

## Qualitative Models

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This is a working draft of the specification for the SBML Level 3 package “qual”. It is not a normative document. Please send comments and other feedback to the Package Working Group mailing list, [sbml-qual@lists.sourceforge.net](mailto:sbml-qual@lists.sourceforge.net).

The latest release, past releases, and other materials related to this specification are available at [http://sbml.org/Community/Wiki/SBML\\_Level\\_3\\_Proposals/Qualitative\\_Models](http://sbml.org/Community/Wiki/SBML_Level_3_Proposals/Qualitative_Models)

*This* release of the specification is available at  
[http://sbml.org/images/a/a7/SBML-L3-qual-specification\\_0.1.pdf](http://sbml.org/images/a/a7/SBML-L3-qual-specification_0.1.pdf)



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# 1 Introduction

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## 1.1 Motivation

Quantitative methods for modelling biological networks require an in-depth knowledge of the biochemical reactions and their stoichiometric and kinetic parameters. In many cases, this knowledge is missing. This has led to the development of several qualitative modelling methods using information such as gene expression data coming from functional genomic experiments. Qualitative models are typically based on the definition of *regulatory* or *influence graph*. The components of these models differ from species and reactions used in current SBML models. For example, qualitative models typically associate discrete levels of activities with entity pools; the processes involving them cannot be described as reactions per se but rather as transitions between states. Boolean networks, logical models and some Petri nets are the most used qualitative formalisms in biology. Despite differences from traditional SBML models, it is desirable to bring these classes of models under a common format scheme. The purpose of this Qualitative Models package for SBML Level 3 is to support qualitative models into SBML.

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## 2 Background and context

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After several attempts to use the existing SBML L2 format, a decision was made to develop an extension for SBML L3. A first proposal written in August 2008 by Duncan Berenguier and Nicolas Le Novère was discussed during a meeting on the 12th and 13th of August 2008<sup>1</sup>. This meeting led to the release of a document (L3F\_extention\_draft\_1.2.pdf) which is a revision of a previous proposal for this package. A summary of the meeting is available at <http://www.ebi.ac.uk/compendium> and a document A second meeting was held at in November 2010 (see <http://compbio.igc.gulbenkian.pt/nmd/node/30>, for the program and participants). A revised version of the proposal was discussed during this meeting. This document accounts for the outcomes of the meeting discussions and of following exchanges.

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<sup>1</sup>Nicolas Le Novère (SBML), Sarah Keating (SBML), Nicolas Rodriguez (SBML), Denis Thieffry (GINSim), Duncan Berenguier (GINSim), Aurélien Naldi (GINSim), Claudine Chaouiya (GINSim, Petri nets), Tomas Helikar (Chemchains), Ioannis Xenarios (SQUAD), Alessandro Di Cara (SQUAD), Mathias John (PiML), Dagmar Koehn (PiML)

## 3 Package syntax and semantics

### 3.1 Graphical and typographical conventions

As this proposal covers various formalisms, the examples are labeled with a token indicating the corresponding formalism : **All** all formalisms, **PN** Petri nets, **LRG** logical regulatory networks or **SYM** symbolic relationships.

### 3.2 Namespace URI and other declarations necessary for using this package

Every SBML Level 3 package is identified uniquely by an XML namespace URI. For an SBML document to be able to use a given SBML Level 3 package, it must declare the use of that package by referencing its URI. The following is the namespace URI for this version of the Qualitative Models package for SBML Level 3 Version 1:

`"http://www.sbml.org/sbml/level3/version1/qual/version1"`

In addition, SBML documents using a given package must indicate whether understanding the package is required for complete mathematical interpretation of a model, or whether the package is optional. This is done using the attribute **required** on the **<sbml>** element in the SBML document. For the Qualitative Models package, the value of this attribute must be set to **"true"**.

The following fragment illustrates the beginning of a typical SBML model using SBML Level 3 Version 1 and this version of the Qualitative Models package:

```
<?xml version="1.0" encoding="UTF-8"?>
<sbml xmlns="http://www.sbml.org/sbml/level3/version1/core" level="3" version="1"
      xmlns:qual="http://www.sbml.org/sbml/level3/version1/qual/version1" qual:required="true">
```

### 3.3 Primitive data types

Section 3.1 of the SBML Level 3 specification defines a number of primitive data types and also uses a number of XML Schema 1.0 data types (?). We assume and use some of them in the rest of this specification, specifically **boolean**, **ID**, **SId**, **SIdRef**, **UnitSId**, **UnitSIdRef**, and **string**. The Qualitative Model package also makes use of or defines other primitive types; they are described below.

#### 3.3.1 Type temporisationType

#### 3.3.2 Type sign

#### 3.3.3 Type transitionInputEffect

#### 3.3.4 Type transitionOutputEffect

### 3.4 The extended Model class

The extension of SBML Level 3 Core's **Model** class is relatively straightforward: the Qualitative Models Package adds two lists, one for holding qualitativeSpecies (**listOfQualitativeSpecies**, of class **ListOfQualitativeSpecies**), and the other for holding transitions (**listOfTransitions**, of class **ListOfTransitions**). Figure ?? on page ?? provides the UML diagram. The **QualitativeSpecies** class and the **Transition** class are defined in Sections Section 3.5 and Section ?? respectively.

## 3.5 The QualitativeSpecies class

### 3.5.1 The SymbolicValue class

## 3.6 The Transition class

### 3.6.1 The Input class

### 3.6.2 The Output class

### 3.6.3 The FunctionTerm class

## 3.7 Not yet worked on

Like **Species** in SBML, the components of qualitative models refer to pools of entities that are considered indistinguishable and are each located in a specific **Compartment**. However, here components are characterised by their qualitative influences rather than by taking parts into reactions. Therefore, we define the **QualitativeSpecies** element to represent such pools of entities, and the **Transition** element to represent their qualitative influences.

This proposal defines the following new main elements: **QualitativeSpecies**, **SymbolicValue**, **Transition**, **Input**, **Output**, **FunctionTerm**, **DefaultTerm**. All inherit from **SBase** and all, except **DefaultTerm**, are contained into the corresponding **ListOfElementName** element, which inherits from **ListOf**.

The SBML element **Model** is extended to include the new elements **ListOfQualitativeSpecies** and **ListOfTransitions**. The SBML elements **EventAssignment** and **AssignmentRule** are extended to refer to **QualitativeSpecies**.

The overall structure of this extension is described in Figure ??.

## Extension of the Model element

The SBML element **Model** is extended to contain at most one **ListOfQualitativeSpecies** and at most one **ListOfTransitions**.

## Definition of QualitativeSpecies

The **Model** element may contain (at most) one **ListOfQualitativeSpecies** that contains at least one **QualitativeSpecies**.

A **QualitativeSpecies** describes a pool of indistinguishable entities in a **Compartment**. It is associated with either a *level* or a *symbol* from its **ListOfSymbolicValues**.

### *The id and name attributes:*

These attributes are used according to the SBML L3v1 Section 3.3. The attribute **id** is mandatory and **name** is optional.

### *The compartment, constant and boundaryCondition attributes:*

These attributes are treated as in **Species** elements.

### *The initialLevel attribute:*

The **initialLevel** is an integer that defines the initial level of the **QualitativeSpecies** in its **Compartment**. This attribute is optional.

### *The maxLevel attribute:*

The **maxLevel** is an integer that sets the maximal level of the **QualitativeSpecies**. This attribute is optional.

## Definition of SymbolicValue

The **QualitativeSpecies** element may contain at most one **ListOfSymbolicValues** that contains zero or more **SymbolicValues**. An empty list is allowed, and useful for e.g. adding annotations. The **SymbolicValue** element defines a non instantiated parameter. Such symbols may represent the different solutions of piecewise linear differential equations, along with different thresholds.

### *The id and name attributes*

These attributes are used according to the SBML L3.1 Section 3.3. The attribute id is mandatory and name is optional.

### *The rank attribute*

The rank is an integer that defines the position of the symbol in the **ListOfSymbolicValues**. This attribute is optional.

## Definition of Transition

The **Model** element may contain at most one **ListOfTransitions** that contains at least one **Transition**. A **Transition** element contains at most one **ListOfInputs**, exactly one **ListOfOutputs** and one **ListOfFunctionTerms**.

### *The id and name attributes:*

These attributes are used according to the SBML L3.1 Section 3.3. They are both optional.

### *The temporisationType attribute:*

The temporisationType is an enumeration the "temporisation" of the **Transition**, that is the updating policy associated with the **Transition**. It can be set to timer, priority, sustain, proportion or rate. This attribute is optional.

## Definition of Input

The **ListOfInputs** contains zero or more **Inputs**. A transition with zero inputs can be useful to define an initial assignment, where the state of an output depends on a function but not on any input values. An empty list is allowed, and useful for e.g. adding annotations. Each **Input** refers to a **QualitativeSpecies** that participates to the corresponding **Transition**.

### *The id and name attributes:*

These attributes are used according to the SBML L3.1 Section 3.3. They are both optional.

### *The qualitativeSpecies attribute:*

The qualitativeSpecies is a SIdRef referring to a **QualitativeSpecies**. This attribute is mandatory.

### *The thresholdLevel and thresholdSymbol attributes:*

The thresholdLevel is an integer and thresholdSymbol is a SIdRef. They are optional and exclusive.

### *The transitionEffect attribute:*

The transitionEffect is an enumeration describing how the qualitativeSpecies is affected by the **Transition**. On inputs, the value of transitionEffect can be either none or consumption. (See section Interpreting transitions). This attribute is mandatory.

### *The sign attribute*

The sign is an enumeration that can be used as an indication on whether the contribution of this input is positive, negative, or both. Thus, possible values can be either **positive**, **negative** or **dual**. The sign is usually used for visualization purposes only. This attribute is optional.

## Definition of Output

The **ListOfOutputs** contains at least one **Output**. Each **Output** refers to a **QualitativeSpecies** that participates to the corresponding **Transition**.

### *The id and name attributes:*

These attributes are used according to the SBML L3.1 Section 3.3. They are both optional.

### *The qualitativeSpecies attribute:*

The qualitativeSpecies is a **SIIDRef** referring to a **QualitativeSpecies**. This attribute is mandatory.

### *The outputLevel attribute:*

The outputLevel is an integer used along with the transitionEffect set to production to specify the effect of the **Transition** on the corresponding **QualitativeSpecies**. This attribute is optional.

### *The transitionEffect attribute:*

The transitionEffect is an enumeration describing how the qualitativeSpecies is affected by the **Transition**. On outputs, the value of transitionEffect can be **production**, **assignmentLevel** or **assignmentSymbol**. (See section Interpreting transitions). This attribute is mandatory.

## Definitions of FunctionTerm and DefaultTerm

The **ListOfFunctionTerms** may contain any number of **FunctionTerm** elements, and exactly one **DefaultTerm**. Each term is associated with a result (symbolic or level) and a **FunctionTerm** is associated with a Boolean function inside a **Math** element. The disjunction of the terms defines the *qualitative function* associated with a **Transition**.

### *The resultLevel and resultSymbol attributes:*

The result of the term is described by a resultLevel or a resultSymbol. Both are optional, but one of them must be defined.

The resultLevel is an integer describing a level. The resultSymbol is a **SIIDRef** referring to a **SymbolicValue**.

### *The temporisationValue attribute and the TemporisationMath element:*

The attribute temporisationValue and the element **TemporisationMath** allow the specification of the "temporisation" of the **Transition** under the corresponding **FunctionTerm**. Both are optional. Depending on the value of the temporisationType, either one or both could be used.

The temporisationValue is a double. The element **TemporisationMath** holds a MathML function returning a double.

### *The Math element:*

Each **FunctionTerm** holds a Boolean function encoded in a **Math** element, using the subset of MathML 2.0 as defined in SBML L3v1 Section 3.4.6. This element encodes the conditions under which the **FunctionTerm** is selected.



## Interpreting transitions

### *Determining the result of a qualitative function:*

The qualitative function associated with a **Transition** is encoded by a **ListOfFunctionTerms**. The **Transition** contains exactly one **DefaultTerm** describing the result of the function by default. A **FunctionTerm** in a **Transition** defines a result (resultLevel or resultSymbol) as well as the conditions (**Math** element) under which this **FunctionTerm** is selected. The conditions are encoded in MathML as a Boolean function that returns true if the conditions are fulfilled. Several **FunctionTerm** elements can have the same result; the qualitative function is then defined as the disjunction of their conditions.

### *Encoding the conditions:*

To encode the conditions of the qualitative function, one can use **ci** elements of MathML to refer to SBML elements. A **ci** referring to the id of a **QualitativeSpecies** then refers to the level or the symbol of this **QualitativeSpecies**, while a **ci** referring to the id of an **Input** then refers to the thresholdLevel or the thresholdSymbol of this **Input**.

### *The transitionEffect:*

The **Input** and **Output** elements refer to a **QualitativeSpecies** using the attribute qualitativeSpecies. They are defined with a transitionEffect attribute that takes one of the following values :

- **none**: Neither the level nor the symbol associated to the qualitativeSpecies is modified.
- **consumption**: The level of the qualitativeSpecies is decreased by the resultLevel of the selected term possibly modified by the thresholdLevel of the **Input**.
- **production**: The level of the qualitativeSpecies is increased by the resultLevel of the selected term possibly modified by the level of the **Output**.
- **assignmentLevel**: The level of the qualitativeSpecies is set to the resultLevel of the selected term.
- **assignmentSymbol**: The symbol associated to the qualitativeSpecies is set to the resultSymbol of the selected term.

## 4 Examples

### Simple Logical Regulatory Graph

**LRG** The following example shows a simple LRG with 3 regulators A, B and C, where A can take three values ( $A = \{0, 1, 2\}$ ), and B, C are Boolean. The logical functions are the following :  $B := 1$  if  $A \geq 1$ ,  $C := 1$  if  $B \geq 1$ ,  $A := 2$  if  $(A \geq 1$  and  $A < 2)$  or  $C \geq 1$ ;  $A := 1$  if  $A < 1$  and  $C \geq 1$ ;  $A := 0$  otherwise.

*Listing 1: Logical Regulatory Graph example*

```
<?xml version="1.0" encoding="UTF8"?>
<sbml xmlns="http://www.sbml.org/sbml/level3/version1" level="3" version="1" xmlns:qual="http://www.sbml.org/sbml/level3/qualitative"
  <model id="example">
    <listOfCompartments>
      <compartment id="cytosol" name="cytosol"/>
      <compartment id="nucleus" name="nucleus"/>
    </listOfCompartments>
    <qual:listOfQualitativeSpecies xmlns="http://sbml.org/Community/Wiki/SBML_Level_3_Proposals/Qualitative_Models">
      <qualitativeSpecies id="A" maxLevel="2" compartment="cytosol"/>
      <qualitativeSpecies id="B" maxLevel="1" compartment="cytosol"/>
      <qualitativeSpecies id="C" maxLevel="1" compartment="nucleus"/>
    </qual:listOfQualitativeSpecies>
    <qual:listOfTransitions xmlns="http://sbml.org/Community/Wiki/SBML_Level_3_Proposals/Qualitative_Models">
      <transition id="tr_B">
        <listOfInputs>
          <input id="theta_B_A" qualitativeSpecies="A" thresholdLevel="1" transitionEffect="none" sboTerm="SBO:0000170" />
        </listOfInputs>
        <listOfOutputs>
          <output qualitativeSpecies="B" transitionEffect="assignmentLevel"/>
        </listOfOutputs>
        <listOfFunctionTerms>
          <functionTerm resultLevel="1">
            <math><!-- A >= 1 -->
              <apply>
                <geq/>
                <ci>A</ci>
                <ci>theta_B_A</ci>
              </apply>
            </math>
          </functionTerm>
          <defaultTerm resultLevel="0"/>
        </listOfFunctionTerms>
      </transition>
      <transition id="tr_A">
        <listOfInputs>
          <input id="theta_A_A1" qualitativeSpecies="A" thresholdLevel="1" transitionEffect="none" sboTerm="SBO:0000170" />
          <input id="theta_A_A2" qualitativeSpecies="A" thresholdLevel="2" transitionEffect="none" sboTerm="SBO:0000170" />
          <input id="theta_A_C" qualitativeSpecies="C" thresholdLevel="1" transitionEffect="none" sboTerm="SBO:0000170" />
        </listOfInputs>
        <listOfOutputs>
          <output qualitativeSpecies="A" transitionEffect="assignmentLevel"/>
        </listOfOutputs>
        <listOfFunctionTerms>
          <functionTerm resultLevel="2">
            <math><!-- (A >= 1 and A < 2) or C < 1 -->
              <apply>
                <or/>
                <apply>
```

```

    <and/>
    <apply>
      <geq/>
      <ci>A</ci>
      <ci>theta_A_A1</ci>
    </apply>
    <apply>
      <lt/>
      <ci>A</ci>
      <ci>theta_A_A2</ci>
    </apply>
  </apply>
  <apply>
    <lt/>
    <ci>C</ci>
    <ci>theta_A_C</ci>
  </apply>
</math>
</functionTerm>
<functionTerm resultLevel="1">
  <math><!-- A < 1 and C >= 1 -->
    <apply>
      <and/>
      <apply>
        <lt/>
        <ci>A</ci>
        <ci>theta_A_A</ci>
      </apply>
      <apply>
        <geq/>
        <ci>C</ci>
        <ci>theta_A_C</ci>
      </apply>
    </apply>
  </math>
</functionTerm>
<defaultTerm resultLevel="0"/>
</listOfFunctionTerms>
</transition>
<transition id="tr_C">
  <listOfInputs>
    <input id="theta_C_B" qualitativeSpecies="B" thresholdLevel="1" transitionEffect="none" sbvTerm="SBO:0000169"
  </listOfInputs>
  <listOfOutputs>
    <output qualitativeSpecies="C" transitionEffect="assignmentLevel"/>
  </listOfOutputs>
  <listOfFunctionTerms>
    <functionTerm resultLevel="1">
      <math><!-- B >= 1 -->
        <apply>
          <geq/>
          <ci>B</ci>
          <ci>theta_C_B</ci>
        </apply>
      </math>
    </functionTerm>
    <defaultTerm resultLevel="0"/>
  </listOfFunctionTerms>

```

```

    </transition>
  </qual:listOfTransitions>
</model>
</sbml>

```

## Simple Petri net

**PN** The following example shows a simple Petri net, containing 4 places A, B, C and D with one transition *t1*.

**Listing 2:** Petri net example

```

<?xml version="1.0" encoding="UTF-8"?>
<sbml xmlns="http://www.sbml.org/sbml/level3/version1" level="3" version="1" xmlns:qual="http://www.sbml.org/sbml/level3/qualitativeModels">
  <model id="PN_exemple">
    <listOfCompartments>
      <compartment id="default" />
    </listOfCompartments>
    <qual:listOfQualitativeSpecies xmlns="http://sbml.org/Community/Wiki/SBML_Level_3_Proposals/Qualitative_Models">
      <qualitativeSpecies id="A" compartment="default" initialLevel="2" />
      <qualitativeSpecies id="B" compartment="default" initialLevel="4" />
      <qualitativeSpecies id="C" compartment="default" initialLevel="2" />
      <qualitativeSpecies id="D" compartment="default" initialLevel="3" />
    </qual:listOfQualitativeSpecies>
    <qual:listOfTransitions xmlns="http://sbml.org/Community/Wiki/SBML_Level_3_Proposals/Qualitative_Models">
      <transition id="t1">
        <listOfInputs>
          <input id="t1_A" qualitativeSpecies="A" thresholdLevel="2" transitionEffect="consumption" />
          <input id="t1_B" qualitativeSpecies="B" thresholdLevel="1" transitionEffect="consumption" />
        </listOfInputs>
        <listOfOutputs>
          <output qualitativeSpecies="C" level="1" transitionEffect="production" />
          <output qualitativeSpecies="D" level="2" transitionEffect="production" />
        </listOfOutputs>
        <listOfFunctionTerms>
          <functionTerm result="1">
            <math><!-- A >= 2 and B >= 1 -->
              <apply>
                <and />
                <apply>
                  <geq />
                  <ci>A</ci>
                  <ci>t1_A</ci>
                </apply>
                <apply>
                  <geq />
                  <ci>A</ci>
                  <ci>t1_B</ci>
                </apply>
              </math>
            </functionTerm>
            <defaultTerm result="0" />
          </listOfFunctionTerms>
        </transition>
      </qual:listOfTransitions>
    </model>
  </sbml>

```

## 5 Best practices

**All** To be valid, the SBML root element must express the requirement of this package: `<sbml ... qual:required="true" ... >`.

**PN** In Petri nets the initial conditions are part of the model, the `initialLevel` must be defined. To represent unbounded places, the `maxLevel` should be not specified.

**LRG** Discussions are still ongoing about the possible (but some times convenient to avoid cumbersome descriptions) incoherency of the **FunctionTerm** elements. For the moment, here are the guidelines to ensure coherent definitions:

- The **FunctionTerm** elements of all the transitions targeting the same output should be "coherent": the conditions of two **FunctionTerm** elements, leading to different effects on the level/symbol of the output, should not be fulfilled at the same time( i.e. they should be exclusive).
- If several **FunctionTerm** elements lead to the same effect on the level/symbol of the same output, then the importing tool should consider the disjunction (OR) on the conditions of the terms.

**LRG** To declare external nodes (ones that have no Boolean expression/truth table associated with them), one should set the attribute `boundaryCondition` of the **QualitativeSpecies** to `TRUE`:

```
<qualitativeSpecies id="EGF" maxLevel="1" boundaryCondition="true"
                    compartment="extracellular"/>
```

**LRG** To declare a "delay" node, which is specified to delay its state update for  $k$  iterations, one should set, for all the **Transition** elements having this node as their (unique) output, the attribute `temporisationType` to the value `timer` and the `temporisationValue` to  $k$ .

**LRG** To declare a "sustain" node, which is specified to sustain (i.e., to remain in) its latest state for the next  $k$  iterations, one should set, for all the **Transition** elements having this node as their (unique) output, the attribute `temporisationType` to the value `sustain` and the `temporisationValue` to  $k$ .

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## A Validation of SBML documents

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## Acknowledgments

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