

---

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

---

Michael Hucka, Andrew Finney, Herbert Sauro, Hamid Bolouri  
{

# 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

The meaning of each component is as follows:

*Unit definition*

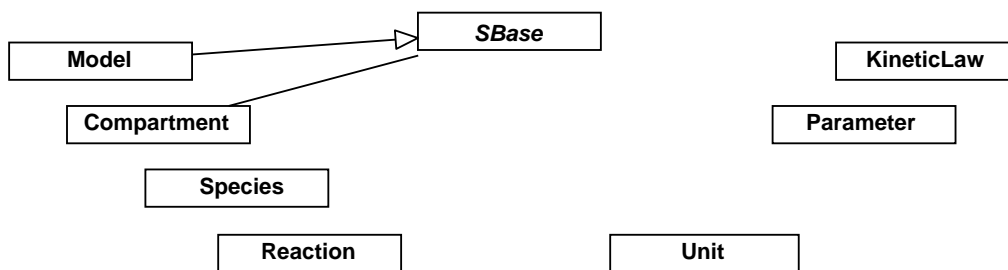


Figure 1:

reference is "http://www.mysim.org/ns" and the prefix is mysim. An example of an annotation might then be as follows:

...

```
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 (*













The optional boolean field `boundaryCondition` determines whether the amount of the `species` is fixed or variable over the course of a simulation. The value of `boundaryCondition` defaults to `false`, indicating



**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**







#### 4.7.2 Kineti cLaw

A ki neti cLaw structure describes the rate of the enclosing reaction. The use of a Ki neti cLaw structure in a Reacti on component is optional. (



The XML encoding shown above is quite straightforward. The outermost container is a tag, <smbl>, that identifies the contents as being Systems Biology Markup Language. The first attribute, xml ns, is required

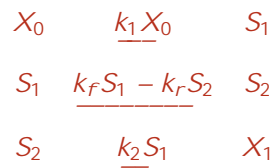
```

        </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 illustrates the use of rules in a model. The model is a simple two-compartment system. The first compartment is at 300 K and the second is at 310 K. The system is modeled using the following 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



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

<species id="T" compartment="cell" initialAmount="0"/>







## Appendix

### A Summary of Notation

```
</xsd:annotation>
<xsd:restriction base="xsd:string">
  <xsd:pattern value="(_|[a-z]|[A-Z])sd:ssns|[0-950_]*"/>sd:string">
  <xsd:string">
```

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

```
</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 name="AlgebraicRuleTJ-9.414-9.315Td[(</xsd:complexType>)]TJ0-9.315Td[(<xsd:complexType>-525(name
```





## C Predefined Functions in SBML

Table 6 lists the basic mathematical functions that are define in SBML Level 1 at this time.

---

Argument
----------

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)	$v = V \frac{S/K_m}{1 + S/K_m + S^2/K_i}$
usir	$S, P, V_f, V_r, K_{ms}, K_{mp}, K_i$	Substrate Inhibition Kinetics (Reversible)	$v = \frac{V_f S/K_{ms} + V_r P/K_{mp}}{1 + S/K_{ms} + P/K_{mp} + S^2/K_i}$
uai	$S, V, K_{sa}, K_{sc}$	Substrate Activation	$v = \frac{V (S/K_{sa})^2}{1 + S/K_{sc} + (S/K_{sa})^2 + S/K_{sa}}$
ucii	$S, I, V, K_m, K_i$	Competitive Inhibition (Irreversible)	$v = \frac{VS/K_m}{1 + S/K_m + I/K_i}$

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	$S, A_c, V, K_m, K_a, K_{ac}$	Mixed Activation Kinetics (Irreversible)	$v = \frac{V S}{K}$

Symbol	Meaning
	Effect of $S$ and

## 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: Dates (W3C candidate recommendation 24 October 2000). Available via , World Wide Web at <http://www.w3.org/TR/xml-schema-2/>.
- Bosak, J. and Bray, T. (1999). XML and the second-generation web. *Scientific American*, 280(5):89–93.

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:

