SBML Frequently Asked Questions

Andrew Finney, Michael Hucka
{afinney, mhucka}@caltech.edu

FAQ Contents

1.8 Where is the SBML web site?

scheme as CellML, introducing support for named function definitions, introducing explicit modifier species

- Using MathML allows us to extend SBML without introducing new non-XML syntax. For example if we wanted to introduce some form of modularity we might want a '.' operator in expressions to reference components of submodel instances. We could agree on the introduction of a MathML operator to do

- Algebraic rules define the point in the model where there is a circular dependency between variables. For instance, the equations $x = 2y$ and $y = x + 1$ have a circular dependancy. It is not possible to form such a dependancy in scalar rules (see the SBML Level 2 specification). At least one of the example equations would have to be encoded as an algebraic rule in SBML.

-

6.2   Is it a good idea to use SBML as my software's native model format?

Depending on the needs of your software, yes, this may be a good idea. JDesigner, JigCell and CellDesigner are examples of software tools that use SBML as their native formats.

6.8   How should I attach standard database identifiers, for example GO terms, to SBML elements?

Database identifier annotations can be created using CellML metadata in SBML Level 2; see the specification for CellML Metadata

6.10.4 Compartment spatial dimensions

Common practice is to allow the `spatialDimensions` attribute to default to 3. In fact the majority of

7.2 Who are the "SBML Editors"?

Currently, the editors are Andrew Finney and Mike Hucka

7.3 What do SBML Editors do?

The following are the roles of the SBML editors:

- assemble proposals into SBML Level specifications
- organize SBML forum meetings
-

standard in the future. The result will be compositional compatibility between CellML and SBML, such that models expressed in one language can be used as components or submodels in the other.

7.10 What is the relationship between SBML and BioPAX?

BioPax is a consortium that is developing a format for the exchange of pathway data between bioinformatics

managed the process until May 2003.

8.4 Who funded the initial editorial work?

The initial development of SBML was funded by the Japan Science And Technology Corporation's *Ex-*