

MIME Media Type for the Systems Biology Markup Language (SBML)

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Abstract

This document registers the MIME sub-type application/sbml+xml, a media type for SBML, the Systems Biology Markup Language. SBML is defined by The SBML Team at the California Institute of Technology and interested members of the systems biology community.

1. Introduction

SBML is an XML format for representing and exchanging models of biochemical reaction networks used in systems biology. SBML:

- o enables researchers in systems biology to use multiple tools, such as simulators, editors, differential-equation solvers, and visualizers, on a single model without rewriting the model for each tool;
- o enables researchers and publishers to make models available on-line to other researchers even if they use a different software environment;
- o enables models, and the intellectual effort put into them, to survive beyond the lifetime of the software tools used to create them.

Currently, about 60 software applications use SBML, and researchers are using these applications to develop quantitative and qualitative computational models, mostly in cell biology. In addition, several consortia and alliances have standardized SBML as their model

definition language. The SBML community hopes that a standardized MIME media type will help researchers share models on a larger scale, drawing more heavily on the capabilities of the world-wide web.

A detailed exposition of SBML and its uses within the systems biology community is available in references [HUCKA2003], [FINNEY2003], and [HUCKA2004].

2. IANA Registration

This section registers application/sbml+xml as a MIME media type according to the parameters set forth in [RFC2048].

MIME media type name: application

MIME subtype name: sbml+xml

Required parameters: none.

Optional parameters: none.

There is no charset parameter. Character handling has identical semantics to the case where the charset parameter of the "application/xml" media type is omitted, as described in section 3.2 of [RFC3023]. Note that SBML level 2 is defined to have UTF-8 encoding [SBML2-1, section 4.1].

Encoding considerations:

Same as described in section 3.2 of [RFC3023].

Security considerations:

The security considerations described in section 7 of [RFC3470] all potentially apply to sbml+xml documents. In particular, sbml+xml documents might contain the results of proprietary biological research that their owner may wish to keep private.

The XML schema for sbml+xml provides for no active or executable content.

Interoperability considerations:

The information in an sbml+xml document describes an abstract model of biochemical reactions. It is not tied to any particular software application, and indeed the primary purpose of SBML is to make these models readable and writable by many different software applications.

This might seem to make sbml+xml more appropriate for the "Model" primary content type [RFC2077], but SBML models are not guaranteed to have the required three orthogonal dimensions. SBML models, rather, involve interacting entities that exist within compartments. However, ideally, browsers and other software that reads sbml+xml would give a human reader multiple choices of how to view the document: in a data-visualization tool, in a model editor, in a differential-equation analyzer, etc.

The systems biology community has and will continue to release new levels and versions of the SBML schema and semantics. New versions attempt to be backward compatible with old versions, but sometimes small incompatibilities are introduced. Every sbml+xml document contains its level and version; programs that read sbml+xml should read this information to be sure they correctly interpret the remainder of the document.

Published specification:

A list of all current SBML specifications and related documents is maintained at:

<http://sbml.org/documents>

Current specifications are:

SBML level 2, version 1

<http://sbml.org/specifications/sbml-level-2-v1.ps>

<http://sbml.org/specifications/sbml-level-2-v1.pdf>

SBML level 1, version 2

<http://sbml.org/specifications/sbml-level-1-v2.ps>

<http://sbml.org/specifications/sbml-level-1-v2.pdf>

SBML level 1, version 1

<http://sbml.org/specifications/sbml-level-1-v1.ps>

<http://sbml.org/specifications/sbml-level-1-v1.pdf>

All specifications are authored by and available in hardcopy form from The SBML Team (see below for mailing information).

Applications which use this media type:

The following application and database projects read and/or write models in sbml+xml format. Currently, most do not encode or decode MIME-format messages. Hopefully the registration of

sbml+xml will make it easier for these projects to connect through a broader infrastructure, such as the creation of repositories of models on the world-wide web.

BALSA
BASIS
BioCharon
biocyc2SBML
BioGrid
BioNetGen
Bio Sketch Pad
BioSpreadsheet
BioUML
BSTLab
CADLIVE
CellDesigner
Cellerator
Cellware
COPASI
Cytoscape
DBsolve
Dizzy
E-CELL
ecellJ
ESS
Gepasi
Jarnac
JDesigner
JigCell
JSIM
JWS
Karyote
KEGG2SBML
Kinsolver (planned)
libSBML
MathSBML
MMT2
Modesto
MOMA (planned)
Monod
NetBuilder
PathArt
PathScout
PaVESy
PathwayBuilder
ProcessDB (planned)
SBW
SCIpath

SigPath
SigTran
Simpathica
SimWiz
StochSim
STOCKS
Trelis
Virtual Cell
VLX Suite
WinSCAMP

A list of SBML-enabled applications, along with URLs for more information about them, is maintained at <http://sbml.org>.

Additional information:

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Intended usage: LIMITED USE

Author/Change Controller:

The SBML specification is a free, open, community effort organized and edited by The SBML Team. The SBML Team has change control over the specification.

The SBML Team and interested members of the systems biology community meet regularly at the "Workshops on Software Platforms for Systems Biology". Information about past and planned workshops is maintained at:

<http://sbml.org/workshops>

3. Security Considerations

Security considerations for sbml+xml are discussed in the "Security Considerations" heading in the IANA registration in section 2.

4. Contributors

The following people contributed to the content of this document: Michael Hucka (Caltech), Andrew Finney (University of Hertfordshire).

5. References

5.1. Normative References

- [SBML2-1] Finney, A. and Hucka, M., "Systems Biology Markup Language (SBML) Level 2: Structures and Facilities for Model Definitions", June 28, 2003. Available from The SBML Team at: <http://sbml.org/specifications/sbml-level-2-v1.pdf>
- [SBML1-2] Hucka, M., Finney, A., Sauro, H. and Bolouri, H., "Systems Biology Markup Language (SBML) Level 1: Structures and Facilities for Basic Model Definitions", August 28, 2003. Available from The SBML Team at: <http://sbml.org/specifications/sbml-level-1-v2.pdf>

5.2. Informative References

- [FINNEY2003] Finney, A. and Hucka, M., "Systems Biology Markup Language: Level 2 and Beyond", Biochemical Society Transactions 31:1472-1473, December, 2003.
- [HUCKA2003] Hucka, M., Finney, A., Sauro, H.M., Bolouri, H., Doyle, J.C., Kitano, H., Arkin, A.P., Bornstein, B.J., Bray, D., Cornish-Bowden, A., Cuellar, A.A., Dronov, S., Gilles, E.D., Ginkel, M., Gor, V., Goryanin, I.I., Hedley, W.J., Hodgman, T.C., Hofmeyr, J.-H., Hunter, P.J., Juty, N.S., Kasberger, J.L., Kremling, A., Kummer, U., Le Novère, N., Loew, L.M., Lucio, D., Mendes, P., Minch, E., Mjolsness, E.D., Nakayama, Y., Nelson, M.R., Nielsen, P.F., Sakurada, T., Schaff, J.C., Shapiro, B.E., Shimizu, T.S., Spence, H.D., Stelling, J., Takahashi, K., Tomita, M., Wagner, J., Wang, J., "The Systems Biology Markup Language (SBML): a Medium for Representation and Exchange of Biochemical Network Models", Bioinformatics 19(4):524-531, 2003.

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- [RFC3023] Murata, M., St. Laurent, S. and D. Kohn, "XML Media Types", RFC 3023, January 2001.
- [RFC3470] Hollenbeck, S., Rose, M. and L. Masinter, "Guidelines for the Use of Extensible Markup Language (XML) within IETF Protocols", BCP 70, RFC 3470, January 2003.

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