# A short description of the main differences between JSBML and LibSBML

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Although the libraries JSBML and LibSBML for working with files and data structures defined in the standard SBML (Systems Biology Markup Language) are very similar and share a common scope, users should be informed about their major differences to switch from one library from the other one more easily. To this end, the document at hand gives a brief overview of the main differences between the Java<sup>TM</sup> application programming interfaces of both libraries.

In addition, JSBML can be used as a communication layer between the widely spread application CellDesigner and an application that works with JSBML as its internal data structure. This document gives an example that demonstrates how to convert between CellDesigner's plug-in data structures and JSBML objects.

In the same way, it is possible to inter-convert between data structures obtained from LibSBML and JSBML data structures. This document also provides an example of how to read SBML files with LibSBML, to turn them into JSBML data structures, manipulate them and to turn it back for writing into the LibSBML format.

Furthermore, JSBML provides a compatibility module, whose member classes show an identical type declaration as defined in LibSBML. In this way, the compatibility module facilitates switching from LibSBML to JSBML and vice versa by simply exchanging the included JAR file in the project. As for the other two modules, this document also gives an example for the usage of the compatibility module.

## 1 An extended type hierarchy

Whenever multiple elements defined in at least one of the SBML specifications (Hucka et al., 2003a, 2008, 2010) share some attributes, JSBML provides a common super class or at least a common interface that gathers methods for manipulation of the shared properties. In this way, the type hierarchy of JSBML has become more complex (see Figs. 1 to 5 on pages 6–11). Just like in LibSBML (Bornstein et al., 2008), all elements extend the abstract type SBase, but in JSBML, SBase has become an interface. This allows more complex relations between derived data types. In contrast to LibSBML, SBase in JSBML extends three other interfaces: Cloneable, Serializable, and TreeNode. As all elements defined in JSBML override the clone() method from the class java.lang.Object, all JSBML elements can be deeply copied and are therefore cloneable. By extending the interface Serializable, it is possible to store JSBML elements in binary form without explicitly writing it to an SBML file. In this way, programs can easily load and save their in-memory objects or send complex data structures through a network connection without the need of additional file encoding and subsequent parsing. The third interface, TreeNode is actually defined in Java's swing package, but defines a data type independent of any graphical information. It basically defines recursive methods on hierarchically structured data types, such as iteration over all of its successors. In this way, all instances of JSBML's SBase interface can be directly passed to the swing class JTree and hence be easily visualized. Listing 1 on page 7 demonstrates in a simple code example how to parse an SBML file and to immediately display its content on a JFrame. Fig. 6 on page 12 shows an example output when applying the program from Listing 1 on page 7 to SBML test model case00026. The ASTNode class in JSBML also implements all these three interfaces and can hence be cloned, serialized, and visualized in the same way.

#### 1.1 The Assignment class

JSBML unifies all those elements that assign values to some other SBase in SBML (Hucka et al., 2003b) under the interface Assignment. This interface uses the term variable for the element whose value is to be changed depending on some mathematical expression that is also present in the Assignment (because Assignment extends the interface MathContainer). Therefore, an Assignment contains methods such as set-/getVariable(Variable v) and also isSetVariable() as well as unsetVariable(). In addition to that, JSBML also provides the method set-/getSymbol(String symbol) in the InitialAssignment class to make sure that switching from LibSBML to JSBML is quite smoothly. However, the preferred way in JSBML is to apply the methods setVariable either with String or Variable instances as arguments.

#### 1.2 The MathContainer interface

This interface gathers all those elements that may contain mathematical expressions encoded in abstract syntax trees (instances of ASTNode). The abstract class AbstractMathContainer serves



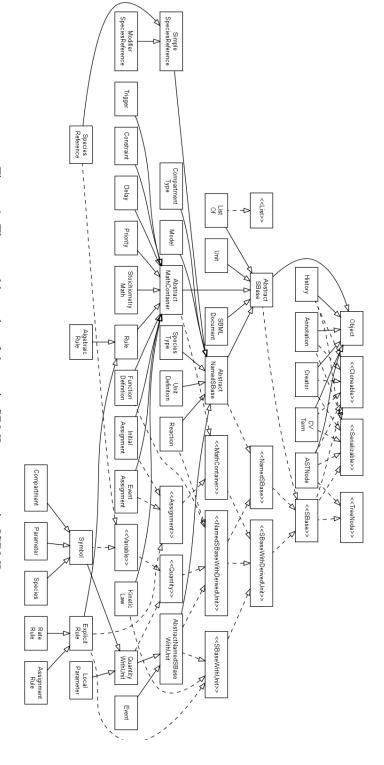


Figure 1: The type hierarchy of the main SBML constructs in JSBML



```
package org.sbml.gui;
1
2
3
   import javax.swing.*;
   import org.sbml.jsbml.*;
6
   public class JSBMLvisualizer extends JFrame {
7
8
     public JSBMLvisualizer(SBMLDocument document) {
9
       super(document.isSetModel() ? document.getModel().getId() : "SBML"
           Visualizer");
10
       getContentPane().add(new JScrollPane(new JTree(document),
11
                JScrollPane.VERTICAL_SCROLLBAR_AS_NEEDED,
12
                JScrollPane.HORIZONTAL_SCROLLBAR_AS_NEEDED));
13
       setDefaultCloseOperation(EXIT_ON_CLOSE);
14
       pack();
15
       setLocationRelativeTo(null);
16
       setVisible(true);
17
18
     /** @param args Expects a valid path to an SBML file. */
19
     public static void main(String[] args) throws Exception {
20
       {\tt UIManager.setLookAndFeel(UIManager.getSystemLookAndFeelClassName());}
21
       new JSBMLvisualizer((new SBMLReader()).readSBML(args[0]));
22
     }
23
24
   }
```

Listing 1: Parsing and visualizing the content of an SBML file



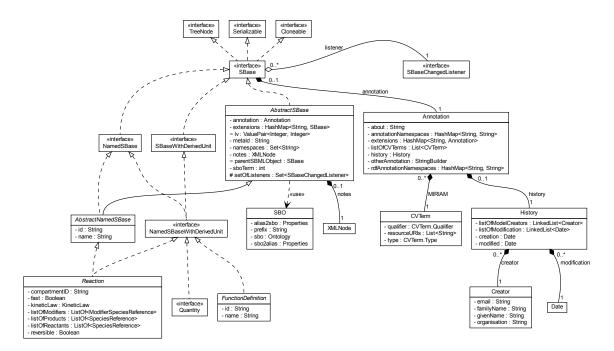


Figure 2: The interface SBase, adapted from (Dräger, 2011). This figure displays the most important top-level data structures of JSBML with main focus on the differences to LibSBML. All other data types that represent SBML constructs in JSBML extend either one of the two abstract classes AbstractSBase or AbstractNamedSBase. The class SB0 parses the ontology file provided on the SBO web site (http://www.ebi.ac.uk/sbo/main/) in OBO format (Open Biomedical Ontologies) using a parser provided by the BioJava project (Holland *et al.*, 2008). For the sake of a clear arrangement, this figure omits methods, fields and other properties.

as actual super class for most of the derived types.

# 2 Differences in the abstract programming interface

JSBML strives to attain an almost complete compatibility to LibSBML. However, the differences in the programming languages C and Java<sup>TM</sup> lead to the necessity of introducing some differences. In some cases, a direct "translation" from C code to Java would not be very elegant. JSBML wants to provide a Java API, whose classes and methods are structured and named and behave like classes and methods in other Java libraries. In this section, we will discuss the most important differences in the APIs of JSBML and LibSBML.



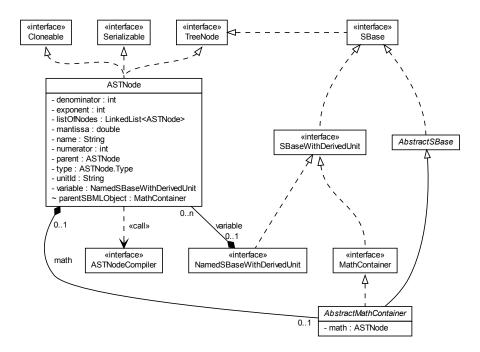


Figure 3: Abstract syntax trees, adapted from (Dräger, 2011). The class AbstractMathContainer severs as the super class for several model components in JSBML. It provides methods to manipulate and access an instance of ASTNode, which can be converted to or read from C-like formula Strings. Internally, AbstractMathContainers only deal with instances of ASTNode. It should be noted that these abstract syntax trees do not implement the SBase interface, but also implement the Java interfaces Cloneable, Serializable, and TreeNode. In this figure, the inheritance relationship between SBase and Cloneable as well as between SBase and Serializable has been omitted for the sake of simplicity.

#### 2.1 Abstract syntax trees

Both libraries define a class ASTNode for in-memory manipulation and evaluation of abstract syntax trees that represent mathematical formulas and equations. These can either be parsed from a representation in C language-like StringsString, or from a MathML representation. The JSBML ASTNode provides various methods to transform these trees to other formats, for instance, LATEX Strings. In JSBML, several static methods allow easy creation of new syntax trees, for instance, the following code

```
ASTNode myNode = ASTNode.plus(myLeftAstNode, myRightASTNode);
```

creates a new instance of ASTNode which represents the sum of the two other ASTNodes. In this way, even complex trees can be easily manipulated.



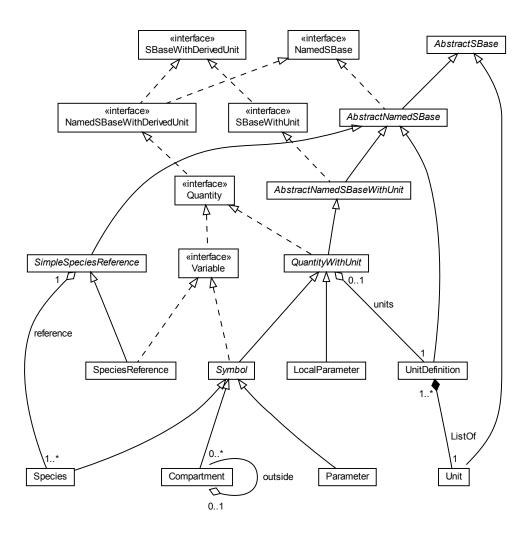


Figure 4: The interface Variable, adapted from (Dräger, 2011). JSBML refers to those components of a model that may change their value during a simulation as Variables. The class Symbol serves as the abstract super class for variables that can also be equipped with a unit. Instances of Parameter do not contain any additional field. In Species a Boolean switch decides whether its value is to be interpreted as an initial amount or as an initial concentration. In contrast to Variables, LocalParameters represent constant unit-value pairs that can only be accessed within their declaring KineticLaw.



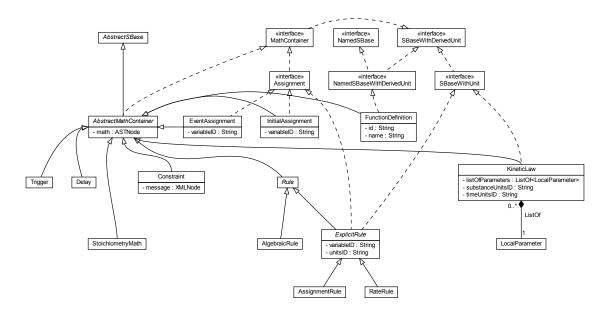


Figure 5: MathContainer, adapted from (Dräger, 2011). Instances of the interface MathContainer, particularly its directly derived class AbstractMathContainer constitute the super class for all elements that store and manipulate mathematical formulas in JSBML, which is done in form of ASTNode objects. These can be evaluated using an implementation of ASTNodeCompiler. Note that some classes that extend AbstractMathContainer do not contain any own fields or methods: Delay, Trigger, StoichiometryMath, and AlgebraicRule.

#### 2.2 The ASTNodeCompiler class

This interface allows users to create customized interpreters for the content of mathematical equations encoded in abstract syntax trees. It is directly and recursively called from the ASTNode class and returns an ASTNodeValue object, which wraps the possible evaluation results of the interpretation. JSBML already provides several implementations of this interface, for instance, ASTNode objects can be directly translated to LATEX or MathML for further processing.

#### 2.3 Cloning when adding child nodes

When adding elements such as a Species to a Model, LibSBML will clone the object and add the clone to the Model. In contrast, JSBML does not automatically perform cloning. The advantage is that modifications on the object belonging to the original pointer will also propagate to the element added to the Model. Furthermore, this is more efficient with respect to the run time and also more intuitive. If cloning is necessary, users should call the clone() method manually. Since all instances of SBase and also Annotation, ASTNode, CVTerm, and History implement the interface Cloneable (see Fig. 1 on page 6), all these elements can be naturally cloned. However,



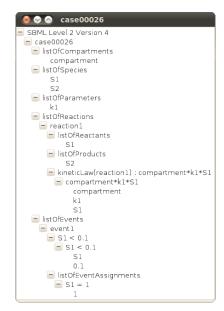


Figure 6: A tree representation of the content of SBML test model case00026

when cloning an object in JSBML, such as an AbstractNamedSBase, all children of this element will recursively be cloned before adding them to the new element. This is necessary, because the data structures specified in SBML define a tree, in which each element has exactly one parental node.

#### 2.4 Deprecation

The intension of JSBML is to provide a Java library for the latest specification of SBML. Hence, JSBML provides methods and classes to cover earlier releases of SBML as well, but these are often marked as being deprecated to avoid creating models that refer to these elements.

#### 2.5 Exceptions

Generally, JSBML throws more exceptions than LibSBML, whose methods often return error codes instead. This behavior helps programmers and users to avoid creating invalid SBML data structures already when dealing with these in memory. Examples are the ParseException that may be thrown if a given formula cannot be parsed properly into an ASTNode data structure, or InvalidArgumentExceptions if inappropriate values are passed to methods. For instance,

- an object representing a constant such as a Parameter whose constant attribute has been set to true cannot be used as the Variable element in an Assignment.
- Another example is the InvalidArgumentException that is thrown when trying to set an invalid identifier String for an instance of AbstractNamedSBase.



• An instance of Priority can only be assigned to an Events if its level attribute has at least been set to three.

Hence, you have to be aware of potential exceptions and errors when using JSBML, on the other hand this will prevent you from doing obvious mistakes.

#### 2.6 Model history

In earlier versions of SBML only the model itself could be associated with a history, i.e., a description about the person(s) who build this model, including names, e-mail addresses, modification and creation dates. Nowadays, it has become possible to annotate each individual construct of an SBML model with such a history. This is reflected by naming the corresponding object History in JSBML, whereas it is still called ModelHistory in LibSBML. Hence, all instances of SBase in JSBML contain methods do access and manipulate its History. Furthermore, you will not find the classes ModelCreator and ModelCreatorList because JSBML gathers its Creator objects in a generic List<Creator> in the History.

#### 2.7 The classes libSBML and JSBML

There is no class libSBML because this library is called JSBML. You can therefore only find a class JSBML. This class provides some similar methods as the libSBML class in LibSBML, such as getJSBMLDottedVersion() to obtain the current version of the JSBML library. However, many other methods that you might expect to find there, if you are used to LibSBML, are located in the actual classes that are related with the function. For instance, the method to convert between a String and a corresponding Unit.Kind can be done by using the method

```
Unit.Kind.valueOf(myString);
```

In a similar way, the ASTNode class provides a method to parse C-like formula Strings according to the specification of SBML Level 1 (Hucka *et al.*, 2003a) into an abstract syntax tree. Therefore, in contrast to the libSBML class, the class JSBML contains only a few methods.

#### 2.8 Replacement of the interface libSBMConstants by Java enums

You won't find a corresponding implementation of this interface in JSBML. The reason is that the JSBML team decided to encode constants using the Java construct enum. For instance, all the fields starting with the prefix AST\_TYPE\_\* have a corresponding field in the ASTNode class itself. There you can find the Type enum. Instead of typing libSBMLConstants.AST\_TYPE\_PLUS, you would therefore type ASTNode.Type.PLUS.

The same holds true for Unit.Kind.\* corresponding to the libSBMLConstants.UNIT\_KIND\_\* fields.



#### 2.9 Various types of ListOf\* classes

In JSBML the ListOf\* objects do not offer a method get(String id) because their generic implementation ListOf<? extends SBase> excepts also elements that do not necessarily have an identifier. Only instances of NamedSBase may have the fields identifier and name set. Hence, generally, the ListOf class cannot assume these fields to be present. To query an instance of ListOf in JSBML for names or identifiers or both, you can apply the following filter:

```
NamedSBase nsb = myList.firstHit(new NameFilter(identifier));
```

This will give you the first element in the list with the given identifier. Various filters are already implemented, but you can easily add your customized filter. To this end, you only have to implement the Filter interface in org.sbml.jsbml.util.filters. There you can also find an OrFilter and an AndFilter, which take as arguments multiple other filters. With the SB0Filter you can query for certain SBO annotations (Le Novère, 2006; Le Novère et al., 2006) in your list, whereas the CVTermFilter helps you to identify SBase instances with a desired MIRIAM (Minimal Information Required In the Annotation of Models) annotation (Le Novère et al., 2005). For instances of ListOf<Species> you can apply the BoundaryConditionFilter to look for those species that operate on the boundary of the reaction system.

#### **2.10 Units**

Since SBML Level 3 (Hucka *et al.*, 2010) the data type of the exponent attribute in the Unit class has been changed from int to double values. JSBML reflects this in the method getExponent() by returning double values only. For a better compatibility with LibSBML, whose corresponding method still returns int values, JSBML also provides the method getExponentAsDouble(). This method returns the value from the getExponent() method and is therefore absolutely redundant.

#### 2.11 Unit Definitions

#### 2.11.1 Predefined unit definitions

A model in JSBML always also contains all predefined units in the model if there are any, i.e., for models encoded of SBML versions before Level 3. These can be accessed from an instance of model by calling the method getPredefinedUnit(String unit).

MIRIAM annotations (Le Novère *et al.*, 2005) have become an integral part of SBML models since Level 2 Version 2. Recently, the Unit Ontology<sup>1</sup> (UO) has been included in the set of supported ontology and online resources of MIRIAM. Since all the predefined units in SBML have corresponding entries in the UO, JSBML automatically equips those predefined units with the correct MIRIAM URI in form of a controlled vocabulary term (CVTerm) if the Level/Version combination of the model supports MIRIAM annotations.



http://www.obofoundry.org/cgi-bin/detail.cgi?id=unit

Note that the enum Unit.Kind also provides methods to directly obtain the entry from the UO that corresponds to a certain unit kind and also to generate MIRIAM URIs accordingly. In this way, JSBML facilitates the annotation of user-defined units and unit definitions with MIRIAM-compliant information.

#### 2.11.2 Access to the units of an element

In JSBML, all SBML elements that can be associated with some unit implement the interface SBaseWithUnit. This interface provides methods for direct access to an object representing their unit. Currently, the following elements implement this interface:

- AbstractNamedSBaseWithUnit
- ExplicitRule
- KineticLaw

Fig. 1 on page 6 provides a better overview about the relationships between all the classes explained here. Note that AbstractNamedSBaseWithUnit serves as the abstract super class for Event and QuantityWithUnit. In Event, all methods to deal with units are already deprecated because only in SBML Level 1 Versions 1 and 2 (Hucka *et al.*, 2003a) Events could be explicitly equipped with units. The same holds true for instances of ExplicitRule and KineticLaw, which both can only explicitly be populated with units for SBML in Level 1, Version 1 and 2. In contrast, QuantityWithUnit serves as the abstract super class for LocalParameter and Symbol, which is then again the super type of Compartment, Species, and (global) Parameter.

With SBaseWithUnit being a subtype of SBaseWithDerivedUnit users can access the units of such an element in two different ways:

getUnit() This method returns the String of the unit kind or the unit definition in the model that has been directly set by the user during the life time of the element. If nothing has been declared, an empty String will be delivered.

getDerivedUnit() This method gives either the same result as getUnit() if some unit has been declared explicitly, or it returns the predefined unit of the element for the given SBML Level/Version combination. Only if neither a user-defined nor a predefined unit is available, this method returns an empty String.

Both methods have corresponding methods to directly obtain an instance of UnitDefinition for convenience.

However, care must be taken when obtaining an instance of UnitDefinition from one of the classes implementing SBaseWithUnit because it might happen that the model containing this SBaseWithUnit does actually not contain the required instance of UnitDefinition and the method returns a UnitDefinition that has just been created for convenience from the information provided by the class. It might therefore be useful to either check if the Model contains this UnitDefinition or to add it to the Model.



In case of KineticLaw it is even more difficult, because SBML Level 1 allows to separately set the substance unit and the time unit of the element. To unify the API, we decided to also provide methods that allow the user to simply pass one UnitDefinition or its identifier to KineticLaw. These methods then try to guess if a substance unit or time unit is given. Furthermore, it is possible to pass a UnitDefinition representing a variant of substance per time directly. In this case, the KineticLaw will memorize a direct link to this UnitDefinition in the model and also try to save separate links to the time unit and the substance unit. However, this may cause a problem if the containing Model does not contain separate UnitDefinitions for both entries.

Generally, this approach provides a more general way to access and to manipulate units of SBML elements.

#### 3 Additional features of JSBML

The JSBML library also provides some features that cannot be found in LibSBML. This section briefly introduces its most important additional capabilities.

#### 3.1 Change events and listeners

JSBML introduces the possibility to listen to change events in the life of an SBML document. To benefit from this advantage, simply let your class implement the interface SBaseChangedListener and add it to the list of listeners in your instance of SBMLDocument. You only have to implement three methods

sbaseAdded(SBase sbase) This method notifies the listener that the given SBase has just been added to the SBMLDocument

sbaseRemoved(SBase sbase) The SBase instance passed to this method is no longer part of the SBMLDocument as it has just been removed.

stateChanged(SBaseChangedEvent event) This method provides detailed information about some value change within the SBMLDocument. The object passed to this method is an SBaseChangedEvent, which provides information about the SBase that has been changed, its property whose value has been changed (this is a String representation of the name of the property), along with the previous value and the new value.

With the help of these methods, you can keep track of what your SBMLDocument does at any time. Furthermore, one could consider to make use of this functionality in a graphical user interface, where the user should be asked if he or she really wants to delete some element or to approve changes before making these persistent. Another idea of using this, would be to write log files of the model building process automatically.

Note that the class SBaseChangedEvent implements the class java.util.EventObject and that the interface SBaseChangedListener extends the interface java.util.EventListener.In



this way, the event and listener data structures fit into the common Java API (Application Programming Interface) and allow users also to make use of, e.g., EventHandlers to deal with changes in a model. It should also be noted that SBaseChangedListeners only keep track of changes in instances of SBase directly. This means that changes inside of, e.g., CVTerm or History may not be traced.

#### 3.2 Logging functionality

JSBML provides logging.

## A Frequently Asked Questions (FAQ)

Why does the class LocalParameter not inherit from Parameter? The reason is the Boolean attribute constant, which is present in Parameter and can be set to false. A parameter in the meaning of SBML is not a constant, it might be some system variable and can therefore be the subject of Rules, Events, InitialAssignments and so on, i.e., all instances of Assignment, whereas a LocalParameter is defined as a constant quantity that never changes its value during the evaluation of a model. It would therefore only be possible to let Parameter inherit from LocalParameter but this could lead to a semantic misinterpretation.

# B An example of how to turn a JSBML-based application into a CellDesigner plug-in

Once an application has been implemented based on JSBML, it can easily be accessed from Cell-Designer's plug-in menu (Funahashi *et al.*, 2003). To this end, it is necessary to extend two classes that are defined in CellDesigner's plug-in API (Application Programming Interface). The Listings 2 to 3 on pages 18–19 show a very simple example of how to pass CellDesigner plug-in model data structures to the translator in JSBML, which creates then a JSBML Model data structure. The examples described by Listings 2 to 3 on pages 18–19 create a plug-in for CellDesigner, which displays the SBML data structure in a tree, like the example in Fig. 6 on page 12. This example only shows how to translate a plug-in data structure from CellDesigner into a corresponding JSBML data structure. With the help of the class PluginSBMLWriter it is possible to notify CellDesigner about changes in the model data structure. Note that Listing 3 on page 19 is only completed by implementing the methods from the super class. In this example it is sufficient to leave the implementation open.



```
package org.sbml.jsbml.cdplugin;
3
   import java.awt.event.ActionEvent;
   import javax.swing.JMenuItem;
   import jp.sbi.celldesigner.plugin.PluginAction;
7
   /** A simple implementation of an action for a CellDesigner plug-in */
8
   public class SimpleCellDesignerPluginAction extends PluginAction {
9
10
     private SimpleCellDesignerPlugin plugin;
11
12
     /** Constructor memorizes the plug-in data structure. */
13
     public SimpleCellDesignerPluginAction(SimpleCellDesignerPlugin plugin) {
14
       this.plugin = plugin;
15
16
17
     /** Executes an action if the given commant occurs. */
18
     public void myActionPerformed(ActionEvent ae) {
19
       if (ae.getSource() instanceof JMenuItem) {
20
         String itemText = ((JMenuItem) ae.getSource()).getText();
21
         if (itemText.equals(SimpleCellDesignerPlugin.ACTION)) {
22
           plugin.startPlugin();
         }
23
24
       } else {
25
         System.err.printf("Unsupported_source_of_action_%\n", ae
26
              .getSource().getClass().getName());
27
     }
28
29
30
   }
```

Listing 2: A simple implementation of CellDesigner's abstract class PluginAction



```
package org.sbml.jsbml.cdplugin;
2
3
   import javax.swing.*;
4
   import jp.sbi.celldesigner.plugin.*;
5
   import org.sbml.jsbml.*;
   import org.sbml.jsbml.gui.*;
8
   /** A very simple implementation of a plug-in for CellDesigner. */
9
   public class SimpleCellDesignerPlugin extends CellDesignerPlugin {
10
     public static final String ACTION = "Display_full_model_tree";
11
12
     public static final String APPLICATION_NAME = "Simple_Plugin";
13
14
     /** Creates a new CellDesigner plug-in with an entry in the menu bar. */
15
     public SimpleCellDesignerPlugin() {
16
       super();
17
       try {
18
         System.out.printf("\n\nLoading_\%s\n\n", APPLICATION_NAME);
19
          SimpleCellDesignerPluginAction action = new
             SimpleCellDesignerPluginAction(this);
20
         PluginMenu menu = new PluginMenu(APPLICATION_NAME);
21
         PluginMenuItem menuItem = new PluginMenuItem(ACTION, action);
22
         menu.add(menuItem);
23
          addCellDesignerPluginMenu(menu);
24
       } catch (Exception exc) {
25
          exc.printStackTrace();
26
27
     }
28
29
     /** This method is to be called by our CellDesignerPluginAction. */
30
     public void startPlugin() {
31
       PluginSBMLReader reader = new PluginSBMLReader(getSelectedModel(), SBO
32
            .getDefaultPossibleEnzymes());
33
       Model model = reader.getModel();
34
       SBMLDocument doc = new SBMLDocument(model.getLevel(), model
35
            .getVersion());
36
       doc.setModel(model);
37
       new JSBMLvisualizer(doc);
38
     }
39
40
     // Include also methods from super class, not needed in this example.
41
     public void addPluginMenu() { }
42
     public void modelClosed(PluginSBase psb) { }
43
     public void modelOpened(PluginSBase psb) { }
44
     public void modelSelectChanged(PluginSBase psb) { }
45
     public void SBaseAdded(PluginSBase psb) { }
46
     public void SBaseChanged(PluginSBase psb) { }
47
     public void SBaseDeleted(PluginSBase psb) { }
48
```

Listing 3: A simple example for a CellDesigner plug-in using JSBML as a communication layer



#### References

- Bornstein, B. J., Keating, S. M., Jouraku, A., and Hucka, M. (2008). LibSBML: an API Library for SBML. *Bioinformatics*, **24**(6), 880–881.
- Dräger, A. (2011). *Computational Modeling of Biochemical Networks*. Ph.D. thesis, University of Tübingen, Sand 1, 720726 Tübingen.
- Funahashi, A., Tanimura, N., Morohashi, M., and Kitano, H. (2003). CellDesigner: a process diagram editor for gene-regulatory and biochemical networks. *BioSilico*, **1**(5), 159–162.
- Holland, R. C. G., Down, T., Pocock, M., Prlić, A., Huen, D., James, K., Foisy, S., Dräger, A., Yates, A., Heuer, M., and Schreiber, M. J. (2008). BioJava: an Open-Source Framework for Bioinformatics. *Bioinformatics*, 24(18), 2096–2097.
- Hucka, M., Finney, A., Sauro, H., and Bolouri, H. (2003a). Systems Biology Markup Language (SBML) Level 1: Structures and Facilities for Basic Model Definitions. Technical Report 2, Systems Biology Workbench Development Group JST ERATO Kitano Symbiotic Systems Project Control and Dynamical Systems, MC 107-81, California Institute of Technology, Pasadena, CA, USA.
- Hucka, M., Finney, A., Sauro, H. M., Bolouri, H., Doyle, J. C., Kitano, H., Arkin, A. P., Bornstein, B. J., Bray, D., Cornish-Bowden, A., Cuellar, A. A., Dronov, S., Gilles, E. D., Ginkel, M., Gor, V., Goryanin, I. I., Hedley, W. J., Hodgman, T. C., Hofmeyr, J.-H. S., Hunter, P. J., Juty, N. S., Kasberger, J. L., Kremling, A., Kummer, U., Le Novère, N., Loew, L. M., Lucio, D., Mendes, P., Minch, E., Mjolsness, E. D., Nakayama, Y., Nelson, M. R., Nielsen, P. F., Sakurada, T., Schaff, J. C., Shapiro, B. E., Shimizu, T. S., Spence, H. D., Stelling, J., Takahashi, K., Tomita, M., Wagner, J. M., Wang, J., and the rest of the SBML Forum (2003b). The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models. *Bioinformatics*, 19(4), 524–531.
- Hucka, M., Finney, A., Hoops, S., Keating, S. M., and Le Novère, N. (2008). Systems biology markup language (SBML) Level 2: structures and facilities for model definitions. Technical report, Nature Precedings.
- Hucka, M., Bergmann, F. T., Hoops, S., Keating, S. M., Sahle, S., Schaff, J. C., Smith, L. P., and Wilkinson, D. J. (2010). The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core. Technical report, Nature Precedings.
- Le Novère, N. (2006). Model storage, exchange and integration. *BMC Neuroscience*, **7 Suppl 1**, S11.
- Le Novère, N., Finney, A., Hucka, M., Bhalla, U. S., Campagne, F., Collado-Vides, J., Crampin, E. J., Halstead, M., Klipp, E., Mendes, P., Nielsen, P., Sauro, H., Shapiro, B. E., Snoep, J. L.,

JSML

- Spence, H. D., and Wanner, B. L. (2005). Minimum information requested in the annotation of biochemical models (MIRIAM). *Nature Biotechnology*, **23**(12), 1509–1515.
- Le Novère, N., Courtot, M., and Laibe, C. (2006). Adding semantics in kinetics models of biochemical pathways. In C. Kettner and M. G. Hicks, editors, 2<sup>nd</sup> International ESCEC Workshop on Experimental Standard Conditions on Enzyme Characterizations. Beilstein Institut, Rüdesheim, Germany, pages 137–153, Rüdessheim/Rhein, Germany. ESEC.



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