

# Package ‘r2sbml’

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**Type** Package

**Title** A Lightweight R Interface to the ‘libsbml’ Library

**Version** 0.1.0

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## Description

Helps explore a model in ‘SBML’ format in R. Allows querying the imported model for information regarding components such species, parameters, reactions, rules, events and function definitions. Also allows exporting model components along with mass-balances in different formats for simulation. Modifications to the exported model in R is not supported.

**License** GPL (>=2)

**Imports** Rcpp (>= 0.12.6)

**LinkingTo** Rcpp

**Biarch** TRUE

**RoxygenNote** 7.2.0

**SystemRequirements** libsbml, libxml2

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convertReactions	<i>convertReactions</i>
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**Description**

convertReactions

**Usage**

```
convertReactions(infile, outfile, format = "R")
```

**Arguments**

infile	input file name
outfile	output file name
format	output code format, should be 'MATLAB', 'mrgsolve', 'rxode' or 'R' (default)

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echoSBML	<i>echoSBML</i>
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**Description**

echoSBML

**Usage**

```
echoSBML(filename)
```

**Arguments**

filename	input file name
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getCmtNames	<i>getCmtNames Outputs the Names of Compartments</i>
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**Description**

getCmtNames Outputs the Names of Compartments

**Usage**

```
getCmtNames(input_model)
```

**Arguments**

input_model	input should be an SBML Model
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getCmtSizes	<i>getCmtSizes Outputs the Sizes of Compartments</i>
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**Description**

getCmtSizes Outputs the Sizes of Compartments

**Usage**

```
getCmtSizes(input_model)
```

**Arguments**

input\_model      input should be an SBML Model

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getEventMath	<i>getEventMath Outputs Model which can be simulated</i>
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**Description**

getEventMath Outputs Model which can be simulated

**Usage**

```
getEventMath(input_model)
```

**Arguments**

input\_model      input should be an SBML Model

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getFunctionDefinition	<i>getFunctionDefinition Outputs Model which can be simulated</i>
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**Description**

getFunctionDefinition Outputs Model which can be simulated

**Usage**

```
getFunctionDefinition(input_model)
```

**Arguments**

input\_model      input should be an SBML Model

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getModel	<i>getModel Outputs an external pointer to the Model from SBML file</i>
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**Description**

getModel Outputs an external pointer to the Model from SBML file

**Usage**

```
getModel(filename)
```

**Arguments**

filename	input file name, should end with .xml
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getNumSpecies	<i>getSpeciesNum Outputs the number of Species in the model</i>
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**Description**

getSpeciesNum Outputs the number of Species in the model

**Usage**

```
getNumSpecies(input_model)
```

**Arguments**

input_model	input should be an SBML model
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getParameterTable	<i>getParameterTable Outputs the Information Table for Parameters</i>
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**Description**

getParameterTable Outputs the Information Table for Parameters

**Usage**

```
getParameterTable(input_model)
```

**Arguments**

input_model	input should be an SBML Model
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getReactionMath	<i>getReactionMath Outputs Model which can be simulated</i>
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**Description**

getReactionMath Outputs Model which can be simulated

**Usage**

```
getReactionMath(input_model)
```

**Arguments**

input\_model      input should be an SBML Model

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getReactionTable	<i>getReactionTable Outputs the Information Table for Reactions</i>
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**Description**

getReactionTable Outputs the Information Table for Reactions

**Usage**

```
getReactionTable(input_model)
```

**Arguments**

input\_model      input should be an SBML Model

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getRuleMath	<i>getRuleMath Outputs Model which can be simulated</i>
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**Description**

getRuleMath Outputs Model which can be simulated

**Usage**

```
getRuleMath(input_model)
```

**Arguments**

input\_model      input should be an SBML Model

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getSpeciesIC	<i>getspeciesIC Outputs the Initial Concentrations of Species</i>
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**Description**

getspeciesIC Outputs the Initial Concentrations of Species

**Usage**

```
getSpeciesIC(input_model)
```

**Arguments**

input_model	input should be an SBML Model
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getSpeciesNames	<i>getSpeciesNames Outputs the Names of Compartments</i>
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**Description**

getSpeciesNames Outputs the Names of Compartments

**Usage**

```
getSpeciesNames(input_model)
```

**Arguments**

input_model	input should be an SBML Model
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getSpeciesTable	<i>getspeciesTable Outputs the Information Table for Species</i>
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**Description**

getspeciesTable Outputs the Information Table for Species

**Usage**

```
getSpeciesTable(input_model)
```

**Arguments**

input_model	input should be an SBML Model
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printSBML

*printSBML*

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### **Description**

printSBML

### **Usage**

printSBML(filename)

### **Arguments**

filename      filename should be the name of the xml file

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