Systems Biology Markup Language (SBML) Level 1: Structures and Facilities for Basic Model Definitions

Michael Hucka, Andrew Finney, Herbert Sauro, Hamid Bolouri
{mhucka,afinney,hsauro,hbolouri}@cds.caltech.edu
Systems Biology Workbench Development Group
JST ERATO Kitano Symbiotic Systems Project
Control and Dynamical Systems, MC 107-81
California Institute of Technology, Pasadena, CA 91125, USA
http://www.cds.caltech.edu/erato

Principal Investigators: John Doyle and Hiroaki Kitano

SBML Level 1, Version 2 (Final Draft)
8 May 2003

1 Introduction

We present the Systems Biology Markup Language (SBML) Level 1

1.2 Scope and Limitations

SBML Level 1 is meant to support non-spatial biochemical models and the kinds of operations that are

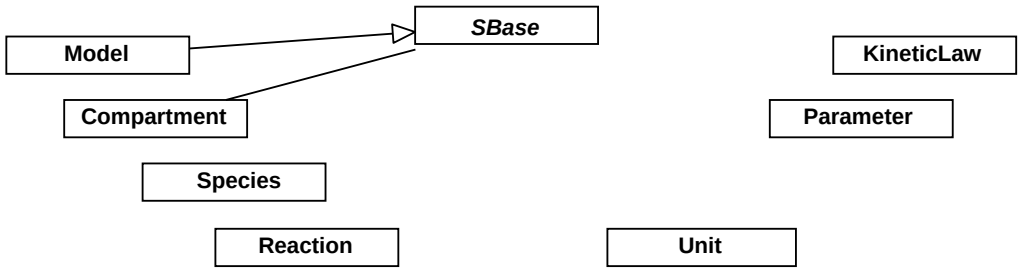
SBase
Model
KineticLaw
Compartment
Parameter
Species
Reaction
Unit

Figure 1:

reference is “http://www.mysim.org/ns” and the prefix is mysim

```
letter   ::= 'a'..'z','A'..'Z'
digit    ::= '0'..'9'
name     ::= ( letter | '_' ) ( letter | digit | '_' )*
```

Figure 3: *The definition of the type SName, expressed in the variant of Extended Backus-Naur Form (EBNF) used by the XML 1.0 specification (Bray et al., 2000). The characters (*

Name	Allowable Units	Default Units
`substance`	moles *or* number of molecules	moles
`volume`	liters	liters
`time`	seconds	seconds

The optional boolean field `boundaryCondition`

The following is an example of parameters defined at the `Model` level:

```
<model>
    ...
    <listOfSpecies>
        ...
    </listOfSpecies>
    <listOfParameters>
        <parameter name="Km1" value="2.3" units="second"/>
        <parameter name="Km2" value="10.7" units="second"/>
    </listOfParameters>
    <listOfReactions>
        ...
    </listOfReactions>
    ...
</model>
```

Figure 9: *The definition of `Rule` and derived types.*

4.6.1 `AlgebraicRule`

The rule type `AlgebraicRule` is used to express equations whose left-hand sides are zero. `AlgebraicRule` does not add any fields to the basic `Rule`; its role is simply to distinguish this case from the other cases.

4.6.2 `SpeciesConcentrationRule`

The `SpeciesConcentrationRule` structure adds one field, `species`, to the basic `AssignmentRule` type. The field `species` has type `SName` and is used to identify the species

Figure 10: *The definitions of* `Reaction`, `KineticLaw` *and*

4.7.2 KineticLaw

A kineticLaw

```
                </listOfProducts>
                <kineticLaw formula="(vm * s1)/(km + s1)"/>
            </reaction>
            <reaction name="v2">
                <listOfReactants>
                    <speciesReference species="s1"/>
                </listOfReactants>
                <listOfProducts>
                    <speciesReference species="s2"/>
                </listOfProducts>
                <kineticLaw formula="(vm * s2)/(km + s2)"/>
            </reaction>
            <reaction name="v3">
                <listOfReactants>
                    <speciesReference species="s2"/>
                </listOfReactants>
                <listOfProducts>
                    <speciesReference species="x1"/>
                </listOfProducts>
                <kineticLaw formula="(vm * s1)/(km + s1)"/>
            </reaction>
        </listOfReactions>
    </model>
</sbml>
```

5.3 An Example of Using Rules

This section contains a model which simulates a system containing a fast reaction. This model uses rules to express the mathematics of the fast react explicitly rather than using the implicit fast field on a reaction element. The system modeled is

"x1"/241"219/100152ds0862es=[(5.3)]TJ-117.682-55.891cm00.compartme0.28k00.890.940.28KBTcompartme0.Td[(<)]TJ
98.399 K 1 0 0 1 0 -15.207229.019 1. fomodel whi21 /F59 8.966 Tf 0.08e

$$X_0 \xrightarrow{k_1 X_0} S_1$$

$$S_1 \xrightarrow{k_f S_1 - k_r S_2} S_2$$

$$S_2 \xrightarrow{k_2 S_1} X_1$$

$$k_1 = 0.1, \quad k_2 = 0.15, \quad k_f = K_{eq} 10000, \quad k_r = 10000, \quad K_{eq} = 2.5.$$

Our vision for SBML is to create an open standard that will enable simulation software to exchange models. SBML is not static; we continue to develop and experiment with it, and we interact with other groups who seek to develop similar markup languages. We plan on continuing to evolve SBML with the help of the systems biology community to make SBML increasingly more powerful, flexible and useful.

6.1 Future Enhancements to SBML: Level 2 and Beyond

As mentioned above, SBML Level 1 is intended to provide the most basic foundations for modeling bio-
eion

Appendix

A Summary of Notation

```
  </xsd:annotation>
  <xsd:restriction base="xsd:string">
    <xsd:pattern value="(_|[a-z]|[A-Z])(_|[a-z]|[A-Z]|[0-9])*"/>
  </xsd:restriction>
</xsd:simpleType>
<!--The definition of SBase follows.-->
<xsd:complexType name="SBase" abstract="true">
  <xsd:annotation>
    <xsd:documentation>The SBase type is the base type of all main
         components in SBML.  It supports attaching notes and annotations
         to components.
    </xsd:documentation>
  </xsd:annotation>
  <xsd:sequence>
    <xsd:element name="notes" minOccurs="0">
```

</xsd:restriction></xsd:simpleType><!--The definition of Unit follows.--><xsd:complexType name="Unit"><xsd:comp

```
  </xsd:restriction>
</xsd:simpleType>
<xsd:complexType name="Rule" abstract="true">
  <xsd:complexContent>
    <xsd:extension base="SBase">
     <xsd:attribute name="formula" type="xsd:string" use="required"/>
    </xsd:extension>
  </xsd:complexContent>
</xsd:complexType>
```

```
        </xsd:complexType>
      </xsd:element>
      <xsd:element name="listOfReactions" minOccurs="0">
        <xsd:complexType>
          <xsd:sequence>
            <xsd:element name="reaction" type="Reaction" maxOccurs="unbounded"/>
          </xsd:sequence>
        </xsd:complexType>
      </xsd:element>
     </xsd:sequence>
     <xsd:attribute name="name" type="SName" use="optional"/>
    </xsd:extension>
  </xsd:complexContent>
</xsd:complexType>
<!-- The following is the type definition for the top-level element in an SBML document.-->
<xsd:complexType name="sbmlDocument">
  <xsd:sequence>
```

Name	Arguments	Meaning	Formula
massi	S_i, k	Irreversible Mass Action Kinetics	$v = k$

Name	Arguments	Meaning	Formula
usii	S, V, K_m, K_i	Substrate Inhibition Kinetics (Irreversible)	$v = V \frac{S/K_m}{1 + S/K_m + S^2/K_i}$

+

Name	Arguments	Meaning	Formula
uctr	S, P, A_c, V_f, V_r, K_{ms}, K_{mp}, K_a	Catalytic Activation (Reversible)	$v = \frac{V_f S/K_{ms} - V_r P/K_{mp}}{1 + K_a/A_c + (S/K_{ms} + P/K_{mp})(1 + K_a/A_c)}$
umai	S, A_c, V, K_m, Kas, Kac	Mixed Activation Kinetics (Irreversible)	$v = VS/K$

Symbol	Meaning
α	

References

Abbott, A. (1999). Alliance of US labs plans to build map of cell signalling pathways. *Nature*, 402:219–200.

Arkin, A. P. (2001). *Simulac* and *Deduce*. Available via the World Wide Web at `http://gobi.lbl.gov/~aparkin/Stuff/Software.html`.

Biron, P. V. and Malhotra, A. (2000). XML Schema part 2: Datatypes (W3C candidate recommendation 24 October 2000). Available via the World Wide Web at `http://www.w3.org/TR/xmlschema-2/`.

Bosak, J. and Bray, T. (1999). XML and the second-generation web. *Scientific American*, 280(5):89–93.

Bray, D., Firth, C., Le Novère, N., and Shimizu, T. (2001). *StochSim*. Available via the World Wide Web at `http://www.zoo.cam.ac.uk/comp-cell/StochSim.html`.

Bray, T., D. Hollander, D., and Layman, A. (1999). Namespaces in XML. World Wide Web Consortium 14-January-1999. Available via the World Wide Web at `http://www.w3.org/TR/1999/REC-xml-names-19990114/`.

Bray, T., Paoli, J., and Sperberg-McQueen, C. M. (1998). Extensible markup language (XML) 1.0, W3C recommendation 10-February-1998. Available via the World Wide Web at `http://www.w3.org/TR/1998/REC-xml-19980210`.

Bray, T., Paoli, J., Sperberg-McQueen, C. M., and Maler, E. (2000). Extensible markup language (XML)

Hucka, M., Finney, A., Sauro, H. M., and Bolouri, H. (2001). Systems Biology Markup Language (SBML) Level 1: Structures and facilities for basic model definitions. Available via the World Wide Web at `http://www.cds.caltech.edu/erato`.

Kernighan, B. W. and Ritchie, D. M. (1988). *The C Programming Language*. Prentice-Hall, New Jersey:

W3C (2000a). Naming and addressing: URIs, URLs, ... Available via the World Wide Web at http://www.w3.org/Addressing/.

W3C (2000b). W3C's math home page. Available via the World Wide Web at http://www.w3.org/Math/.