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

Status of this Memo

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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

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5.2. Informative References

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