AlgebraicRule-class

SBML type "AlgebraicRule"

Description

Expresses equations that are not assignments nor rates of change.

Instantiation

Objects can be created by calls of the form new("AlgebraicRule", ...).

Slots

math: Object of class "expression" specifying the equation.
metaId: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
notes: Object of class "character" containing user-readable XHTML notes about an element.
annotation: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
cvTerms: Object of class "list" containing instances of CVTerm associated with this element.
sboTerm: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "Rule", directly. Class "SBase", by class "Rule", distance 2.

Methods

No methods defined with class "AlgebraicRule" in the signature.

Author(s)

Michael Lawrence
AssignmentRule-class

SBML type "AssignmentRule"

Description

An equation that assigns a value to the quantity of a Species, the size of a Compartment or the value of a Parameter.

Instantiation

Objects can be created by calls of the form `new("AssignmentRule", ...)`.

Slots

- **variable**: Object of class "character" naming the variable (the id of a Species, Compartment or Parameter) to set.
- **type**: Object of class "character", deprecated.
- **math**: Object of class "expression" specifying the equation.
- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
- **notes**: Object of class "character" containing user-readable XHTML notes about an element.
- **annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- **cvTerms**: Object of class "list" containing instances of CVTerm associated with this element.
- **sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "Rule", directly. Class "SBase", by class "Rule", distance 2.

Methods

- **variable** signature(object = "AssignmentRule"): gets the variable slot
- **variable<-** signature(object = "AssignmentRule"): sets the variable slot
- **type** signature(object = "AssignmentRule"): gets the type slot
- **type<-** signature(object = "AssignmentRule"): sets the type slot

Author(s)

Michael Lawrence
BoundingBox-class

**SBML type** "BoundingBox"

**Description**
Species the size and position of an SBML layout object.

**Instantiation**
Objects can be created by calls of the form `new("BoundingBox", ...)`.

**Slots**
- **id**: Object of class "character" uniquely identifying this component.
- **position**: Object of class "Point" specifying the position.
- **dimensions**: Object of class "Dimensions" specifying the size.
- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
- **notes**: Object of class "character" containing user-readable XHTML notes about an element.
- **annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- **cvTerms**: Object of class "list" containing instances of `CVTerm` associated with this element.
- **sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

**Extends**
Class "SBase", directly.

**Methods**
- `id` signature `(object = "BoundingBox")`: gets the id slot
- `id<-` signature `(object = "BoundingBox")`: sets the id slot
- `dimensions` signature `(object = "BoundingBox")`: gets the dimensions slot
- `dimensions<-` signature `(object = "BoundingBox")`: sets the dimensions slot
- `position` signature `(object = "BoundingBox")`: gets the position slot
- `position<-` signature `(object = "BoundingBox")`: sets the position slot

**Author(s)**
Michael Lawrence

**References**
- [http://projects.villa-bosch.de/bcb/sbml](http://projects.villa-bosch.de/bcb/sbml)
- [http://sbml.org/documents/](http://sbml.org/documents/)
CVTerm-class  

SBML Type "CVTerm"

Description

A MIRIAM annotation, consisting of a qualifier ("model", "biological" or something else) and a resource (URI).

Objects from the Class

Objects can be created by calls of the form new("CVTerm", ...).

Slots

* **qualifierType**: Object of class "character" specifying the type of qualifier for this term. Types "model" and "biological" have special meaning, but any string may be specified.

* **modelQualifierType**: Object of class "character" specifying the type of model qualifier, if qualifierType is set to "model". Types "is" and "isDescribedBy" are formally defined in MIRIAM, but any string may be specified.

* **biologicalQualifierType**: Object of class "character" specifying the type of biological qualifier, if qualifierType is set to "biological". Types "is", "hasPart", "isPartOf", "isVersionOf", "hasVersion", "isHomologTo", and "isDescribedBy" are formally defined in MIRIAM, though any string may be specified.

* **resources**: Object of class "character" specifying a URI that identifies some resource related an SBML element by the qualifier.

Methods

* **biologicalQualifierType** signature(object = "CVTerm"): gets the biologicalQualifierType slot.

* **biologicalQualifierType<-** signature(object = "CVTerm"): sets the biologicalQualifierType slot.

* **modelQualifierType** signature(object = "CVTerm"): gets the modelQualifierType slot.

* **modelQualifierType<-** signature(object = "CVTerm"): sets the modelQualifierType slot.

* **qualifierType** signature(object = "CVTerm"): gets the qualifierType slot.

* **qualifierType<-** signature(object = "CVTerm"): sets the qualifierType slot.

* **resources** signature(object = "CVTerm"): gets the resources slot.

* **resources<-** signature(object = "CVTerm"): sets the resources slot.

Author(s)

Michael Lawrence

References

http://sbml.org/documents/
**Compartment-class**

**SBML type** "Compartment"

### Description

A bounded space that contains Species.

### Instantiation

Objects can be created by calls of the form `new("Compartment", ...)`. 

### Slots

- **id**: Object of class "character" uniquely identifying this component.
- **name**: Object of class "character" naming this component.
- **spatialDimensions**: Object of class "integer" indicating the number of dimensions (0, 1, 2, or 3)
- **size**: Object of class "numeric" indicating the size in the given units.
- **units**: Object of class "character" indicating the units (built-in or the id of a UnitDefinition).
- **outside**: Object of class "character" identifying the compartment containing this compartment.
- **constant**: Object of class "logical" indicating whether the size changes during simulation.
- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource.
  This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
- **notes**: Object of class "character" containing user-readable XHTML notes about an element.
- **annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- **cvTerms**: Object of class "list" containing instances of CVTerm associated with this element.
- **sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

### Extends

Class "SBase", directly.

### Methods

- **id** signature(object = "Compartment"): gets the id slot
- **id<-** signature(object = "Compartment"): sets the id slot
- **name** signature(object = "Compartment"): gets the name slot
- **name<-** signature(object = "Compartment"): sets the name slot
- **constant** signature(object = "Compartment"): gets the constant slot
- **constant<-** signature(object = "Compartment"): sets the constant slot
CompartmentGlyph-class

outside signature(object = "Compartment"): gets the outside slot
outside<- signature(object = "Compartment"): sets the outside slot
size signature(object = "Compartment"): gets the size slot
size<- signature(object = "Compartment"): sets the size slot
units signature(object = "Compartment"): gets the constant slot
units<- signature(object = "Compartment"): sets the constant slot
spatialDimensions signature(object = "Compartment"): gets the spatialDimensions slot
spatialDimensions<- signature(object = "Compartment"): sets the spatialDimensions slot

Author(s)
Michael Lawrence

References
http://sbml.org/documents/

CompartmentGlyph-class
SBML type "CompartmentGlyph"

Description
A glyph representing a Compartment.

Instantiation
Objects can be created by calls of the form new("CompartmentGlyph", ...).

Slots

compartment: Object of class "character" identifying the compartment this glyph represents.

id: Object of class "character" uniquely identifying this component.

boundingBox: Object of class "BoundingBox" describing the position and size of the graphical object.

metaId: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.

notes: Object of class "character" containing user-readable XHTML notes about an element.

annotation: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

cvTerms: Object of class "list" containing instances of CVTerm associated with this element.

sboTerm: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).
CompartmentType-class

Extends

Class "GraphicalObject", directly. Class "SBase", by class "GraphicalObject", distance 2.

Methods

compartment signature(object = "CompartmentGlyph"): gets the compartment slot

compartment<- signature(object = "CompartmentGlyph"): sets the compartment slot

Author(s)

Michael Lawrence

References

http://projects.villa-bosch.de/bcb/sbml
CompartmentVolumeRule-class

Methods

**id** signature(object = "CompartmentType"): gets the id slot

**id<-** signature(object = "CompartmentType"): sets the id slot

**name** signature(object = "CompartmentType"): gets the name slot

**name<-** signature(object = "CompartmentType"): sets the name slot

Note

Requires libsbml >= 3.0

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

See Also

Compartment

CompartmentVolumeRule-class

SBML type "CompartmentVolumeRule"

Description

**Obsolete** way to assign a volume to a Compartment.

Instantiation

Objects can be created by calls of the form `new("CompartmentVolumeRule", ...).

Slots

**compartment**: Object of class "character" identifying the compartment

**variable**: Object of class "character", ignored.

**type**: Object of class "character", deprecated.

**math**: Object of class "expression" specifying the equation.

**metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.

**notes**: Object of class "character" containing user-readable XHTML notes about an element.

**annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

**cvTerms**: Object of class "list" containing instances of CVTerm associated with this element.

**sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).
Constraint-class

Extends


Methods

compartment signature(object = "CompartmentVolumeRule"): gets the compartment slot

compartment<- signature(object = "CompartmentVolumeRule"): sets the compartment slot

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

---

Constraint-class  SBML Type "Constraint"

Description

A constraint that must be continuously satisfied throughout the simulation of a model. Once a constraint is no longer met, the simulation must halt.

Objects from the Class

Objects can be created by calls of the form new("Constraint", ...).

Slots

math: Object of class "expression" that evaluates to FALSE if the constraint is not satisfied, otherwise evaluates to TRUE.

message: Object of class "character", formatted in XHTML, that is displayed to the user by an application when the constraint is not satisfied.

metaId: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.

notes: Object of class "character" containing user-readable XHTML notes about an element.

annotation: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

cvTerms: Object of class "list" containing instances of CVTerm associated with this element.

sboTerm: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).
Exteses
Class "SBase", directly.

Methods
math signature(domain = "Constraint"): gets the math slot.
math<- signature(object = "Constraint"): sets the math slot.
msg signature(domain = "Constraint"): gets the msg slot.
msg<- signature(object = "Constraint"): sets the msg slot.

Note
Requires libsbml >= 3.0

Author(s)
Michael Lawrence

References
http://sbml.org/documents/

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CubicBezier-class  SBML type "CubicBezier"

Description
A cubic bezier curve in an SBML layout.

Instantiation
Objects can be created by calls of the form new("CubicBezier", ...).

Slots

basePoint1: Object of class "Point" indicating the position of the base point closest to the
starting point.

basePoint2: Object of class "Point" indicating the position of the base point farthest from
the starting point.

start: Object of class "Point" ~~

end: Object of class "Point" ~~

metaId: Object of class "character" that is an XML ID "described" by an RDF resource.
This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML
element, but is usually placed inside the annotation element.

notes: Object of class "character" containing user-readable XHTML notes about an ele-
ment.

annotation: Object of class "character" containing additional machine-readable information
about an element, usually as RDF, such as BioPAX. This is where application-specific
data belongs.
Curve-class

**cvTerms**: Object of class "list" containing instances of CVTerm associated with this element.

**sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "LineSegment", directly. Class "SBase", by class "LineSegment", distance 2.

Methods

- `basePoint1` signature(object = "CubicBezier"): gets the basePoint1 slot
- `basePoint1<-` signature(object = "CubicBezier"): sets the basePoint1 slot
- `basePoint2` signature(object = "CubicBezier"): gets the basePoint2 slot
- `basePoint2<-` signature(object = "CubicBezier"): sets the basePoint2 slot

Author(s)

Michael Lawrence

References

http://projects.villa-bosch.de/bcb/sbml

Curve-class SBML type "Curve"

Description

A curve (list of line segments) in an SBML layout.

Instantiation

Objects can be created by calls of the form `new("Curve", ...)`.

Slots

- **curveSegments**: Object of class "list" containing the LineSegments that compose the curve.
- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
- **notes**: Object of class "character" containing user-readable XHTML notes about an element.
- **annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- **cvTerms**: Object of class "list" containing instances of CVTerm associated with this element.
- **sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).
Delay-class

Extends

Class "SBase", directly.

Methods

curveSegments signature(object = "Curve"): gets the curveSegments slot
curveSegments<- signature(object = "Curve"): sets the curveSegments slot

Author(s)

Michael Lawrence

References

http://projects.villa-bosch.de/bcb/sbml

Delay-class

SBML Type "Delay"

Description

The length of time between the Triggering of an Event and the execution of its EventAssignments.

Objects from the Class

Objects can be created by calls of the form new("Delay", ...).

Slots

math: Object of class "expression" that evaluates to a quantity of time.
metaId: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
notes: Object of class "character" containing user-readable XHTML notes about an element.
annotation: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
cvTerms: Object of class "list" containing instances of CVTerm associated with this element.
sboTerm: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "SBase", directly.
Methods

math signature(domain = "Delay"): gets the math slot.

math<- signature(object = "Delay"): sets the math slot.

Note
Requires libsbml >= 3.0

Author(s)
Michael Lawrence

References
http://sbml.org/documents/

See Also
Event

describe Describing objects

describe (object, ...)

Arguments

object The object to be described.

... Additional arguments for methods.

Value
A short textual (string) representation of object.

Describable objects
An object that extends Describable has a method for the describe generic, and by default Describable objects are shown by printing the output of describe. Note that Describable is a virtual tag class, no objects may be created from it.
Dimensions-class

Describable methods

show signature(object = "Describable"): outputs the return value of describe.

Author(s)

Michael Lawrence

Dimensions-class  SBML type "Dimensions"

Description

Holds the size of an SBML layout object.

Instantiation

Objects can be created by calls of the form new("Dimensions", ...).

Slots

width: Object of class "numeric" indicating the width, in pixels
height: Object of class "numeric" indicating the height, in pixels
depth: Object of class "numeric" indicating the depth, in pixels
metaId: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
notes: Object of class "character" containing user-readable XHTML notes about an element.
annotation: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

Extends

Class "SBase", directly.

Methods

depth signature(object = "Dimensions"): gets the depth slot
depth<- signature(object = "Dimensions"): sets the depth slot
height signature(object = "Dimensions"): gets the height slot
height<- signature(object = "Dimensions"): sets the height slot
width signature(object = "Dimensions"): gets the width slot
width<- signature(object = "Dimensions"): sets the width slot
Event-class

Author(s)

Michael Lawrence

References

http://projects.villa-bosch.de/bcb/sbml

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### Event-class

**SBML type** "Event"

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### Description

Description of a instantaneous, discontinuous change in the model state.

---

### Instantiation

Objects can be created by calls of the form `new("Event", ...)`. 

---

### Slots

- **id**: Object of class "character" uniquely identifying this component. 
- **name**: Object of class "character" naming this component. 
- **trigger**: Object of class "expression" that evaluates to TRUE when the event is to be fired. 
- **eventDelay**: Object of class "expression" that evaluates to the time until execution of this event after it has been fired. 
- **timeUnits**: Object of class "character" identifying the units of the delay. 
- **eventAssignments**: Object of class "list" containing EventAssignments that are performed at execution. 
- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element. 
- **notes**: Object of class "character" containing user-readable XHTML notes about an element. 
- **annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs. 
- **cvTerms**: Object of class "list" containing instances of CVTerm associated with this element. 
- **sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO). 

---

### Extends

Class "SBase", directly.
Methods

id signature(object = "Event"): gets the id slot
id< signature(object = "Event"): sets the id slot
name signature(object = "Event"): gets the name slot
name< signature(object = "Event"): sets the name slot
timeUnits signature(object = "Event"): gets the timeUnits slot
timeUnits< signature(object = "Event"): sets the timeUnits slot
eventDelay signature(x = "Event"): ...
eventDelay< signature(object = "Event"): sets the delay slot
eventAssignments signature(object = "Event"): gets the eventAssignments slot
eventAssignments< signature(object = "Event"): sets the eventAssignments slot
trigger signature(object = "Event"): gets the trigger slot
trigger< signature(object = "Event"): sets the trigger slot

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

EventAssignment-class

SBML type "EventAssignment"

Description

As part of an event, assigns a value to the quantity of a Species, the size of a Compartment or the value of a Parameter.

Instantiation

Objects can be created by calls of the form new("EventAssignment", ...).

Slots

variable: Object of class "character" ~
math: Object of class "expression" that evaluates to the value to assign.
metaId: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
notes: Object of class "character" containing user-readable XHTML notes about an element.
annotation: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
Experiment-class

cvTerms: Object of class "list" containing instances of CVTerm associated with this element.

sboTerm: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "SBase", directly.

Methods

math signature(object = "EventAssignment"): gets the math slot

math<- signature(object = "EventAssignment"): sets the math slot

variable signature(object = "EventAssignment"): gets the variable slot

variable<- signature(object = "EventAssignment"): sets the variable slot

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

Experiment-class  Experiment

Description

This class is an abstraction for an experiment, e.g. in a simulation. An experiment consists of a
ExperimentProtocol, ExperimentDesign, ExperimentSubject and ExperimentResult.

Objects from the Class

A virtual Class: No objects may be created from it.

Slots

protocol: Object of empty virtual class ExperimentProtocol, how the experiment was or
is to be performed.

design: Object of empty virtual class ExperimentDesign, the design of the experiment.

subject: Object of empty virtual class ExperimentSubject, the object being observed by
the experiment.

result: Object of empty virtual class ExperimentResult, the result of the experiment.
Methods

- **design** signature(object = "Experiment") : Gets the design slot.
- **design**<- signature(object = "Experiment") : Sets the design slot.
- **protocol** signature(object = "Experiment") : Gets the protocol slot.
- **protocol**<- signature(object = "Experiment") : Sets the protocol slot.
- **result** signature(object = "Experiment") : Gets the result slot.
- **result**<- signature(object = "Experiment") : Sets the result slot.
- **subject** signature(object = "Experiment") : Gets the subject slot.
- **subject**<- signature(object = "Experiment") : Sets the subject slot.

Author(s)

Michael Lawrence

See Also

*SOSExperiment*, an implementation that simulates SBML modules using the SBML ODE Solver library.

---

**FunctionDefinition-class**

*SBML type "FunctionDefinition"

Description

Identifies a mathematical expression so that it may be referenced in other expressions.

Instantiation

Objects can be created by calls of the form `new("FunctionDefinition", ...)`.

Slots

- **id** : Object of class "character" uniquely identifying this component.
- **name** : Object of class "character" naming this component.
- **math** : Object of class "expression" that defines the function.
- **metaId** : Object of class "character" that is an XML ID "described" by an RDF resource.
  This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
- **notes** : Object of class "character" containing user-readable XHTML notes about an element.
- **annotation** : Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- **cvTerms** : Object of class "list" containing instances of CVTerm associated with this element.
- **sboTerm** : Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).
GraphicalObject-class

Extends

Class "SBase", directly.

Methods

- **id** signature(object = "FunctionDefinition"): gets the id slot
- **id<-** signature(object = "FunctionDefinition"): sets the id slot
- **name** signature(object = "FunctionDefinition"): gets the name slot
- **name<-** signature(object = "FunctionDefinition"): sets the name slot
- **math** signature(object = "FunctionDefinition"): gets the math slot
- **math<-** signature(object = "FunctionDefinition"): sets the math slot

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

GraphicalObject-class

*SBML type "GraphicalObject"*

Description

The base class for graphical objects (e.g. glyphs) in SBML layouts.

Instantiation

Objects can be created by calls of the form `new("GraphicalObject", ...)`. 

Slots

- **id**: Object of class "character" uniquely identifying this component.
- **boundingBox**: Object of class "BoundingBox" describing the position and size of the graphical object.
- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
- **notes**: Object of class "character" containing user-readable XHTML notes about an element.
- **annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- **cvTerms**: Object of class "list" containing instances of **CVTerm** associated with this element.
- **sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).
InitialAssignment-class

Extends
Class "SBase", directly.

Methods

\texttt{id} \ signature(object = "GraphicalObject") \colon \text{gets the id slot}

\texttt{id<-} \ signature(object = "GraphicalObject") \colon \text{sets the id slot}

\texttt{boundingBox} \ signature(object = "GraphicalObject") \colon \text{gets the boundingBox slot}

\texttt{boundingBox<-} \ signature(object = "GraphicalObject") \colon \text{sets the boundingBox slot}

Author(s)
Michael Lawrence

References
http://projects.villa-bosch.de/bcb/sbml

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InitialAssignment-class

\textit{SBML Type "InitialAssignment"}

Description
Calculates the value of a symbol when the model is initialized.

Objects from the Class
Objects can be created by calls of the form \texttt{new("InitialAssignment", ...}).

Slots

\texttt{symbol}: Object of class "character" to which the value is assigned.

\texttt{math}: Object of class "expression" that evaluates to the assigned value.

\texttt{metaId}: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the \texttt{annotation} element.

\texttt{notes}: Object of class "character" containing user-readable XHTML notes about an element.

\texttt{annotation}: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

\texttt{cvTerms}: Object of class "list" containing instances of \texttt{CVTerm} associated with this element.

\texttt{sboTerm}: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).
KineticLaw-class

Extends

Class "SBase", directly.

Methods

math signature(object = "InitialAssignment"): gets the math slot.
math<- signature(object = "InitialAssignment"): sets the math slot.
symbol signature(object = "InitialAssignment"): gets the symbol slot.
symbol<- signature(object = "InitialAssignment"): sets the symbol slot.

Note

Requires libsbml >= 3.0

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

See Also

AssignmentRule, which can set a value at any time but cannot set constants.

---

**KineticLaw-class**

*SBML type "KineticLaw"

**Description**

Describes the rate of a Reaction.

**Instantiation**

Objects can be created by calls of the form `new("KineticLaw", ...)`. 

**Slots**

math: Object of class "expression" defining the rate of the reaction.

parameters: Object of class "list" containing Parameters that may be used in math.

timeUnits: Object of class "character" indicating the units for time.

substanceUnits: Object of class "character" indicating the units for substance.

metaId: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.

notes: Object of class "character" containing user-readable XHTML notes about an element.
annotation: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

cvTerms: Object of class "list" containing instances of CVTerm associated with this element.

sboTerm: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "SBase", directly.

Methods

math signature(object = "KineticLaw"): gets the math slot

math<- signature(object = "KineticLaw"): sets the math slot

substanceUnits signature(object = "KineticLaw"): gets the substanceUnits slot

substanceUnits<- signature(object = "KineticLaw"): sets the substanceUnits slot

timeUnits signature(object = "KineticLaw"): gets the timeUnits slot

timeUnits<- signature(object = "KineticLaw"): sets the timeUnits slot

parameters signature(object = "KineticLaw"): gets the parameters slot

parameters<- signature(object = "KineticLaw"): sets the parameters slot

Author(s)

Michael Lawrence

References

http://sbml.org/documents/
Slots

**id**: Object of class "character" uniquely identifying this component.

**dimensions**: Object of class "Dimensions" specifying the size of the layout.

**compartmentGlyphs**: Object of class "list" containing the CompartmentGlyphs.

**speciesGlyphs**: Object of class "list" containing the SpeciesGlyphs.

**reactionGlyphs**: Object of class "list" containing the ReactionGlyphs.

**textGlyphs**: Object of class "list" containing the TextGlyphs.

**additionalGraphicalObjects**: Object of class "list" containing the additional GraphicalObjects that are not bound to any model component.

**metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.

**notes**: Object of class "character" containing user-readable XHTML notes about an element.

**annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

**cvTerms**: Object of class "list" containing instances of CVTerm associated with this element.

**sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "SBase", directly.

Methods

**id** signature(object = "Layout"): gets the id slot

**id<-** signature(object = "Layout"): sets the id slot

**additionalGraphicalObjects** signature(object = "Layout"): gets the additionalGraphicalObjects slot

**additionalGraphicalObjects<-** signature(object = "Layout"): sets the additionalGraphicalObjects slot

**compartmentGlyphs** signature(object = "Layout"): gets the compartmentGlyphs slot

**compartmentGlyphs<-** signature(object = "Layout"): sets the compartmentGlyphs slot

**dimensions** signature(object = "Layout"): gets the dimensions slot

**dimensions<-** signature(object = "Layout"): sets the dimensions slot

**reactionGlyphs** signature(object = "Layout"): gets the reactionGlyphs slot

**reactionGlyphs<-** signature(object = "Layout"): sets the reactionGlyphs slot

**speciesGlyphs** signature(object = "Layout"): gets the speciesGlyphs slot

**speciesGlyphs<-** signature(object = "Layout"): sets the speciesGlyphs slot

**textGlyphs** signature(object = "Layout"): gets the textGlyphs slot

**textGlyphs<-** signature(object = "Layout"): sets the textGlyphs slot
LineSegment-class

Author(s)

Michael Lawrence

References

http://projects.villa-bosch.de/bcb/sbml

LineSegment-class  SBML type "LineSegment"

Description

Describes a simple A-B line.

Instantiation

Objects can be created by calls of the form new("LineSegment", ...).

Slots

start: Object of class "Point" indicating the start position.

end: Object of class "Point" indicating the end position.

metaId: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.

notes: Object of class "character" containing user-readable XHTML notes about an element.

annotation: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

cvTerms: Object of class "list" containing instances of CVTerm associated with this element.

sboTerm: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "SBase", directly.

Methods

end signature(x = "LineSegment"): ...

dend signature(object = "LineSegment"): sets the end slot

start signature(x = "LineSegment"): ...

start signature(object = "LineSegment"): sets the start slot

Author(s)

Michael Lawrence
References

http://projects.villa-bosch.de/bcb/sbml

---

Model-class  

SBML type "Model"

---

Description

The central SBML element. Contains the Species, Reactions, Compartments and other components of the model. See the SBML specification, at the reference, for further details.

Instantiation

Objects can be created by calls of the form `new("Model", ...)`. 

Slots

- `id`: Object of class "character" uniquely identifying this component.
- `name`: Object of class "character" naming this component.
- `functionDefinitions`: Object of class "list" containing `FunctionDefinitions`.
- `unitDefinitions`: Object of class "list" containing `UnitDefinitions`.
- `compartments`: Object of class "list" containing `Compartments`.
- `species`: Object of class "list" containing `Species`.
- `parameters`: Object of class "list" containing `Parameters`.
- `rules`: Object of class "list" containing `Rules`.
- `reactions`: Object of class "list" containing `Reactions`.
- `events`: Object of class "list" containing `Events`.
- `layouts`: Object of class "list" containing `Layouts`.
- `speciesTypes`: Object of class "list" containing `SpeciesTypes`.
- `compartmentTypes`: Object of class "list" containing `CompartmentTypes`.
- `constraints`: Object of class "list" containing `Constraints`.
- `initialAssignments`: Object of class "list" containing `InitialAssignments`.
- `modelHistory`: Object of class `ModelHistory` recording the history of the model.
- `metaId`: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the `annotation` element.
- `notes`: Object of class "character" containing user-readable XHTML notes about an element.
- `annotation`: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- `cvTerms`: Object of class "list" containing instances of `CVTerm` associated with this element.
- `sboTerm`: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).
Extends

Class "SBase", directly.

Methods

id signature(object = "Model"): gets the id slot
id<- signature(object = "Model"): sets the id slot
name signature(object = "Model"): gets the name slot
name<- signature(object = "Model"): sets the name slot
compartments signature(object = "Model"): gets the compartments slot
compartments<- signature(object = "Model"): sets the compartments slot
events signature(object = "Model"): gets the events slot
events<- signature(object = "Model"): sets the events slot
functionDefinitions signature(object = "Model"): gets the functionDefinitions slot
functionDefinitions<- signature(object = "Model"): sets the functionDefinitions slot
layouts signature(object = "Model"): gets the layouts slot
layouts<- signature(object = "Model"): sets the layouts slot
parameters signature(object = "Model"): gets the parameters slot
parameters<- signature(object = "Model"): sets the parameters slot
species signature(object = "Model"): gets the species slot
species<- signature(object = "Model"): sets the species slot
reactions signature(object = "Model"): gets the reactions slot
reactions<- signature(object = "Model"): sets the reactions slot
rules signature(object = "Model"): gets the rules slot
rules<- signature(object = "Model"): sets the rules slot
unitDefinitions signature(object = "Model"): gets the unitDefinitions slot
unitDefinitions<- signature(object = "Model"): sets the unitDefinitions slot
compartメントTypes signature(object = "Model"): gets the compartmentTypes slot
compartメントTypes<- signature(object = "Model"): sets the compartmentTypes slot
constraints signature(object = "Model"): gets the constraints slot
constraints<- signature(object = "Model"): sets the constraints slot
initialAssignments signature(object = "Model"): gets the initialAssignments slot
initialAssignments<- signature(object = "Model"): sets the initialAssignments slot
speciesTypes signature(object = "Model"): gets the speciesTypes slot
speciesTypes<- signature(object = "Model"): sets the speciesTypes slot
modelHistory signature(object = "Model"): gets the modelHistory slot
modelHistory<- signature(object = "Model"): sets the modelHistory slot
ModelCreator-class

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

ModelCreator-class  SBML Type "ModelCreator"

Description

Information, such as name, email and organization, about a creator of an SBML model.

Objects from the Class

Objects can be created by calls of the form new("ModelCreator", ...).

Slots

- **familyName**: Object of class "character" specifying the family name of the creator.
- **givenName**: Object of class "character" specifying the given name of the creator.
- **email**: Object of class "character" specifying the email address of the creator.
- **organization**: Object of class "character" specifying the name of the organization to which the creator belongs.

Methods

- **email** signature(object = "ModelCreator") : gets the email slot.
- **email<-** signature(object = "ModelCreator") : sets the email<- slot.
- **familyName** signature(object = "ModelCreator") : gets the familyName slot.
- **familyName<-** signature(object = "ModelCreator") : sets the familyName<- slot.
- **givenName** signature(object = "ModelCreator") : gets the givenName slot.
- **givenName<-** signature(object = "ModelCreator") : sets the givenName<- slot.
- **organization** signature(object = "ModelCreator") : gets the organization slot.
- **organization<-** signature(object = "ModelCreator") : sets the organization<- slot.

Author(s)

Michael Lawrence

References

http://sbml.org/documents/
ModelHistory-class  SBML Type "ModelHistory"

Description

Stores the history of an SBML model, including the created/modified dates and the creators.

Objects from the Class

Objects can be created by calls of the form `new("ModelHistory", ...)`.

Slots

- **createdDate**: Object of class "character" representing the date/time of creation, in W3CDTF format: YYYY-MM-DDTh:mm:ssTZD, e.g. "1997-07-16T19:20:30+01:00".
- **modifiedDate**: Object of class "character" representing the date/time of last modification, in W3CDTF format: YYYY-MM-DDTh:mm:ssTZD, e.g. "1997-07-16T19:20:30+01:00".
- **creators**: Object of class "list" of instances of `ModelCreator`, one for each creator of the model.

Methods

- **createdDate** signature(object = "ModelHistory"): get the createdDate slot.
- **createdDate<-** signature(object = "ModelHistory", value = "character"): Set the createdDate slot to a correctly formatted string.
- **createdDate<-** signature(object = "ModelHistory", value = "POSIXt"): Set the createdDate slot with a POSIXt instance, obtained e.g. from `Sys.time`.
- **creators** signature(object = "ModelHistory"): gets the creators slot.
- **creators<-** signature(object = "ModelHistory"): sets the creators slot.
- **modifiedDate** signature(object = "ModelHistory"): get the modifiedDate slot.
- **modifiedDate<-** signature(object = "ModelHistory", value = "character"): Set the modifiedDate slot to a correctly formatted string.
- **modifiedDate<-** signature(object = "ModelHistory", value = "POSIXt"): Set the modifiedDate slot with a POSIXt instance, obtained e.g. from `Sys.time`.

Author(s)

Michael Lawrence

References

[http://sbml.org/documents/](http://sbml.org/documents/)
ModifierSpeciesReference-class

SBML type "ModifierSpeciesReference"

Description

Identifies a Species that modifies the parent Reaction.

Instantiation

Objects can be created by calls of the form `new("ModifierSpeciesReference", ...)`.

Slots

- **id**: Object of class "character" uniquely identifying this component.
- **species**: Object of class "character" identifying the Species being referenced.
- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
- **notes**: Object of class "character" containing user-readable XHTML notes about an element.
- **annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- **cvTerms**: Object of class "list" containing instances of CVTerm associated with this element.
- **sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends


Methods

No methods defined with class "ModifierSpeciesReference" in the signature.

Author(s)

Michael Lawrence

References

http://sbml.org/documents/
Parameter-class  

**SBML type "Parameter"**

**Description**
Declares a variable to be used in a mathematical expression.

**Instantiation**
Objects can be created by calls of the form `new("Parameter", ...)`.

**Slots**
- **id**: Object of class "character" uniquely identifying this component.
- **name**: Object of class "character" naming this component.
- **value**: Object of class "numeric" specifying the initial value.
- **units**: Object of class "character" identifying the units.
- **constant**: Object of class "logical" indicating whether the value of this parameter is constant.
- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
- **notes**: Object of class "character" containing user-readable XHTML notes about an element.
- **annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- **cvTerms**: Object of class "list" containing instances of `CVTerm` associated with this element.
- **sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

**Extends**
Class "SBase", directly.

**Methods**
- **id** signature(object = "Parameter"): gets the id slot
- **id<-** signature(object = "Parameter"): sets the id slot
- **name** signature(object = "Parameter"): gets the name slot
- **name<-** signature(object = "Parameter"): sets the name slot
- **units** signature(object = "Parameter"): gets the units slot
- **units<-** signature(object = "Parameter"): sets the units slot
- **constant** signature(object = "Parameter"): gets the constant slot
- **constant<-** signature(object = "Parameter"): sets the constant slot
- **value** signature(object = "Parameter"): gets the value slot
- **value<-** signature(object = "Parameter"): sets the value slot
ParameterRule-class

SBML type "ParameterRule"

Description

Obsolete rule that controls the value of a Parameter.

Instantiation

Objects can be created by calls of the form new("ParameterRule", ...).

Slots

name: Object of class "character" naming this component.
units: Object of class "character" identifying the units of the assigned value.
variable: Object of class "character", ignored.
type: Object of class "character", deprecated.
math: Object of class "expression" specifying the equation.
metaId: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
notes: Object of class "character" containing user-readable XHTML notes about an element.
annotation: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
cvTerms: Object of class "list" containing instances of CVTerm associated with this element.
sboTerm: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Point-class

Methods

  name signature(object = "Parameter"): gets the name slot
  name<- signature(object = "Parameter"): sets the name slot
  units signature(object = "Parameter"): gets the units slot
  units<- signature(object = "Parameter"): sets the units slot
  variable signature(object = "Parameter"): gets the variable slot
  variable<- signature(object = "Parameter"): sets the variable slot
  type signature(object = "Parameter"): gets the type slot
  type<- signature(object = "Parameter"): sets the type slot
  math signature(object = "Parameter"): gets the math slot
  math<- signature(object = "Parameter"): sets the math slot

Author(s)

  Michael Lawrence

References

  http://sbml.org/documents/

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Point-class  SBML type "Point"

Description

  Specifies a position in 3D space.

Instantiation

  Objects can be created by calls of the form new("Point", ...).

Slots

  x: Object of class "numeric" indicating the X coordinate
  y: Object of class "numeric" indicating the Y coordinate
  z: Object of class "numeric" indicating the Z coordinate
  metaId: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
  notes: Object of class "character" containing user-readable XHTML notes about an element.
  annotation: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
  cvTerms: Object of class "list" containing instances of CVTerm associated with this element.
  sboTerm: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).
RateRule-class

Extends

Class "SBase", directly.

Methods

\texttt{x signature(object = "Point")}: gets the \texttt{x} slot
\texttt{x<- signature(object = "Point")}: sets the \texttt{x} slot
\texttt{y signature(object = "Point")}: gets the \texttt{y} slot
\texttt{y<- signature(object = "Point")}: sets the \texttt{y} slot
\texttt{z signature(object = "Point")}: gets the \texttt{z} slot
\texttt{z<- signature(object = "Point")}: sets the \texttt{z} slot

Author(s)

Michael Lawrence

References

http://projects.villa-bosch.de/bcb/sbml

RateRule-class SBML type "RateRule"

Description

An equation that describes the rate of change in the quantity of a \texttt{Species}, the size of a \texttt{Compartment} or the value of a \texttt{Parameter}.

Instantiation

Objects can be created by calls of the form \texttt{new("RateRule", ...)}.

Slots

\texttt{variable}: Object of class "character" naming the variable (the id of a \texttt{Species}, \texttt{Compartment} or \texttt{Parameter}) being described.
\texttt{math}: Object of class "expression" specifying the equation.
\texttt{metaId}: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the \texttt{annotation} element.
\texttt{notes}: Object of class "character" containing user-readable XHTML notes about an element.
\texttt{annotation}: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
\texttt{cvTerms}: Object of class "list" containing instances of \texttt{CVTerm} associated with this element.
\texttt{sboTerm}: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).
Reaction-class

Extends

Class "Rule", directly. Class "SBase", by class "Rule", distance 2.

Methods

variable signature(object = "RateRule"): gets the variable slot
variable<- signature(object = "RateRule"): sets the variable slot

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

Reaction-class

SBML type "Reaction"

Description

Any transformation, transportation or binding process that changes the quantity of one or more Species.

Instantiation

Objects can be created by calls of the form new("Reaction", ...).

Slots

id: Object of class "character" uniquely identifying this component.
name: Object of class "character" naming this component.
reactants: Object of class "list" containing SpeciesReferences specifying the Species that are reactants for this reaction.
products: Object of class "list" containing SpeciesReferences specifying the Species that are products for this reaction.
modifiers: Object of class "list" containing ModifierSpeciesReferences specifying the Species that are modifiers for this reaction.
kineticLaw: Object of class "KineticLaw" that dynamically defines the rate of the reaction.
reversible: Object of class "logical" indicating whether the direction of this reaction is reversible.
fast: Object of class "logical" indicating whether this reaction should be considered instantaneous relative to non-fast reactions.
metaId: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
notes: Object of class "character" containing user-readable XHTML notes about an element.
**Reaction-class**

**annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

**cvTerms**: Object of class "list" containing instances of CVTerm associated with this element.

**sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

**Extends**

Class "SBase", directly.

**Methods**

id signature(object = "Reaction"): gets the id slot
id<- signature(object = "Reaction"): sets the id slot
name signature(object = "Reaction"): gets the name slot
name<- signature(object = "Reaction"): sets the name slot
fast signature(object = "Reaction"): gets the fast slot
fast<- signature(object = "Reaction"): sets the fast slot
kineticLaw signature(object = "Reaction"): gets the kineticLaw slot
kineticLaw<- signature(object = "Reaction"): sets the kineticLaw slot
modifiers signature(object = "Reaction"): gets the modifiers slot
modifiers<- signature(object = "Reaction"): sets the modifiers slot
products signature(object = "Reaction"): gets the products slot
products<- signature(object = "Reaction"): sets the products slot
reactants signature(object = "Reaction"): gets the reactants slot
reactants<- signature(object = "Reaction"): sets the reactants slot
reversible signature(object = "Reaction"): gets the reversible slot
reversible<- signature(object = "Reaction"): sets the reversible slot

**Author(s)**

Michael Lawrence

**References**

http://sbml.org/documents/
ReactionGlyph-class

SBML type "ReactionGlyph"

Description

A glyph representing a Reaction in the SBML layout.

Instantiation

Objects can be created by calls of the form \texttt{new("ReactionGlyph", ...)}.

Slots

- \texttt{reaction}: Object of class "character" identifying the reaction represented by this glyph.
- \texttt{glyphCurve}: Object of class "Curve" describing this glyph as a curve (optional).
- \texttt{speciesReferenceGlyphs}: Object of class "list" containing \texttt{SpeciesReferenceGlyphs} that represent the \texttt{SpeciesReferences} of the underlying \texttt{Reaction}.
- \texttt{id}: Object of class "character" uniquely identifying this component.
- \texttt{boundingBox}: Object of class "BoundingBox" describing the position and size of the graphical object.
- \texttt{metaId}: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the \texttt{annotation} element.
- \texttt{notes}: Object of class "character" containing user-readable XHTML notes about an element.
- \texttt{annotation}: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- \texttt{cvTerms}: Object of class "list" containing instances of \texttt{CVTerm} associated with this element.
- \texttt{sboTerm}: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "GraphicalObject", directly. Class "SBase", by class "GraphicalObject", distance 2.

Methods

\begin{verbatim}
glyphCurve signature(expr = "ReactionGlyph"): gets the glyphCurve slot
glyphCurve<- signature(object = "ReactionGlyph"): sets the glyphCurve slot
reaction signature(object = "ReactionGlyph"): gets the reaction slot
reaction<- signature(object = "ReactionGlyph"): sets the reaction slot
speciesReferenceGlyphs signature(object = "ReactionGlyph"): gets the speciesReferenceGlyphs slot
speciesReferenceGlyphs<- signature(object = "ReactionGlyph"): sets the speciesReferenceGlyphs slot
\end{verbatim}


Description

A mathematical equation.

Instantiation

A virtual Class: No objects may be created from it.

Slots

- **math**: Object of class "expression" specifying the equation.
- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
- **notes**: Object of class "character" containing user-readable XHTML notes about an element.
- **annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- **cvTerms**: Object of class "list" containing instances of CVTerm associated with this element.
- **sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "SBase", directly.

Methods

- `math signature(object = "Rule")`: gets the math slot
- `math<- signature(object = "Rule")`: sets the math slot

Author(s)

Michael Lawrence

References

http://sbml.org/documents/
Description

The root element of an SBML document. An actual SBML Model may be retrieved from an instance of this class.

Instantiation

Objects can be created by calls of the form `new("SBML", ...)`. 

Slots

- **level**: Object of class "integer" indicating the level of the SBML standard (currently at 2).
- **ver**: Object of class "integer" indicating the version of the level (currently at 2 for level 2).
- **model**: Object of class "Model" the SBML model itself.
- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
- **notes**: Object of class "character" containing user-readable XHTML notes about an element.
- **annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- **cvTerms**: Object of class "list" containing instances of CVTerm associated with this element.
- **sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "SBase", directly.

Methods

- `coerce` signature(from = "SBMLDocument", to = "SBML"): constructs the S4 object model from a low-level libsbml document.
- `coerce` signature(from = "SBML", to = "SBMLDocument"): converts the S4 object model to a low-level libsbml document.
- `coerce` signature(from = "SBML", to = "graph"): converts the S4 object model to a graph.
- **level** signature(object = "SBML"): gets the level slot
- **level<-** signature(object = "SBML"): sets the level slot
- **model** signature(object = "SBML"): gets the model slot
- **model<-** signature(object = "SBML"): sets the model slot
- **rsbml_doc** signature(model = "SBML"): converts the S4 object model to a low-level libsbml document.
SBMLDocument-class

rsbml_write signature(object = "SBML"): writes this document to a file as SBML.
rsbml_xml signature(object = "SBML"): converts this document to a string as SBML.
rsbml_graph signature(object = "SBML"): converts this document to a graph object.
simulate signature(object = "SBML"): converts this document to an internal SBMLDocument and calls simulate on it.
ver signature(object = "SBML"): gets the ver slot
ver<- signature(object = "SBML"): sets the ver slot

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

Examples

# Get a DOM
dom <- rsbml_read(system.file("sbml", "GlycolysisLayout.xml", package = "rsbml"))

# Get the species ID's
sapply(species(model(dom)), id)

# Convert DOM back to a low-level document for checking
doc <- rsbml_doc(dom)
rsbml_check(doc)

# Write a DOM to a file
## Not run: rsbml_write(dom, "my.xml")

SBMLDocument-class "SBMLDocument" from libsbml

Description

Low-level libsbml document structure.

Instantiation

A virtual Class: No objects may be created from it.

Extends

Class "oldClass", directly.
Methods

rsbml_check signature(object = "SBMLDocument"): rsbml_check(object, quiet = FALSE, verbose = FALSE): semantically validates the document. If quiet is TRUE, emits warnings describing errors and fatal failures encountered when the document was parsed. If verbose is also TRUE, reports less critical warnings about problems in the model, such as internal inconsistencies.

rsbml_dom signature(doc = "SBMLDocument"): Constructs an S4 object model from a libsbml document.

rsbml_graph signature(doc = "SBMLDocument"): Converts a libsbml document to a graph.

rsbml_probs signature(object = "SBMLDocument"): reports problems encountered during parsing and/or validation.

rsbml_write signature(object = "SBMLDocument"): writes this document to a file as SBML.

rsbml_xml signature(object = "SBMLDocument"): converts this document to a string as SBML.

simulate signature(object = "SBMLDocument"): simulate(object, nsim = 10, seed, ...): a shortcut for simulating the model in this document using the SBML ODE Solver library. Arguments in ... should match slots of SOSProtocol. See simulate for more details.

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

Examples

# Read a document into an R DOM
dom <- rsbml_read(system.file("sbml", "GlycolysisLayout.xml", package = "rsbml"))

# Convert to a graph
graph <- rsbml_graph(dom)

# Write it out to a file
## Not run: rsbml_write(dom, "my.xml")

# Or convert it to a string of XML
rsbml_xml(dom)

# Read into external libsbml data structure
doc <- rsbml_read(system.file("sbml", "GlycolysisLayout.xml", package = "rsbml"), dom = FALSE)

# Convert it explicitly to an S4 DOM
dom <- rsbml_dom(doc)
SBMLProblem-class  SBMLProblem

Description

Represents an exception thrown during SBML parsing.

Details

There are trivial subclasses for fatal errors (SBMLFatal), recoverable errors (SBMLError), warnings (SBMLWarning) and informational messages (SBMLInfo). Errors become R error conditions, warnings become R warning conditions and messages are output via message.

Slots

- **line**: The "numeric" line number in the SBML file where the problem was detected.
- **column**: Object of class "numeric" column number in the SBML file where the problem was detected.
- **msg**: Object of class "character", a human-readable description of the problem.

Methods

- **condition** signature(object = "SBMLProblem"): constructs a condition object representing the exception.

Author(s)

Michael Lawrence

See Also

SBMLProblems, a container for instances of this class.

SBMLProblems-class  SBMLProblems

Description

A class representing errors encountered during parsing of SBML.

Slots

- **fatsals**: A list of SBMLFatal instances.
- **errors**: A list of SBMLError instances.
- **warnings**: A list of SBMLWarning instances.
- **infos**: A list of SBMLInfo instances.
Methods

`.throw` signature(object = "SBMLProblems"): Throws each `SBMLProblem` in this object.
`errors` signature(object = "SBMLProblems"): Gets the errors slot.
`fatal` signature(object = "SBMLProblems"): Gets the fatals slot.
`infos` signature(object = "SBMLProblems"): Gets the infos slot.
`warns` signature(object = "SBMLProblems"): Gets the warns slot.

Author(s)

Michael Lawrence

See Also

The `rsbml_problems` function for obtaining an instance of this class describing any problems encountered during parsing.

---

**SBase-class**

**SBML type** "SBase"

Description

The abstract type from which all other SBML types are derived.

Instantiation

A virtual Class: No objects may be created from it.

Slots

- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the `annotation` element.

- **notes**: Object of class "character" containing user-readable XHTML notes about an element.

- **annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

- **cvTerms**: Object of class "list" containing instances of `CVTerm` associated with this element.

- **sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).
SOSDesign-class

Methods

annotation signature(object = "SBase"): gets the annotation slot
annotation<- signature(object = "SBase"): sets the annotation slot
metaId signature(object = "SBase"): gets the metaId slot
metaId<- signature(object = "SBase"): sets the metaId slot
notes signature(object = "SBase"): gets the notes slot
notes<- signature(object = "SBase"): sets the notes slot
cvTerms signature(object = "SBase"): gets the cvTerms slot.
cvTerms<- signature(object = "SBase"): sets the cvTerms slot.
sboTerm signature(object = "SBase"): gets the sboTerm slot.
sboTerm<- signature(object = "SBase"): sets the sboTerm slot.

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

Description

Specifies the reaction names and their parameter settings for each run in a batch experiment. It extends matrix; each column corresponds to a parameter in the model and each row should hold the parameter settings for one run of the experiment.

Details

It is often desirable to explore the state space of a model by adjusting its initial parameter settings. One could do this by modifying the model itself for each experiment, but this class aims to provide a more convenient and systematic means of running experiments in batch, over a range of parameter settings. The results of the experiment will then contain the output from each run, which may then be compared.

The design is specified as a matrix, and each column in the matrix should correspond to a parameter defined in an SBML model. The column names should identify the parameters. These are not to be confused with the simulation parameters specified in SOSProtocol, which control how the simulation is executed. These should be kept constant across the runs.

There are two different types of parameters: global and local (reaction) parameters. Global parameters may correspond to a Species quantity, Compartiment size, or model-level Parameter value. These should be identified in the column names by the id of the corresponding SBML element. The element in the reactions slot for one of these parameters should be the empty string.

The second type of parameter specifies the value of a Parameter element within the KineticLaw of a reaction. These should be named by the id of the Parameter. They also should be namespaced by the containing Reaction id, which is stored in the corresponding element of the reactions slot.
Objects from the Class

Objects can be created by calls of the form `new("SOSDesign", data, nrow, ncol, byrow, dimnames, ...)`. This is the same as initializing a `matrix`.

Slots

`.Data`: Object of class "matrix", holding the parameter settings.

`reactions`: Object of class "character" of length the number of columns, holding the reaction IDs for parameters local to a reaction (i.e. KineticLaw Parameters). For global parameters, the corresponding value should be the empty string.

Extends


Methods

`reactions` signature(object = "SOSDesign"): gets the reactions slot.

`reactions<-` signature(object = "SOSDesign"): sets the reactions slot.

Author(s)

Michael Lawrence

References


See Also

`SOSEperiment`, the container of this class, for configuring and running a simulation.
Details
The general workflow for running a simulation:

1. Create or import an SBML Model.
2. Customize the model, for example by adding perturbation Events.
3. Wrap the model in a SOSSubject, e.g. new("SOSSubject", model).
4. Optionally construct a SOSDesign for running the experiment in batch over several sets of model parameter settings.
5. Optionally construct a SOSProtocol for specifying the time points and other parameters controlling the simulation.
6. Construct an instance of this class that groups the subject, design and protocol.
7. Run simulate on the SOSEperiment, optionally specifying the number of iterations and the random seed.
8. Analyze the returned SOSResult, perhaps starting by converting it to a time series with as.ts and making some plots.

Objects from the Class
Objects can be created by calls of the form new("SOSEperiment", ...).

Slots
- **protocol**: Object of class SOSProtocol, where the simulation parameters are specified.
- **design**: Object of class SOSDesign, specifying model parameters for each run of a batch experiment.
- **subject**: Object of class SOSSubject, containing the Model to be simulated.
- **result**: Object of class SOSResult containing the result of the simulation.

Extends
Class Experiment, directly.

Methods
- **simulate** signature(object = "SOSEperiment"): simulate(object, nsim = 10, seed, ...): Simulates the model in the subject slot according to the design points in design and parameters in protocol for nsim iterations, using seed as the random seed. Returns an instance of SOSEperiment, which now should include a SOSResult for analysis.

Author(s)
Michael Lawrence

References
See http://www.tbi.univie.ac.at/~raim/odeSolver/ for more information on the SBML ODE Solver library.
SOSProtocol-class  

**Description**

Holds the parameters controlling the execution of the simulation using the SBML ODE Solver library.

**Details**

Most users will probably set only the `times` slot, either directly or through the `timeStep` slot and the `nsim` parameter to `simulate`.

**Objects from the Class**

Objects can be created by calls of the form `new("SOSProtocol", ...)`. Each argument in `...` should correspond to one of the slots described below.

**Slots**

- **`times`**: A "numeric" vector indicating the time points at which to evaluate the model. Defaults to `tail(seq(0, by = timeStep, length.out = nsim + 1), -1)`. The model is always evaluated at \( t = 0 \). This slot is ignored when `indefinite` (below) is `TRUE`.

- **`timeStep`**: A scalar "numeric" value, giving the length in time between model evaluations. This is used when calculating the default value of `times`, above, but is otherwise only relevant when the `indefinite` slot, below, is `TRUE`. Defaults to 1.

- **`indefinite`**: A scalar "logical", indicating whether the simulation should run indefinitely, i.e. until one of the stopping conditions is met. See `haltOnEvent` and `haltOnSteadyState` below. Defaults to `FALSE`.

- **`atol`**: Scalar "numeric", the absolute tolerance in integration error. Defaults to `1e-18`.

- **`rtol`**: Scalar "numeric", the relative tolerance in integration error. Defaults to `1e-10`.

- **`maxStep`**: Scalar "numeric", the maximum number of steps for integration. Not to be confused with `timeStep`, etc, above, which control the simulation time points. Defaults to 10000.

- **`odeMethod`**: Scalar "character" naming the method for solving ODEs. Either "bdf" (the default) or "adams-moulton".

- **`iterMethod`**: Scalar "character", naming the iteration method used by the ODE solver, either "newton" (the default) or "functional".

- **`maxOrder`**: Scalar "numeric" indicating maximum order for the ODE solver. Defaults to 5.

- **`sensMethod`**: Scalar "character" naming the method for sensitivity analysis. One of "none" (the default and currently the only valid option), "simultaneous", "staggered" or "staggered1".

- **`haltOnEvent`**: Scalar "logical" indicating whether the simulation should halt when the model emits an `Event`. This allows the model to stop the simulation when some state is reached. Defaults to `FALSE`.

See Also

The `simulate` method on `SBMLDocument` is a shortcut, but most users will probably find the above approach most useful.
haltOnSteadyState: Scalar "logical", indicating whether to halt when a steady state is detected. Defaults to FALSE.

useJacobian: Scalar "logical" indicating whether to use Jacobian ASTs (TRUE, the default) or the internal approximation in the CVODES library.

storeResults: Scalar "logical" indicating whether to store the entire time course (TRUE, the default) or just the last time point. Just for performance.

Extends

Class "ExperimentProtocol", directly.

Methods

No methods defined with class "SOSProtocol" in the signature.

Author(s)

Michael Lawrence

References


See Also

The SOSExperiment class, which contains a SOSProtocol instance, for setting up and running a simulation.
SOSSubject-class

Extends

Class "ExperimentResult", directly.

Methods

\texttt{as.ts} signature(x = "SOSResult"): converts this object to a time course object of class ts. This allows analysis of the results with existing R infrastructure for time course analysis.

\texttt{compartments} signature(object = "SOSResult"): returns a subset containing only the Compartment size courses.

\texttt{parameters} signature(object = "SOSResult"): returns a subset containing only the global Parameter value courses.

\texttt{reactions} signature(object = "SOSResult"): returns a subset containing only the Reaction rate courses.

\texttt{species} signature(object = "SOSResult"): returns a subset containing only the Species quantity courses.

Author(s)

Michael Lawrence

References

See \url{http://www.tbi.univie.ac.at/~raim/odeSolver/} for more information on the SBML ODE Solver library.

See Also

\texttt{SOSExperiment} for running a simulation and obtaining an instance of this class.

\begin{verbatim}
SOSSubject-class  SOSSubject
\end{verbatim}

Description

This just marks a \texttt{Model} as being a valid subject for simulation using the SBML ODE Solver library.

Objects from the Class

Normally created from a \texttt{Model} with: \texttt{new("SOSSubject", model)}.

Extends

Class "ExperimentSubject", directly. Class "Model", directly. Class "SBase", by class "Model", distance 2. Class "Describable", by class "Model", distance 3.

Author(s)

Michael Lawrence
SimpleSpeciesReference-class

References


See Also

*SSEExperiment* for running a simulation on a SOSSubject.

SimpleSpeciesReference-class

*SBML type "SimpleSpeciesReference"*

Description

Base class for bindings between a *Species* and a *Reaction*.

Instantiation

Objects can be created by calls of the form `new("SimpleSpeciesReference", ...)`.

Slots

- **id**: Object of class "character" uniquely identifying this component.
- **species**: Object of class "character" identifying the *Species* being referenced.
- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the *annotation* element.
- **notes**: Object of class "character" containing user-readable XHTML notes about an element.
- **annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- **cvTerms**: Object of class "list" containing instances of *CVTerm* associated with this element.
- **sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "SBase", directly.

Methods

- **id** signature(object = "SpeciesGlyph"): gets the id slot
- **id<-** signature(object = "SpeciesGlyph"): sets the id slot
- **species** signature(object = "SpeciesGlyph"): gets the species slot
- **species<-** signature(object = "SpeciesGlyph"): sets the species slot
Description

A participant in an SBML model.

Instantiation

Objects can be created by calls of the form `new("Species", ...)`.

Slots

- **id**: Object of class "character" uniquely identifying this component.
- **name**: Object of class "character" naming this component.
- **compartment**: Object of class "character" identifying the compartment in which this species is located.
- **initialAmount**: Object of class "numeric" indicating the initial amount for this species (mutually exclusive with `initialConcentration`).
- **initialConcentration**: Object of class "numeric" indicating the initial concentration for this species (mutually exclusive with `initialAmount`).
- **substanceUnits**: Object of class "character" identifying the units for the amount of this species or the numerator of the concentration.
- **spatialSizeUnits**: Object of class "character" identifying the units for the denominator of the species concentration.
- **hasOnlySubstanceUnits**: Object of class "logical" indicating whether the quantity of this species is specified as an amount or a concentration.
- **boundaryCondition**: Object of class "logical". If TRUE, indicates that the quantity of this species cannot be changed by a reaction.
- **charge**: Object of class "integer" indicating the electrical charge of this species.
- **constant**: Object of class "logical" indicating whether the quantity of this species can change.
- **units**: Object of class "character", deprecated.
- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
- **notes**: Object of class "character" containing user-readable XHTML notes about an element.
Species-class

**annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

**cvTerms**: Object of class "list" containing instances of CVTerm associated with this element.

**sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

**Extends**

Class "SBase", directly.

**Methods**

- `id` signature(object = "Species"): gets the id slot
- `id<-` signature(object = "Species"): sets the id slot
- `name` signature(object = "Species"): gets the name slot
- `name<-` signature(object = "Species"): sets the name slot
- `boundaryCondition` signature(object = "Species"): gets the boundaryCondition slot
- `boundaryCondition<-` signature(object = "Species"): sets the boundaryCondition slot
- `charge` signature(object = "Species"): gets the charge slot
- `charge<-` signature(object = "Species"): sets the charge slot
- `compartment` signature(object = "Species"): gets the compartment slot
- `compartment<-` signature(object = "Species"): sets the compartment slot
- `constant` signature(object = "Species"): gets the constant slot
- `constant<-` signature(object = "Species"): sets the constant slot
- `units` signature(object = "Species"): gets the constant slot
- `units<-` signature(object = "Species"): sets the constant slot
- `hasOnlySubstanceUnits` signature(object = "Species"): gets the hasOnlySubstanceUnits slot
- `hasOnlySubstanceUnits<-` signature(object = "Species"): sets the hasOnlySubstanceUnits slot
- `initialAmount` signature(object = "Species"): gets the initialAmount slot
- `initialAmount<-` signature(object = "Species"): sets the initialAmount slot
- `initialConcentration` signature(object = "Species"): gets the initialConcentration slot
- `initialConcentration<-` signature(object = "Species"): sets the initialConcentration slot
- `spatialSizeUnits` signature(object = "Species"): gets the spatialSizeUnits slot
- `spatialSizeUnits<-` signature(object = "Species"): sets the spatialSizeUnits slot
- `substanceUnits` signature(object = "Species"): gets the substanceUnits slot
- `substanceUnits<-` signature(object = "Species"): sets the substanceUnits slot
SpeciesConcentrationRule-class

Author(s)
Michael Lawrence

References
http://sbml.org/documents/

SpeciesConcentrationRule-class

SBML type "SpeciesConcentrationRule"

Description
Obsolete type of rule that describes the concentration of Species.

Instantiation
Objects can be created by calls of the form new("SpeciesConcentrationRule", ...).

Slots

species: Object of class "character" identifying the Species.
variable: Object of class "character", ignored.
type: Object of class "character", deprecated.
math: Object of class "expression" specifying the equation.
metaId: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
notes: Object of class "character" containing user-readable XHTML notes about an element.
annotation: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
.cvTerms: Object of class "list" containing instances of CVTerm associated with this element.
sboTerm: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Methods

species signature(object = "SpeciesConcentrationRule"): gets the species slot
species<- signature(object = "SpeciesConcentrationRule"): sets the species slot
SpeciesGlyph-class

Author(s)
Michael Lawrence

References
http://sbml.org/documents/

SpeciesGlyph-class  SBML type "SpeciesGlyph"

Description
A glyph representing a Species in an SBML layout.

Instantiation
Objects can be created by calls of the form new("SpeciesGlyph", ...).

Slots

  species: Object of class "character" identifying the species this glyph represents.
  id: Object of class "character" uniquely identifying this component.
  boundingBox: Object of class "BoundingBox" describing the position and size of the graphical object.
  metaId: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
  notes: Object of class "character" containing user-readable XHTML notes about an element.
  annotation: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
  cvTerms: Object of class "list" containing instances of CVTerm associated with this element.
  sboTerm: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends
Class "GraphicalObject", directly. Class "SBase", by class "GraphicalObject", distance 2.

Methods

  species signature(object = "SpeciesGlyph"): gets the species slot
  species<- signature(object = "SpeciesGlyph"): sets the species slot

Author(s)
Michael Lawrence

References
http://projects.villa-bosch.de/bcb/sbml
SpeciesReference-class

SBML type "SpeciesReference"

Description

Binds a reactant or product Species to a Reaction.

Instantiation

Objects can be created by calls of the form new("SpeciesReference", ...).

Slots

- **stoichiometry**: Object of class "numeric" indicating the (static) stoichiometric coefficient.
- **stoichiometryMath**: Object of class "StoichiometryMath" that dynamically calculates the stoichiometric coefficient.
- **id**: Object of class "character" uniquely identifying this component.
- **species**: Object of class "character" identifying the Species being referenced.
- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
- **notes**: Object of class "character" containing user-readable XHTML notes about an element.
- **annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- **cvTerms**: Object of class "list" containing instances of CVTerm associated with this element.
- **sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends


Methods

- **stoichiometry** signature(object = "SpeciesReference"): gets the stoichiometry slot
- **stoichiometry<-.signature** signature(object = "SpeciesReference"): sets the stoichiometry slot
- **stoichiometryMath** signature(object = "SpeciesReference"): gets the stoichiometryMath slot
- **stoichiometryMath<-.signature** signature(object = "SpeciesReference"): sets the stoichiometryMath slot
SpeciesReferenceGlyph-class

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

SpeciesReferenceGlyph-class

SBML type "SpeciesReferenceGlyph"

Description

A glyph representing a SpeciesReference in an SBML layout.

Instantiation

Objects can be created by calls of the form new("SpeciesReferenceGlyph", ...).

Slots

speciesGlyph: Object of class "character" identifying the SpeciesGlyph representing the Species that is referenced by the underlying SpeciesReference.

speciesReference: Object of class "character" identifying the linkS4class{SpeciesReference} represented by this glyph.

role: Object of class "character" indicating how this glyph should represent the "role" of the underlying SpeciesReference.

glyphCurve: Object of class "Curve" describing this glyph as a curve (optional).

id: Object of class "character" uniquely identifying this component.

boundingBox: Object of class "BoundingBox" describing the position and size of the graphical object.

metaId: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.

notes: Object of class "character" containing user-readable XHTML notes about an element.

annotation: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

cvTerms: Object of class "list" containing instances of CVTerm associated with this element.

sboTerm: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "GraphicalObject", directly. Class "SBasis", by class "GraphicalObject", distance 2.
Methods

- **role** signature(object = "SpeciesReferenceGlyph"): gets the role slot
- **role<-** signature(object = "SpeciesReferenceGlyph"): sets the role slot
- **speciesGlyph** signature(object = "SpeciesReferenceGlyph"): gets the speciesGlyph slot
- **speciesGlyph<-** signature(object = "SpeciesReferenceGlyph"): sets the speciesGlyph slot
- **speciesReference** signature(object = "SpeciesReferenceGlyph"): gets the speciesReference slot
- **speciesReference<-** signature(object = "SpeciesReferenceGlyph"): sets the speciesReference slot
- **glyphCurve** signature(expr = "SpeciesReferenceGlyph"): gets the glyphCurve slot
- **glyphCurve<-** signature(object = "SpeciesReferenceGlyph"): sets the glyphCurve slot

Author(s)

Michael Lawrence

References

http://projects.villa-bosch.de/bcb/sbml
cvTerms: Object of class "list" containing instances of CVTerm associated with this element.

sboTerm: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "SBase", directly.

Methods

id signature(object = "SpeciesType"): gets the id slot
id<- signature(object = "SpeciesType"): sets the id slot
name signature(object = "SpeciesType"): gets the name slot
name<- signature(object = "SpeciesType"): sets the name slot

Note

Requires libsbml >= 3.0

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

See Also

Species

StoichiometryMath-class

SBML type "StoichiometryMath"

Description

Dynamically defines the stoichiometry of a SpeciesReference.

Instantiation

Objects can be created by calls of the form new("StoichiometryMath", ...).
Slots

**math**: Object of class "expression" that evaluates to the stoichiometric coefficient.

**metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the `annotation` element.

**notes**: Object of class "character" containing user-readable XHTML notes about an element.

**annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

**cvTerms**: Object of class "list" containing instances of `CVTerm` associated with this element.

**sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "SBase", directly.

Methods

```r
math signature(object = "StoichiometryMath"): gets the math slot
math<- signature(object = "StoichiometryMath"): sets the math slot
```

Author(s)

Michael Lawrence

References

[http://sbml.org/documents/](http://sbml.org/documents/)

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**TextGlyph-class**

SBML type "TextGlyph"

Description

A run of text in an SBML layout.

Instantiation

Objects can be created by calls of the form `new("TextGlyph", ...)`.
Slots

**graphicalObject**: Object of class "character" identifying the `GraphicalObject` that this glyph labels (optional).

**text**: Object of class "character" containing the text shown by the glyph (mutually exclusive with `originOfText`).

**originOfText**: Object of class "character" identifying an SBML component whose name is used as the text (mutually exclusive with `text`).

**id**: Object of class "character" uniquely identifying this component.

**boundingBox**: Object of class "BoundingBox" describing the position and size of the graphical object.

**metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the `annotation` element.

**notes**: Object of class "character" containing user-readable XHTML notes about an element.

**annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

**cvTerms**: Object of class "list" containing instances of `CVTerm` associated with this element.

**sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "`GraphicalObject`", directly. Class "`SBase`", by class "`GraphicalObject`", distance 2.

Methods

**graphicalObject** signature(object = "TextGlyph"): gets the `graphicalObject` slot

**graphicalObject<-** signature(object = "TextGlyph"): sets the `graphicalObject` slot

**originOfText** signature(object = "TextGlyph"): gets the `originOfText` slot

**originOfText<-** signature(object = "TextGlyph"): sets the `originOfText` slot

**text** signature(x = "TextGlyph"):...

**text<-** signature(object = "TextGlyph"): sets the `text` slot

Author(s)

Michael Lawrence

References

[http://projects.villa-bosch.de/bcb/sbml](http://projects.villa-bosch.de/bcb/sbml)
Trigger-class  \textit{SBML Type "Trigger"}

\textbf{Description}

Expresses when an \texttt{Event} should be fired.

\textbf{Objects from the Class}

Objects can be created by calls of the form \texttt{new("Trigger", \ldots)}.

\textbf{Slots}

\begin{itemize}
  \item \texttt{math}: Object of class "expression" that evaluates to \texttt{TRUE} when the event should be fired.
  \item \texttt{metaId}: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the \texttt{annotation} element.
  \item \texttt{notes}: Object of class "character" containing user-readable XHTML notes about an element.
  \item \texttt{annotation}: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
  \item \texttt{cvTerms}: Object of class "list" containing instances of \texttt{CVTerm} associated with this element.
  \item \texttt{sboTerm}: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).
\end{itemize}

\textbf{Extends}

Class "\texttt{SBase}", directly.

\textbf{Methods}

\begin{itemize}
  \item \texttt{math signature(domain = "Trigger")}: gets the math slot.
  \item \texttt{math<- signature(object = "Trigger")}: sets the math slot.
\end{itemize}

\textbf{Note}

Requires \texttt{libsbml} >= 3.0

\textbf{Author(s)}

Michael Lawrence

\textbf{References}

\url{http://sbml.org/documents/}

\textbf{See Also}

\texttt{Event}, the parent of this element.
Description

A (possibly transformed) reference to a base UnitKind. The transformation is of the form:
\[
multiplier \times 10^{scale} \times x^{exponent} + offset.
\]

Instantiation

Objects can be created by calls of the form `new("Unit", ...)`.

Slots

- **kind**: Object of class "character" identifying a SBML UnitKind. For possible values see Table 2 in the SBML specification.
- **exponent**: Object of class "integer" indicating the exponent to use in the transformation.
- **unitScale**: Object of class "integer" indicating the order of magnitude of the scaling to use in the transformation.
- **multiplier**: Object of class "numeric" indicating the factor to use for scaling in the transformation.
- **offset**: Object of class "numeric" indicating the amount of constant shift in the transformation.
- **metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.
- **notes**: Object of class "character" containing user-readable XHTML notes about an element.
- **annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.
- **cvTerms**: Object of class "list" containing instances of CVTerm associated with this element.
- **sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "SBase", directly.

Methods

- **exponent** signature(object = "Unit"): gets the exponent slot
- **exponent<-** signature(object = "Unit"): sets the exponent slot
- **kind** signature(object = "Unit"): gets the kind slot
- **kind<-** signature(object = "Unit"): sets the kind slot
- **multiplier** signature(object = "Unit"): gets the multiplier slot
- **multiplier<-** signature(object = "Unit"): sets the multiplier slot
offset signature(object = "Unit"): gets the offset slot

offset<- signature(object = "Unit"): sets the offset slot

unitScale signature(x = "Unit"): ...  

unitScale<- signature(object = "Unit"): sets the unitScale slot

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

UnitDefinition-class

---

**SBML type** "UnitDefinition"

---

Description

Associates one or more Units with an ID and name.

Instantiation

Objects can be created by calls of the form `new("UnitDefinition", ...)`.  

Slots

**id**: Object of class "character" uniquely identifying this component.

**name**: Object of class "character" naming this component.

**units**: Object of class "list" containing equivalent Units that are all associated with the same ID and name.

**metaId**: Object of class "character" that is an XML ID "described" by an RDF resource. This links an SBML element to an RDF resource. RDF may appear anywhere in an SBML element, but is usually placed inside the annotation element.

**notes**: Object of class "character" containing user-readable XHTML notes about an element.

**annotation**: Object of class "character" containing additional machine-readable information about an element, usually as RDF, such as BioPAX. This is where application-specific data belongs.

**cvTerms**: Object of class "list" containing instances of CVTerm associated with this element.

**sboTerm**: Object of class "integer" identifying a term in the Systems Biology Ontology (SBO).

Extends

Class "SBase", directly.
Methods

id signature(object = "UnitDefinition"): gets the id slot
id<- signature(object = "UnitDefinition"): sets the id slot
name signature(object = "UnitDefinition"): gets the name slot
name<- signature(object = "UnitDefinition"): sets the name slot
units signature(object = "UnitDefinition"): gets the units slot
units<- signature(object = "UnitDefinition"): sets the units slot

Author(s)

Michael Lawrence

References

http://sbml.org/documents/

Description

Each of these functions implements a trigonometry function found in the MathML specification but not found in base R. These are all simple wrappers around existing R trig functions.

Usage

acot(x)
acoth(x)
acsc(x)
acsch(x)
asec(x)
asech(x)
cot(x)
coth(x)
csc(x)
csch(x)
sec(x)
sech(x)

Arguments

x The numeric value(s) for the trigonometry operation

Value

A numeric vector, the same length as x.

Author(s)

Michael Lawrence
SBML import  

Read in an SBML file (start here)

Description

Read an SBML file into R.

Usage

rsbml_read(filename, text, dom = TRUE, strict = FALSE, schema = FALSE)

Arguments

- **filename**: the name of the SBML file to parse
- **text**: a string of SBML text to parse (instead of file)
- **dom**: whether to convert directly to the S4 DOM (TRUE, the default) or leave as the internal `SBMLDocument`
- **strict**: whether to report warnings in addition to errors or not (FALSE, the default)
- **schema**: whether to perform XML schema validation

Value

- a SBML object, or a `SBMLDocument` if `dom` is FALSE.

Author(s)

Michael Lawrence

Examples

# Read an SBML file
file <- system.file("sbml", "GlycolysisLayout.xml", package = "rsbml")
doc <- rsbml_read(file)

# Read an SBML string
string <- paste(readLines(file), collapse="\n")
doc <- rsbml_read(text = string)
Index

*Topic IO
  SBML import, 64

*Topic classes
  AlgebraicRule-class, 1
  AssignmentRule-class, 2
  BoundingBox-class, 3
  Compartment-class, 5
  CompartmentGlyph-class, 6
  CompartmentType-class, 7
  CompartmentVolumeRule-class, 8
  Constraint-class, 9
  CubicBezier-class, 10
  Curve-class, 11
  CVTerm-class, 4
  Delay-class, 12
  describe, 13
  Dimensions-class, 14
  Event-class, 15
  EventAssignment-class, 16
  Experiment-class, 17
  FunctionDefinition-class, 18
  GraphicalObject-class, 19
  InitialAssignment-class, 20
  KineticLaw-class, 21
  Layout-class, 22
  LineSegment-class, 24
  Model-class, 25
  ModelCreator-class, 27
  ModelHistory-class, 28
  ModifierSpeciesReference-class, 29
  Parameter-class, 30
  ParameterRule-class, 31
  Point-class, 32
  RateRule-class, 33
  Reaction-class, 34
  ReactionGlyph-class, 36
  Rule-class, 37
  SBase-class, 42
  SBML-class, 38
  SBMLDocument-class, 39
  SBMLProblem-class, 41
  SBMLProblems-class, 41
  SimpleSpeciesReference-class, 49
  SOSDesign-class, 43
  SOSExperiment-class, 44
  SOSProtocol-class, 46
  SOSResult-class, 47
  SOSSubject-class, 48
  Species-class, 50
  SpeciesConcentrationRule-class, 52
  SpeciesGlyph-class, 53
  SpeciesReference-class, 54
  SpeciesReferenceGlyph-class, 55
  SpeciesType-class, 56
  StoichiometryMath-class, 57
  TextGlyph-class, 58
  Trigger-class, 60
  Unit-class, 61
  UnitDefinition-class, 62

*Topic math
  acot (math), 63
  acoth (math), 63
  acsc (math), 63
  acsch (math), 63
  additionalGraphicalObjects
    (Layout-class), 22
  additionalGraphicalObjects, Layout-method (Layout-class), 22
INDEX

additionalGraphicalObjects<-(Layout-class), 22
additionalGraphicalObjects<-,Layout-method (Layout-class), 22
AlgebraicRule-class, 1
annotation (SBase-class), 42
annotation, SBase-method (SBase-class), 42
annotation<- (SBase-class), 42
annotation<-, SBase-method (SBase-class), 42
array, 44
as.character.SBML (SBML-class), 38
as.character.SBMLDocument (SBMLDocument-class), 39
as.ts, 45
as.ts, SOSResult-method (SOSResult-class), 47
asec (math), 63
asech (math), 63
AssignmentRule, 9, 21, 31, 52
AssignmentRule-class, 2
basePoint1 (CubicBezier-class), 10
basePoint1,CubicBezier-method (CubicBezier-class), 10
basePoint1<-(CubicBezier-class), 10
basePoint1<-,CubicBezier-method (CubicBezier-class), 10
basePoint2 (CubicBezier-class), 10
basePoint2,CubicBezier-method (CubicBezier-class), 10
basePoint2<-(CubicBezier-class), 10
basePoint2<-,CubicBezier-method (CubicBezier-class), 10
biologicalQualifierType (CVTerm-class), 4
biologicalQualifierType,CVTerm-method (CVTerm-class), 4
biologicalQualifierType<-(CVTerm-class), 4
biologicalQualifierType<-,CVTerm-method (CVTerm-class), 4
boundaryCondition (Species-class), 50
boundaryCondition, Species-method (Species-class), 50
boundaryCondition<-(Species-class), 50
boundaryCondition<-, Species-method (Species-class), 50
boundingBox (GraphicalObject-class), 19
boundingBox, GraphicalObject-method (GraphicalObject-class), 19
BoundingBox-class, 3
boundingBox<-(GraphicalObject-class), 19
boundingBox<-, GraphicalObject-method (GraphicalObject-class), 19
charge (Species-class), 50
charge, Species-method (Species-class), 50
charge<-(Species-class), 50
charge<-, Species-method (Species-class), 50
coerce (SBML-class), 38
coerce, SBML, graph-method (SBML-class), 38
coerce, SBMLDocument, graph-method (SBMLDocument-class), 38
coerce, SBMLDocument, SBML-method (SBMLDocument-class), 39
Compartment, 2, 6–8, 16, 25, 33, 43, 47, 48
compartment (Species-class), 50
compartment, CompartmentGlyph-method (CompartmentGlyph-class), 6
compartment, CompartmentVolumeRule-method (CompartmentVolumeRule-class), 8
compartment, Species-method (Species-class), 50
Compartment-class, 5
compartment<-(Species-class), 50
compartment<-, CompartmentGlyph-method (CompartmentGlyph-class), 6
compartment<-, CompartmentVolumeRule-method (CompartmentVolumeRule-class), 8
compartment<-, Species-method (Species-class), 50
CompartmentGlyph-class, 23
CompartmentGlyphs (Layout-class), 22
compartmentGlyphs, Layout-method (Layout-class), 22
compartmentGlyphs<-(Layout-class), 22
compartmentGlyphs<-, Layout-method (Layout-class), 22
compartments (Model-class), 25
compartments, Model-method (Model-class), 25
compartments, SOSResult-method (SOSResult-class), 25
compartments<-(Model-class), 25
compartments<-, Model-method (Model-class), 25
CompartmentType, 25
CompartmentType-class, 25
compartmentTypes (Model-class), 25
compartmentTypes, Model-method (Model-class), 25
compartmentTypes<-(Model-class), 25
compartmentTypes<-, Model-method (Model-class), 25
CompartmentVolumeRule-class, 25
csc (math), 63
csch (math), 63
CubicBezier-class, 25
Curve-class, 25
curveSegments (Curve-class), 25
curveSegments, Curve-method (Curve-class), 25
curveSegments<-(Curve-class), 25
curveSegments<-, Curve-method (Curve-class), 25
CVTerm-class, 25
cvTerms (SBase-class), 25
cvTerms, SBase-method (SBase-class), 25
cvTerms<-(SBase-class), 25
cvTerms<-, SBase-method (SBase-class), 25
Delay-class, 25
depth (Dimensions-class), 25
depth, Dimensions-method (Dimensions-class), 25
depth<-(Dimensions-class), 25
depth<-, Dimensions-method (Dimensions-class), 25
Describable, 25
Describable-class (describe), 25
describe, 25
describe, AlgebraicRule-method (describe), 25
describe, AssignmentRule-method (describe), 25
describe, BoundingBox-method (describe), 25
describe, Compartment-method (describe), 25
describe, CompartmentGlyph-method (describe), 25
describe, CompartmentType-method (describe), 25
describe, CompartmentVolumeRule-method (describe), 25
createdDate (ModelHistory-class), 25
createdDate, ModelHistory-method (ModelHistory-class), 25
createdDate<-(ModelHistory-class), 25
createdDate<-, ModelHistory-method (ModelHistory-class), 25
createdDate<-, ModelHistory, character-method (ModelHistory-class), 25
createdDate<-, ModelHistory, POSIXt-method (ModelHistory-class), 25
index
INDEX

errors (SBMLProblems-class), 41
errors, SBMLProblems-method (SBMLProblems-class), 41
Event, 12, 13, 25, 45, 46, 60
Event-class, 15
EventAssignment, 12, 15
EventAssignment-class, 16
eventAssignments (Event-class), 15
eventAssignments, Event-method (Event-class), 15
eventAssignments<- (Event-class), 15
eventAssignments<-, Event-method (Event-class), 15
eventDelay (Event-class), 15
eventDelay, Event-method (Event-class), 15
eventDelay<- (Event-class), 15
eventDelay<-, Event-method (Event-class), 15
events (Model-class), 25
events, Model-method (Model-class), 25
events<- (Model-class), 25
events<-, Model-method (Model-class), 25
Experiment, 44, 45
Experiment-class, 17
ExperimentDesign, 44
ExperimentDesign-class (Experiment-class), 17
ExperimentProtocol, 47
ExperimentProtocol-class (Experiment-class), 17
ExperimentResult, 48
ExperimentResult-class (Experiment-class), 17
ExperimentSubject, 48
ExperimentSubject-class (Experiment-class), 17
exponent (Unit-class), 61
exponent, Unit-method (Unit-class), 61
exponent<- (Unit-class), 61
exponent<-, Unit-method (Unit-class), 61
familyName (ModelCreator-class), 27
familyName, ModelCreator-method (ModelCreator-class), 27
familyName<-, ModelCreator-method (ModelCreator-class), 27
fast (Reaction-class), 34
fast, Reaction-method (Reaction-class), 34
fast<- (Reaction-class), 34
fast<-, Reaction-method (Reaction-class), 34
fatals (SBMLProblems-class), 41
fatals, SBMLProblems-method (SBMLProblems-class), 41
FunctionDefinition, 25
FunctionDefinition-class, 18
functionDefinitions (Model-class), 25
functionDefinitions, Model-method (Model-class), 25
functionDefinitions<- (Model-class), 25
functionDefinitions<-, Model-method (Model-class), 25
givenName (ModelCreator-class), 27
givenName, ModelCreator-method (ModelCreator-class), 27
givenName<-, ModelCreator-method (ModelCreator-class), 27
glyphCurve (ReactionGlyph-class), 36
glyphCurve, ReactionGlyph-method (ReactionGlyph-class), 36
glyphCurve, SpeciesReferenceGlyph-method (SpeciesReferenceGlyph-class), 55
glyphCurve<-, ReactionGlyph-class), 36
glyphCurve<-, SpeciesReferenceGlyph-method (SpeciesReferenceGlyph-class), 55
graph, 40
GraphicalObject, 7, 23, 36, 53, 55, 59
graphicalObject (TextGlyph-class), 58
graphicalObject, TextGlyph-method (TextGlyph-class), 58
GraphicalObject-class, 19
graphicalObject<-, (TextGlyph-class), 58
graphicObject<-,TextGlyph-method (TextGlyph-class), 58
hasOnlySubstanceUnits (Species-class), 50
hasOnlySubstanceUnits, Species-method (Species-class), 50
hasOnlySubstanceUnits<- (Species-class), 50
hasOnlySubstanceUnits<-, Species-method (Species-class), 50
height (Dimensions-class), 14
height, Dimensions-method (Dimensions-class), 14
height<-, Dimensions-method (Dimensions-class), 14
id (UnitDefinition-class), 62
id, BoundingBox-method (BoundingBox-class), 3
id, Compartment-method (Compartment-class), 5
id, CompartmentType-method (CompartmentType-class), 7
id, Event-method (Event-class), 15
id, FunctionDefinition-method (FunctionDefinition-class), 18
id<-, GraphicalObject-method (GraphicalObject-class), 19
id<-, Layout-method (Layout-class), 22
id<-, Model-method (Model-class), 25
id<-, Parameter-method (Parameter-class), 30
id<-, Reaction-method (Reaction-class), 34
id<-, SimpleSpeciesReference-method (SimpleSpeciesReference-class), 49
id<-, Species-method (Species-class), 50
id<-, SpeciesType-method (SpeciesType-class), 56
id<-, UnitDefinition-method (UnitDefinition-class), 62
infos (SBMLProblems-class), 41
infos, SBMLProblems-method (SBMLProblems-class), 41
initialAmount (Species-class), 50
initialAmount, Species-method (Species-class), 50
initialAmount<-, Species-method (Species-class), 50
initialAssignments, Model-method (Model-class), 25
initialAssignments<-, Model-method (Model-class), 25
initialAssignments<-, Model-method (Model-class), 25
initialAssignments<-, Model-method (Model-class), 25
initialAssignments<-, Model-method (Model-class), 25
initialConcentration (Species-class), 50
initialConcentration, Species-method (Species-class), 50
initialConcentration<-, Species-class), 50
initialAssignments, Model-method (Model-class), 25
initialConcentration<-, Species-method
( Species-class), 50

kind(Unit-class), 61
kind, Unit-method(Unit-class), 61
kind<-, Unit-method(Unit-class), 61

KineticLaw, 43, 44
kineticLaw(Reaction-class), 34
kineticLaw, Reaction-method
(Reaction-class), 34

Layout, 25
Layout-class, 22
layouts(Model-class), 25
layouts, Model-method
(Model-class), 25
layouts<-, Model-method
(Model-class), 25

level(SBML-class), 38
level, SBML-method(SBML-class), 38
level<-, SBML-method(SBML-class), 38

LineSegment, 11
LineSegment-class, 24

math, 63
math(KineticLaw-class), 21
math, Constraint-method
(Constraint-class), 9
math, Delay-method(Delay-class), 12
math, EventAssignment-method
(EventAssignment-class), 16
math, FunctionDefinition-method
(FunctionDefinition-class), 18

math, InitialAssignment-method
(InitialAssignment-class), 20

math, KineticLaw-method
(KineticLaw-class), 21
math, ParameterRule-method
(ParameterRule-class), 31
math, Rule-method(Rule-class), 37

math, Trigger-method
(Trigger-class), 60
math<-, (KineticLaw-class), 21
math<-, Constraint-method
(Constraint-class), 9
math<-, Delay-method
(Delay-class), 12
math<-, EventAssignment-method
(EventAssignment-class), 16
math<-, FunctionDefinition-method
(FunctionDefinition-class), 18

math<-, InitialAssignment-method
(InitialAssignment-class), 20

math<-, KineticLaw-method
(KineticLaw-class), 21
math<-, ParameterRule-method
(ParameterRule-class), 31
math<-, Rule-method(Rule-class), 37
math<-, StoichiometryMath-method
(StoichiometryMath-class), 57

math<-, Trigger-method
(Trigger-class), 60

matrix, 44
message, 41

metaId(SBase-class), 42
metaId, SBase-method
(SBase-class), 42
metaId<-, SBase-method
(SBase-class), 42

Model, 38, 45, 48
model(SBML-class), 38
model, SBML-method(SBML-class), 38

Model-class, 25
model<-, SBML-method(SBML-class), 38

ModelCreator, 28
ModelCreator-class, 27

ModellHistory, 25
modelHistory(Model-class), 25
modelHistory, Model-method
(Model-class), 25

ModelHistory-class, 28
modelHistory<-, (Model-class), 25
modelHistory<-,Model-method (Model-class), 25
modelQualifierType (CVTerm-class), 4
modelQualifierType,CVTerm-method (CVTerm-class), 4
modelQualifierType<-, (CVTerm-class), 4
modelQualifierType<-,CVTerm-method (CVTerm-class), 4
modifiedDate (ModelHistory-class), 28
modifiedDate,ModelHistory-method (ModelHistory-class), 28
modifiedDate<-, (ModelHistory-class), 28
modifiedDate<-,ModelHistory,character-method (ModelHistory-class), 28
modifiedDate<-,ModelHistory,POSIXt-method (ModelHistory-class), 28
modifiedDate<-,ModelHistory-method (ModelHistory-class), 28
modifiedDate<-, (ModelHistory-class), 28
modifiers (Reaction-class), 34
modifiers,Reaction-method (Reaction-class), 34
modifiers<-,Reaction-method (Reaction-class), 34
modifiers<-, (Reaction-class), 34
ModifierSpeciesReference, 34
ModifierSpeciesReference-class, 29
msg (Constraint-class), 9
msg,Constraint-method (Constraint-class), 9
msg<-, (Constraint-class), 9
msg<-,Constraint-method (Constraint-class), 9
multiplier (Unit-class), 61
multiplier,Unit-method (Unit-class), 61
multiplier<-,Unit-method (Unit-class), 61
name (UnitDefinition-class), 62
name,Compartment-method (Compartment-class), 5
name,CompartmentType-method (CompartmentType-class), 7
name,Event-method (Event-class), 15
name<-,Reaction-method (Reaction-class), 34
name<-,Parameter-method (Parameter-class), 30
name<-,ParameterRule-method (ParameterRule-class), 31
name<-,Species-method (Species-class), 50
name<-,SpeciesType-method (SpeciesType-class), 56
msg<-,UnitDefinition-method (UnitDefinition-class), 62
notes (SBase-class), 42
notes<-,SBase-method (SBase-class), 42
notes<-,SBase-method (SBase-class), 42
offset (Unit-class), 61
offset,Unit-method (Unit-class), 61
offset<-,Unit-method (Unit-class), 61
offset<-, (Unit-class), 61
oldClass, 39
<table>
<thead>
<tr>
<th>Class/Method</th>
</tr>
</thead>
<tbody>
<tr>
<td>OptionalCurve-class</td>
</tr>
<tr>
<td>(Curve-class), 11</td>
</tr>
<tr>
<td>OptionalDelay-class</td>
</tr>
<tr>
<td>(Delay-class), 12</td>
</tr>
<tr>
<td>OptionalKineticLaw-class</td>
</tr>
<tr>
<td>(KineticLaw-class), 21</td>
</tr>
<tr>
<td>OptionalModelHistory-class</td>
</tr>
<tr>
<td>(ModelHistory-class), 28</td>
</tr>
<tr>
<td>OptionalStoichiometryMath-class</td>
</tr>
<tr>
<td>(StoichiometryMath-class), 57</td>
</tr>
<tr>
<td>organization</td>
</tr>
<tr>
<td>(ModelCreator-class), 27</td>
</tr>
<tr>
<td>organization, ModelCreator-method</td>
</tr>
<tr>
<td>(ModelCreator-class), 27</td>
</tr>
<tr>
<td>organization-, ModelCreator-method</td>
</tr>
<tr>
<td>(ModelCreator-class), 27</td>
</tr>
<tr>
<td>originOfText (TextGlyph-class), 58</td>
</tr>
<tr>
<td>originOfText, TextGlyph-method</td>
</tr>
<tr>
<td>(TextGlyph-class), 58</td>
</tr>
<tr>
<td>originOfText-, TextGlyph-method</td>
</tr>
<tr>
<td>(TextGlyph-class), 58</td>
</tr>
<tr>
<td>outside (Compartment-class), 5</td>
</tr>
<tr>
<td>outside, Compartment-method</td>
</tr>
<tr>
<td>(Compartment-class), 5</td>
</tr>
<tr>
<td>outside-, Compartment-method</td>
</tr>
<tr>
<td>(Compartment-class), 5</td>
</tr>
<tr>
<td>Parameter, 2, 16, 21, 25, 31, 33, 43, 44, 47, 48</td>
</tr>
<tr>
<td>Parameter-class, 30</td>
</tr>
<tr>
<td>ParameterRule-class, 31</td>
</tr>
<tr>
<td>parameters (Model-class), 25</td>
</tr>
<tr>
<td>parameters, KineticLaw-method</td>
</tr>
<tr>
<td>(KineticLaw-class), 21</td>
</tr>
<tr>
<td>parameters, Model-method</td>
</tr>
<tr>
<td>(Model-class), 25</td>
</tr>
<tr>
<td>parameters, SOSResult-method</td>
</tr>
<tr>
<td>(SOSResult-class), 47</td>
</tr>
<tr>
<td>parameters-, Model-class</td>
</tr>
<tr>
<td>(Model-class), 25</td>
</tr>
<tr>
<td>Point-class, 32</td>
</tr>
<tr>
<td>position (BoundingBox-class), 3</td>
</tr>
<tr>
<td>position-, BoundingBox-method</td>
</tr>
<tr>
<td>(BoundingBox-class), 3</td>
</tr>
<tr>
<td>POSIXt, 28</td>
</tr>
<tr>
<td>products (Reaction-class), 34</td>
</tr>
<tr>
<td>products, Reaction-method</td>
</tr>
<tr>
<td>(Reaction-class), 34</td>
</tr>
<tr>
<td>products-, Reaction-method</td>
</tr>
<tr>
<td>(Reaction-class), 34</td>
</tr>
<tr>
<td>protocol (Experiment-class), 17</td>
</tr>
<tr>
<td>protocol, Experiment-method</td>
</tr>
<tr>
<td>(Experiment-class), 17</td>
</tr>
<tr>
<td>protocol-, Experiment-method</td>
</tr>
<tr>
<td>(Experiment-class), 17</td>
</tr>
<tr>
<td>qualifierType (CVTerm-class), 4</td>
</tr>
<tr>
<td>qualifierType, CVTerm-method</td>
</tr>
<tr>
<td>(CVTerm-class), 4</td>
</tr>
<tr>
<td>qualifierType-, CVTerm-method</td>
</tr>
<tr>
<td>(CVTerm-class), 4</td>
</tr>
<tr>
<td>RateRule-class, 33</td>
</tr>
<tr>
<td>reactants (Reaction-class), 34</td>
</tr>
<tr>
<td>reactants, Reaction-method</td>
</tr>
<tr>
<td>(Reaction-class), 34</td>
</tr>
<tr>
<td>reactants-, Reaction-method</td>
</tr>
<tr>
<td>(Reaction-class), 34</td>
</tr>
<tr>
<td>Reaction, 21, 25, 29, 36, 47–49, 54</td>
</tr>
<tr>
<td>reaction (ReactionGlyph-class), 36</td>
</tr>
<tr>
<td>reaction, ReactionGlyph-method</td>
</tr>
<tr>
<td>(ReactionGlyph-class), 36</td>
</tr>
<tr>
<td>Reaction-class, 34</td>
</tr>
<tr>
<td>reaction-, ReactionGlyph-method</td>
</tr>
<tr>
<td>(ReactionGlyph-class), 36</td>
</tr>
<tr>
<td>ReactionGlyph, 23</td>
</tr>
<tr>
<td>ReactionGlyph-class, 36</td>
</tr>
<tr>
<td>reactionGlyphs (Layout-class), 22</td>
</tr>
<tr>
<td>reactionGlyphs, Layout-method</td>
</tr>
<tr>
<td>(Layout-class), 22</td>
</tr>
<tr>
<td>reactionGlyphs-, Layout-method</td>
</tr>
<tr>
<td>(Layout-class), 22</td>
</tr>
<tr>
<td>reactions (Model-class), 25</td>
</tr>
<tr>
<td>reactions, Model-method</td>
</tr>
<tr>
<td>(Model-class), 25</td>
</tr>
</tbody>
</table>
reactions, SOSDesign-method
(SOSDesign-class), 43
reactions, SOSResult-method
(SOSResult-class), 47
reactions <- (Model-class), 25
reactions <- , Experiment-method
(Experiment-class), 17
reactions <- , Method
(Model-class), 25
reactions <- , SOSDesign-method
(SOSDesign-class), 43
resources (CVTerm-class), 4
resources, CVTerm-method
(CVTerm-class), 4
resources <- (CVTerm-class), 4
resources <- , CVTerm-method
(CVTerm-class), 4
result (Experiment-class), 17
result, Experiment-method
(Experiment-class), 17
result <- , Experiment-method
(Experiment-class), 17
reversible (Reaction-class), 34
reversible, Reaction-method
(Reaction-class), 34
reversible <- (Reaction-class), 34
reversible <- , Reaction-method
(Reaction-class), 34
role
(SpeciesReferenceGlyph-class), 55
role, SpeciesReferenceGlyph-method
(SpeciesReferenceGlyph-class), 55
role <-
(SpeciesReferenceGlyph-class), 55
role <- , SpeciesReferenceGlyph-method
(SpeciesReferenceGlyph-class), 55
rsbml_check (SBMLDocument-class), 39
rsbml_check, SBMLDocument-method
(SBMLDocument-class), 39
rsbml_doc (SBML-class), 38
rsbml_doc, SBML-method
(SBML-class), 38
rsbml_dom (SBMLDocument-class), 39
rsbml_dom, SBMLDocument-method
(SBMLDocument-class), 39
rsbml_graph (SBMLDocument-class), 39
INDEX

SBMLWarning-class
(SBMLProblem-class), 41
sboTerm(SBase-class), 42
sboTerm(SBase-method
(SBase-class), 42
sboTerm<- (SBase-class), 42
sboTerm<-, SBase-method
(SBase-class), 42
sec(math), 63
sech(math), 63
show,Describable-method
(describe), 13
show,SBMLProblem-method
(SBMLProblem-class), 41
SimpleSpeciesReference, 29, 34
SimpleSpeciesReference-class, 49
simulate, 40, 46
simulate (SOSExperiment-class), 44
simulate, SBML-method
(SBML-class), 38
simulate, SBMLDocument-method
(SBMLDocument-class), 39
simulate, SOSExperiment-method
(SOSExperiment-class), 44
size (Compartment-class), 5
size, Compartment-method
(Compartment-class), 5
size<- (Compartment-class), 5
size<-, Compartment-method
(Compartment-class), 5
SOSDesign, 45, 47
SOSDesign-class, 43
SOSExperiment, 18, 44, 47–49
SOSExperiment-class, 44
SOSProtocol, 40, 43, 45
SOSProtocol-class, 46
SOSResult, 45
SOSResult-class, 47
SOSSubject, 45
SOSSubject-class, 48
spatialDimensions
(Compartment-class), 5
spatialDimensions, Compartment-method
(Compartment-class), 5
spatialDimensions<- (Compartment-class), 5
spatialDimensions<-, Compartment-method
(Compartment-class), 5
spatialSizeUnits (Species-class), 50
spatialSizeUnits, Species-method
(Species-class), 50
spatialSizeUnits<-
(Species-class), 50
spatialSizeUnits<-, Species-method
(Species-class), 50
Species, 2, 5, 16, 25, 29, 33, 34, 43, 47–49,
52–57
species (SpeciesGlyph-class), 53
species, Model-method
(Model-class), 25
species, SimpleSpeciesReference-method
(SimpleSpeciesReference-class), 49
species, SOSResult-method
(SOSResult-class), 47
species, SpeciesConcentrationRule-method
(SpeciesConcentrationRule-class), 52
species, SpeciesGlyph-method
(SpeciesGlyph-class), 53
Species-class, 50
species<- (SpeciesGlyph-class), 53
species<-, Model-method
(Model-class), 25
species<-, SimpleSpeciesReference-method
(SimpleSpeciesReference-class), 49
species<-, SpeciesConcentrationRule-method
(SpeciesConcentrationRule-class), 52
species<-, SpeciesGlyph-method
(SpeciesGlyph-class), 53
SpeciesConcentrationRule-class, 52
SpeciesGlyph, 23, 55
speciesGlyph
(SpeciesReferenceGlyph-class), 55
speciesGlyph, SpeciesReferenceGlyph-method
(SpeciesReferenceGlyph-class), 55
SpeciesGlyph-class, 53
speciesGlyph<-
(SpeciesReferenceGlyph-class), 55
speciesGlyph<-, SpeciesReferenceGlyph-method
(SpeciesReferenceGlyph-class), 55
speciesGlyphs (Layout-class), 22
speciesGlyphs, Layout-method
(Layout-class), 22
speciesGlyphs<-, Layout-method
warns(SBMLProblems-class), 41
warns,SBMLProblems-method
  (SBMLProblems-class), 41
width(Dimensions-class), 14
width,Dimensions-method
  (Dimensions-class), 14
width<-(Dimensions-class), 14
width<-,Dimensions-method
  (Dimensions-class), 14

x(Point-class), 32
x,Point-method(Point-class), 32
x<-(Point-class), 32
x<-,Point-method(Point-class), 32

y(Point-class), 32
y,Point-method(Point-class), 32
y<-(Point-class), 32
y<-,Point-method(Point-class), 32

z(Point-class), 32
z,Point-method(Point-class), 32
z<-(Point-class), 32
z<-,Point-method(Point-class), 32