

# sybilSBML – Quick Start

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## 1 Introduction

The package *sybilSBML* is an addition to package *sybil*<sup>1</sup> providing support for metabolic networks written in SBML (Systems Biology Markup Language), in particular those developed by Bernhard Ø. Palsson's lab<sup>2</sup> and those from the BiGG database<sup>3</sup> [Schellenberger et al., 2010].

## 2 Installation

The package *sybilSBML* depends on a working installation of LibSBML [Bornstein et al., 2008] available from the SBML homepage<sup>4</sup> (in particular libraries and header files). See `INSTALL` for installation instructions and platform specific details.

## 3 Usage

The package *sybilSBML* provides the command `readSBMLmod()` which reads SBML formatted files and returns instances of class `modelorg`.

```
> library(sybilSBML)
> model <- readSBMLmod("<model>.xml")
```

## 4 Input files

The function `readSBMLmod()` reads metabolic network models written in SBML format (Systems Biology Markup Language). Among the models available in this de-facto standard format are in particular those developed by Bernhard Ø. Palsson's lab.

The file `ecoli_core_model.xml` (in `extdata/`) contains an exemplarily metabolic network written in SBML for the core energy metabolism of *E. coli* [Palsson, 2006, Orth

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<sup>1</sup><http://CRAN.R-project.org/package=sybil>

<sup>2</sup><http://gcrg.ucsd.edu/>

<sup>3</sup><http://bigg.ucsd.edu/>

<sup>4</sup><http://www.sbml.org/>, libSBML version 5.6.0 or higher

et al., 2010]. The exact location of the file can be retrieved with the `system.file()` command:

```
> library(sybilSBML)
> mp      <- system.file(package = "sybilSBML", "extdata")
> ec_mod <- file.path(mp, "ecoli_core_model.xml")
```

The model can be read in by using the command `readSBMLmod()`:

```
> mod <- readSBMLmod(ec_mod, bndCond = FALSE)

model name:          Ecoli_core_model
number of compartments 2
                    C_c
                    C_e
number of reactions:  95
number of metabolites: 72
number of unique genes: 137
objective function:   +1 Biomass_Ecoli_core_w_GAM
```

The metabolite id's of the SBML files are written in the format `M_<metabolite abbreviation>_<compartment abbreviation>`. The compartment abbreviation is a one letter abbreviation, e.g. `c` for cytosol. All metabolites outside the system boundary belong to compartment `b`. Those metabolites are transported into or outside the system. As long as they are mentioned, the network is closed. The function `readSBMLmod()` will remove them in order to produce an open network.

## 5 Validation of input files

SBML files can be validated by using the command `validateSBMLdocument()`:

```
> err <- validateSBMLdocument(ec_mod)
```

The variable `err` is of class `sbmlError`, storing error messages generated by the validation procedure.

## References

- S. A. Becker et al. Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. *Nat Protoc*, 2(3):727–738, 2007. doi: 10.1038/nprot.2007.99.
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