SBML Level 3 Package Specification

# Multistate, Multicomponent and Multicompartment Species Package for SBML Level 3

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This is a draft specification for the SBML Level 3 package called "*Multi*". It is not a normative document. Please send feedback to the package mailing list at sbml-multi@lists.sourceforge.net.

The latest release, past releases, and other materials related to this specification are available at http://sbml.org/Documents/Specifications/SBML_Level_3/Packages/Multistate_and_Multicomponent_Species_(multi)

*This* release of the specification is available at
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And all the people who contributed to the discussions on the sbml-multi mailing list.

# Contents

# 1 Introduction

This Multistate, Multicomponent and Multicompartment Species (Multi) package provides an extension of SBML Level 3 [Hucka et al. (2010)] that supports encoding `models` with molecular complexes that have multiple components and can exist in multiple states and in multiple `compartments`. One of its goals also is to provide a platform for sharing `models` based on the specifications of bi-molecular interactions and the rules governing such interactions[Angermann et al. (2012); Feret et al. (2009); Hlavacek et al. (2006); Zhang et al. (2013)]. This specification covers the goals and features described in the previous Multi proposal [Novère and Oellrich (2010)] for extending SBML to carry the information for *multistate multicomponent* `species` with revised data structure. In addition, this specification includes the feature for *multicompartment* `species` as described in the most recent releases of the Multi proposal[Zhang and Meier-Schellersheim (2013a), Zhang et al. (2012)].

## 1.1 Proposal corresponding to this package specification

This specification for Multi in SBML Level 3 Version 1 is mainly based on the new Multi proposal (May 2013, Rev 280) located at the following URL:

`http://goo.gl/2375K`

## 1.2 Package dependencies

The Multi package has no dependencies on other SBML Level 3 packages.

## 1.3 Document conventions

UML 1.0 notation is used in this document to define the constructs provided by this package. Colors in the diagrams carry the following additional information for the benefit of those viewing the document on media that can display color:

- *Black* Items colored black are components taken unchanged from their definitions in the SBML Level 3 Core specification document.
- *Green* Items colored green are components that exist in SBML Level 3 Core, but are extended by this package. Class boxes are also drawn with with dashed lines to further distinguish them.
- Blue Items colored blue are new components introduced in this package specification. They have no equivalent in the SBML Level 3 Corespecification.

For other matters involving the use of UML, XML and typographical conventions, this document follows the conventions used in the SBML Level 3 Core specification document[Hucka et al. (2010)].

For simplicity, "`...`" in all example code refers to some unspecified code content, that is not important for the purpose of illustrating the issue at hand.

# 2 Background and context

Rule-based modeling (more specific: "Domain-detailed reaction rule modeling") approaches (*BioNetGen*[Faeder et al. (2009)], *Kappa*[Danos and Laneve (2004)], and *Simmune*[Angermann et al. (2012); Meier-Schellersheim et al. (2006)]) define rules for interactions between pairs of molecule domains, specifying how the interactions depend on particular states of the molecules (pattern) and their locations in specific compartments. In order to generate networks of biochemical reactions these rules are applied to the molecular components of the systems to be modeled, either at the beginning of the modeling (simulation) process or "on the fly" (as molecule complexes emerge from the interaction rules). Expressing such rule-based reaction networks using the concepts of **Species** and **Compartment** in SBML (L3 core and L2) can be difficult for rules and molecule sets that lead to large numbers of resulting molecular complexes. It would therefore be desirable to have an SBML standard for encoding rule-based `models` using their "native" concepts for describing reactions instead of having to apply the rules and unfold the networks prior to encoding in an SBML format.

We proposed a revised proposal of the Multi: "Multistate, Multicomponent and Multicompartment Species Package for SBML Level 3" (abbreviated as Multi)[Zhang et al. (2012) and Zhang and Meier-Schellersheim (2013a)] which takes the scopes and some data structures developed in the previous Multi proposal [Novère and Oellrich (2010)] and addresses main issues arising from a rule-based modeling point of view with the data structures consistent with that used in the available rule-based modeling tools.

## 2.1 Revision history

### *2.1.1 Current version: 1.0.6.0*

Remove the recurrsively referencing relationship in the **ListOfSpeciesFeatures** class by adding a **SubListOfSpeciesFeatures** class. See the details in **Species**.

### *2.1.2 Version: 1.0.5.1 - released in Dec 2015*

Minor document revision from v1.0.5 based on the online discussion with Nicolas Rodriguez.

### *2.1.3 Version: 1.0.5 - released in Nov 2015*

This version has been developed from the previous release v1.0.4 with the following modifications based on the discussion during and after COMBINE 2015 [Zhang (2015)]:

- Drop the `occur` attribute in the class of **SpeciesTypeInstance**.
- Drop the `occur` attribute in the class of **SpeciesTypeComponentIndex**.
- Drop the class of **DenotedSpeciesTypeComponentIndex**.
- Revise the scope of **PossibleSpeciesFeatureValue** ids to be global.

### *2.1.4 Version: 1.0.4 - released in June 2015*

This version has been developed from the previous release v1.0.3 with minor document update and complete validation rules.

### *2.1.5 Version: 1.0.3 - released in April 2015*

This version has been developed from the previous release v1.0.2 mainl based on the discussion in COMBINE 2014 with the focus on how to facilitate tools to export and import `models` encoded in the Multi format[Zhang and Meier-Schellersheim (2014)]

### 2.1.6 Version: 1.0.2 - released in Nov 2014

This version has been developed from the previous release v1.0.1 with the following modifications:

- A new **BindingSiteSpeciesType** sub-class inheritting the **SpeciesType** class for `binding sites`. Accordingly, the `isBindingSite` attribute has been dropped from **SpeciesType**.
- Restriction on `binding sites` which have to be atomic.
- Restriction on **SpeciesType** that a `speciesType` can not have a `listOfSpeciesFeatureTypes` if it has a `listOfInSpeciesTypeBonds`.
- A new **IntraSpeciesReaction** sub-class inheritting the **Reaction** class for the reactions happening within a **Species** object. Accordingly, the `isIntraSpeciesReaction` attribute has been dropped from **Reaction**.
- Validation rules.

### 2.1.7 Revision history before version 1.0.2

See the past work (Section 2.2).

## 2.2 Past work on this problem or similar topics

- Nicolas Le Novère and Anika Oellrich proposed the previous version of the Multi proposal[Novère and Oellrich (2010)]. The development became stalled after 2010.
- In August 2012, Fengkai Zhang from the *Simmune* group presented " Draft for discussion SBML Proposals for Revised Multi, Simple Spatial and Multi-Spatial Extensions" at COMBINE 2012[Zhang et al. (2012)]. The three proposals cover the goals and scope of the previous Multi proposal (2010), revise it and add some new features that improve usage of the proposal for rule-based approaches.
- Based on the discussions and suggestions received during COMBINE 2012 as well as on feedback from the SBML discussion forum, the new Multi proposal [Rev 221, Zhang and Meier-Schellersheim (2012)] was released to the SBML-Multi community, which integrates and covers most of the features in the three previous proposals of Aug 2012.
- In May 2013, a new reversion of the Multi proposal [Zhang and Meier-Schellersheim (2013a)] was released before the meeting of HARMONY 2013. The extended **Compartment** class and its related classes have been reorganized. All optional boolean attributes have been removed/replaced. A new optional Multi attribute, "`whichValue`", was added to the `ci` elements in **KineticLaw** to identify the sources of `species`. (Lucian Smith gave many comments/suggestions about this proposal and William Hlavacek gave thoughtful feedback about the *BioNetGen* example in this proposal). This revision 280 was presented at HARMONY 2013 [Zhang and Meier-Schellersheim (2013c)] with new features to configure multiple occurrences of **SpeciesFeatureType**. Several new or revised features were discussed during and after HARMONY 2013, including multiple occurrences of **SpeciesFeatureType**, multiple copies of **SpeciesTypeInstance**, the `numericValue` attribute for **PossibleSpeciesFeatureValue** and concentration summation of pattern `species`. These features are covered or updated in this specification.
- A draft specification V1.0.1 was released in Sep 2013 [Zhang and Meier-Schellersheim (2013b)] and was presented in COMBINE 2013 [Zhang and Meier-Schellersheim (2013d)]. This version of the specification addresses the scenario of multiple occurrences of identical components and/or identical features.

# 3 Package syntax and semantics

This section contains a definition of the syntax and semantics of the Multi package for SBML Level 3 Core.

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

The following is the namespace URI for this version of the Multi package for SBML Level 3 Core:

"http://www.sbml.org/sbml/level3/version1/multi/version1"

In addition, SBML documents using a given package must indicate whether the package can be used to change the mathematical interpretation of a model. This is done using the attribute `required` on the <sbml> element in the SBML document. For the Multi package, the value of this attribute must be "`true`".

The following fragment illustrates the beginning of a typical SBML model using SBML Level 3 Core and this version of the Multi package:

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

## 3.2 Primitive data types

The Multi package uses a number of the primitive data types described in Section 3.1 of the SBML Level 3 Core [Hucka et al. (2010)] specification such as `SId`, `SIdRef`, `string`, `boolean`, `int` and `positiveInteger`, and adds three additional primitive types described below.

### 3.2.1 *Type* `BindingStatus`

The `BindingStatus` primitive data type is used in the definition of the **OutwardBindingSite** class. `BindingStatus` is derived from type `string` and its values are restricted to be one of the following possibilities: "`bound`", "`unbound`", and "`either`". Attributes of type `BindingStatus` cannot take on any other values. The meaning of these three values is discussed in the context of the **OutwardBindingSite** class in Section 3.16 on page 26.

### 3.2.2 *Type* `Relation`

The `Relation` primitive data type is used in the definition of the **SubListOfSpeciesFeatures** class. `Relation` is derived from type `string` and its values are restricted to be one of the following possibilities: "`and`", "`or`", and "`not`". Attributes of type `Relation` cannot take on any other values. The meaning of these three values is discussed in the context of the **SubListOfSpeciesFeatures** class in Section 3.17 on page 27.

### 3.2.3 *Type* `RepresentationType`

The `RepresentationType` primitive data type is used in the extension of the `ci` element. `RepresentationType` is derived from type `string` and its values are restricted to be one of the following possibilities: "`sum`" or "`numericValue`". If present, attributes of type `RepresentationType` cannot take on any other values. The meaning of these values is discussed in the context of the `ci` element in Section 3.27 on page 41.

## 3.3 The new and extended classes in the Multi Package

The Multi package defines or extends the following object classes, **Model**, **ListOfSpeciesTypes**, **Compartment**, **ListOfCompartmentReferences**, **CompartmentReference**, **SpeciesType**, **ListOfSpeciesTypeInstances**, **ListOfSpeciesFeatureTypes**, **ListOfInSpeciesTypeBonds**, **ListOfSpeciesTypeComponentIndexes**, **SpeciesFeatureType**, **ListOfPossibleSpeciesFeatureValues**, **PossibleSpeciesFeatureValue**, **SpeciesTypeInstance**, **InSpeciesTypeBond**, **SpeciesTypeComponent-**

**Index**, **Species**, **ListOfOutwardBindingSites**, **ListOfSpeciesFeatures**, **SubListOfSpeciesFeatures**, **OutwardBindingSite**, **SpeciesFeature**, **ListOfSpeciesFeatureValues**, **SpeciesFeatureValue**, **Reaction**, **SimpleSpeciesReference**, **SpeciesReference**, **ListOfSpeciesTypeComponentMapsInProduct**, **SpeciesTypeComponentMapInProduct**, **ListOfSpeciesFeatureChanges**, and **SpeciesFeatureChange**.

All the classes in the Multi package are directly or indirectly derived from ***SBase***, and ***SBase*** provides the ability to attach `SBO` terms as well as `MIRIAM` annotations, the semantics of a given class in the Multi package can be made more precise by referencing to external controlled vocabularies and ontologies.

Like the classes in SBML Level 3 Core, most new Multi classes have the attribute `id` (typically mandatory but not all, and of type `SId`), which serves as an identifier to provide a way to identify the class object. The identifier of a class object reference may or may not carry mathematical interpretation or be used in mathematical formulas, depending on its class and the class object referencing it. The scope of `id`s is described in the section of "Namespace scoping rules for identifiers"(Section 3.28 on page 44).

## 3.4 Model

The Multi package extends the **Model** class of SBML Level 3 Core and adds an optional **ListOfSpeciesTypes** child to **Model**. Figure 1 provides the UML diagram for the extended **Model** class.

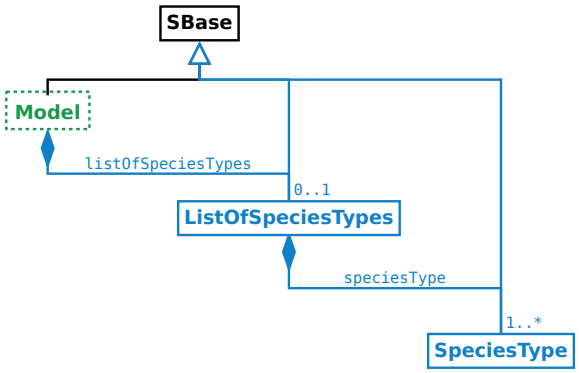


***Figure 1:*** *The extension of the* ***Model*** *class.*

### 3.4.1 *ListOfSpeciesTypes*

**ListOfSpeciesTypes** is defined in Figure 1. If present, a **ListOfSpeciesTypes** object must contain at least one **SpeciesType** object. Since **ListOfSpeciesTypes** is derived from **SBase**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

## 3.5 Extended Compartment

A **Compartment** object in SBML Level 3 Core represents a bounded space in which *species* are located. In the Multi package, **Compartment** is extended. A Multi `compartment` can be a `type` that multiple referencing `compartments` can map to. A Multi `compartment` can also be a composite `compartment` or a container that includes other `compartments`.

The extension of **Compartment** is defined in Figure 2. The extended **Compartment** class has a new required attribute `isType`, a new optional attribute `compartmentType` and an optional **ListOfCompartmentReferences** child. The example at Section 4.1 on page 45 illustrates the use of the extended **Compartment** class.

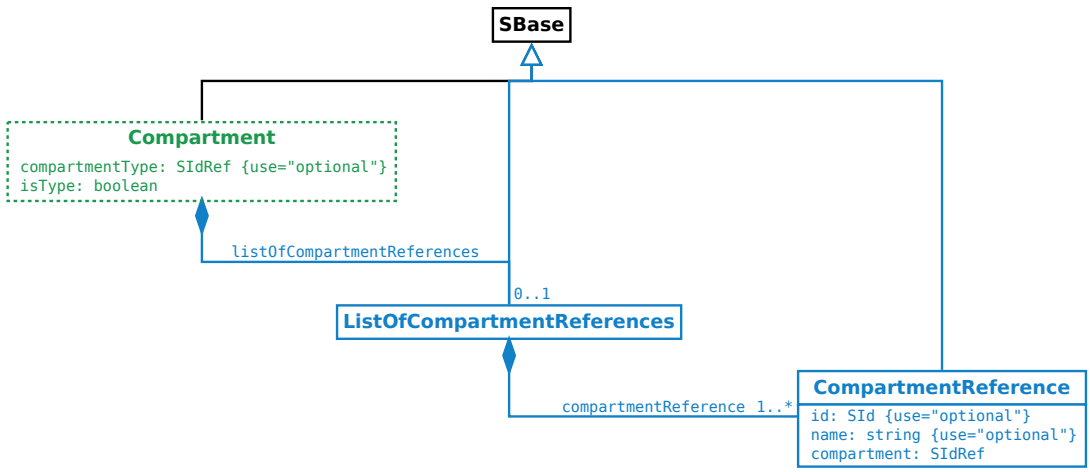


***Figure 2:*** *The definitions of **Compartment**, **ListOfCompartmentReferences** and **CompartmentReference***

### 3.5.1 *The* `isType` *attribute*

The required attribute `isType`, of type `boolean`, on the **Compartment** class serves to provide a way to indicate whether the **Compartment** object is a compartment type.

A **Compartment** object is a compartment type if the value of its `isType` attribute is "`true`". A `compartment type` is a template (in the sense of prototype) for all **Compartment** objects referencing it (via `compartmentType` attributes). A **Species** object directly referencing a compartment type is not a "`fully defined`" species (see Section 3.19 on page 33).

If the value of the `isType` attribute is "`false`", the **Compartment** object is a "`not-a-type`" *compartment* , and it is similar to a SBML core `compartment` except it can reference a compartment type and can have a **ListOfCompartmentReferences** child.

### 3.5.2 *The* `compartmentType` *attribute*

The optional attribute `compartmentType`, of type `SIdRef`, is used for a "`not-a-type`" `compartment` to reference a compartment type. A `compartment` with the "`true`" value of its `isType` attribute can not have the `compartmentType` attribute defined.

### 3.5.3 *ListOfCompartmentReferences*

**ListOfCompartmentReferences** is defined in Figure 2, and is extended from the **ListOf** class. A `listOfCompartmentReferences` must have one or more **CompartmentReference** children. Since **ListOfCompartmentReferences** is derived from **SBase** through **ListOf**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

## 3.6 CompartmentReference

**CompartmentReference** is defined in Figure 2 on the preceding page. It has two optional attributes `id` and `name`, and a required attribute `compartment`. Since **CompartmentReference** is derived from **SBase**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

### *3.6.1 The* `id` *and* `name` *attributes*

The optional `id` attribute, of type `SId`, serves to provide a way to identify a `compartmentReference`. **CompartmentReference** also has an optional `name` attribute, of type `string`.

If some or all `compartmentReferences` within a **ListOfCompartmentReferences** object reference the same `compartment`, those `compartmentReferences` are required to have their `id` attributes defined to distinguish different `compartmentReferences`.

### *3.6.2 The* `compartment` *attribute*

The required `compartment` attribute, of type `SIdRef`, serves to provide a way to reference a **Compartment** object.

## 3.7 The relationship of Compartment, CompartmentReference and ListOfCompartmentReferences

In a **ListOfCompartmentReferences** object, every children `compartmentReferences` must exclusively reference, directly or indirectly, "`not-a-type`" `compartment` which can be of the same compartment type. See the extended **Compartment** objects in the example in Section 4.1 on page 45.

All `compartments` referenced by a `listOfCompartmentReferences` must have the values of their `isType` attributes the same as that in the parent `compartment` of the `listOfCompartmentReferences`. For example, a compartment "`A`" with `isType`="`true`" has a `listOfCompartmentReferences` referencing two compartments "`A1`" and "`A2`". Then, "`A1`" and "`A2`" must have `isType`="`true`".

## 3.8 SpeciesType

**SpeciesType** is defined in Figure 3 and serves to provide backbone structures for `species`. **SpeciesType** has one required attribute, `id`, two optional attributes, `name` and `compartment` and four optional **ListOf**__ objects of **ListOfSpeciesFeatureTypes**, **ListOfSpeciesTypeInstances**, **ListOfInSpeciesTypeBonds** and **ListOfSpeciesTypeComponentIndexes** respectively. Since **SpeciesType** is derived from **SBase**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

The **ListOfSpeciesTypeInstances** subobject provides a way to define multicomponents which are instances of other **SpeciesType** objects.

The **ListOfSpeciesFeatureTypes** subobject and its **SpeciesFeatureType** children set up a framework for the referencing `species` or the instances of `speciesTypes` to be able to have multistates. The **ListOfSpeciesTypeComponentIndexes** subobject provides a flexible way to reference any `component` in a `speciesType`.

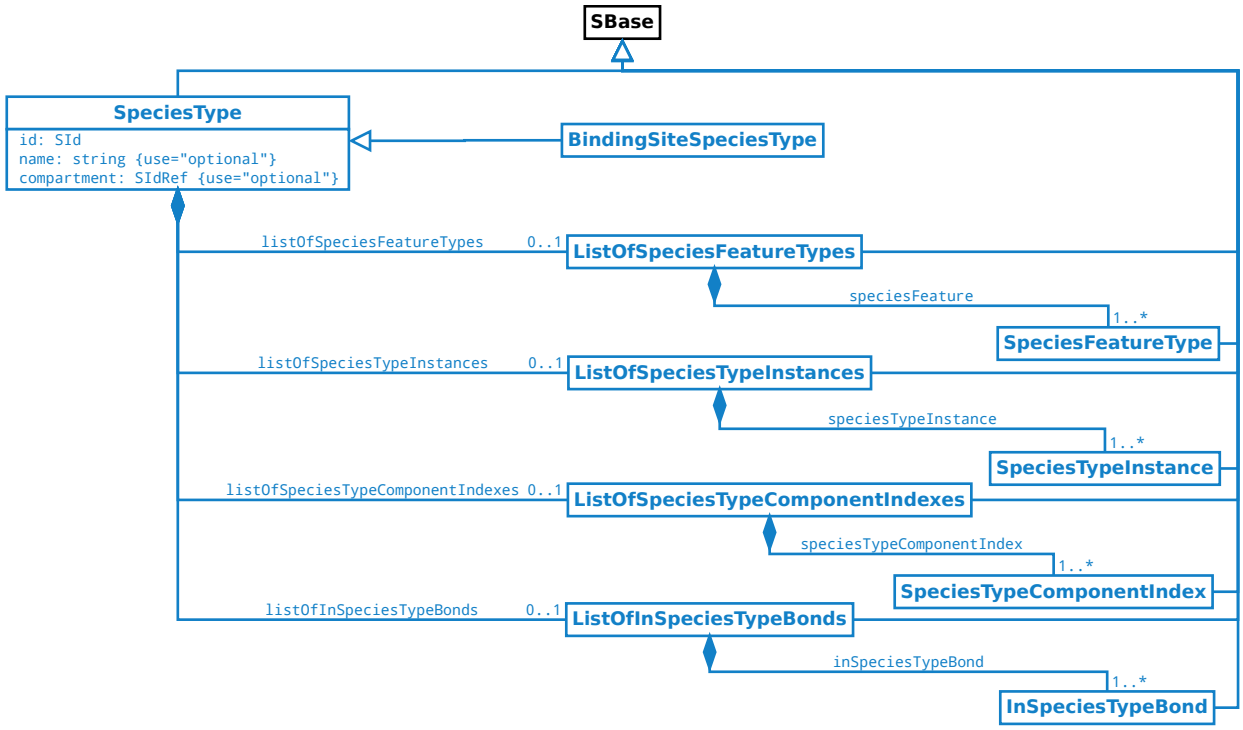


***Figure 3:*** *The definition of the **SpeciesType** class.*

### 3.8.1 The `id` and `name` attributes

The required `id` attribute, of type `SId`, serves to provide a way to identify a `speciesType`. **SpeciesType** also has an optional `name` attribute, of type `string`.

### 3.8.2 The `compartment` attribute

**SpeciesType** has an optional attribute `compartment`, of type `SIdRef`, to be used to identify the `compartment` where the `speciesType` is located. The attribute value must be the identifier of an existing `compartment` in the `model`. If present, it must be consistent with the `compartment` attributes of the referencing `species` (see Section 3.15 on page 24) and the `compartmentReference` attributes of its instances (see Section 3.11.3 on page 17). The example in Section 4.1 on page 45 illustrates how to keep the consistency of this attribute.

### 3.8.3 ListOfSpeciesFeatureTypes

**ListOfSpeciesFeatureTypes** is defined in Figure 3 on the preceding page, and is extended from the **ListOf** class. If present, a `listOfSpeciesFeatureTypes` must have one or more **SpeciesFeatureType** children. Since **ListOfSpeciesFeatureTypes** is derived from **SBase** through **ListOf**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

### 3.8.4 ListOfSpeciesTypeInstances

**ListOfSpeciesTypeInstances** is defined in Figure 3 on the previous page, and is extended from the **ListOf** class. If present, a `listOfSpeciesTypeInstances` must have one or more **SpeciesTypeInstance** children. Since **ListOfSpeciesTypeInstances** is derived from **SBase** through **ListOf**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

### 3.8.5 ListOfInSpeciesTypeBonds

**ListOfInSpeciesTypeBonds** class is defined in Figure 3 on the preceding page, and is extended from the **ListOf** class. If present, a `listOfInSpeciesTypeBonds` must have one or more **InSpeciesTypeBond** children. Since **ListOfInSpeciesTypeBonds** is derived from **SBase** through **ListOf**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

### 3.8.6 ListOfSpeciesTypeComponentIndexes

**ListOfSpeciesTypeComponentIndexes** is defined in Figure 3 on the previous page, and is extended from the **ListOf** class. If present, a `listOfSpeciesTypeComponentIndexes` must have one or more **SpeciesTypeComponentIndex** children. Since **ListOfSpeciesTypeComponentIndexes** is derived from **SBase** through **ListOf**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

### 3.8.7 BindingSiteSpeciesType

**BindingSiteSpeciesType** inherits the **SpeciesType** class and is defined in Figure 3 on the preceding page. A **BindingSiteSpeciesType** object is a `binding site`, and therefore its instance can further define the `bindingStatus` attribute and can participate a binding internally and explicitly in an **InSpeciesTypeBond** object, or externally and implicitly defined by an **OutwardBindingSite** object. A `binding site` must be an atomic component which means that a **BindingSiteSpeciesType** object can not contain a **ListOfSpeciesTypeInstances** subobject.

☞ *Note:*
*In the Multi package, a* `binding site` *can participate one binding at a time. That means a* `binding site` *can not bind two partners at the same time. The binding relationship is one-to-one.*

## 3.9 SpeciesFeatureType

**SpeciesFeatureType** is defined in Figure 4, and serves to provide frameworks or templates to define the referencing **SpeciesFeature** objects. **SpeciesFeatureType** has two required attributes `id` and `occur`, an optional attribute `name`, and a required child `listOfPossibleSpeciesFeatureValues`. The multiple `possibleSpeciesFeatureValues` of the **ListOfPossibleSpeciesFeatureValues** object permit constructing multistate `species` via its `speciesFeatures` under the **ListOfSpeciesFeatures** or **SubListOfSpeciesFeatures** object. Since **SpeciesFeatureType** is derived from **SBase**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

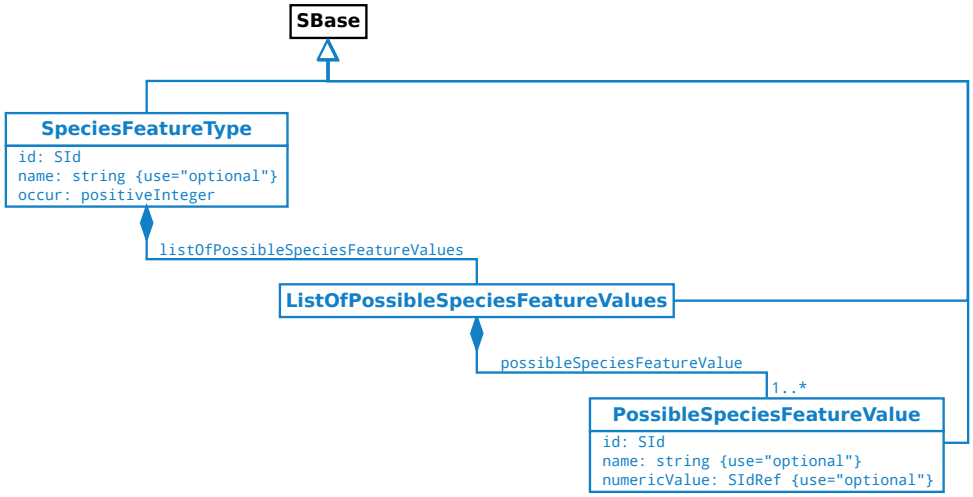


***Figure 4:*** *The definitions of **SpeciesFeatureType**, **ListOfPossibleSpeciesFeatureValues** and **PossibleSpeciesFeatureValue** classes.*

### 3.9.1 The `id` and `name` attributes

The required `id` attribute, of type `SId`, serves to provide a way to identify a `speciesFeatureType`. Its value must be unique within its direct parent `speciesType`. When a `speciesFeatureType` is referenced by a `speciesFeature`, a **SpeciesTypeComponentIndex** object indexing the containing `component` can be used to avoid ambiguity.

**SpeciesFeatureType** also has an optional `name` attribute, of type `string`.

### 3.9.2 The `occur` attribute

**SpeciesFeatureType** has a required attribute `occur`, of type `positiveInteger`, used to indicate the number of instances of the `speciesFeatureType`. This attribute can be used to infer the number of the instances in "`don't care`" state with the use of the `occur` attribute in a referencing `speciesFeature` (also see Section 3.18.3 on page 29).

### 3.9.3 ListOfPossibleSpeciesFeatureValues

**ListOfPossibleSpeciesFeatureValues** is defined in Figure 4, and is extended from the **ListOf** class. A `listOfPossibleSpeciesFeatureValues` must have one or more **PossibleSpeciesFeatureValue** children. Since **ListOfPossibleSpeciesFeatureValues** is derived from **SBase** through **ListOf**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

## 3.10 PossibleSpeciesFeatureValue

**PossibleSpeciesFeatureValue** is defined in Figure 4 on the preceding page, and is used to define the possible values a `speciesFeature` can take. It has a required attribute `id` and two optional attributes `name` and `numericValue`. Since **PossibleSpeciesFeatureValue** is derived from **SBase**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

### *3.10.1 The* `id` *and* `name` *attributes*

The required `id` attribute, of type `SId`, serves to provide a way to identify a `possibleSpeciesFeatureValue`.

If the `id` of a `possibleSpeciesFeatureValue` is the content of a `ci` element in a MathML expression, it can either represent the `numericValue` ( when the `ci` has `representationType`="`numericValue`") or the count of the feature instances (default) which have this value. Also see the example at Section 3.27.1 on page 41.

**PossibleSpeciesFeatureValue** also has an optional `name` attribute, of type `string`.

### *3.10.2 The* `numericValue` *attribute*

**PossibleSpeciesFeatureValue** has an optional attribute `numericValue` to be used to provide a reference to a numeric value that the **PossibleSpeciesFeatureValue** object can have. This attribute has type of `SIdRef`, and the value must be the identifier of a **Parameter** object in the `model`. The numeric value along with the unit can be defined in the **Parameter** object.

The modeler can either use the identifier of the `parameter`, or the identifier of the `possibleSpeciesFeatureValue` (with `ci`'s `representationType` and `speciesReference` attribute) as the content of a `ci` element to represent its value in `MathML` expressions in SBML.

## 3.11 SpeciesTypeInstance

**SpeciesTypeInstance** serves to provide a way to construct `speciesTypes` and `species` with multiple components. A `speciesType` can contain a list of instances of other `speciesTypes` which can also have their own `speciesTypeInstances`, so the complete structure of a `speciesType` can be like a tree. A `speciesType` can not contain an instance of any other `speciesType` that already contains the instance of it. In other words, circular references are not allowed when constructing `speciesTypes`. For example, if a speciesType "`A`" contains the instance of another speciesType "`B`", "`B`" must not contain the instance of "`A`" anywhere in the complete structure of "`B`".

**SpeciesTypeInstance** is defined in Figure 5. It has two required attributes, `id`, and `speciesType`, and two optional attributes `name` and `compartmentReference`. Since **SpeciesTypeInstance** is derived from **SBase**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

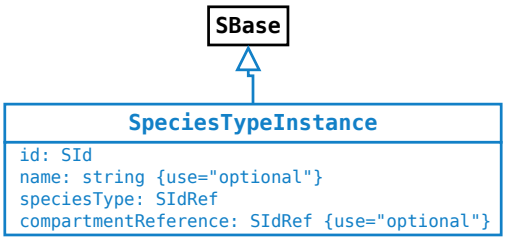


***Figure 5:*** *The definition of the* ***SpeciesTypeInstance*** *class*

### 3.11.1 *The* `id` *and* `name` *attributes*

The required `id` attribute, of type `SId`, serves to provide a way to identify a `speciesTypeInstance`. Its value must be unique within its direct parent `speciesType`.

**SpeciesTypeInstance** also has an optional `name` attribute of type `string`.

### 3.11.2 *The* `speciesType` *attribute*

**SpeciesTypeInstance** has a required attribute `speciesType`, of type `SIdRef`, is used to reference a `speciesType`.

### 3.11.3 *The* `compartmentReference` *attribute*

**SpeciesTypeInstance** has an optional attribute `compartmentReference`, of type `SIdRef`, can be used to indicate which sub-compartment in a composite `compartment` the `speciesTypeInstance` is located in.

For example, a compartment "`cA`" has two sub-compartments "`cB1`" (referenced by compartmentReference "`crB1`") and "`cB2`" (referenced by compartmentReference "`crB2`") of the same compartment type "`cB`". A speciesType "`stA`" has two speciesTypeInstances "`stiB1`" and "`stiB2`" of the same speciesType "`stB`". The speciesType "`stA`" references the compartment "`cA`" and the speciesType "`stB`" references the compartment "`cB`". The speciesTypeInstance "`stiB1`" is located in "`cB1`" via the compartmentReference "`crB1`" and the speciesTypeInstance "`stiB2`" is located in "`cB2`" via the compartmentReference "`crB2`". The SBML code can be as follows:

```
<listOfCompartments>
   <compartment id="cB" multi:isType="true" ... />
   <compartment id="cB1" multi:isType="false" multi:compartmentType="cB" ... />
   <compartment id="cB2" multi:isType="false" multi:compartmentType="cB" ... />
   <compartment id="cA" multi:isType="false" ... >
      <multi:listOfCompartmentReferences>
         <multi:compartmentReference multi:id="crB1" multi:compartment="cB1" />
         <multi:compartmentReference multi:id="crB2" multi:compartment="cB2" />
      </multi:listOfCompartmentReferences>
   </compartment>
```

```
</listOfCompartments>
<multi:listOfSpeciesTypes>
   <multi:speciesType multi:id="stB" multi:compartment="cB" ... />
   <multi:speciesType multi:id="stA" multi:compartment="cA" ... >
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="stiB1" multi:speciesType="stB"
            multi:compartmentReference="crB1" ... />
         <multi:speciesTypeInstance multi:id="stiB2" multi:speciesType="stB"
            multi:compartmentReference="crB2" ... />
      </multi:listOfSpeciesTypeInstances>
   </multi:speciesType>
</multi:listOfSpeciesTypes>
```

## 3.12 SpeciesTypeComponentIndex

**SpeciesTypeComponentIndex** provides a way to identify or index a `component` within a `speciesType`. A **SpeciesTypeComponentIndex** object can be referenced by other class objects, such as **InSpeciesTypeBond**, **OutwardBindingSite**, **SpeciesFeature** or **SpeciesTypeComponentMapInProduct** objects, which needs to identify a component in a particular `speciesType`.

**SpeciesTypeComponentIndex** is defined in Figure 6. It has two required attributes, `id`, and `component`, and an optional attribute `identifyingParent`. Since **SpeciesTypeComponentIndex** is derived from **SBase**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

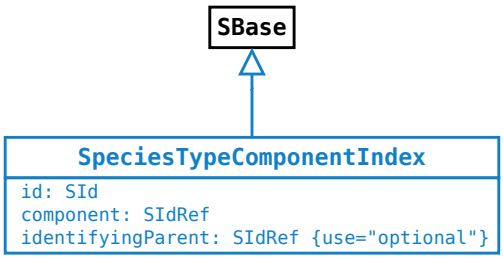


***Figure 6:*** *The definition of the **SpeciesTypeComponentIndex** class*

See Section 3.16.2 on page 26 about how to use **SpeciesTypeComponentIndex** in an `outwardBindingSite`.

### 3.12.1 The `id` attribute

The `id` attribute, of type `SId`, provides a way to identify a `speciesTypeComponentIndex`. The value must be unique within the direct parent `speciesType`.

### 3.12.2 The `component` attribute

The `component` attribute, of type of `SIdRef`, references a `speciesTypeInstance` in the `speciesType`, or the `speciesType` itself. The value of this attribute can be the `id` of a `speciesTypeInstance` or a `speciesTypeComponentIndex` that is defined in the `speciesType` of a `speciesTypeInstance`.

### 3.12.3 The `identifyingParent` attribute

The `component` attribute itself may not be sufficient to uniquely reference a component in a `speciesType`. The `identifyingParent` attribute provides assistance for the identification of a **component**. It references a parent of the component and the value can be the `id` of an object of **SpeciesTypeInstance**, **SpeciesTypeComponentIndex** or **SpeciesType**.

This example illustrates the use of the `identifyingParent` attribute. There are three speciesTypes "`stA`", "`stB`" and "`stC`". The speciesType "`stB`" contains two speciesTypeInstances "`C1`" and "`C2`" of the same speciesType "`stC`". The speciesType "`stA`" contains two speciesTypeInstances "`B1`" and "`B2`" of the same speciesType "`stB`". The speciesType "`A`" may be required to index every "`C1`" and "`C2`" by its **ListOfInSpeciesTypeBonds** child or referencing `species`. The following SBML code demonstrates how to do the indexing with assistance from the `identifyingParent` attribute.

```
<multi:listOfSpeciesTypes>
   <multi:speciesType multi:id="stC" ... />
   <multi:speciesType multi:id="stB" ... >
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="C1" multi:speciesType="stC" />
         <multi:speciesTypeInstance multi:id="C2" multi:speciesType="stC" />
      </multi:listOfSpeciesTypeInstances>
```

```
   </multi:speciesType>
   <multi:speciesType multi:id="stA" ... >
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="B1" multi:speciesType="stB" />
         <multi:speciesTypeInstance multi:id="B2" multi:speciesType="stB" />
      </multi:listOfSpeciesTypeInstances>
      <multi:listOfSpeciesTypeComponentIndexes>
         <multi:speciesTypeComponentIndex multi:id="B1C1"
            multi:component="C1" multi:identifyingParent="B1" />
         <multi:speciesTypeComponentIndex multi:id="B1C2"
            multi:component="C2" multi:identifyingParent="B1" />
         <multi:speciesTypeComponentIndex multi:id="B2C1"
            multi:component="C1" multi:identifyingParent="B2" />
         <multi:speciesTypeComponentIndex multi:id="B2C2"
            multi:component="C2" multi:identifyingParent="B2" />
      </multi:listOfSpeciesTypeComponentIndexes>
      ...
   </multi:speciesType>
   ...
</multi:listOfSpeciesTypes>
```

In the speciesType "`stA`", "`B1C1`" identifies the "`C1`" in "`B1`" and "`B2C1`" identifies the "`C1`" in "`B2`". Similarly, "`B1C2`" identifies the "`C2`" in "`B1`" and "`B2C2`" identifies "`C2`" in "`B2`".

### *3.12.4 Reference a* `component` *in a* `speciesType` *or a* `species`

In the Multi package, a component of a `speciesType` may be a `speciesTypeInstance` in the `speciesType` or the `speciesType` itself. This permits, for example, to define the `bindingStatus` of a binding site which may be a `speciesTypeInstance` in a `species` or a `speciesType` directly referenced by a `species`. The second case will be to reference a `speciesFeatureType` of a `speciesTypeInstance` in a `speciesType` or a `speciesType` itself.

In many cases, to reference a component, the `id` of the `component` will be sufficient and it is not necessary to create an index (`speciesTypeComponentIndex`). The example in Section 3.12.3 on the previous page illustrates two equivalent ways to reference a component, for example, the "`B1`" component in the "`stA`" speciesType. The creation of a `speciesTypeComponentIndex` cannot be avoided when a `speciesType` (indirectly) has two `speciesTypeInstances` that have the same `id`.

## 3.13 InSpeciesTypeBond

An **InSpeciesTypeBond** object defines a bond existing within a `speciesType`. The bond therefore exists in every `species` that references the `speciesType`.

**InSpeciesTypeBond** is defined in Figure 7. It has two optional attributes, `id` and `name`, and two required attributes, `bindingSite1` and `bindingSite2`. Since **InSpeciesTypeBond** is derived from **SBase**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

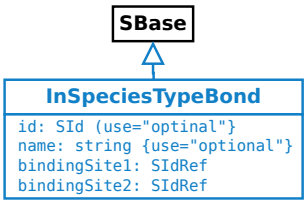


***Figure 7:*** *The definition of the* ***InSpeciesTypeBond*** *class*

### *3.13.1 The* `id` *and* `name` *attributes*

The optional `id` attribute, of type `SId`, provides a way to identify an `inSpeciesTypeBond`. If present, the value of the `id` attribute must be unique within its directly parent `speciesType`.

**InSpeciesTypeBond** also has an optional `name` attribute, of type `string`.

### *3.13.2 The* `bindingSite1` *and* `bindingSite2` *attributes*

**InSpeciesTypeBond** has two required attributes, `bindingSite1` and `bindingSite2`, both of type `SIdRef`, used to reference a pair of binding sites of the **InSpeciesTypeBond** object in a `speciesType`. The referenced identifiers of the binding sites can be the `id`s of the `speciesTypeInstances` (binding sites), or the `id`s of the `speciesTypeComponentIndexes` indexing the binding sites and the ultimately referenced components must be the **BindingSiteSpeciesType** objects. Obviously, `bindingSite1` and `bindingSite2` must not reference the same **BindingSiteSpeciesType** object.

## 3.14 Uniqueness of SpeciesType definitions

In some special cases, it may be possible to define a `speciesType` in multiple equivalent ways.

Figure 8 shows an example of a `speciesType` constructed in two different formats. The two "`st_x`" speciesTypes in the diagram can be the results of different reaction paths, but they are equivalent and define the same `speciesType`.

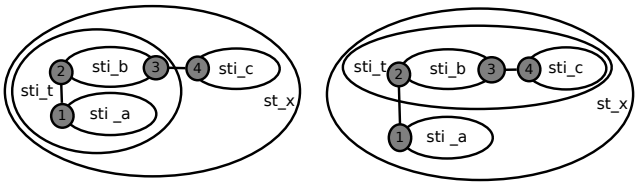


***Figure 8:*** *Different formats of the same* `speciesType`

Construct 1: The definition of speciesType "`st_x`" on the left in Figure 8.

```
<multi:listOfSpeciesTypes>
   <multi:bindingSiteSpeciesType multi:id="st1" />
   <multi:bindingSiteSpeciesType multi:id="st2" />
   <multi:bindingSiteSpeciesType multi:id="st3" />
   <multi:bindingSiteSpeciesType multi:id="st4" />
   <multi:speciesType multi:id="st_a">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="_1" multi:speciesType="st1" />
      </multi:listOfSpeciesTypeInstances>
   </multi:speciesType>
   <multi:speciesType multi:id="st_b">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="_2" multi:speciesType="st2" />
         <multi:speciesTypeInstance multi:id="_3" multi:speciesType="st3" />
      </multi:listOfSpeciesTypeInstances>
   </multi:speciesType>
   <multi:speciesType multi:id="st_c">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="_4" multi:speciesType="st4" />
      </multi:listOfSpeciesTypeInstances>
   </multi:speciesType>
   <multi:speciesType multi:id="st_t">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="sti_a" multi:speciesType="st_a" />
         <multi:speciesTypeInstance multi:id="sti_b" multi:speciesType="st_b" />
      </multi:listOfSpeciesTypeInstances>
      <multi:listOfInSpeciesTypeBonds>
         <multi:inSpeciesTypeBond multi:bindingSite1="_1" multi:bindingSite2="_2" />
      </multi:listOfInSpeciesTypeBonds>
   </multi:speciesType>
   <multi:speciesType multi:id="st_x">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="sti_t" multi:speciesType="st_t" />
         <multi:speciesTypeInstance multi:id="sti_c" multi:speciesType="st_c" />
      </multi:listOfSpeciesTypeInstances>
      <multi:listOfInSpeciesTypeBonds>
         <multi:inSpeciesTypeBond multi:bindingSite1="_3" multi:bindingSite2="_4" />
      </multi:listOfInSpeciesTypeBonds>
   </multi:speciesType>
</multi:listOfSpeciesTypes>
```

Construct 2: The definition of speciesType "`st_x`" on the right in Figure 8 on the previous page.

```
<multi:listOfSpeciesTypes>
   <multi:bindingSiteSpeciesType multi:id="st1" />
   <multi:bindingSiteSpeciesType multi:id="st2" />
   <multi:bindingSiteSpeciesType multi:id="st3" />
   <multi:bindingSiteSpeciesType multi:id="st4" />
   <multi:speciesType multi:id="st_a">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="_1" multi:speciesType="st1" />
      </multi:listOfSpeciesTypeInstances>
   </multi:speciesType>
   <multi:speciesType multi:id="st_b">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="_2" multi:speciesType="st2" />
         <multi:speciesTypeInstance multi:id="_3" multi:speciesType="st3" />
      </multi:listOfSpeciesTypeInstances>
   </multi:speciesType>
   <multi:speciesType multi:id="st_c">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="_4" multi:speciesType="st4" />
      </multi:listOfSpeciesTypeInstances>
   </multi:speciesType>
   <multi:speciesType multi:id="st_t">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="sti_b" multi:speciesType="st_b" />
         <multi:speciesTypeInstance multi:id="sti_c" multi:speciesType="st_c" />
      </multi:listOfSpeciesTypeInstances>
      <multi:listOfInSpeciesTypeBonds>
         <multi:inSpeciesTypeBond multi:bindingSite1="_3" multi:bindingSite2="_4" />
      </multi:listOfInSpeciesTypeBonds>
   </multi:speciesType>
   <multi:speciesType multi:id="st_x">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="sti_a" multi:speciesType="st_a" />
         <multi:speciesTypeInstance multi:id="sti_t" multi:speciesType="st_t" />
      </multi:listOfSpeciesTypeInstances>
      <multi:listOfInSpeciesTypeBonds>
         <multi:inSpeciesTypeBond multi:bindingSite1="_1" multi:bindingSite2="_2" />
      </multi:listOfInSpeciesTypeBonds>
   </multi:speciesType>
</multi:listOfSpeciesTypes>
```

This kind of ambiguity cannot be avoided for `speciesTypes` involving more than two subcomponents connected by `inSpeciesTypeBonds`, for example, the `speciesType` referenced by the product `species` in an association `reaction`. It is up to the modeler (parser) to identify whether the two `speciesTypes` such as those in the example above are identical.

## 3.15 Species

A `species` in SBML Level 3 Core refers a pool of entities. A `species` in the Multi package is extended from a pool to a template or pattern which multiple pools may map to. An extended `species` can reference a `speciesType` that provides the backbone for the `species` such as `components` (including `binding sites`) and `speciesFeatureTypes`. When referencing a `speciesType`, a `species` can be further defined with regard to the binding statuses of its `outwardBindingSites` and the `speciesFeatures`. With the options to have variable values selected, such as "`either`" for the `bindingStatus` attribute and multiple `possibleSpeciesFeatureValues` for a `speciesFeature`, an extended `species` can work as a template or pattern how `species` participate in `reactions`.

The extension of the **Species** class is illustrated in Figure 9. The extended **Species** class has a new optional attribute `speciesType`, and two extra optional **ListOfOutwardBindingSites** and **ListOfSpeciesFeatures** children. A `species` may have a `listOfOutwardBindingSites` child and/or a `listOfSpeciesFeatures` child only when its `speciesType` attribute has been defined.

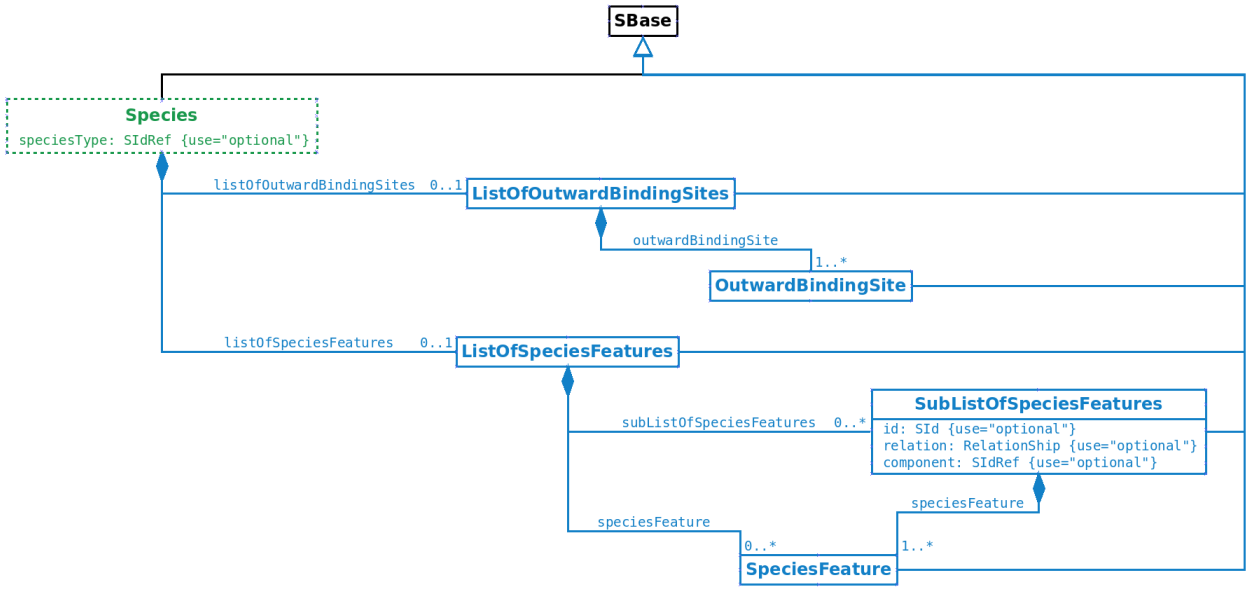


***Figure 9:*** *The extension of the* ***Species*** *class*

### 3.15.1 *The* `speciesType` *attribute*

The optional attribute `speciesType`, of type `SIdRef`, references a **SpeciesType** object.

### 3.15.2 *ListOfOutwardBindingSites*

**ListOfOutwardBindingSites** is defined in Figure 9 and is extended from the **ListOf** class. A `listOfOutwardBindingSites` can only be defined when the `speciesType` attribute is defined. If present, it must have one or more **OutwardBindingSite** children. Since **ListOfOutwardBindingSites** is derived from **SBase** through **ListOf**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

☞ *Note:*
*The* `listOfOutwardBindingSites` *of a* `species` *is not necessary to list all the* `outwardBindingSites` *(the binding sites not involved in any* `inSpeciesTypeBond`*) defined by the referenced* `speciesType`*. If an* `outwardBindingSite` *is not listed in the* `listOfOutwardBindingSites`*, the value of its* `bindingStatus` *is "*`either`*", in other words, the binding site is in a "*`don't care`*" state.*

### 3.15.3 *ListOfSpeciesFeatures*

**ListOfSpeciesFeatures** is defined in Figure 9 on the preceding page and is extended from the **ListOf** class. A `listOfSpeciesFeatureTypes` can only be defined when the `speciesType` attribute is defined. If present, it must have one or more children. A child can be a **SpeciesFeature**, or a **SubListOfSpeciesFeatures** object.

☞ *Note:*
*The* `listOfSpeciesFeatures` *of a* `species` *does not have to cover all the* `speciesFeatures` *corresponding to all* `speciesFeatureTypes` *(see Section 3.9 on page 15) of every* `component` *defined by the referenced* `speciesType`. *If a* `speciesFeatureType` *is defined and there is no* `speciesFeature` *explicitly referencing it, the* `species` *has an implicit* `speciesFeature` *having all the* `listOfPossibleSpeciesFeatureValues` *and "*`or`*" relationships between them. In other words, the implicit* `speciesFeature` *has a "*`don't care`*" state for the* `species`.

Since **ListOfSpeciesFeatures** is derived from **SBase** through **ListOf**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

The example at Section 3.18.7 on page 29 illustrates the usage of the **ListOfSpeciesFeatures** class.

## 3.16 OutwardBindingSite

**OutwardBindingSite** is defined in Figure 10. It has two required attributes, `bindingStatus` and `component`. A `binding site` not involved in any **InSpeciesTypeBond** object in the `speciesType` referenced by a `species` is an `outwardBindingSite`. Since **OutwardBindingSite** is derived from **SBase**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

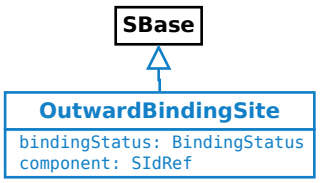


***Figure 10:*** *The definition of the **OutwardBindingSite** class*

### 3.16.1 *The* `bindingStatus` *attribute*

The `bindingStatus` attribute takes a value of type `BindingStatus`.

### 3.16.2 *The* `component` *attribute*

The `component` attribute, of type `SIdRef`, references a `component` which ultimately reference a **BindingSiteSpeciesType** object. The attribute value must be the identifier of a **SpeciesTypeInstance**, **SpeciesTypeComponentIndex** or **SpeciesType** object.

There are three scenarios for the `component` attribute to have the value of an identifier of **SpeciesType**, **SpeciesTypeInstance**, or **SpeciesTypeComponentIndex** respectively.

(1) When a `species` references a simple `bindingSiteSpeciesType`, the value of the `component` attribute of the `outwardBindingSite` of the `species` can only be the `id` of the referenced `speciesType`.

(2) When a `species` references a `speciesType` with a `speciesTypeInstance` being a binding site (have an `id` of **BindingSiteSpeciesType** as its `speciesType` attribute) and the `id` of the `speciesTypeInstance` can identify the binding site within the `speciesType` (referenced by the `species`) unambiguously, and therefore, the value of the `component` attribute of an `outwardBindingSite` of the `species` can be the `id` of the `speciesTypeInstance`.

(3) When a `species` references a `speciesType` with a `speciesTypeInstance` being a binding site (directly or indirectly) and `id` of the `speciesTypeInstance` can NOT identify the binding site without ambiguity, an `id` of **SpeciesTypeComponentIndex** can be used as the value of the `component` attribute of an `outwardBindingSite`of the `species`.

### 3.16.3 *Example*

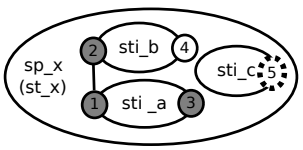


***Figure 11:*** *An example of **OutwardBindingSite***

Figure 11 illustrates the usage of the **OutwardBindingSite** class. Species "`sp_x`" references speciesType "`st_x`", which has three speciesTypeInstances "`sti_a`", "`sti_b`" and "`sti_c`". SpeciesTypeInstance "`sti_a`" has bindingSites "`_1`"

and "_3", speciesTypeInstance "sti_b" has bindingSites "_2" and "_4", and speciesTypeInstance "sti_c" has bindingSite "_5". The inSpeciesTypeBond in "st_x" involves two bindingSites "_1" and "_2". The other three bindingSites, "_3", "_4" and "_5", in the species "sp_x" are outwardBindingSites. The outwardBindingSite "_3" is "bound" (filled circle with solid line in the diagram), the outwardBindingSite "_4" is "unbound" (empty circle with solid line) and the outwardBindingSite "_5" has binding status "either" (empty circle with dotted line). The corresponding SBML code would be as follows:

```
<multi:listOfSpeciesTypes>
   <multi:bindingSiteSpeciesType multi:id="st_1" />
   <multi:bindingSiteSpeciesType multi:id="st_2" />
   <multi:bindingSiteSpeciesType multi:id="st_3" />
   <multi:bindingSiteSpeciesType multi:id="st_4" />
   <multi:bindingSiteSpeciesType multi:id="st_5" />
   <multi:speciesType multi:id="st_a">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="_1" multi:speciesType="st_1" />
         <multi:speciesTypeInstance multi:id="_3" multi:speciesType="st_3" />
      </multi:listOfSpeciesTypeInstances>
   </multi:speciesType>
   <multi:speciesType multi:id="st_b">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="_2" multi:speciesType="st_2" />
         <multi:speciesTypeInstance multi:id="_4" multi:speciesType="st_4" />
      </multi:listOfSpeciesTypeInstances>
   </multi:speciesType>
   <multi:speciesType multi:id="st_c">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="_5" multi:speciesType="st_5" />
      </multi:listOfSpeciesTypeInstances>
   </multi:speciesType>
   <multi:speciesType multi:id="st_x">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="sti_a" multi:speciesType="st_a" />
         <multi:speciesTypeInstance multi:id="sti_b" multi:speciesType="st_b" />
         <multi:speciesTypeInstance multi:id="sti_c" multi:speciesType="st_c" />
      </multi:listOfSpeciesTypeInstances>
      <multi:listOfInSpeciesTypeBonds>
         <multi:inSpeciesTypeBond  multi:bindingSite1="_1" multi:bindingSite2="_2" />
      </multi:listOfInSpeciesTypeBonds>
   </multi:speciesType>
</multi:listOfSpeciesTypes>
<listOfSpecies>
   <species id="sp_x" multi:speciesType="st_x">
      <multi:listOfOutwardBindingSites>
         <multi:outwardBindingSite multi:component="_3" multi:bindingStatus="bound" />
         <multi:outwardBindingSite multi:component="_4" multi:bindingStatus="unbound" />
         <multi:outwardBindingSite multi:component="_5" multi:bindingStatus="either" />
      </multi:listOfOutwardBindingSites>
   </species>
</listOfSpecies>
```

## 3.17 SubListOfSpeciesFeatures

**SubListOfSpeciesFeatures** is defined in Figure 9 on page 24, and is extended from the **ListOf** class. If present, a subListOfSpeciesFeatures must have one or more **SpeciesFeature** children. Since **SubListOfSpeciesFeatures** is derived from **SBase** through **ListOf**, it inherits the sboTerm and metaid attributes, as well as the optional children **Notes** and **Annotation** objects.

### 3.17.1 The `id` attribute

The optional `id` attribute, of type `SId`, can serve to provide a way to identify a `subListOfSpeciesFeatures`. If present, the value must be unique within the `species`.

### 3.17.2 The `relation` attribute

**SubListOfSpeciesFeatures** has an optional attribute `relation`, of type `Relation`, to define the logic relationship among its children. The `relation` attribute can not be defined if a `subListOfSpeciesFeatures` has only one child.

### 3.17.3 The `component` attribute

The optional `component` attribute, of type `SIdRef`, can be used to indicate which `component` of a `species` the `subListOfSpeciesFeatures` belongs to. It is required when the `component` of any `speciesFeature` contained in this `subListOfSpeciesFeatures` can not be identified only based on its `speciesFeatureType` attribute.

## 3.18 SpeciesFeature

**SpeciesFeature** is defined in Figure 12. It has two optional attributes, `id` and `component`, two required attributes, `speciesFeatureType` and `occur`, and a required child `listOfSpeciesFeatureValues`. Since **SpeciesFeature** is derived from **SBase**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects. **SpeciesFeature** serves to define the state of a `component` in a `species` by selecting values from the `listOfPossibleSpeciesFeatureValues` of the referenced `speciesFeatureType`.

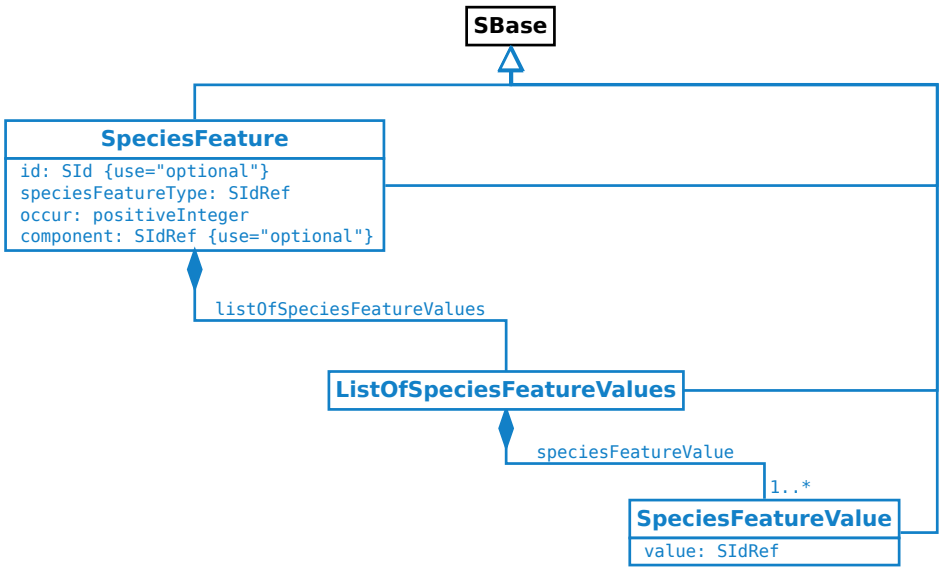


***Figure 12:*** *The definitions of the **SpeciesFeature** class and the **SpeciesFeatureValue** class*

### 3.18.1 The `id` attribute

The optional `id` attribute, of type `SId`, can serve to provide a way to identify a `speciesFeature`. If present, the value must be unique within the `species`.

### 3.18.2 The `speciesFeatureType` attribute

**SpeciesFeature** has a required attribute `speciesFeatureType`, of type `SIdRef`, used to reference a `speciesFeatureType`.

### 3.18.3 *The* occur *attribute*

**SpeciesFeature** has a required attribute occur, of type of positiveInteger, used to define the number of instances of the referenced speciesFeatureType.

The value of the occur attribute can not be larger than the occur of the referenced speciesFeatureType. When a speciesFeatureType has multiple instances (speciesFeatureType's occur > "1"), the speciesFeature's occur attribute provides a way for a species to define the instances of the speciesFeatureType differently.

For example, in a speciesType, speciesFeatureType "ftA" has occur="2" and two possibleSpeciesFeatureValues "fva1" and "fva2". A species referencing the speciesType can be defined to have two speciesFeatures "sfA1" and "sfA2" both referencing "ftA". The speciesFeature "sfA1" has occur="1" and its value is "fva1". The speciesFeature "sfA2" has occur="1" and its value is "fva2".

If the occur of a speciesFeature is less than the occur of the referenced speciesFeatureType, the rest of the unspecified instances of the speciesFeatureType are in "don't care" state which means that the value of an unspecified instance can be any from the listOfPossibleSpeciesFeatureValues.

For example, in a speciesType, a speciesFeatureType "phosphorylation" has two possibleSpeciesFeatureValues "phosphorylated" and "unphosphorylated" and the occur is "5". A species referencing the speciesType can be defined to have a speciesFeature of the "phosphorylation" with the value of "phosphorylated" and the occur of "1". Then, the species is a pattern species with at least one "phosphorylated" site (the other four "phosphorylation" sites are in "don't care" state). (See the example in Section 3.25.4 on page 38.) This pattern species can be mapped by anyone of the "fully defined" species (see Section 3.19 on page 33) of the same type and with any of "1" to "5" phosphorylated sites.

### 3.18.4 *The* component *attribute*

The optional component attribute, of type SIdRef, can be used to indicate which **component** of a species the speciesFeature belongs to. It is required when the component can not be identified only based on the speciesFeatureType attribute.

### 3.18.5 *ListOfSpeciesFeatureValues*

**ListOfSpeciesFeatureValues** is defined in Figure 12 on the previous page, and is extended from the **ListOf** class. A listOfSpeciesFeatureValues must have one or more **SpeciesFeatureValue** children. If a listOfSpeciesFeatures has multiple speciesFeatureValues, the interpretation of the relationship between them is "or". Since **ListOfSpeciesFeatureValues** is derived from **SBase** through **ListOf**, it inherits the sboTerm and metaid attributes, as well as the optional children **Notes** and **Annotation** objects.

### 3.18.6 *SpeciesFeatureValue*

**SpeciesFeatureValue** is defined in Figure 12 on the preceding page. A speciesFeatureValue serves to specify a value for a speciesFeature to select from the listOfPossibleSpeciesFeatureValues defined in the referenced speciesFeatureType. The **SpeciesFeatureValue** class has only one attribute value of type SIdRef, used to reference a **PossibleSpeciesFeatureValue** object. Since **SpeciesFeatureValue** is derived from **SBase**, it inherits the sboTerm and metaid attributes, as well as the optional children **Notes** and **Annotation** objects.

### 3.18.7 *Example*

Figure 13 on the next page is an example speciesType to illustrate the usage of the **ListOfSpeciesFeatures**, **SubListOfSpeciesFeatures** and **SpeciesFeature** classes. SpeciesType "st_X" has two speciesTypeInstance "sti_A" and "sti_B". which have speciesFeatureTypes "fA", "fB1" and "fB2" respectively. The speciesFeatureType "fA" has possibleSpeciesFeatureValues "v1" and "v2". The speciesFeatureType "fB1" has "v3" and "v4", and "fB2" has "v5" and "v6". Here are several ways to construct the listOfSpeciesFeatures of a species referencing the speciesType "st_A":

- listOfSpeciesFeatures ("fA"="v1", "fB1"="v3", "fB2"="v5") is a state:
  "[fA=v1] AND [fB1=v3] AND [fB2=v5]"

- listOfSpeciesFeatures ("fA"="v1", "fB1"="v3" is a state:
  "[fA=v1] AND [fB1=v3] AND ([fB2=v5] OR fB2=v6)"
  "fB2" has a value of "don't care"

- listOfSpeciesFeatures (children=
  "fA=v1",
  subListOfSpeciesFeatures (relation="not", children="fB1=v3", "fB2=v5")
  ) is a state:
  "[fA=v1] and [fB1=v4] and [fB2=V5]" or
  "[fA=v1] and [fB1=v4] and [fB2=V6]" or
  "[fA=v1] and [fB1=v3] and [fB2=V6]"

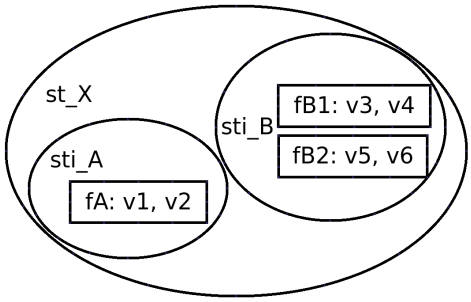


***Figure 13:*** *An example* speciesFeatureType *to illustrate the usage of* ***ListOfSpeciesFeatures****,* ***SubListOfSpecies-Features*** *and the* ***SpeciesFeature***

The SBML code can be as follows and the species "sp_A1", "sp_A2" and "sp_A3" contain the tree listOfSpecies-Features above respectively.

```
<multi:listOfSpeciesTypes>
   <multi:bindingSiteSpeciesType multi:id="st_A">
      <multi:listOfSpeciesFeatureTypes>
         <multi:speciesFeatureType multi:id="fA" multi:occur="1">
            <multi:listOfPossibleSpeciesFeatureValues>
               <multi:possibleSpeciesFeatureValue multi:id="v1" />
               <multi:possibleSpeciesFeatureValue multi:id="v2" />
            </multi:listOfPossibleSpeciesFeatureValues>
         </multi:speciesFeatureType>
      </multi:listOfSpeciesFeatureTypes>
   </multi:bindingSiteSpeciesType>
   <multi:bindingSiteSpeciesType multi:id="st_B">
      <multi:listOfSpeciesFeatureTypes>
         <multi:speciesFeatureType multi:id="fB1" multi:occur="1">
            <multi:listOfPossibleSpeciesFeatureValues>
               <multi:possibleSpeciesFeatureValue multi:id="v3" />
               <multi:possibleSpeciesFeatureValue multi:id="v4" />
            </multi:listOfPossibleSpeciesFeatureValues>
         </multi:speciesFeatureType>
         <multi:speciesFeatureType multi:id="fB2" multi:occur="1">
            <multi:listOfPossibleSpeciesFeatureValues>
               <multi:possibleSpeciesFeatureValue multi:id="v5" />
               <multi:possibleSpeciesFeatureValue multi:id="v6" />
            </multi:listOfPossibleSpeciesFeatureValues>
         </multi:speciesFeatureType>
      </multi:listOfSpeciesFeatureTypes>
```

```
   </multi:bindingSiteSpeciesType>
   <multi:speciesType multi:id="st_X">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="sti_A" multi:speciesType="st_A" />
         <multi:speciesTypeInstance multi:id="sti_B" multi:speciesType="st_B" />
      </multi:listOfSpeciesTypeInstances>
   </multi:speciesType>
</multi:listOfSpeciesTypes>
<listOfSpecies>
   <species id="sp_A1" multi:speciesType="st_A" .>
      <!-- [v1] AND [v3] AND [v5] -->
      <multi:listOfSpeciesFeatures>
         <multi:speciesFeature multi:speciesFeatureType="fA" multi:occur="1"
            multi:component="sti_A">
            <multi:listOfSpeciesFeatureValues>
               <multi:speciesFeatureValue multi:value="v1" />
            </multi:listOfSpeciesFeatureValues>
         </multi:speciesFeature>
         <multi:speciesFeature multi:speciesFeatureType="fB1" multi:occur="1"
            multi:component="sti_B">
            <multi:listOfSpeciesFeatureValues>
               <multi:speciesFeatureValue multi:value="v3" />
            </multi:listOfSpeciesFeatureValues>
         </multi:speciesFeature>
         <multi:speciesFeature multi:speciesFeatureType="fB2" multi:occur="1"
            multi:component="sti_B">
            <multi:listOfSpeciesFeatureValues>
               <multi:speciesFeatureValue multi:value="v5" />
            </multi:listOfSpeciesFeatureValues>
         </multi:speciesFeature>
      </multi:listOfSpeciesFeatures>
      <multi:listOfOutwardBindingSites>
         ...
    </multi:listOfOutwardBindingSites>
   </species>
   <species id="sp_A2" multi:speciesType="st_A" .>
      <!-- [v1] AND [v3] -->
      <multi:listOfSpeciesFeatures>
         <multi:speciesFeature multi:speciesFeatureType="fA" multi:occur="1"
            multi:component="sti_A">
            <multi:listOfSpeciesFeatureValues>
               <multi:speciesFeatureValue multi:value="v1" />
            </multi:listOfSpeciesFeatureValues>
         </multi:speciesFeature>
         <multi:speciesFeature multi:speciesFeatureType="fB1" multi:occur="1"
            multi:component="sti_B">
            <multi:listOfSpeciesFeatureValues>
               <multi:speciesFeatureValue multi:value="v3" />
            </multi:listOfSpeciesFeatureValues>
         </multi:speciesFeature>
      </multi:listOfSpeciesFeatures>
      <multi:listOfOutwardBindingSites>
         ...
    </multi:listOfOutwardBindingSites>
   </species>
   <species id="sp_A3" multi:speciesType="st_A" .>
      <!-- [v1] AND NOT([v3] and [v5]) -->
      <multi:listOfSpeciesFeatures>
         <multi:speciesFeature multi:speciesFeatureType="fA" multi:occur="1"
            multi:component="sti_A">
            <multi:listOfSpeciesFeatureValues>
               <multi:speciesFeatureValue multi:value="v1" />
            </multi:listOfSpeciesFeatureValues>
         </multi:speciesFeature>
         <multi:subListOfSpeciesFeatures multi:id="sf_B" multi:relation="not" multi:component="sti_B">
           <multi:speciesFeature multi:speciesFeatureType="fB1" multi:occur="1">
```

```
            <multi:listOfSpeciesFeatureValues>
               <multi:speciesFeatureValue multi:value="v3" />
            </multi:listOfSpeciesFeatureValues>
         </multi:speciesFeature>
         <multi:speciesFeature multi:speciesFeatureType="fB2" multi:occur="1">
            <multi:listOfSpeciesFeatureValues>
               <multi:speciesFeatureValue multi:value="v5" />
            </multi:listOfSpeciesFeatureValues>
         </multi:speciesFeature>
      </multi:subListOfSpeciesFeatures>
   </multi:listOfSpeciesFeatures>
   <multi:listOfOutwardBindingSites>
      ...
 </multi:listOfOutwardBindingSites>
</species>
</listOfSpecies>
```

## 3.19 "Fully defined" species and the mapping to "pattern" species

An extended **Species** object functions as a template or a pattern which allows multiple pools of entities to map to it. A species is "fully defined" if there is only one pool mapping to it. A "fully defined" species can be considered the same as a SBML core species, and can be initialized with the initialAmount attribute, or the initialConcentration attribute, or via an **InitialAssignment** object. In the Multi package, a species is "fully defined" if the following conditions are fulfilled.

- All outwardBindingSites must be free (bindingStatus="unbound"), since "bound" sites imply that there is a non-specified binding partner.
- Each speciesFeature occurrence can only have one speciesFeatureValue, and every occurrences of every speciesFeatureTypes of every components of the referenced speciesType must be referenced by exactly one speciesFeature occurrence.
- If applicable, only "and" values are allowed for the relation attributes of the **SubListOfSpeciesFeatures** objects.
- Only one single **SpeciesFeatureValue** object is allowed for any speciesFeature.
- The referenced compartment can not be a compartment type, which means the value of the isType attribute of the referenced compartment can only be "false".

The mapping from a "fully defined" species to a "pattern" species is implicit and can be inferred from the structure of the species. For example, a speciesType "stA" has one speciesFeatureType with two possibleSpeciesFeatureValues "v1" and "v2". A species "spA1" references "stA" and has the speciesFeature with the value of "v1". Another species "spA" also references "stA" and has no speciesFeature explicitly defined. Thus, the species "spA1" is a "fully defined" species and can map to the "pattern" species "spA" because species "spA" has an implicit speciesFeature which can take either value "v1" or value "v2" (see the note in Section A on page 69).

## 3.20 Reaction

**Reaction** itself in the Multi package is not extended, but it may use the Multi **Species** objects to construct `reactions`. The **Reaction** class in the Multi package can not only define the relations among pools (SBML core `species`), but also the relations among patterns (Multi extended `species`). Several related classes including **SimpleSpeciesReference** and **SpeciesReference** are extended to handle some issues specific to the Multi package. A new class, **IntraSpeciesReaction**, is derived from **Reaction** to explicitly define those reactions within the same **Species** object.

The changes under the **Reaction** class in the Multi package are illustrated in Figure 14.

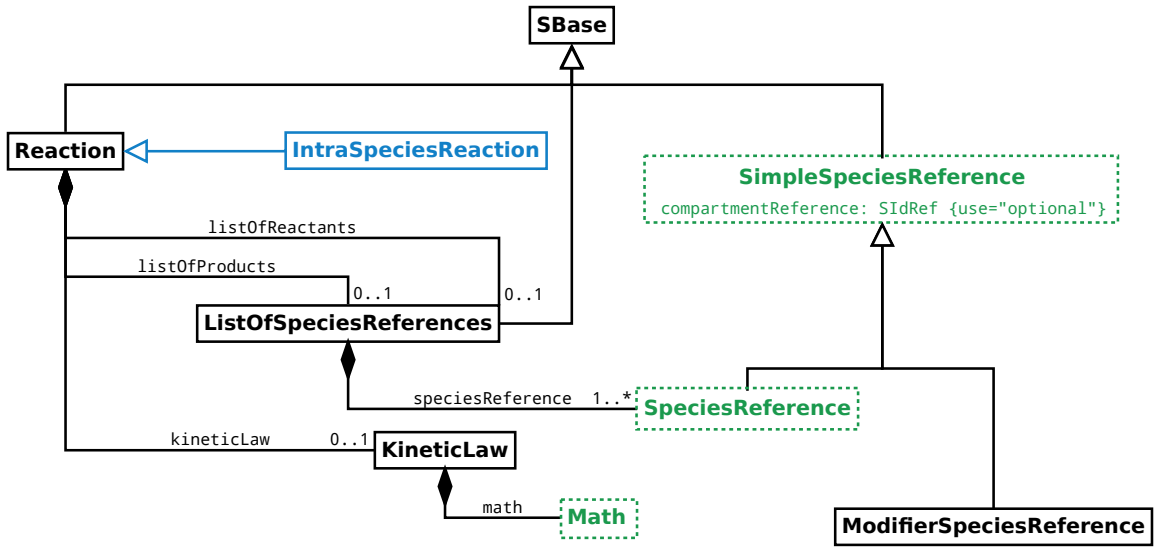


***Figure 14:*** *The changes under the **Reaction** class including **IntraSpeciesReaction**, **SimpleSpeciesReference**, **SpeciesReference** and **Math***

## 3.21 IntraSpeciesReaction

**IntraSpeciesReaction** is derived from **Reaction** for the `reactions` happening within a `species` (see the example "`Extended Reaction class`" at page 23 of the slides at HARMONY 2013 [Zhang and Meier-Schellersheim (2013c)]).

A particular `reaction` may happen within a `species` as an `intraSpeciesReaction` if the following conditions are fulfilled.

- The `reaction` is either an association `reaction` or a dissociation `reaction`.
- If it is an association `reaction`, each of the two reactant `species` has at least one `outwardBindingSite` free ("unbound").
- If it is a dissociation `reaction`, each of the two product `species` has at least one `outwardBindingSite` free ("unbound").

☞ *Note:*
*Technically, transformations are also reactions happening with one* `species`*, but they do not have the ambiguity of association and dissociation* `reactions`*. Therefore, transformation* `reactions` *do not have to be defined as* `intraSpeciesReactions`.

## 3.22 Extended SimpleSpeciesReference

The **SimpleSpeciesReference** class is extended with a new optional attribute `compartmentReference`, of type `SIdRef`, to reference a `compartmentReference`. The `compartmentReference` attribute can serve to indicate which sub-compartment where an object of a class (**SpeciesReference** or **ModifierSpeciesReference**) inheriting **SimpleSpeciesReference** is located.

This example illustrates the use of the `compartmentReference` attribute. A model has a compartment type "`c`" and a composite compartment type "`cc`" with two compartmentReferences "`cr1`" and "`cr2`" both referencing the "`c`" compartment type. Both species "`spA`" and "`spM`" reference the "`c`" compartment type. A reaction happens between two "`spA`" species from the two compartments respectively and results in a cross-compartment product. One condition for this reaction is that two "`spM`" species work as modifiers in the two "`c`" compartments respectively. The situation described here could correspond to interactions among species located on two adjacent membranes. Without the `compartmentReference` attribute in the **SimpleSpeciesReference** class, it is impossible to distinguish the two "`spA`" species as well as the two "`spM`" species. The SBML code can be as follows:

```
<listOfCompartments>
   <compartment id="c" constant="true" multi:isType="true" />
   <compartment id="cc" constant="true" multi:isType="true">
      <multi:listOfCompartmentReferences>
         <multi:compartmentReference multi:id="cr1" multi:compartment="c" />
         <multi:compartmentReference multi:id="cr2" multi:compartment="c" />
      </multi:listOfCompartmentReferences>
   </compartment>
</listOfCompartments>
<multi:listOfSpeciesTypes>
   <multi:bindingSiteSpeciesType multi:id="stA" multi:compartment="c" />
   <multi:speciesType multi:id="stM" multi:compartment="c" />
   <multi:speciesType multi:id="stAA" multi:compartment="cc">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="stiA1" multi:speciesType="stA"
            multi:compartmentReference="cr1" />
         <multi:speciesTypeInstance multi:id="stiA2" multi:speciesType="stA"
            multi:compartmentReference="cr2" />
      </multi:listOfSpeciesTypeInstances>
      <multi:listOfInSpeciesTypeBonds>
         <multi:inSpeciesTypeBond multi:bindingSite1="stiA1" multi:bindingSite2="stiA2" />
      </multi:listOfInSpeciesTypeBonds>
   </multi:speciesType>
</multi:listOfSpeciesTypes>
<listOfSpecies>
   <species id="spA" multi:speciesType="stA" compartment="c" ... />
   <species id="spM" multi:speciesType="stM" compartment="c" ... />
   <species id="spAA" multi:speciesType="stAA" compartment="cc" ... />
</listOfSpecies>
<reaction id="reaction" ...>
   <listOfReactants>
      <speciesReference id="r1" species="spA" multi:compartmentReference="cr1" ... />
      <speciesReference id="r2" species="spA" multi:compartmentReference="cr2" ... />
   </listOfReactants>
   <listOfProducts>
      <speciesReference species="spAA" ... />
   </listOfProducts>
   <listOfModifiers>
      <modifierSpeciesReference id="m1" species="spM" multi:compartmentReference="cr1" />
      <modifierSpeciesReference id="m2" species="spM" multi:compartmentReference="cr2" />
   </listOfModifiers>
   ...
</reaction>
```

## 3.23 Extended SpeciesReference

The **SpeciesReference** class is extended from SBML Level 3 Core and can establish `component` mappings between the reactant `species` and the product `species` when the mappings can not be inferred from the `id`s of the **SpeciesTypeInstance** objects. The **SpeciesReference** class has an optional **ListOfSpeciesTypeComponentMapsInProduct** child, as defined in Figure 15. Only a `reaction` `product` can contain the **ListOfSpeciesTypeComponentMapsInProduct** child and it is not necessary to store the mappings again in the `reactants`.

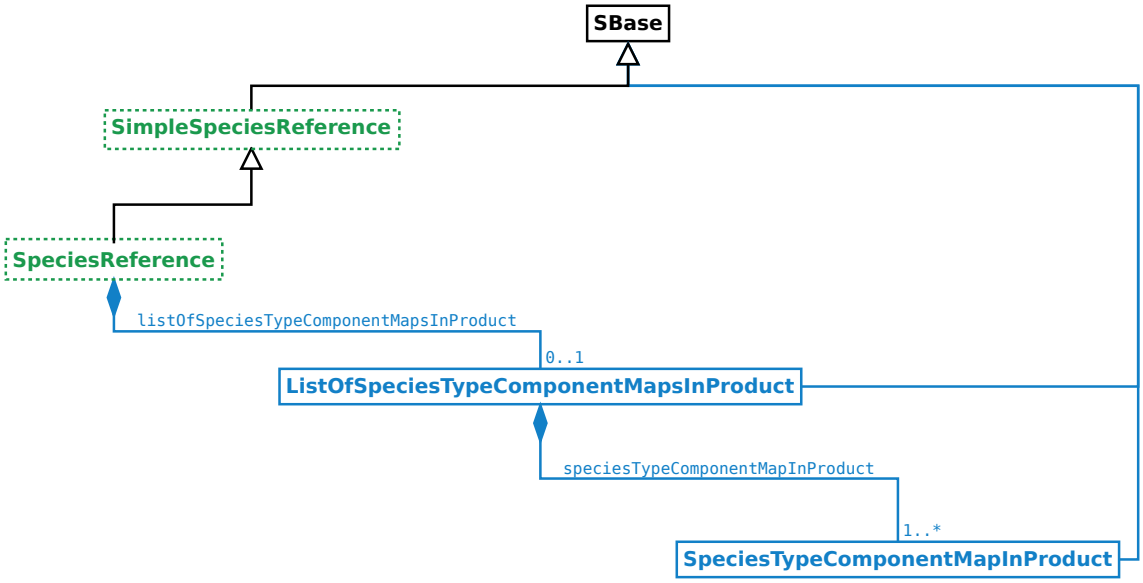


***Figure 15:*** *The extension of the **SpeciesReference** class*

### 3.23.1 ListOfSpeciesTypeComponentMapsInProduct

**ListOfSpeciesTypeComponentMapsInProduct** is defined in Figure 15, and is extended from the **ListOf** class. If present, a `listOfSpeciesTypeComponentMapsInProduct` must have one or more **SpeciesTypeComponentMapInProduct** children. Since **ListOfSpeciesTypeComponentMapsInProduct** is derived from **SBase** through **ListOf**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

## 3.24 SpeciesTypeComponentMapInProduct

**SpeciesTypeComponentMapInProduct** is defined in Figure 16. Since **SpeciesTypeComponentMapInProduct** is derived from **SBase**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

A `speciesTypeComponentMapInProduct` defines the mapping between a `component` in a reactant and a `component` in a product. The identifications of a **`component`** and the `speciesReference` should be sufficient to identify the `component` in the context of a `reaction`. The attributes `reactant` and `reactantComponent` can identify the `component` in a `reactant`, and the `productComponent` attribute and the product storing the mapping information can identify the `component` in a `product`.

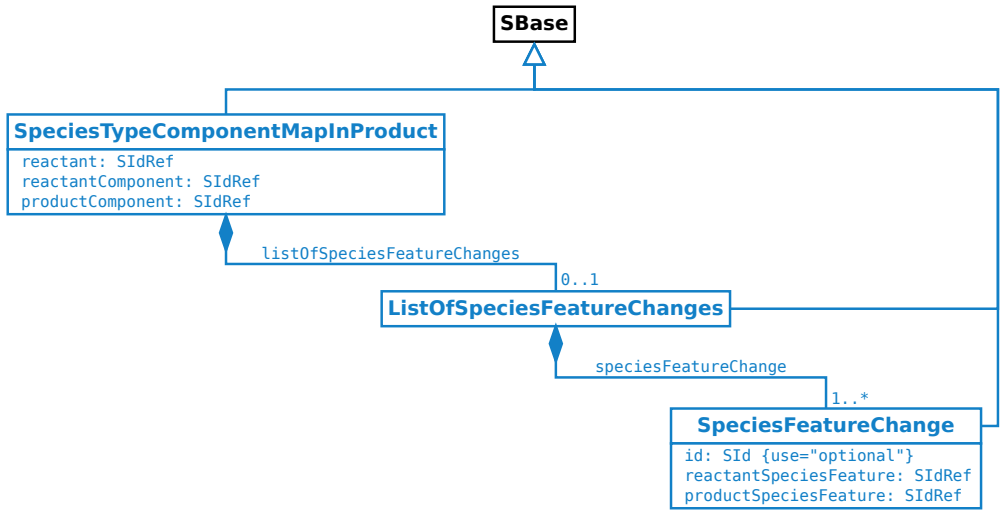


***Figure 16:*** *The definitions of the **SpeciesTypeComponentMapInProduct** and **SpeciesFeatureChange** classes*

### 3.24.1 The `reactant` attribute

**SpeciesTypeComponentMapInProduct** has a required `reactant` attribute, of type `SIdRef`, to reference the `id` of a reactant `speciesReference` in a `reaction`.

### 3.24.2 The `reactantComponent` attribute

**SpeciesTypeComponentMapInProduct** has a required `reactantComponent` attribute, of type `SIdRef`, to reference a **`component`** in a reactant `species`.

### 3.24.3 The `productComponent` attribute

**SpeciesTypeComponentMapInProduct** has a required `productComponent` attribute, of type `SIdRef`, to reference a **`component`** in a product `species`.

### 3.24.4 ListOfSpeciesFeatureChanges

**SpeciesTypeComponentMapInProduct** also has an optional **ListOfSpeciesFeatureChanges** child to explicitly define changes of `speciesFeatures` in a `reaction`. **ListOfSpeciesFeatureChanges** is extended from the **ListOf** class. If present, a `listOfSpeciesFeatureChanges` must have one or more **SpeciesFeatureChange** children. Since **ListOfSpeciesFeatureChanges** is derived from **SBase** through **ListOf**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

## 3.25 SpeciesFeatureChange

**SpeciesFeatureChange** is defined in Figure 16 on the previous page and provides a way to specify how some of or all instances of a `speciesFeatureType` to change. This class should only be used when the `occur` of the referenced `speciesFeatureType` is larger than "`1`". The parent `components` of the changed `speciesFeatures` are identified in the **SpeciesTypeComponentMapInProduct** object. **SpeciesFeatureChange** has one optional attribute `id` and two required attributes, `reactantSpeciesFeature` and `productSpeciesFeature`. The `occur` attributes of the changed `speciesFeatures` in `reactant` and `product` respectively must have the same value.

Since **SpeciesFeatureChange** is derived from **SBase**, it inherits the `sboTerm` and `metaid` attributes, as well as the optional children **Notes** and **Annotation** objects.

### 3.25.1 *The* `id` *attribute*

The optional `id` attribute, of type `SId`, provides a way to identify a `speciesFeatureChange`.

### 3.25.2 *The* `reactantSpeciesFeature` *attribute*

The `reactantSpeciesFeature` attribute, of type `SIdRef`, references a `speciesFeature` in the reactant **component** in a reaction mapping.

### 3.25.3 *The* `productSpeciesFeature` *attribute*

The `productSpeciesFeature` attribute, of type `SIdRef`, references a `speciesFeature` in the product **component** in a reaction mapping.

### 3.25.4 *Example*

Here is an example to illustrate the use of the **SpeciesFeatureChange** class in a phosphorylation reaction. One among the five sites in a species is transformed from "`unphosphorylated`" to "`phosphorylated`" and the phosphorylation sites are defined as the referenced speciesFeatureType with `occur`="`5`". The SBML code can be as follows:

```
<multi:listOfSpeciesTypes>
   <multi:speciesType multi:id="stX" ... >
      <multi:listOfSpeciesFeatureTypes>
         <multi:speciesFeatureType multi:id="phosphorylation" multi:occur="5">
            <mulit:listOfPossibleSpeciesFeatureValues>
               <multi:possibleSpeciesFeatureValue multi:id="phosphorylated" />
               <multi:possibleSpeciesFeatureValue multi:id="unphosphorylated" />
            </mulit:listOfPossibleSpeciesFeatureValues>
         </multi:speciesFeatureType>
      </multi:listOfSpeciesFeatureTypes>
   </multi:speciesType>
</multi:listOfSpeciesTypes>
<listOfSpecies>
   <species id="spX1" multi:speciesType="stX">
      <multi:listOfSpeciesFeatures>
         <multi:speciesFeature multi:id="U"
               multi:speciesFeatureType="phosphorylation" multi:occur="1" >
            <multi:listOfSpeciesFeatureValues>
               <multi:speciesFeatureValue multi:value="unphosphorylated" />
            </multi:listOfSpeciesFeatureValues>
         </multi:speciesFeature>
      </multi:listOfSpeciesFeatures>
      ...
   </species>
   <species id="spX2" multi:speciesType="stX">
      <multi:listOfSpeciesFeatures>
         <multi:speciesFeature multi:id="P"
               multi:speciesFeatureType="phosphorylation" multi:occur="1" >
```

```
            <multi:listOfSpeciesFeatureValues>
               <multi:speciesFeatureValue multi:value="phosphorylated" />
            </multi:listOfSpeciesFeatureValues>
         </multi:speciesFeature>
      </multi:listOfSpeciesFeatures>
      ...
   </species>
</listOfSpecies>
<listOfReactions>
   <reaction id="transformation" ... >
      <listOfReactants>
         <speciesReference id="reactant" species="spX1" ... />
      </listOfReactants>
      <listOfProducts>
         <speciesReference id="product" species="spX2" ...>
            <multi:listOfSpeciesTypeComponentMapsInProduct>
               <multi:speciesTypeComponentMapInProduct multi:reactant="reactant"
                     multi:reactantComponent="stX" multi:productComponent="stX">
                  <multi:listOfSpeciesFeatureChanges>
                     <multi:speciesFeatureChange multi:reactantSpeciesFeature="U"
                        multi:productSpeciesFeature="P" />
                  </multi:listOfSpeciesFeatureChanges>
               </multi:speciesTypeComponentMapInProduct>
            </multi:listOfSpeciesTypeComponentMapsInProduct>
         </speciesReference>
      </listOfProducts>
   </reaction>
</listOfReactions>
```

## 3.26 The outwardBindingSites and speciesFeatures in "don't care" state in a reaction product

An outwardBindingSite is in "don't care" state if its bindingStatus is "either" or is not specified (also see Section 3.15.2 on page 24). A speciesFeature or an instance of a speciesFeature (the occur of its speciesFeatureType is larger than "1") is in "don't care" state if it has all the possibleSpeciesFeatureValues under its speciesFeatureType, or it is not specified in the species (also see Section 3.15.3 on page 25).

For a species as a product in a reaction, if it has "don't care" outwardBindingSites or "don't care" speciesFeatures, the interpretation of the "don't care" is "don't change". In a product, a "don't care" outwardBindingSite has the same bindingStatus as the mapped outwardBindingSite in the reactant, and a "don't care" speciesFeature or instance of a speciesFeature has the same value as the mapped speciesFeature or the mapped speciesFeature instance in the reactant.

For the phosphorylation example in Section 3.25.4 on page 38, the reactant species has one "unphosphorylated" site and four "don't care" sites, and the product species has one "phosphorylated" site and four don't care sites. The "phosphorylation" reaction can apply to the following reactions of "fully defined" species.

- Reactant: a species with "0" phosphorylated site and "5" unphosphorylated sites.
  Product: a species with "1" phosphorylated site and "4" unphosphorylated sites.
- Reactant: a species with "1" phosphorylated site and "4" unphosphorylated sites.
  Product: a species with "2" phosphorylated sites and "3" unphosphorylated sites.
- Reactant: a species with "2" phosphorylated sites and "3" unphosphorylated sites.
  Product: a species with "3" phosphorylated sites and "2" unphosphorylated sites.
- Reactant: a species with "3" phosphorylated sites and "2" unphosphorylated sites.
  Product: a species with "4" phosphorylated sites and "1" unphosphorylated site.
- Reactant: a species with "4" phosphorylated sites and "1" unphosphorylated site.
  Product: a species with "5" phosphorylated sites and "0" unphosphorylated site.

## 3.27 Extended ci elements in Math objects

The Multi package extends the ci element in **Math** in **Reaction** with optional attributes speciesReference and representationType.

### 3.27.1 *The* speciesReference *attribute*

The optional speciesReference attribute, of type SIdRef, can only be used when the content of the ci element is a species id, or when the content of the ci element is a speciesFeature id. The speciesReference attribute can identify which species is referenced in a reaction, and the speciesReference attribute must have a value of a speciesReference id within the same reaction.

If the ci content references a species' id, the id represent the concentration of the species.

If the ci content references a speciesFeature's id, the id represent the count of the speciesFeature instances with the speciesFeatureValue (also see Section 3.18.1 on page 28).

The example in Section 3.22 on page 35 can be further extended with a block of kineticLaw in the reaction to illustrate the use of the speciesReference attribute with a species' id.

```
<reaction id="reaction" ... >
   ...
   <kineticLaw>
      <math xmlns="http://www.w3.org/1998/Math/MathML">
         <apply>
            <times />
            <ci> k </ci>
            <ci multi:speciesReference="r1"> spA </ci>
            <ci multi:speciesReference="m1"> spM </ci>
            <ci multi:speciesReference="r2"> spA </ci>
            <ci multi:speciesReference="m2"> spM </ci>
         </apply>
      </math>
      <listOfLocalParameters>
         <localParameter id="k" value="0.1" ... />
      </listOfLocalParameters>
   </kineticLaw>
</reaction>
```

Two "spA" species and two "spM" species are distinguished by the "r1" and "r2" speciesReferences respectively.

Here is another example to show the use of the speciesReference attribute for a possibleSpeciesFeatureValue. This example is a simplified adaptation of published models [Malleshaiah et al. (2010), Barik et al. (2010)]. A speciesType "stY" has 10 phosphorylation sites. A species "Yu" referencing speciesType "stY" can be phosphorylated by another species "M" one site one time and the phosphorylation rate depends on the number of sites already phosphorylated in species "Yu". The SBML code can be as follows:

```
<multi:listOfSpeciesTypes>
   <multi:speciesType multi:id="stY" >
      <multi:listOfSpeciesFeatureType multi:id="phosphorylation" multi:occur="10" >
         <multi:listOfPossibleSpeciesFeatureValues>
            <multi:possibleSpeciesFeatureValue multi:id="P" multi:name="phosphorylated" />
            <multi:possibleSpeciesFeatureValue multi:id="U" multi:name="unphosphorylated" />
         </multi:listOfPossibleSpeciesFeatureValues>
      </multi:listOfSpeciesFeatureType>
   </multi:speciesType>
</multi:listOfSpeciesTypes>
<listOfSpecies>
   <species id="Yu" multi:speciesType="stY" ...>
      <multi:listOfSpeciesFeatures>
         <multi:speciesFeature multi:id="fU" multi:occur="1">
            <multi:listOfSpeciesFeatureValues>
```

```
               <multi:speciesFeatureValue value="U" />
            </multi:listOfSpeciesFeatureValues>
         </multi:speciesFeature>
      </multi:listOfSpeciesFeatures>
   </species>
   <species id="Yp" multi:speciesType="stY" ...>
      <multi:listOfSpeciesFeatures>
         <multi:speciesFeature multi:id="fP" multi:occur="1">
            <multi:listOfSpeciesFeatureValues>
               <multi:speciesFeatureValue value="P" />
            </multi:listOfSpeciesFeatureValues>
         </multi:speciesFeature>
      </multi:listOfSpeciesFeatures>
   </species>
   <species id="M" ... />
</listOfSpecies>
<listOfReactions>
   <reaction id="reaction" .>
      <listOfReactants>
         <speciesReference id="r" species="Yu" />
      </listOfReactants>
      <listOfProducts>
         <speciesReference id="p" species="Yp" >
            <multi:listOfSpeciesTypeComponentMapsInProduct>
               <multi:speciesTypeComponentMapInProduct multi:reactant="r"
                     multi:reactantComponent="stY" multi:productReactant="stY" >
                  <multi:listOfSpeciesFeatureChanges>
                     <multi:speciesFeatureChange multi:reactantSpeciesFeature="fU"
                        multi:productSpeciesFeature="fP" />
                  </multi:listOfSpeciesFeatureChanges>
               </multi:speciesTypeComponentMapInProduct>
            </multi:listOfSpeciesTypeComponentMapsInProduct>
         </speciesReference>
      </listOfProducts>
      <listOfModifierSpeciesReferences>
         <modifierSpeciesReference species="M" />
      </listOfModifierSpeciesReferences>
      <kineticLaw>
         <math xmlns="http://www.w3.org/1998/Math/MathML">
            <apply>
               <times />
               <ci> k </ci>
               <ci> Yu </ci>
               <ci> M </ci>
               <ci multi:speciesReference="r"> P </ci>
            </apply>
         </math>
         <listOfLocalParameters>
            <localParameter id="k" ... />
         </listOfLocalParameters>
      </kineticLaw>
   </reaction>
</listOfReactions>
```

Any "`fully defined`" species referencing "`stY`" with at least one unphosphorylated site maps to the species "`Yu`". Any "`fully defined`" species referencing "`stY`" with at least one phosphorylated site maps to the species "`Yp`". The `speciesFeatureChange` references speciesFeatures "`fU`" and "`fP`" and the value of "`1`" for both `occur` attributes of "`fU`" and "`fP`" indicates that one site is phosphorylated in the `reaction`. The `<ci multi:speciesReference="r"> P </ci>` depends on the "`fully defined`" species mapping to the species "`Yu`" which is referenced by the speciesReference "`r`". If the "`fully defined`" species has 1 site phosphorylated, the `ci` is "`1`" in the math, similarly, `ci` is 2 for 2 phosphorylated sites, ...., `ci` is 9 for 9 phosphorylated sites.

### 3.27.2 The representationType attribute

The optional representationType attribute, of type RepresentationType, can only be used when the content of the ci element is a species' id or a possibleSpeciesFeatureValue's id. The representationType and speciesReference attributes can both be used for the same ci element at the same time.

The representationType attribute can only have the value of "sum" when the content of the ci is species. The interpretation of such a ci element is the total concentration or amount of all "fully defined" species (see Section 3.19 on page 33) mapping to the referenced pattern species.

The representationType attribute can have the value of "numericValue" when the content of the ci is possibleSpeciesFeatureVa and the speciesReference attribute must be defined. The interpretation of such a ci is the same as a ci element having a parameter which the possibleSpeciesFeatureValue links via its numericValue attribute.

The following example demonstrates the use of this attribute for "sum" of species concentrations.

```
    k1*Si/(k2+SUM(Si))
```

In this example, the reactant "Si" is a pattern species which may have multiple "fully defined" species mapping to it, for example species "S1", "S2", ..., "Sn". "SUM(Si)" is a function to calculate the total concentration of all "fully defined" species mapping to "Si". The product can be another pattern species "Pi". The SBML code for the math expression can be as follows:

```
<reaction id="r">
   <listOfReactants>
      <speciesReference species="Si" />
   </listOfReactants>
   <listOfProducts>
      <speciesReference species="Pi" />
   </listOfProducts>
   <kineticLaw>
      <math xmlns="http://www.w3.org/1998/Math/MathML">
         <apply>
            <divide>
               <apply>
                  <times />
                  <ci>Si</ci>
                  <ci>k1</ci>
               </apply>
               <apply>
                  <plus />
                  <ci>k2</ci>
                  <ci multi:representationType="sum">Si</ci>
               </apply>
            </divide>
         </apply>
      </math>
      <listOfLocalParameters>
         <localParameter id="k1" ... />
         <localParameter id="k2" .... />
      </listOfLocalParameters>
   </kineticLaw>
</reaction>
```

The math expressions for the individual species in the example can be:

```
For species S1:    k1*S1/(k2 + (S1 + S2 + ... + Sn))
For species S2:    k1*S2/(k2 + (S1 + S2 + ... + Sn))
...
For species Sn:    k1*Sn/(k2 + (S1 + S2 + ... + Sn))
```

## 3.28 Namespace scoping rules for identifiers

In the Multi package, as in SBML Level 3 Version 1 Core, the **Model** object contains the main components of an SBML model, such as the species, compartments and reactions. The package defines new classes within a model and the scope of identifiers of those new classes should be defined to prevent identifier collisions. In this section, we describe the scoping rules for all of the types and classes defined in Section 3.4 to Section 3.27 on pages 10–41.

1. The namespace for `SId` identifiers defined within a **Model** object used in the Multi package follows the same rules as those defined in SBML Level 3 Version 1 Core for plain **Model** objects. The scope of the identifiers is limited to the enclosing **Model** object.

2. The identifier of every **SpeciesType** and **PossibleSpeciesFeatureValue** object defined in the Multi package must be unique across the set of all identifiers in the **Model** object in which it is located.

3. The identifier of every **SpeciesTypeInstance**, **SpeciesTypeComponentIndex**, **InSpeciesTypeBond** and **SpeciesFeatureType** object defined in the Multi package must be unique across the set of all identifiers of the same class under the direct parent **SpeciesType** object in which it is located.

4. The identifier of every **SpeciesFeature** and **SubListOfSpeciesFeatures** object defined in the Multi package must be unique across the set of all identifiers in the **Species** object in which it is located.

5. The identifier, if defined, of every **SpeciesFeatureChange** object defined in the Multi package must be unique across the set of all identifiers in the **SpeciesTypeComponentMapInProduct** object in which it is located.

6. The identifier, if defined, of every **CompartmentReference** object defined in the Multi package must be unique across the set of all identifiers in the **Compartment** object in which it is located.

# 4 Examples

This section contains examples employing the Multi package for SBML Level 3.

## 4.1 Example: Compartment, SpeciesType and Species

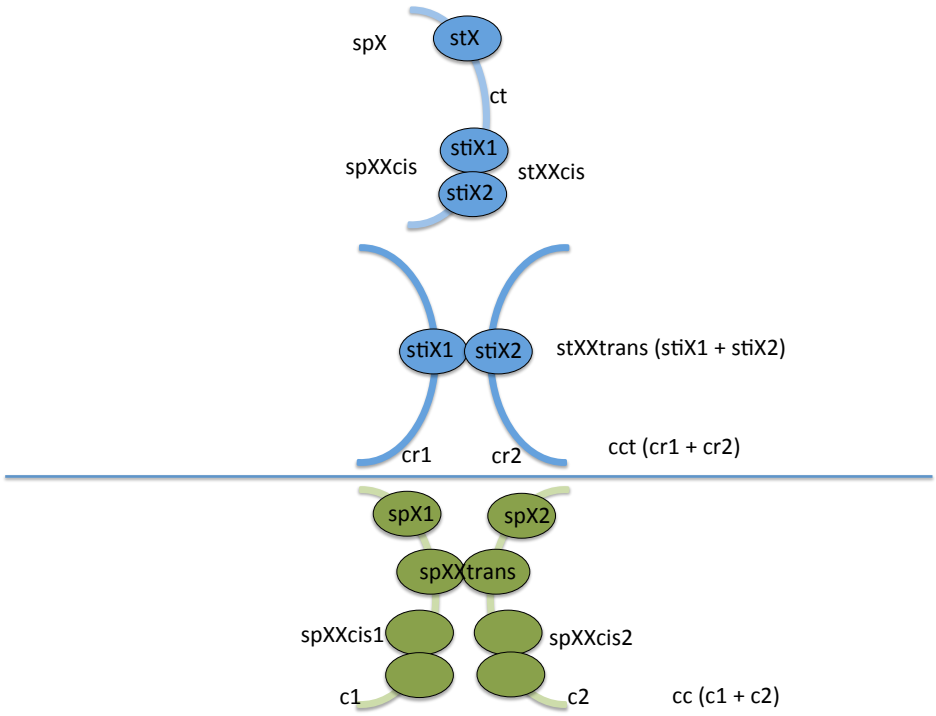


***Figure 17:*** *Diagram for an example of **Compartment**, **SpeciesType** and **Species***

Figure 17 shows an example illustrating the usages of and relations among the **Compartment**, **SpeciesType** and **Species** classes.

"`ct`" is a `compartment` type. "`cct`" is a composite `compartment` type with two `compartmentReferences` "`cr1`" and "`cr2`" both referencing "`ct`". "`c1`" is a "`not-a-type`" `compartment` and references "`ct`". Similarly, "`c2`" is also a "`not-a-type`" `compartment` and references "`ct`". "`cc`" is a composite "`not-a-type`" `compartment` composed of "`c1`" and "`c2`".

"`stX`" is a `speciesType` on the "`ct`" `compartment`. "`stXXcis`" is a `speciesType` on the "`ct`" `compartment`, and has two `speciesTypeInstances` "`stiX1`" and "`stX2`" both of that reference the "`stX`" speciesType. "`stXXtrans`" is a `speciesType` on the "`cct`" `compartment` with two `speciesTypeInstances` "`stiX1`" and "`stiX2`" sitting in different sub-compartments.

"`spX`" is a `species` referencing `speciesType` "`stX`". "`spXXcis`" is a `species` referencing "`stXXcis`". "`spX1`" is a `species` referencing "`stX`" and sitting in the "`c1`" `compartment`. "`spX2`" is a `species` also referencing "`stX`", but sitting in "`c2`". "`spXXtrans`" is a `species` referencing "`stXXtrans`". "`spXXcis1`" is a `species` referencing "`stXXtrans`" and sitting in "`c1`"."`spXXcis1`" is a `species` referencing "`stXXtrans`" and sitting in "`c2`".

"spX1", "spX2", "spXXtrans", "spXXcis1" and "spXXcis2" are "fully defined" species (see Section 3.19 on page 33).

The SBML code can be as follows:

```
<listOfCompartments>
   <compartment id="ct" multi:isType="true" />
   <compartment id="cct" multi:isType="true">
      <multi:listOfCompartmentReferences>
         <multi:compartmentReference multi:id="cr1" multi:compartment="ct" />
         <multi:compartmentReference multi:id="cr2" multi:compartment="ct" />
      </multi:listOfCompartmentReferences>
   </compartment>
   <compartment id="c1" multi:isType="false" multi:compartmentType="ct" />
   <compartment id="c2" multi:isType="false" multi:compartmentType="ct" />
   <compartment id="cc" multi:isType="false" multi:compartmentType="cct">
      <multi:listOfCompartmentReferences>
         <multi:compartmentReference multi:compartment="c1" />
         <multi:compartmentReference multi:compartment="c2" />
      </multi:listOfCompartmentReferences>
   </compartment>
</listOfCompartments>
<multi:listOfSpeciesTypes>
   <multi:bindingSiteSpeciesType multi:id="stX" multi:compartment="ct" />
   <multi:speciesType multi:id="stXXcis" multi:compartment="ct">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="stiX1" multi:speciesType="stX" />
         <multi:speciesTypeInstance multi:id="stiX2" multi:speciesType="stX" />
      </multi:listOfSpeciesTypeInstances>
      <multi:listOfInSpeciesTypeBonds>
         <multi:inSpeciesTypeBond multi:bindingSite1="stiX1" multi:bindingSite2="stiX2" />
      </multi:listOfInSpeciesTypeBonds>
   </multi:speciesType>
   <multi:speciesType multi:id="stXXtrans" multi:compartment="cct">
      <multi:listOfSpeciesTypeInstances>
         <multi:speciesTypeInstance multi:id="stiX1" multi:speciesType="stX"
            multi:compartmentReference="cr1" />
         <multi:speciesTypeInstance multi:id="stiX2" multi:speciesType="stX"
            multi:compartmentReference="cr2" />
      </multi:listOfSpeciesTypeInstances>
      <multi:listOfInSpeciesTypeBonds>
         <multi:inSpeciesTypeBond multi:bindingSite1="stiX1" multi:bindingSite2="stiX2" />
      </multi:listOfInSpeciesTypeBonds>
   </multi:speciesType>
</multi:listOfSpeciesTypes>
<listOfSpecies>
   <species id="spX" multi:speciesType="stX" compartment="ct" />
   <species id="spXXcis" multi:speciesType="stXXcis" compartment="ct" />
   <species id="spX1" multi:speciesType="stX" compartment="c1" /> <!-- Fully defined -->
   <species id="spX2" multi:speciesType="stX" compartment="c2" /> <!-- Fully defined -->
   <species id="spXXtrans" multi:speciesType="stXXtrans" compartment="cc" /> <!-- Fully defined -->
   <species id="spXXcis1" multi:speciesType="stXXcis" compartment="c1" /> <!-- Fully defined -->
   <species id="spXXcis2" multi:speciesType="stXXcis" compartment="c2" /> <!-- Fully defined -->
</listOfSpecies>
```

## 4.2 *Simmune* example: the Ecad model

The *Simmune* toolset (http://go.usa.gov/QeH) has some example models including the published Ecad model [Angermann et al. (2012)]. The Ecad model describes the interactions between E-cadherin receptors that can associate either with other E-cadherin receptors within the same membrane (in "cis") or with E-cadherin receptors on adjacent membranes (in "trans"). This model is transformed into the SBML Level 3 format with use of the Multi package.

```
<?xml version="1.0" encoding="UTF-8"?>
```

```
<sbml xmlns="http://www.sbml.org/sbml/level3/version1/core" level="3" version="1"
   xmlns:multi="http://www.sbml.org/sbml/level3/version1/multi/version1" multi:required="true">
   <model name="E-cadherin_mediated_adhesion">

      <!-- Definitions -->
      <listOfUnitDefinitions>
         <unitDefinition id="litre_per_mole_per_sec">
            <listOfUnits>
               <unit kind="litre" exponent="1" scale="0" multiplier="1" />
               <unit kind="mole" exponent="-1" scale="0" multiplier="1" />
               <unit kind="second" exponent="-1" scale="0" multiplier="1" />
            </listOfUnits>
         </unitDefinition>
         <unitDefinition id="micron_square_per_sec">
            <listOfUnits>
               <unit kind="metre" exponent="2" scale="-6" multiplier="1" />
               <unit kind="second" exponent="-1" scale="0" multiplier="1" />
            </listOfUnits>
         </unitDefinition>
         <unitDefinition id="micrometre_per_sec">
            <listOfUnits>
               <unit kind="metre" exponent="1" scale="-6" multiplier="1" />
               <unit kind="second" exponent="-1" scale="0" multiplier="1" />
            </listOfUnits>
         </unitDefinition>
         <unitDefinition id="per_sec">
            <listOfUnits>
               <unit kind="second" exponent="-1" scale="0" multiplier="1" />
            </listOfUnits>
         </unitDefinition>
      </listOfUnitDefinitions>

      <!-- Compartments -->
      <listOfCompartments>
         <compartment id="membrane" constant="true" multi:isType="true" />
         <compartment id="inter_membrane" constant="true" multi:isType="true">
            <multi:listOfCompartmentReferences>
               <multi:compartmentReference multi:id="m1" multi:compartment="membrane" />
               <multi:compartmentReference multi:id="m2" multi:compartment="membrane" />
            </multi:listOfCompartmentReferences>
         </compartment>
      </listOfCompartments>

      <!-- SpeciesTypes -->
      <multi:listOfSpeciesTypes>

         <!-- Ecad with cis-binding site and trans-binding site: -->
         <multi:bindingSiteSpeciesType multi:id="st_Cis_Interface" />
         <multi:bindingSiteSpeciesType multi:id="st_Trans_Interface" />
         <multi:speciesType multi:id="st_Ecad" multi:compartment="membrane">
            <multi:listOfSpeciesTypeInstances>
               <multi:speciesTypeInstance multi:id="cis" multi:speciesType="st_Cis_Interface" />
               <multi:speciesTypeInstance multi:id="trans" multi:speciesType="st_Trans_Interface" />
            </multi:listOfSpeciesTypeInstances>
         </multi:speciesType>

         <!-- cis dimer: -->
         <multi:speciesType multi:id="st_Ecad_cis_dimer" multi:compartment="membrane">
            <multi:listOfSpeciesTypeInstances>
               <multi:speciesTypeInstance multi:id="Ecad1" multi:speciesType="st_Ecad" />
               <multi:speciesTypeInstance multi:id="Ecad_2" multi:speciesType="st_Ecad" />
            </multi:listOfSpeciesTypeInstances>
            <multi:listOfSpeciesTypeComponentIndexes>
               <multi:speciesTypeComponentIndex multi:id="Ecad1cis"
                  multi:component="cis" multi:identifyingParent="Ecad1" />
               <multi:speciesTypeComponentIndex multi:id="Ecad2cis"
```

```
                multi:component="cis" multi:identifyingParent="Ecad2" />
            <multi:speciesTypeComponentIndex multi:id="Ecad1trans"
                multi:component="trans" multi:identifyingParent="Ecad1" />
            <multi:speciesTypeComponentIndex multi:id="Ecad2trans"
                multi:component="trans" multi:identifyingParent="Ecad2" />
         </multi:listOfSpeciesTypeComponentIndexes>
         <multi:listOfInSpeciesTypeBonds>
            <multi:inSpeciesTypeBond multi:bindingSite1="Ecad1cis"
                multi:bindingSite2="Ecad2cis" />
         </multi:listOfInSpeciesTypeBonds>
      </multi:speciesType>

      <!-- trans dimer: -->
      <multi:speciesType multi:id="st_Ecad_trans_dimer" multi:compartment="inter_membrane">
         <multi:listOfSpeciesTypeInstances>
            <multi:speciesTypeInstance multi:id="Ecad1" multi:speciesType="st_Ecad"
                multi:compartmentReference="m1" />
            <multi:speciesTypeInstance multi:id="Ecad2" multi:speciesType="st_Ecad"
                multi:compartmentReference="m2" />
         </multi:listOfSpeciesTypeInstances>
         <multi:listOfSpeciesTypeComponentIndexes>
            <multi:speciesTypeComponentIndex multi:id="Ecad1trans"
                multi:component="trans" multi:identifyingParent="Ecad1" />
            <multi:speciesTypeComponentIndex multi:id="Ecad2trans"
                multi:component="trans" multi:identifyingParent="Ecad2" />
            <multi:speciesTypeComponentIndex multi:id="Ecad1cis"
                multi:component="cis" multi:identifyingParent="Ecad1" />
            <multi:speciesTypeComponentIndex multi:id="Ecad2cis"
                multi:component="cis" multi:identifyingParent="Ecad2" />
         </multi:listOfSpeciesTypeComponentIndexes>
         <multi:listOfInSpeciesTypeBonds>
            <multi:inSpeciesTypeBond multi:bindingSite1="Ecad1trans"
                multi:bindingSite2="Ecad2trans" />
         </multi:listOfInSpeciesTypeBonds>
      </multi:speciesType>

      <!-- trimer: -->
      <multi:speciesType multi:id="st_Ecad_trimer" multi:compartment="inter_membrane">
         <multi:listOfSpeciesTypeInstances>
            <multi:speciesTypeInstance multi:id="Ecad1" multi:speciesType="st_Ecad"
                multi:compartmentReference="m1" />
            <multi:speciesTypeInstance multi:id="Ecad2" multi:speciesType="st_Ecad"
                multi:compartmentReference="m1" />
            <multi:speciesTypeInstance multi:id="Ecad3" multi:speciesType="st_Ecad"
                multi:compartmentReference="m2" />
         </multi:listOfSpeciesTypeInstances>
         <multi:listOfSpeciesTypeComponentIndexes>
            <multi:speciesTypeComponentIndex multi:id="Ecad1cis"
                multi:component="cis" multi:identifyingParent="Ecad1" />
            <multi:speciesTypeComponentIndex multi:id="Ecad1trans"
                multi:component="trans" multi:identifyingParent="Ecad1" />
            <multi:speciesTypeComponentIndex multi:id="Ecad2cis"
                multi:component="cis" multi:identifyingParent="Ecad2" />
            <multi:speciesTypeComponentIndex multi:id="Ecad2trans"
                multi:component="trans" multi:identifyingParent="Ecad2" />
            <multi:speciesTypeComponentIndex multi:id="Ecad3cis"
                multi:component="cis" multi:identifyingParent="Ecad3" />
            <multi:speciesTypeComponentIndex multi:id="Ecad3trans"
                multi:component="trans" multi:identifyingParent="Ecad3" />
         </multi:listOfSpeciesTypeComponentIndexes>
         <multi:listOfInSpeciesTypeBonds>
            <multi:inSpeciesTypeBond multi:bindingSite1="Ecad1cis"
                multi:bindingSite2="Ecad2cis" />
            <multi:inSpeciesTypeBond multi:bindingSite1="Ecad1trans"
                multi:bindingSite2="Ecad3trans" />
         </multi:listOfInSpeciesTypeBonds>
```

```
      </multi:speciesType>
    </multi:listOfSpeciesTypes>

    <!-- Species -->
    <listOfSpecies>

      <!-- free Ecad -->
      <species id="sp_Ecad_unbound" name="Ecad_unbound" compartment="membrane"
        hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false"
        multi:speciesType="st_Ecad">
        <multi:listOfOutwardBindingSites>
          <multi:outwardBindingSite multi:component="cis"
            multi:bindingStatus="unbound" />
          <multi:outwardBindingSite multi:component="trans"
            multi:bindingStatus="unbound" />
        </multi:listOfOutwardBindingSites>
      </species>

      <!-- Pattern species: Ecad trans unbnd -->
      <species id="sp_Ecad_trans_unbnd" name="Ecad_trans_unbnd" compartment="membrane"
        hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false"
        multi:speciesType="st_Ecad">
        <multi:listOfOutwardBindingSites>
          <multi:outwardBindingSite multi:component="trans"
            multi:bindingStatus="unbound" />
        </multi:listOfOutwardBindingSites>
      </species>

      <!-- Pattern species: Ecad trans bnd -->
      <species id="sp_Ecad_trans_bnd" name="Ecad_trans_bnd" compartment="membrane"
        hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false"
        multi:speciesType="st_Ecad">
        <multi:listOfOutwardBindingSites>
          <multi:outwardBindingSite multi:component="trans"
            multi:bindingStatus="bound" />
        </multi:listOfOutwardBindingSites>
      </species>

      <!-- Pattern species: Ecad all -->
      <species id="sp_Ecad_all" name="Ecad_all" compartment="membrane"
        hasOnlySubstanceUnits="false"
        boundaryCondition="false" constant="false" multi:speciesType="st_Ecad" />

      <!-- Pattern species: Ecad cis unbnd -->
      <species id="sp_Ecad_cis_unbnd" name="Ecad_cis_unbnd" compartment="membrane"
        hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false"
        multi:speciesType="st_Ecad">
        <multi:listOfOutwardBindingSites>
          <multi:outwardBindingSite multi:component="cis"
            multi:bindingStatus="unbound" />
        </multi:listOfOutwardBindingSites>
      </species>

      <!-- Pattern species: Ecad cis unbnd, trans bnd -->
      <species id="sp_Ecad_6" name="Ecad_6" compartment="membrane" hasOnlySubstanceUnits="false"
        boundaryCondition="false" constant="false" multi:speciesType="st_Ecad">
        <multi:listOfOutwardBindingSites>
          <multi:outwardBindingSite multi:component="cis"
            multi:bindingStatus="unbound" />
          <multi:outwardBindingSite multi:component="trans"
            multi:bindingStatus="bound" />
        </multi:listOfOutwardBindingSites>
      </species>

      <!-- Pattern species: Ecad cis bnd, trans unbnd -->
      <species id="sp_Ecad_7" name="Ecad_7" compartment="membrane" hasOnlySubstanceUnits="false"
```

```
            boundaryCondition="false" constant="false" multi:speciesType="st_Ecad">
            <multi:listOfOutwardBindingSites>
               <multi:outwardBindingSite multi:component="cis"
                  multi:bindingStatus="bound" />
               <multi:outwardBindingSite multi:component="trans"
                  multi:bindingStatus="unbound" />
            </multi:listOfOutwardBindingSites>
         </species>

         <!-- Pattern species: Ecad cis dimer -->
         <species id="sp_Ecad_cis_dimer" name="Ecad_cis_dimer" compartment="membrane"
            hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false"
            multi:speciesType="st_Ecad_cis_dimer" />

         <!-- Pattern species: Ecad cis dimer: all trans bnd -->
         <species id="sp_EcadEcad_2" name="Ecad.Ecad_2" compartment="membrane"
            hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false"
            multi:speciesType="st_Ecad_cis_dimer">
            <multi:listOfOutwardBindingSites>
               <multi:outwardBindingSite multi:component="Ecad1trans"
                  multi:bindingStatus="bound" />
               <multi:outwardBindingSite multi:component="Ecad2trans"
                  multi:bindingStatus="bound" />
            </multi:listOfOutwardBindingSites>
         </species>

         <!-- Pattern species: Ecad trans dimer -->
         <species id="sp_EcadEcad_1" name="Ecad.Ecad_1" compartment="inter_membrane"
            hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false"
            multi:speciesType="st_Ecad_trans_dimer" />

         <!-- Pattern species: Ecad trans dimer: all cis bnd -->
         <species id="sp_Ecad_trans_dimer_2" name="Ecad_trans_dimer_2" compartment="inter_membrane"
            hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false"
            multi:speciesType="st_Ecad_trans_dimer">
            <multi:listOfOutwardBindingSites>
               <multi:outwardBindingSite multi:component="Ecad1cis"
                  multi:bindingStatus="bound" />
               <multi:outwardBindingSite multi:component="Ecad2cis"
                  multi:bindingStatus="bound" />
            </multi:listOfOutwardBindingSites>
         </species>

         <!-- Pattern species: Ecad True Trimer -->
         <species id="sp_Ecad_True_Trimer" compartment="inter_membrane" hasOnlySubstanceUnits="false"
            boundaryCondition="false" constant="false" multi:speciesType="st_Ecad_trimer">
            <multi:listOfOutwardBindingSites>
               <multi:outwardBindingSite multi:component="Ecad2trans"
                  multi:bindingStatus="unbound" />
               <multi:outwardBindingSite multi:component="Ecad3cis"
                  multi:bindingStatus="unbound" />
            </multi:listOfOutwardBindingSites>
         </species>

         <!-- Pattern species: Ecad All Trimer -->
         <species id="sp_Ecad_All_Trimer" compartment="inter_membrane" hasOnlySubstanceUnits="false"
            boundaryCondition="false" constant="false" multi:speciesType="st_Ecad_trimer" />
      </listOfSpecies>

      <!-- Reactions -->
      <listOfReactions>

         <!-- cis association: -->
         <reaction id="rc_Cis_Association" name="Cis_Association" reversible="false" fast="false"
            compartment="membrane">
            <listOfReactants>
```

```
            <speciesReference id="Cis_Association_r1" species="sp_Ecad_6"
               stoichiometry="1" constant="false" />
            <speciesReference id="Cis_Association_r2" species="sp_Ecad_6"
               stoichiometry="1" constant="false" />
         </listOfReactants>
         <listOfProducts>
            <speciesReference species="sp_EcadEcad_2" constant="false" />
         </listOfProducts>
         <kineticLaw>
            <math xmlns="http://www.w3.org/1998/Math/MathML">
               <apply>
                  <times />
                  <ci> kon </ci>
                  <ci multi:speciesReference="Cis_Association_r1"> sp_Ecad_6 </ci>
                  <ci multi:speciesReference="Cis_Association_r2"> sp_Ecad_6 </ci>
               </apply>
            </math>
            <listOfLocalParameters>
               <localParameter id="kon" value="9000" units="litre_per_mole_per_sec" />
            </listOfLocalParameters>
         </kineticLaw>
      </reaction>

      <!-- In species cis association: Here the model requires that the two interacting molecules
        are part of one connected complex already prior to the association. Since the necessary
        connectivity can only be mediated by the trans binding sites here, these sites must be
        bound to the subcomplex (not shown) linking the two interacting molecules.
        -->
      <multi:intraSpeciesReaction id="rc_Intra_Complex_Cis_Association"
       name="Intra-Complex_Cis_Association"
         reversible="false" fast="false" compartment="membrane">
         <listOfReactants>
            <speciesReference id="Intra_Complex_Cis_Association_r1" species="sp_Ecad_6"
               stoichiometry="1" constant="false" />
            <speciesReference id="Intra_Complex_Cis_Association_r2" species="sp_Ecad_6"
               stoichiometry="1" constant="false" />
         </listOfReactants>
         <listOfProducts>
            <speciesReference species="sp_EcadEcad_2" constant="false" />
         </listOfProducts>
         <kineticLaw>
            <math xmlns="http://www.w3.org/1998/Math/MathML">
               <apply>
                  <times />
                  <ci> kon </ci>
                  <ci multi:speciesReference="Intra_Complex_Cis_Association_r1"> sp_Ecad_6 </ci>
               </apply>
            </math>
            <listOfLocalParameters>
               <localParameter id="kon" value="100" units="per_sec" />
            </listOfLocalParameters>
         </kineticLaw>
      </multi:intraSpeciesReaction>

      <!-- trans association: -->
      <reaction id="rc_Trans_Association" name="Trans_Association" reversible="false" fast="false"
         compartment="inter_membrane">
         <listOfReactants>
            <speciesReference id="Trans_Association_r1" species="sp_Ecad_trans_unbnd"
               multi:compartmentReference="m1" constant="false" />
            <speciesReference id="Trans_Association_r2" species="sp_Ecad_trans_unbnd"
               multi:compartmentReference="m2" constant="false" />
         </listOfReactants>
         <listOfProducts>
            <speciesReference species="sp_EcadEcad_1" constant="false" />
         </listOfProducts>
```

```
            <kineticLaw>
               <math xmlns="http://www.w3.org/1998/Math/MathML">
                  <apply>
                     <times />
                     <ci> kon </ci>
                     <ci multi:speciesReference="Trans_Association_r1"> sp_Ecad_trans_unbnd </ci>
                     <ci multi:speciesReference="Trans_Association_r2"> sp_Ecad_trans_unbnd </ci>
                  </apply>
               </math>
               <listOfLocalParameters>
                  <localParameter id="kon" value="90000" units="litre_per_mole_per_sec" />
               </listOfLocalParameters>
            </kineticLaw>
         </reaction>

         <!-- In complex trans association: Here the model requires that the two interacting molecules
           are part of one connected complex already prior to the association. Since the necessary
           connectivity can only be mediated by the cis binding sites here, these sites must be bound
           to the subcomplex (not shown) linking the two interacting molecules.
           -->
         <multi:intraSpeciesReaction id="rc_Intra_Complex_Trans_Association"
          name="Intra-Complex_Trans_Association"
            reversible="false" fast="false" compartment="inter_membrane" >
            <listOfReactants>
               <speciesReference id="Intra_Complex_Trans_Association_r1" species="sp_Ecad_7"
                  multi:compartmentReference="m1" constant="false" />
               <speciesReference id="Intra_Complex_Trans_Association_r2" species="sp_Ecad_7"
                  multi:compartmentReference="m2" constant="false" />
            </listOfReactants>
            <listOfProducts>
               <speciesReference species="sp_Ecad_trans_dimer_2" constant="false" />
            </listOfProducts>
            <kineticLaw>
               <math xmlns="http://www.w3.org/1998/Math/MathML">
                  <apply>
                     <times />
                     <ci> kon </ci>
                     <ci multi:speciesReference="Intra_Complex_Trans_Association_r1"> sp_Ecad_7 </ci>
                  </apply>
               </math>
               <listOfLocalParameters>
                  <localParameter id="kon" value="100" units="per_sec" />
               </listOfLocalParameters>
            </kineticLaw>
         </multi:intraSpeciesReaction>

         <!-- cis dissociation: -->
         <reaction id="rc_Cis_dissociation" name="Cis_dissociation" reversible="false" fast="false"
            compartment="membrane">
            <listOfReactants>
               <speciesReference species="sp_Ecad_cis_dimer" constant="false" />
            </listOfReactants>
            <listOfProducts>
               <speciesReference id="Cis_dissociation_p1" species="sp_Ecad_cis_unbnd"
                  stoichiometry="1" constant="false" />
               <speciesReference id="Cis_dissociation_p2" species="sp_Ecad_cis_unbnd"
                  stoichiometry="1" constant="false" />
            </listOfProducts>
            <kineticLaw>
               <math xmlns="http://www.w3.org/1998/Math/MathML">
                  <apply>
                     <times />
                     <ci> koff </ci>
                     <ci> sp_Ecad_cis_unbnd </ci>
                  </apply>
               </math>
```

```
            <listOfLocalParameters>
               <localParameter id="koff" value="1" units="per_sec" />
            </listOfLocalParameters>
         </kineticLaw>
      </reaction>

      <!-- In-species cis dissociation: By specifying that this reaction breaks only an inner bond,
        the model limits the application of this reaction to dissociations that result in only one
        reaction product. The complex is still connected through a subcomplex that is not shown
        here but that links the two molecules involved in the reaction at their trans binding
        sites. Note that the modeler application has to ensure the correct application of this
        rule and its consistent definition. For instance, specifying the one or both of the trans
        binding sites to be unbound would lead to a rule that could never be applied because the
        trans bindings are required for the connectivity of the result complex.
        -->
      <multi:intraSpeciesReaction id="rc_Intra_Complex_Cis_dissociation"
       name="Intra-Complex_Cis_dissociation"
         reversible="false" fast="false" compartment="membrane" >
         <listOfReactants>
            <speciesReference species="sp_EcadEcad_2" constant="false" />
         </listOfReactants>
         <listOfProducts>
            <speciesReference id="Intra_Complex_Cis_dissociation_p1" species="sp_Ecad_6"
               stoichiometry="2" constant="false" />
            <speciesReference id="Intra_Complex_Cis_dissociation_p2" species="sp_Ecad_6"
               stoichiometry="2" constant="false" />
         </listOfProducts>
         <kineticLaw>
            <math xmlns="http://www.w3.org/1998/Math/MathML">
               <apply>
                  <times />
                  <ci> koff </ci>
                  <ci> sp_Ecad_6 </ci>
               </apply>
            </math>
            <listOfLocalParameters>
               <localParameter id="koff" value="0.01" units="per_sec" />
            </listOfLocalParameters>
         </kineticLaw>
      </multi:intraSpeciesReaction>

      <!-- trans dissociation: -->
      <reaction id="rc_Trans_dissociation" name="Trans_dissociation" reversible="false"
         fast="false" compartment="inter_membrane">
         <listOfReactants>
            <speciesReference species="sp_EcadEcad_1" constant="false" />
         </listOfReactants>
         <listOfProducts>
            <speciesReference id="Trans_dissociation_p1" species="sp_Ecad_trans_unbnd"
               multi:compartmentReference="m1" constant="false" />
            <speciesReference id="Trans_dissociation_p2" species="sp_Ecad_trans_unbnd"
               multi:compartmentReference="m2" constant="false" />
         </listOfProducts>
         <kineticLaw>
            <math xmlns="http://www.w3.org/1998/Math/MathML">
               <apply>
                  <times />
                  <ci> koff </ci>
                  <ci> sp_Ecad_trans_unbnd </ci>
               </apply>
            </math>
            <listOfLocalParameters>
               <localParameter id="koff" value="1" units="per_sec" />
            </listOfLocalParameters>
         </kineticLaw>
      </reaction>
```

```
        <!-- In species trans dissociation: By specifying that this reaction breaks only an inner
          bond, the model limits the application of this reaction to dissociations that result in
          only one reaction product. The complex is still connected through a subcomplex that is
          not shown here but that links the two molecules involved in the reaction at their cis
          binding sites. Note that the modeler application has to ensure the correct application
          of this rule and its consistent definition. For instance, specifying the one or both of
          the cis binding sites to be unbound would lead to a rule that could never be applied
          because the cis bindings are required for the connectivity of the result complex.
          -->
        <multi:intraSpeciesReaction id="rc_Intra_Complex_Trans_dissociation"
         name="Intra-Complex_Trans_dissociation"
           reversible="false" fast="false" compartment="inter_membrane" >
           <listOfReactants>
              <speciesReference species="sp_Ecad_trans_dimer_2" constant="false" />
           </listOfReactants>
           <listOfProducts>
              <speciesReference id="Intra_Complex_Trans_dissociation_p1" species="sp_Ecad_7"
                 multi:compartmentReference="m1" constant="false" />
              <speciesReference id="Intra_Complex_Trans_dissociation_p2" species="sp_Ecad_7"
                 multi:compartmentReference="m2" constant="false" />
           </listOfProducts>
           <kineticLaw>
              <math xmlns="http://www.w3.org/1998/Math/MathML">
                 <apply>
                    <times />
                    <ci> koff </ci>
                    <ci> sp_Ecad_7 </ci>
                 </apply>
              </math>
              <listOfLocalParameters>
                 <localParameter id="koff" value="0.01" units="per_sec" />
              </listOfLocalParameters>
           </kineticLaw>
        </multi:intraSpeciesReaction>
      </listOfReactions>
   </model>
</sbml>
```

## 4.3 A *BioNetGen* example from its user manual

egfr_simple.bngl (http://bionetgen.org/index.php/BNGManual:Listing_1)

```
begin parameters
  NA 6.02e23                # Avogadro's number (molecules/mol)
  f  1                      # Fraction of the cell to simulate
  Vo f*1.0e-10              # Extracellular volume=1/cell_density (L)
  V  f*3.0e-12              # Cytoplasmic volume (L)

  EGF_init 20*1e-9*NA*Vo    # Initial amount of ligand (20 nM)
                            # converted to copies per cell

  # Initial amounts of cellular components (copies per cell)
  EGFR_init f*1.8e5
  Grb2_init f*1.5e5
  Sos1_init f*6.2e4

  # Rate constants
  # Divide by NA*V to convert bimolecular rate constants
  # from /M/sec to /(molecule/cell)/sec
  kp1 9.0e7/(NA*Vo)   # ligand-monomer binding
  km1 0.06            # ligand-monomer dissociation
  kp2 1.0e7/(NA*V)    # aggregation of bound monomers
  km2 0.1             # dissociation of bound monomers
```

```
  kp3 0.5             # dimer transphosphorylation
  km3 4.505           # dimer dephosphorylation
  kp4 1.5e6/(NA*V)    # binding of Grb2 to receptor
  km4 0.05            # dissociation of Grb2 from receptor
  kp5 1.0e7/(NA*V)    # binding of Grb2 to Sos1
  km5 0.06            # dissociation of Grb2 from Sos1
  deg 0.01            # degradation of receptor dimers
end parameters

begin molecule types
  EGF(R)
  EGFR(L,CR1,Y1068~U~P)
  Grb2(SH2,SH3)
  Sos1(PxxP)
  Trash()
end molecule types

begin seed species
  EGF(R)               0
  EGFR(L,CR1,Y1068~U) EGFR_init
  Grb2(SH2,SH3)       Grb2_init
  Sos1(PxxP)          Sos1_init
end seed species

begin observables
  1 Molecules   EGFR_tot  EGFR()
  2 Molecules   Lig_free  EGF(R)
  3 Species     Dim       EGFR(CR1!+)
  4 Molecules   RP        EGFR(Y1068~P!?)
  5 Molecules   Grb2Sos1  Grb2(SH2,SH3!1).Sos1(PxxP!1)
  6 Molecules   Sos1_act  EGFR(Y1068!1).Grb2(SH2!1,SH3!2).Sos1(PxxP!2)
end observables

begin reaction rules
  # Ligand-receptor binding
  1 EGFR(L,CR1) + EGF(R) <-> EGFR(L!1,CR1).EGF(R!1) kp1, km1

  # Receptor-aggregation
  2 EGFR(L!+,CR1) + EGFR(L!+,CR1) <-> EGFR(L!+,CR1!1).EGFR(L!+,CR1!1) kp2,km2

  # Transphosphorylation of EGFR by RTK
  3 EGFR(CR1!+,Y1068~U) -> EGFR(CR1!+,Y1068~P) kp3

  # Dephosphorylation
  4 EGFR(Y1068~P) -> EGFR(Y1068~U) km3

  # Grb2 binding to pY1068
  5 EGFR(Y1068~P) + Grb2(SH2) <-> EGFR(Y1068~P!1).Grb2(SH2!1) kp4,km4

  # Grb2 binding to Sos1
  6 Grb2(SH3) + Sos1(PxxP) <-> Grb2(SH3!1).Sos1(PxxP!1) kp5,km5

  # Receptor dimer internalization/degradation
  7 EGF(R!1).EGF(R!2).EGFR(L!1,CR1!3).EGFR(L!2,CR1!3) -> Trash()
end reaction rules

#actions
generate_network({overwrite=>1});

# Equilibration
simulate_ode({suffix=>equil,t_end=>100000,n_steps=>10,sparse=>1,steady_state=>1});
setConcentration("EGF(R)","EGF_init");
saveConcentrations(); # Saves concentrations for future reset

# Kinetics
writeSBML({});
```

```
simulate_ode({t_end=>120,n_steps=>120});
resetConcentrations(); # reverts to saved Concentrations
simulate_ssa({suffix=>ssa,t_end=>120,n_steps=>120});
```

The SBML code can be as follows. Please note, the SBML code does not cover the content other than the model in the bngl file, such as the "`actions`", "`Equilibration`" and "`Kinetics`" sections.

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

   <model name="bionetgen_example_egfr_simple">

      <listOfUnitDefinitions>
         <unitDefinition id="molecules_per_mol">
            <listOfUnits>
               <unit kind="mole" scale="0" mulitplier="1" exponent="-1" />
            </listOfUnits>
         </unitDefinition>
      </listOfUnitDefinitions>

      <!-- compartments -->
      <listOfCompartments>
         <compartment id="Vo" constant="true" spatialDimensions="3" units="liter"
            multi:isType="false" />
         <compartment id="V" constant="true" spatialDimensions="3" units="liter"
            multi:isType="false" />
      </listOfCompartments>

      <!-- speciesType -->
      <multi:listOfSpeciesTypes>

         <!-- EGF(R) -->
         <multi:bindingSiteSpeciesType multi:id="st_EGF_bs_R" />
         <multi:speciesType multi:id="st_EGF">
            <multi:listOfSpeciesTypeInstances>
               <multi:component multi:id="R" multi:speciesType="st_EGF_bs_R" />
            </multi:listOfSpeciesTypeInstances>
         </multi:speciesType>

         <!-- EGFR(L,CR1,Y1068~U~P) -->
         <multi:bindingSiteSpeciesType multi:id="st_EGFR_bs_L" />
         <multi:bindingSiteSpeciesType multi:id="st_EGFR_bs_CR1" />
         <multi:bindingSiteSpeciesType multi:id="st_EGFR_bs_Y1068">
            <multi:listOfSpeciesFeatureTypes>
               <multi:speciesFeatureType multi:id="sft_Y1068">
                  <multi:listOfPossibleSpeciesFeatureValues>
                     <multi:possibleSpeciesFeatureValue multi:id="U" />
                     <multi:possibleSpeciesFeatureValue multi:id="P" />
                  </multi:listOfPossibleSpeciesFeatureValues>
               </multi:speciesFeatureType>
            </multi:listOfSpeciesFeatureTypes>
         </multi:bindingSiteSpeciesType>
         <multi:speciesType multi:id="st_EGFR">
            <multi:listOfSpeciesTypeInstances>
               <multi:component multi:id="L" multi:speciesType="st_EGFR_bs_L" />
               <multi:component multi:id="CR1" multi:speciesType="st_EGFR_bs_CR1" />
               <multi:component multi:id="Y1068" multi:speciesType="st_EGFR_bs_Y1068" />
            </multi:listOfSpeciesTypeInstances>
         </multi:speciesType>

         <!-- EGFR dimer: [EGFR(CR1!1).EGFR(CR1!1)] -->
         <multi:speciesType multi:id="st_EGFR_dimer">
            <multi:listOfSpeciesTypeInstances>
               <multi:component multi:id="EGFR1" multi:speciesType="st_EGFR" />
```

```
            <multi:component multi:id="EGFR2" multi:speciesType="st_EGFR" />
         </multi:listOfSpeciesTypeInstances>
         <multi:listOfSpeciesTypeComponentIndexes>
            <multi:speciesTypeComponentIndex multi:id="EGFR1CR1"
               multi:component="CR1" identifyingParent="EGFR1" />
            <multi:speciesTypeComponentIndex multi:id="EGFR2CR1"
               multi:component="CR1" identifyingParent="EGFR2" />
         </multi:listOfSpeciesTypeComponentIndexes>
         <multi:listOfInSpeciesTypeBonds>
            <multi:inSpeciesTypeBond multi:bindingSite1="EGFR1CR1"
               multi:bindingSite2="EGFR2CR1" />
         </multi:listOfInSpeciesTypeBonds>
      </multi:speciesType>

      <!-- EGFR-EGF dimer: [EGF(R!1).EGF(R!2).EGFR(L!1,CR1!3).EGFR(L!2,CR1!3)] -->
      <multi:speciesType multi:id="st_EGFR_EGF_dimer">
         <multi:listOfSpeciesTypeInstances>
            <multi:component multi:id="EGF1" multi:speciesType="st_EGF" />
            <multi:component multi:id="EG2" multi:speciesType="st_EGF" />
            <multi:component multi:id="EGFR1" multi:speciesType="st_EGFR" />
            <multi:component multi:id="EGFR2" multi:speciesType="st_EGFR" />
         </multi:listOfSpeciesTypeInstances>
         <multi:listOfSpeciesTypeComponentIndexes>
            <multi:speciesTypeComponentIndex multi:id="EGF1R"
               multi:component="R" identifyingParent="EGF1" />
            <multi:speciesTypeComponentIndex multi:id="EGF2R"
               multi:component="R" identifyingParent="EGF2" />
            <multi:speciesTypeComponentIndex multi:id="EGFR1L"
               multi:component="L" identifyingParent="EGFR1" />
            <multi:speciesTypeComponentIndex multi:id="EGFR2L"
               multi:component="L" identifyingParent="EGFR2" />
            <multi:speciesTypeComponentIndex multi:id="EGFR1CR1"
               multi:component="CR1" identifyingParent="EGFR1" />
            <multi:speciesTypeComponentIndex multi:id="EGFR2CR1"
               multi:component="CR1" identifyingParent="EGFR2" />
         </multi:listOfSpeciesTypeComponentIndexes>
         <multi:listOfInSpeciesTypeBonds>
            <multi:inSpeciesTypeBond multi:bindingSite1="EGFR1CR1" multi:bindingSite2="EGFR2CR1" />
            <multi:inSpeciesTypeBond multi:bindingSite1="EGF1R" multi:bindingSite2="EGFR1L" />
            <multi:inSpeciesTypeBond multi:bindingSite1="EGF2R" multi:bindingSite2="EGFR2L" />
         </multi:listOfInSpeciesTypeBonds>
      </multi:speciesType>

      <!-- Grb2(SH2, SH3) -->
      <multi:bindingSiteSpeciesType multi:id="st_Grb2_bs_SH2" />
      <multi:bindingSiteSpeciesType multi:id="st_Grb2_bs_SH3" />
      <multi:speciesType multi:id="st_Grb2">
         <multi:listOfSpeciesTypeInstances>
            <multi:component multi:id="SH2" multi:speciesType="st_Grb2_bs_SH2" />
            <multi:component multi:id="SH3" multi:speciesType="st_Grb2_bs_SH3" />
         </multi:listOfSpeciesTypeInstances>
      </multi:speciesType>

      <!-- Sos1 -->
      <multi:bindingSiteSpeciesType multi:id="st_Sos1_bs_PxxP" />
      <multi:speciesType multi:id="st_Sos1">
         <multi:listOfSpeciesTypeInstances>
            <multi:component multi:id="PxxP" multi:speciesType="st_Sos1_bs_PxxP" />
         </multi:listOfSpeciesTypeInstances>
      </multi:speciesType>

      <!-- Trash -->
      <multi:speciesType multi:id="trash" />

      <!-- Grb2-Sos1 -->
      <multi:speciesType multi:id="st_Grb2_Sos1">
```

```
            <multi:listOfSpeciesTypeInstances>
               <multi:component multi:id="Grb2" multi:speciesType="st_Grb2" />
               <multi:component multi:id="Sos1" multi:speciesType="st_Sos1" />
            </multi:listOfSpeciesTypeInstances>
            <multi:listOfInSpeciesTypeBonds>
               <multi:inSpeciesTypeBond multi:bindingSite1="SH3" multi:bindingSite2="PxxP" />
            </multi:listOfInSpeciesTypeBonds>
         </multi:speciesType>

         <!-- EGFR(Y1068!1).Grb1(SH2!1,SH3!2).Sos1(PxxP!2) -->
         <multi:speciesType multi:id="st_EGFR_Grb2_Sos1">
            <multi:listOfSpeciesTypeInstances>
               <multi:component multi:id="EGFR" multi:speciesType="st_EGFR" />
               <multi:component multi:id="Grb2" multi:speciesType="st_Grb2" />
               <multi:component multi:id="Sos1" multi:speciesType="st_Sos1" />
            </multi:listOfSpeciesTypeInstances>
            <multi:listOfInSpeciesTypeBonds>
               <multi:inSpeciesTypeBond multi:bindingSite1="Y1068" multi:bindingSite2="SH2" />
               <multi:inSpeciesTypeBond multi:bindingSite1="SH3" multi:bindingSite2="PxxP" />
            </multi:listOfInSpeciesTypeBonds>
         </multi:speciesType>

         <!-- EGFR(L!1).EGF(R!1) -->
         <multi:speciesType multi:id="st_EGFR_EGF">
            <multi:listOfSpeciesTypeInstances>
               <multi:component multi:id="EGFR" multi:speciesType="st_EGFR" />
               <multi:component multi:id="EGF" multi:speciesType="st_EGF" />
            </multi:listOfSpeciesTypeInstances>
            <multi:listOfInSpeciesTypeBonds>
               <multi:inSpeciesTypeBond multi:bindingSite1="L" multi:bindingSite2="R" />
            </multi:listOfInSpeciesTypeBonds>
         </multi:speciesType>

         <!-- EGFR(Y1068!1).Grb2(SH2!1) -->
         <multi:speciesType multi:id="st_EGFR_Grb2">
            <multi:listOfSpeciesTypeInstances>
               <multi:component multi:id="EGFR" multi:speciesType="st_EGFR" />
               <multi:component multi:id="Grb2" multi:speciesType="st_Grb2" />
            </multi:listOfSpeciesTypeInstances>
            <multi:listOfInSpeciesTypeBonds>
               <multi:inSpeciesTypeBond multi:bindingSite1="Y1068" multi:bindingSite2="SH2" />
            </multi:listOfInSpeciesTypeBonds>
         </multi:speciesType>

      </multi:listOfSpeciesTypes>

      <!-- species -->
      <listOfSpecies>

         <species id="sp_EGF_free" name="EGF(R)" multi:speciesType="st_EGF"
            hasOnlySubstanceUnits="false"
            boundaryCondition="false" constant="false">
            <multi:listOfOutwardBindingSites>
               <multi:outwardBindingSite multi:component="R" multi:bindingStatus="unbound" />
            </multi:listOfOutwardBindingSites>
         </species>

         <species id="sp_EGFR_free_U" name="EGFR(L,CR1,Y1068~U)" multi:speciesType="st_EGFR"
            hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
            <multi:listOfOutwardBindingSites>
               <multi:outwardBindingSite multi:component="L" multi:bindingStatus="unbound" />
               <multi:outwardBindingSite multi:component="CR1" multi:bindingStatus="unbound" />
               <multi:outwardBindingSite multi:component="Y1068" multi:bindingStatus="unbound" />
            </multi:listOfOutwardBindingSites>
            <multi:listOfSpeciesFeatures>
               <multi:speciesFeature multi:speciesFeatureType="sft_Y1068">
```

```
                <multi:listOfSpeciesFeatureValues>
                   <multi:speciesFeatureValue multi:value="U" />
                </multi:listOfSpeciesFeatureValues>
             </multi:speciesFeature>
          </multi:listOfSpeciesFeatures>
       </species>
       <species id="sp_Grb2_free" name="Grb2(SH2,SH3)" multi:speciesType="st_Grb2"
          hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
          <multi:listOfOutwardBindingSites>
             <multi:outwardBindingSite multi:component="SH2" multi:bindingStatus="unbound" />
             <multi:outwardBindingSite multi:component="SH3" multi:bindingStatus="unbound" />
          </multi:listOfOutwardBindingSites>
       </species>
       <species id="sp_Grb2_SH2" name="Grb2(SH2)" multi:speciesType="st_Grb2"
          hasOnlySubstanceUnits="false"
          boundaryCondition="false" constant="false">
          <multi:listOfOutwardBindingSites>
             <multi:outwardBindingSite multi:component="SH2" multi:bindingStatus="unbound" />
          </multi:listOfOutwardBindingSites>
       </species>
       <species id="sp_Grb2_SH3" name="Grb2(SH3)" multi:speciesType="st_Grb2"
          hasOnlySubstanceUnits="false"
          boundaryCondition="false" constant="false">
          <multi:listOfOutwardBindingSites>
             <multi:outwardBindingSite multi:component="SH3" multi:bindingStatus="unbound" />
          </multi:listOfOutwardBindingSites>
       </species>
       <species id="sp_Sos1_free" name="Sos1(PxxP)" multi:speciesType="st_Sos1"
          hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
          <multi:listOfOutwardBindingSites>
             <multi:outwardBindingSite multi:component="PxxP" multi:bindingStatus="unbound" />
          </multi:listOfOutwardBindingSites>
       </species>
       <species id="sp_EGF_tot" name="EGF()" multi:speciesType="st_EGF"
          hasOnlySubstanceUnits="false"
          boundaryCondition="false" constant="false" />
       <species id="sp_EGFR_dimerized" name="EGFR(CR1!+)" multi:speciesType="st_EGFR"
          hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
          <multi:listOfOutwardBindingSites>
             <multi:outwardBindingSite multi:component="CR1" multi:bindingStatus="bound" />
          </multi:listOfOutwardBindingSites>
       </species>
       <species id="sp_EGFR_U" name="EGFR(Y1068~P!?)" multi:speciesType="st_EGFR"
          hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
          <multi:listOfSpeciesFeatures>
             <multi:speciesFeature multi:speciesFeatureType="sft_Y1068">
                <multi:listOfSpeciesFeatureValues>
                   <multi:speciesFeatureValue multi:value="P" />
                </multi:listOfSpeciesFeatureValues>
             </multi:speciesFeature>
          </multi:listOfSpeciesFeatures>
       </species>
       <species id="sp_EGFR_L_CR1" name="EGFR(L,CR1)" multi:speciesType="st_EGFR"
          hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
          <multi:listOfOutwardBindingSites>
             <multi:outwardBindingSite multi:component="L" multi:bindingStatus="unbound" />
             <multi:outwardBindingSite multi:component="CR1" multi:bindingStatus="unbound" />
          </multi:listOfOutwardBindingSites>
       </species>
       <species id="sp_EGFR_EGF_CR1" name="EGFR(L!1,CR1).EGF(R!1)" multi:speciesType="st_EGFR_EGF"
          hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
          <multi:listOfOutwardBindingSites>
             <multi:outwardBindingSite multi:component="CR1" multi:bindingStatus="unbound" />
          </multi:listOfOutwardBindingSites>
       </species>
       <species id="sp_EGFR_bL_CR1" name="EGFR(L!+,CR1)" multi:speciesType="st_EGFR"
```

```
            hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
            <multi:listOfOutwardBindingSites>
               <multi:outwardBindingSite multi:component="L" multi:bindingStatus="bound" />
               <multi:outwardBindingSite multi:component="CR1" multi:bindingStatus="unbound" />
            </multi:listOfOutwardBindingSites>
         </species>
         <species id="sp_EGFR_dimer_bL" name="EGFR(L!+,CR1!1).EGFR(L!+,CR1!1)"
            multi:speciesType="st_EGFR_dimer"
            hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
            <multi:listOfOutwardBindingSites>
               <multi:outwardBindingSite multi:component="EGFR1L"
                  multi:bindingStatus="bound" />
               <multi:outwardBindingSite multi:component="EGFR2L"
                  multi:bindingStatus="bound" />
            </multi:listOfOutwardBindingSites>
         </species>
         <species id="sp_EGFR_EGF_dimer" name="EGF(R!1).EGF(R!2).EGFR(L!1,CR1!3).EGFR(L!2,CR1!3)"
            multi:speciesType="st_EGFR_EGF_dimer" hasOnlySubstanceUnits="false"
            boundaryCondition="false"
            constant="false" />
         <species id="sp_EGFR_bCR1_Y1068_U" name="EGFR(CR1!+,Y1068~U)" multi:speciesType="st_EGFR"
            hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
            <multi:listOfOutwardBindingSites>
               <multi:outwardBindingSite multi:component="CR1" multi:bindingStatus="bound" />
               <multi:outwardBindingSite multi:component="Y1068" multi:bindingStatus="unbound" />
            </multi:listOfOutwardBindingSites>
            <multi:listOfSpeciesFeatures>
               <multi:speciesFeature multi:speciesFeatureType="sft_Y1068">
                  <multi:listOfSpeciesFeatureValues>
                     <multi:speciesFeatureValue multi:value="U" />
                  </multi:listOfSpeciesFeatureValues>
               </multi:speciesFeature>
            </multi:listOfSpeciesFeatures>
         </species>
         <species id="sp_EGFR_bCR1_Y1068_P" name="EGFR(CR1!+,Y1068~P)" multi:speciesType="st_EGFR"
            hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
            <multi:listOfOutwardBindingSites>
               <multi:outwardBindingSite multi:component="CR1" multi:bindingStatus="bound" />
               <multi:outwardBindingSite multi:component="Y1068" multi:bindingStatus="unbound" />
            </multi:listOfOutwardBindingSites>
            <multi:listOfSpeciesFeatures>
               <multi:speciesFeature multi:speciesFeatureType="sft_Y1068">
                  <multi:listOfSpeciesFeatureValues>
                     <multi:speciesFeatureValue multi:value="P" />
                  </multi:listOfSpeciesFeatureValues>
               </multi:speciesFeature>
            </multi:listOfSpeciesFeatures>
         </species>
         <species id="sp_EGFR_Y1068_P" name="EGFR(Y1068~P)" multi:speciesType="st_EGFR"
            hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
            <multi:listOfOutwardBindingSites>
               <multi:outwardBindingSite multi:component="Y1068" multi:bindingStatus="unbound" />
            </multi:listOfOutwardBindingSites>
            <multi:listOfSpeciesFeatures>
               <multi:speciesFeature multi:speciesFeatureType="sft_Y1068">
                  <multi:listOfSpeciesFeatureValues>
                     <multi:speciesFeatureValue multi:value="P" />
                  </multi:listOfSpeciesFeatureValues>
               </multi:speciesFeature>
            </multi:listOfSpeciesFeatures>
         </species>
         <species id="sp_EGFR_Y1068_U" name="EGFR(Y1068~U)" multi:speciesType="st_EGFR"
            hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
            <multi:listOfOutwardBindingSites>
               <multi:outwardBindingSite multi:component="Y1068" multi:bindingStatus="unbound" />
            </multi:listOfOutwardBindingSites>
```

```
            <multi:listOfSpeciesFeatures>
               <multi:speciesFeature multi:speciesFeatureType="sft_Y1068">
                  <multi:listOfSpeciesFeatureValues>
                     <multi:speciesFeatureValue multi:value="U" />
                  </multi:listOfSpeciesFeatureValues>
               </multi:speciesFeature>
            </multi:listOfSpeciesFeatures>
         </species>
         <species id="sp_EGFR_Grb2_P" name="EGFR(Y1068~P!1).Grb2(SH2!1)"
            multi:speciesType="st_EGFR_Grb2"
            hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
            <multi:listOfSpeciesFeatures>
               <multi:speciesFeature multi:speciesFeatureType="sft_Y1068">
                  <multi:listOfSpeciesFeatureValues>
                     <multi:speciesFeatureValue multi:value="P" />
                  </multi:listOfSpeciesFeatureValues>
               </multi:speciesFeature>
            </multi:listOfSpeciesFeatures>
         </species>
         <species id="sp_Grb2_Sos1" name="Grb2(SH3!1).Sos1(PxxP!1)" multi:speciesType="st_Grb2_Sos1"
            hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false" />

         <species id="sp_Trash" name="Trash()" multi:speciesType="st_Trash"
            hasOnlySubstanceUnits="false"
            boundaryCondition="false" constant="false" />
      </listOfSpecies>

      <!-- parameters -->
      <listOfParameters>
         <parameter id="NA" value="6.02e23" constant="true" units="molecules_per_mol" />
         <parameter id="f" value="1" constant="true" />
         <parameter id="kp1" constant="true" />
         <parameter id="km1" value="0.06" constant="true" />
         <parameter id="kp2" constant="true" />
         <parameter id="km2" value="0.1" constant="true" />
         <parameter id="kp3" value="0.5" constant="true" />
         <parameter id="km3" value="4.505" constant="true" />
         <parameter id="kp4" constant="true" />
         <parameter id="km4" value="0.05" constant="true" />
         <parameter id="kp5" constant="true" />
         <parameter id="km5" value="0.06" constant="true" />
         <parameter id="deg" value="0.01" constant="true" />
      </listOfParameters>

      <!-- intiialAssignments -->
      <listOfIntialAssignments>

         <initialAssignment symbol="Vo">
            <math xmls="http://www.w3.org/1998/Math/MathML">
               <apply>
                  <times />
                  <ci>f</ci>
                  <cn> 1e-10 </cn>
               </apply>
            </math>
         </initialAssignment>
         <initialAssignment symbol="V">
            <math xmls="http://www.w3.org/1998/Math/MathML">
               <apply>
                  <times />
                  <ci>f</ci>
                  <cn> 3e-12 </cn>
               </apply>
            </math>
         </initialAssignment>
         <initialAssignment symbol="kp1">
```

```
            <math xmls="http://www.w3.org/1998/Math/MathML">
               <apply>
                  <divide />
                  <cn>9.02e7</cn>
                  <apply>
                     <times />
                     <ci>NA</ci>
                     <ci>Vo</ci>
                  </apply>
               </apply>
            </math>
         </initialAssignment>
         <initialAssignment symbol="kp2">
            <math xmls="http://www.w3.org/1998/Math/MathML">
               <apply>
                  <divide />
                  <cn>1.0e7</cn>
                  <apply>
                     <times />
                     <ci>NA</ci>
                     <ci>V</ci>
                  </apply>
               </apply>
            </math>
         </initialAssignment>
         <initialAssignment symbol="kp4">
            <math xmls="http://www.w3.org/1998/Math/MathML">
               <apply>
                  <divide />
                  <cn>1.5e6</cn>
                  <apply>
                     <times />
                     <ci>NA</ci>
                     <ci>V</ci>
                  </apply>
               </apply>
            </math>
         </initialAssignment>
         <initialAssignment symbol="kp5">
            <math xmls="http://www.w3.org/1998/Math/MathML">
               <apply>
                  <divide />
                  <cn>1.0e7</cn>
                  <apply>
                     <times />
                     <ci>NA</ci>
                     <ci>V</ci>
                  </apply>
               </apply>
            </math>
         </initialAssignment>
         <initialAssignment symbol="sp_EGF_free">
            <math xmls="http://www.w3.org/1998/Math/MathML">
               <apply>
                  <times />
                  <cn>20</cn>
                  <cn>1e-9</cn>
                  <ci>NA</ci>
                  <ci>Vo</ci>
               </apply>
            </math>
         </initialAssignment>
         <initialAssignment symbol="sp_EGFR_free_U">
            <math xmls="http://www.w3.org/1998/Math/MathML">
               <apply>
                  <times />
```

```
                <ci>f</ci>
                <cn>1.8e5</cn>
             </apply>
          </math>
       </initialAssignment>
       <initialAssignment symbol="sp_Grb2_free">
          <math xmls="http://www.w3.org/1998/Math/MathML">
             <apply>
                <times />
                <ci>f</ci>
                <cn>1.5e5</cn>
             </apply>
          </math>
       </initialAssignment>
       <initialAssignment symbol="sp_Sos1_free">
          <math xmls="http://www.w3.org/1998/Math/MathML">
             <apply>
                <times />
                <ci>f</ci>
                <cn>6.2e4</cn>
             </apply>
          </math>
       </initialAssignment>
    </listOfIntialAssignments>

    <!-- reactions -->
    <listOfReactions>

       <!-- # Ligand-receptor binding -->
       <!-- 1 EGFR(L,CR1) + EGF(R) <-> EGFR(L!1,CR1).EGF(R!1) kp1, km1 -->
       <reaction id="rc_Ligand_receptor_binding" reversible="true" fast="false">
          <listOfReactants>
             <speciesReference species="sp_EGFR_L_CR1" constant="false" />
             <speciesReference species="sp_EGF_free" constant="false" />
          </listOfReactants>
          <listOfProducts>
             <speciesReference species="sp_EGFR_EGF_CR1" constant="false" />
          </listOfProducts>
          <kineticLaw>
             <math xmlns="http://www.w3.org/1998/Math/MathML">
                <apply>
                   <minus />
                   <apply>
                      <times />
                      <ci> kp1 </ci>
                      <ci> sp_EGFR_L_CR1 </ci>
                      <ci> sp_EGF_free </ci>
                   </apply>
                   <apply>
                      <times />
                      <ci> km1 </ci>
                      <ci> sp_EGFR_EGF_CR1 </ci>
                   </apply>
                </apply>
             </math>
          </kineticLaw>
       </reaction>

       <!-- # Receptor-aggregation -->
       <!-- 2 EGFR(L!+,CR1) + EGFR(L!+,CR1) <-> EGFR(L!+,CR1!1).EGFR(L!+,CR1!1) kp2,km2 -->
       <reaction id="rc_Receptor_aggregation" reversible="true" fast="false">
          <listOfReactants>
             <speciesReference species="sp_EGFR_bL_CR1" constant="false" stoichiometry="2" />
          </listOfReactants>
          <listOfProducts>
             <speciesReference species="sp_EGFR_dimer_bL" constant="false" />
```

```
            </listOfProducts>
            <kineticLaw>
               <math xmlns="http://www.w3.org/1998/Math/MathML">
                  <apply>
                     <minus />
                     <apply>
                        <times />
                        <ci> kp2 </ci>
                        <ci> sp_EGFR_bL_CR1 </ci>
                        <ci> sp_EGFR_bL_CR1 </ci>
                     </apply>
                     <apply>
                        <times />
                        <ci> km3 </ci>
                        <ci> sp_EGFR_dimer_bL </ci>
                     </apply>
                  </apply>
               </math>
            </kineticLaw>
         </reaction>

         <!-- # Transphosphorylation of EGFR by RTK -->
         <!-- 3 EGFR(CR1!+,Y1068~U) -> EGFR(CR1!+,Y1068~P) kp3 -->
         <reaction id="rc_Transphosphorylation" reversible="false" fast="false">
            <listOfReactants>
               <speciesReference species="sp_EGFR_bCR1_Y1068_U" constant="false" />
            </listOfReactants>
            <listOfProducts>
               <speciesReference species="sp_EGFR_bCR1_Y1068_P" constant="false" />
            </listOfProducts>
            <kineticLaw>
               <math xmlns="http://www.w3.org/1998/Math/MathML">
                  <apply>
                     <times />
                     <ci>kp3</ci>
                     <ci>sp_EGFR_bCR1_Y1068_U</ci>
                  </apply>
               </math>
            </kineticLaw>
         </reaction>

         <!-- # Dephosphorylation -->
         <!-- 4 EGFR(Y1068~P) -> EGFR(Y1068~U) km3 -->
         <reaction id="rc_Dephosphorylation" reversible="false" fast="false">
            <listOfReactants>
               <speciesReference species="sp_EGFR_Y1068_P" constant="false" />
            </listOfReactants>
            <listOfProducts>
               <speciesReference species="sp_EGFR_Y1068_U" constant="false" />
            </listOfProducts>
            <kineticLaw>
               <math xmlns="http://www.w3.org/1998/Math/MathML">
                  <apply>
                     <times />
                     <ci>km3</ci>
                     <ci>sp_EGFR_Y1068_P</ci>
                  </apply>
               </math>
            </kineticLaw>
         </reaction>

         <!-- # Grb2 binding to pY1068 -->
         <!-- 5 EGFR(Y1068~P) + Grb2(SH2) <-> EGFR(Y1068~P!1).Grb2(SH2!1) kp4,km4 -->
         <reaction id="rc_Grb2_binding_to_pY1068" reversible="true" fast="false">
            <listOfReactants>
               <speciesReference species="sp_EGFR_Y1068_P" constant="false" />
```

```
            <speciesReference species="sp_Grb2_SH2" constant="false" />
         </listOfReactants>
         <listOfProducts>
            <speciesReference species="sp_EGFR_Grb2_P" constant="false" />
         </listOfProducts>
         <kineticLaw>
            <math xmlns="http://www.w3.org/1998/Math/MathML">
               <apply>
                  <minus />
                  <apply>
                     <times />
                     <ci> kp4 </ci>
                     <ci> sp_EGFR_Y1068_P </ci>
                     <ci> sp_Grb2_SH2 </ci>
                  </apply>
                  <apply>
                     <times />
                     <ci> km4 </ci>
                     <ci> sp_EGFR_Grb2_P </ci>
                  </apply>
               </apply>
            </math>
         </kineticLaw>
      </reaction>

      <!-- # Grb2 binding to Sos1 -->
      <!-- 6 Grb2(SH3) + Sos1(PxxP) <-> Grb2(SH3!1).Sos1(PxxP!1) kp5,km5 -->
      <reaction id="rc_Grb2_binding_to_Sos1" reversible="true" fast="false">
         <listOfReactants>
            <speciesReference species="sp_Grb2_SH3" constant="false" />
            <speciesReference species="sp_Sos1_free" constant="false" />
         </listOfReactants>
         <listOfProducts>
            <speciesReference species="sp_Grb2_Sos1" constant="false" />
         </listOfProducts>
         <kineticLaw>
            <math xmlns="http://www.w3.org/1998/Math/MathML">
               <apply>
                  <minus />
                  <apply>
                     <times />
                     <ci> kp5 </ci>
                     <ci> sp_Grb2_SH3 </ci>
                     <ci> sp_Sos1_free </ci>
                  </apply>
                  <apply>
                     <times />
                     <ci> km5 </ci>
                     <ci> sp_Grb2_Sos1 </ci>
                  </apply>
               </apply>
            </math>
         </kineticLaw>
      </reaction>

      <!-- # Receptor dimer internalization/degradation -->
      <!-- 7 EGF(R!1).EGF(R!2).EGFR(L!1,CR1!3).EGFR(L!2,CR1!3) -> Trash() -->
      <reaction id="rc_EGFR_EGF_dimer_degration" reversible="false" fast="false">
         <listOfReactants>
            <speciesReference species="sp_EGFR_EGF_dimer" constant="false" />
         </listOfReactants>
         <listOfProducts>
            <speciesReference species="sp_Trash" constant="false" />
         </listOfProducts>
         <kineticLaw>
            <math xmlns="http://www.w3.org/1998/Math/MathML">
```

```
                  <apply>
                     <times />
                     <ci>deg</ci>
                     <ci>sp_EGFR_EGF_dimer</ci>
                  </apply>
               </math>
            </kineticLaw>
         </reaction>
      </listOfReactions>
   </model>
</sbml>
```

## 4.4 Example from *Kappa*'s documentation

Here is the example "An Introduction to Kappa Syntax" at *Kappa* website (http://www.kappalanguage.org/syntax.html).

Rule in English: "Unphosphorylated Site1 of A binds to Site1 of B"

Kappa Rule: A(Site1 u),B(Site1) -> A(Site1 u!1),B(Site1!1)

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

   <model name="An␣Introduction␣to␣Kappa␣Syntax">
      ...
      <!-- speciesType -->
      <multi:listOfSpeciesTypes>

         <!-- A:Site1 -->
         <multi:bindingSiteSpeciesType multi:id="st_A_Site1">
            <multi:listOfSpeciesFeatureTypes>
               <multi:speciesFeatureType multi:id="phosphorylation">
                  <multi:listOfPossibleSpeciesFeatureValues>
                     <multi:possibleSpeciesFeatureValue multi:id="U" />
                     <multi:possibleSpeciesFeatureValue multi:id="P" />
                  </multi:listOfPossibleSpeciesFeatureValues>
               </multi:speciesFeatureType>
            </multi:listOfSpeciesFeatureTypes>
         </multi:bindingSiteSpeciesType>

         <!-- A -->
         <multi:speciesType multi:id="st_A">
            <multi:listOfSpeciesTypeInstances>
               <multi:speciesTypeInstance multi:id="Asite1" multi:speciesType="st_A_Site1" />
            </multi:listOfSpeciesTypeInstances>
         </multi:speciesType>

         <!-- B:Site1 -->
         <multi:bindingSiteSpeciesType multi:id="st_B_Site1" />

         <!-- B -->
         <multi:speciesType multi:id="st_B">
            <multi:listOfSpeciesTypeInstances>
               <multi:speciesTypeInstance multi:id="Bsite1" multi:speciesType="st_B_Site1" />
            </multi:listOfSpeciesTypeInstances>
         </multi:speciesType>

         <!-- A.B -->
         <multi:speciesType multi:id="st_AB">
            <multi:listOfSpeciesTypeInstances>
               <multi:speciesTypeInstance multi:id="A" multi:speciesType="st_A" />
               <multi:speciesTypeInstance multi:id="B" multi:speciesType="st_B" />
```

```
            </multi:listOfSpeciesTypeInstances>
            <multi:listOfInSpeciesTypeBonds>
               <multi:inSpeciesTypeBond multi:bindingSite1="Asite1"
                  multi:bindingSite2="Bsite1" />
            </multi:listOfInSpeciesTypeBonds>
         </multi:speciesType>
         ...
      </multi:listOfSpeciesTypes>

      <!-- species -->
      <listOfSpecies>
         <!-- species A with free unphosphorylated Site1 -->
         <species id="sp_A" name="A␣with␣Unphosphorylated␣Site␣1" multi:speciesType="st_A"
            hasOnlySubstanceUnits="false" boundaryCondition="false" constant="false">
            <multi:listOfOutwardBindingSites>
               <multi:outwardBindingSite multi:component="Asite1"
                  multi:bindingStatus="unbound" />
            </multi:listOfOutwardBindingSites>
            <multi:listOfSpeciesFeatures>
               <multi:speciesFeature multi:speciesFeatureType="phosphorylation">
                  <multi:listOfSpeciesFeatureValues>
                     <multi:speciesFeatureValue multi:value="U" />
                  </multi:listOfSpeciesFeatureValues>
               </multi:speciesFeature>
            </multi:listOfSpeciesFeatures>
         </species>

         <!-- species B with free Site 1 -->
         <species id="sp_B" name="B" multi:speciesType="st_B" hasOnlySubstanceUnits="false"
            boundaryCondition="false" constant="false">
            <multi:listOfOutwardBindingSites>
               <multi:outwardBindingSite multi:component="sti_B_Site1"
                  multi:bindingStatus="unbound" />
            </multi:listOfOutwardBindingSites>
         </species>

         <!-- species AB: unphosphorylated -->
         <species id="sp_AB" name="AB" multi:speciesType="st_AB" hasOnlySubstanceUnits="false"
            boundaryCondition="false" constant="false">
            <multi:listOfSpeciesFeatures>
               <multi:speciesFeature multi:speciesFeatureType="phosphorylation">
                  <multi:listOfSpeciesFeatureValues>
                     <multi:speciesFeatureValue multi:value="U" />
                  </multi:listOfSpeciesFeatureValues>
               </multi:speciesFeature>
            </multi:listOfSpeciesFeatures>
         </species>
         ...
      </listOfSpecies>

      <!-- reactions -->
      <listOfReactions>

         <!-- Unphosphorylated Site1 of A binds to Site1 of B -->
         <!-- Kappa Rule: A(Site1~u),B(Site1) -> A(Site1~u!1),B(Site1!1) -->
         <reaction id="rc_AB" reversible="false" fast="false">
            <listOfReactants>
               <speciesReference species="sp_A" constant="false" />
               <speciesReference species="sp_B" constant="false" />
            </listOfReactants>
            <listOfProducts>
               <speciesReference species="sp_AB" constant="false" />
            </listOfProducts>
            <kineticLaw>
               ...
            </kineticLaw>
```

```
        </reaction>
        ...
      </listOfReactions>
   </model>
</sbml>
```

# A Validation of SBML documents using Multi constructs

☞ *Note:*
*The whole validation section is new in this version of the specification of the Multi package.*

This section summarizes all the conditions that should be true of an SBML Level 3 Version 1 model that uses the Multi package. We use the same conventions that are used in the SBML Level 3 Version 1 Core specification document. In particular, there are different degrees of rule strictness. Formally, the differences are expressed in the statement of a rule: either a rule states that a condition *must* be true, or a rule states that it *should* be true. Rules of the former kind are strict SBML validation rules—a model encoded in SBML must conform to all of them in order to be considered valid. Rules of the latter kind are consistency rules. To help highlight these differences, we use the three symbols (☑ - `requirement`, ▲ - `recommendation`, and ★ - `strong recommendation`) next to the rule numbers as described in section A of the SBML Level 3 Version 1 Core specification document.

The validation rules listed in the following subsections are all stated or implied in the rest of this specification document. They are enumerated here for convenience. Unless explicitly stated, all validation rules concern objects and attributes specifically defined in the Multi package.

☞ For convenience and brevity, we use the shorthand "`multi:x`" to stand for an attribute or element name `x` in the namespace for the Multi package, using the namespace prefix `multi`. We use "`multi:x`" because it is shorter than to write a full explanation everywhere we refer to an attribute or element in the Multi package namespace.

## General rules about the Multi package

**multi-10101** ☑ To conform to Version 1 of the Multi package specification for SBML Level 3, an SBML document must declare the use of the following XML Namespace: "`http://www.sbml.org/sbml/level3/version1/multi/version1`". (References: SBML Level 3 Package Specification for Multi Version 1, Section 3.1 on page 8.)

**multi-10102** ☑ Wherever they appear in an SBML document, elements and attributes from the Multi package must be declared either implicitly or explicitly to be in the XML namespace "`http://www.sbml.org/sbml/level3/version1/multi/version1`". (References: SBML Level 3 Package Specification for Multi Version 1, Section 3.1 on page 8.)

**multi-10103** ☑ The `multi:required` attribute is required on the <sbml> element in the Multi package. (References: SBML Level 3 Package Specification for Multi Version 1, Section 3.1 on page 8.)

**multi-10104** ☑ The `multi:required` attribute on the <sbml> element must be `Boolean`. (References: SBML Level 3 Package Specification for Multi Version 1, Section 3.1 on page 8.)

**multi-10105** ☑ The value of the `multi:required` attribute on the <sbml> element must be "`true`". (References: SBML Level 3 Package Specification for Multi Version 1, Section 3.1 on page 8.)

## General rules about identifiers

**multi-10301** ☑ (Extends validation rule #10301 in the SBML Level 3 Version 1 Core specification.) Within a **Model** object, the values of the attributes `id` and `multi:id` on every instance of the following classes of objects must be unique across the set of all `id` and `multi:id` attribute values of all such objects in a model: the **Model** itself, plus all contained **FunctionDefinition**, **Compartment**, **Species**, **Reaction**, **SpeciesReference**, **ModifierSpeciesReference**, **Event**, and **Parameter** objects, plus the **SpeciesType** and **PossibleSpeciesFeatureValue** objects defined by the Multi package, and any objects defined by any other package with `package:id` attributes defined as falling in the 'SId' namespace. (References: Section 3.28 on page 44.)

**multi-10302** ☑ The value of a `multi:id` attribute must always conform to the syntax of the SBML data type

`SId`. (References: SBML Level 3 Version 1 Core, Section 3.1.7.)

**multi-10303** ☑ The value of a `multi:name` attribute must always conform to the syntax of type `string`. (References: SBML Level 3 Version 1 Core, Section 3.1.1.)

**multi-10401** ☑ The value of a `multi:id` attribute on **SpeciesTypeInstance** objects must be unique across the set of all `multi:id` attribute values of all the **SpeciesTypeInstance** objects under the direct parent **SpeciesType** object in which it is located. (References: Section 3.11.1 on page 17 and Section 3.28 on page 44.)

**multi-10402** ☑ The value of a `multi:id` attribute on **SpeciesTypeComponentIndex** objects must be unique across the set of all `multi:id` attribute values of all the **SpeciesTypeComponentIndex** objects under the direct parent **SpeciesType** object in which it is located. (References: Section 3.12.1 on page 19 and Section 3.28 on page 44.)

**multi-10403** ☑ The value of a `multi:id` attribute on **InSpeciesTypeBond** objects must be unique across the set of all `multi:id` attribute values of all the **InSpeciesTypeBond** objects under the direct parent **SpeciesType** object in which it is located. (References: Section 3.13.1 on page 21 and Section 3.28 on page 44.)

**multi-10404** ☑ The value of a `multi:id` attribute on **SpeciesFeatureType** objects must be unique across the set of all `multi:id` attribute values of all the **SpeciesFeatureType** objects under the direct parent **SpeciesType** object in which it is located. (References: Section 3.9.1 on page 15 and Section 3.28 on page 44.)

**multi-10405** ☑ The value of a `multi:id` attribute on **SubListOfSpeciesFeatures** objects must be unique across the set of all `id` and `multi:id` attribute values of all objects in the **Species** object in which it is located. (References: Section 3.17.1 on page 28 and Section 3.28 on page 44.)

**multi-10406** ☑ The value of a `multi:id` attribute on **SpeciesFeature** objects must be unique across the set of all `id` and `multi:id` attribute values of all objects in the **Species** object in which it is located. (References: Section 3.18.1 on page 28 and Section 3.28 on page 44.)

**multi-10407** ☑ The value of a `multi:id` attribute on **SpeciesFeatureChange** objects must be unique across the set of all `multi:id` attribute values of all objects in the **SpeciesTypeComponentMapInProduct** object in which it is located. (References: Section 3.25.1 on page 38 and Section 3.28 on page 44.)

**multi-10408** ☑ The value of a `multi:id` attribute on **CompartmentReference** objects must be unique across the set of all `id` and `multi:id` attribute values of all objects in the **Compartment** object in which it is located. (References: Section 3.6.1 on page 12 and Section 3.28 on page 44.)

**multi-10501** ☑ The value of a `multi:compartment` attribute on **SpeciesType** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.8.2 on page 13.)

**multi-10502** ☑ The value of a `multi:numericValue` attribute on **PossibleSpeciesFeatureValue** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.10.2 on page 16.)

**multi-10503** ☑ The value of a `multi:speciesType` attribute on **SpeciesTypeInstance** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.11.2 on page 17.)

**multi-10504** ☑ The value of a `multi:compartmentReference` attribute on **SpeciesTypeInstance** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.11.3 on page 17.)

**multi-10505** ☑ The value of a `multi:component` attribute on **SpeciesTypeComponentIndex** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.12.2 on page 19.)

**multi-10506** ☑ The value of a `multi:identifyingParent` attribute on **SpeciesTypeComponentIndex** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.12.3 on page 19.)

**multi-10508** ☑ The value of a `multi:bindingSite1` attribute on **InSpeciesTypeBond** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.13.2 on page 21.)

**multi-10509** ☑ The value of a `multi:bindingSite2` attribute on **InSpeciesTypeBond** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.13.2 on page 21.)

**multi-10601** ☑ The value of a `multi:speciesType` attribute on **Species** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.15.1 on page 24.)

**multi-10602** ☑ The value of a `multi:component` attribute on **OutwardBindingSite** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.16.2 on page 26.)

**multi-10603** ☑ The value of a `multi:speciesFeatureType` attribute on **SpeciesFeature** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.18.2 on page 28.)

**multi-10604** ☑ The value of a `multi:component` attribute on **SpeciesFeature** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.18.4 on page 29.)

**multi-10605** ☑ The value of a `multi:value` attribute on **SpeciesFeatureValue** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.18.6 on page 29.)

**multi-10701** ☑ The value of a `multi:compartmentReference` attribute on **SimpleSpeciesReference** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.22 on page 35.)

**multi-10702** ☑ The value of a `multi:reactant` attribute on **SpeciesTypeComponentMapInProduct** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.24.1 on page 37.)

**multi-10703** ☑ The value of a `multi:reactantComponent` attribute on **SpeciesTypeComponentMapInProduct** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.24.2 on page 37.)

**multi-10704** ☑ The value of a `multi:productComponent` attribute on **SpeciesTypeComponentMapInProduct** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.24.3 on page 37.)

**multi-10705** ☑ The value of a `multi:reactantSpeciesFeature` attribute on **SpeciesFeatureChange** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.25.2 on page 38.)

**multi-10706** ☑ The value of a `multi:productSpeciesFeature` attribute on **SpeciesFeatureChange** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.25.3 on page 38.)

**multi-10801** ☑ The value of a `multi:compartmentType` attribute on **Compartment** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.5.2 on page 11.)

**multi-10802** ☑ The value of a `multi:compartment` attribute on **CompartmentReference** objects must conform to the syntax of the SBML data type `SIdRef`. (References: Section 3.6.2 on page 12.)

## Rules for extended Model objects

**multi-20101** ☑ There may be at most one **ListOfSpeciesTypes** container object within a **Model** object. (References: Section 3.4 on page 10.)

**multi-20102** ☑ A **ListOfSpeciesTypes** object within an extended **Model** object is optional, but if present, must not be empty. (References: Section 3.4 on page 10.)

**multi-20103** ☑ A **ListOfSpeciesTypes** object may have the optional SBML core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace or the Multi namespace are permitted on a **ListOfSpeciesTypes** object. (References: Section 3.4.1 on page 10.)

**multi-20104** ☑ Apart from the general `notes` and `annotation` subobjects permitted on all SBML objects, a **ListOfSpeciesTypes** container object may only contain **SpeciesType** objects. (References: Section 3.4.1 on page 10.)

## Rules for extended Compartment objects

**multi-20201** ☑ An extended **Compartment** object must have the required attribute `multi:isType`, and may also have the optional attribute `multi:comparetmentType`. No other attributes from the Multi namespace are permitted on an extended **Compartment** object.(References: Section 3.5 on page 11.)

**multi-20202** ☑ The value of a `multi:isType` attribute on an extended **Compartment** object must always confirm to the syntax of the SBML data type `boolean`. (References: Section 3.5.1 on page 11.)

**multi-20203** ☑ The `multi:isType` attribute on an extended **Compartment** object is required. (References: Section 3.5.1 on page 11.)

**multi-20204** ☑ The value of the `multi:isType` attribute of the **Compartment** object referenced by a **CompartmentReference** object must be the same as that of the `multi:isType` attribute of the parent **Compartment** object of the **ListOfCompartmentReferences** object which contains the **CompartmentReference** object. (References: Section 3.7 on page 12.)

**multi-20205** ☑ The `multi:compartmentType` attribute on a **Compartment** object must not be defined if the value of the `multi:isType` is "`true`". (References: Section 3.5.2 on page 11.)

**multi-20206** ☑ There may be at most one **ListOfCompartmentReferences** container object within a **Compartment** object. (References: Section 3.5.3 on page 11.)

**multi-20207** ☑ A **ListOfCompartmentReferences** object within a **Compartment** object is optional, but if present, must not be empty. (References: Section 3.5.3 on page 11.)

**multi-20208** ☑ A **ListOfCompartmentReferences** object may have the optional SBML core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace or the Multi namespace are permitted on a **ListOfCompartmentReferences** object. (References: Section 3.5.3 on page 11.)

**multi-20209** ☑ Apart from the general `notes` and `annotation` subobjects permitted on all SBML objects, a **ListOfCompartmentReferences** container object may only contain **CompartmentReference** objects. (References: Section 3.5.3 on page 11.)

## Rules for CompartmentReference objects

**multi-20301** ☑ A **CompartmentReference** object may have the optional SBML Level 3 Core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace are permitted on a **CompartmentReference** object. (References: Section 3.6 on page 12).

**multi-20302** ☑ A **CompartmentReference** object may have the optional SBML Level 3 Core subobjects for `notes` and `annotation`. No other elements from the SBML Level 3 Core namespace are permitted on a **CompartmentReference** object. (References: Section 3.6 on page 12).

**multi-20303** ☑ A **CompartmentReference** object must have the required attribute `multi:compartment`, and may have the optional attributes `multi:id` and `multi:name`. No other attributes from the Multi namespace are permitted on a **CompartmentReference** object. (References: Section 3.6 on page 12.)

**multi-20304** ☑ The value of the `multi:compartment` attribute must be the value of an `id` attribute on an existing **Compartment** object in the `SId` namespace of the parent **Model**. (References: Section 3.6 on page 12.)

**multi-20305** ☑ If some or all **CompartmentReference** objects within a **ListOfCompartmentReferences** object reference the same **Compartment** object, those `compartmentReferences` are required to have its `multi:id` attribute defined. (References: Section 3.6.1 on page 12.)

## Rules for SpeciesType objects

**multi-20401** ☑ A **SpeciesType** object may have the optional SBML Level 3 Core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace are permitted on a **SpeciesType** object. (References: Section 3.8 on page 13).

**multi-20402** ☑ A **SpeciesType** object may have the optional SBML Level 3 Core subobjects for `notes` and `annotation`. No other elements from the SBML Level 3 Core namespace are permitted on a **SpeciesType** object. (References: Section 3.8 on page 13).

**multi-20403** ☑ A **SpeciesType** object must have the required attribute `multi:id`, and may have the optional attributes `multi:name` and `multi:compartment`. No other attributes from the Multi namespace are permitted on a **SpeciesType** object. (References: Section 3.8 on page 13.)

**multi-20404** ☑ The value of the `multi:compartment` attribute, if set on a given **SpeciesType** object, must be the value of an `id` attribute on an existing **Compartment** object in the `SId` namespace of the parent **Model** object. (References: Section 3.8.2 on page 13.)

**multi-20405** ☑ The various **ListOf**___ subobjects within a **SpeciesType** object are optional, but if present, these container objects must not be empty. Specifically, if any of the following classes of objects are present with a **SpeciesType** object, it must not be empty: **ListOfSpeciesFeatureTypes**, **ListOfSpeciesTypeInstances**, **ListOfSpeciesTypeComponentIndexes** and **ListOfInSpeciesTypeBonds**. (References: Section 3.8 on page 13.)

**multi-20406** ☑ There may be at most one **ListOfSpeciesFeatureTypes** container object within a **SpeciesType** object. (References: Section 3.8 on page 13.)

**multi-20407** ☑ Apart from the general `notes` and `annotation` subobjects permitted on all SBML objects, a **ListOfSpeciesFeatureTypes** container object may only contain **SpeciesFeatureType** objects. (References: Section 3.8.3 on page 14.)

**multi-20408** ☑ A **ListOfSpeciesFeatureTypes** object may have the optional SBML core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace or the Multi namespace are permitted on a **ListOfSpeciesFeatureTypes** object. (References: Section 3.8.3 on page 14.)

**multi-20409** ☑ There may be at most one **ListOfSpeciesTypeInstances** container object within a **SpeciesType** object. (References: Section 3.8 on page 13.)

**multi-20410** ☑ Apart from the general `notes` and `annotation` subobjects permitted on all SBML objects, a **ListOfSpeciesTypeInstances** container object may only contain **SpeciesTypeInstance** objects. (References: Section 3.8.4 on page 14.)

**multi-20411** ☑ A **ListOfSpeciesTypeInstances** object may have the optional SBML core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace or the Multi namespace are permitted on a **ListOfSpeciesTypeInstances**. (References: Section 3.8.4 on page 14.)

**multi-20412** ☑ There may be at most one **ListOfSpeciesTypeComponentIndexes** container object within a **SpeciesType** object. (References: Section 3.8 on page 13.)

**multi-20413** ☑ Apart from the general `notes` and `annotation` subobjects permitted on all SBML objects, a **ListOfSpeciesTypeComponentIndexes** container object may only contain **SpeciesTypeComponentIndex** objects. (References: Section 3.8.6 on page 14.)

**multi-20414** ☑ A **ListOfSpeciesTypeComponentIndexes** object may have the optional SBML core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace or the Multi namespace are permitted on a **ListOfSpeciesTypeComponentIndexes** object. (References: Section 3.8.6 on page 14.)

**multi-20415** ☑ There may be at most one **ListOfInSpeciesTypeBonds** container object within a **SpeciesType** object. (References: Section 3.8 on page 13.)

**multi-20416** ☑ Apart from the general `notes` and `annotation` subobjects permitted on all SBML objects, a **ListOfInSpeciesTypeBonds** container object may only contain **InSpeciesTypeBond** objects. (References: Section 3.8.5 on page 14.)

**multi-20417** ☑ A **ListOfInSpeciesTypeBonds** object may have the optional SBML core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace or the Multi namespace are permitted on a **ListOfInSpeciesTypeBonds** object. (References: Section 3.8.5 on page 14.)

## Rules for BindingSiteSpeciesType objects

**multi-20501** ☑ A **BindingSiteSpeciesType** object is not permitted to have any **ListOfSpeciesTypeInstances** subobject. (References: Section 3.8.7 on page 14).

## Rules for SpeciesFeatureType objects

**multi-20601** ☑ A **SpeciesFeatureType** object may have the optional SBML Level 3 Core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace are permitted on a **SpeciesFeatureType** object. (References: Section 3.9 on page 15).

**multi-20602** ☑ A **SpeciesFeatureType** object may have the optional SBML Level 3 Core subobjects for `notes` and `annotation`. No other elements from the SBML Level 3 Core namespace are permitted on a **SpeciesFeatureType** object. (References: Section 3.9 on page 15).

**multi-20603** ☑ A **SpeciesFeatureType** object must have the required attributes `multi:id` and `multi:occur`, and may have the optional attribute `multi:name`. No other attributes from the Multi namespace are permitted on a **SpeciesFeatureType** object. (References: Section 3.9 on page 15.)

**multi-20604** ☑ The value of the `multi:occur` attribute on a given **SpeciesFeatureType** object must conform to the syntax of the SBML data type `positiveInteger`. (References: Section 3.9.2 on page 15.)

**multi-20605** ☑ One **ListOfPossibleSpeciesFeatureValues** subobject in a **SpeciesFeatureType** object is required. (References: Section 3.9.3 on page 15.)

**multi-20606** ☑ A **ListOfPossibleSpeciesFeatureValues** object may have the optional SBML core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace or the Multi namespace are permitted on a **ListOfPossibleSpeciesFeatureValues** object. (References: Section 3.9.3 on page 15.)

**multi-20607** ☑ Apart from the general `notes` and `annotation` subobjects permitted on all SBML objects, a **ListOfPossibleSpeciesFeatureValues** container object may only contain **PossibleSpeciesFeatureValue** objects. (References: Section 3.9.3 on page 15.)

**multi-20608** ☑ A **ListOfPossibleSpeciesFeatureValues** object must not be empty. (References: Section 3.9.3 on page 15.)

## Rules for PossibleSpeciesFeatureValue objects

**multi-20701** ☑ A **PossibleSpeciesFeatureValue** object may have the optional SBML Level 3 Core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace are permitted on a **PossibleSpeciesFeatureValue** object. (References: Section 3.10 on page 16).

**multi-20702** ☑ A **PossibleSpeciesFeatureValue** object may have the optional SBML Level 3 Core subobjects for `notes` and `annotation`. No other elements from the SBML Level 3 Core namespace are permitted on a **PossibleSpeciesFeatureValue** object. (References: Section 3.10 on page 16).

**multi-20703** ☑ A **PossibleSpeciesFeatureValue** object must have the required attribute `multi:id`, and may have the optional attributes `multi:name` and `multi:numericValue`. No other attributes from the Multi namespace are permitted on a **PossibleSpeciesFeatureValue** object. (References: Section 3.10 on page 16.)

**multi-20704** ☑ The value of the `multi:numericValue` attribute on a given **PossibleSpeciesFeatureValue** object must be the identifier of a **Parameter** object defined in the same **Model** object. (References: Section 3.10.2 on page 16.)

## Rules for SpeciesTypeInstance objects

**multi-20801** ☑ A **SpeciesTypeInstance** object may have the optional SBML Level 3 Core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace are permitted on a **SpeciesTypeInstance** object. (References: Section 3.11 on page 17).

**multi-20802** ☑ A **SpeciesTypeInstance** object may have the optional SBML Level 3 Core subobjects for `notes` and `annotation`. No other elements from the SBML Level 3 Core namespace are permitted on a **SpeciesTypeInstance** object. (References: Section 3.11 on page 17).

**multi-20803** ☑ A **SpeciesTypeInstance** object must have the required attributes `multi:id` and `multi:speciesType`, and may have the optional attributes `multi:name` and `multi:compartmentReference`. No other attributes from the Multi namespace are permitted on a **SpeciesTypeInstance** object. (References: Section 3.11 on page 17.)

**multi-20805** ☑ The value of the `multi:speciesType` attribute on a given **SpeciesTypeInstance** object must be the identifier of a **SpeciesType** object defined in the same **Model** object. (References: Section 3.11.2 on page 17.)

**multi-20806** ☑ The value of the `multi:compartmentReference` attribute, if present on a given **SpeciesTypeInstance** object, must be the identifier of a **CompartmentReference** object defined in the same **Model** object. (References: Section 3.11.3 on page 17.)

## Rules for SpeciesTypeComponentIndex objects

**multi-20901** ☑ A **SpeciesTypeComponentIndex** object may have the optional SBML Level 3 Core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace are permitted on a **SpeciesTypeComponentIndex** object. (References: Section 3.12 on page 19).

**multi-20902** ☑ A **SpeciesTypeComponentIndex** object may have the optional SBML Level 3 Core subobjects for `notes` and `annotation`. No other elements from the SBML Level 3 Core namespace are permitted on a **SpeciesTypeComponentIndex** object. (References: Section 3.12 on page 19).

**multi-20903** ☑ A **SpeciesTypeComponentIndex** object must have the required attributes `multi:id` and `multi:compartment`, and may have the optional attribute `multi:identifyingParent`. No other attributes from the Multi namespace are permitted on a **SpeciesTypeComponentIndex** object. (References: Section 3.12 on page 19.)

**multi-20904** ☑ The value of the `multi:component` attribute on a given **SpeciesTypeComponentIndex** object must be the identifier of a **SpeciesTypeInstance** object, or a **SpeciesTypeComponentIndex** object under the **SpeciesType** object that this **SpeciesTypeComponentIndex** object belongs to, or the **SpeciesType** object itself. (References: Section 3.12.2 on page 19.)

**multi-20907** ☑ The value of the `multi:identifyingParent` attribute on a given **SpeciesTypeComponentIndex** object must be the identifier of a `component` object under the **SpeciesType** object that this **SpeciesTypeComponentIndex** object belongs to. A `component` object can be an object of **SpeciesTypeInstance**, **SpeciesTypeComponentIndex** or **SpeciesType**. (References: Section 3.12.3 on page 19.)

## Rules for InSpeciesTypeBond objects

**multi-21101** ☑ An **InSpeciesTypeBond** object may have the optional SBML Level 3 Core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace are permitted on an **InSpeciesTypeBond** object. (References: Section 3.13 on page 21).

**multi-21102** ☑ An **InSpeciesTypeBond** object may have the optional SBML Level 3 Core subobjects for `notes` and `annotation`. No other elements from the SBML Level 3 Core namespace are permitted on an **InSpeciesTypeBond** object. (References: Section 3.13 on page 21).

**multi-21103** ☑ An **InSpeciesTypeBond** object must have the required attributes, `multi:bindingSite1` and `multi:bindingSite2`, and may have the optional attributes, `multi:id` and `multi:name`. No other attributes from the Multi namespace are permitted on an **InSpeciesTypeBond** object. (References: Section 3.13 on page 21.)

**multi-21104** ☑ The value of the `multi:bindingSite1` attribute on a given **InSpeciesTypeBond** object must be the identifier of a **SpeciesTypeInstance** object or **SpeciesTypeComponentIndex** which ultimately reference a object of **BindingSiteSpeciesType**. (References: Section 3.13.2 on page 21.)

**multi-21105** ☑ The value of the `multi:bindingSite2` attribute on a given **InSpeciesTypeBond** object must be the identifier of a **SpeciesTypeInstance** object or **SpeciesTypeComponentIndex** which ultimately reference a object of **BindingSiteSpeciesType**. (References: Section 3.13.2 on page 21.)

**multi-21106** ☑ The `multi:bindingSite1` and `multi:bindingSite2` attributes must not reference the same **BindingSiteSpeciesType** object. (References: Section 3.13.2 on page 21.)

## Rules for extended Species objects

**multi-21201** ☑ A **Species** object may have the optional attribute, `multi:speciesType`. No other attributes from the Multi namespace are permitted on a **Species** object. (References: Section 3.15 on page 24.)

**multi-21202** ☑ The value of a `multi:speciesType` attribute, if present on a **Species** object, must be the identifier of a **SpeciesType** object. (References: Section 3.15.1 on page 24.)

**multi-21203** ☑ Two **ListOf**__ subobjects with a **Species** object are optional, but if present, these container object must not be empty. Specifically, if any of the following two classes of objects are present on the **Species** object, it must not be empty: **ListOfOutwardBindingSites** and **ListOfSpeciesFeatures**. (References: Section 3.15 on page 24.)

**multi-21204** ☑ A **ListOfOutwardBindingSites** object may have the optional SBML core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace or the Multi namespace are permitted on a **ListOfOutwardBindingSites** object. (References: Section 3.15.2 on page 24.)

**multi-21205** ☑ Apart from the general `notes` and `annotation` subobjects permitted on all SBML objects, a **ListOfOutwardBindingSites** container object may only contain **OutwardBindingSite** objects. (References: Section 3.15.2 on page 24.)

**multi-21206** ☑ A **ListOfSpeciesFeatures** object may have the optional SBML core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace or the Multi namespace are permitted on a **ListOfSpeciesFeatures** object. (References: Section 3.15.3 on page 25.)

**multi-21207** ☑ A **SubListOfSpeciesFeatures** object may have the optional attributes `multi:id`, `multi:relation` and `multi:component`. No other attributes from the Multi namespace are permitted on a **SubListOfSpeciesFeatures** object. (References: Section 3.17 on page 27.)

**multi-21208** ☑ The value of the `multi:relation` attribute, if presented on a **SubListOfSpeciesFeatures** object, must conform to the syntax of the Multi data type **`Relation`**. (References: Section 3.17.2 on page 28.)

**multi-21209** ☑ Apart from the general `notes` and `annotation` subobjects permitted on all SBML objects, a **ListOfSpeciesFeatures** container object may only contain **SpeciesFeature** and/or **SubListOfSpeciesFeatures** objects. (References: Section 3.15.3 on page 25.)

**multi-21210** ☑ A **SubListOfSpeciesFeatures** object may have the optional SBML core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace are permitted on a **SubListOfSpeciesFeatures** object. (References: Section 3.17 on page 27.)

**multi-21211** ☑ Apart from the general `notes` and `annotation` subobjects permitted on all SBML objects, a **SubListOfSpeciesFeatures** container object may only contain **SpeciesFeature** objects. (References: Section 3.17 on page 27.)

**multi-21212** ☑ The value of the `multi:component` attribute on a given **SubListOfSpeciesFeatures** object must be the identifier of an object of **SpeciesTypeInstance**, **SpeciesTypeComponentIndex** or **SpeciesType** which contains the **SpeciesFeature** objects in this `subListOfSpeciesFeatures`. (References: Section 3.17.3 on page 28.)

## Rules for OutwardBindingSite objects

**multi-21301** ☑ An **OutwardBindingSite** object may have the optional SBML Level 3 Core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace are permitted on an **OutwardBindingSite** object. (References: Section 3.16 on page 26).

**multi-21302** ☑ An **OutwardBindingSite** object may have the optional SBML Level 3 Core subobjects for `notes` and `annotation`. No other elements from the SBML Level 3 Core namespace are permitted on an **OutwardBindingSite** object. (References: Section 3.16 on page 26).

**multi-21303** ☑ An **OutwardBindingSite** object must have the required attributes, `multi:bindingStatus` and `multi:component`. No other attributes from the Multi namespace are permitted on an **OutwardBindingSite** object. (References: Section 3.16 on page 26.)

**multi-21304** ☑ The value of the `multi:bindingStatus` attribute on a given **OutwardBindingSite** object must confirm to the syntax of the Multi data type `BindingStatus`. (References: Section 3.16.1 on page 26.)

**multi-21305** ☑ The value of the `multi:component` attribute on a given **OutwardBindingSite** object must be the identifier of an object of **SpeciesTypeInstance**, **SpeciesTypeComponentIndex** or **SpeciesType** which ultimately reference an object of **BindingSiteSpeciesType**. (References: Section 3.16.2 on page 26.)

## Rules for SpeciesFeature objects

**multi-21401** ☑ A **SpeciesFeature** object may have the optional SBML Level 3 Core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace are permitted on a **SpeciesFeature** object. (References: Section 3.18 on page 28).

**multi-21402** ☑ A **SpeciesFeature** object may have the optional SBML Level 3 Core subobjects for `notes` and `annotation`. No other elements from the SBML Level 3 Core namespace are permitted on a **SpeciesFeature** object. (References: Section 3.18 on page 28).

**multi-21403** ☑ A **SpeciesFeature** object must have the required attributes, `multi:speciesFeatureType` and `multi:occur`, and may have the optional attributes, `multi:id` and `multi:component`. No other attributes from the Multi namespace are permitted on a **SpeciesFeature** object. (References: Section 3.18 on page 28.)

**multi-21404** ☑ The value of the `multi:speciesFeatureType` attribute on a given **SpeciesFeature** object must be the identifier of a **SpeciesFeatureType** object which is in the **SpeciesType** object referenced by the **Species** object containing this **SpeciesFeature** object. (References: Section 3.18.2 on page 28.)

**multi-21405** ☑ The value of the `multi:occur` attribute on a given **SpeciesFeature** object must conform to the syntax of the SBML data type `positiveInteger`. The value of the `multi:occur` attribute must not be larger than that of the `multi:occur` attribute of the **SpeciesFeatureType** object referenced by this **SpeciesFeature** object. (References: Section 3.18.3 on page 29.)

**multi-21406** ☑ The value of the `multi:component` attribute on a given **SpeciesFeature** object must be the identifier of an object of **SpeciesTypeInstance**, **SpeciesTypeComponentIndex** or **SpeciesType** which contains this **SpeciesFeature** object. (References: Section 3.18.4 on page 29.)

**multi-21407** ☑ One and only one **ListOfSpeciesFeatureValues** subobject within a **SpeciesFeature** object is required. (References: Section 3.18.5 on page 29.)

**multi-21408** ☑ A **ListOfSpeciesFeatureValues** object must not be empty. (References: Section 3.18.5 on page 29.)

**multi-21409** ☑ A **ListOfSpeciesFeatureValues** object may have the optional SBML core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace or the Multi namespace are permitted on a **ListOfSpeciesFeatureValues** object. (References: Section 3.18.5 on page 29.)

**multi-21410** ☑ Apart from the general `notes` and `annotation` subobjects permitted on all SBML objects, a **ListOfSpeciesFeatureValues** container object may only contain **SpeciesFeatureValue** objects. (References: Section 3.18.5 on page 29.)

## Rules for SpeciesFeatureValue objects

**multi-21501** ☑ A **SpeciesFeatureValue** object may have the optional SBML Level 3 Core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace are permitted on a **SpeciesFeatureValue** object. (References: Section 3.18.6 on page 29).

**multi-21502** ☑ A **SpeciesFeatureValue** object may have the optional SBML Level 3 Core subobjects for `notes` and `annotation`. No other elements from the SBML Level 3 Core namespace are permitted on a **SpeciesFeatureValue** object. (References: Section 3.18.6 on page 29).

**multi-21503** ☑ A **SpeciesFeatureValue** object must have the required attribute `multi:value`. No other attributes from the Multi namespace are permitted on a **SpeciesFeatureValue** object. (References: Section 3.18.6 on page 29.)

**multi-21504** ☑ The value of the `multi:value` attribute on a given **SpeciesFeatureValue** object must be the identifier of a **PossibleSpeciesFeatureValue** object defined in the **SpeciesFeatureType** object referenced by the **SpeciesFeature** object containing this **SpeciesFeatureValue** object. (References: Section 3.18.6 on page 29.)

## Rules for IntraSpeciesReaction objects

**multi-21601** ☑ An **IntraSpeciesReaction** object may have the optional SBML Level 3 Core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace and the Multi namespace are permitted on an **IntraSpeciesReaction** object. (References: Section 3.21 on page 34).

**multi-21602** ☑ An **IntraSpeciesReaction** object may have the optional SBML Level 3 Core subobjects for `notes` and `annotation`. No other elements from the SBML Level 3 Core namespace are permitted on an **IntraSpeciesReaction** object. (References: Section 3.21 on page 34).

## Rules for extended SimpleSpeciesReference objects

**multi-21701** ☑ An extended **SimpleSpeciesReference** object may have the optional attribute, `multi:compartmentReference`. No other attributes from the Multi namespace are permitted on a **SimpleSpeciesReference** object. (References: Section 3.22 on page 35.)

**multi-21702** ☑ The value of a `multi:compartmentReference` attribute, if present on a **SimpleSpeciesReference** object, must be the identifier of a **CompartmentReference** object. (References: Section 3.22 on page 35.)

## Rules for extended SpeciesReference objects

**multi-21801** ☑ A **ListOfSpeciesTypeComponentMapsInProduct** object within an extended **SpeciesReference** object is optional, but if present, must not be empty. (References: Section 3.23.1 on page 36.)

**multi-21802** ☑ A **ListOfSpeciesTypeComponentMapsInProduct** object may have the optional SBML core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace or the Multi namespace are permitted on a **ListOfSpeciesTypeComponentMapsInProduct** object. (References: Section 3.23.1 on page 36.)

**multi-21803** ☑ Apart from the general `notes` and `annotation` subobjects permitted on all SBML objects, a **ListOfSpeciesTypeComponentMapsInProduct** container object may only contain **SpeciesTypeComponentMapInProduct** objects. (References: Section 3.23.1 on page 36.)

## Rules for SpeciesTypeComponentMapInProduct objects

**multi-21901** ☑ A **SpeciesTypeComponentMapInProduct** object may have the optional SBML Level 3 Core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace are permitted on a **SpeciesTypeComponentMapInProduct** object. (References: Section 3.24 on page 37).

**multi-21902** ☑ A **SpeciesTypeComponentMapInProduct** object may have the optional SBML Level 3 Core subobjects for `notes` and `annotation`. No other elements from the SBML Level 3 Core namespace are permitted on a **SpeciesTypeComponentMapInProduct** object. (References: Section 3.24 on page 37).

**multi-21903** ☑ A **SpeciesTypeComponentMapInProduct** object must have the required attributes `multi:reactant`, `multi:reactantComponent`, and `multi:productComponent`. No other attributes from the Multi namespace are permitted on a **SpeciesTypeComponentMapInProduct** object. (References: Section 3.24 on page 37.)

**multi-21904** ☑ The value of the `multi:reactant` attribute on a given **SpeciesTypeComponentMapInProduct** object must be the identifier of a reactant **SpeciesReference** object within a reaction. (References: Section 3.24.1 on page 37.)

**multi-21905** ☑ The value of the `multi:reactantComponent` attribute on a given **SpeciesTypeComponentMapInProduct** object must be the identifier of an object of **SpeciesTypeInstance**, **SpeciesTypeComponentIndex** or **SpeciesType**. (References: Section 3.24.2 on page 37.)

**multi-21906** ☑ The value of the `multi:productComponent` attribute on a given **SpeciesTypeComponentMapInProduct** object must be the identifier of an object of **SpeciesTypeInstance**, **SpeciesTypeComponentIndex** or **SpeciesType**. (References: Section 3.24.3 on page 37.)

**multi-21907** ☑ A **ListOfSpeciesFeatureChanges** object within a **SpeciesTypeComponentMapInProduct** object is optional, but if present, must not be empty. (References: Section 3.24.4 on page 37.)

**multi-21908** ☑ A **ListOfSpeciesFeatureChanges** object may have the optional SBML core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace or the Multi namespace are permitted on a **ListOfSpeciesFeatureChanges** object. (References: Section 3.24.4 on page 37.)

**multi-21909** ☑ Apart from the general `notes` and `annotation` subobjects permitted on all SBML objects, a **ListOfSpeciesFeatureChanges** container object may only contain **SpeciesFeatureChange** objects. (References: Section 3.24.4 on page 37.)

## Rules for SpeciesFeatureChange objects

**multi-22001** ☑ A **SpeciesFeatureChange** object may have the optional SBML Level 3 Core attributes `metaid` and `sboTerm`. No other attributes from the SBML Level 3 Core namespace are permitted on a **SpeciesFeatureChange** object. (References: Section 3.25 on page 38).

**multi-22002** ☑ A **SpeciesFeatureChange** object may have the optional SBML Level 3 Core subobjects for `notes` and `annotation`. No other elements from the SBML Level 3 Core namespace are permitted on a **SpeciesFeatureChange** object. (References: Section 3.25 on page 38).

**multi-22003** ☑ A **SpeciesFeatureChange** object must have the required attributes `multi:reactantSpeciesFeature` and `multi:productSpeciesFeature`. No other attributes from the Multi namespace are permitted on a **SpeciesFeatureChange** object. (References: Section 3.25 on page 38.)

**multi-22004** ☑ The value of the `multi:reactantSpeciesFeature` attribute on a given **SpeciesFeatureChange** object must be the identifier of a **SpeciesFeature** object. (References: Section 3.25.2 on page 38.)

**multi-22005** ☑ The value of the `multi:productSpeciesFeature` attribute on a given **SpeciesFeatureChange** object must be the identifier of a **SpeciesFeature** object. (References: Section 3.25.3 on page 38.)

## Rules for extended `ci` elements in Math objects

**multi-22101** ☑ A `ci` element in a **Math** object may have the optional attributes `multi:speciesReference` and `multi:representationType`. No other attributes from the Multi namespace are permitted on a `ci` element. (References: Section 3.27 on page 41).

**multi-22102** ☑ The value of the `multi:speciesReference` attribute on a given `ci` element must be the identifier of a **SpeciesReference** object within the same reaction. (References: Section 3.27.1 on page 41.)

**multi-22103** ☑ The value of the `multi:representationType` attribute on a given `ci` element must conform to the syntax of the Multi data type **`RepresentationType`**. (References: Section 3.27.2 on page 43.)

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