

libSBML

Frank Bergmann and Sarah Keating

Getting started ...

libsbml-5.0.0

examples

c

c++

csharp

java

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python

ruby

sample-models

from-spec

level-2

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convertSBML

evaluateMath

extractReactionInfo

extractReactions

printMath

printSBML

readSBML

translateMath

validateSBML

libsbml-5.0.0

examples

c

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level-2

level-3

convertSBML

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extractReactionInfo

extractReactions

printMath

printSBML

readSBML

translateMath

validateSBML

```

#!/usr/bin/perl

use File::Basename;
use blib '../src/bindings/perl';
use LibSBML;
use strict;

my $filename = shift()
  || do { printf STDERR "\n usage: @{{basename($0)}}<filename>\n\n";
          exit (1);
        };

my $rd = new LibSBML::SBMLReader();
my $d = $rd->readSBML($filename);

$d->printErrors();

my $m = $d->getModel() || exit (2);

my $level = $d->getLevel();
my $version = $d->getVersion();

printf("\n");
printf("File: %s (Level %u, version %u)\n",
       basename($filename), $level, $version);
printf( "      ");

($level == 1) ? printf("model name: %s\n", $m->getName()) : printf(" model id: %s\n",
    $m->isSetId() ? $m->getId() : '(empty)');

printf( "      compartments: %d\n", $m->getNumCompartments    ( ) );
printf( "      species: %d\n", $m->getNumSpecies              ( ) );
printf( "      parameters: %d\n", $m->getNumParameters        ( ) );
printf( "      reactions: %d\n", $m->getNumReactions          ( ) );
printf( "\n" );

```

```
#!/usr/bin/perl
```

```
use File::Basename;  
use blib '../src/bindings/perl';  
use LibSBML;  
use strict;
```

```
my $filename = shift()  
  || do { printf STDERR "\n usage: @{{basename($0)}}<filename>\n\n";  
          exit (1);  
        };
```

```
my $rd = new LibSBML::SBMLReader();  
my $d = $rd->readSBML($filename);
```

```
$d->printErrors();
```

```
my $m = $d->getModel() || exit (2);
```

```
my $level = $d->getLevel();  
my $version = $d->getVersion();
```

```
printf("\n");  
printf("File: %s (Level %u, version %u)\n",  
       basename($filename), $level, $version);  
printf( "      ");
```

```
($level == 1) ? printf("model name: %s\n", $m->getName()) : printf(" model id: %s\n",  
$m->isSetId() ? $m->getId() : '(empty)');
```

```
printf( " compartments: %d\n", $m->getNumCompartments    ( ) );  
printf( " species: %d\n", $m->getNumSpecies              ( ) );  
printf( " parameters: %d\n", $m->getNumParameters        ( ) );  
printf( " reactions: %d\n", $m->getNumReactions          ( ) );  
printf( "\n" );
```

```
#!/usr/bin/perl
```

```
use File::Basename;  
use blib '../src/bindings/perl';  
use LibSBML;  
use strict;
```

```
my $filename = shift()  
  || do { printf STDERR "\n usage: @{{basename($0)}}<filename>\n\n";  
          exit (1);  
        };
```

```
my $rd = new LibSBML::SBMLReader();  
my $d = $rd->readSBML($filename);
```

```
$d->printErrors();
```

```
my $m = $d->getModel() || exit (2);
```

```
my $level = $d->getLevel();  
my $version = $d->getVersion();
```

```
printf("\n");  
printf("File: %s (Level %u, version %u)\n",  
       basename($filename), $level, $version);  
printf(" ");
```

```
($level == 1) ? printf("model name: %s\n", $m->getName()) : printf(" model id: %s\n",  
    $m->isSetId() ? $m->getId() : '(empty)');
```

```
printf(" compartments: %d\n", $m->getNumCompartments    ( ) );  
printf(" species: %d\n", $m->getNumSpecies              ( ) );  
printf(" parameters: %d\n", $m->getNumParameters        ( ) );  
printf(" reactions: %d\n", $m->getNumReactions          ( ) );  
printf("\n");
```



```
#!/usr/bin/perl
```

```
use File::Basename;  
use blib '../src/bindings/perl';  
use LibSBML;  
use strict;
```

```
my $filename = shift()  
  || do { printf STDERR "\n usage: @{{basename($0)}}<filename>\n\n";  
          exit (1);  
        };
```

```
my $rd = new LibSBML::SBMLReader();  
my $d = $rd->readSBML($filename);
```

```
$d->printErrors();
```

```
my $m = $d->getModel() || exit (2);
```

```
my $level = $d->getLevel();  
my $version = $d->getVersion();
```

```
printf("\n");  
printf("File: %s (Level %u, version %u)\n",  
       basename($filename), $level, $version);  
printf(" ");
```

```
($level == 1) ? printf("model name: %s\n", $m->getName()) : printf(" model id: %s\n",  
$m->isSetId() ? $m->getId() : '(empty)');
```

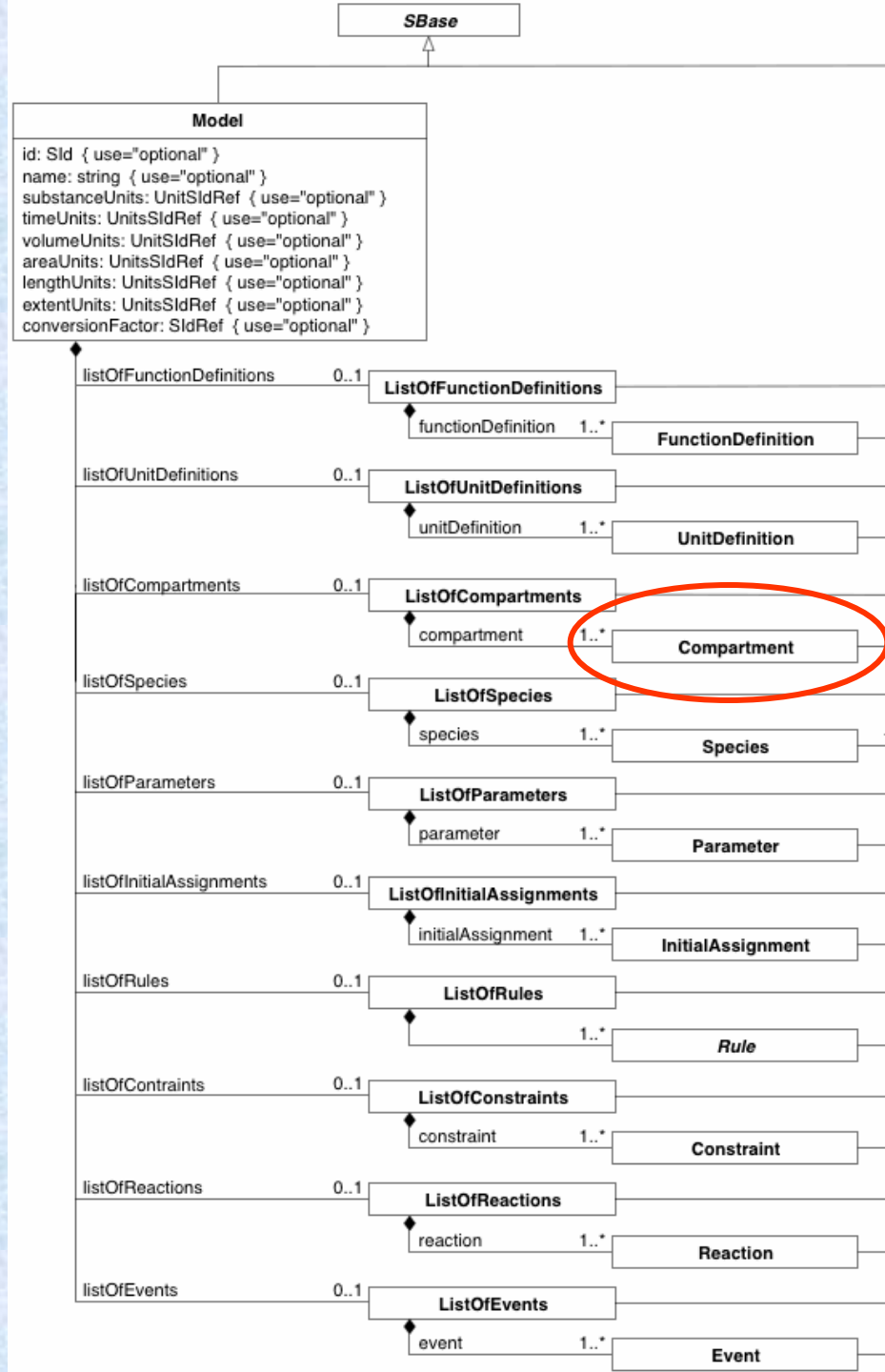
```
printf(" compartments: %d\n", $m->getNumCompartments ());  
printf(" species: %d\n", $m->getNumSpecies ());  
printf(" parameters: %d\n", $m->getNumParameters ());  
printf(" reactions: %d\n", $m->getNumReactions ());  
printf("\n");
```


Manipulating SBML – the API



Components in SBML specification

Components in SBML specification

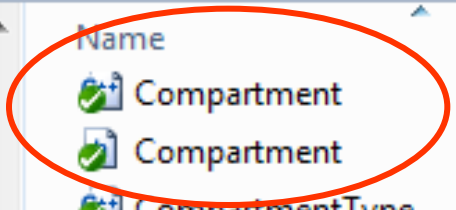


Navigation icons: back, forward, refresh, search. Address bar: << src >> sbml >. Search: Search sbml

Organize > Include in library >> View icons: list, compare, help

- src
 - .svn
 - bindings
 - common
 - sbml (selected)
 - .svn
 - annotation
 - common
 - compress
 - extension
 - math
 - packages
 - test
 - units
 - util
 - validator
 - xml

- | Name |
|--------------------|
| Compartment |
| Compartment |
| CompartmentType |
| CompartmentType |
| Constraint |
| Constraint |
| Delay |
| Delay |
| Event |
| Event |
| EventAssignment |
| EventAssignment |
| FunctionDefinition |
| FunctionDefinition |
| InitialAssignment |



90 items

SBase



Compartment

id : SId
name : string {use="optional"}
spatialDimensions : integer {use="optional"}
size : double {use="optional"}
units : SId {use="optional"}
constant : boolean {use="optional"}

```
<compartment id="Yeast" units="litre" constant="true"/>
```


(Unknown Scope)

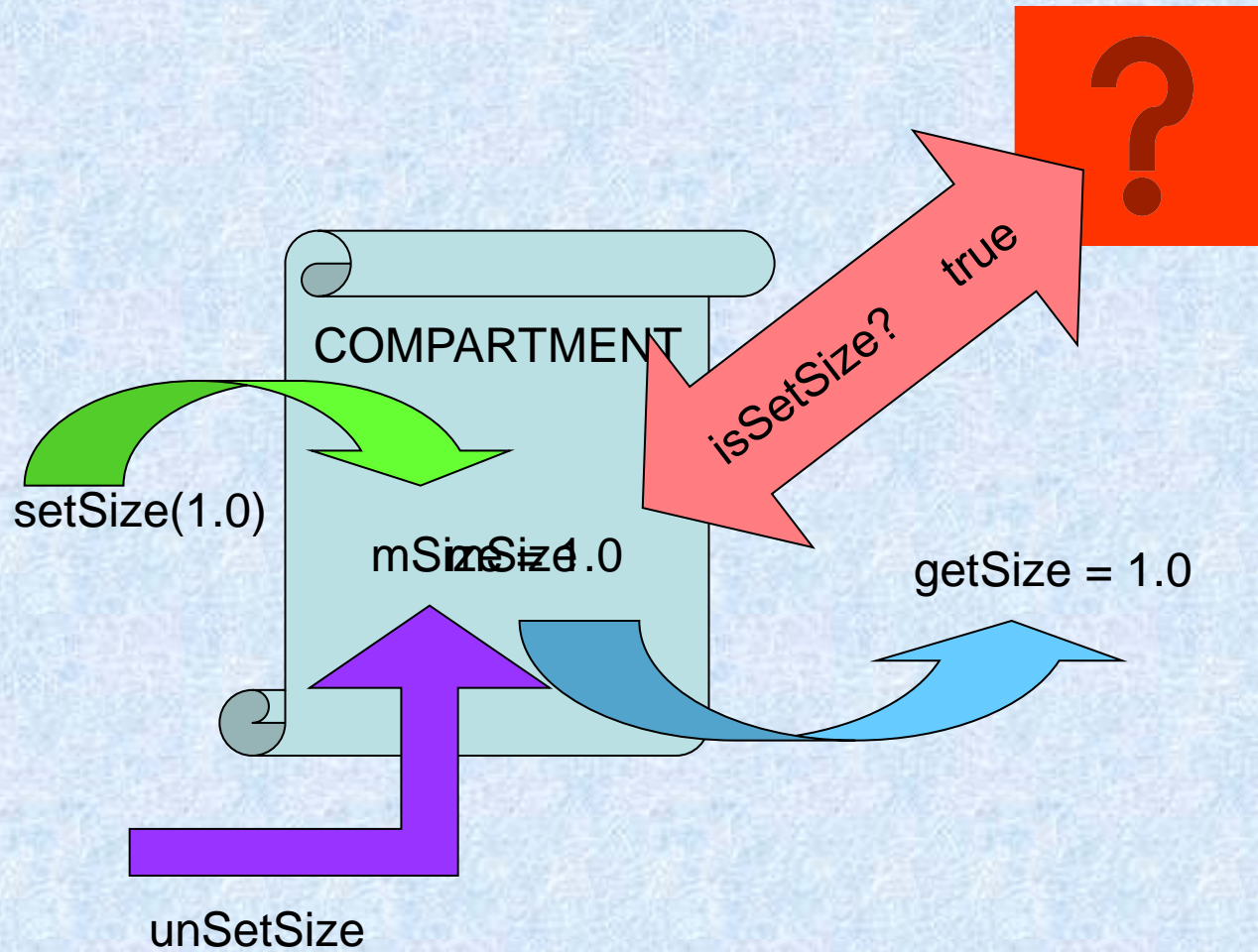
```
1  #ifndef Compartment_h
2  #define Compartment_h
3
4  class LIBSBML_EXTERN Compartment : public SBase
5  {
6  public:
7
8      ...
9
10 protected:
11
12     std::string      mId;
13     std::string      mName;
14     double           mSpatialDimensionsDouble;
15     double           mSize;
16     std::string      mUnits;
17     std::string      mOutside;
18     bool             mConstant;
19
20     bool             mIsSetSize;
21     bool             mIsSetSpatialDimensions;
22     bool             mIsSetConstant;
23 };
24
```

Compartment

```
id : SId
name : string {use="optional"}
spatialDimensions : integer {use="optional"}
size : double {use="optional"}
units : SId {use="optional"}
constant : boolean {use="optional"}
```

```
1
2
3
4
5
6 public:
7
8   ...
9
10 protected:
11
12     std::string    mId;
13     std::string    mName;
14     double         mSpatialDimensionsDouble;
15     double         mSize;
16     std::string    mUnits;
17     std::string    mOutside;
18     bool           mConstant;
19
20     bool           mIsSetSize;
21     bool           mIsSetSpatialDimensions;
22     bool           mIsSetConstant;
23 };
24
```


Attribute API



File Edit Shell Debug Options Windows Help

Python 2.6.6 (r266:84297, Aug 24 2010, 18:13:38) [MSC v.1500 64 bit (AMD64)] on win32

Type "copyright", "credits" or "license()" for more information.

```
*****
Personal firewall software may warn about the connection IDLE
makes to its subprocess using this computer's internal loopback
interface. This connection is not visible on any external
interface and no data is sent to or received from the Internet.
*****
```

IDLE 2.6.6

```
>>> import libsbml
>>> r = libsbml.SBMLReader()
>>> doc = r.readSBML("C:\working\sbml-files\compOnly.xml")
>>> comp = doc.getModel().getCompartment(0)
>>> print("Compartment id: %s" % (comp.getId()))
Compartment id: c
>>> comp.isSetSize()
False
>>> comp.getSize()
nan
>>> comp.setSize(2.3)
0
>>> comp.isSetSize()
True
>>> comp.getSize()
2.2999999999999998
>>> comp.isSetUnits()
False
>>> comp.isSetSpatialDimensions()
False
>>> comp.setUnits("litre")
0
>>> comp.setSpatialDimensions(3)
0
>>> comp.isSetUnits()
True
>>> |
```

```
>>> import libsbml
>>> r = libsbml.SBMLReader()
>>> doc = r.readSBML("C:\working\sbml-files\compOnly.xml")
>>> comp = doc.getModel().getCompartment(0)
>>> print("Compartment id: %s" % (comp.getId()))
Compartment id: c
```

```
>>> comp.setSize()  
False  
>>> comp.getSize()  
nan  
>>> comp.setSize(2.3)  
0  
>>> comp.setSize()  
True  
>>> comp.getSize()  
2.2999999999999998
```

```
>>> comp.isSetUnits ()
False
>>> comp.isSetSpatialDimensions ()
False
>>> comp.setUnits ("litre")
0
>>> comp.setSpatialDimensions (3)
0
>>> comp.isSetUnits ()
True
>>> |
```

Public Member Functions

...

const std::string & [getCompartmentType](#) () const

Get the compartment type of this Compartment, as indicated by the Compartment object's "compartmentType" attribute value.

unsigned int [getSpatialDimensions](#) () const

Get the number of spatial dimensions of this Compartment object.

double [getSize](#) () const

Get the size of this Compartment.

...

bool [isSetCompartmentType](#) () const

*Predicate returning **true** or **false** depending on whether this Compartment's "compartmentType" attribute has been set.*

bool [isSetSize](#) () const

*Predicate returning **true** or **false** depending on whether this Compartment's "size" attribute has been set.*

...

void [setCompartmentType](#) (const std::string &sid)

Sets the "compartmentType" attribute of this Compartment.

void [setSpatialDimensions](#) (unsigned int value)

Sets the "spatialDimensions" attribute of this Compartment.

void [setSize](#) (double value)

Sets the "size" attribute (or "volume" in SBML Level 1) of this Compartment.

...

void [unsetCompartmentType](#) ()

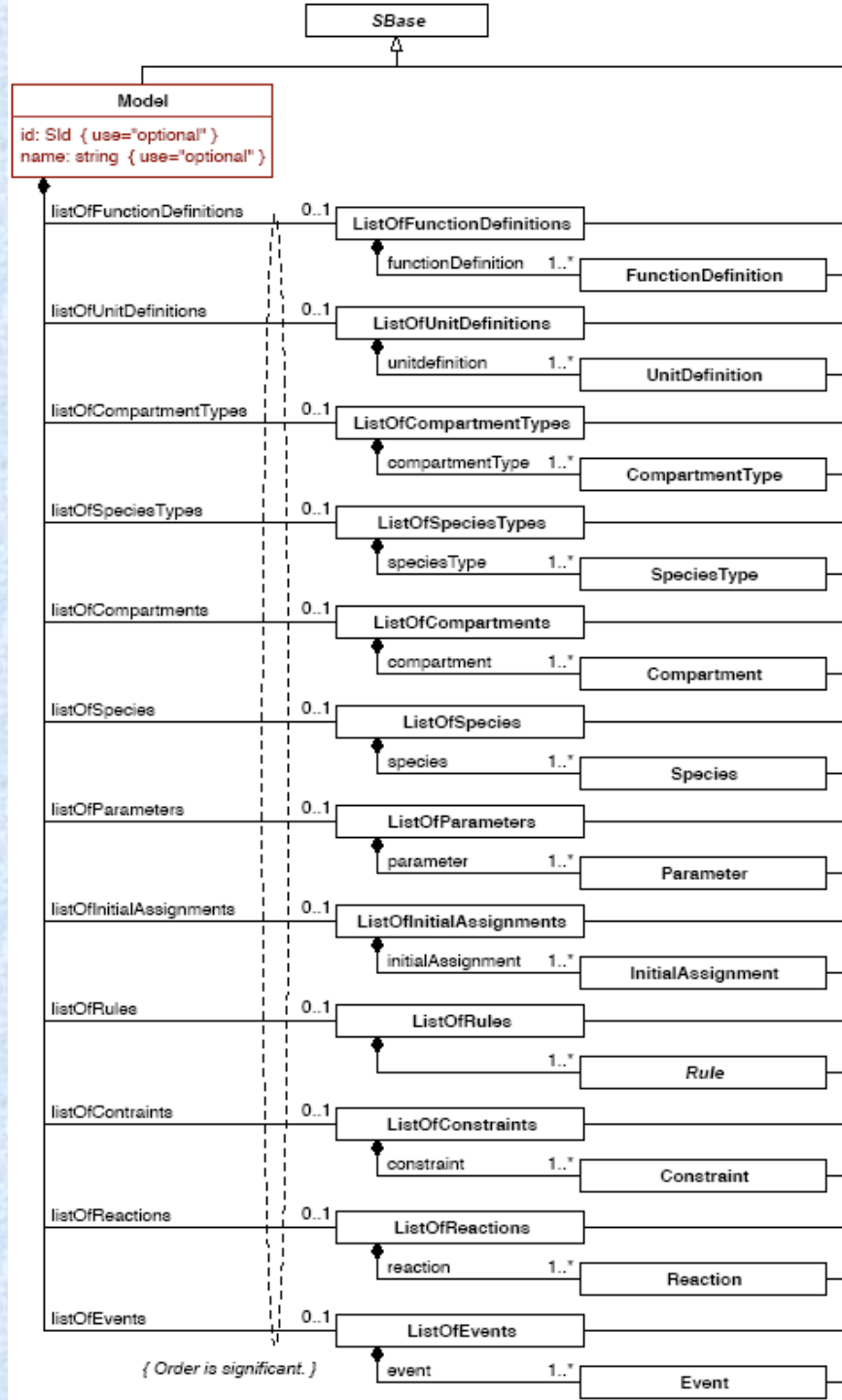
Unsets the value of the "compartmentType" attribute of this Compartment.

void [unsetSize](#) ()

Unsets the value of the "size" attribute of this Compartment.

...

ListOf...Elements



Model.h

Model

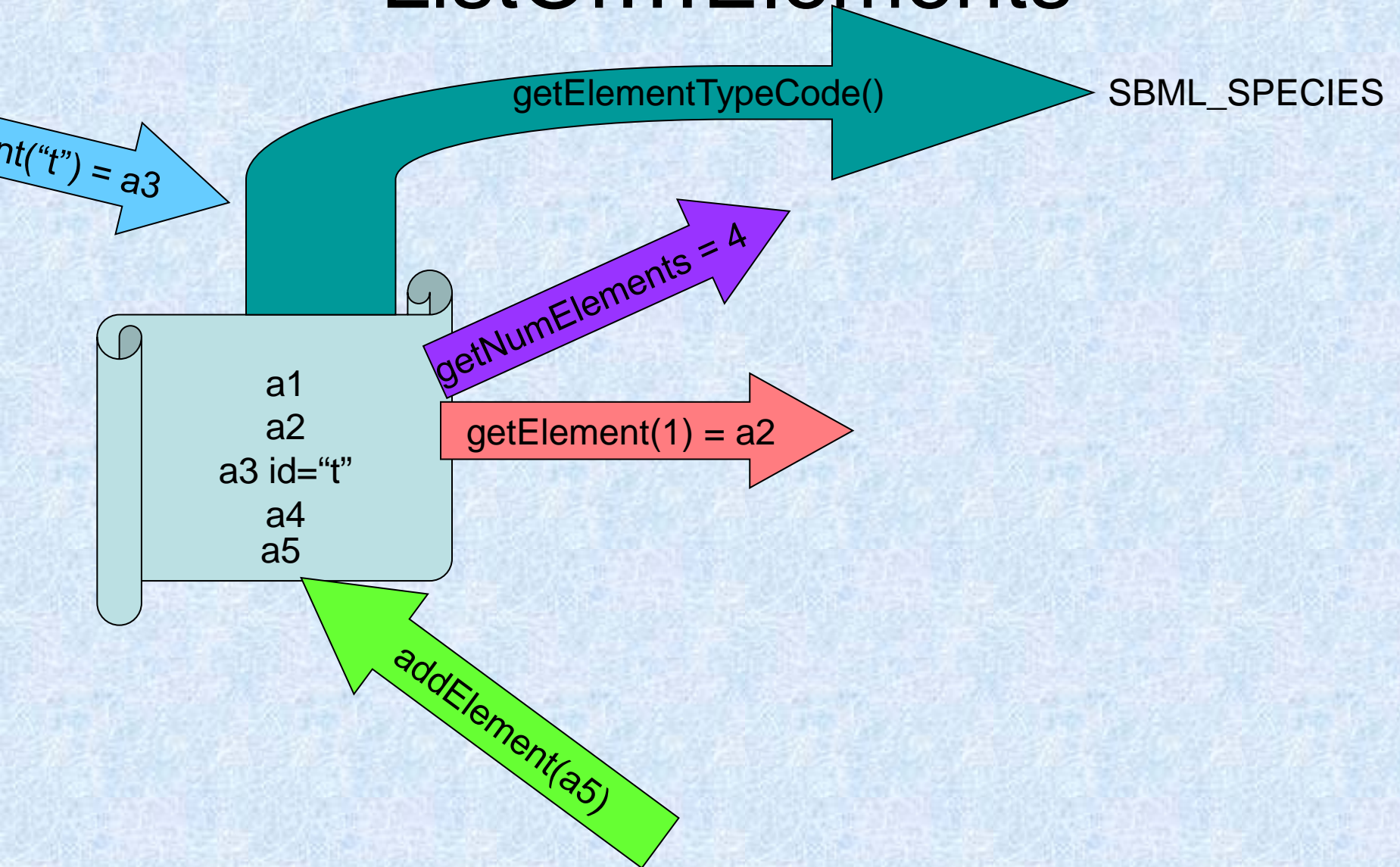
```
ModelHistory*    mHistory;

ListOfFunctionDefinitions    mFunctionDefinitions;
ListOfUnitDefinitions       mUnitDefinitions;
ListOfCompartmentTypes     mCompartmentTypes;
ListOfSpeciesTypes         mSpeciesTypes;
ListOfCompartments         mCompartments;
ListOfSpecies               mSpecies;
ListOfParameters           mParameters;
ListOfInitialAssignments   mInitialAssignments;
ListOfRules                 mRules;
ListOfConstraints           mConstraints;
ListOfReactions             mReactions;
ListOfEvents                mEvents;

ListFormulaUnitsData       mFormulaUnitsData;

#ifdef USE_LAYOUT
    ListOfLayouts mLayouts;
#endif /* USE_LAYOUT */
```

ListOf...Elements



Public Member Functions

	ListOf () <i>Creates a new ListOf items.</i>
virtual	~ListOf () <i>Destroys the given ListOf and its constituent items.</i>
	ListOf (const ListOf &orig) <i>Copy constructor.</i>
ListOf &	operator= (const ListOf &rhs) <i>Assignment operator.</i>
virtual bool	accept (SBMLVisitor &v) const <i>Accepts the given SBMLVisitor.</i>
virtual SBase *	clone () const
void	append (const SBase *item) <i>Adds item to the end of this ListOf items.</i>
void	appendAndOwn (SBase *item) <i>Adds item to the end of this ListOf items.</i>
const SBase *	get (unsigned int n) const
SBase *	get (unsigned int n)
const SBase *	get (const std::string &sid) const
SBase *	get (const std::string &sid)
SBase *	remove (unsigned int n) <i>Removes the nth item from this ListOf items and returns a pointer to it.</i>
SBase *	remove (const std::string &sid) <i>Removes item in this ListOf items with the given id or NULL if no such item exists.</i>
unsigned int	size () const
virtual void	setSBMLDocument (SBMLDocument *d) <i>Sets the parent SBMLDocument of this SBML object.</i>
virtual SBMLTypeCode_t	getTypeCode () const
virtual SBMLTypeCode_t	getItemTypeCode () const
virtual const std::string &	getElementName () const



Which reactions produce a particular species ?

```
unsigned int n;
Model* model = document->getModel();
std::string speciesId;
for (n = 0; n < model->getNumSpecies(); n++)
{
    if (model->getSpecies(n)->getName() == "Glucose-6-Phosphate")
    {
        speciesId = model->getSpecies(n)->getId();
        break;
    }
}
ListOfReactions * myReactions = new ListOfReactions();

for (n = 0; n < model->getNumReactions(); n++)
{
    Reaction * r = model->getReaction(n);

    if (r->getProduct(speciesId) != NULL)
    {
        myReactions->appendAndOwn(r);
    }
}

cout << "Reactions containing Glucose-6-Phosphate as a product:\n";
for (n = 0; n < myReactions->size(); n++)
{
    cout << "Reaction id: " << myReactions->get(n)->getId() << endl;
}
```

C:\ "c:\libsaml_3\win32\bin\validateSBMLD.exe" BIOMD000000000...

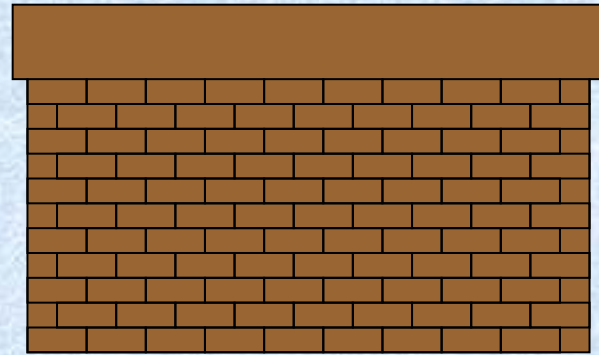
filename: BIOMD000000000051.xml

Reactions containing Glucose-6-Phosphate as a product:

Reaction id: vPTS

Press any key to continue_

Creating SBML – the API




```
use blib '../..'/src/bindings/perl';  
use LibSBML;  
use strict;
```



```
use blib '../..../src/bindings/perl';  
use LibSBML;  
use strict;
```

create the namespace for the level and
version of SBML

```
my $sbmlns = new  
    LibSBML::SBMLNamespaces(3, 1);
```

create the document

```
my $document=new  
    LibSBML::SBMLDocument($sbmlns);
```



```
my $document=new LibSBML::SBMLDocument($sbmlIns);
```

```
# create the Model
```

```
my $model=$document->createModel();
```

```
$model->setId("TestModel");
```

```
my $document=new LibSBML::SBMLDocument($sbmlns);
```

```
my $model=$document->createModel();
```

```
# create the Compartment
```

```
my $compartment=
```

```
    $model->createCompartment();
```

```
$compartment->setId("Compartment_1");
```

```
$compartment->setConstant(1);
```

```
my $document=new LibSBML::SBMLDocument($sbmlns);
```

```
my $model=$document->createModel();
```

```
my $compartment=$model->createCompartment();
```

```
# create the Species
```

```
my $species1=$model->createSpecies();
```

```
$species1->setId("Species_1");
```

```
$species1->setCompartment  
                                ($compartment->getId());
```

```
$species1->setHasOnlySubstanceUnits(0);
```

```
$species1->setBoundaryCondition(0);
```

```
$species1->setConstant(0);
```



```
my $document=new LibSBML::SBMLDocument($sbmlns);
```

```
my $model=$document->createModel();
```

```
my $compartment=$model->createCompartment();
```

```
my $species1=$model->createSpecies();
```

```
my $species2=$model->createSpecies();
```

create the Reactions

```
my $reaction1=$model->createReaction();
```

```
$reaction1->setId("Reaction_1");
```

```
$reaction1->setReversible(0);
```

```
$reaction1->setFast(0);
```

```
my $reaction1=$model->createReaction();  
$reaction1->setId("Reaction_1");  
$reaction1->setReversible(0);  
$reaction1->setFast(0);
```

create the Reactant

```
my $reference1=$reaction1->createReactant();  
$reference1->setSpecies($species1->getId());  
$reference1->setId("SpeciesReference_1");  
$reference1->setConstant(0);
```



```
my $reaction1=$model->createReaction();
```

```
my $reference1=$reaction1->createReactant();
```

create the Product

```
my $reference2= $reaction1->createProduct();
```

```
$reference2->setSpecies($species2->getId());
```

```
$reference2->setId("SpeciesReference_2");
```

```
$reference2->setConstant(0);
```

```
my $reaction1=$model->createReaction();  
my $reference1=$reaction1->createReactant();  
my $reference2= $reaction1->createProduct();
```

create the KineticLaw

```
my $kineticLaw=  
    $reaction1->createKineticLaw();
```

```
my $KLmath=  
    LibSBML::parseFormula('species2 * 2');
```

```
$kineticLaw->setMath($KLmath);
```

Documentation

Add File Add Folder

Home / libsbml / 5.0.0

Name ▾

↑ Parent folder

Mac OS X

Linux

Windows

libSBML-5.0.0-docs.zip

libSBML-5.0.0-docs.tar.gz

libSBML-5.0.0-src.tar.gz


libSBML-5.0.0-src.zip


README.txt


Totals: 8 Items

DOWNLOAD


ONLINE


 [Download libSBML](#)

 [How to install libSBML](#)

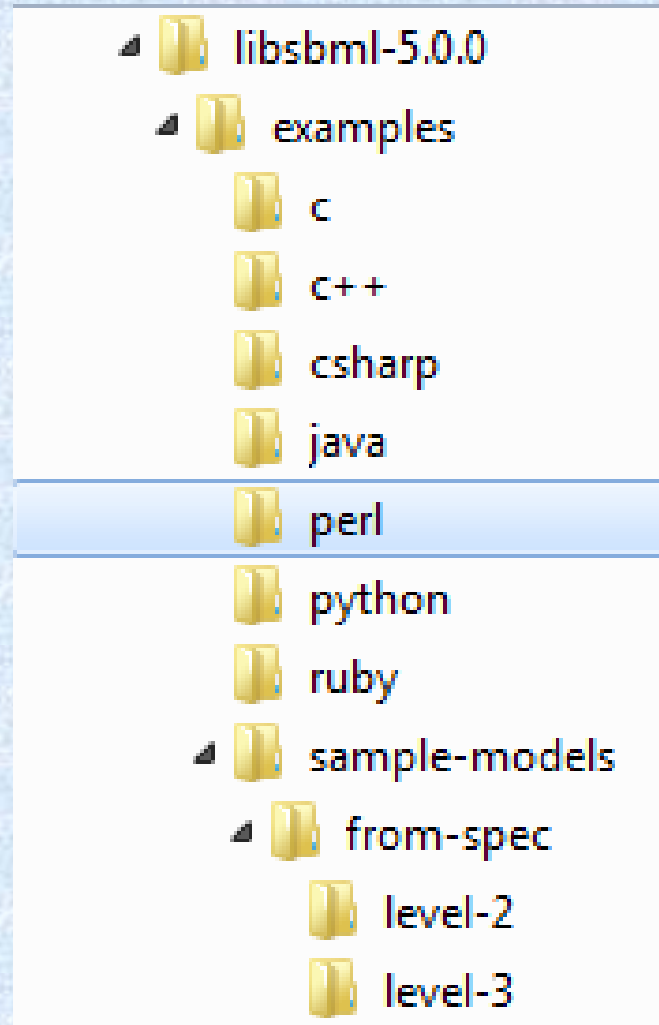
 *Language API docs:*

- C++
- C#
- Java
- Matlab
- Octave
- Python
- C (docs unfinished)
- Perl (docs unfinished)
- Ruby (docs unfinished)

 [Release notes](#)

 [Known issues](#)

Getting started ...



<http://sbml.org/Software/libSBML/Tutorials>