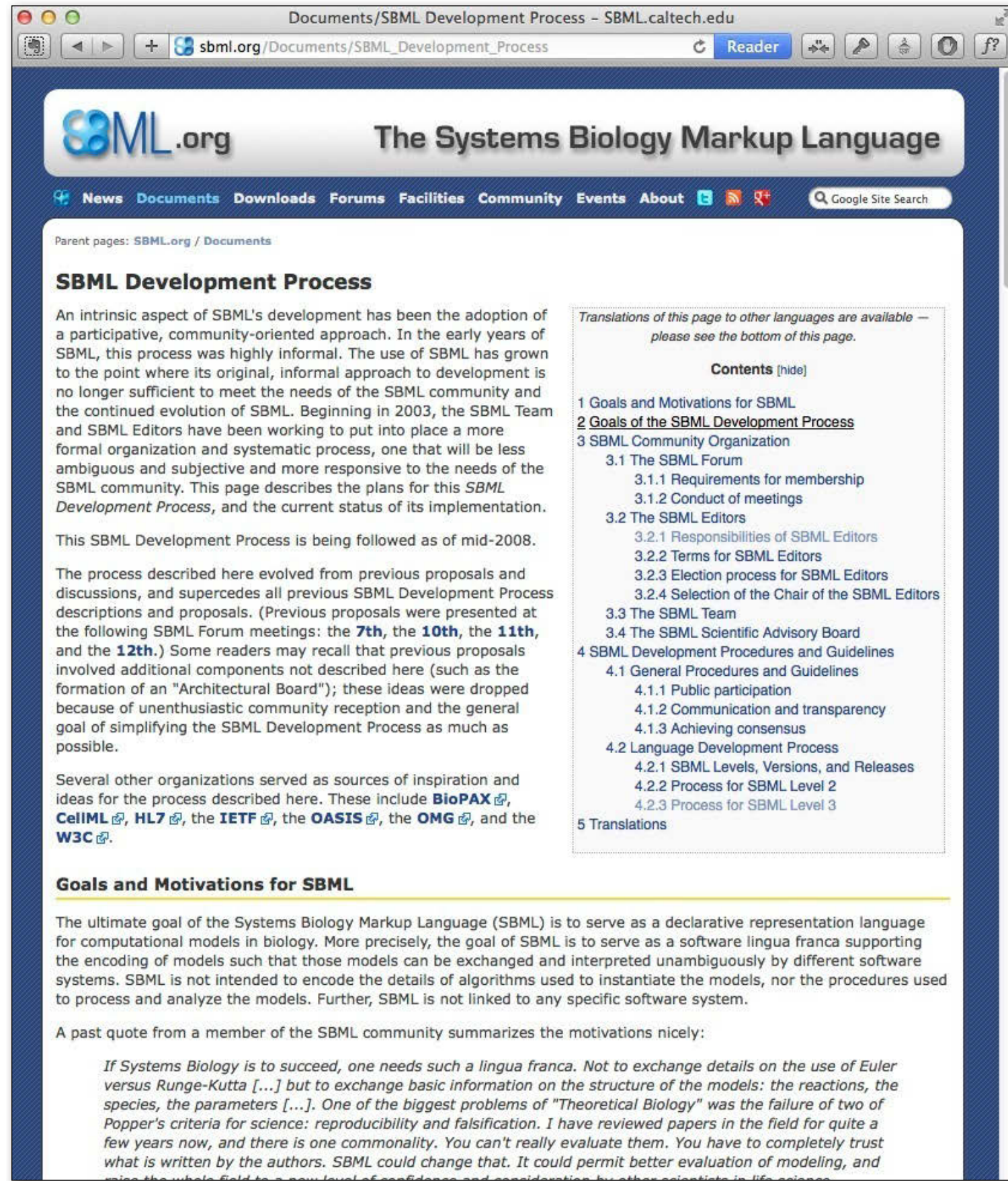


# Community-based development process

Defines process for

- **Proposing** changes and additions to SBML and SBML packages
- **Developing** specifications
- **Voting**
- The **roles** of editors

**Small changes forthcoming**  
*in package requirements and procedures*



The screenshot shows a web browser window with the address bar displaying "Documents/SBML Development Process - SBML.caltech.edu" and "sbml.org/Documents/SBML\_Development\_Process". The page features the SBML.org logo and the title "The Systems Biology Markup Language". A navigation bar includes links for News, Documents, Downloads, Forums, Facilities, Community, Events, and About, along with a Google Site Search box. The main content area is titled "SBML Development Process" and contains an introductory paragraph about the community-oriented approach. A sidebar on the right lists the page's contents, including goals, community organization, and development procedures. The main text continues with a paragraph about the process's evolution and a list of organizations that inspired it.

Documents/SBML Development Process - SBML.caltech.edu  
sbml.org/Documents/SBML\_Development\_Process

SBML.org The Systems Biology Markup Language

News Documents Downloads Forums Facilities Community Events About Google Site Search

Parent pages: SBML.org / Documents

## SBML Development Process

An intrinsic aspect of SBML's development has been the adoption of a participative, community-oriented approach. In the early years of SBML, this process was highly informal. The use of SBML has grown to the point where its original, informal approach to development is no longer sufficient to meet the needs of the SBML community and the continued evolution of SBML. Beginning in 2003, the SBML Team and SBML Editors have been working to put into place a more formal organization and systematic process, one that will be less ambiguous and subjective and more responsive to the needs of the SBML community. This page describes the plans for this *SBML Development Process*, and the current status of its implementation.

This SBML Development Process is being followed as of mid-2008.

The process described here evolved from previous proposals and discussions, and supercedes all previous SBML Development Process descriptions and proposals. (Previous proposals were presented at the following SBML Forum meetings: the **7th**, the **10th**, the **11th**, and the **12th**.) Some readers may recall that previous proposals involved additional components not described here (such as the formation of an "Architectural Board"); these ideas were dropped because of unenthusiastic community reception and the general goal of simplifying the SBML Development Process as much as possible.

Several other organizations served as sources of inspiration and ideas for the process described here. These include [BioPAX](#), [CellML](#), [HL7](#), the [IETF](#), the [OASIS](#), the [OMG](#), and the [W3C](#).

### Goals and Motivations for SBML

The ultimate goal of the Systems Biology Markup Language (SBML) is to serve as a declarative representation language for computational models in biology. More precisely, the goal of SBML is to serve as a software lingua franca supporting the encoding of models such that those models can be exchanged and interpreted unambiguously by different software systems. SBML is not intended to encode the details of algorithms used to instantiate the models, nor the procedures used to process and analyze the models. Further, SBML is not linked to any specific software system.

A past quote from a member of the SBML community summarizes the motivations nicely:

*If Systems Biology is to succeed, one needs such a lingua franca. Not to exchange details on the use of Euler versus Runge-Kutta [...] but to exchange basic information on the structure of the models: the reactions, the species, the parameters [...]. One of the biggest problems of "Theoretical Biology" was the failure of two of Popper's criteria for science: reproducibility and falsification. I have reviewed papers in the field for quite a few years now, and there is one commonality. You can't really evaluate them. You have to completely trust what is written by the authors. SBML could change that. It could permit better evaluation of modeling, and raise the whole field to a new level of confidence and consideration by other scientists in life sciences.*

Translations of this page to other languages are available — please see the bottom of this page.

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- 1 Goals and Motivations for SBML
- 2 Goals of the SBML Development Process
- 3 SBML Community Organization
  - 3.1 The SBML Forum
    - 3.1.1 Requirements for membership
    - 3.1.2 Conduct of meetings
  - 3.2 The SBML Editors
    - 3.2.1 Responsibilities of SBML Editors
    - 3.2.2 Terms for SBML Editors
    - 3.2.3 Election process for SBML Editors
    - 3.2.4 Selection of the Chair of the SBML Editors
  - 3.3 The SBML Team
  - 3.4 The SBML Scientific Advisory Board
- 4 SBML Development Procedures and Guidelines
  - 4.1 General Procedures and Guidelines
    - 4.1.1 Public participation
    - 4.1.2 Communication and transparency
    - 4.1.3 Achieving consensus
  - 4.2 Language Development Process
    - 4.2.1 SBML Levels, Versions, and Releases
    - 4.2.2 Process for SBML Level 2
    - 4.2.3 Process for SBML Level 3
- 5 Translations

# SBML Editors



**Frank Bergmann**



**Michael Hucka**  
*(chair)*



**Nicolas Le Novère**



**Brett Olivier**



**Sven Sahle**



**Dagmar Waltemath**

**Current**

Past

Stefan Hoops

Sarah Keating

Chris Myers

James Schaff

Lucian Smith

Darren Wilkinson



# Google Summer of Code 2014

*Open Bioinformatics Foundation (OBF) as mentoring organization*



**Victor Kofia**

Redesign the implementation of the JSBML math class ASTNode



**Ibrahim Vazirabad**

Create a CellDesigner plugin for JSBML that will convert between the layout format used by CellDesigner and SBML Level 3 layout



**Leandro Watanabe**

Implement support in JSBML for the SBML Level 3 *Arrays* package



# Acknowledgments

Mike Hucka, Sarah Keating, Frank Bergmann, Lucian Smith,  
*SBML & JSBML Team:* Andrew Finney, Herbert Sauro, Hamid Bolouri, Ben Bornstein, Maria Schilstra, Jo Matthews, Bruce Shapiro, Linda Taddeo, Akira Funahashi, Akiya Juraku, Ben Kovitz, Nicolas Rodriguez, Andreas Dräger, Alex Thomas

Mike Hucka, Frank Bergmann, Sarah Keating, Nicolas Le Novère, Chris Myers,  
*SBML Editors:* Lucian Smith, Stefan Hoops, Sven Sahle, James Schaff, Dagmar Waltemath, Darren Wilkinson, Brett Olivier

*GoSC students:* Victor Kofia, Ibrahim Vazirabad, Leandro Watanabe

*And a huge thanks to everyone in the SBML and COMBINE communities for massive contributions to SBML development and continuing support*





## **National Institute of General Medical Sciences (USA)**

Google Summer of Code

European Molecular Biology Laboratory (EMBL)

Drug Disease Model Resources (EU-EFPIA Innovative Medicine Initiative)

JST ERATO Kitano Symbiotic Systems Project (Japan) (to 2003)

JST ERATO-SORST Program (Japan)

ELIXIR (UK)

Beckman Institute, Caltech (USA)

Keio University (Japan)

International Joint Research Program of NEDO (Japan)

Japanese Ministry of Agriculture

Japanese Ministry of Educ., Culture, Sports, Science and Tech.

BBSRC (UK)

National Science Foundation (USA)

DARPA IPTO Bio-SPIICE Bio-Computation Program (USA)

Air Force Office of Scientific Research (USA)

STRI, University of Hertfordshire (UK)

Molecular Sciences Institute (USA)

**SBML funding sources over the past 14 years**