Package 'sybil'

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Type Package

Title sybil - Efficient Constrained Based Modelling in R

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Depends R (>= 2.14.2), Matrix, lattice

Imports methods

Suggests
glpkAPI (>= 1.2.8), cplexAPI (>= 1.2.4), clpAPI (>= 1.2.4),lpSolveAPI (>= 5.5.2.0), parallel, grid

URL http://www.cs.hhu.de/en/research-groups/bioinformatics/software/sybil.html

Description The package sybil is a Systems Biology Library for R, implementing algorithms for constraint based analyses of metabolic networks (e.g. flux-balance analysis (FBA), minimization of metabolic adjustment (MOMA), regulatory on/off minimization (ROOM), robustness analysis and flux variability analysis).

LazyLoad yes

License GPL-3

Collate generics.R validmodelorg.R validoptsol.R validreactId.R
validreactId_Exch.R validsysBiolAlg.R addAlgorithm.R
addExchReact.R addReact.R addSolver.R blockedReact.R
bracket_pairs.R ceilValues.R changeBounds.R changeGPR.R
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sysBiolAlg_lmomaClass.R sysBiolAlg_momaClass.R
sysBiolAlg_mtfClass.R sysBiolAlg_roomClass.R sybilLogClass.R

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NeedsCompilation no

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R topics documented:

`sybil-package` *sybil – Efficient Constrained Based Modelling in R*

Description

The package **sybil** is a collection of functions designed for in silico analysis—in particular constrained based analysis—of metabolic networks.

Details

The package sybil is designed to read metabolic networks from csv files. This is done by the function `readTSVmod`. The function returns an object of the class `modelorg`.

Read csv files (example files included):

```
mpath <- system.file(package = "sybil", "extdata")
model <- readTSVmod(prefix = "Ec_core",
                    fpath = mpath, quote = "\"")
```

Perform flux balance analysis (FBA):
`ec_f <- optimizeProb(model)`

Perform single gene deletion analysis:
`ec_g <- oneGeneDel(model)`

Plot the values of the objective function after optimization in a histogram:
`plot(ec_g)`

Perform flux variability analysis:
`ec_v <- fluxVar(model)`

Plot the result:
`plot(ec_v)`

Author(s)

Gabriel Gelius-Dietrich

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References

The BiGG database http://bigg.ucsd.edu/.

Schellenberger, J., Park, J. O., Conrad, T. C., and Palsson, B. Ø., (2010) BiGG: a Biochemical Genetic and Genomic knowledgebase of large scale metabolic reconstructions. *BMC Bioinformatics* **11**, 213.

The openCOBRA project http://opencobra.sourceforge.net/.

Becker, S. A., Feist, A. M., Mo, M. L., Hannum, G., Palsson, B. Ø. and Herrgard, M. J. (2007) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. *Nat Protoc* **2**, 727–738.

Schellenberger, J., Que, R., Fleming, R. M. T., Thiele, I., Orth, J. D., Feist, A. M., Zielinski, D. C., Bordbar, A., Lewis, N. E., Rahmanian, S., Kang, J., Hyduke, D. R. and Palsson, B. Ø. (2011) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. *Nat Protoc* **6**, 1290–1307.

See Also

Package **sybilSBML** and there the function `readSBMLmod` to read metabolic models written in SBML language.

Examples

```
data(Ec_core)
Ec_ofd <- oneGeneDel(Ec_core)
plot(Ec_ofd)
```

`addAlgorithm` *Add a New Algorithm Name to sybil*

Description

Certain simulations can be run using different algorithms. For example, genetic perturbations can be studied with FBA, MOMA or the like. With this funktion you can add a new algorithm to an existing kind of simulation.

Usage

```
addAlgorithm(alg, purpose)
```

Arguments

`alg`	A single character string containing the name of the new algorithm.
`purpose`	Purpose of the new algorithm.

Value

Returns `NULL` invisibly.

Author(s)

Gabriel Gelius-Dietrich

See Also

checkAlgorithm, getsybilenv

---

addCols-methods *Add Columns to an Optimization Problem*

Description

Add columns to an optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI,numeric'
addCols(lp, ncols)

## S4 method for signature 'optObj_cplexAPI,numeric'
addCols(lp, ncols)

## S4 method for signature 'optObj_glpkAPI,numeric'
addCols(lp, ncols)

## S4 method for signature 'optObj_lpSolveAPI,numeric'
addCols(lp, ncols)
```

Arguments

lp	An object extending class optObj.
ncols	Number of columns (variables) to add to the problem object.

Methods

signature(lp = "optObj_clpAPI", ncols = "numeric") method to use with package **optObj_clpAPI**.

signature(lp = "optObj_cplexAPI", ncols = "numeric") method to use with package **optObj_cplexAPI**.

signature(lp = "optObj_glpkAPI", ncols = "numeric") method to use with package **optObj_glpkAPI**.

signature(lp = "optObj_lpSolveAPI", ncols = "numeric") method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

addColsToProb-methods *Add New Columns (Variables) to an Optimization Problem*

Description

Add new columns (variables) to an optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI'
addColsToProb(lp, j, obj, lb, ub, rind, nzval)

## S4 method for signature 'optObj_cplexAPI'
addColsToProb(lp, j, obj, lb, ub, rind, nzval)

## S4 method for signature 'optObj_glpkAPI'
addColsToProb(lp, j, obj, lb, ub, rind, nzval)

## S4 method for signature 'optObj_lpSolveAPI'
addColsToProb(lp, j, obj, lb, ub, rind, nzval)
```

Arguments

lp	An object extending class optObj.
j	A numeric vector containing the new column indices.
obj	A numeric vector containing the objective coefficients of the new variables.
lb	A numeric vector containing the lower bounds of the new variables.
ub	A numeric vector containing the upper bounds of the new variables.
rind	A list containing the row indices of the new non-zero elements.
nzval	A list containing the new non-zero elements.

Methods

signature(lp = "optObj_clpAPI") method to use with package **optObj_clpAPI**.

signature(lp = "optObj_cplexAPI") method to use with package **optObj_cplexAPI**.

signature(lp = "optObj_glpkAPI") method to use with package **optObj_glpkAPI**.

signature(lp = "optObj_lpSolveAPI") method to use with package **optObj_lpSolveAPI**.

Note

Arguments j, obj, lb, lu, rind and nzval must have the same length.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

addExchReact *Add Exchange Reactions to a Model*

Description

The function addExchReact adds exchange reactions for a set of metabolites to a metabolic model.

Usage

```
addExchReact(model, met, lb, ub)
```

Arguments

model	An object of class modelorg.
met	A vector of character strings containing the metabolite id's to add exchange reactions for.
lb	A vector of numeric values of the same length as met containing the lower bounds for the exchange reactions. Default: rep(0, length(met)).
ub	A vector of numeric values of the same length as met containing the upper bounds for the exchange reactions. Default: rep(SYBIL_SETTINGS("MAXIMUM"), length(met)).

Details

If lb[i] < 0, the exchange reaction for the metabolite in met[i] is considered to be reversible, otherwise irreversible. A reaction id is generated for each exchange reaction by prepending the metabolite id's with the string "Ex_".

Value

An object of class modelorg

Author(s)

Gabriel Gelius-Dietrich

References

Becker, S. A., Feist, A. M., Mo, M. L., Hannum, G., Palsson, B. Ø. and Herrgard, M. J. (2007) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. *Nat Protoc* **2**, 727–738.

Schellenberger, J., Que, R., Fleming, R. M. T., Thiele, I., Orth, J. D., Feist, A. M., Zielinski, D. C., Bordbar, A., Lewis, N. E., Rahmanian, S., Kang, J., Hyduke, D. R. and Palsson, B. Ø. (2011) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. *Nat Protoc* **6**, 1290–1307.

See Also

modelorg and addReact

Examples

```
# add exchange reactions (allowing input) for the metabolites
# malate and oxalacetate
data(Ec_core)
mod <- addExchReact(Ec_core,
                    met = c("mal_L[c]", "oaa[c]"),
                    lb = c(-20, -20))
findExchReact(mod)
```

---

addReact *Add/Change Reactions in a Model*

Description

The function addReact adds one reaction to a metabolic model, or changes one reaction in a metabolic model.

Usage

```
addReact(model,
         id,
         met,
         Scoef,
         reversible = FALSE,
         lb = 0,
         ub = SYBIL_SETTINGS("MAXIMUM"),
         obj = 0,
         subSystem = NA,
         gprAssoc = NA,
         reactName = NA,
         metName = NA,
         metComp = NA)
```

Arguments

model	An object of class modelorg.
id	A single character string containing a reaction id (see details below).
met	A vector of character strings containing the metabolite id's used in the reaction given in Scoef.
Scoef	A numeric vector of the same length as met of stoichiometric coefficients for the metabolites in met. The value in Scoef[i] is the stoichiometric coefficient of the metabolite in met[i].
reversible	A Boolean value, indicating if the reaction is reversible or not. Default: FALSE.
lb	A single numeric value giving the lower bound of the reaction. Default: 0.
ub	A single numeric value giving the upper bound of the reaction. Default: SYBIL_SETTINGS("MAXIMUM").
obj	A single numeric value giving the objective coefficient of the reaction. Default: 0.
subSystem	A vector of character strings containing the sub systems to which the reaction belongs. All values must be available in subSys(model). If NA, the reaction will not be associated to any sub system. Default: NA.
gprAssoc	A single character string giving the gpr association for the reaction. If NA, no gpr association is created.p Default: NA.
reactName	A single character string giving the name for the reaction. If NA, the value of argument id is used. Default: NA.
metName	A vector of character strings of the same length as met containing the the metabolites names for the metabolites given in argument met. If set to NA, the metabolite id's are used. Default: NA.
metComp	A vector of character strings or integers of the same length as met containing a compartment name (as in mod_compart(model)) or an index pointing to a value in mod_compart(model) (as in met_comp(model)). If NA, the metabolites will not be associated to any compartment. Default: NA.

Details

The function addReact can be used to add reactions and/or metabolites to a given metabolic model, or to change parameters of a reaction already present in a given metabolic model. If the reaction id in argument idis already present in the given model, this reaction will be changed, no new column will be added to the stoichiometric matrix. If any of the metabolite id's of argument met are not present in the model, they will be added (new rows in the stoichiometric matrix will be added).

Arguments subSystem, gprAssoc and reactName are only used, if a new reaction is added to the model (if id is not in react_id(model), exact matching is used).

Value

An object of class modelorg, or modelorg_irrev, if model is of class modelorg_irrev.

Author(s)

Gabriel Gelius-Dietrich

References

Becker, S. A., Feist, A. M., Mo, M. L., Hannum, G., Palsson, B. Ø. and Herrgard, M. J. (2007) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. *Nat Protoc* **2**, 727–738.

Schellenberger, J., Que, R., Fleming, R. M. T., Thiele, I., Orth, J. D., Feist, A. M., Zielinski, D. C., Bordbar, A., Lewis, N. E., Rahmanian, S., Kang, J., Hyduke, D. R. and Palsson, B. Ø. (2011) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. *Nat Protoc* **6**, 1290–1307.

See Also

modelorg and rmReact

---

addRows-methods *Add Rows to an Optimization Problem*

Description

Add rows to an optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI,numeric'
addRows(lp, nrows)

## S4 method for signature 'optObj_cplexAPI,numeric'
addRows(lp, nrows)

## S4 method for signature 'optObj_glpkAPI,numeric'
addRows(lp, nrows)

## S4 method for signature 'optObj_lpSolveAPI,numeric'
addRows(lp, nrows)
```

Arguments

lp	An object extending class optObj.
nrows	Number of rows (constraints) to add to the problem object.

Methods

`signature(lp = "optObj_clpAPI", nrows = "numeric")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI", nrows = "numeric")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI", nrows = "numeric")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI", nrows = "numeric")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

---

addRowsCols-methods *Add Rows and Columns to an Optimization Problem*

Description

Add rows and columns to an optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI,numeric,numeric'
addRowsCols(lp, nrows, ncols)

## S4 method for signature 'optObj_cplexAPI,numeric,numeric'
addRowsCols(lp, nrows, ncols)

## S4 method for signature 'optObj_glpkAPI,numeric,numeric'
addRowsCols(lp, nrows, ncols)

## S4 method for signature 'optObj_lpSolveAPI,numeric,numeric'
addRowsCols(lp, nrows, ncols)
```

Arguments

`lp`	An object extending class `optObj`.
`nrows`	Number of rows (constraints) to add to the problem object.
`ncols`	Number of columns (variables) to add to the problem object.

Methods

`signature(lp = "optObj_clpAPI", nrows = "numeric", ncols = "numeric")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI", nrows = "numeric", ncols = "numeric")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI", nrows = "numeric", ncols = "numeric")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI", nrows = "numeric", ncols = "numeric")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

---

addRowsToProb-methods *Add New Rows (Constraints) to an Optimization Problem*

Description

Add new rows (constraints) to an optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI'
addRowsToProb(lp, i, type, lb, ub, cind, nzval, rnames = NULL)

## S4 method for signature 'optObj_cplexAPI'
addRowsToProb(lp, i, type, lb, ub, cind, nzval, rnames = NULL)

## S4 method for signature 'optObj_glpkAPI'
addRowsToProb(lp, i, type, lb, ub, cind, nzval, rnames = NULL)

## S4 method for signature 'optObj_lpSolveAPI'
addRowsToProb(lp, i, type, lb, ub, cind, nzval, rnames = NULL)
```

Arguments

`lp`	An object extending class `optObj`.
`i`	A numeric vector containing the new row indices.

type	A character vector giving the constraint type: "F": free constraint (**optObj_glpkAPI** only), "L": >= (lower bound), "U": <= (upper bound) or "D": lb <= r <= ub (double bound) or "E": = (equality). If type[k] is not F, "L", "U", "D" or "E", the value of type[k] will be set to "E".
lb	A numeric vector containing the lower bound of the new constraints.
ub	A numeric vector containing the upper bound of the new constraints.
cind	A list containing the column indices of the new non-zero elements.
nzval	A list containing the new non-zero elements.
rnames	A character vector containing names for the new rows/constraints. Default: NULL.

Methods

signature(lp = "optObj_clpAPI") method to use with package **optObj_clpAPI**. Parameter rnames is currently unused.

signature(lp = "optObj_cplexAPI") method to use with package **optObj_cplexAPI**.

signature(lp = "optObj_glpkAPI") method to use with package **optObj_glpkAPI**.

signature(lp = "optObj_lpSolveAPI") method to use with package **optObj_lpSolveAPI**.

Note

Arguments i, type, lb, cind, nzval and rnames (if not NULL) must have the same length.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

addSolver *Add a New Mathematical Programming Solver to sybil*

Description

Make a new mathematical programming solver available to sybil via the SYBIL_SETTINGS command.

Usage

```
addSolver(solver, method, probType)
```

Arguments

solver	A single character string giving the name of the desiered solver.
method	A character vector of algorithms supported by the solver given in solver.
probType	A list of hte same length as method containing a vector of character strings for each method which types of problems can be solved with that method: method[i] of solver can solve problems of type probType[[i]]. Problem types could be "lp": linear programming, "mip": mixed integer programming or "qp": quadratic programming.

Details

The parameters to the algorithms given in method are set to NA, which means, the default parameters of the solver software will be used. If a solver already exists, an error message will be given.

Value

The function returns NULL invisibly.

Author(s)

Gabriel Gelius-Dietrich

See Also

SYBIL_SETTINGS

---

applyChanges-methods *Generic Function to Apply Changes to Objects of Class sysBiolAlg*

Description

Use method applyChanges to apply changes in objects of class sysBiolAlg. Changes can be coefficients of the objective function, variable bounds or the optimization direction.

Usage

```
## S4 method for signature 'sysBiolAlg'
applyChanges(object, del, obj, ld,
             react    = NULL,
             lb       = NULL,
             ub       = NULL,
             obj_coef = NULL,
             lpdir    = NULL)

## S4 method for signature 'sysBiolAlg_room'
applyChanges(object, del, obj, ld,
             react    = NULL,
```

```
lb       = NULL,
ub       = NULL,
obj_coef = NULL,
lpdir    = NULL)
```

Arguments

object	An object of class sysBiolAlg.
del	A logical value indicating whether variable bounds should be altered or not.
obj	A logical value indicating whether objective coefficients should be altered or not.
ld	A logical value indicating whether the direction of optimization should be altered or not.
react	A numeric vector containing indices to reactions which should be changed (in terms of variable bounds or objective coefficients). Default: NULL.
lb	Numeric vector of the same length as react, containing the new lower variable bounds. Default: NULL.
ub	Numeric vector of the same length as react, containing the new upper variable bounds. Default: NULL.
obj_coef	Numeric vector of the same length as react, containing the new objective coefficients. Default: NULL.
lpdir	A single character value indicating the new direction of optimization. Default: NULL.

Value

Returns a list containing the original values in order to undo the changes with resetChanges:

react	A numeric vector containing variable id's to apply changes to.
lb	A numeric vector of the same length as react containing the original variable lower bounds.
ub	A numeric vector of the same length as react containing the original variable upper bounds.
obj_coef	A numeric vector of the same length as react containing the original objective coefficients.
lpdir	A single character value giving the original optimization direction.
ri	A numeric vector of the same length as react containing row indices of the stoichiometric matrix required to apply changes in variable bounds when algorithm "room" is used. (only used by the sysBiolAlg_room method).
ci	A numeric vector of the same length as react containing column indices of the stoichiometric matrix required to apply changes in variable bounds when algorithm "room" is used. (only used by the sysBiolAlg_room method).

Methods

`signature(object = "sysBiolAlg")` Method used with objects extending class `sysBiolAlg`

`signature(object = "sysBiolAlg_room")` Method used with objects of class `sysBiolAlg_room`

Author(s)

Gabriel Gelius-Dietrich

See Also

Class `sysBiolAlg` and `resetChanges`

`backupProb-methods` *Copies a Problem Object to a New Problem Object*

Description

Copies a problem object into a new problem object.

Usage

```
## S4 method for signature 'optObj_clpAPI'
backupProb(lp)

## S4 method for signature 'optObj_cplexAPI'
backupProb(lp)

## S4 method for signature 'optObj_glpkAPI'
backupProb(lp)

## S4 method for signature 'optObj_lpSolveAPI'
backupProb(lp)
```

Arguments

`lp`	An object extending class `optObj`.

Value

An object of the same class as given in argument `lp` (extending class `optObj`).

Methods

`signature(lp = "optObj_clpAPI")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**. The new problem object will be in the same CPLEX environment like the original one.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**. Building a new problem object will reset all parameters to their default. After backing up, set all parameters which are not at their default values again.

`signature(lp = "optObj_lpSolveAPI")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

---

blockedReact *Find Blocked Reactions in a Metabolic Network*

Description

A blocked Reaction in a metabolic network can not be used by the network, given the stiochiometric matrix of the network and a set of input and output fluxes.

Usage

```
blockedReact(model,
             tol = SYBIL_SETTINGS("TOLERANCE"),
             exex = TRUE,
             fld = FALSE,
             retOptSol = FALSE,
             verboseMode = 2,
             ...)
```

Arguments

`model`	An object of class `modelorg`.
`tol`	Tolerance value. Default: `SYBIL_SETTINGS("TOLERANCE")`.
`exex`	Boolean, if set to `TRUE`, exchange reactions found by `findExchReact` are excluded from the analysis. Default: `TRUE`.
`fld`	Boolean. Save the resulting flux distributions. Default: `FALSE`

retOptSol	Boolean. Return an object of class optsol_blockedReact or just a list containing the results. Default: FALSE.
verboseMode	An integer value indicating the amount of output to stdout: 0: nothing, 1: status messages, 2: like 1 plus a progress indicator. Default: 2.
...	Further arguments passed to sysBiolAlg. Argument solverParm is a good candidate.

Details

A reaction i is considered to be 'blocked', if its calculated reaction rate v_i is $-\mathrm{tol} < v_i < \mathrm{tol}$. Reaction rates are calculated via linear optimization: maximizing and minimizing each reaction rate. If the difference of the maximum and the minimum is not larger than tol, that particular reaction is blocked, given the current side conditions (exchange fluxes).

Value

If argument retOptsol is set to TRUE, an object of class optsol_blockedReact is returned, otherwise a logical vector with length equal to the number of reactions of the network. If element i equals TRUE, reaction i is blocked.

Author(s)

Gabriel Gelius-Dietrich

See Also

modelorg, optsol_blockedReact and SYBIL_SETTINGS.

---

changeBounds *Change Variable Bounds in a Metabolic Network*

Description

The function changes the upper and/or lower bounds of a given metabolic network model to new values.

Usage

```
changeBounds(model, react, lb = NULL, ub = NULL)
```

Arguments

model	An object of class modelorg.
react	An object of class reactId, character or integer. Specifies the fluxes (variables) for which to change the upper and/or lower bounds.
lb	Numeric vector giving the lower bounds for the fluxes mentioned in react. If missing, lower bounds are set to zero. If lb has a length of 1, the value of lb will be used for all reactions in react.
ub	Numeric vector giving the upper bounds for the fluxes mentioned in react. If missing, upper bounds are set to zero. If ub has a length of 1, the value of ub will be used for all reactions in react.

Details

The argument react will be evaluated by the function checkReactId.

Value

Returns the given model (an object of the same class as the argument lpmodel) containing the new objective function.

Author(s)

Gabriel Gelius-Dietrich

See Also

checkReactId

Examples

```
## change the E.coli core model to lactate input:
data(Ec_core)
Ec_new <- changeBounds(Ec_core,
                       c("EX_glc", "EX_lac"),
                       lb = c(0, -20), ub = 1000)
```

---

changeColsBnds-methods

Change Column (Variable) Bounds in the Optimization Problem

Description

Change column (variable) bounds in the optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI'
changeColsBnds(lp, j, lb, ub)

## S4 method for signature 'optObj_cplexAPI'
changeColsBnds(lp, j, lb, ub)

## S4 method for signature 'optObj_glpkAPI'
changeColsBnds(lp, j, lb, ub)

## S4 method for signature 'optObj_lpSolveAPI'
changeColsBnds(lp, j, lb, ub)
```

Arguments

lp	An object extending class optObj.
j	A numeric vector containing the column indices of the variables to change.
lb	A numeric vector of the same length as j containing the lower bounds of the variables to change.
ub	A numeric vector of the same length as j containing the upper bounds of the variables to change.

Methods

signature(lp = "optObj_clpAPI") method to use with package **optObj_clpAPI**.

signature(lp = "optObj_cplexAPI") method to use with package **optObj_cplexAPI**.

signature(lp = "optObj_glpkAPI") method to use with package **optObj_glpkAPI**.

signature(lp = "optObj_lpSolveAPI") method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

changeColsBndsObjCoefs-methods

Change Column (Variable) Bounds and Objective Coefficients in the Optimization Problem

---

Description

Change column (variable) bounds and objective coefficients in the optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI'
changeColsBndsObjCoefs(lp, j, lb, ub, obj_coef)

## S4 method for signature 'optObj_cplexAPI'
changeColsBndsObjCoefs(lp, j, lb, ub, obj_coef)

## S4 method for signature 'optObj_glpkAPI'
changeColsBndsObjCoefs(lp, j, lb, ub, obj_coef)

## S4 method for signature 'optObj_lpSolveAPI'
changeColsBndsObjCoefs(lp, j, lb, ub, obj_coef)
```

Arguments

`lp`	An object extending class `optObj`.
`j`	A numeric vector containing the column indices of the variables to change.
`lb`	A numeric vector of the same length as `j` containing the lower bounds of the variables to change.
`ub`	A numeric vector of the same length as `j` containing the upper bounds of the variables to change.
`obj_coef`	A numeric vector of the same length as `j` containing the objective coefficients of the variables to change.

Methods

`signature(lp = "optObj_clpAPI")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

changeGPR *Check and Change the GPR Rules*

Description

Checks and Changes the GPR Rules for the chosen reactions

Usage

```
changeGPR(model, react, gprRules = "logicalExpression", verboseMode = 1)
```

Arguments

model	An object of class modelorg
react	An object of class reactId, a numeric vector, or a character vector containing reaction id's.
gprRules	character: contains logical expressions.
verboseMode	integer: verbosity level.

Details

The function changes the expressions for the chosen reactions.

The function stops if any logic expressions is not correct. Then the changes are executed.

Author(s)

Benjamin Braasch

---

changeMatrixRow-methods

Change a Row in the Constraint Matrix of the Optimization Problem

Description

Change a row in the constraint matrix of the optimization problem.

Usage

```
## S4 method for signature 'optObj_cplexAPI'
changeMatrixRow(lp, i, j, val)

## S4 method for signature 'optObj_glpkAPI'
changeMatrixRow(lp, i, j, val)

## S4 method for signature 'optObj_lpSolveAPI'
changeMatrixRow(lp, i, j, val)
```

Arguments

lp	An object extending class optObj.
i	A single numeric value giving the row index of the constraint matrix to change.
j	A numeric vector containing the column indices of the new non-zero elements.
val	A numeric vector of the same length as j containing the new non-zero elements.

Methods

signature(lp = "optObj_cplexAPI") method to use with package **optObj_cplexAPI**. Only the columns given in argument j will be changed. All other columns stay the same.

signature(lp = "optObj_glpkAPI") method to use with package **optObj_glpkAPI**. The row given in argument i will be reset completely.

signature(lp = "optObj_lpSolveAPI") method to use with package **optObj_lpSolveAPI**. The row given in argument i will be reset completely.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

changeObjCoefs-methods

Change Column (Variable) Objective Coefficients in the Optimization Problem

---

Description

Change column (variable) objective coefficients in the optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI'
changeObjCoefs(lp, j, obj_coef)

## S4 method for signature 'optObj_cplexAPI'
changeObjCoefs(lp, j, obj_coef)

## S4 method for signature 'optObj_glpkAPI'
changeObjCoefs(lp, j, obj_coef)

## S4 method for signature 'optObj_lpSolveAPI'
changeObjCoefs(lp, j, obj_coef)
```

Arguments

lp	An object extending class optObj.
j	A numeric vector containing the column indices of the variables to change.
obj_coef	A numeric vector of the same length as j containing the objective coefficients of the variables to change.

Methods

signature(lp = "optObj_clpAPI") method to use with package **optObj_clpAPI**.

signature(lp = "optObj_cplexAPI") method to use with package **optObj_cplexAPI**.

signature(lp = "optObj_glpkAPI") method to use with package **optObj_glpkAPI**.

signature(lp = "optObj_lpSolveAPI") method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

changeObjFunc *Sets/changes the Objective Function*

Description

The function changeObjFunc changes or sets the objective function for a specified model.

Usage

```
changeObjFunc(model, react, obj_coef = rep(1, length(react)))
```

Arguments

model	An object of class modelorg.
react	An object of class reactId, character or integer. Specifies the fluxes (variables) for which to change the objective coefficients.
obj_coef	A numerical vector with length equal to the number of reaction id's given in argument react containing the objective coefficients. Default: a value of one for each reaction given in argument react.

Details

The argument react will be evaluated by the function checkReactId. The return value is used to change the objective function.

All reactions not given in argument react will get an objective value of zero.

Value

Returns the given model containing the new objective function.

Author(s)

Gabriel Gelius-Dietrich

See Also

checkReactId

Examples

```
## sets the objective function to the ATP maintenance reaction:
data(Ec_core)
Ec_new <- changeObjFunc(Ec_core, "ATPM")
```

---

changeRowsBnds-methods

Change Row Bounds in the Optimization Problem

Description

Change row bounds in the optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI'
changeRowsBnds(lp, i, lb, ub)

## S4 method for signature 'optObj_cplexAPI'
changeRowsBnds(lp, i, lb, ub)

## S4 method for signature 'optObj_glpkAPI'
changeRowsBnds(lp, i, lb, ub)

## S4 method for signature 'optObj_lpSolveAPI'
changeRowsBnds(lp, i, lb, ub)
```

Arguments

lp	An object extending class optObj.
i	A numeric vector containing the row indices of the constraints to change.
lb	A numeric vector of the same length as i containing the lower bounds of the constraints to change.
ub	A numeric vector of the same length as i containing the upper bounds of the constraints to change.

Methods

`signature(lp = "optObj_clpAPI")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI")` method to use with package **optObj_lpSolveAPI**.

Note

Changing row bounds does not change the constraint type.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

---

changeUptake-methods *Change Uptake Reactions*

Description

Switch uptake reactions in metabolic networks on and off.

Usage

```
## S4 method for signature 'modelorg'
changeUptake(object, off = NULL, on = NULL,
                                    rate = SYBIL_SETTINGS("MAXIMUM") * -1)
```

Arguments

`object`	An object of class `modelorg`.
`off`	A numeric or character vector or an object of class `reactId_Exch` containing the metabolite id's of metabolites to not use for uptake. If they have an exchange reaction with a lower bound less than zero, this lower bound is set to `0`. If `off` is set to `NULL`, all uptake reactions will be deactivated. If `off` is set to `FALSE`, no uptake reaction will be deactivated. If you just want to add an uptake reaction, set `off` to `FALSE`. Default: `NULL`.
`on`	A numeric or character vector or an object of class `reactId_Exch` containing the metabolite id's of metabolites to use for uptake. Default: `NULL`.
`rate`	A numeric vector containing the uptake rates for metabolites given in `on`. Default: `SYBIL_SETTINGS("MAXIMUM") * -1`.

Value

An object of class modelorg.

Methods

signature(object = "modelorg") method to use with objects of class modelorg.

Author(s)

Gabriel Gelius-Dietrich

See Also

Class modelorg

---

checkAlgorithm *Check Algorithm*

Description

Test, if a given algorithm can has a certain purpose.

Usage

```
checkAlgorithm(alg, purpose)
```

Arguments

alg	A single character string containing the name of the algorithm.
purpose	Purpose of the new algorithm.

Value

Returns TRUE if successful, otherwise FALSE.

Author(s)

Gabriel Gelius-Dietrich

See Also

addAlgorithm, getsybilenv

checkDefaultMethod *Validate Solver and Method*

Description

The function checkDefaultMethod returns the default method for a desired solver, or a default solver – method pair. A "solver" is always the name of a R package offering facilities for solving optimization problems.

Usage

```
checkDefaultMethod(solver, method, probType, loadPackage = TRUE)
```

Arguments

solver	A single character string, containing the solver name (must be identical to the name of an R-package), see SYBIL_SETTINGS.
method	A single character string, containing the method name, see SYBIL_SETTINGS.
probType	A single character string, containing the problem type, see optObj.
loadPackage	A single Boolean value. If set to TRUE, load the given solver package via require.

Details

In order to run simulations (optimizations) with sybil, additional software offering facilities for solving optimization problems is required. Supported R packages are described in SYBIL_SETTINGS. At first, the function checks if argument solver contains a valid solver. If that is not the case, a corresponding library will be loaded, if one exists (this library must have the same name as given in solver). If this failes too, the default solver will be returned (see SYBIL_SETTINGS). Next the same is done for the argument method, regarding the current value of solver. Additionally, it will be checked, wether or not the given problem type can be solved using the given method and solver.

Value

sol	Validated solver name.
met	Validated method name.
parm	Default prarmeter set for the validated method.

Note

Arguments "glpk", "cplex" and "clp" not used anymore; valid arguments must be the name of the desired solver package like "glpkAPI", "cplexAPI" and "cplAPI".

Author(s)

Gabriel Gelius-Dietrich

Maintainer: Gabriel Gelius-Dietrich <geliudie@uni-duesseldorf.de>

See Also

SYBIL_SETTINGS and getsybilenv

---

checkOptSol-methods *Summarized Information About an Object of Class Optsol*

Description

The function checkOptSol evaluates the results of the solution of optimizations; the returned objects e.g. from optimizeProb.

Usage

```
## S4 method for signature 'optsol'
checkOptSol(opt, onlywarn = FALSE)
```

Arguments

opt	An object of class optsol.
onlywarn	A single Boolean value. If set to TRUE, the method will check, if all optimizations ended successfully. Default: FALSE.

Details

The function checkOptSol is used by functions performing a linear optimization (e.g. optimizeProb). In that case, the argument onlywarn is set to TRUE. If the optimization ends unsuccesfull, a warning will be produced.

It is also possible to use the function directly, with onlywarn set to FALSE (the default). In that case, an object of class checksol will be retuned. This object contains a summary with the exit status of the optimization.

Value

TRUE or FALSE if onlywarn is set to TRUE, otherwisw an object of class checksol.

Methods

signature(opt = "optsol") method to use with objects of class optsol.

Author(s)

Gabriel Gelius-Dietrich

See Also

checksol, optimizeProb and oneGeneDel

Examples

```
data(Ec_core)
Ec_f <- optimizeProb(Ec_core, retOptSol = TRUE)
Ec_check <- checkOptSol(Ec_f)
```

---

checkReactId *Check if a Reaction Id is Valid*

Description

The function checkReactId evaluates a vector of reaction id's if they are unique and appear in a given model.

Usage

```
checkReactId(model, react)
```

Arguments

model	A model. An object of class modelorg, or a problem object of a lp solver.
react	Character vector containing reaction id's, or a numerical vector containing indices of reaction id's.

Details

If argument react is numeric, the maximun value will be inspected, if it is larger than the number of reactions in the model.

In case of a character vector, react is matched to the reaction id's residing in the model. If they are not found, grep is used.

If argument react is of class reactId, it will be returned without checking.

Value

An object of class reactId or NULL if argument react contains any reactions not in model.

Author(s)

Gabriel Gelius-Dietrich

See Also

reactId

Examples

```
data(Ec_core)

## Example with react as character vector
ids <- c("ATPM", "ACK")
idc <- checkReactId(Ec_core, ids)

## Example with react as numerical vector
ids <- c(1:4)
idc <- checkReactId(Ec_core, ids)
```

---

checksol-class *Structure of the Class "checksol"*

Description

Structure of the class "checksol". Objects of that class are returned by the function checkOptSol.

Objects from the Class

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

Slots

exit_code: Object of class "integer" containing the exit code of the lp solver.

exit_num: Object of class "integer" containing the number of appearance of a specific exit code.

exit_meaning: Object of class "character" containing the meaning of the exit code.

num_of_prob: Object of class "integer" indicating the number of optimization problems.

status_code: Object of class "integer" containing the solution status of the lp problem.

status_num: Object of class "integer" containing the number of appearance of a specific solution status.

status_meaning: Object of class "character" containing the meaning of the solution status.

Methods

exit_code<-: signature(object = "checksol"): sets the exit_code slot.

exit_code: signature(object = "checksol"): gets the exit_code slot.

exit_meaning<-: signature(object = "checksol"): sets the exit_meaning slot.

exit_meaning: signature(object = "checksol"): gets the exit_meaning slot.

exit_num<-: signature(object = "checksol"): sets the exit_num slot.

exit_num: signature(object = "checksol"): gets the exit_num slot.

num_of_prob<-: signature(object = "optsol"): sets the num_of_prob slot.

num_of_prob: signature(object = "optsol"): gets the num_of_prob slot.

show: signature(object = "checksol"): prints some details specific to the instance of class checksol.

status_code<-: signature(object = "checksol"): sets the status_code slot.

status_code: signature(object = "checksol"): gets the status_code slot.

status_meaning<-: signature(object = "checksol"): sets the status_meaning slot.

status_meaning: signature(object = "checksol"): gets the status_meaning slot.

status_num<-: signature(object = "checksol"): sets the status_num slot.

status_num: signature(object = "checksol"): gets the status_num slot.

Author(s)

Gabriel Gelius-Dietrich

See Also

checkOptSol

Examples

```
showClass("checksol")
```

---

deadEndMetabolites-methods

Identify Dead End Metabolites

Description

Search a metabolic network for metabolites, which are produced, but not consumed and vice versa.

Usage

```
## S4 method for signature 'modelorg'
deadEndMetabolites(object,retIds)
```

Arguments

object	An object of class modelorg.
retIds	Boolean. If set to TRUE, a list containing metabolite id's will be returned, otherwise a list of logical vectors. Default: TRUE.

Value

A list will be returned:

dem	dead end metabolites
der	reactions containing dead end metabolites

Methods

`signature(object = "modelorg")` method to use with class `modelorg`.

Author(s)

Gabriel Gelius-Dietrich

See Also

Class `modelorg` and `readTSVmod`.

`delProb-methods` *Free Memory Associated to the Pointer to the Problem Object*

Description

Delete (free) memory associated to the pointer to the problem object.

Usage

```
## S4 method for signature 'optObj_clpAPI'
delProb(lp, ...)

## S4 method for signature 'optObj_cplexAPI'
delProb(lp, closeEnv = TRUE)

## S4 method for signature 'optObj_glpkAPI'
delProb(lp, ...)

## S4 method for signature 'optObj_lpSolveAPI'
delProb(lp, ...)
```

Arguments

`lp`	An object extending class `optObj`.
`closeEnv`	A Boolean value. If set to `TRUE`, the CPLEX environment associated with the problem object will be closed also. Otherwise not. Default: `TRUE`.
`...`	Further arguments passed to the deletion function of the solver package.

Methods

`signature(lp = "optObj_clpAPI")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

doubleFluxDel *Double Flux Deletion Experiment*

Description

Double reaction (flux) deletion analysis.

Usage

```
doubleFluxDel(model, react1, react2, lb = NULL, ub = NULL,
              allComb = FALSE, exex = FALSE, checkOptSolObj = FALSE, ...)
```

Arguments

model	An object of class modelorg.
react1	An object of class reactId or character or integer containing reaction id's to constrain to zero. Default: react_id(model).
react2	An object of class reactId or character or integer containing reaction id's to constrain to zero. Default: react_id(model).
lb	A numeric vector containing the lower bounds for the reaction rates of reactions (variables) given in arguments react1 and react2. If set to NULL, all reactions will be constrained to zero. Default: NULL.
ub	A numeric vector containing the upper bounds for the reaction rates of reactions (variables) given in arguments react1 and react2. If set to NULL, all reactions will be constrained to zero. Default: NULL.
allComb	A single Boolean value. If set to TRUE, every possible pairwise combination of reactions given in arguments react1 and react2 will be constrained to zero flux. If set to FALSE, arguments react1 and react2 must have the same length. The deletions will be computed pair-wise: first react1[1] and react2[1], second react1[2] and react2[2] and so on. Default: FALSE.
exex	A single Boolean value. If set to TRUE, exchange reactions will be excluded from the analysis. They are identified by the function findExchReact. Default: FALSE.

checkOptSolObj A single logical value. If set to TRUE, a warning will be generated, if not all optimizations ended successful.
Default: FALSE.

... Further arguments passed to optimizer. Important ones are algorithm in order to set the algorithm to use or solverParm in order to set parameter values for the optimization software.

Details

The function doubleFluxDel studies the effect of double flux deletions on the phenotype of the metabolic network. The function performs n optimizations with n being either the number of reaction id's in argument react1 times the number of reaction id's in argument react2, if argument allComb is set to TRUE, or the length of one of these vectors if argument allComb is set to FALSE. Each optimization corresponds to the simultaneous deletion of two fluxes.

Value

An object of class optsol_fluxdel.

Author(s)

Gabriel Gelius-Dietrich

See Also

modelorg, optsol, optsol_fluxdel, checkOptSol, optimizer and SYBIL_SETTINGS.

Examples

```
data(Ec_core)
Ec_dfd <- doubleFluxDel(Ec_core)
```

---

doubleGeneDel *Double Gene Deletion Experiment*

Description

Predict the metabolic phenotype of of double-gene knock out mutants.

Usage

```
doubleGeneDel(model, geneList1, geneList2, lb = NULL, ub = NULL,
              allComb = FALSE, exLethal = TRUE,
              tol = SYBIL_SETTINGS("TOLERANCE"),
              checkOptSolObj = FALSE, ...)
```

Arguments

model	An object of class modelorg.
geneList1	A character vector containing the set of genes to be deleted. Default: allGenes(model).
geneList2	A character vector containing the set of genes to be deleted. Default: allGenes(model).
lb	A numeric vector containing the lower bounds for the reaction rates of reactions (variables) affected by the genes given in arguments geneList1 and geneList2. If set to NULL, all reactions affected will be constrained to zero. Default: NULL.
ub	A numeric vector containing the upper bounds for the reaction rates of reactions (variables) affected by the genes given in arguments geneList1 and geneList2. If set to NULL, all reactions affected will be constrained to zero. Default: NULL.
allComb	A single Boolean value. If set to TRUE, every possible pairwise combination of genes given in arguments geneList1 and geneList2 will be knocked-out. If set to FALSE, arguments geneList1 and geneList2 must have the same length. The knock-outs will be computed pair-wise: first geneList1[1] and geneList2[1], second geneList1[2] and geneList2[2] and so on. Default: FALSE.
exLethal	A single Boolean value. If set to TRUE, lethal genes are removed from the analysis. A unique set of genes in geneList1 and geneList2 will be scanned for lethal genes. A particular gene i is considered as lethal, if the deletion of this gene results in a zero flux rate in the objective function given in model. Default: TRUE.
tol	A single numeric value, containing an absolute threshold value for a gene being lethal or not. Default: SYBIL_SETTINGS("TOLERANCE").
checkOptSolObj	A single logical value. If set to TRUE, a warning will be generated, if not all optimizations ended successful. Default: FALSE.
...	Further arguments passed to optimizer. Important ones are algorithm in order to set the algorithm to use or solverParm in order to set parameter values for the optimization software.

Details

The function doubleGeneDel studies the effect of genetic perturbations by double gene deletions on the phenotype of the metabolic network. The function performs n optimizations with n being either the length of the character vector in argument geneList1 times the length of the character vector in argument geneList2, if argument allComb is set to TRUE, or the length of one of these vectors if argument allComb is set to FALSE. For each gene deletion i, j the set of fluxes effected by the simultaneous deletion of genes i and j is constrained to zero flux. If the deletion of a certain pair of genes has an effect, is tested with the function geneDel. Each optimization corresponds to the simultaneous deletion of two genes.

Value

An object of class optsol_genedel.

Author(s)

Gabriel Gelius-Dietrich

See Also

modelorg, optsol, optsol_genedel, checkOptSol, optimizer and SYBIL_SETTINGS.

Examples

```
## Not run:
  ## compute all possible pairwise gene deletions
  # load example data set
  data(Ec_core)

  # compute all possible pairwise gene deletions via
  # FBA (default)
  Ec_dgd <- doubleGeneDel(Ec_core, allComb = TRUE)

  # or MOMA (linearized version)
  Ec_dgd <- doubleGeneDel(Ec_core,
                          allComb = TRUE,
                          algorithm = "lmoma")

## End(Not run)
```

---

doubleReact *Identifies Identical Reactions*

Description

The function doubleReact identifies identical reactions (isoenzymes) in a model.

Usage

```
doubleReact(model, checkRev = TRUE, linInd = FALSE)
```

Arguments

model	An object of class modelorg.
checkRev	A single logical value. If set to TRUE, two reactions are identical, if, additionally to the stoichiometric coefficients, the direction of the reactions is the same (the corresponding value of slot react_rev of the model). Default: TRUE.

`linInd` A single logical value. If set to `TRUE`, two reactions are identical, if the vectors of stoichiometric coefficients are linear dependent. For example, two reactions with coefficients $(1, 1, -1)$ and $(2, 2, -2)$ are linear dependent. If the coefficients have different signs, for example $(-1, 1)$ and $(1, -1)$ (the first reaction being forward direction and the second one being backward direction), they are not identical. If `linInd` is set to `FALSE`, the stoichiometric must be identical, for two reactions considered to be identical. Default: `FALSE`.

Details

In the first step, the stoichiometric matrix S is divided into groups of reactions containing the same number of metabolites. After that, the row indices of the non-zero elements of these matrices are compared. If identical pairs are found, we check the corresponding values in S. If they are also identical, the reversibility of the reactions are examined. If they are the same, the two reactions are called identical.

Value

If no identical reactions were found, the return value is FALSE. Otherwise a list is returned, ordered by the number of metabolites used in each reaction. Each element is a numerical vector containing the indices (column number fo the stoichiometrix matrix) of identical reactions.

Note

At the moment, the directions of a pair of reactions is not compared. Meaning, that if concerning to the values in S the reaction is in forward direction, but not when including the flux values, `doubleReact` will not find it.

Author(s)

Gabriel Gelius-Dietrich

Examples

```
data(Ec_core)
Ec_dr <- doubleReact(Ec_core)
```

Ec_core *Escherichia coli Core Metabolic Model*

Description

The dataset is a network representation of the *E. coli* core metabolism. It consists of 95 internal reactions, 20 exchange reactions and a biomass objective function.

Usage

```
data(Ec_core)
```

Format

An object of class `modelorg`

Source

http://gcrg.ucsd.edu/Downloads/EcoliCore

References

Bernhard Ø. Palsson (2006). *Systems Biology: Properties of Reconstructed Networks*. Cambridge University Press.

Orth, J. D., Fleming, R. M. T. and Palsson, B. Ø. (2010). Reconstruction and Use of Microbial Metabolic Networks: the Core Escherichia coli Metabolic Model as an Educational Guide *in* EcoSal Chapter 10.2.1.

---

editEnvir *Environment Editor for Metabolic Networks*

Description

Environment editor for metabolic networks. The function `editEnvir` opens the exchange reactions of a metabolic network in R's data editor. Changes in upper and lower bounds will be set in the given model.

Usage

```
editEnvir(model, newKey = FALSE, ...)
```

Arguments

`model`	An object of class `modelorg`.
`newKey`	If set to `TRUE`, a new model key will be generated.
`...`	Further arguments passed to `edit`.

Value

An object of class `modelorg`.

Author(s)

Gabriel Gelius-Dietrich

See Also

`checkReactId`

Examples

```
## Not run:
## change environment of E.coli core model:
data(Ec_core)
mod <- editEnvir(Ec_core)

## End(Not run)
```

`findExchReact` *Find Exchange Reactions*

Description

This function identifies reactions in a metabolic network which transport metabolites accross the network boundary. Only the stroichiometric matrix is taken into account, so the identified reactions are basically those, having only one non-zero entry in their column of the stroichiometric matrix. In order to work, the network must be "open", it must not contain boundary metabolites.

Usage

```
findExchReact(model)
```

Arguments

`model`	An object of class `modelorg`, `Matrix` or `matrix`.

Details

A exchange reaction j for a particular metabolite i has exactly one non-zero entry in the stoichiometric matrix $S_{ij} \in \{-1, 1\}$. If $S_{ij} = -1$, reaction j is considered to be an uptake (source) reaction.

Value

If `model` is of class `modelorg` an object of class `reactId_Exch` is returned. Otherwise, if `model` is of class `matrix` or of class `Matrix`, a logical vector is returned. If element `i` equals `TRUE`, column `i` of `model` is an exchange reaction.

Author(s)

Gabriel Gelius-Dietrich

References

Becker, S. A., Feist, A. M., Mo, M. L., Hannum, G., Palsson, B. Ø. and Herrgard, M. J. (2007) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. *Nat Protoc* **2**, 727–738.

Schellenberger, J., Que, R., Fleming, R. M. T., Thiele, I., Orth, J. D., Feist, A. M., Zielinski, D. C., Bordbar, A., Lewis, N. E., Rahmanian, S., Kang, J., Hyduke, D. R. and Palsson, B. Ø. (2011) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. *Nat Protoc* **6**, 1290–1307.

Examples

```
data(Ec_core)
ex  <- findExchReact(Ec_core)

# run FBA
opt <- optimizeProb(Ec_core)

# get flux distribution of exchange reactions
getFluxDist(opt, ex)
```

---

fluxDistribution-class

Class "fluxDistribution"

Description

Structure of the class "fluxDistribution". Objects of that class are used by class "optsol" in order to store flux distributions. Flux distributions are stored column by column; each flux corresponds to one row and the optimizations correspond to the columns.

Objects from the Class

Objects can be created by calls of the form `test <- fluxDistribution(fluxes, nrow = 1, ncol = 1`.

If argument `fluxes` is of class `Matrix` or `matrix`, `num_of_fluxes` is set to `ncol(fluxes) * nrow(fluxes)`. If argument `fluxes` is a vector, a matrix will be generated according to `nrow` and `ncol`.

Slots

`fluxes`: Object of class "Matrix" containing fluxdistributions column by column.

`num_of_fluxes`: Object of class "integer" containing the number of elements in `fluxes`.

Methods

`[ signature(x = "fluxDistribution")`: subsetting operator for the matrix of flux distributions.

`fluxes signature(object = "fluxDistribution")`: gets the `fluxes` slot.

`fluxes<- signature(object = "fluxDistribution")`: sets the `fluxes` slot.

`num_of_fluxes signature(object = "fluxDistribution")`: gets the `num_of_fluxes` slot.

`nnzero signature(object = "fluxDistribution")`: gets the number of non-zero elements in slot `fluxes`.

`nvar signature(object = "fluxDistribution")`: gets the number of fluxes in the fluxdistribution in slot `fluxes` (the number of rows of slot `fluxes`).

`plot signature(x = "fluxDistribution", y = "missing")`: heatmap like plotting method for fluxdistributions. Not finished yet.

Author(s)

Gabriel Gelius-Dietrich

Examples

```
showClass("fluxDistribution")
```

`fluxVar` *Flux Variability Analysis*

Description

Performs flux variability analysis for a given model.

Usage

```
fluxVar(model, react = c(1:react_num(model)), exex = FALSE, ...)
```

Arguments

`model`	An object of class `modelorg`.
`react`	An object of class `reactId`, character or integer. Specifies the fluxes (variables) to analyse. Default: all reactions present in `model`.
`exex`	Boolean. Exclude exchange reactions from analysis. If set to `TRUE`, argument `react` will be ignored. All reactions present in `model` will be used, except for the exchange reactions. Default: `FALSE`
`...`	Further arguments passed to `optimizer`. Argument `algorithm` is set to `"fv"`, further possible arguments are `fld`, arguments for pre and post processing commands, `verboseMode` and further arguments passed to the constructor for objects of class `sysBiolAlg_fv`, see there for details.

Details

The algorithm is described in `sysBiolAlg_fv`.

Value

An object of class optsol_fluxVar. The first 1 to n (with n being the number of elements in argument react) solutions are from the minimizations, and the last $n + 1$ to $2n$ solutions are from the maximizations.

Author(s)

Gabriel Gelius-Dietrich

References

Becker, S. A., Feist, A. M., Mo, M. L., Hannum, G., Palsson, B. Ø. and Herrgard, M. J. (2007) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. *Nat Protoc* **2**, 727–738.

Schellenberger, J., Que, R., Fleming, R. M. T., Thiele, I., Orth, J. D., Feist, A. M., Zielinski, D. C., Bordbar, A., Lewis, N. E., Rahmanian, S., Kang, J., Hyduke, D. R. and Palsson, B. Ø. (2011) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. *Nat Protoc* **6**, 1290–1307.

Bernhard Ø. Palsson (2006). *Systems Biology: Properties of Reconstructed Networks*. Cambridge University Press.

Examples

```
data(Ec_core)
fv <- fluxVar(Ec_core)
plot(fv)
```

---

geneDel *Get Gene-Reaction Association*

Description

The function geneDel returns the fluxes which are effected by a particular combination of genes.

Usage

```
geneDel(model, genes, checkId = FALSE)
```

Arguments

model	An object of class modelorg.
genes	A vector of character strings of gene id's used in model, or an integer vector with indices to gene id's in allGenes(model).
checkId	Boolean. If set to TRUE, argument genes will be checked wether it fits to model (e.g. are all genes existing). If set to FALSE, genes must contain indices of gene id's in model, e.g. in calls from optimizer.

Details

The function geneDel checks for a set of gene id's in gene on which fluxes a deletion of this set of genes has an effect.

Value

An numeric vector of pointers to reaction id's in model or NULL, if no fluxes are effected by the gene deletion.

Author(s)

Gabriel Gelius-Dietrich

References

Edwards, J. S., Ibarra, R. U. and Palsson, B. Ø. (2001) In silico predictions of *Escherichia coli* metabolic capabilities are consistent with experimental data. *Nat Biotechnol* **19**, 125–130.

See Also

optimizer

---

geneDeletion *Gene Deletion Experiments*

Description

The function geneDeletion studies the effect of n in silico gene deletions on the phenotype of a metabolic network. The value of n is the number of genes knocked-out simultaneously.

Usage

```
geneDeletion(model, genes, combinations = 1,
             lb = NULL, ub = NULL, checkOptSolObj = FALSE, ...)
```

Arguments

model	An object of class modelorg.
genes	Character or Integer: the genes to delete (see Details below).
combinations	A single integer value. If combinations > 1 and genes is not a matrix, combinations is the number of elements from genes taken at a time while building all combinations of the elements in genes (see Details below). Default: 1.
lb	A numeric vector containing the lower bounds for the reaction rates of reactions (variables) affected by the genes given in argument genes. If set to NULL, all reactions affected will be constrained to zero. Default: NULL.

ub	A numeric vector containing the upper bounds for the reaction rates of reactions (variables) affected by the genes given in argument genes. If set to NULL, all reactions affected will be constrained to zero. Default: NULL.
checkOptSolObj	A single logical value. If set to TRUE, a warning will be generated, if not all optimizations ended successful. Default: FALSE.
...	Further arguments passed to optimizer. Important ones are algorithm in order to set the algorithm to use or solverParm in order to set parameter values for the optimization software.

Details

If argument genes is a matrix of character values (gene id's) or integers (pointers to gene id's), each column is treated as one deletion experiment. If the matrix is made up of integers, a zero entry means no gene.

If argument genes is a character vector or integer, the argument combinations gives the number of gene id's taken each time in order to build all possible combinations of genes. A matrix is constructed using combn. The value of argument combinations gives the number of genes, which are knocked-out simultaneously. The default value 1 performs a single gene deletion experiment, like the function oneGeneDel does. A value of 2 performs a double gene deletion as described in doubleGeneDel. A value of n performs an n gene deletion experiment. Keep in mind, that the number of optimizations will get very high for increasing values of combinations.

If argument genes is empty, the number of unique genes present in model is used.

The required length of arguments lb and ub (if not NULL) depends on the values given in arguments genes and combinations. If genes is a matrix, lb and ub must be of length equal to the number of columns in genes. If genes is a vector, lb and ub must be of length equal to length(genes) * combinations.

Value

An object of class optsol_genedel.

Author(s)

Gabriel Gelius-Dietrich

See Also

modelorg, optsol, optsol_genedel, checkOptSol, oneGeneDel, optimizer, optimizeProb, combn and SYBIL_SETTINGS.

Examples

```
## load the dataset
data(Ec_core)

## perform a single gene deletion analysis
```

```
  ## (delete every gene one by one) via FBA
  gd <- geneDeletion(Ec_core)

  ## or via MOMA (linearized version)
  gd <- geneDeletion(Ec_core, algorithm = "lmoma")

  ## triple gene deletion analysis using the first ten genes
  gd <- geneDeletion(Ec_core, genes = 10, combinations = 3)

## Not run:
  ## perform a double gene deletion analysis
  ##(delete all possible pairwise combinations of all genes)
  gd <- geneDeletion(Ec_core, combinations = 2)

  ## perform a triple gene deletion analysis
  ## (very high number of optimizations)
  gd <- geneDeletion(Ec_core, combinations = 3)

## End(Not run)
```

`getColPrim-methods` *Get Primal Value of Variables After Optimization*

Description

Get primal value of variables after optimization.

Usage

```
## S4 method for signature 'optObj_clpAPI,numeric'
getColPrim(lp, j)

## S4 method for signature 'optObj_cplexAPI,numeric'
getColPrim(lp, j)

## S4 method for signature 'optObj_glpkAPI,numeric'
getColPrim(lp, j)

## S4 method for signature 'optObj_lpSolveAPI,numeric'
getColPrim(lp, j)
```

Arguments

`lp`	An object extending class `optObj`.
`j`	A numeric vector containing the column (variable) indices.

Value

A numeric vector containing the desired primal values.

Methods

`signature(lp = "optObj_clpAPI", j = "numeric")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI", j = "numeric")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI", j = "numeric")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI", j = "numeric")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

`getColsLowBnds-methods` *Get Lower Bounds of the Columns (Variables) of the Optimization Problem*

Description

Get lower bounds of the columns (variables) of the optimization Problem.

Usage

```
## S4 method for signature 'optObj_clpAPI,numeric'
getColsLowBnds(lp, j)

## S4 method for signature 'optObj_cplexAPI,numeric'
getColsLowBnds(lp, j)

## S4 method for signature 'optObj_glpkAPI,numeric'
getColsLowBnds(lp, j)

## S4 method for signature 'optObj_lpSolveAPI,numeric'
getColsLowBnds(lp, j)
```

Arguments

`lp`	An object extending class `optObj`.
`j`	A numeric vector containing the column (variable) indices.

Value

A numeric vector containing the desired column bounds.

Methods

`signature(lp = "optObj_clpAPI", j = "numeric")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI", j = "numeric")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI", j = "numeric")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI", j = "numeric")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

`getColsNames-methods` *Retrieve Variable Names*

Description

Get names of variables (columns) used in a optimization problem.

Usage

```
## S4 method for signature 'optObj_cplexAPI,numeric'
getColsNames(lp, j)

## S4 method for signature 'optObj_glpkAPI,numeric'
getColsNames(lp, j)

## S4 method for signature 'optObj_lpSolveAPI,numeric'
getColsNames(lp, j)
```

Arguments

`lp`	An object extending class `optObj`.
`j`	A numeric vector of column indices.

Value

A character vector of column names, if names are existing.

Methods

`signature(lp = "optObj_cplexAPI", j = "numeric")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI", j = "numeric")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI", j = "numeric")` method to use with package **optObj_lpSolveAPI**.

Note

For the optObj_glpkAPI method: the result vector may be shorter than j, if some names are missing.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

getColsUppBnds-methods

Get Upper Bounds of the Columns (Variables) of the Optimization Problem

---

Description

Get upper bounds of the columns (variables) of the optimization Problem.

Usage

```
## S4 method for signature 'optObj_clpAPI,numeric'
getColsUppBnds(lp, j)

## S4 method for signature 'optObj_cplexAPI,numeric'
getColsUppBnds(lp, j)

## S4 method for signature 'optObj_glpkAPI,numeric'
getColsUppBnds(lp, j)

## S4 method for signature 'optObj_lpSolveAPI,numeric'
getColsUppBnds(lp, j)
```

Arguments

lp	An object extending class optObj.
j	A numeric vector containing the column (variable) indices.

Value

A numeric vector containing the desired column bounds.

Methods

`signature(lp = "optObj_clpAPI", j = "numeric")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI", j = "numeric")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI", j = "numeric")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI", j = "numeric")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

`getFluxDist-methods` *Retrieve Flux Distribution*

Description

Get all primal values of variables after optimization (the resulting flux distribution).

Usage

```
## S4 method for signature 'optObj_clpAPI'
getFluxDist(lp)

## S4 method for signature 'optObj_cplexAPI'
getFluxDist(lp)

## S4 method for signature 'optObj_glpkAPI'
getFluxDist(lp)

## S4 method for signature 'optObj_lpSolveAPI'
getFluxDist(lp)

## S4 method for signature 'optsol'
getFluxDist(lp, react = NULL, opt = NULL, drop = TRUE)
```

Arguments

`lp`	An object extending class `optObj` or class `optsol`.
`react`	Numeric vector or object of class `reactId` indicating the reactions (rows of the flux distribution) to return. Default: `NULL`.

opt	Numeric vector indicating the optimizations (columns of the flux distribution) to return. Default: NULL.
drop	Used for array subsetting like in [. Default: TRUE.

Value

A numeric matrix or vector containing all primal values (the flux distribution).

Methods

signature(lp = "optObj_clpAPI") method to use with package **optObj_clpAPI**.

signature(lp = "optObj_cplexAPI") method to use with package **optObj_cplexAPI**.

signature(lp = "optObj_glpkAPI") method to use with package **optObj_glpkAPI**.

signature(lp = "optObj_lpSolveAPI") method to use with package **optObj_lpSolveAPI**.

signature(lp = "optsol") method to use with objects of class optsol. Returns a subset of the flux distribution stored in slot fluxdist as object of class Matrix. If arguments react and opt are both set to NULL (default), the flux distribution corresponding to the variable indices in slot fldind will be returned.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

getNumCols-methods *Get Number of Columns (Variables) of the Optimization Problem*

Description

Get number of columns (variables) of the optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI'
getNumCols(lp)

## S4 method for signature 'optObj_cplexAPI'
getNumCols(lp)

## S4 method for signature 'optObj_glpkAPI'
getNumCols(lp)
```

```
## S4 method for signature 'optObj_lpSolveAPI'
getNumCols(lp)
```

Arguments

lp	An object extending class optObj.

Value

A single numeric value.

Methods

`signature(lp = "optObj_clpAPI")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

getNumNnz-methods *Retrieve the Number of Non-Zero Elements of the Constraint Matrix*

Description

Retrieve the number of non-zero elements in the constraint matrix of the optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI'
getNumNnz(lp)

## S4 method for signature 'optObj_cplexAPI'
getNumNnz(lp)

## S4 method for signature 'optObj_glpkAPI'
getNumNnz(lp)
```

Arguments

lp	An object extending class optObj.

Value

A single numeric value.

Methods

`signature(lp = "optObj_clpAPI")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

---

getNumRows-methods *Get Number of Rows (Constraints) of the Optimization Problem*

Description

Get number of rows (constraints) of the optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI'
getNumRows(lp)

## S4 method for signature 'optObj_cplexAPI'
getNumRows(lp)

## S4 method for signature 'optObj_glpkAPI'
getNumRows(lp)

## S4 method for signature 'optObj_lpSolveAPI'
getNumRows(lp)
```

Arguments

`lp`	An object extending class `optObj`.

Value

A single numeric value.

Methods

`signature(lp = "optObj_clpAPI")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

`getObjCoefs-methods` *Get Objective Coefficients of the Optimization Problem*

Description

Get objective coefficients of the optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI,numeric'
getObjCoefs(lp, j)

## S4 method for signature 'optObj_cplexAPI,numeric'
getObjCoefs(lp, j)

## S4 method for signature 'optObj_glpkAPI,numeric'
getObjCoefs(lp, j)

## S4 method for signature 'optObj_lpSolveAPI,numeric'
getObjCoefs(lp, j)
```

Arguments

`lp`	An object extending class `optObj`.
`j`	A numeric vector containing the column (variable) indices.

Value

A numeric vector containing the desired objective coefficients.

Methods

`signature(lp = "optObj_clpAPI", j = "numeric")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI", j = "numeric")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI", j = "numeric")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI", j = "numeric")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

`getObjDir-methods` *Get Direction of Optimization.*

Description

Get direction of optimization.

Usage

```
## S4 method for signature 'optObj_clpAPI'
getObjDir(lp)

## S4 method for signature 'optObj_cplexAPI'
getObjDir(lp)

## S4 method for signature 'optObj_glpkAPI'
getObjDir(lp)

## S4 method for signature 'optObj_lpSolveAPI'
getObjDir(lp)
```

Arguments

`lp`	An object extending class `optObj`.

Value

Returns a single character string indicating the direction of optimization: `"max"`: maximization, or `"min"`: minimization.

Methods

`signature(lp = "optObj_clpAPI")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

`getObjVal-methods` *Get Value of the Objective Function After Optimization*

Description

Get value of the objective function after optimization.

Usage

```
## S4 method for signature 'optObj_clpAPI'
getObjVal(lp)

## S4 method for signature 'optObj_cplexAPI'
getObjVal(lp)

## S4 method for signature 'optObj_glpkAPI'
getObjVal(lp)

## S4 method for signature 'optObj_lpSolveAPI'
getObjVal(lp)
```

Arguments

`lp`	An object extending class `optObj`.

Value

Returns a single numeric value.

Methods

`signature(lp = "optObj_clpAPI")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**. For problems of type `"mip"`: if no solution exists, the **cplexAPI** function `getBestObjValCPLEX` will be used.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

`getRedCosts-methods` *Get Reduced Costs of all Variables After Optimization*

Description

Get reduced costs of all variables after optimization.

Usage

```
## S4 method for signature 'optObj_clpAPI'
getRedCosts(lp)

## S4 method for signature 'optObj_cplexAPI'
getRedCosts(lp)

## S4 method for signature 'optObj_glpkAPI'
getRedCosts(lp)

## S4 method for signature 'optObj_lpSolveAPI'
getRedCosts(lp)
```

Arguments

`lp`	An object extending class `optObj`.

Value

A numeric vector containing the reduced costs of all variables.

Methods

`signature(lp = "optObj_clpAPI")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

`getRowsLowBnds-methods` *Get Lower Bounds of the Rows (Constraints) of the Optimization Problem*

Description

Get lower bounds of the rows (constraints) of the optimization Problem.

Usage

```
## S4 method for signature 'optObj_clpAPI,numeric'
getRowsLowBnds(lp, i)

## S4 method for signature 'optObj_cplexAPI,numeric'
getRowsLowBnds(lp, i)

## S4 method for signature 'optObj_glpkAPI,numeric'
getRowsLowBnds(lp, i)

## S4 method for signature 'optObj_lpSolveAPI,numeric'
getRowsLowBnds(lp, i)
```

Arguments

`lp`	An object extending class `optObj`.
`i`	A numeric vector containing the row indices.

Value

A numeric vector containing the desired row bounds.

Methods

`signature(lp = "optObj_clpAPI", i = "numeric")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI", i = "numeric")` method to use with package **optObj_cplexAPI**. This method returns always `FALSE`.

`signature(lp = "optObj_glpkAPI", i = "numeric")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI", i = "numeric")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

`getRowsNames-methods` *Retrieve Constraint Names*

Description

Get names of constraints (rows) used in a optimization problem.

Usage

```
## S4 method for signature 'optObj_cplexAPI,numeric'
getRowsNames(lp, i)

## S4 method for signature 'optObj_glpkAPI,numeric'
getRowsNames(lp, i)

## S4 method for signature 'optObj_lpSolveAPI,numeric'
getRowsNames(lp, i)
```

Arguments

`lp`	An object extending class `optObj`.
`i`	A numeric vector of row indices.

Value

A character vector of row names, if names are existing.

Methods

`signature(lp = "optObj_cplexAPI", i = "numeric")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI", i = "numeric")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI", i = "numeric")` method to use with package **optObj_lpSolveAPI**.

Note

For the optObj_glpkAPI method: the result vector may be shorter than i, if some names are missing.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

getRowsUppBnds-methods

Get Upper Bounds of the Rows (Constraints) of the Optimization Problem

---

Description

Get upper bounds of the rows (constraints) of the optimization Problem.

Usage

```
## S4 method for signature 'optObj_clpAPI,numeric'
getRowsUppBnds(lp, i)

## S4 method for signature 'optObj_cplexAPI,numeric'
getRowsUppBnds(lp, i)

## S4 method for signature 'optObj_glpkAPI,numeric'
getRowsUppBnds(lp, i)

## S4 method for signature 'optObj_lpSolveAPI,numeric'
getRowsUppBnds(lp, i)
```

Arguments

lp	An object extending class optObj.
i	A numeric vector containing the row indices.

Value

A numeric vector containing the desired row bounds.

Methods

`signature(lp = "optObj_clpAPI", i = "numeric")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI", i = "numeric")` method to use with package **optObj_cplexAPI**. This method returns always `FALSE`.

`signature(lp = "optObj_glpkAPI", i = "numeric")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI", i = "numeric")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

`getSolStat-methods` *Get Solution Status After Optimization*

Description

Get solution status after optimization.

Usage

```
## S4 method for signature 'optObj_clpAPI'
getSolStat(lp)

## S4 method for signature 'optObj_cplexAPI'
getSolStat(lp)

## S4 method for signature 'optObj_glpkAPI'
getSolStat(lp)

## S4 method for signature 'optObj_lpSolveAPI'
getSolStat(lp)
```

Arguments

`lp`	An object extending class `optObj`.

Value

Returns a single numeric value indicating the solution status after optimization.

Methods

`signature(lp = "optObj_clpAPI")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI")` method to use with package **optObj_lpSolveAPI**. This method returns `NA`. Package **lpSolveAPI** does not provide a solution status.

Author(s)

Gabriel Gelius-Dietrich

See Also

Function `getMeanStatus` and superclass `optObj` and constructor function `optObj`.

---

getSolverParm-methods *Retrieve Current Parameter Settings Used By The Optimization Software*

Description

Retrieve current parameter settings used by the optimization software.

Usage

```
## S4 method for signature 'optObj_clpAPI'
getSolverParm(lp)

## S4 method for signature 'optObj_cplexAPI'
getSolverParm(lp)

## S4 method for signature 'optObj_glpkAPI'
getSolverParm(lp)

## S4 method for signature 'optObj_lpSolveAPI'
getSolverParm(lp)
```

Arguments

`lp`	An object extending class `optObj`.

Value

Returns a list containing the current parameter settings or zero/non-zero.

Methods

`signature(lp = "optObj_clpAPI")` method to use with package **optObj_clpAPI**. This method is currently unused. It is not possible to provide parameters for package **clpAPI**. Always `FALSE` will be returned.

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**. This method writes the current parameter settings to the file `"cplex_parameters.prm"`. The method returns zero if successfull, otherwise non-zero.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

---

getsybilenv *Print sybil Environment*

Description

Prints current settings in the sybil environment.

Usage

```
getsybilenv(part)
```

Arguments

`part`	A character vector containing names of elements in the sybil environment. Possible values are: `"solvers"` supported R packages for solving optimization problems. `"methods"` methods to solve optimization problems included in the R packages. `"ptype"` methods required for a particular problem type. `"purpose"` algorithms used in systems biology to use with a particular purpose.

Details

Typical usages are

```
getsybilenv(part)
getsybilenv()
```

If argument `part` is not given, all elements described above will be printed.

Value

Returns NULL invisibly.

Author(s)

Gabriel Gelius-Dietrich

See Also

addSolver, checkDefaultMethod and SYBIL_SETTINGS.

---

initProb-methods *Initialize Problem Object*

Description

Initialize Problem Object.

Usage

```
## S4 method for signature 'optObj_clpAPI'
initProb(lp, to = NULL, ...)

## S4 method for signature 'optObj_cplexAPI'
initProb(lp, to = FALSE, ...)

## S4 method for signature 'optObj_glpkAPI'
initProb(lp, to = FALSE, ...)

## S4 method for signature 'optObj_lpSolveAPI'
initProb(lp, to = NULL, nrows, ncols)
```

Arguments

lp	An object extending class optObj.
to	A single boolean, numeric or character value, controling the amount of terminal output of the solver software. Default: FALSE or NULL.
nrows	Number of rows (constraints) of the new problem object.
ncols	Number of columns (variables) of the new problem object.
...	Further arguments passed to the initialization function of the solver package.

Methods

`signature(lp = "optObj_clpAPI")` method to use with package **optObj_clpAPI**, argument `to` can be a single numeric value: `0` – "none", `1` – "just final", `2` – "just factorizations", `3` – "as 2 plus a bit more", code4 – "verbose". See COIN-OR Clp documentation for more details.

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**, argument `to` can be `TRUE` or `FALSE`. Setting CPLEX parameter `CPX_PARAM_SCRIND` to `CPX_ON` or `CPX_OFF` has the same effect.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**, argument `to` can be `TRUE` or `FALSE`, setting GLPK function `termOutGLPK` to `GLP_ON` or `GLP_OFF`. The amount of output is controlled by the GLPK parameter `MSG_LEV`.

`signature(lp = "optObj_lpSolveAPI")` method to use with package **optObj_lpSolveAPI**, argument `to` can be a single character value, see **lpSolveAPI** documentation for more details (`lp.control.options`, section `verbose`).

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

`loadLPprob-methods` *Load Data to Optimization Problem*

Description

Load data to the problem object (extending class `optObj`). Use this method to generate problem objects.

Usage

```
## S4 method for signature 'optObj_clpAPI'
loadLPprob(lp,
           nCols, nRows, mat, ub, lb, obj, rlb, rtype,
           lpdir = "max", rub = NULL, ctype = NULL,
           cnames = NULL, rnames = NULL, pname = NULL,
           defLowerBnd = SYBIL_SETTINGS("MAXIMUM") * -1,
           defUpperBnd = SYBIL_SETTINGS("MAXIMUM")
)

## S4 method for signature 'optObj_cplexAPI'
loadLPprob(lp,
           nCols, nRows, mat, ub, lb, obj, rlb, rtype,
           lpdir = "max", rub = NULL, ctype = NULL,
           cnames = NULL, rnames = NULL, pname = NULL)
```

```
## S4 method for signature 'optObj_glpkAPI'
loadLPprob(lp,
           nCols, nRows, mat, ub, lb, obj, rlb, rtype,
           lpdir = "max", rub = NULL, ctype = NULL,
           cnames = NULL, rnames = NULL, pname = NULL)

## S4 method for signature 'optObj_lpSolveAPI'
loadLPprob(lp,
           nCols, nRows, mat, ub, lb, obj, rlb, rtype,
           lpdir = "max", rub = NULL, ctype = NULL,
           cnames = NULL, rnames = NULL, pname = NULL)
```

Arguments

lp	An object of class optObj_clpAPI, optObj_cplexAPI, optObj_glpkAPI or optObj_lpSolveAPI.
nCols	Number of columns (variables) of the constraint matrix.
nRows	Number of rows (constraints) of the constraint matrix.
mat	An object of class Matrix. The constraint matrix of the problem object. The number of columns in mat must be nCols and the number of rows in mat must be nRows.
ub	A numeric vector of length nCols giving the upper bounds of the variables of the problem object.
lb	A numeric vector of length nCols giving the lower bounds of the variables of the problem object.
obj	A numeric vector of length nCols giving the objective coefficients of the variables of the problem object.
rlb	A numeric vector of length nRows giving the right hand side of the problem object. If argument rub is not NULL, rlb contains the lower bounds of the constraints of the problem object. See Details.
rtype	A character vector of length nRows giving the constraint type:

"F":	free constraint (GLPK only)	$-\infty < x < \infty$
"L":	constraint with lower bound	$\text{lb} \leq x < \infty$
"U":	constraint with upper bound	$-\infty < x \leq \text{ub}$
"D":	double-bounded (ranged) constraint	$\text{lb} \leq x \leq \text{ub}$
"E":	fixed (equality) constraint	$\text{lb} = x = \text{ub}$

If rtype[i] is not one of "F", "L", "U", "D" or "E", the value of rtype[i] will be set to "E". See Details.

lpdir	Single character string containing the direction of optimization. Can be set to "min" or "max". Default: "max".
rub	A numeric vector of length nRows giving the right hand side of the problem

object. If not NULL, it contains the upper bounds of the constraints of the problem object. See Details.
Default: NULL.

ctype
: A character vector of length nCols giving the variable type. If set to NULL, no specific variable type is set, which usually means, all variables are treated as continuous variables.
Default: NULL.

"C":	continuous variable
"B":	binary variable
"I":	integer variable
"S":	semi-continuous variable
"N":	semi-integer variable

Values "S" and "N" are not available for every solver software. Check documentation of the solver software if semi-continuous and semi-integer variables are supported. If ctype[j] is not "C", "B", "I", "S", or "N", the value of ctype[j] will be set to "C".

cnames
: A character vector of length nCols containing symbolic names for the variable of the problem object.
Default: NULL.

rnames
: A character vector of length nRows containing symbolic names for the constraints of the problem object.
Default: NULL.

pname
: A single character string containing a name for the problem object.
Default: NULL.

defLowerBnd
: For the optObj_clpAPI method only: a single numeric value containing a default value for an lower bound to a constraint in an optimization problem.
Default: SYBIL_SETTINGS("MAXIMUM") * -1.

defUpperBnd
: For the optObj_clpAPI method only: a single numeric value containing a default value for an upper bound to a constraint in an optimization problem.
Default: SYBIL_SETTINGS("MAXIMUM").

Details

Method loadLPprob can be used any time after a problem object is initialized by initProb.

In order so set constraints, usually only parameter rlb is required and parameter rub can be left at NULL (which is the default). If rub is not NULL, rlb and rub must have the same length. Parameter rub is required, if a particular constraint is a ranged or double bounded constraint. The general idea is, for any constraint i, the value in rlb[i] gives the lower bound and the value in rub[i] gives the upper bound. If the constraints of the optimization problem do only have one bound (type "L", "U" and "E"), all bounds can be set via rlb and rub is not required. If any constraint is of type "D" (a double-bounded or ranged constraint) additionally rub is required. It is of course also possible to use rlb strictly for all lower bounds and rub for all upper bounds. Again, if both rlb and rub are given (not NULL), they must have the same length. For equality constraints (type "E"), allways the value in rlb is used.

For the optObj_cplexAPI method: CPLEX uses so called ranged constraints for double bounded constraints. The values in rlb and rub will be transformed into range values for ranged constraints. The range for a ranged constraint i is given as abs(rub[i] - rlb[i]), so that the valid interval is denoted as [rlb[i], rlb[i] + range].

For the optObj_glpkAPI method: if cnames or rnames is not NULL, an index will be created.

For the optObj_clpAPI method: if cnames is not NULL, rnames must be also not NULL and vice versa.

For the optObj_lpSolveAPI method: if cnames is not NULL, rnames must be also not NULL and vice versa. Round brackets ("(" and ")") will be replaced by underscores "_".

Methods

signature(lp = "optObj_clpAPI") method to use with package **clpAPI**.

signature(lp = "optObj_cplexAPI") method to use with package **cplexAPI**.

signature(lp = "optObj_glpkAPI") method to use with package **glpkAPI**.

signature(lp = "optObj_lpSolveAPI") method to use with package **lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

loadQobj-methods *Load Quadratic Part of the Objective Function to the Optimization Problem*

Description

load quadratic part of the objective function to the optimization problem.

Usage

```
## S4 method for signature 'optObj_cplexAPI,Matrix'
loadQobj(lp, mat)
## S4 method for signature 'optObj_cplexAPI,numeric'
loadQobj(lp, mat)
```

Arguments

lp	An object extending class optObj.
mat	An object of class Matrix or a numeric vector containing the quadratic objective Matrix Q.

Methods

`signature(lp = "optObj_cplexAPI", mat = "Matrix")` method to use with package **optObj_cplexAPI** and if `mat` is of class `Matrix`.

`signature(lp = "optObj_cplexAPI", mat = "numeric")` method to use with package **optObj_cplexAPI** and if `mat` is a `numeric` vector.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

`makeOptsolMO` *Constructor Function for Objects of Class* `optsol_optimizeProb`.

Description

This function is a constructor function generating objects of class `optsol_optimizeProb`.

Usage

```
makeOptsolMO(mod, sol)
```

Arguments

`mod`	An object of class `modelorg`.
`sol`	A list returned by function `optimizer`.

Value

An object of class `optsol_optimizeProb`.

Author(s)

Gabriel Gelius-Dietrich

See Also

Class `optsol_optimizeProb`, class `modelorg` and function `optimizer`.

mod2irrev *Produces a Model in Irreversible Format*

Description

The function mod2irrev produces a model with all reactions moving in positive direction.

Usage

```
mod2irrev(model, exex = FALSE)
```

Arguments

model	An object of class modelorg.
exex	Boolean. Exclude exchange fluxes (default: FALSE).

Details

The returned model consists only of reactions moving in positive direction. Reactions with a negative direction in the original model are transferred to positive direction; the corresponding reaction id gets extended by "_r".

Reversible reactions are split into two reactions. The corresponding reaction ids gets extended by "_f", or "_b" indicating the original direction.

If exex = TRUE, the exchange reactions were obtained by findExchReact.

Value

An object of class modelorg_irrev.

Author(s)

Gabriel Gelius-Dietrich, Markus Herrgard

References

Becker, S. A., Feist, A. M., Mo, M. L., Hannum, G., Palsson, B. Ø. and Herrgard, M. J. (2007) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. *Nat Protoc* **2**, 727–738.

Schellenberger, J., Que, R., Fleming, R. M. T., Thiele, I., Orth, J. D., Feist, A. M., Zielinski, D. C., Bordbar, A., Lewis, N. E., Rahmanian, S., Kang, J., Hyduke, D. R. and Palsson, B. Ø. (2011) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. *Nat Protoc* **6**, 1290–1307.

See Also

modelorg_irrev

Examples

```
data(Ec_core)
Ec_ir <- mod2irrev(Ec_core)
```

`modelorg-class` *Structure of Class "modelorg"*

Description

Structure of the class `"modelorg"`. Objects of that class are returned by functions like `readTSVmod`.

Objects from the Class

Objects can be created by calls of the function `modelorg`:

`test <- modelorg(id = "foo", name = "bar")`.

`id`: a single character string giving the model id.

`name`: a single character string giving the model name.

This constructor also generates the model key used in slot `mod_key`.

Slots

`mod_desc`: Object of class `"character"` containing a description of the model.

`mod_name`: Object of class `"character"` indicating the model name.

`mod_id`: Object of class `"character"` indicating the model id.

`mod_key`: Object of class `"character"` containing a single character string functioning as a unique key to a model object.

`mod_compart`: Object of class `"character"` containing the model compartments.

`met_num`: Object of class `"integer"` indicating the number of metabolites.

`met_id`: Object of class `"character"` containing the metabolite id's.

`met_name`: Object of class `"character"` containing the metabolite names.

`met_comp`: Object of class `"integer"` containing the metabolites compartment.

`met_single`: Object of class `"logical"` with length `met_num`. Element `i` is `TRUE`, if metabolite `i` appears only once in S.

`met_de`: Object of class `"logical"` with length `met_num`. Element `i` is `TRUE`, if metabolite `i` is a dead end metabolite.

`react_num`: Object of class `"integer"` indicating the number of reactions.

`react_rev`: Object of class `"logical"` indicating whether a reaction is reversible or not.

`react_id`: Object of class `"character"` containing the reaction id's.

`react_name`: Object of class `"character"` containing the reaction names.

`react_single`: Object of class `"logical"` with length `react_num`. Element `i` is `TRUE`, if reaction `i` uses metabolites appearing only once in S.

react_de: Object of class "logical" with length react_num. Element i is TRUE, if reaction i uses dead end metabolites.

S: Object of class "matrix" containing the stoichiometric matrix.

lowbnd: Object of class "numeric" containing the reactions lower bounds.

uppbnd: Object of class "numeric" containing the reactions upper bounds.

obj_coef: Object of class "numeric" containing the objective coefficients.

gprRules: Object of class "character" containing the gene-reaction association rules in computable form.

genes: Object of class "list" containing the genes corresponding to each reaction. Every list element is a vector of the type character.

gpr: Object of class "character" containing the gene-reaction association rules for each reaction.

allGenes: Object of class "character" containing a unique list of all genes.

rxnGeneMat: Object of class "matrix" containing a reaction to gene mapping.

subSys: Object of class "matrix" giving one or more subsystem name for each reaction.

Methods

allGenes<-: signature(object = "modelorg"): sets the allGenes slot.

allGenes: signature(object = "modelorg"): gets the allGenes slot.

dim: signature(object = "modelorg"): gets the dimension attribute of slot S.

genes<-: signature(object = "modelorg"): sets the genes slot.

genes: signature(object = "modelorg"): gets the genes slot.

gpr<-: signature(object = "modelorg"): sets the gpr slot.

gpr: signature(object = "modelorg"): gets the gpr slot.

gprRules<-: signature(object = "modelorg"): sets the gprRules slot.

gprRules: signature(object = "modelorg"): gets the gprRules slot.

lowbnd<-: signature(object = "modelorg"): sets the lowbnd slot.

lowbnd: signature(object = "modelorg"): gets the lowbnd slot.

met_comp<-: signature(object = "modelorg"): sets the met_comp slot.

met_comp: signature(object = "modelorg"): gets the met_comp slot.

met_de<-: signature(object = "modelorg"): sets the met_de slot.

met_de: signature(object = "modelorg"): gets the met_de slot.

met_id<-: signature(object = "modelorg"): sets the met_id slot.

met_id: signature(object = "modelorg"): gets the met_id slot.

met_name<-: signature(object = "modelorg"): sets the met_name slot.

met_name: signature(object = "modelorg"): gets the met_name slot.

met_num<-: signature(object = "modelorg"): sets the met_num slot.

met_num: signature(object = "modelorg"): gets the met_num slot.

met_single<-: signature(object = "modelorg"): sets the met_single slot.

met_single: signature(object = "modelorg"): gets the met_single slot.

mod_compart<-: signature(object = "modelorg"): sets the mod_compart slot.

mod_compart: signature(object = "modelorg"): gets the mod_compart slot.

mod_desc<-: signature(object = "modelorg"): sets the mod_desc slot.

mod_desc: signature(object = "modelorg"): gets the mod_desc slot.

mod_id<-: signature(object = "modelorg"): sets the mod_id slot.

mod_id: signature(object = "modelorg"): gets the mod_id slot.

mod_key<-: signature(object = "modelorg"): sets the mod_key slot.

mod_key: signature(object = "modelorg"): gets the mod_key slot.

mod_name<-: signature(object = "modelorg"): sets the mod_name slot.

mod_name: signature(object = "modelorg"): gets the mod_name slot.

obj_coef<-: signature(object = "modelorg"): sets the obj_coef slot.

obj_coef: signature(object = "modelorg"): gets the obj_coef slot.

printObjFunc: signature(object = "modelorg"): prints the objective function in a human readable way.

react_de<-: signature(object = "modelorg"): sets the react_de slot.

react_de: signature(object = "modelorg"): gets the react_de slot.

react_id<-: signature(object = "modelorg"): sets the react_id slot.

react_id: signature(object = "modelorg"): gets the react_id slot.

react_name<-: signature(object = "modelorg"): sets the react_name slot.

react_name: signature(object = "modelorg"): gets the react_name slot.

react_num<-: signature(object = "modelorg"): sets the react_num slot.

react_num: signature(object = "modelorg"): gets the react_num slot.

react_rev<-: signature(object = "modelorg"): sets the react_rev slot.

react_rev: signature(object = "modelorg"): gets the react_rev slot.

react_single<-: signature(object = "modelorg"): sets the react_single slot.

react_single: signature(object = "modelorg"): gets the react_single slot.

rxnGeneMat<-: signature(object = "modelorg"): sets the rxnGeneMat slot.

rxnGeneMat: signature(object = "modelorg"): gets the rxnGeneMat slot.

show: signature(object = "modelorg"): prints some details specific to the instance of class modelorg.

Snnz: signature(object = "modelorg"): prints the number of non-zero elements in S.

S<-: signature(object = "modelorg"): sets the S slot as matrix, see Details below.

S: signature(object = "modelorg"): gets the S slot as matrix.

subSys<-: signature(object = "modelorg"): sets the subSys slot.

subSys: signature(object = "modelorg"): gets the subSys slot.

uppbnd<-: signature(object = "modelorg"): sets the uppnds slot.

uppbnd: signature(object = "modelorg"): gets the uppbnd slot.

Author(s)

Gabriel Gelius-Dietrich

See Also

modelorg_irrev for models in irreversible format.

Examples

```
showClass("modelorg")

## print human readable version of the objective function
data(Ec_core)
printObjFunc(Ec_core)

## change objective function and print
Ec_objf <- changeObjFunc(Ec_core, c("EX_etoh(e)", "ETOHt2r"), c(1, 2))
printObjFunc(Ec_objf)
```

---

modelorg2ExPA *Write an Instance of Class modelorg to File in ExPA Format*

Description

The function modelorg2ExPA writes the content of an instance of class modelorg to text files in a format which can be read by the program ExPA to compute extreme pathways.

Usage

```
modelorg2ExPA(model, fname = NULL, exIntReact = NULL,
              filepath = ".", suffix = "expa",
              tol = SYBIL_SETTINGS("TOLERANCE"))
```

Arguments

model	An object of class modelorg.
fname	An single character string giving the filename to write to. Default: <model_id>.expa.
exIntReact	An object of class reactId, character or integer, giving id's of internal reactions to exclude in the ExPA file. Default: NULL.
filepath	A single character string giving the path to a certain directory in which the output files will be stored. Default: ".".
suffix	A single character string giving the file name extension. Default: "expa".

`tol` A single numeric value giving the limit of tolerance. An element S_{ij} of the stoichiometric matrix is treated as non-zero, if $|S_{ij}| >$ tol is true.
Default: `"expa"`.

Details

The function `modelorg2ExPA` produces input files for the program ExPA. With ExPA, it is possible to calculate extreme pathways in metabolic networks.

The function produces a warning, if a reaction contains non-integer stoichiometric values, because they are not compatible with the ExPA program.

Value

Returns `TRUE` invisibly on success.

Author(s)

Gabriel Gelius-Dietrich, C. Jonathan Fritzemeier

References

Bell, S. L. and Palsson, B. Ø. (2005) Expa: a program for calculating extreme pathways in biochemical reaction networks. *Bioinformatics* **21**, 1739–1740.

The ExPA homepage http://gcrg.ucsd.edu/Downloads/ExtremePathwayAnalysis.

---

modelorg2tsv *Write an Instance of Class modelorg to File*

Description

The function `modelorg2tsv` writes the content of an instance of class `modelorg` to text files in a character-separated value format adopted from the BiGG database output.

Usage

```
modelorg2tsv(model, prefix, suffix, extMetFlag = "b",
             fielddelim = "\t", entrydelim = ", ",
             makeClosedNetwork = FALSE,
             onlyReactionList = FALSE,
             minimalSet = FALSE,
             fpath = SYBIL_SETTINGS("PATH_TO_MODEL"), ...)
```

Arguments

model	An object of class modelorg.
prefix	A single character string giving the prefix for three possible output files (see Details below).
suffix	A single character string giving the file name extension. If missing, the value of suffix depends on the argument fielddelim, see Details below. Default: "tsv".
extMetFlag	A single character string giving the identificator for metabolites which are outside the system boundary. Only necessary, if the model is a closed one. Default: "b".
fielddelim	A single character string giving the value separator. Default: "\t".
entrydelim	A single character string giving the a separator for values containing more than one entry. Default: ", ".
makeClosedNetwork	Boolean. If set to TRUE, external metabolites (which are outside the system boundary) will be added to the model. These metabolites participate in reactions, transporting metabolites across the system boundary. The metabolite id will be the same as for the metabolite inside the system, but the compartment type is set to the value of argument extMetFlag. For example, most models contain a transport reaction for glucose: glc[c] <==> If makeClosedNetwork is set to TRUE, this reaction will be written as glc[c] <==> glc[b] with the letter b being the default value for extMetFlag. Default: FALSE.
onlyReactionList	Boolean. If set to TRUE, only one file containing all reaction equations will be produced (output file has one column). Default: FALSE.
minimalSet	Boolean. If set to TRUE, only one file containing the fields "abbreviation", "equation", "lowbnd", "uppbnd" and "obj_coef" will be produced (output file has five columns). Default: FALSE.
fpath	A single character string giving the path to a certain directory in which the output files will be stored. Default: SYBIL_SETTINGS("PATH_TO_MODEL").
...	Further arguments passed to write.table, e.g. the Boolean argument quote can be used here.

Details

The function modelorg2tsv produces three output files: a reactions list, a metabolites list and a model description file.

The reactions list has the following columns:

"abbreviation"	react_id(model)
"name"	react_name(model)
"equation"	the reaction equations
"reversible"	react_rev(model)
"compartment"	reaction compartment(s)
"lowbnd"	lowbnd(model)
"uppbnd"	uppbnd(model)
"obj_coef"	obj_coef(model)
"rule"	gpr(model)
"subsystem"	subSys(model)

The metabolites list has the following columns:

"abbreviation"	met_id(model)
"name"	met_name(model)
"compartment"	met_comp(model)

The model description file has the following columns:

"name"	mod_name(model)
"id"	mod_id(model)
"description"	mod_desc(model)
"compartment"	mod_compart(model)
"abbreviation"	unique compartment abbreviations
"Nmetabolites"	number of metabolites
"Nreactions"	number of reactions
"Ngenes"	number of independend genes
"Nnnz"	number of non-zero elements in the stoichiometric matrix

If `onlyReactionList` is set to `TRUE`, only the reactions list containing the column `"equation"` is produced.

Please read the package vignette for detailed information about file formats and examples.

All fields in the output files are in double quotes. In order to read them in with `readTSVmod`, set argument `quoteChar` to `"\""`.

Value

Returns `TRUE` on success.

Author(s)

Gabriel Gelius-Dietrich

References

The BiGG database http://bigg.ucsd.edu/.

See Also

read.table, modelorg2tsv, modelorg.

---

modelorg_irrev-class *Class for Metabolic Networks in Irreversible Format.*

Description

Structure of the class "modelorg_irrev". Objects of that class are returned by the function mod2irrev.

Objects from the Class

Objects can be created by calls of the function modelorg_irrev:

test <- modelorg_irrev(id = "foo", name = "bar").

Slots

irrev: Object of class "logical" indicating if the model is in irreversible format.

matchrev: Object of class "integer" matching of forward and backward reactions of a reversible reaction.

rev2irrev: Object of class "matrix" containing the reaction id's of the corresponding reactions in irreversible format.

irrev2rev: Object of class "integer" containing the reaction id's of the corresponding reaction in reversible format.

Extends

Class "modelorg", directly.

Methods

irrev<-: signature(object = "modelorg_irrev"): sets the irrev slot.

irrev: signature(object = "modelorg_irrev"): gets the irrev slot.

matchrev<-: signature(object = "modelorg_irrev"): sets the matchrev slot.

matchrev: signature(object = "modelorg_irrev"): gets the matchrev slot.

rev2irrev<-: signature(object = "modelorg_irrev"): sets the rev2irrev slot.

rev2irrev: signature(object = "modelorg_irrev"): gets the rev2irrev slot.

irrev2rev<-: signature(object = "modelorg_irrev"): sets the irrev2rev slot.

irrev2rev: signature(object = "modelorg_irrev"): gets the irrev2rev slot.

Author(s)

Gabriel Gelius-Dietrich

See Also

modelorg

Examples

```
showClass("modelorg_irrev")
```

---

multiDel *Parallel Support for sybil*

Description

Parallel computation support for the functions oneGeneDel, doubleGeneDel, oneFluxDel, doubleFluxDel and fluxVar.

Usage

```
multiDel(model, nProc = 2, todo = "oneGeneDel", del1 = NA, del2 = NA, ...)
```

Arguments

model	An object of class modelorg.
nProc	Number of cores (processes) to use.
todo	A single character value giving the function name, which should be parallelised. Can be one of "oneGeneDel", "doubleGeneDel", "oneFluxDel", "doubleFluxDel" or "fluxVar".
del1	Vector of genes/reactions to consider.
del2	Vector of genes/reactions to consider (for use with doubleGeneDel or doubleFluxDel).
...	Further arguments passed to oneGeneDel, doubleGeneDel, oneFluxDel, doubleFluxDel or fluxVar.

Details

The function loads the package **parallel** if available. Argument nProc should be the number of cores to use. This number is veryfied via a call to detectCores (of **parallel**) and is set to the return value of detectCores, if nProc > detectCores() evaluates to TRUE. Arguments del1 and del2 are split into lists, each list element containing nProc/del1 elements. These are passed to mclapply.

Value

A list of length nProc (or less, depending of the numbers of available cores), each element containing the return value of the function called (on object of a class extending optsol).

Author(s)

Gabriel Gelius-Dietrich

See Also

mclapply, optsol, oneGeneDel, doubleGeneDel, oneFluxDel, doubleFluxDel and fluxVar.

Examples

```
## Not run:
## The examples here require the packages glpkAPI and parallel to be
## installed.

## perform single gene deletion analysis using the E. coli core
## metabolic model
data(Ec_core)
ad <- multiDel(Ec_core)
mapply(checkOptSol, ad)

## End(Not run)
```

---

netFlux-class *Class* "netFlux"

Description

Class "netFlux" groups exchange reaction rates according to their sign in uptake, excretion and unused reactions.

Objects from the Class

Objects can be created by calls of the form getNetFlux(rates, tol), with argument rates being a named numeric vector containing reaction rates of exchange fluxes and corresponding reaction id's. Argument rates can be obtained by a call to optimizeProb. The second argument tol is a tolerance value (default: SYBIL_SETTINGS("TOLERANCE")). Reaction rates less than tol * -1 are uptake reactions, reaction rates greater than tol are excretion reactions and all others (abs(rates) < tol) are unused reactions.

Slots

uptake: Object of class "logical" indicating uptake reactions.

product: Object of class "logical" indicating excretion reactions.

unused: Object of class "logical" indicating unused reactions.

react_id: Object of class "character" containing the reaction id's of the exchange reactions.

rate: Object of class "numeric" containing the reaction rates of the exchange reactions.

Methods

length `signature(x = "netFlux")`: number of exchange reactions.

rate `signature(object = "netFlux")`: gets the `rate` slot.

react_id `signature(object = "netFlux")`: gets the `react_id` slot.

react_id<- `signature(object = "netFlux")`: sets the `react_id` slot.

Author(s)

Gabriel Gelius-Dietrich

See Also

`optimizeProb`, `getFluxDist`

Examples

```
data(Ec_core)
# retrieve all exchange reactions
ex  <- findExchReact(Ec_core)
# perform flux balance analysis
opt <- optimizeProb(Ec_core, algorithm = "fba")
# get flux distribution of all exchange reactions
fd  <- getFluxDist(opt, ex)
# group exchange reactions
getNetFlux(fd)
```

---

oneFluxDel *Single Flux Deletion Experiment*

Description

Single reaction (flux) deletion analysis.

Usage

```
oneFluxDel(model, react = c(1:react_num(model)),
           lb = rep(0, length(react)),
           ub = rep(0, length(react)),
           checkOptSolObj = FALSE, ...)
```

Arguments

`model`	An object of class `modelorg`.
`react`	An object of class `reactId` or character or integer containing reaction id's to constrain to zero one by one. Default: all reactions present in argument `model`.

lb	A numeric vector of the same length as react containing the lower bounds for the reaction rates of reactions (variables) given in argument react. Default: 0 for all reactions in react, zero flux through all reactions.
ub	A numeric vector of the same length as react containing the lower bounds for the reaction rates of reactions (variables) given in argument react. Default: 0 for all reactions in react, zero flux through all reactions.
checkOptSolObj	A single logical value. If set to TRUE, a warning will be generated, if not all optimizations ended successful. Default: FALSE.
...	Further arguments passed to optimizer. Important ones are algorithm in order to set the algorithm to use or solverParm in order to set parameter values for the optimization software.

Details

The function oneFluxDel studies the effect of constraining single fluxes to zero flux rates on the phenotype of the metabolic network. The function performs n optimizations with n being the number of reaction id's given in argument react. Each optimization corresponds to the removal of one reaction.

Value

An object of class optsol_fluxdel.

Author(s)

Gabriel Gelius-Dietrich

See Also

modelorg, optsol, optsol_fluxdel, checkOptSol, optimizer and SYBIL_SETTINGS.

Examples

```
data(Ec_core)
Ec_ofd <- oneFluxDel(Ec_core)
```

---

oneGeneDel *Single Gene Deletion Experiment*

Description

Predict the metabolic phenotype of single-gene knock out mutants.

Usage

```
oneGeneDel(model, geneList,
           lb = rep(0, length(geneList)),
           ub = rep(0, length(geneList)),
           checkOptSolObj = FALSE, ...)
```

Arguments

model	An object of class modelorg.
geneList	A character vector containing the set of genes to be deleted one by one. Default: allGenes(model).
lb	A numeric vector of the same length as geneList containing the lower bounds for the reaction rates of reactions (variables) affected by the genes given in argument geneList. Default: 0 for all genes in geneList, simulating knock-out mutants.
ub	A numeric vector of the same length as geneList containing the upper bounds for the reaction rates of reactions (variables) affected by the genes given in argument geneList. Default: 0 for all genes in geneList, simulating knock-out mutants.
checkOptSolObj	A single logical value. If set to TRUE, a warning will be generated, if not all optimizations ended successful. Default: FALSE.
...	Further arguments passed to optimizer. Important ones are algorithm in order to set the algorithm to use or solverParm in order to set parameter values for the optimization software.

Details

The function oneGeneDel studies the effect of genetic perturbations by single gene deletions on the phenotype of the metabolic network. The function performs n optimizations with n being the length of the character vector in argument geneList. For each gene deletion j the set of fluxes effected by the deletion of gene given in geneList[j] is constrained to zero flux. If the deletion of a certain gene has an effect, is tested with the function geneDel. Each optimization corresponds to the deletion of one gene.

Value

An object of class optsol_genedel.

Author(s)

Gabriel Gelius-Dietrich

See Also

modelorg, optsol, optsol_genedel, checkOptSol, optimizer and SYBIL_SETTINGS.

Examples

```
# load example data set
data(Ec_core)

# compute phenotypes of genetic perturbations via
# FBA (default)
Ec_ogd <- oneGeneDel(Ec_core)

# or MOMA (linearized version)
Ec_ogd <- oneGeneDel(Ec_core, algorithm = "lmoma")
```

---

onlyChangeGPR *Change the GPR Rules*

Description

Changes the GPR Rules for the chosen reactions

Usage

```
onlyChangeGPR(model, gprRules, reactNr, verboseMode = 0)
```

Arguments

model	An object of class modelorg
gprRules	character: contains logical expressions.
reactNr	An object of class reactId, a numeric vector, or a character vector containing reaction id's.
verboseMode	integer: verbosity level.

Details

The function changes the expressions for the chosen reactions.

Use onlyCheckGPR first to check the expressions.

Author(s)

Benjamin Braasch

onlyCheckGPR *Check the GPR Rules*

Description

Checks the GPR Rules for the chosen reactions

Usage

```
onlyCheckGPR(model, gprRules, reactNr, verboseMode = 1)
```

Arguments

model	An object of class modelorg
gprRules	character: contains logical expressions.
reactNr	An object of class reactId, a numeric vector, or a character vector containing reaction id's.
verboseMode	integer: verbosity level.

Details

The function checks the expressions for the chosen reactions.

Author(s)

Benjamin Braasch

optimizeProb-methods *Optimize Problem Object*

Description

The generic optimizeProb performs the optimization of a mathematical programming object.

Usage

```
## S4 method for signature 'modelorg'
optimizeProb(object,
             algorithm = SYBIL_SETTINGS("ALGORITHM"),
             gene = NULL,
             react = NULL,
             lb = NULL,
             ub = NULL,
             retOptSol = TRUE,
             obj_coef = NULL,
```

```
              lpdir = NULL,
              mtfobj = NULL,
              prCmd = NA,
              poCmd = NA,
              prCil = NA,
              poCil = NA,
              ...)

## S4 method for signature 'sysBiolAlg'
optimizeProb(object,
              react = NULL,
              lb = NULL,
              ub = NULL,
              obj_coef = NULL,
              lpdir = NULL,
              resetChanges = TRUE,
              prCmd = NA,
              poCmd = NA,
              prCil = NA,
              poCil = NA)
```

Arguments

object	An object of class modelorg or sysBiolAlg.
algorithm	A single character string giving the name of the algorithm to use. See parameter "ALGORITHM" in SYBIL_SETTINGS for possible values. Default: SYBIL_SETTINGS("ALGORITHM").
gene	A character or integer vector containing gene id's or indices of gene id's in allGenes(model). If arguments lb and/or ub are additionally used (not NULL), upper and lower bounds will be applied to all fluxes on which the deletion of the genes given in gene have an effect. In this case, the first value in lb and ub is used. Default: NULL.
react	An object of class reactId, character or integer. Specifies the fluxes (variables) for which to change the upper and lower bound (see also arguments lb and ub) or objective coefficients (see also argument obj_coef). For class sysBiolAlg, it must be numeric. For class modelorg, setting react as no effect, if gene is also not NULL. Default: NULL.
lb	Numeric vector, must have the same length as react. Contains the new values for the lower bounds of fluxes (variables) mentioned in react. If set to NULL, lower bounds for variables in react will be left unchanged. Default: NULL.
ub	Same functionality as lb, but for upper bounds. Default: NULL.
obj_coef	Numeric vector, must have the same length as react. Contains the new values for the objective coefficients of fluxes (variables) mentioned in react. All other objective coefficients stay untouched. If set to NULL, objective coefficients for

variables in react will be left unchanged.
Default: NULL.

lpdir — Character value, direction of optimization. Can be set to "min" for minimization or "max" for maximization.
Default: SYBIL_SETTINGS("OPT_DIRECTION").

mtfobj — Only used, if argument algorithm is set to "mtf". A single numeric value giving a previously calculated optimized value of the objective function given in the model. The objective function of the model will be fixed to this value during optimization. If set to NULL, it will be computed by means of the "fba" algorithm. If additionally arguments solver and method are set, they will be used here too.
Default: NULL.

resetChanges — Boolean value. If set to TRUE, (default) modifications of the problem object will be reset to their original values (e.g. changing upper and lower bounds for certain reactions). If set to FALSE, modifications will stay in the model.
Default: TRUE.

prCmd — A list of preprocessing commands. See Details below.
Default: NA.

poCmd — A list of postprocessing commands. See Details below.
Default: NA.

prCil — Can be used if optimizeProb is called several times (like in optimizer). The argument prCil gets the value of the loop variable and passes it to the preprocessing function. There, one can access it via the keyword "LOOP_VAR". See also optimizer.
Default: NA.

poCil — Same as prCil, but for postprocessing.
Default: NA.

retOptSol — Boolean. Return an object of class optsol_optimizeProb or just a list containing the results.
Default: TRUE.

... — Only for the modelorg-method: further arguments passed to sysBiolAlg. See Details below.

Details

The arguments prCmd and poCmd can be used to execute R commands working on the problem object. All commands in prCmd are executed immediately before solving the problem; all commands in poCmd are executed after the problem has been solved. In all other aspects, the arguments work the same. The value of prCmd or poCmd are lists of character vectors (each list element is one command). Each command is a character vector and should be built as follows:

- The first element is the name of the function to call.
- All other elements are arguments to the function named in the first element.
- If any argument is character, enclose it in single quotes ' '.
- Use the keyword LP_PROB in order to refer to the variable name of the problem object (object of class optObj).

- If the length of the character vector is one, it is treated as a function call with the problem object (object of class optObj) as single argument.

The result will be an object of class ppProc. A few examples for arguments prCmd or poCmd (all arguments must be lists, see examples section below):

```
sensitivityAnalysis
```

will be translated to the command

```
sensitivityAnalysis(LP_PROB)
```

with LP_PROB being the placeholder for the variable name of the problem object. The vector

```
c("writeProb", "LP_PROB", "'Ec_core.lp'", "'lp'")
```

will be translated to the command

```
writeProb(LP_PROB, 'Ec_core.lp', 'lp')
```

The first element will be the function name and the others the arguments to that function. The list of commands

```
list("sensitivityAnalysis",
     c("getDjCPLEX", "LP_PROB@oobj@env",
       "LP_PROB@oobj@lp", "0", "react_num(Ec_core)-1"
     )
)
```

will be translated to the commands

```
sensitivityAnalysis(LP_PROB)
getDjCPLEX(LP_PROB@oobj@env, LP_PROB@oobj@lp,
           0, react_num(Ec_core)-1)
```

For more information on the usage of prCmd and poCmd, see the examples section below.

The method optimizeProb for class modelorg generates a subclass of class sysBiolAlg and calls optimizeProb for that object again. Argument MoreArgs is used to transport arguments to the second optimizeProb call. Argument ... instead is used to transport arguments to the constructor function sysBiolAlg, for example algorithm, solver, method and solverParm. See SYBIL_SETTINGS for possible values.

Arguments gene, react, lb, ub and react cause changes in the problem object (object of class optObj, slot problem of class sysBiolAlg). These changes will be reset immediately after optimization if argument resetChanges is set to TRUE, otherwise changes will persist.

Value

Calls to optimizeProb returns either an object of class optsol_optimizeProb of length one if argument retOptSol is set to TRUE and object is of class modelorg, or a list containing the results of the optimization:

ok	Return value of the optimizer (e.g. "solution process was successful" or "time limit exceeded").
obj	Value of the objective function after optimization.
stat	Status value of the optimization (e.g. "solution is optimal" or "no feasible solution exists").
fluxes	The resulting flux distribution.
fldind	Pointers to columns (variables) representing a flux (reaction) in the original network. The variable fldind[i] in the solution object represents reaction i in the original network.
preP	An object of class ppProc if a preprocessing command was given.
postP	An object of class ppProc if a postprocessing command was given.

Methods

signature(object = "modelorg") Translates the object of class modelorg into an object of class sysBiolAlg and calls optimizeProb again.

signature(object = "sysBiolAlg") Run optimization with the given problem object.

Author(s)

Gabriel Gelius-Dietrich

See Also

modelorg and sysBiolAlg.

Examples

```
## Not run:
## The examples here require the package glpkAPI to be
## installed. If that package is not available, you have to set
## the argument 'solver' (the default is: solver = SYBIL_SETTINGS("SOLVER")).

## load the example data set
data(Ec_core)

## run optimizeProb(), Ec_sf will be an object of
## class optsol_optimizeProb
Ec_sf <- optimizeProb(Ec_core)

## run optimizeProb(), Ec_sf will be a list
Ec_sf <- optimizeProb(Ec_core, retOptSol = FALSE)
```

```
## do FBA, change the upper and lower bounds for the reactions
## "ATPM" and "PFK".
optimizeProb(Ec_core, react = c("ATPM", "PFK"),
             lb = c(3, -3), ub = c(5, 6))

## do FBA, perform sensitivity analysis after optimization
optimizeProb(Ec_core, poCmd = list("sensitivityAnalysis"))

## do FBA, write the problem object to file in lp-format
optimizeProb(Ec_core,
             poCmd = list(c("writeProb", "LP_PROB",
                            "'Ec_core.lp'", "'lp'")))

## do FBA, use "cplexAPI" as lp solver. Get all lower bounds before
## solving the problem. After solving, perform a sensitivity
## analysis and retrieve the reduced costs
opt <- optimizeProb(Ec_core, solver = "cplexAPI",
                    prCmd = list(c("getColsLowBnds", "LP_PROB", "1:77")),
                    poCmd = list("sensitivityAnalysis",
                                 c("getDjCPLEX",
                                 "LP_PROB@oobj@env",
                                 "LP_PROB@oobj@lp",
                                 "0", "react_num(Ec_core)-1")))
## get lower bounds
preProc(opt)
## get results of sensitivity analysis
postProc(opt)

## End(Not run)
```

---

optimizer *Performs Series of Optimizations*

Description

The function optimizer is a wrapper to the sysBiolAlg-method optimizeProb. While optimizeProb runs one optimization, optimizer is designed to run a series of optimization by re-optimizing a given problem object (successive calls to optimizeProb.

Usage

```
optimizer(model, react, lb, ub, obj_coef, lpdir,
          algorithm = SYBIL_SETTINGS("ALGORITHM"),
          mtfobj = NULL,
          setToZero = FALSE,
          rebuildModel = FALSE,
          fld = "none",
          prCmd = NA, poCmd = NA,
          prDIR = NULL, poDIR = NULL,
```

```
            verboseMode = 2,
            ...)
```

Arguments

model	An object of class modelorg.
react	A list of numeric vectors. Each value must point to a reaction id present in model. The length of the list in react determines the number of optimizations to run. Each list element can be used in conjunction with arguments lb and ub or obj_coef and lpdir. The parameters given in this arguments will be set temporarily for each optimization.
lb	A numeric vector or list of the same length as react or a matrix with the number of rows equal to the length of react containing the lower bounds for the reaction rates of reactions (variables) given in argument react. If set to NULL, no lower bounds will be changed. If lb is a vector, lb[k] is used as lower bound for all reactions given in react[k]. If lb is a list, lb[k] must have the same length as react[k]. If lb is a matrix, each row serves as lower bound for the reactions given in each element of react (all elements in react must have the same length). Default: NULL.
ub	A numeric vector or list of the same length as react or a matrix with the number of rows equal to the length of react containing the upper bounds for the reaction rates of reactions (variables) given in argument react. If set to NULL, no upper bounds will be changed. If ub is a vector, ub[k] is used as upper bound for all reactions given in react[k]. If ub is a list, ub[k] must have the same length as react[k]. If ub is a matrix, each row serves as upper bound for the reactions given in each element of react (all elements in react must have the same length). Default: NULL.
obj_coef	A numeric vector or list of the same length as react or a matrix with the number of rows equal to the length of react containing the objective coefficients for the reactions (variables) given in argument react. If set to NULL, no objective coefficients will be changed. If obj_coef is a vector, obj_coef[k] is used as objective coefficients for all reactions given in react[k]. If obj_coef is a list, obj_coef[k] must have the same length as react[k]. If obj_coef is a matrix, each row serves as objective coefficient for the reactions given in each element of react (all elements in react must have the same length). Default: NULL.
lpdir	A character vector of the same length as react containing the direction of optimization for each optimization. Possible values are "min" for minimization, or "max" for maximization. If set to NULL, optimization direction will not change. Default: NULL.
algorithm	A single character value giving the algorithm to compute genetic perturbations. Can be "fba": flux-balance analysis, "mtf": minimization of absolute total flux (see Details below), "moma": minimization of metabolic adjustment (MOMA), "lmoma": linear version of MOMA, "room": regulatory on/off minimization (ROOM) or "fv": flux variability analysis. Default: SYBIL_SETTINGS("ALGORITHM").

mtfobj — Only used, if argument algorithm is set to "mtf". A numeric vector of the same length as react containing previously calculated optimized values of the objective function given in the model. The objective function of the model will be fixed to this values in each optimization. If set to NULL, they will be computed by means of the "fba" algorithm. If additionally arguments solver and method are set, they will be used here too.
Default: NULL.

setToZero — Logical: If the mathematical programming software returns a solution status which is not optimal, set the corresponding objective value to zero.
Default: FALSE.

rebuildModel — Logical. If set to TRUE, the problem object will be rebuilt prior each round of optimization. Default: FALSE.

fld — Type of flux distribution to return. If set to "none", no flux distribution will be returned. If set to "fluxes", only the real flux distribution is returned, meaning all variable values after optimization representing a flux (reaction) in the model. If set to "all", all variable values are returned. If algorithm is set to "mtf" and fld equals "none", argument fld will be changed to "fluxes".
Default: "none".

prCmd — A list of preprocessing commands passed to optimizeProb. See there for details.
Default: NA.

poCmd — A list of postprocessing commands passed to optimizeProb. See there for details.
Default: NA.

prDIR — A numeric or character vector, indicating in which round of optimization the preprocessing command(s) will be executed. prDIR = c(2, 5, 10) executes the commands in prCmd before the second, 5th and 10th optimization.

If prDIR is a character vector, for example prDIR = c("10"), the preprocessing commands given in prCmd will pe executed every 10th round of optimization.

If prDIR is character and has length 2, the first element is an offset to the following elements. prDIR = c("-2", "10") will do the preprocessing on every 10th round of optimization, beginning in round number 10 - 2 = 8.
Default: NULL.

poDIR — The same as prDIR, but for postprocessing. Default: NULL.

verboseMode — Single integer value, giving the amount of output to the console. Use sink to redirect output to a file. If verboseMode == 1 status messages will be printed, if verboseMode == 2 additionally a progress bar will be produced. If verboseMode > 2, intermediate results will be printed. Use suppressMessages to disable any output to the console.
Default: 2.

... — Further arguments passed to sysBiolAlg.

Value

A list containing the results of the optimization:

solver	A single character string indicating the used mathematical programming software.
method	A single character string indicating the used optimization method by the mathematical programming software.
algorithm	A single character string indicating the used algorithm.
lp_num_cols	Number of columns (variables) in the problem object.
lp_num_rows	Number of rows (constraints) in the problem object.
obj	A numeric vector containing the values of the objective function after optimization.
ok	A numeric vector containing the return values of the optimizer (e.g. "solution process was successful" or "time limit exceeded").
stat	A numeric vector containing the status value of the optimization (e.g. "solution is optimal" or "no feasible solution exists").
lp_dir	A factor variable indicating the direction of optimization for each optimization.
fldind	Pointers to columns (variables) representing a flux (reaction) in the original network. The variable `fldind[i]` in the solution object represents reaction `i` in the original network.
fluxdist	The resulting flux distribution.
prAna	An object of class `ppProc` if a preprocessing command was given.
poAna	An object of class `ppProc` if a postprocessing command was given.
alg_par	A named list of algorithm specific parameters.

Author(s)

Gabriel Gelius-Dietrich

References

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See Also

Class `sysBiolAlg`, and constructor function `sysBiolAlg`, `optimizeProb` and `SYBIL_SETTINGS`.

optObj *General Constructor Function For Objects of Class* optObj

Description

This function serves as a user constructor function for objects of class optObj.

Usage

```
optObj(solver = SYBIL_SETTINGS("SOLVER"),
       method = SYBIL_SETTINGS("METHOD"),
       pType = "lp", prefix = "optObj", sep = "_")
```

Arguments

solver	A single character string giving the name of the solver package to use. See SYBIL_SETTINGS for possible values. Default: SYBIL_SETTINGS("SOLVER").
method	A single character string containing the name of the method used by solver. See SYBIL_SETTINGS for possible values. If missing or not available, the default method for solver is used (see also checkDefaultMethod). Default: SYBIL_SETTINGS("METHOD").
pType	A single character string containing the type of optimization problem. Can be "lp": linear programming, "mip": mixed integer programming or "qp": quadratic programming. Default: "lp".
prefix	A single character string containing a prefix for the new class name. Default: "optObj".
sep	A single character string containing a separator for prefix and solver. Default: "_".

Details

If argument solver is set to "foo" and prefix is set to "optObj" (default), optObj will try to build an instance of class optObj_foo. If solver does not contain a valid name of a solver package (this is checked by checkDefaultMethod), the default solver package will be used (see SYBIL_SETTINGS). For the name of the class, the arguments prefix and solver are stick together separated by sep (default: a single underscore "_"): prefix_solver.

Value

An instance of a subclass of class optObj.

Author(s)

Gabriel Gelius-Dietrich

See Also

Class optObj, SYBIL_SETTINGS and checkDefaultMethod.

---

optObj-class *Class* "optObj"

Description

Structure of the class "optObj". Objects extending optObj returned by the constructor function optObj. These objects are used as part of class sysBiolAlg.

Details

The intention of class optObj is, to provide a flexible user interface to several optimization software products. The methods here working on the slot oobj are interface functions to low level functions invoking corresponding C functions. Basically, the user has not to care about the nature of the solver, or solver-specific functions. That is done by the class.

Objects from the Class

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

Slots

oobj: Object of class "pointerToProb" containing a pointer to a problem object (see section Note).

solver: Object of class "character" containing the name of the solver software (see SYBIL_SETTINGS for suitable values).

method: Object of class "character" containing the method (algorithm) used by the solver software (see SYBIL_SETTINGS for suitable values).

probType: Object of class "character" giving the problem type (see optObj argument pType for suitable values).

Methods

dim signature(x = "optObj"): returns a vector d of length two with d[1] and d[2] containing the number of rows and columns of the constraint matrix.

method signature(object = "optObj"): gets the method slot.

probType signature(object = "optObj"): gets the probType slot.

solver signature(object = "optObj"): gets the solver slot.

Further usefull Functions

`checkSolStat`: `checkSolStat(stat, solver = SYBIL_SETTINGS("SOLVER"))`
Returns the indices of problems with a non-optimal solution status, or `NA` if it is not possible to retrieve a solution status.

`stat` Vector of integer values containing the solution status.

`solver` Single character string specifying the used solver (see `SYBIL_SETTINGS`).

`getMeanReturn`: `getMeanReturn(code, solver = SYBIL_SETTINGS("SOLVER"))`
Translates the return value (`code`) of a solver in a human readable string. Returns `NA` if hte translation is not possible.

`getMeanStatus`: `getMeanStatus(code, solver = SYBIL_SETTINGS("SOLVER"), env = NULL)`
Translates the soluton status value (`code`) of a solver in a human readable string. Returns `NA` if hte translation is not possible. Argument `env` is for use with IBM ILOG CPLEX holding an object of class `cplexPtr` pointing to a IBM ILOG CPLEX environment.

`wrong_type_msg`: `wrong_type_msg(lp)`
prints a warning message, if slot `oobj` from `lp` (an instance of class `optObj`) does not contain a pointer to a valid solver. See also `SYBIL_SETTINGS` for possible solvers.

`wrong_solver_msg`: `wrong_solver_msg(lp, method, printOut = TRUE)`
if `printOut == TRUE`, it will print a warning message, if `method` is not available for `solver` in `lp`.

Additional methods used by classes extending class `optObj`

`addCols`: add columns to the problem object.

`addRows`: add rows to the problem object.

`addRowsCols`: add rows and columns to the problem object.

`addColsToProb`: add new columns (variables) to the problem object.

`addRowsToProb`: add new rows (constraints) to the problem object.

`backupProb`: copies a problem object into a new problem object.

`changeColsBnds`: change column (variable) bounds in the problem object.

`changeColsBndsObjCoefs`: change column (variable) bounds and objective coefficients in the problem object.

`changeMatrixRow`: change a row in the constraint matrix of the problem object.

`changeObjCoefs`: change objective coefficients in the problem object.

`changeRowsBnds`: change row bounds in the problem object.

`delProb`: delete (free) memory associated to the pointer to the problem object.

`getColPrim`: get primal value of variables after optimization.

`getColsLowBnds`: get lower bounds of variables.

`getColsUppBnds`: get upper bounds of variables.

`getFluxDist`: get all primal values of variables after optimization (resulting flux distribution).

`getNumCols`: get number of columns in the problem object.

`getNumNnz`: get number of non zero elements in the constraint matrix of the problem object.

getNumRows: get number of rows in the problem object.

getObjCoefs: get objective coefficients in the problem object.

getObjDir: get direction of optimization.

getObjVal: get value of the objective function after optimization.

getRedCosts: get reduced costs of all variables after optimization.

getRowsLowBnds: get lower row bounds of the problem object.

getRowsUppBnds: get lower bounds of the rows (constraints) of the problem object.

getSolStat: get solution status after optimization.

getSolverParm: get current parameter settings of the used solver.

initProb: initialize problem object.

loadLPprob: load data to the problem object. Use this method to generate problem objects.

loadQobj: load quadratic part of the objective function to the problem object.

readProb: read problem object from file (e.g. lp formated).

scaleProb: scaling of the constraint matrix.

sensitivityAnalysis: perform sensitivity analysis.

setObjDir: set direction of optimization.

setRhsZero: set right hand side of the problem object to zero: $\boldsymbol{Sv} = 0$.

setSolverParm: set parameters for the used solver.

solveLp: run optimization with the solver mentioned in slot solver and with the method given by slot method.

writeProb: write problem object to file (e.g. in lp format).

Note

The class pointerToProb contains an external pointer to a problem object (usually a C/C++ pointer). This is for **glpkAPI** an object of class glpkPtr, for **clpAPI** an object of class externalptr, for **lpSolveAPI** an object of class lpExtPtr and for **cplexAPI** an object of class cplexPointer.

The class cplexPointer has two slots env and lp, each of class cplexPtr. To access for example the environment pointer from an object of class optObj, one can write lp@oobj@env.

Author(s)

Gabriel Gelius-Dietrich

See Also

The constructor function sysBiolAlg for objects extending class sysBiolAlg; The constructor function optObj; SYBIL_SETTINGS and checkDefaultMethod.

Examples

```
showClass("optObj")
```

optObj_clpAPI-class *Class* "optObj_clpAPI"

Description

Structure of the class "optObj_clpAPI".

Objects from the Class

Objects can be created by calls of the constructor function optObj:

```
test <- optObj(solver = "clpAPI").
```

Slots

oobj: Object of class "pointerToProb" containing a pointer to a **clpAPI** problem object.

solver: Object of class "character" containing the name of the solver software (see SYBIL_SETTINGS for suitable values).

method: Object of class "character" containing the method (algorithm) used by the solver software (see SYBIL_SETTINGS for suitable values).

probType: Object of class "character" giving the problem type (see optObj for suitable values).

Extends

Class "optObj", directly.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj

Examples

```
showClass("optObj_clpAPI")
```

optObj_cplexAPI-class *Class* "optObj_cplexAPI"

Description

Structure of the class "optObj_cplexAPI".

Objects from the Class

Objects can be created by calls of the constructor function optObj:

test <- optObj(solver = "cplexAPI").

Slots

oobj: Object of class "pointerToProb" containing a pointer to a **cplexAPI** problem object.

solver: Object of class "character" containing the name of the solver software (see SYBIL_SETTINGS for suitable values).

method: Object of class "character" containing the method (algorithm) used by the solver software (see SYBIL_SETTINGS for suitable values).

probType: Object of class "character" giving the problem type (see optObj for suitable values).

Extends

Class "optObj", directly.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj

Examples

```
showClass("optObj_cplexAPI")
```

optObj_glpkAPI-class *Class* "optObj_glpkAPI"

Description

Structure of the class "optObj_glpkAPI".

Objects from the Class

Objects can be created by calls of the constructor function optObj:

```
test <- optObj(solver = "glpkAPI").
```

Slots

oobj: Object of class "pointerToProb" containing a pointer to a **glpkAPI** problem object.

solver: Object of class "character" containing the name of the solver software (see SYBIL_SETTINGS for suitable values).

method: Object of class "character" containing the method (algorithm) used by the solver software (see SYBIL_SETTINGS for suitable values).

probType: Object of class "character" giving the problem type (see optObj for suitable values).

Extends

Class "optObj", directly.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj

Examples

```
showClass("optObj_glpkAPI")
```

optObj_lpSolveAPI-class

Class "optObj_lpSolveAPI"

Description

Structure of the class "optObj_lpSolveAPI".

Objects from the Class

Objects can be created by calls of the constructor function optObj:

```
test <- optObj(solver = "lpSolveAPI").
```

Slots

oobj: Object of class "pointerToProb" containing a pointer to a **lpSolveAPI** problem object.

solver: Object of class "character" containing the name of the solver software (see SYBIL_SETTINGS for suitable values).

method: Object of class "character" containing the method (algorithm) used by the solver software (see SYBIL_SETTINGS for suitable values).

probType: Object of class "character" giving the problem type (see optObj for suitable values).

Extends

Class "optObj", directly.

Further usefull Functions

return_codeLPSOLVE: (code) prints a human readable translation of return codes of lpSolveAPI.

loadMatrixPerColumnLPSOLVE: (lpmod, constMat) load a constraint matrix (an object of class Matrix) to a **lpSolveAPI** problem object column by column.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj

Examples

```
showClass("optObj_lpSolveAPI")
```

optsol-class *Class optsol*

Description

The class optsol provides data structures to store and access the results of optimizations. This class is extended by other classes and will not be used as is. The representation of class optsol is used as superclass.

Objects from the Class

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

Slots

mod_id: Object of class "character" containing the model id of the used model.

mod_key: Object of class "character" containing the model key of the used model.

solver: Object of class "character" indicating the used solver.

method: Object of class "character" indicating the used method.

algorithm: Object of class "character" containing the name of the algorithm used for optimizations.

num_of_prob: Object of class "integer" indicating the number of optimization problems.

lp_num_cols: Object of class "integer" indicating the number of columns.

lp_num_rows: Object of class "integer" indicating the number of rows.

lp_obj: Object of class "numeric" containing the optimal values of the objective function after optimization. If no flux distribution is available, slot lp_obj contains the cross-product of the objective coefficients in slot obj_coef and the part of the flux distribution in slot fluxdist containing the values representing fluxes in the entire metabolic network (slot fldind).

lp_ok: Object of class "integer" containing the exit code of the optimization.

lp_stat: Object of class "integer" containing the solution status of the optimization.

lp_dir: Object of class "character" indicating the direction of optimization.

obj_coef: Object of class "numeric" containing the objective coefficients of the used model (slot obj_coef of an object of class modelorg). These are not necessarily the objective coefficients of the used algorithm.

obj_func: Object of class "character" containing the objective function of the used model. Usually, it contains the return value of printObjFunc.

fldind: Object of class "integer" pointers to columns (variables) representing a flux (reaction) in the original network. The variable fldind[i] in the problem object represents reaction i in the original network.

fluxdist: Object of class "fluxDistribution" containing the solutions flux distributions.

alg_par: Object of class "list" containing a named list containing algorithm specific parameters.

Methods

`algorithm<-`: `signature(object = "optsol")`: sets the `algorithm` slot.

`algorithm`: `signature(object = "optsol")`: gets the `algorithm` slot.

alg_par `signature(object = "optsol")`: gets the `alg_par` slot.

alg_par<- `signature(object = "optsol")`: sets the `alg_par` slot.

`checkStat`: `signature(opt = "optsol")`: returns the indices of problems with a non optimal solution status.

`fldind<-`: `signature(object = "optsol")`: sets the `fldind` slot.

`fldind`: `signature(object = "optsol")`: gets the `fldind` slot.

`fluxdist<-`: `signature(object = "optsol")`: sets the `fluxdist` slot.

`fluxdist`: `signature(object = "optsol")`: gets the `fluxdist` slot.

`fluxes<-`: `signature(object = "optsol")`: sets the `fluxes` slot of slot `fluxdist`.

`fluxes`: `signature(object = "optsol")`: gets the `fluxes` slot of slot `fluxdist`.

`plot`: `signature(x = "optsol")`: plots a `histogram` of the values of the objective function given in the model in optimal state. Additional arguments can be passed to `histogram` via the `...` argument.

`length`: `signature(x = "optsol")`: returns the number of optimizations.

`lp_dir<-`: `signature(object = "optsol", value = "character")`: sets the `lp_dir` slot. Argument `value` can be `"min"` (minimization) or `"max"` (maximization).

`lp_dir<-`: `signature(object = "optsol", value = "factor")`: sets the `lp_dir` slot.

`lp_dir<-`: `signature(object = "optsol", value = "numeric")`: sets the `lp_dir` slot. Argument `value` can be `1` (minimization) or `-1` (maximization).

`lp_dir`: `signature(object = "optsol")`: gets the `lp_dir` slot.

`lp_num_cols<-`: `signature(object = "optsol")`: sets the `lp_num_cols` slot.

`lp_num_cols`: `signature(object = "optsol")`: gets the `lp_num_cols` slot.

`lp_num_rows<-`: `signature(object = "optsol")`: sets the `lp_num_rows` slot.

`lp_num_rows`: `signature(object = "optsol")`: gets the `lp_num_rows` slot.

`lp_obj<-`: `signature(object = "optsol")`: sets the `lp_obj` slot.

`lp_obj`: `signature(object = "optsol")`: gets the `lp_obj` slot.

`lp_ok<-`: `signature(object = "optsol")`: sets the `lp_ok` slot.

`lp_ok`: `signature(object = "optsol")`: gets the `lp_ok` slot.

`lp_stat<-`: `signature(object = "optsol")`: sets the `lp_stat` slot.

`lp_stat`: `signature(object = "optsol")`: gets the `lp_stat` slot.

`method<-`: `signature(object = "optsol")`: sets the `method` slot.

`method`: `signature(object = "optsol")`: gets the `method` slot.

`mod_id<-`: `signature(object = "optsol")`: sets the `mod_id` slot.

`mod_id`: `signature(object = "optsol")`: gets the `mod_id` slot.

`mod_key<-`: `signature(object = "optsol")`: sets the `mod_key` slot.

`mod_key`: `signature(object = "optsol")`: gets the `mod_key` slot.

`mod_obj`: `signature(object = "optsol_fluxdel")`: returns always the cross-product of the objective coefficients in slot `obj_coef` and the part of the flux distribution in slot `fluxdist` containing the values representing fluxes in the entire metabolic network (slot `fldind`). If slot `obj_coef` is `NA`, the content of slot `lp_obj` is returned. In contrast, method `lp_obj` always returns the value of the objective function of the used algorithm after optimization.

`nfluxes`: `signature(object = "optsol")`: gets the number of elements in the flux distribution matrix.

`num_of_prob<-`: `signature(object = "optsol")`: sets the `num_of_prob` slot.

`num_of_prob`: `signature(object = "optsol")`: gets the `num_of_prob` slot.

`obj_coef<-`: `signature(object = "optsol")`: sets the `obj_coef` slot.

`obj_coef`: `signature(object = "optsol")`: gets the `obj_coef` slot.

`obj_func<-`: `signature(object = "optsol")`: sets the `obj_func` slot.

`obj_func`: `signature(object = "optsol")`: gets the `obj_func` slot.

`react_id<-`: `signature(object = "optsol")`: sets the `react_id` slot.

`react_id`: `signature(object = "optsol")`: gets the `react_id` slot.

`show`: `signature(object = "optsol")`: prints a summary of the content of instance of class `optsol`.

`solver<-`: `signature(object = "optsol")`: sets the `solver` slot.

`solver`: `signature(object = "optsol")`: gets the `solver` slot.

Author(s)

Gabriel Gelius-Dietrich

See Also

`checkOptSol`, `optsol_optimizeProb` `optsol_fluxdel`, `optsol_genedel`, `optsol_robAna` and `optsol_fluxVar`

Examples

```
showClass("optsol")
```

---

optsol_blockedReact-class

Class "optsol_blockedReact"

Description

Structure of the class "optsol_blockedReact". Objects of that class are returned by the function `blockedReact`.

Objects from the Class

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

Slots

`blocked`: Object of class `"logical"` indicating if a reaction is blocked, or not.

`react`: Object of class `"reactId"` containing the reaction id's of checked reactions.

`mod_id`: Object of class `"character"` containing the model id of the used model.

`mod_key`: Object of class `"character"` containing the model key of the used model.

`solver`: Object of class `"character"` indicating the used solver.

`method`: Object of class `"character"` indicating the used method.

`algorithm`: Object of class `"character"` containing the name of the algorithm used for optimizations.

`num_of_prob`: Object of class `"integer"` indicating the number of optimization problems.

`lp_num_cols`: Object of class `"integer"` indicating the number of columns.

`lp_num_rows`: Object of class `"integer"` indicating the number of rows.

`lp_obj`: Object of class `"numeric"` containing the optimal values of the objective function after optimization. If no flux distribution is available, slot `lp_obj` contains the cross-product of the objective coefficients in slot `obj_coef` and the part of the flux distribution in slot `fluxdist` containing the values representing fluxes in the entire metabolic network (slot `fldind`).

`lp_ok`: Object of class `"integer"` containing the exit code of the optimization.

`lp_stat`: Object of class `"integer"` containing the solution status of the optimization.

`lp_dir`: Object of class `"character"` indicating the direction of optimization.

`obj_coef`: Object of class `"numeric"` containing the objective coefficients of the used model (slot `obj_coef` of an object of class `modelorg`). These are not necessarily the objective coefficients of the used algorithm.

`obj_func`: Object of class `"character"` containing the objective function of the used model. Usually, it contains the return value of `printObjFunc`.

`fldind`: Object of class `"integer"` pointers to columns (variables) representing a flux (reaction) in the original network. The variable `fldind[i]` in the problem object represents reaction `i` in the original network.

`fluxdist`: Object of class `"fluxDistribution"` containing the solutions flux distributions.

`alg_par`: Object of class `"list"` containing a named list containing algorithm specific parameters.

Extends

Class `"optsol"`, directly.

Methods

`blocked`: `signature(object = "optsol_blockedReact")`: gets the `blocked` slot.

`blocked<-`: `signature(object = "optsol_blockedReact")` sets the `blocked` slot.

`react`: `signature(object = "optsol_blockedReact")`: gets the `react` slot.

`react<-`: `signature(object = "optsol_blockedReact")` sets the `react` slot.

`maxSol`: `signature(object = "optsol_blockedReact")(slot)`: returns the values in the slot given in `slot` for optimizations in "max" direction.

`minSol`: `signature(object = "optsol_blockedReact")(slot)`: returns the values in the slot given in `slot` for optimizations in "min" direction.

Author(s)

Gabriel Gelius-Dietrich

See Also

`checkOptSol` and `optsol`

Examples

```
showClass("optsol_blockedReact")
```

---

optsol_fluxdel-class *Class* "optsol_fluxdel"

Description

Structure of the class "optsol_fluxdel". Objects of that class are returned by the function `oneFluxDel`.

Objects from the Class

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

Slots

`chlb`: Object of class "numeric" containing the new (changed) values for the columns lower bounds.

`chub`: Object of class "numeric" containing the new (changed) values for the columns upper bounds.

`dels`: Object of class "matrix" containing the reaction id's of constrained reactions. Each row of the matrix represents one set of simultaneously constrained reactions.

`preProc`: Object of class "ppProc" containing the results of pre-processing. See also `optimizeProb`.

`postProc`: Object of class "ppProc" containing the results of post-processing. See also `optimizeProb`.

`mod_id`: Object of class "character" containing the model id of the used model.

`mod_key`: Object of class `"character"` containing the model key of the used model.

`solver`: Object of class `"character"` indicating the used solver.

`method`: Object of class `"character"` indicating the used method.

`algorithm`: Object of class `"character"` containing the name of the algorithm used for optimizations.

`num_of_prob`: Object of class `"integer"` indicating the number of optimization problems.

`lp_num_cols`: Object of class `"integer"` indicating the number of columns.

`lp_num_rows`: Object of class `"integer"` indicating the number of rows.

`lp_obj`: Object of class `"numeric"` containing the optimal values of the objective function after optimization. If no flux distribution is available, slot `lp_obj` contains the cross-product of the objective coefficients in slot `obj_coef` and the part of the flux distribution in slot `fluxdist` containing the values representing fluxes in the entire metabolic network (slot `fldind`).

`lp_ok`: Object of class `"integer"` containing the exit code of the optimization.

`lp_stat`: Object of class `"integer"` containing the solution status of the optimization.

`lp_dir`: Object of class `"character"` indicating the direction of optimization.

`obj_coef`: Object of class `"numeric"` containing the objective coefficients of the used model (slot `obj_coef` of an object of class `modelorg`). These are not necessarily the objective coefficients of the used algorithm.

`obj_func`: Object of class `"character"` containing the objective function of the used model. Usually, it contains the return value of `printObjFunc`.

`fldind`: Object of class `"integer"` pointers to columns (variables) representing a flux (reaction) in the original network. The variable `fldind[i]` in the problem object represents reaction `i` in the original network.

`fluxdist`: Object of class `"fluxDistribution"` containing the solutions flux distributions.

`alg_par`: Object of class `"list"` containing a named list containing algorithm specific parameters.

Extends

Class `"optsol_optimizeProb"`, directly. Class `"optsol"`, by class "optsol_optimizeProb", distance 2.

Methods

`react_id`: `signature(object = "optsol_fluxdel")`: gets the `react_id` slot.

`react_id<-`: `signature(object = "optsol_fluxdel")` sets the `react_id` slot.

`allGenes`: `signature(object = "optsol_fluxdel")`: gets the `allGenes` slot.

`allGenes<-`: `signature(object = "optsol_fluxdel")` sets the `allGenes` slot.

`chlb`: `signature(object = "optsol_fluxdel")`: gets the `chlb` slot.

`chlb<-`: `signature(object = "optsol_fluxdel")` sets the `chlb` slot.

`chub`: `signature(object = "optsol_fluxdel")`: gets the chub slot.

`chub<-`: `signature(object = "optsol_fluxdel")`: sets the chub slot.

`dels`: `signature(object = "optsol_fluxdel")`: gets the `dels` slot.

`dels<-`: `signature(object = "optsol_fluxdel")` sets the `dels` slot.

`algorithm`: `signature(object = "optsol_fluxdel")`: gets the `algorithm` slot.

`algorithm<-`: `signature(object = "optsol_fluxdel")` sets the `algorithm` slot.

`lethal`: `signature(object = "optsol_fluxdel")(wt, tol)`: returns a logical vector of length `num_of_prob(object)`. Argument `wt` is an optimal (wild type) growth rate, e.g. computed via FBA. If the absolute growth ratio (`mod_obj(object)/wt`) of knock-out `i` is less than `tol`, the deletion is considered as lethal. If `lethal(object)[i]` is `TRUE`, deletion [i] is lethal.

`deleted`: `signature(object = "optsol_fluxdel")(i)`: gets the `i`th element of the `dels` slot.

`[`: `signature(x = "optsol_fluxdel")`: access like a vector. `x[i]` returns a new object of class `optsol_fluxdel` containing the `i`th deletion experiment.

Author(s)

Gabriel Gelius-Dietrich

See Also

`checkOptSol`, `optsol`, `optsol_genedel` and `optsol_optimizeProb`

Examples

```
showClass("optsol_fluxdel")
```

---

optsol_fluxVar-class *Class* "optsol_fluxVar"

Description

Structure of the class "optsol_fluxVar". Objects of that class are returned by the function `fluxVar`.

Objects from the Class

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

Slots

`react`: Object of class "reactId" containing reaction id's for which ranges were calculated.

`preProc`: Object of class "ppProc" containing the results of pre-processing. See also `optimizeProb`.

`postProc`: Object of class "ppProc" containing the results of post-processing. See also `optimizeProb`.

`mod_id`: Object of class "character" containing the model id of the used model.

`mod_key`: Object of class "character" containing the model key of the used model.

`solver`: Object of class "character" indicating the used solver.

`method`: Object of class "character" indicating the used method.

`algorithm`: Object of class "character" containing the name of the algorithm used for optimizations.

num_of_prob: Object of class "integer" indicating the number of optimization problems.

lp_num_cols: Object of class "integer" indicating the number of columns.

lp_num_rows: Object of class "integer" indicating the number of rows.

lp_obj: Object of class "numeric" containing the optimal values of the objective function after optimization.

lp_ok: Object of class "integer" containing the exit code of the optimization.

lp_stat: Object of class "integer" containing the solution status of the optimization.

lp_dir: Object of class "character" indicating the direction of optimization.

obj_coef: Object of class "numeric" containing the objective coefficients of the used model (slot obj_coef of an object of class modelorg). These are not necessarily the objective coefficients of the used algorithm.

obj_func: Object of class "character" containing the objective function of the used model. Usually, it contains the return value of printObjFunc.

fldind: Object of class "integer" pointers to columns (variables) representing a flux (reaction) in the original network. The variable fldind[i] in the problem object represents reaction i in the original network.

fluxdist: Object of class "fluxDistribution" containing the solutions flux distributions.

alg_par: Object of class "list" containing a named list containing algorithm specific parameters.

Extends

Class "optsol_optimizeProb", directly. Class "optsol", by class "optsol_optimizeProb", distance 2.

Methods

react: signature(object = "optsol_fluxVar"): gets the react slot.

react<-: signature(object = "optsol_fluxVar"): sets the react slot.

maxSol: signature(object = "optsol_fluxVar")(slot): returns the values in the slot given in slot for optimizations in "max" direction.

minSol: signature(object = "optsol_fluxVar")(slot): returns the values in the slot given in slot for optimizations in "min" direction.

plot signature(x = "optsol_fluxVar", y = "missing")(ylim, xlab = "", ylab = "Value", pch = 20, col = "b
plots the range of values each flux can have still giving an optimal objective function value.

ylim scaling of y-axis, if missing, the maximum and minimum value of all optimizations is used (rounded to the next smaller/larger integer value).

xlab label of x-axis, see also par.

ylab label of y-axis, see also par.

pch how to plot the points, see also par.

col color of the plot, see also par.

collower color of the minimum range value. Default col.

colupper color of the maximum range value. Default col.

pchupper how to plot the point for the maximum range value. Default pch.

`pchlower` how to plot the point for the minimum range value. Default `pch`.

`dottedline` if set to `FALSE`, from each minimum range value a dotted line to the corresponding x-axis label will be plotted. Default `FALSE`.

`baseline` plot a horizontal dashed line at the value of `baseline`. Default `0`. If set to `NA`, no baseline will be plotted.

`connect` if set to `TRUE`, a solid connecting line will be drawn between the minimum and maximum value of one reaction. Default `TRUE`.

`colconnect` color of the connecting line. Default `"black"`.

`...` further arguments to the `plot` function.

`plotRangeVar signature(object = "optsol_fluxVar")(...)`: plot a histogram of the span of the minimum and maximum range values for each flux.

`...` further arguments to the `hist` function.

`blReact signature(object = "optsol_fluxVar")(tol = SYBIL_SETTINGS("TOLERANCE"))`: returns a logical vector of length equal to the number of reactions analyzed during flux variance analysis (number of optimizations divided by two). If `blReact(object)[j]` equals `TRUE`, reaction `j` is considered to be blocked (zero flux rate) given the used conditions. A reaction j is considered to be 'blocked', if its calculated range of reaction rates does not exceed `0 +/- tol`.

`tol` limit of tolerance.

Author(s)

Gabriel Gelius-Dietrich

See Also

`checkOptSol` and `optsol`

Examples

```
showClass("optsol_fluxVar")
```

---

optsol_genedel-class *Class* "optsol_genedel"

Description

Structure of the class `"optsol_genedel"`. Objects of that class are returned by the function `geneDel`.

Objects from the Class

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

Slots

`fluxdels`: Object of class `"list"` containing the reaction id's of constrained reactions (fluxes). `fluxdels(optsol_genedel)[[i]][j] = l`: The deletion of gene `i` requires the deletion of a set of fluxes `1..k` ($j \leq k$), `j` being the j'th reaction of that set.

`hasEffect`: Object of class `"logical"` indicating whether deletion of gene `i` has an effect or not.

`chlb`: Object of class `"numeric"` containing the new (changed) values for the columns lower bounds.

`chub`: Object of class `"numeric"` containing the new (changed) values for the columns upper bounds.

`dels`: Object of class `"matrix"` containing the gene id of constrained genes. Each row of the matrix represents one set of simultaneously constrained genes.

`preProc`: Object of class `"ppProc"` containing the results of pre-processing. See also `optimizeProb`.

`postProc`: Object of class `"ppProc"` containing the results of post-processing. See also `optimizeProb`.

`mod_id`: Object of class `"character"` containing the model id of the used model.

`mod_key`: Object of class `"character"` containing the model key of the used model.

`solver`: Object of class `"character"` indicating the used solver.

`method`: Object of class `"character"` indicating the used method.

`algorithm`: Object of class `"character"` containing the name of the algorithm used for optimizations.

`num_of_prob`: Object of class `"integer"` indicating the number of optimization problems.

`lp_num_cols`: Object of class `"integer"` indicating the number of columns.

`lp_num_rows`: Object of class `"integer"` indicating the number of rows.

`lp_obj`: Object of class `"numeric"` containing the optimal values of the objective function after optimization. If no flux distribution is available, slot `lp_obj` contains the cross-product of the objective coefficients in slot `obj_coef` and the part of the flux distribution in slot `fluxdist` containing the values representing fluxes in the entire metabolic network (slot `fldind`).

`lp_ok`: Object of class `"integer"` containing the exit code of the optimization.

`lp_stat`: Object of class `"integer"` containing the solution status of the optimization.

`lp_dir`: Object of class `"character"` indicating the direction of optimization.

`obj_coef`: Object of class `"numeric"` containing the objective coefficients of the used model (slot `obj_coef` of an object of class `modelorg`). These are not necessarily the objective coefficients of the used algorithm.

`obj_func`: Object of class `"character"` containing the objective function of the used model. Usually, it contains the return value of `printObjFunc`.

`fldind`: Object of class `"integer"` pointers to columns (variables) representing a flux (reaction) in the original network. The variable `fldind[i]` in the problem object represents reaction `i` in the original network.

`fluxdist`: Object of class `"fluxDistribution"` containing the solutions flux distributions.

`alg_par`: Object of class `"list"` containing a named list containing algorithm specific parameters.

Extends

Class "optsol_fluxdel", directly. Class "optsol_optimizeProb", by class "optsol_fluxdel", distance 2. Class "optsol", by class "optsol_fluxdel", distance 3.

Methods

`fluxdels`: `signature(object = "optsol_genedel")`: gets the `fluxdels` slot.

`fluxdels<-`: `signature(object = "optsol_genedel")` sets the `fluxdels` slot.

`hasEffect`: `signature(object = "optsol_genedel")`: gets the `hasEffect` slot.

`hasEffect<-`: `signature(object = "optsol_genedel")`: sets the `hasEffect` slot.

`deleted`: `signature(object = "optsol_genedel")(i)`: gets the `i`th element of the `dels` slot.

Author(s)

Gabriel Gelius-Dietrich

See Also

checkOptSol, optsol, optsol_fluxdel and optsol_optimizeProb

Examples

```
showClass("optsol_genedel")
```

---

optsol_optimizeProb-class

Class "optsol_optimizeProb"

Description

Structure of the class "optsol_optimizeProb". Objects of that class are returned by the function optimizeProb with the argument `retOptSol` set to `TRUE`.

Objects from the Class

Objects can be created by calls of the form `new("optsol_optimizeProb", ...)`, or via the constructor function makeOptsolMO.

Slots

`preProc`: Object of class "ppProc" containing the results of pre-processing. See also optimizeProb.

`postProc`: Object of class "ppProc" containing the results of post-processing. See also optimizeProb.

`mod_id`: Object of class "character" containing the model id of the used model.

`mod_key`: Object of class "character" containing the model key of the used model.

`solver`: Object of class "character" indicating the used solver.

`method`: Object of class `"character"` indicating the used method.

`algorithm`: Object of class `"character"` containing the name of the algorithm used for optimizations.

`num_of_prob`: Object of class `"integer"` indicating the number of optimization problems.

`lp_num_cols`: Object of class `"integer"` indicating the number of columns.

`lp_num_rows`: Object of class `"integer"` indicating the number of rows.

`lp_obj`: Object of class `"numeric"` containing the optimal values of the objective function after optimization. If no flux distribution is available, slot `lp_obj` contains the cross-product of the objective coefficients in slot `obj_coef` and the part of the flux distribution in slot `fluxdist` containing the values representing fluxes in the entire metabolic network (slot `fldind`).

`lp_ok`: Object of class `"integer"` containing the exit code of the optimization.

`lp_stat`: Object of class `"integer"` containing the solution status of the optimization.

`lp_dir`: Object of class `"character"` indicating the direction of optimization.

`obj_coef`: Object of class `"numeric"` containing the objective coefficients of the used model (slot `obj_coef` of an object of class `modelorg`). These are not necessarily the objective coefficients of the used algorithm.

`obj_func`: Object of class `"character"` containing the objective function of the used model. Usually, it contains the return value of `printObjFunc`.

`fldind`: Object of class `"integer"` pointers to columns (variables) representing a flux (reaction) in the original network. The variable `fldind[i]` in the problem object represents reaction `i` in the original network.

`fluxdist`: Object of class `"fluxDistribution"` containing the solutions flux distributions.

`alg_par`: Object of class `"list"` containing a named list containing algorithm specific parameters.

Extends

Class `"optsol"`, directly.

Methods

`preProc`: `signature(object = "optsol_optimizeProb")`: gets the `preProc` slot.

`preProc<-`: `signature(object = "optsol_optimizeProb")`: sets the `preProc` slot.

`postProc`: `signature(object = "optsol_optimizeProb")`: gets the `postProc` slot.

`postProc<-`: `signature(object = "optsol_optimizeProb")`: sets the `postProc` slot.

Author(s)

Gabriel Gelius-Dietrich

See Also

`checkOptSol`, `optsol`, `optsol_genedel` and `optsol_fluxdel`

Examples

```
showClass("optsol_optimizeProb")
```

optsol_phpp-class *Class* "optsol_phpp"

Description

Structure of the class "optsol_robAna". Objects of that class are returned by the function phpp.

Objects from the Class

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

Slots

ctrlflm: Object of class "matrix" containing the control flux values.

redCosts: Object of class "matrix" containing the reduced costs of the two control flux values.

ctrlr: Object of class "reactId" containing the reaction id of the control reaction.

ctrlfl: Object of class "numeric" unused, see ctrlflm.

preProc: Object of class "ppProc" containing the results of pre-processing. See also optimizeProb.

postProc: Object of class "ppProc" containing the results of post-processing. See also optimizeProb.

mod_id: Object of class "character" containing the model id of the used model.

mod_key: Object of class "character" containing the model key of the used model.

solver: Object of class "character" indicating the used solver.

method: Object of class "character" indicating the used method.

algorithm: Object of class "character" containing the name of the algorithm used for optimizations.

num_of_prob: Object of class "integer" indicating the number of optimization problems.

lp_num_cols: Object of class "integer" indicating the number of columns.

lp_num_rows: Object of class "integer" indicating the number of rows.

lp_obj: Object of class "numeric" containing the optimal values of the objective function after optimization. If no flux distribution is available, slot lp_obj contains the cross-product of the objective coefficients in slot obj_coef and the part of the flux distribution in slot fluxdist containing the values representing fluxes in the entire metabolic network (slot fldind).

lp_ok: Object of class "integer" containing the exit code of the optimization.

lp_stat: Object of class "integer" containing the solution status of the optimization.

lp_dir: Object of class "character" indicating the direction of optimization.

obj_coef: Object of class "numeric" containing the objective coefficients of the used model (slot obj_coef of an object of class modelorg). These are not necessarily the objective coefficients of the used algorithm.

obj_func: Object of class "character" containing the objective function of the used model. Usually, it contains the return value of printObjFunc.

`fldind`: Object of class `"integer"` pointers to columns (variables) representing a flux (reaction) in the original network. The variable `fldind[i]` in the problem object represents reaction `i` in the original network.

`fluxdist`: Object of class `"fluxDistribution"` containing the solutions flux distributions.

`alg_par`: Object of class `"list"` containing a named list containing algorithm specific parameters.

Extends

Class "optsol_robAna", directly. Class "optsol_optimizeProb", by class "optsol_robAna", distance 2. Class "optsol", by class "optsol_robAna", distance 3.

Methods

ctrlfl `signature(object = "optsol_phpp")`: gets the `ctrlflm` slot.

ctrlfl<- `signature(object = "optsol_phpp")`: sets the `ctrlflm` slot.

getRedCosts `signature(lp = "optsol_phpp")`: gets the `ctrlflm` slot.

plot `signature(x = "optsol_phpp", y = "character")`: `(main = paste("Reduced Costs:", y), xlab =` plots the reduced costs of the control fluxes as `levelplot`.

`y` reaction id of one control reaction.

`main` plot title, see also `levelplot`.

`xlab` label of x-axis, see also `levelplot`.

`ylab` label of y-axis, see also `levelplot`.

`shrink` scale of rectangles to plot, see `levelplot`.

`col.regions` a vector of colors (default greyscale) see `levelplot`.

`...` further graphical parameters to the `levelplot` function.

plot `signature(x = "optsol_phpp", y = "missing")`: `(xlab = list(label = react_id(ctrlr(x)[1]), rot = 30, grey(w * irr + (1 - w) * (1-(1-ref)^0.75)) }, ...)`: plots the optimal values of the objective function vs. the control flux values in a `wireframe` plot.

`xlab` label of x-axis, see also `wireframe`.

`ylab` label of y-axis, see also `wireframe`.

`zlab` label of z-axis, see also `wireframe`.

`scales` parameters describing scales, see `wireframe`.

`par.settings` additional parameters, see `wireframe`.

`shade` enable/disable shading, see `wireframe`.

`shade.colors` a function for the shading color (default greyscale), see `wireframe`.

`...` further graphical parameters to the `wireframe` function.

Author(s)

Gabriel Gelius-Dietrich

See Also

`phpp`, `checkOptSol` and `optsol`

Examples

```
showClass("optsol_phpp")
```

---

optsol_robAna-class *Class* "optsol_robAna"

Description

Structure of the class "optsol_robAna". Objects of that class are returned by the function robAna.

Objects from the Class

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

Slots

ctrlr: Object of class "reactId" containing the reaction id of the control reaction.

ctrlfl: Object of class "numeric" containing the control flux values.

preProc: Object of class "ppProc" containing the results of pre-processing. See also optimizeProb.

postProc: Object of class "ppProc" containing the results of post-processing. See also optimizeProb.

mod_id: Object of class "character" containing the model id of the used model.

mod_key: Object of class "character" containing the model key of the used model.

solver: Object of class "character" indicating the used solver.

method: Object of class "character" indicating the used method.

algorithm: Object of class "character" containing the name of the algorithm used for optimizations.

num_of_prob: Object of class "integer" indicating the number of optimization problems.

lp_num_cols: Object of class "integer" indicating the number of columns.

lp_num_rows: Object of class "integer" indicating the number of rows.

lp_obj: Object of class "numeric" containing the optimal values of the objective function after optimization. If no flux distribution is available, slot lp_obj contains the cross-product of the objective coefficients in slot obj_coef and the part of the flux distribution in slot fluxdist containing the values representing fluxes in the entire metabolic network (slot fldind).

lp_ok: Object of class "integer" containing the exit code of the optimization.

lp_stat: Object of class "integer" containing the solution status of the optimization.

lp_dir: Object of class "character" indicating the direction of optimization.

obj_coef: Object of class "numeric" containing the objective coefficients of the used model (slot obj_coef of an object of class modelorg). These are not necessarily the objective coefficients of the used algorithm.

obj_func: Object of class "character" containing the objective function of the used model. Usually, it contains the return value of printObjFunc.

`fldind`: Object of class `"integer"` pointers to columns (variables) representing a flux (reaction) in the original network. The variable `fldind[i]` in the problem object represents reaction `i` in the original network.

`fluxdist`: Object of class `"fluxDistribution"` containing the solutions flux distributions.

`alg_par`: Object of class `"list"` containing a named list containing algorithm specific parameters.

Extends

Class `"optsol_optimizeProb"`, directly. Class `"optsol"`, by class "optsol_optimizeProb", distance 2.

Methods

`ctrlfl`: `signature(object = "optsol_robAna")`: gets the `ctrlfl` slot.

`ctrlfl<-`: `signature(object = "optsol_robAna")`: sets the `ctrlfl` slot.

`ctrlr`: `signature(object = "optsol_robAna")`: gets the `ctrlr` slot.

`ctrlr<-`: `signature(object = "optsol_robAna")`: sets the `ctrlr` slot.

`plot signature(x = "optsol_robAna", y = "missing")(xlab = paste("Control Flux:", react_id(ctrlr(x))),` plots the optimal values of the objective function vs. the control flux values.

`xlab` label of x-axis, see also `par`.

`ylab` label of y-axis, see also `par`.

`type` plot type, see also `par`.

`pch` how to plot the points, see also `par`.

`fillColorBg` color of the area below the curve.

`fillBg` logical: color the area below the curve.

`absCtrl` if set to `TRUE`, the control flux values (x axis) are plotted as absolute values.

`...` further graphical parameters to the `points` function.

Author(s)

Gabriel Gelius-Dietrich

See Also

`robAna`, `checkOptSol` and `optsol`

Examples

```
showClass("optsol_robAna")
```

phpp *Phenotypic Phase Plane Analysis*

Description

Performs phenotypic phase plane analysis for a given metabolic model.

Usage

```
phpp(model, ctrlreact, rng = c(0, 0, 20, 20),
     numP = 50, setToZero = TRUE, redCosts = FALSE, ...)
```

Arguments

`model`	An object of class `modelorg`.
`ctrlreact`	An object of class `reactId`, character or integer. Specifies two control reactions.
`rng`	A numeric vector of length four, giving the lower and upper bounds of the control reactions. The first two values contain the lower bounds, the last two values the upper bounds. Default: `c(0, 0, 20, 20)`
`numP`	The number of points to analyse. Default: `50`
`setToZero`	Logical: If the mathematical programming software returns a solution status which is not optimal, set the corresponding objective value to zero (see also `optimizer`). Default: `TRUE`.
`redCosts`	Logical: store reduced costs of the control variables. Default: `FALSE`.
`...`	Further arguments passed to `optimizer`.

Details

The two control reactions given in argument `ctrlreact` are treated as uptake reactions: reactions that transport metabolites into the metabolic network. That means, the optimizations are performed using `abs(rng) * -1`.

Value

An object of class `optsol_phpp`.

Author(s)

Gabriel Gelius-Dietrich

References

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Bernhard Ø. Palsson (2006). *Systems Biology: Properties of Reconstructed Networks*. Cambridge University Press.

Examples

```
data(Ec_core)

# switch off glucose input
Ec_core_wo_glc <- changeUptake(Ec_core, off = "glc_D[e]")
opt <- phpp(Ec_core_wo_glc, ctrlreact = c("EX_succ(e)", "EX_o2(e)"))

# plot phenotypic phase plane
plot(opt)

# plot reduced costs of the two control reactions
plot(opt, "EX_succ(e)")
plot(opt, "EX_o2(e)")
```

---

ppProc-class *Class* "ppProc"

Description

Structure of the class "ppProc". Objects of that class are returned as part of class optsol when performing pre- or post-processing of an optimization, e.g. in optimizeProb.

Objects from the Class

Objects can be created by calls of the function ppProc:

test <- ppProc(cmd).

cmd: Object of class "list".

Slots

`cmd`: Object of class `"list"` a character vector or a list of character strings containing pre- or postprocessing commands.

`pa`: Object of class `"list"` return values of the pre- or postprocessing commands. They can be numeric, integer, character, list or of class `sybilError`.

`ind`: Object of class `"integer"` giving the indices of the optimizations when pre- or postprocessing was performed.

Methods

`cmd`: `signature(object = "ppProc")`: gets the `cmd` slot.

`cmd<-`: `signature(object = "ppProc")`: sets the `cmd` slot.

`pa`: `signature(object = "ppProc")`: gets the `pa` slot.

`pa<-`: `signature(object = "ppProc")`: sets the `pa` slot.

`ind`: `signature(object = "ppProc")`: gets the `ind` slot.

`ind<-`: `signature(object = "ppProc")`: sets the `ind` slot.

Author(s)

Gabriel Gelius-Dietrich

See Also

`optimizeProb` and `optimizer`

Examples

```
showClass("ppProc")
```

---

printMetabolite-methods

Print Rows of the Stoichiometric Matrix

Description

Print the rows of the stoichiometric matrix or an FBA model in CPLEX LP file format.

Usage

```
## S4 method for signature 'modelorg'
printMetabolite(object, met, FBAlp = FALSE, printOut = TRUE, ...)
```

Arguments

object	An object of class modelorg.
met	A numeric or character vector containing the metabolite id's of metabolites to print out. If missing, all metabolites given in the model are used.
FBAlp	A single logical value. If set to TRUE, the output will be in CPLEX LP file format, including the objective function given in the model and reaction bounds. Additionally, if set to TRUE, argument met will be ignored; all metabolites present in the model are used. See also Details. Default: FALSE.
printOut	A single Boolean value. If set to TRUE, the desired reactions will be printed via the cat function. Default: TRUE.
...	Further arguments passed to cat, e.g. argument file.

Details

Metabolite id's beginning with a digit or period will be prefixed by the letter "r", reaction id's beginning with a digit or period will be prefixed by the letter "x" and square brackets in reaction or metabolite id's will be replaced by round brackets.

Value

The modelorg method returns a character vector of length equal to the number of metabolites given in argument met, invisibly. Each string represents the reaction participation of one particular metabolite.

Methods

signature(object = "modelorg") method to use with objects of class modelorg.

Author(s)

Gabriel Gelius-Dietrich

See Also

Class modelorg

---

printReaction-methods *Print Columns of the Stoichiometric Matrix*

Description

Print the columns of the stoichiometric matrix.

Usage

```
## S4 method for signature 'modelorg,ANY'
printReaction(object, react, printOut = TRUE, ...)
## S4 method for signature 'summaryOptsol,modelorg'
printReaction(object, mod, j, ...)
```

Arguments

object	An object of class modelorg or of class summaryOptsol.
mod	An object of class modelorg.
react	A numeric of character vector or an object of class reactId containing the reaction id's of reactions to print out.
j	A numeric of character vector indicating the simulations to consider, see Details.
printOut	A single Boolean value. If set to TRUE, the desired reactions will be printed via the cat function. Default: TRUE.
...	Further arguments passed to cat, e.g. argument file.

Details

The output of the modelorg method is compatible to the file format produced by modelorg2tsv. Two columns are used: "abbreviation" containing the reaction id's and "equation" containing the reaction equation.

The summaryOptsol method prints the limiting reactions generated in simulations and stored in objects of class summaryOptsol. Slot react_id of class summaryOptsol contains a list of reaction id's: list element j gives the reaction id's limiting simulation number j.

Value

The modelorg method returns invisibly a character vector of length equal to the number of reactions given in argument react. Each string consists of two tab-delimited values: first, the reaction id, second, the reaction equation.

The summaryOptsol returns invisibly a list of length equal to the number of elements in argument j. Each list element is of the same type as the return value of the modelorg method.

Methods

signature(object = "modelorg") method to use with objects of class modelorg.

signature(object = "summaryOptsol", mod = "modelorg") method to use with objects of class summaryOptsol.

Author(s)

Gabriel Gelius-Dietrich

See Also

Class modelorg and class summaryOptsol.

---

promptSysBiolAlg *Generate A Skeletal Structure of Subclasses of sysBiolAlg*

Description

Generates a skeletal structure of new subclasses of class sysBiolAlg, in particular for the constructor method initialize.

Usage

```
promptSysBiolAlg(algorithm, prefix = "sysBiolAlg", sep = "_",
                 suffix = "R", fpath = ".", ...)
```

Arguments

algorithm	A single character string containing the name of the new algorithm.
prefix	A single character string containing a prefix for the new algorithm, see Details below. Default: "sysBiolAlg".
sep	A single character string containing a separator for prefix and algorithm. Default: "_".
suffix	A single character string containing a file name suffix. Default: "R".
fpath	A single character string containing a file path. Default: ... .
...	Further arguments passed to file.

Details

The arguments prefix algorithm are stick together separated by sep (default: a single underscore "_") to get the new class name: prefix_algorithm. The filename will be: prefix_algorithmClass.R.

The class definition in the new file will extend class sysBiolAlg directly and will not add any slots. Additionally a skeletal structure for method initialize will be generated. In this method, the user should create all arguments to the initialize method described in the base class sysBiolAlg and put them all to callNextMethod. Or, alternatively, generate an instance of class optObj "by hand".

Value

Returns NULL invisible.

Author(s)

Gabriel Gelius-Dietrich

See Also

sysBiolAlg

---

reactId-class *Structure of Class "reactId"*

Description

Structure of the class "reactId". Objects of that class are returned by the function checkReactId.

Objects from the Class

Objects can be created by calls of the form new("reactId", mod_id, pnt, id = NULL, mod_key = "").

mod_id: Object of class "character" containing the model id.

pnt: Object of class "numeric" containing the column indices in a stoichiometric matrix of the reactions given in react.

id: Object of class "character" containing the reaction id's corresponding to argument pos. If set to NULL (default), no reaction id's are used.

mod_key: Object of class "character" containing the model key.

Slots

mod_id: Object of class "character" containing the model id.

mod_key: Object of class "character" containing the model key of the used model.

react_pos: Object of class "integer" containing the column indices of reaction id's in the stoichiometric matrix of the metabolic model with id mod_id.

react_id: Object of class "character" containing the reaction id's corresponding to the indices given in slot react_pos.

react_num: Object of class "integer" containing the number of reaction id's.

Methods

mod_id<-: signature(object = "reactId"): sets the mod_id slot.

mod_id: signature(object = "reactId"): gets the mod_id slot.

mod_key<-: signature(object = "reactId"): sets the mod_key slot.

mod_key: signature(object = "reactId"): gets the mod_key slot.

react_pos<-: signature(object = "reactId"): sets the react_pos slot.

react_pos: signature(object = "reactId"): gets the react_pos slot.

react_id<-: signature(object = "reactId"): sets the react_id slot.

react_id: signature(object = "reactId"): gets the react_id slot.

length signature(object = "reactId"): returns the number of reaction id's.

[: signature(x = "reactId"): access like a vector. x[i] returns a new object of class reactId containing the ith reaction id.

Author(s)

Gabriel Gelius-Dietrich

See Also

checkReactId

Examples

```
showClass("reactId")
```

---

reactId_Exch-class *Class* "reactId_Exch"

Description

Structure of the class "reactId_Exch". Objects of that class are returned by the function findExchReact.

Objects from the Class

Objects can be created by calls of the form new("reactId_Exch", mod_id, mod_key, rpnt, rid, upt, mpnt, mid, lb,

mod_id: Object of class "character" containing the model id.

mod_key: Object of class "character" containing the model key.

rpnt: Object of class "numeric" containing the column indices in a stoichiometric matrix of the reactions given in rid.

rid: Object of class "character" containing the reaction id's corresponding to argument rpnt.

upt: Object of class "logical": upt[j] equals TRUE if reaction j in rid is an uptake reaction (an exchange reaction with a lower bound less than zero).

mpnt: Object of class "numeric" containing the row indices in a stoichiometric matrix of the metabolites given in mid. The reaction given in rid[j] transports metabolite mid[j] across the system boundary of the model.

mid: Object of class "character" containing the metabolite id's corresponding to argument mpnt.

lb: Object of class "numeric" containing the lower bounds of the reactions given in rpnt.

ub: Object of class "numeric" containing the upper bounds of the reactions given in rpnt.

Slots

uptake: Object of class "logical" indicating if a certain reaction is an uptake reaction or not.

met_pos: Object of class "integer" containing the row indices of metabolite id's in the stoichiometric matrix of the metabolic model with id mod_id.

met_id: Object of class "character" containing the metabolite id's corresponding to the indices given in slot met_pos.

`lowbnd`: Object of class `"numeric"` containing the lower bounds of the reactions given in slot `react_pos`.

`uppbnd`: Object of class `"numeric"` containing the upper bounds of the reactions given in slot `react_pos`.

`mod_id`: Object of class `"character"` containing the model id.

`mod_key`: Object of class `"character"` containing the model key of the used model.

`react_pos`: Object of class `"integer"` containing the column indices of reaction id's in the stoichiometric matrix of the metabolic model with id `mod_id`.

`react_id`: Object of class `"character"` containing the reaction id's corresponding to the indices given in slot `react_pos`.

`react_num`: Object of class `"integer"` containing the number of reaction id's.

Extends

Class `"reactId"`, directly.

Methods

met_pos `signature(object = "reactId_Exch")`: gets the `met_pos` slot.

met_pos<- `signature(object = "reactId_Exch")`: sets the `met_pos` slot.

met_id `signature(object = "reactId_Exch")`: gets the `met_id` slot.

met_id<- `signature(object = "reactId_Exch")`: sets the `met_id` slot.

met_pos `signature(object = "reactId_Exch")`: gets the `met_pos` slot.

met_pos<- `signature(object = "reactId_Exch")`: sets the `met_pos` slot.

lowbnd `signature(object = "reactId_Exch")`: gets the `lowbnd` slot.

lowbnd<- `signature(object = "reactId_Exch")`: sets the `lowbnd` slot.

uppbnd `signature(object = "reactId_Exch")`: gets the `uppbnd` slot.

uppbnd<- `signature(object = "reactId_Exch")`: sets the `uppbnd` slot.

uptake `signature(object = "reactId_Exch")`: gets the `uptake` slot.

uptake<- `signature(object = "reactId_Exch")`: sets the `uptake` slot.

uptReact `signature(object = "reactId_Exch")`: gets the id's of uptake reactions.

uptMet `signature(object = "reactId_Exch")`: gets the metabolite id's of metabolites used by uptake reactions.

`[`: `signature(x = "reactId_Exch")`: access like a vector. `x[i]` returns a new object of class `reactId_Exch` containing the `i`th exchange reaction id.

`show`: `signature(x = "reactId_Exch")`: prints a table of all exchange reactions. If an upper or lower bound is equal or greater than `abs(SYBIL_SETINGS("MAXIMUM"))`, it will be shown as `Inf` or `-Inf`.

Author(s)

Gabriel Gelius-Dietrich

See Also

checkReactId

Examples

```
showClass("reactId")
```

---

readProb-methods *Read Problem Object From File*

Description

Read problem object from file.

Usage

```
## S4 method for signature 'optObj_clpAPI,character'
readProb(lp, fname, ff = "mps", ...)

## S4 method for signature 'optObj_cplexAPI,character'
readProb(lp, fname, ff = "lp")

## S4 method for signature 'optObj_glpkAPI,character'
readProb(lp, fname, ff = "lp", ...)

## S4 method for signature 'optObj_lpSolveAPI,character'
readProb(lp, fname, ff = "lp", ...)
```

Arguments

lp	An object extending class optObj.
fname	A single character string giving the file name to read from.
ff	A single character string giving the file format to use, see Details. Default: "lp".
...	Further arguments passed to the corresponding API routine.

Details

Argument "ff" in conjunction with **clpAPI** can be mps for MPS file format or "clp" for COIN-OR Clp file mormat. Valid values for **cplexAPI** and lpSolveAPI are available in their documentations. For **glpkAPI**, argument "ff" can be "lp" for LP file format, "mps" for MPS file format or "glpk" for GLPK file format.

Methods

`signature(lp = "optObj_clpAPI", fname = "character")` method to use with package **optObj_clpAPI**. Argument `ff` is not used here.

`signature(lp = "optObj_cplexAPI", fname = "character")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI", fname = "character")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI", fname = "character")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

---

readTSVmod *Read a Metabolic Network in a TSV (CSV) Format*

Description

The function `readTSVmod` reads metabolic networks in text files, following a character-separated value format. Each line should contain one entry; the default value separator is a tab. Output files from the BiGG database are compatible.

Usage

```
readTSVmod(prefix, suffix,
           reactList, metList = NA, modDesc = NA,
           fielddelim = "\t", entrydelim = ", ", extMetFlag = "b",
           excludeComments = TRUE,
           oneSubSystem = TRUE,
           mergeMet = TRUE,
           balanceReact = TRUE,
           remUnusedMetReact = TRUE,
           singletonMet = FALSE,
           deadEndMet = FALSE,
           remMet = FALSE,
           constrMet = FALSE,
           tol = SYBIL_SETTINGS("TOLERANCE"),
           fpath = SYBIL_SETTINGS("PATH_TO_MODEL"),
           def_bnd = SYBIL_SETTINGS("MAXIMUM"),
           arrowlength = NULL,
           quoteChar = "",
           commentChar, ...)
```

Arguments

prefix	A single character string giving the prefix for three possible input files (see Details below).
suffix	A single character string giving the file name extension. If missing, the value of suffix depends on the argument fielddelim, see Details below. Default: "tsv".
reactList	A single character vector giving a file name containing a reaction list. Only necessary, if argument suffix is empty.
metList	A single character vector giving a file name containing a metabolite list. Default: NA.
modDesc	A single character vector giving a file name containing a model description. Default: NA.
fielddelim	A single character string giving the value separator. Default: "\t".
entrydelim	A single character string giving the a separator for values containing more than one entry. Default: ", ".
extMetFlag	A single character string giving the identificator for metabolites which are outside the system boundary. Only necessary, if the model is a closed one. Default: "b".
excludeComments	A Boolean value. Sometimes, the reaction abbreviations and/or the metabolite abbreviations contain comments in square brackets. If set to TRUE, these comments will be removed. If set to FALSE, whitespaces included in comments in metabolite abbreviations will be removed. Comments in reaction abbreviations stay unchanged. A reaction id with comment is, for example, the string: pfk [comment], with [comment] being the comment. There must be at least one whitespace between id and comment, otherwise it will be considered as compartment flag. Default: TRUE.
oneSubSystem	A Boolean value. Ignore parameter entrydelim for the field 'subsystem', if every reaction belongs to exactly one sub system. Default: TRUE.
mergeMet	Boolean: if set to TRUE, metabolites used more than once as reactand or product in a particular reaction are added up, see details below. If set to FALSE, the last value is used without warning. Default: TRUE.
balanceReact	Boolean: if set to TRUE, metabolites used as reactand and product in a particular reaction at the same time are balanced, see details below. If set to FALSE the last value is used without warning (reactands before products). Default: TRUE.
remUnusedMetReact	Boolean: if set to TRUE, metabolites and reactions which are not used in the stoichiometric matrix will be removed. A metabolite or a reaction is considered as unused, if the corresponding element of rowSums (metabolites) or colSums

(reactions) of the binary version of the stoichiometric matrix is zero, see details below. If set to FALSE, only a warning is given.
Default: FALSE.

singletonMet — Boolean: if set to TRUE, metabolites appearing only once in the stoichiometric matrix are identified. Metabolites appear only once, if rowSums of the binary stoichiometric matrix is one in the corresponding row, see details below.
Default: FALSE.

deadEndMet — Boolean: if set to TRUE, metabolites which are produced but not consumed, or vice versa are identified, see details below. If both arguments singletonMet and deadEndMet are set to TRUE, the function will first look for singleton metabolites, and exclude them (and the corresponding reactions) from the search list. Afterwards, dead end metabolites are searched only in the smaller model.
Default: FALSE.

remMet — Boolean: if set to TRUE, metabolites identified as singleton or dead end metabolites will be removed from the model. Additionally, reactions containing such metabolites will be removed also.
Default: FALSE.

constrMet — Boolean: if set to TRUE, reactions containing metabolites identified as singleton or dead end metabolites will be constrained to zero.
Default: FALSE.

tol — A single numeric value, giving the smallest positive floating point number unequal to zero, see details below.
Default: SYBIL_SETTINGS("TOLERANCE").

fpath — A single character string giving the path to a certain directory containing the model files.
Default: SYBIL_SETTINGS("PATH_TO_MODEL").

def_bnd — A single numeric value. Absolute value for uppper and lower bounds for reaction bounds.
Default: SYBIL_SETTINGS("MAXIMUM").

arrowlength — A single numeric or character value or NULL. This argument controls the number of "-" and "=" used in reaction arrows in the equation strings. If set to NULL, one or more symbols are used. The regular expression used is "<?[=-]+>". If numeric, all reaction arrows must consist of exactly arrowlength signs. The regular expression used is "<?[=-]{arrowlength}>". If character, arrowlength must be a regular expression and will be used as "<?[=-]arrowlength>". For example, if arrowlength is "{1,2}" the regular expression is "<?[=-]{1,2}>", meaning the reaction arrow can consist of one or two signs. In any case, the completed regular expression will always used with argument perl = TRUE.
Default: NULL.

quoteChar — Set of quoting characters used for the argument quote in read.table, see there for details.
Default: "" (disable quoting).

commentChar — A single character used for the argument comment.char in read.table, see there for details. If a comment char is needed, e.g. "@" (at) seems to be a good one.
Default: "".

... Further arguments passed to read.table, e.g. argument quote, comment.char or argument fill, if some lines do not have enough elements. If all fields are in double quotes, for example, set quote to "\"".

Details

A metabolic model consists of three input files:

1. <prefix>_react.<suffix> containing all reactions.
2. <prefix>_met.<suffix> containing all metabolites.
3. <prefix>_desc.<suffix> containing a model description.

All of these files must be character separated value files (for a detailed format description and examples, see package vignette). The argument prefix is the part of the filenames, all three have in common (e.g. if they where produced by modelorg2tsv). Alternatively, the arguments reactList, metList and modDesc can be used. A file containing all reactions must be there, everything else is optional.

If suffix is missing, it is set according to the value of fielddelim:

"\t"	"tsv"
";"	"csv"
","	"csv"
"|"	"dsv"
anything else	"dsv"

The argument ... is passed to read.table.

In some cases, it could be necessary, to turn off quoting quoteChar = "" (default), if e.g. metabolite names contain quoting characters "'" like in 3',5'-bisphosphate nucleotidase. If all fields are in quotes (e.g. files generated by modelorg2tsv), use quoteChar = "\"" for example.

The input files are read using the function read.table. The argument header is set to TRUE and the argument sep is set to the value of fielddelim. Everything else can be passed via the ... argument.

The header for the reactions list may have the following columns:

"abbreviation"	a unique reaction id
"name"	a reaction name
"equation"	the reaction equation
"reversible"	TRUE, if the reaction is reversible
"compartment"	reaction compartment(s) (currently unused)
"lowbnd"	lower bound
"uppbnd"	upper bound
"obj_coef"	objective coefficient
"rule"	gene to reaction association
"subsystem"	subsystem of the reaction

Every entry except for "equation" is optional. If there are missing values in field "lowbnd", they will be set to -1 * def_bnd; if there are missing values in field "uppbnd", they will be set to def_bnd; if there are missing values in field "obj_coef", they will be set to 0.

The header for the metabolites list may have the following columns:

"abbreviation"	a unique metabolite id
"name"	a metabolite name
"compartment"	metabolite compartment (currently unused)

If a metabolite list is provided, it is supposed to contain at least the entries "abbreviation" and "name".

The header for the model description file may have the following columns:

"name"	a name for the model
"id"	a shorter model id
"description"	a model description
"compartment"	the compartments
"abbreviation"	unique compartment abbreviations
"Nmetabolites"	number of metabolites
"Nreactions"	number of reactions
"Ngenes"	number of independend genes
"Nnnz"	number of non-zero elements in the stoichiometric matrix

If a file contains a certain column name, there must be no empty entries.

If a model description file is provided, it is supposed to contain at least the entries "name" and "id". Otherwise, the filename of the reactions list will be used (the filename extension and the string _react at the end of the filename will be removed).

The compartments in which a reaction takes place is determined by the compartment flags of the participating metabolites.

All fields in the output files of modelorg2tsv are in double quotes. In order to read them, set argument quoteChar to "\"".

Please read the package vignette for detailed information about input formats and examples.

If a metabolite is used more than once as product or reactand of a particular reaction, it is merged: a + (2) a is converted to (3) a and a warning will be given.

If a metabolite is used first as reactand and then as product of a particular reaction, the reaction is balanced: (2) b + a -> b + c is converted to b + a -> c

A binary version of the stoichiometric matrix S is constructed via $|S| > tol$.

A binary version of the stoichiometric matrix S is scanned for reactions and metabolites which are not used in S. If there are some, a warning will be given and the corresponding reactions and metabolites will be removed from the model if remUnusedMetReact is set to TRUE.

The binary version of the stoichiometric matrix S is scanned for metabolites, which are used only once in S. If there are some, at least a warning will be given. If either constrMet or remMet is set

to TRUE, the binary version of S is scanned for paths of singleton metabolites. If constrMet is set to TRUE, reactions containing those metabolites will be constrained to zero; if remMet is set to TRUE, the metabolites and the reactions containing those metabolites will be removed from the network.

In order to find path of singleton metabolites a binary version of the stoichiometric matrix S is used. Sums of rows gives the vector of metabolite usage, each element is the number of reactions a metabolite participates. A single metabolite (singleton) is a metabolite with a row sum of zero. All columns in S (reactions) containing singleton metabolites will be set to zero. And again, singleton metabolites will be searched until none are found.

The algorithm to find dead end metabolites works in a quite similar way, but not in the binary version of the stroichiometric matrix. Here, metabolite i is considered as dead end, if it is for example produced by reaction j but not used by any other reaction k.

Value

An instance of class modelorg.

Author(s)

Gabriel Gelius-Dietrich

References

The BiGG database http://bigg.ucsd.edu/.

Schellenberger, J., Park, J. O., Conrad, T. C., and Palsson, B. Ø., (2010) BiGG: a Biochemical Genetic and Genomic knowledgebase of large scale metabolic reconstructions. *BMC Bioinformatics* **11**, 213.

Becker, S. A., Feist, A. M., Mo, M. L., Hannum, G., Palsson, B. Ø. and Herrgard, M. J. (2007) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. *Nat Protoc* **2**, 727–738.

Schellenberger, J., Que, R., Fleming, R. M. T., Thiele, I., Orth, J. D., Feist, A. M., Zielinski, D. C., Bordbar, A., Lewis, N. E., Rahmanian, S., Kang, J., Hyduke, D. R. and Palsson, B. Ø. (2011) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. *Nat Protoc* **6**, 1290–1307.

See Also

read.table, modelorg2tsv, modelorg

Examples

```
## read example dataset
mp  <- system.file(package = "sybil", "extdata")
mod <- readTSVmod(prefix = "Ec_core", fpath = mp, quoteChar = "\"")

## redirect warnings to a log file
sink(file = "warn.log")
mod <- readTSVmod(prefix = "Ec_core", fpath = mp, quoteChar = "\"")
warnings()
sink()
```

```
  unlink("warn.log")

  ## print no warnings
  suppressWarnings(
    mod <- readTSVmod(prefix = "Ec_core", fpath = mp, quoteChar = "\""))

  ## print no messages
  suppressMessages(
    mod <- readTSVmod(prefix = "Ec_core", fpath = mp, quoteChar = "\""))

## Not run:
  ## set number of warnings to keep
  options(nwarnings = 1000)

  ## redirect every output to a file
  zz <- file("log.Rout", open = "wt")
  sink(zz)
  sink(zz, type = "message")
  mod <- readTSVmod(prefix = "Ec_core", fpath = mp, quoteChar = "\"")
  warnings()
  sink(type = "message")
  sink()
  close(zz)

## End(Not run)
```

`resetChanges-methods` *Generic Function to Reset Temporary Changes in Objects of Class sysBiolAlg*

Description

Use method `resetChanges` to undo changes in objects of class `sysBiolAlg` made by `applyChanges`.

Usage

```
## S4 method for signature 'sysBiolAlg'
resetChanges(object, old_val)

## S4 method for signature 'sysBiolAlg_room'
resetChanges(object, old_val)
```

Arguments

`object`	An object of class `sysBiolAlg`.
`old_val`	A list containing the original values of the model. This list is returned by `applyChanges`.

Value

Invisibly TRUE will be returned.

Methods

signature(object = "sysBiolAlg") Method used with objects extending class sysBiolAlg

signature(object = "sysBiolAlg_room") Method used with objects of class sysBiolAlg_room

Author(s)

Gabriel Gelius-Dietrich

See Also

Class sysBiolAlg and applyChanges

---

rmReact *Remove Reactions From a Model*

Description

The function rmReact removes reactions from a model.

Usage

```
rmReact(model, react, rm_met = TRUE)
```

Arguments

model	An object of class modelorg
react	An object of class reactId, a numeric vector, or a character vector containing reaction id's.
rm_met	Logical: also remove unused metabolites (default: TRUE).

Details

The argument react is evaluated by the function checkReactId.

Value

An object of class modelorg.

Author(s)

Gabriel Gelius-Dietrich

References

Becker, S. A., Feist, A. M., Mo, M. L., Hannum, G., Palsson, B. Ø. and Herrgard, M. J. (2007) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. *Nat Protoc* **2**, 727–738.

Schellenberger, J., Que, R., Fleming, R. M. T., Thiele, I., Orth, J. D., Feist, A. M., Zielinski, D. C., Bordbar, A., Lewis, N. E., Rahmanian, S., Kang, J., Hyduke, D. R. and Palsson, B. Ø. (2011) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. *Nat Protoc* **6**, 1290–1307.

See Also

modelorg, reactId and checkReactId

Examples

```
data(Ec_core)
Ec_r <- rmReact(Ec_core, c("ATPM", "Biomass"))
```

---

robAna *Robustness Analysis*

Description

Performs robustness analysis for a given metabolic model.

Usage

```
robAna(model, ctrlreact, rng = NULL,
       numP = 20, verboseMode = 1, ...)
```

Arguments

model	An object of class modelorg.
ctrlreact	An object of class reactId, character or integer. Specifies the control reaction – the parameter to vary.
rng	A numeric vector of length two, giving the lower and upper bound of the control reaction. If set to NULL (the default), the range will be computed by flux variability analysis for the reaction given in ctrlreact. Default: NULL
numP	The number of points to analyse. Default: 20
verboseMode	An integer value indicating the amount of output to stdout, see optimizer for details. Default: 1.
...	Further arguments passed to optimizer.

Details

The function robAna performs a robustness analysis with a given model. The flux of ctrlreact will be varied in numP steps between the maximum and minimum value the flux of ctrlreact can reach. For each of the numP datapoints the followong lp problem is solved

$$\begin{aligned} \max \quad & \boldsymbol{c}^{\mathrm{T}}\boldsymbol{v} \\ \text{s.t.} \quad & \boldsymbol{S}\boldsymbol{v} = 0 \\ & v_j = c_k \\ & \alpha_i \leq v_i \leq \beta_i \qquad \forall i \in \{1, \ldots, n\}, i \neq j \end{aligned}$$

with $\boldsymbol{S}$ being the stoichiometric matrix, α_i and β_i being the lower and upper bounds for flux (variable) i. The total number of variables of the optimization problem is denoted by n. The parameter c_k is varied numP times in the range of $v_{j,\min}$ to $v_{j,\max}$. The result of the optimization is returned as object of class optsol_robAna containing the objective value for each datapoint.

The extreme points of the range for ctrlreact are calculated via flux balance analysis (see also sysBiolAlg_fba) with the objective function being minimization and maximization of the flux through ctrlreact.

Value

An object of class optsol_robAna.

Author(s)

Gabriel Gelius-Dietrich

References

Becker, S. A., Feist, A. M., Mo, M. L., Hannum, G., Palsson, B. Ø. and Herrgard, M. J. (2007) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. *Nat Protoc* **2**, 727–738.

Schellenberger, J., Que, R., Fleming, R. M. T., Thiele, I., Orth, J. D., Feist, A. M., Zielinski, D. C., Bordbar, A., Lewis, N. E., Rahmanian, S., Kang, J., Hyduke, D. R. and Palsson, B. Ø. (2011) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. *Nat Protoc* **6**, 1290–1307.

Bernhard Ø. Palsson (2006). *Systems Biology: Properties of Reconstructed Networks*. Cambridge University Press.

Examples

```
data(Ec_core)
rb <- robAna(Ec_core, ctrlreact = "EX_o2(e)")
plot(rb)
```

scaleProb-methods *Scaling of the Constraint Matrix of an Optimization Problem*

Description

Scaling of the constraint matrix of an optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI'
scaleProb(lp, opt)

## S4 method for signature 'optObj_cplexAPI'
scaleProb(lp, opt)

## S4 method for signature 'optObj_glpkAPI'
scaleProb(lp, opt)

## S4 method for signature 'optObj_lpSolveAPI'
scaleProb(lp, opt)
```

Arguments

lp	An object extending class optObj.
opt	Scaling option depending on the used solver software.

Methods

signature(lp = "optObj_clpAPI") method to use with package **optObj_clpAPI**.

signature(lp = "optObj_cplexAPI") method to use with package **optObj_cplexAPI**.

signature(lp = "optObj_glpkAPI") method to use with package **optObj_glpkAPI**.

signature(lp = "optObj_lpSolveAPI") method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

`sensitivityAnalysis-methods` *Sensitivity Analysis*

Description

Perform sensitivity analysis.

Usage

```
## S4 method for signature 'optObj_cplexAPI'
sensitivityAnalysis(lp, ...)

## S4 method for signature 'optObj_glpkAPI'
sensitivityAnalysis(lp, ...)
```

Arguments

`lp`	An object extending class `optObj`.
`...`	Further arguments passed to the initialization function of the solver package.

Value

The **glpkAPI** method generates a file `"sar.txt"` and the **cplexAPI** method returns a list.

Methods

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass `optObj` and constructor function `optObj`.

setColsNames-methods *Set/Change Variable Names*

Description

Set or change names of variables (columns) used in a optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI,numeric,character'
setColsNames(lp, j, names)

## S4 method for signature 'optObj_cplexAPI,numeric,character'
setColsNames(lp, j, names)

## S4 method for signature 'optObj_glpkAPI,numeric,character'
setColsNames(lp, j, names)

## S4 method for signature 'optObj_lpSolveAPI,numeric,character'
setColsNames(lp, j, names)
```

Arguments

lp	An object extending class optObj.
j	A numeric vector of column indices.
names	A character vector of the same length as j containing the column names.

Value

NULL is invisibly returned.

Methods

signature(lp = "optObj_clpAPI", j = "numeric", names = "character") method to use with package **optObj_clpAPI**.

signature(lp = "optObj_cplexAPI", j = "numeric", names = "character") method to use with package **optObj_cplexAPI**.

signature(lp = "optObj_glpkAPI", j = "numeric", names = "character") method to use with package **optObj_glpkAPI**.

signature(lp = "optObj_lpSolveAPI", j = "numeric", names = "character") method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

setObjDir-methods *Set Direction of Optimization*

Description

Set direction of optimization.

Usage

```
## S4 method for signature 'optObj_clpAPI,character'
setObjDir(lp, lpdir)

## S4 method for signature 'optObj_clpAPI,numeric'
setObjDir(lp, lpdir)

## S4 method for signature 'optObj_cplexAPI,character'
setObjDir(lp, lpdir)

## S4 method for signature 'optObj_cplexAPI,integer'
setObjDir(lp, lpdir)

## S4 method for signature 'optObj_cplexAPI,numeric'
setObjDir(lp, lpdir)

## S4 method for signature 'optObj_glpkAPI,character'
setObjDir(lp, lpdir)

## S4 method for signature 'optObj_glpkAPI,integer'
setObjDir(lp, lpdir)

## S4 method for signature 'optObj_glpkAPI,numeric'
setObjDir(lp, lpdir)

## S4 method for signature 'optObj_lpSolveAPI,character'
setObjDir(lp, lpdir)

## S4 method for signature 'optObj_lpSolveAPI,numeric'
setObjDir(lp, lpdir)
```

Arguments

lp	An object extending class optObj.

lpdir — A single character string, numeric or integer value. Can be set to "max" or -1 for maximization, or "min" or 1 for minimization. For packages **cplexAPI** and glpkAPI it is also possible to use the corresponding constant given by the package.

Methods

signature(lp = "optObj_clpAPI", lpdir = "character") method to use with package **optObj_clpAPI**. Set lpdir to "max" for maximization or "min" for minimization.

signature(lp = "optObj_clpAPI", lpdir = "numeric") method to use with package **optObj_clpAPI**. Set lpdir to -1 for maximization or 1 for minimization.

signature(lp = "optObj_cplexAPI", lpdir = "character") method to use with package **optObj_cplexAPI**. Set lpdir to "max" for maximization or "min" for minimization.

signature(lp = "optObj_cplexAPI", lpdir = "integer") method to use with package **optObj_cplexAPI**. Set lpdir to CPX_MAX for maximization or CPX_MIN for minimization.

signature(lp = "optObj_cplexAPI", lpdir = "numeric") method to use with package **optObj_cplexAPI**. Set lpdir to -1 for maximization or 1 for minimization.

signature(lp = "optObj_glpkAPI", lpdir = "character") method to use with package **optObj_glpkAPI**. Set lpdir to "max" for maximization or "min" for minimization.

signature(lp = "optObj_glpkAPI", lpdir = "integer") method to use with package **optObj_glpkAPI**. Set lpdir to GLP_MAX for maximization or GLP_MIN for minimization.

signature(lp = "optObj_glpkAPI", lpdir = "numeric") method to use with package **optObj_glpkAPI**. Set lpdir to -1 for maximization or 1 for minimization.

signature(lp = "optObj_lpSolveAPI", lpdir = "character") method to use with package **optObj_lpSolveAPI**. Set lpdir to "max" for maximization or "min" for minimization.

signature(lp = "optObj_lpSolveAPI", lpdir = "numeric") method to use with package **optObj_lpSolveAPI**. Set lpdir to -1 for maximization or 1 for minimization.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

setRhsZero-methods *Set Right Hand Side of the Optimization Problem To Zero*

Description

Set right hand side of the optimization problem to zero: $\boldsymbol{Sv} = 0$.

Usage

```
## S4 method for signature 'optObj_clpAPI'
setRhsZero(lp)

## S4 method for signature 'optObj_cplexAPI'
setRhsZero(lp)

## S4 method for signature 'optObj_glpkAPI'
setRhsZero(lp)

## S4 method for signature 'optObj_lpSolveAPI'
setRhsZero(lp)
```

Arguments

lp	An object extending class optObj.

Methods

`signature(lp = "optObj_clpAPI")` method to use with package **optObj_clpAPI**.

`signature(lp = "optObj_cplexAPI")` method to use with package **optObj_cplexAPI**.

`signature(lp = "optObj_glpkAPI")` method to use with package **optObj_glpkAPI**.

`signature(lp = "optObj_lpSolveAPI")` method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

setRowsNames-methods *Set/Change Constraint Names*

Description

Set or change names of constraints (rows) used in a optimization problem.

Usage

```
## S4 method for signature 'optObj_clpAPI,numeric,character'
setRowsNames(lp, i, names)

## S4 method for signature 'optObj_cplexAPI,numeric,character'
setRowsNames(lp, i, names)
```

```
## S4 method for signature 'optObj_glpkAPI,numeric,character'
setRowsNames(lp, i, names)

## S4 method for signature 'optObj_lpSolveAPI,numeric,character'
setRowsNames(lp, i, names)
```

Arguments

lp	An object extending class optObj.
i	A numeric vector of row indices.
names	A character vector of the same length as i containing the row names.

Value

NULL is invisibly returned.

Methods

signature(lp = "optObj_clpAPI", i = "numeric", names = "character") method to use with package **optObj_clpAPI**.

signature(lp = "optObj_cplexAPI", i = "numeric", names = "character") method to use with package **optObj_cplexAPI**.

signature(lp = "optObj_glpkAPI", i = "numeric", names = "character") method to use with package **optObj_glpkAPI**.

signature(lp = "optObj_lpSolveAPI", i = "numeric", names = "character") method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

setSolverParm-methods *Set Parameters Used By The Optimization Software*

Description

Set parameters used by the optimization software. Parameters are set on a key-value basis. Sets of parameters can be set via a named list or a named data frame. The names of the parameters itself and possible values differ from solver to solver. Please consult the documentation of your solver software to get information about available parameters.

Usage

```
## S4 method for signature 'optObj_clpAPI'
setSolverParm(lp, solverParm)

## S4 method for signature 'optObj_cplexAPI'
setSolverParm(lp, solverParm)

## S4 method for signature 'optObj_glpkAPI'
setSolverParm(lp, solverParm)

## S4 method for signature 'optObj_lpSolveAPI'
setSolverParm(lp, solverParm)
```

Arguments

lp	An object extending class optObj.
solverParm	A named list or data frame containing sets of parameters. They must not contain NA values and every list or data frame element must have length one.

Methods

signature(lp = "optObj_clpAPI") method to use with package **optObj_clpAPI**. This method is currently unused. It is not possible to provide parameters for package **clpAPI**. Always FALSE will be returned.

signature(lp = "optObj_cplexAPI") method to use with package **optObj_cplexAPI**. In order to set integer parameters (parameters of type CPXINT), the value must be of type integer. For example, like as.integer(42) or 23L.

signature(lp = "optObj_glpkAPI") method to use with package **optObj_glpkAPI**.

signature(lp = "optObj_lpSolveAPI") method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

shrinkMatrix-methods *Get a Subset of Matrix Like Objects*

Description

Generate subsets of matrix-like objects.

Usage

```
## S4 method for signature 'modelorg'
shrinkMatrix(X, i = NULL, j = NULL,
                                    tol = SYBIL_SETTINGS("TOLERANCE"))
```

Arguments

X	An object treated to be matrix-like.
i	A numeric or character vector containing row indices of the matrix given in argument X. For the modelorg method, this can be an object of class reactId_Exch. Default: NULL.
j	A numeric or character vector containing column indices of the matrix given in argument X. For the modelorg method, this can be an object of class reactId. Default: NULL.
tol	A tolerance value. An element X_{ij} of the matrix given in argument X is considered to be zero, if $\|X_{ij}\| > tol$ is true. Default: SYBIL_SETTINGS("TOLERANCE").

Value

The modelorg method will return an object of class Matrix, with columns named by their reaction id's and rows named by their metabolite id's.

Methods

signature(X = "modelorg") method to use with objects of class modelorg for subsets of the stoichiometric matrix. Either argument i or argument j can be used, not both at the same time. If they are of type character, they must contain metabolite or reaction id's existing in the modelorg object. Use i to get the reactions in which the metabolites given in i participate (the metabolites given in i will be located in the first rows of the result). Use j to get all reactions given in j. The method will remove all non-zero rows and columns from the result.

Author(s)

Claus Jonathan Fritzemeier, Gabriel Gelius-Dietrich

See Also

Class modelorg.

Examples

```
# get the part of the stoichiometric containing
# the exchange reactions
data(Ec_core)
ex <- findExchReact(Ec_core)
shrinkMatrix(Ec_core, j = ex)
```

singletonMetabolites-methods
Identify Singleton Metabolites

Description

Search a metabolic network for metabolites, which appear only once in the stoichiometric matrix.

Usage

```
## S4 method for signature 'modelorg'
singletonMetabolites(object,tol,retIds)
```

Arguments

object	An object of class modelorg.
tol	A numeric tolerance value: an entry of the stoichiometric matrix s_ij is considered to be non-zero if $abs(s_ij) > tol$ is TRUE. Default: SYBIL_SETTINGS("TOLERANCE").
retIds	Boolean. If set to TRUE, a list containing metabolite id's will be returned, otherwise a list of logical vectors. Default: TRUE.

Value

A list will be returned:

smet	singleton metabolites
sreact	reactions containing singleton metabolites

Methods

signature(object = "modelorg") method to use with class modelorg.

Author(s)

Gabriel Gelius-Dietrich

See Also

Class modelorg and readTSVmod.

solveLp-methods *Optimize Problem Object*

Description

Optimize problem object.

Usage

```
## S4 method for signature 'optObj_clpAPI'
solveLp(lp)

## S4 method for signature 'optObj_cplexAPI'
solveLp(lp)

## S4 method for signature 'optObj_glpkAPI'
solveLp(lp)

## S4 method for signature 'optObj_lpSolveAPI'
solveLp(lp)
```

Arguments

lp	An object extending class optObj.

Methods

signature(lp = "optObj_clpAPI") method to use with package **optObj_clpAPI**.

signature(lp = "optObj_cplexAPI") method to use with package **optObj_cplexAPI**.

signature(lp = "optObj_glpkAPI") method to use with package **optObj_glpkAPI**.

signature(lp = "optObj_lpSolveAPI") method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

summaryOptsol *Summarize Objects of Class Optsol*

Description

Generates a quick overview of results of simulations stored in objects of class optsol.

Usage

```
summaryOptsol(opt, mod, perc = 1, tol = SYBIL_SETTINGS("TOLERANCE"))
```

Arguments

opt	An object of class optsol.
mod	An object of class modelorg.
perc	A single numeric value in between zero and one indicating how close a flux value has to reach a flux boundary in order to be called "limiting", see Details below. Default: 1.
tol	A tolerance value, see Details below. Default: SYBIL_SETTINGS("TOLERANCE").

Details

The function summaryOptsol generates a summary of the simulations resulting in the object given in argument opt. Both model id's, of the optsol object and of the modelorg object must be identical. The resulting object of class summaryOptsol contains information about the number of zeros and non-zeros in the flux distribution, the substrates and products and about the limiting reactions.

A reaction i is called "limiting", if its flux value v_i is non-zero: $|v_i| > tol$ and if its flux value hits the flux boundaries: $v_i \leq v_{i,\text{min}} \cdot perc \vee v_i \geq v_{i,\text{max}} \cdot perc$.

Value

An object of class summaryOptsol if a flux distribution exists in argument opt, otherwise a summary of the objective values (mod_obj) is returned.

Author(s)

Gabriel Gelius-Dietrich

See Also

Class optsol, class modelorg and class summaryOptsol.

summaryOptsol-class *Class* "summaryOptsol"

Description

Class summaryOptsol stores a summary of instances of class optsol.

Objects from the Class

Objects can be created by calls of the form summaryOptsol(opt, mod).

Slots

mod_id: Object of class "character" containing the model id of the analyzed model.

mod_key: Object of class "character" containing the model key of the used model.

nzeros: Object of class "integer" giving the number of zeros in the flux distribution.

nnonzero: Object of class "integer" giving the number of non-zeros in the flux distribution.

mod_obj: Object of class "numeric" containing the objective coefficients of the model.

ex_met: Object of class "character" containing the id's of exchange metabolites. These are metabolites which are transported across the system boundary.

ex_val: Object of class "Matrix" with each column being the flux distribution of the exchange metabolites of one optimization.

react_id: Object of class "list" with each list element containing a set of reaction id's limiting one optimization. A reactions is considered as "limiting", if it has a non-zero flux value and if its flux value hits an upper or lower bound.

chksol: Object of class "checksol" describing return values of the mathematical programming software and solution status.

Methods

ex_met signature(object = "summaryOptsol"): gets the ex_met slot.

ex_val signature(object = "summaryOptsol"): gets the ex_val slot.

plot: signature(x = "summaryOptsol"): plots a histogram of the values of the objective function in optimal state. Additional arguments can be passed to histogram via the ... argument.

image signature(x = "summaryOptsol"): plots a grey-scale representation of the exchange fluxes of the flux distribution. Black: metabolite is produced, grey: metabolite is imported. Further arguments are:

printOut A single logical value. If set to FALSE, a trellis.object is returned invisibly. Otherwise, a plot is drawn additionally.
Default: TRUE.

... Further arguments to image-methods.

mod_id signature(object = "summaryOptsol"): gets the mod_id slot.

mod_id<- `signature(object = "summaryOptsol")`: sets the `mod_id` slot.

mod_key `signature(object = "summaryOptsol")`: gets the `mod_key` slot.

mod_key<- `signature(object = "summaryOptsol")`: sets the `mod_key` slot.

mod_obj `signature(object = "summaryOptsol")`: gets the `mod_obj` slot.

mod_obj<- `signature(object = "summaryOptsol")`: sets the `mod_obj` slot.

nnzero `signature(object = "summaryOptsol")`: gets the `nnonzero` slot.

nzeros `signature(object = "summaryOptsol")`: gets the `nzeros` slot.

printExchange `signature(object = "summaryOptsol")`: prints a matrix indicating wether a particular metabolite is taken up or produced by the metabolic network given certain conditions. Each line corresponds to one metabolite and each column to one optimization. A `"-"` indicates uptake and `"+"` indicates excretion. A whitespace character `" "` is used, if the metabolite is unused. Further arguments are:

`i` A numeric vector indicating the metabolites (rows) to print: `i[x]` points to matabolite `ec_met(object)[x]`.

`j` A numeric vector indicating the optimizations (columns) to print.

`dense` A single Boolean value. If set to `TRUE`, each column has a column with of one letter.

Author(s)

Gabriel Gelius-Dietrich

See Also

Constructor function `summaryOptsol`, class `optsol` and class `modelorg`.

Examples

```
showClass("summaryOptsol")
```

`sybil-deprecated` *Deprecated Functions and Methods in Package* `sybil`

Description

These functions and methods will be defunct in the next release.

Details

- Function `blockedReact`

Author(s)

Gabriel Gelius-Dietrich

See Also

`Deprecated`

sybilError-class *Class* "sybilError"

Description

Structure of the class "sybilError".

Objects from the Class

Objects can be created by calls of the function sybilError:

test <- sybilError(errmsg = "", number = NA).

errmsg: Object of class "character" containing an error message.

number: Object of class "integer" containing an error number.

Slots

emsg: Object of class "character" error message.

enum: Object of class "integer" error number.

Methods

emsg: signature(object = "sybilError"): gets the emsg slot.

emsg<-: signature(object = "sybilError"): sets the emsg slot.

enum: signature(object = "sybilError"): gets the enum slot.

enum<-: signature(object = "sybilError"): sets the enum slot.

Author(s)

Gabriel Gelius-Dietrich

See Also

optimizeProb

Examples

```
showClass("sybilError")
```

sybilLog-class *Class* "sybilLog"

Description

Handles log files, messages warnings and errors.

Objects from the Class

Objects can be created by calls of the function sybilLog:

logObj <- sybilLog(filename).

Slots

fh: Object of class file which is a connection to a file to print to.

fname: Object of class "character" being the name of the file to print to. If set to NA, no logfile is used. Default: NA.

fpath: Object of class "character" giving the path to the file mentioned in fname. Default: ".".

fenc: Object of class "character" encoding of the log file. Default: "".

loglevel: Object of class "integer" controlling the amount of details to log: If set to 0, nothing will be written to the logfile. If set to > 0, all warnings are logged; if set do > 1, also messages are logged. If loglevel is > 2, the used function call will be printed. Default: 0.

verblevel: Object of class "integer" controlling the amount of details to log: If set to 0, nothing will be written to the standard output connection. If set to > 0, all warnings are logged; if set do > 1, also messages are logged. Default: 0.

lastStep: Object of class "list" which is a stack, containing character strings describing performed steps. See also sybilStack.

lstname: Object of class "list" giving the name of the stack in lastStep.

didFoot: Object of class "logical" which is FALSE, if the footer of the log file is not yet printed, otherwise TRUE. This is useful if the function which is logged, stops unexpected.

Methods

didFoot signature(object = "sybilLog"): gets the didFoot slot.

didFoot<- signature(object = "sybilLog"): sets the didFoot slot.

fenc signature(object = "sybilLog"): gets the fenc slot.

fenc<- signature(object = "sybilLog"): sets the fenc slot.

fh signature(object = "sybilLog"): gets the fh slot.

fh<- signature(object = "sybilLog"): sets the fh slot.

fname signature(object = "sybilLog"): gets the fname slot.

fname<- signature(object = "sybilLog"): sets the fname slot.

fpath signature(object = "sybilLog"): gets the fpath slot.

`fpath<- signature(object = "sybilLog")`: sets the `fpath` slot.

`loglevel signature(object = "sybilLog")`: gets the `loglevel` slot.

`loglevel<- signature(object = "sybilLog")`: sets the `loglevel` slot.

`lstname signature(object = "sybilLog")`: gets the `lstname` slot.

`verblevel signature(object = "sybilLog")`: gets the `verblevel` slot.

`verblevel<- signature(object = "sybilLog")`: sets the `verblevel` slot.

`logCall signature(object = "sybilLog")` (`nog`): writes all arguments and values of the function call to be logged to the log file. Nothing is printed to the standard output; `verblevel` has no meaning here; `verblevel` must be `> 2`.

`nog`	number of generations to go back

`logClose<- signature(object = "sybilLog")`: close the connection in slot `fh` and set it to `NA`. If slot `didFoot` is not `TRUE`, it prints a log comment to the connection in `fh` mentioning, that the logging ended unexpected.

`logComment signature(object = "sybilLog")` (`cmt, commentChar`): add a comment to the log file if `loglevel` is `> 2` and to `stdout` if `verblevel` is `> 2`.

`cmt`	the comment text
`cmtChar`	a string to prefix `cmt`, default: `#`

`logError signature(object = "sybilLog")` (`msg, num`): add an error message to the log file. Returns an object of class `sybilError`.

`msg`	the error message
`num`	an error number

`logFH signature(object = "sybilLog")`: Returns `TRUE`, if slot `fh` is of class `file`, otherwise `FALSE`.

`logFoot<- signature(object = "sybilLog")`: Print a head for your log file.

`logHead signature(object = "sybilLog")`: Print a foot for your log file.

`logMessage signature(object = "sybilLog")`: add a message to the log file if `loglevel` is `> 1`.

`...`	strings pasted to the log file

`logOptimization signature(object = "sybilLog")`: (`ok, stat, obj, del, i`): add a row containing results of an optimization to the log file if `loglevel` is `> 2` and to `stdout` if `verblevel` is `> 2`.

`opt no.`

ret	
stat	
obj value	(numeric) val
dir	if not given, it is a global value of the algorithm (here empty), otherwise the c
obj c	if not given, it is a globel value of the model (here empty), otherwise the current setting of the objective coefficie
flux no.	fluxes (variables) wh

`logOptimizationTH signature(object = "sybilLog")`: add a row containing a table header for results of an optimization to the log file if `loglevel` is `> 2` and to `stdout` if `verblevel` is `> 2`. This should be used prior `logOptimization`.

`logStep<- signature(object = "sybilLog")`: (`value`): add a status message to the log file if `loglevel` is `> 1`, like "performing step x".

`value`	strings giving the status

If `is.na(value)` evaluates to `TRUE`, the current process is assumed to have finished as expected. If `verblevel` is `> 1`, "`OK`" will be printed on the command line end if `loglevel` is `> 1`, "`# done step x`" will be printed to the log file.

`logWarning signature(object = "sybilLog")`: (`...`): add a warning to the log file if `loglevel` is `> 0`.

`...`	strings pastes to the log file

Author(s)

Gabriel Gelius-Dietrich

Examples

```
showClass("sybilLog")
```

---

sybilStack *A Data Type Providing Stack (LIFO) And Queue (FIFO) Functionality*

Description

These functions implement simple stack or queue functionality.

Usage

```
stinit(stname)
stclear(stname)
stpush(stname, value)
```

```
stpop(stname)
stunshift(stname, value)
stshift(stname)
stseek(stname)
stfirst(stname)
stlist(stname)
stlength(stname)
stexists(stname)
```

Arguments

stname	A single character string, giving the name of the stack or queue.
value	Value to add to the stack or queue.

Details

The funtion stinit creates an empty stack named stname.

The funtion stclear removes the stack named stname.

The funtion stpush appends element value at the end of the stack named stname.

The funtion stpop removes the last element of the stack named stname and returns it invisible.

The funtion stunshift appends element value at the beginning of the stack stname.

The funtion stshift removes the first element of the stack named stname and returns it invisible.

The funtion stseek returns the last element of the stack named stname but does not remove it.

The funtion stfirst returns the first element of the stack named stname but does not remove it.

The funtion stlist returns the stack named stname as list.

The funtion stlength returns the number of elements stored in the stack named stname.

The funtion stexists returns TRUE if a stack named stname exists, otherwise FALSE.

Value

The functions stpop and stshift return the last/first element of the stack invisibly. The functions stseek and stfirst just return the last/first element.

Author(s)

Gabriel Gelius-Dietrich

Maintainer: Gabriel Gelius-Dietrich <geliudie@uni-duesseldorf.de>

Examples

```
## initialize empty stack named test
stinit("test")

## add a few elemets
stpush("test", 9)
stpush("test", 3)
```

```
stpush("test", 7)

## get last element
stpop("test")

## remove stack
stclear("test")
```

SYBIL_SETTINGS *Set and Get sybil Parameters*

Description

Manage a set of default parameter settings for sybil.

Usage

```
SYBIL_SETTINGS(parm, value, ...)
```

Arguments

parm	A character string giving the name of the parameter to set.
value	The corresponding value.
...	Further arguments passed to checkDefaultMethod. Only used if parameters "SOLVER" or "METHOD" are set.

Details

Typical usages are

```
SYBIL_SETTINGS(parm, value)
SYBIL_SETTINGS(parm)
SYBIL_SETTINGS()
```

Possible parameters are:

"SOLVER" The default solver for lp problems. Possible values are depend on your installed API package.

glpkAPI: "glpkAPI",
cplexAPI: "cplexAPI",
clpAPI: "clpAPI",
lpSolveAPI: "lpSolveAPI".

Default: "glpkAPI".

"METHOD" The default method to solve lp problems. Possible values are

glpkAPI: "simplex", "interior", "exact" or mip.

cplexAPI: "lpopt", "primopt" "dualopt", "baropt", "hybbaropt", "hybnetopt", "siftopt", mipopt or qpopt.

clpAPI: "general_solve", "inidual" "iniprimal", "inibarrier", "inibarriernoc", "idiot", "dual" or "primal".

lpSolveAPI: "lp_solve".

Default: "simplex".
If the parameter "SOLVER" is changed, the corrsponding default "METHOD" is the first one mentioned, e.g. for "cplexAPI", it will be "lpopt". This change is done automatically when changing the solver. It is not possible, to set a not existing "METHOD" for a particular "SOLVER", the corresponding default value will be used in such a case.

"TOLERANCE" Tolerance value.
Default: 1E-6.

"MAXIMUM" Absolute maximum value.
Default: 1000.

"ALGORITHM" Algorithm to use in order to analyze metabolic networks. Possible values are:

"fba" flux-balance analysis,

"fv" flux-variance analysis,

"mtf" minimize total flux,

"moma" minimization of metabolic adjustment (MOMA),

"lmoma" linear version of MOMA,

"room" regulatory on/off minimization (ROOM).

Default: "fba".

"OPT_DIRECTION" Direction of optimization. Can be "max" or "min".
Default: "max".

"USE_NAMES" A logical value indicating if reaction id's and metabolite id's (or other names) should be used as names for variables and constraints in objects of class sysBiolAlg.
Default: FALSE.

"PATH_TO_MODEL" Path to a directory to read or write files.
Default: ".".

"SOLVER_CTRL_PARM" A data.frame giving parameters to the optimizer software (e.g. GLPK).
Default: as.data.frame(NA).

Value

If successful, a set of parameters to sybil will be returned.

Author(s)

Gabriel Gelius-Dietrich

Maintainer: Gabriel Gelius-Dietrich <geliudie@uni-duesseldorf.de>

See Also

checkDefaultMethod

Examples

```
  ## show all current parameters
  SYBIL_SETTINGS()

  ## show current setting for "SOLVER"
  SYBIL_SETTINGS("SOLVER")

  ## change current solver to glpkAPI
  SYBIL_SETTINGS("SOLVER", "glpkAPI")
## Not run:
  ## this needs cplexAPI installed
  ## change current solver to cplexAPI
  SYBIL_SETTINGS("SOLVER", "cplexAPI")

## End(Not run)
```

---

sysBiolAlg *General Constructor Function For Objects of Class* sysBiolAlg

---

Description

This function serves as a user constructor function for objects of class sysBiolAlg.

Usage

```
sysBiolAlg(model,
           algorithm = SYBIL_SETTINGS("ALGORITHM"),
           prefix = "sysBiolAlg", sep = "_",
           ...)
```

Arguments

model	An object of class modelorg.
algorithm	A single character string giving the name of the algorithm to use. See parameter "ALGORITHM" in SYBIL_SETTINGS for possible values. Default: SYBIL_SETTINGS("ALGORITHM").
prefix	A single character string containing a prefix for the new class name. Default: "sysBiolAlg".
sep	A single character string containing a separator for prefix and algorithm. Default: "_".
...	Further arguments passed to the initialize method depending on the desired algorithm (see Details below).

Details

If argument algorithm is set to "foo" and prefix is set to "sysBiolAlg" (default), sysBiolAlg will try to build an instance of class sysBiolAlg_foo. If no such class definition exists, an error will be returned. For the name of the class, the values of arguments prefix and algorithm are stick together separated by the value of argument sep: prefix_algorithm.

Additional arguments required by the initialize method are for example solver, method and solverParm.

Value

An instance of a subclass of class sysBiolAlg.

Author(s)

Gabriel Gelius-Dietrich

See Also

Class sysBiolAlg

Examples

```
## Not run:
## The examples here require the package glpkAPI to be
## installed. If that package is not available, you have to set
## the argument 'solver' (the default is: solver = SYBIL_SETTINGS("SOLVER")).

data(Ec_core)

## algorithm: fba (flux balance analysis)
fb <- sysBiolAlg(Ec_core, algorithm = "fba")

## algorithm: lmoma (linearized version of MOMA)
fb <- sysBiolAlg(Ec_core, algorithm = "lmoma")

## End(Not run)
```

---

sysBiolAlg-class *Class* "sysBiolAlg"

Description

The class sysBiolAlg holds an object of class optObj which is generated concerning a particular algorithm, e.g. FBA or ROOM. This class is extended by other classes and will not be used as is. The representation of class sysBiolAlg is used as superclass.

Details

The `initialize` method has the following arguments:

solver Single character string giving the solver package to use. See `SYBIL_SETTINGS` for possible values.
Default: `SYBIL_SETTINGS("SOLVER")`.

method Single character string giving the method the desired solver has to use. `SYBIL_SETTINGS` for possible values.
Default: `SYBIL_SETTINGS("METHOD")`.

solverParm A named data frame or list containing parameters for the specified solver. Parameters can be set as data frame or list: `solverParm = list(parm1 = val1, parm2 = val2)` with `parm1` and `parm2` being the names of two different parameters and `val1` and `val2` the corresponding values. For possible parameters and values see the documentation of the used solver package (e.g. **glpkAPI**).
Default: `SYBIL_SETTINGS("SOLVER_CTRL_PARM")`.

termOut A single boolean, numeric or character value, controling the amount of terminal output of the solver software. See also `initProb` (argument `to`) for more details.
Default: `NULL`.

sbalg Single character string containing the name of the algorithm to use.

pType Single character string containing the type of the problem object. Can be `"lp"`: linear program, `mip`: mixed integer program or `"qp"`: quadratic program.
Default: `"lp"`.

scaling Scaling options used to scale the constraint matrix. If set to `NULL`, no scaling will be performed (see `scaleProb`).
Default: `NULL`.

fi Pointers to columns (variables) representing a flux (reaction) in the original network. The variable `fldind[i]` in the problem object represents reaction `i` in the original network.

nCols Number of columns (variables) of the problem object.

nRows Number of rows (constraints) of the problem object.

mat An object of class `Matrix`. The constraint matrix of the problem object. The number of columns in `mat` must be `nCols` and the number of rows in `mat` must be `nRows`.

ub A numeric vector of length `nCols` giving the upper bounds of the variables of the problem object.

lb A numeric vector of length `nCols` giving the lower bounds of the variables of the problem object.

obj A numeric vector of length `nCols` giving the objective coefficients of the variables of the problem object.

rlb A numeric vector of length `nRows` giving the right hand side of the problem object. If argument `rub` is not `NULL`, `rlb` contains the lower bounds of the constraints of the problem object.

rtype A character vector of length `nRows` giving the constraint type. See `loadLPprob` for details.

lpdir Single character string containing the direction of optimization. Can be set to `"min"` or `"max"`.
Default: `"max"`.

rub A numeric vector of length nRows giving the right hand side of the problem object. If not NULL, it contains the upper bounds of the constraints of the problem object.
Default: NULL.

ctype A character vector of length nCols giving the variable type. If set to NULL, no specific variable type is set, which usually means, all variables are treated as continuous variables. See loadLPprob for details.
Default: NULL.

cnames A character vector of length nCols giving the variable names. If set to NULL, no specific variable names are set.
Default: NULL.

rnames A character vector of length nRows giving the constraint names. If set to NULL, no specific constraint names are set.
Default: NULL.

pname A single character string containing a name for the problem object.
Default: NULL.

retAlgPar A single boolean flag, if algorithm specific parameters should be saved in the object extending class sysBiolAlg.
Default: TRUE.

algPar A named list containing algorithm specific parameters.
Default: NULL.

Objects from the Class

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

Slots

problem**:** Object of class "optObj" containing the problem object.

algorithm**:** Object of class "character" containing the name of the algorithm.

nr**:** Object of class "integer" containing the number of rows of the problem object.

nc**:** Object of class "integer" containing the number of columns of the problem object

fldind**:** Object of class "integer" pointers to columns (variables) representing a flux (reaction) in the original network. The variable fldind[i] in the problem object represents reaction i in the original network.

alg_par**:** Object of class "list" containing a named list of algorithm specific parameters.

Methods

algorithm signature(object = "sysBiolAlg"): gets the algorithm slot.

algorithm<- signature(object = "sysBiolAlg"): sets the algorithm slot.

alg_par signature(object = "sysBiolAlg"): gets the alg_par slot.

alg_par<- signature(object = "sysBiolAlg"): sets the alg_par slot.

fldind signature(object = "sysBiolAlg"): gets the fldind slot.

fldind<- signature(object = "sysBiolAlg"): sets the fldind slot.

nc `signature(object = "sysBiolAlg")`: gets the nc slot.

nc<- `signature(object = "sysBiolAlg")`: sets the nc slot.

nr `signature(object = "sysBiolAlg")`: gets the nr slot.

nr<- `signature(object = "sysBiolAlg")`: sets the nr slot.

optimizeProb `signature(object = "sysBiolAlg")`: runs optimization on the given problem object (see optimizeProb for details).

problem `signature(object = "sysBiolAlg")`: gets the problem slot.

initialize `signature(object = "sysBiolAlg")`: default constructor method for objects inheriting from class sysBiolAlg. It gets all data structures necessary to built a problem object (object of class optObj) representing a particular algorithm. This method can be used in constructor methods for subclasses of sysBiolAlg via callNextMethod. In this case, the constructor has to generate all the data structures, pass them to callNextMethod and let the constructor of the superclass do all the work in generating the problem object and interacting with the solver software. See also the Details section.

Author(s)

Gabriel Gelius-Dietrich

See Also

The general constructor function sysBiolAlg, and classes sysBiolAlg_fba, sysBiolAlg_fv, sysBiolAlg_mtf, sysBiolAlg_lmoma, sysBiolAlg_moma and sysBiolAlg_room.

Examples

```
showClass("sysBiolAlg")
```

---

sysBiolAlg_fba-class *Class* "sysBiolAlg_fba"

Description

The class sysBiolAlg_fba holds an object of class optObj which is generated to meet the requirements of the FBA algorithm.

Details

The initialize method has the following arguments:

model An object of class modelorg.

lpdir Single character string containing the direction of optimization. Can be set to "min" or "max".
Default: "max".

useNames A single boolean value. If set to `TRUE`, variables and constraints will be named according to `cnames` and `rnames`. If set to `NULL`, no specific variable or constraint names are set.
Default: `SYBIL_SETTINGS("USE_NAMES")`.

cnames A character vector giving the variable names. If set to `NULL`, the reaction id's of `model` are used.
Default: `NULL`.

rnames A character vector giving the constraint names. If set to `NULL`, the metabolite id's of `model` are used.
Default: `NULL`.

pname A single character string containing a name for the problem object.
Default: `NULL`.

scaling Scaling options used to scale the constraint matrix. If set to `NULL`, no scaling will be performed (see `scaleProb`).
Default: `NULL`.

writeProbToFileName A single character string containing a file name to which the problem object will be written in LP file format.
Default: `NULL`.

... Further arguments passed to the initialize method of `sysBiolAlg`. They are `solver`, `method` and `solverParm`.

The problem object is built to be capable to perform flux balance analysis (FBA) with a given model, which is basically the solution of a linear programming problem

$$\begin{aligned} \max \quad & \boldsymbol{c}^{\mathrm{T}}\boldsymbol{v} \\ \text{s.t.} \quad & \boldsymbol{S}\boldsymbol{v} = 0 \\ & \alpha_i \leq v_i \leq \beta_i \qquad \forall i \in \{1, \ldots, n\} \end{aligned}$$

with $\boldsymbol{S}$ being the stoichiometric matrix, α_i and β_i being the lower and upper bounds for flux (variable) i respectively. The total number of variables of the optimization problem is denoted by n. The solution of the optimization is a flux distribution maximizing the objective function $\boldsymbol{c}^{\mathrm{T}}\boldsymbol{v}$ under the a given environment and the assumption of steady state. The optimization can be executed by using `optimizeProb`.

Objects from the Class

Objects can be created by calls of the form

`sysBiolAlg(model, algorithm = "fba", ...)`.

Arguments to `...` which are passed to method `initialize` of class `sysBiolAlg_fba` are described in the Details section.

Slots

`problem`**:** Object of class `"optObj"` containing the problem object.

`algorithm`**:** Object of class `"character"` containing the name of the algorithm.

`nr`**:** Object of class `"integer"` containing the number of rows of the problem object.

`nc`: Object of class `"integer"` containing the number of columns of the problem object

`fldind`: Object of class `"integer"` pointers to columns (variables) representing a flux (reaction) in the original network. The variable `fldind[i]` in the problem object represents reaction `i` in the original network.

`alg_par`: Object of class `"list"` containing a named list containing algorithm specific parameters.

Extends

Class `"sysBiolAlg"`, directly.

Methods

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

Author(s)

Gabriel Gelius-Dietrich

References

Edwards, J. S., Covert, M and Palsson, B. Ø. (2002) Metabolic modelling of microbes: the flux-balance approach. *Environ Microbiol* **4**, 133–140.

Edwards, J. S., Ibarra, R. U. and Palsson, B. Ø. (2001) In silico predictions of *Escherichia coli* metabolic capabilities are consistent with experimental data. *Nat Biotechnol* **19**, 125–130.

See Also

Constructor function `sysBiolAlg` and superclass `sysBiolAlg`.

Examples

```
showClass("sysBiolAlg_fba")
```

---

sysBiolAlg_fv-class *Class* "sysBiolAlg_fv"

Description

The class `sysBiolAlg_fv` holds an object of class `optObj` which is generated to meet the requirements of the flux variance algorithm.

Details

The initialize method has the following arguments:

model An object of class modelorg.

percentage Consider solutions with x percent of the optimal solution.
Default: 100.

Zopt A single numeric value giving the optimal value to be fixed during all other optimizations (see argument fixObjVal). If Zopt is set to NULL and model has an objective function, a default value is computed based on FBA. If given, arguments solver, method and solverParm are used during FBA.
Default: NULL.

fixObjVal A single Boolean value. If set to TRUE and if the model contains an objective function, an optimal value of this objective function will be fixed during all other optimizations. The optimal value can be controlled by argument Zopt.
Default: TRUE.

tol Single numeric value giving the tolerance value.
Default: SYBIL_SETTINGS("TOLERANCE").

lpdir Single character string containing the direction of optimization. Can be set to "min" or "max".
Default: SYBIL_SETTINGS("OPT_DIRECTION").

useNames A single boolean value. If set to TRUE, variables and constraints will be named according to cnames and rnames. If set to NULL, no specific variable or constraint names are set.
Default: SYBIL_SETTINGS("USE_NAMES").

cnames A character vector giving the variable names. If set to NULL, the reaction id's of model are used.
Default: NULL.

rnames A character vector giving the constraint names. If set to NULL, the metabolite id's of model are used. If an objective value has to be fixed (see argument fixObjVal), the corresponding constrained is named "Z".
Default: NULL.

pname A single character string containing a name for the problem object.
Default: NULL.

scaling Scaling options used to scale the constraint matrix. If set to NULL, no scaling will be performed (see scaleProb).
Default: NULL.

writeProbToFileName A single character string containing a file name to which the problem object will be written in LP file format.
Default: NULL.

... Further arguments passed to the initialize method of sysBiolAlg. They are solver, method and solverParm.

The problem object is built to be capable to perform the flux variance algorithm with a given model, which is basically the solution of a linear program

$$\begin{aligned} \max \text{ or } \min \quad & v_i \\ \text{s.t.} \quad & Z = Z_{\text{opt}} \\ & \boldsymbol{S}\boldsymbol{v} = 0 \\ & \alpha_i \leq v_i \leq \beta_i \qquad \forall i \in \{1, \ldots, n\} \end{aligned}$$

with $\boldsymbol{S}$ being the stoichiometric matrix, α_i and β_i being the lower and upper bounds for flux (variable) i. The total number of variables of the optimization problem is denoted by n. The optimization can be executed by using `optimizeProb`.

Objects from the Class

Objects can be created by calls of the form

`sysBiolAlg(model, algorithm = "fv", ...)`.

Arguments to `...` which are passed to method `initialize` of class `sysBiolAlg_fv` are described in the Details section.

Slots

`problem`: Object of class `"optObj"` containing the problem object.

`algorithm`: Object of class `"character"` containing the name of the algorithm.

`nr`: Object of class `"integer"` containing the number of rows of the problem object.

`nc`: Object of class `"integer"` containing the number of columns of the problem object

`fldind`: Object of class `"integer"` pointers to columns (variables) representing a flux (reaction) in the original network. The variable `fldind[i]` in the problem object represents reaction `i` in the original network.

`alg_par`: Object of class `"list"` containing a named list containing algorithm specific parameters.

Extends

Class `"sysBiolAlg"`, directly.

Methods

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

Author(s)

Gabriel Gelius-Dietrich

References

Becker, S. A., Feist, A. M., Mo, M. L., Hannum, G., Palsson, B. Ø. and Herrgard, M. J. (2007) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. *Nat Protoc* **2**, 727–738.

Schellenberger, J., Que, R., Fleming, R. M. T., Thiele, I., Orth, J. D., Feist, A. M., Zielinski, D. C., Bordbar, A., Lewis, N. E., Rahmanian, S., Kang, J., Hyduke, D. R. and Palsson, B. Ø. (2011) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. *Nat Protoc* **6**, 1290–1307.

Bernhard Ø. Palsson (2006). *Systems Biology: Properties of Reconstructed Networks*. Cambridge University Press.

See Also

Constructor function `sysBiolAlg` and superclass `sysBiolAlg`.

Examples

```
showClass("sysBiolAlg_fv")
```

---

sysBiolAlg_lmoma-class

Class "sysBiolAlg_lmoma"

Description

The class `sysBiolAlg_lmoma` holds an object of class `optObj` which is generated to meet the requirements of a lineraized versoin of the MOMA algorithm.

Details

The `initialize` method has the following arguments:

model An object of class `modelorg`.

wtflux A numeric vector holding an optimal wild type flux distribution for the given model. If missing, a default value is computed based on FBA. If given, arguments `solver` and `method` are used, but `solverParm` is not.

COBRAflag Boolean, prepare problem object in order to perform minimization of metabolic adjustment as in COBRA Toolbox.
Default: `FALSE`.

wtobj Only used if argument `COBRAflag` is set to `TRUE`: A single numeric value giving the optimized value of the objective function of the wild type problem. If missing, a default value is computed based on FBA. If given, arguments `solver` and `method` are used, but `solverParm` is not.

wtobjLB Only used if argument `COBRAflag` is set to `TRUE`: Boolean. If set to `TRUE`, the value of argument `wtobj` is treated as lower bound. If set to `FALSE`, `wtobj` serves as an upper bound.
Default: `TRUE`.

obj_coefD A numeric vector of length two times the number of reactions in the model containing the non-zero part of the objective function. If set to NULL, the vector is filled with ones.
Default: NULL.

useNames A single boolean value. If set to TRUE, variables and constraints will be named according to cnames and rnames. If set to NULL, no specific variable or constraint names are set.
Default: SYBIL_SETTINGS("USE_NAMES").

cnames A character vector giving the variable names. If set to NULL, the reaction id's of model are used.
Default: NULL.

rnames A character vector giving the constraint names. If set to NULL, the metabolite id's of model are used.
Default: NULL.

pname A single character string containing a name for the problem object.
Default: NULL.

scaling Scaling options used to scale the constraint matrix. If set to NULL, no scaling will be performed (see scaleProb).
Default: NULL.

writeProbToFileName A single character string containing a file name to which the problem object will be written in LP file format.
Default: NULL.

... Further arguments passed to the initialize method of sysBiolAlg. They are solver, method and solverParm.

The problem object is built to be capable to perform a linearized version of the MOMA algorithm with a given model, which is basically the solution of a linear programming problem

$$
\begin{aligned}
\min \quad & \sum_{i,j=1}^{n} \left| v_{j,\mathrm{del}} - v_{i,\mathrm{wt}} \right| \\
\text{s. t.} \quad & \boldsymbol{S}\boldsymbol{v}_{\mathrm{del}} = 0 \\
& v_i = v_{i,\mathrm{wt}} \qquad \forall i \in \{1, \ldots, n\} \\
& \alpha_j \leq v_{j,\mathrm{del}} \leq \beta_j \qquad \forall j \in \{1, \ldots, n\}
\end{aligned}
$$

Here, $\boldsymbol{v}_{\mathrm{wt}}$ is the optimal wild type flux distribution. This can be set via the argument wtflux. If wtflux is NULL (the default), the wild type flux distribution will be calculated by a standard FBA.

If argument COBRAflag is set to TRUE, the linear programm is formulated differently. Wild type and knock-out strain will be computed simultaneously.

$$
\begin{aligned}
\min \quad & \sum_{i,j=1}^{n} \left| v_{j,\mathrm{del}} - v_{i,\mathrm{wt}} \right| \\
\text{s.t.} \quad & \boldsymbol{S}\boldsymbol{v}_{\mathrm{wt}} = 0 \\
& \alpha_i \leq v_{i,\mathrm{wt}} \leq \beta_i \qquad \forall i \in \{1, \ldots, n\} \\
& \boldsymbol{S}\boldsymbol{v}_{\mathrm{del}} = 0 \\
& \alpha_j \leq v_{j,\mathrm{del}} \leq \beta_j \qquad \forall j \in \{1, \ldots, n\} \\
& \mu_{\mathrm{wt}} = \boldsymbol{c}^{\mathrm{T}} \boldsymbol{v}_{\mathrm{wt}}
\end{aligned}
$$

with $\boldsymbol{S}$ being the stoichiometric matrix, α_i and β_i being the lower and upper bounds for flux (variable) i (j for the deletion strain). The total number of variables of the optimization problem is denoted by n. Here, μ_{wt} is the optimal wild type growth rate. This can be set via the argument wtobj. If wtobj is NULL (the default), the wild type growth rate will be calculated by a standard FBA. The optimization can be executed by using optimizeProb.

Objects from the Class

Objects can be created by calls of the form

sysBiolAlg(model, algorithm = "lmoma", ...).

Arguments to ... which are passed to method initialize of class sysBiolAlg_lmoma are described in the Details section.

Slots

problem: Object of class "optObj" containing the problem object.

algorithm: Object of class "character" containing the name of the algorithm.

nr: Object of class "integer" containing the number of rows of the problem object.

nc: Object of class "integer" containing the number of columns of the problem object

fldind: Object of class "integer" pointers to columns (variables) representing a flux (reaction) in the original network. The variable fldind[i] in the problem object represents reaction i in the original network.

alg_par: Object of class "list" containing a named list containing algorithm specific parameters.

Extends

Class "sysBiolAlg", directly.

Methods

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

Author(s)

Gabriel Gelius-Dietrich

References

Becker, S. A., Feist, A. M., Mo, M. L., Hannum, G., Palsson, B. Ø. and Herrgard, M. J. (2007) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. *Nat Protoc* **2**, 727–738.

Edwards, J. S., Covert, M and Palsson, B. Ø. (2002) Metabolic modelling of microbes: the flux-balance approach. *Environ Microbiol* **4**, 133–140.

Edwards, J. S., Ibarra, R. U. and Palsson, B. Ø. (2001) In silico predictions of *Escherichia coli* metabolic capabilities are consistent with experimental data. *Nat Biotechnol* **19**, 125–130.

Schellenberger, J., Que, R., Fleming, R. M. T., Thiele, I., Orth, J. D., Feist, A. M., Zielinski, D. C., Bordbar, A., Lewis, N. E., Rahmanian, S., Kang, J., Hyduke, D. R. and Palsson, B. Ø. (2011) Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. *Nat Protoc* **6**, 1290–1307.

Segrè, D., Vitkup, D. and Church, G. M. (2002) Analysis or optimality in natural and pertubed metabolic networks. *PNAS* **99**, 15112–15117.

See Also

Constructor function `sysBiolAlg` and superclass `sysBiolAlg`.

Examples

```
showClass("sysBiolAlg_lmoma")
```

---

sysBiolAlg_moma-class *Class* "sysBiolAlg_moma"

Description

The class `sysBiolAlg_moma` holds an object of class `optObj` which is generated to meet the requirements of the MOMA algorithm.

Details

The `initialize` method has the following arguments:

model An object of class `modelorg`.

wtflux A numeric vector holding an optimal wild type flux distribution for the given model. If set to `NULL`, a default value is computed based on flux-balance analysis. If given, arguments `solver` and `method` are used, but `solverParm` is not. Default: `NULL`.

Qmat A numeric vector or matrix (of class `Matrix`) holding the quadratic part of the objective function. If set to `NULL`, a quadratic unity matrix with number of columns and rows equal to the number of reactions given in the model is used. Default: `NULL`.

scaleDist A numeric vector containing scaling factors for each reaction in the objective function. If `scaleDist[j]` is set to `0`, reaction `j` will be ignored. The quadratic and the linear part of the objective function are multiplied by this factor. If set to `NULL`, the reactions are not scaled.
Default: `NULL`.

useNames A single boolean value. If set to `TRUE`, variables and constraints will be named according to `cnames` and `rnames`. If set to `NULL`, no specific variable or constraint names are set.
Default: `SYBIL_SETTINGS("USE_NAMES")`.

cnames A character vector giving the variable names. If set to `NULL`, the reaction id's of `model` are used.
Default: `NULL`.

rnames A character vector giving the constraint names. If set to `NULL`, the metabolite id's of `model` are used.
Default: `NULL`.

pname A single character string containing a name for the problem object.
Default: `NULL`.

scaling Scaling options used to scale the constraint matrix. If set to `NULL`, no scaling will be performed (see `scaleProb`).
Default: `NULL`.

writeProbToFileName A single character string containing a file name to which the problem object will be written in LP file format.
Default: `NULL`.

... Further arguments passed to the initialize method of `sysBiolAlg`. They are `solver`, `method` and `solverParm`.

The problem object is built to be capable to perform the MOMA algorithm with a given model, which is basically the solution of a quadratic programming problem

$$\begin{aligned} \min \quad & \sum_{j=1}^{n} \left((v_{j,\mathrm{del}} - v_{j,\mathrm{wt}}) \cdot sd_j \right)^2 \\ \text{s.t.} \quad & \boldsymbol{S}\boldsymbol{v} = 0 \\ & \alpha_j \leq v_j \leq \beta_j \qquad \forall j \in \{1, \ldots, n\} \end{aligned}$$

with $\boldsymbol{S}$ being the stoichiometric matrix, α_j and β_j being the lower and upper bounds for flux (variable) j and sd_j being the scaling factor for reaction j (default: $sd_j = 1, \forall j$). The total number of variables of the optimization problem is denoted by n. Here, $\boldsymbol{v}_{\mathrm{wt}}$ is the optimal wild type flux distribution. This can be set via the argument `wtflux`. If `wtflux` is `NULL` (the default), the wild type flux distribution will be calculated by a standard FBA. The optimization can be executed by using `optimizeProb`.

Objects from the Class

Objects can be created by calls of the form

`sysBiolAlg(model, algorithm = "moma", ...)`.

Arguments to `...` which are passed to method `initialize` of class `sysBiolAlg_moma` are described in the Details section.

Slots

`problem`: Object of class `"optObj"` containing the problem object.

`algorithm`: Object of class `"character"` containing the name of the algorithm.

`nr`: Object of class `"integer"` containing the number of rows of the problem object.

`nc`: Object of class `"integer"` containing the number of columns of the problem object

`fldind`: Object of class `"integer"` pointers to columns (variables) representing a flux (reaction) in the original network. The variable `fldind[i]` in the problem object represents reaction `i` in the original network.

`alg_par`: Object of class `"list"` containing a named list containing algorithm specific parameters.

Extends

Class `"sysBiolAlg"`, directly.

Methods

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

Author(s)

Gabriel Gelius-Dietrich

References

Segrè, D., Vitkup, D. and Church, G. M. (2002) Analysis or optimality in natural and pertubed metabolic networks. *PNAS* **99**, 15112–15117.

See Also

Constructor function `sysBiolAlg` and superclass `sysBiolAlg`.

Examples

```
showClass("sysBiolAlg_moma")
```

---

sysBiolAlg_mtf-class *Class* "sysBiolAlg_mtf"

Description

The class `sysBiolAlg_mtf` holds an object of class `optObj` which is generated to meet the requirements of the minimize total flux algorithm: minimize the absolute sum of all fluxes given a previously calculated objective value.

Details

The initialize method has the following arguments:

model An object of class modelorg.

wtobj A single numeric value giving the optimal value. If missing, a default value is computed based on FBA. If given, arguments solver and method are used, but solverParm is not.
Default: NULL.

react Arguments react, lb and ub are used, if argument wtobj is NULL, meaning: no previous objective value is given. Objective values will be calculated via fba using the parameters given in react, lb and ub.
Default: NULL.

lb See argument react.
Default: NULL.

ub See argument react.
Default: NULL.

costcoeffw A numeric vector containing cost coefficients for all variables (forward direction). If set to NULL, all cost coefficients are set to 1, so that all variables have the same impact on the objective function.
Default: NULL.

costcoefbw A numeric vector containing cost coefficients for all variables (backward direction). If set to NULL, all cost coefficients are set to the values given in costcoeffw.
Default: NULL.

useNames A single boolean value. If set to TRUE, variables and constraints will be named according to cnames and rnames. If set to NULL, no specific variable or constraint names are set.
Default: SYBIL_SETTINGS("USE_NAMES").

cnames A character vector giving the variable names. If set to NULL, the reaction id's of model are used.
Default: NULL.

rnames A character vector giving the constraint names. If set to NULL, the metabolite id's of model are used.
Default: NULL.

pname A single character string containing a name for the problem object.
Default: NULL.

scaling Scaling options used to scale the constraint matrix. If set to NULL, no scaling will be performed (see scaleProb).
Default: NULL.

writeProbToFileName A single character string containing a file name to which the problem object will be written in LP file format.
Default: NULL.

... Further arguments passed to the initialize method of sysBiolAlg. They are solver, method and solverParm.

The problem object is built to be capable to perform minimize total flux with a given model, which is basically the solution of a linear programming problem

$$\begin{aligned} \min \quad & \sum_{i=1}^{n} cost_i |v_i| \\ \text{s.t.} \quad & \boldsymbol{S}\boldsymbol{v} = 0 \\ & \alpha_i \leq v_i \leq \beta_i \qquad \forall i \in \{1, \ldots, n\} \\ & \boldsymbol{c}_{\text{wt}} \geq \boldsymbol{c}^{\text{T}} \boldsymbol{v}_{\text{wt}} \end{aligned}$$

with $\boldsymbol{c}^{\text{T}} \boldsymbol{v}_{\text{wt}}$ being the previously computed optimized value of the objective function (argument `wtobj`). The variable $\boldsymbol{S}$ denotes the stoichiometric matrix, α_i and β_i being the lower and upper bounds for flux (variable) i. The total number of variables of the optimization problem is denoted by n. The optimization can be executed by using `optimizeProb`.

Objects from the Class

Objects can be created by calls of the form

`sysBiolAlg(model, algorithm = "mtf", ...)`.

Arguments to `...` which are passed to method `initialize` of class `sysBiolAlg_mtf` are described in the Details section.

Slots

`maxobj`: Object of class `"numeric"` containing optimized objective values.

`problem`: Object of class `"optObj"` containing the problem object.

`algorithm`: Object of class `"character"` containing the name of the algorithm.

`nr`: Object of class `"integer"` containing the number of rows of the problem object.

`nc`: Object of class `"integer"` containing the number of columns of the problem object

`fldind`: Object of class `"integer"` pointers to columns (variables) representing a flux (reaction) in the original network. The variable `fldind[i]` in the problem object represents reaction `i` in the original network.

`alg_par`: Object of class `"list"` containing a named list containing algorithm specific parameters.

Extends

Class `"sysBiolAlg"`, directly.

Methods

changeMaxObj `signature(object = "sysBiolAlg_mtf")`: change current objective value to the jth value given in slot `maxobj`. Argument `j` must be in `[1:length(maxobj)]`.

Author(s)

Gabriel Gelius-Dietrich

References

Edwards, J. S., Covert, M and Palsson, B. Ø. (2002) Metabolic modelling of microbes: the flux-balance approach. *Environ Microbiol* **4**, 133–140.

Edwards, J. S., Ibarra, R. U. and Palsson, B. Ø. (2001) In silico predictions of *Escherichia coli* metabolic capabilities are consistent with experimental data. *Nat Biotechnol* **19**, 125–130.

See Also

Constructor function `sysBiolAlg` and superclass `sysBiolAlg`.

Examples

```
showClass("sysBiolAlg_mtf")
```

---

sysBiolAlg_room-class *Class* "sysBiolAlg_room"

Description

The class `sysBiolAlg_room` holds an object of class `optObj` which is generated to meet the requirements of the ROOM algorithm.

Details

The `initialize` method has the following arguments:

model An object of class `modelorg`.

wtflux A numeric vector holding an optimal wild type flux distribution for the given model. If missing, a default value is computed based on FBA. If given, arguments `solver` and `method` are used to calculate the dafault, but `solverParm` is not.

delta A single numeric value giving the relative range of tolerance, see Details below.
Default: `0.03`.

epsilon A single numeric value giving the absolute range of tolerance, see Details below.
Default: `0.001`.

LPvariant Boolean. If `TRUE`, the problem object is formulated as linear program. See Details below.
Default: `FALSE`.

useNames A single boolean value. If set to `TRUE`, variables and constraints will be named according to `cnames` and `rnames`. If set to `NULL`, no specific variable or constraint names are set.
Default: `SYBIL_SETTINGS("USE_NAMES")`.

cnames A character vector giving the variable names. If set to `NULL`, the reaction id's of `model` are used.
Default: `NULL`.

rnames A character vector giving the constraint names. If set to NULL, the metabolite id's of model are used.
Default: NULL.

pname A single character string containing a name for the problem object.
Default: NULL.

scaling Scaling options used to scale the constraint matrix. If set to NULL, no scaling will be performed (see scaleProb).
Default: NULL.

writeProbToFileName A single character string containing a file name to which the problem object will be written in LP file format.
Default: NULL.

... Further arguments passed to the initialize method of sysBiolAlg. They are solver, method and solverParm.

The problem object is built to be capable to perform the ROOM algorithm with a given model, which is basically the solution of a mixed integer programming problem

$$
\begin{aligned}
\min \quad & \sum_{i=1}^{n} y_i \\
\text{s.t.} \quad & \boldsymbol{S}\boldsymbol{v} = 0 \\
& \alpha_i \leq v_i \leq \beta_i && \forall i \in \{1, \ldots, n\} \\
& v_i - y(\beta_i - w_i^u) \leq w_i^u \\
& v_i - y(\alpha_i - w_i^l) \geq w_i^l \\
& y_i \in \{0, 1\} \\
& w_i^u = w_i + \delta|w_i| + \epsilon \\
& w_i^l = w_i - \delta|w_i| - \epsilon
\end{aligned}
$$

with $\boldsymbol{S}$ being the stoichiometric matrix, α_i and β_i being the lower and upper bounds for flux (variable) i. The total number of fluxes of the optimization problem is denoted by n. Here, w is the optimal wild type flux distribution. This can be set via the argument wtflux. If wtflux is NULL (the default), the wild type flux distribution will be calculated by a standard FBA. All variables y_i are binary, with $y_i = 1$ for a significant flux change in v_i and $y_i = 0$ otherwise. Thresholds determining the significance of a flux change are given in w^u and w^l, with δ and ϵ specifying absolute and relative ranges in tolerance [Shlomi et al. 2005].

The Boolean argument LPvariant relax the binary contraints to $0 \leq y_i \leq 1$ so that the problem becomes a linear program. The optimization can be executed by using optimizeProb.

Objects from the Class

Objects can be created by calls of the form

sysBiolAlg(model, algorithm = "room", ...).

Arguments to ... which are passed to method initialize of class sysBiolAlg_room are described in the Details section.

Slots

`wu`: Object of class `"numeric"` containing the upper threshold for a significant flux change, see Details below.

`wl`: Object of class `"numeric"` containing the lower threshold for a significant flux change, see Details below.

`fnc`: Object of class `"integer"` containing the number of reactions in the entire metabolic network (argument `model` to the constructor function `sysBiolAlg`).

`fnr`: Object of class `"integer"` containing the number of metabolites in the entire metabolic network (argument `model` to the constructor function `sysBiolAlg`).

`problem`: Object of class `"optObj"` containing the problem object.

`algorithm`: Object of class `"character"` containing the name of the algorithm.

`nr`: Object of class `"integer"` containing the number of rows of the problem object.

`nc`: Object of class `"integer"` containing the number of columns of the problem object

`fldind`: Object of class `"integer"` pointers to columns (variables) representing a flux (reaction) in the original network. The variable `fldind[i]` in the problem object represents reaction `i` in the original network.

`alg_par`: Object of class `"list"` containing a named list containing algorithm specific parameters.

Extends

Class `"sysBiolAlg"`, directly.

Methods

optimizeProb `signature(object = "sysBiolAlg_room")`: runs optimization on the given problem object (see `optimizeProb` for details).

Note

If using **glpkAPI** as MIP solver, consider to set parameter `PRESOLVE` to `GLP_ON`.

Author(s)

Gabriel Gelius-Dietrich

References

Shlomi, T., Berkman, O. and Ruppin, E. (2005) Regulatory on/off minimization of metabolic flux changes after genetic pertubations. *PNAS* **102**, 7695–7700.

See Also

Constructor function `sysBiolAlg` and superclass `sysBiolAlg`.

Examples

```
showClass("sysBiolAlg_room")
```

writeProb-methods *Write Problem Object to File*

Description

Write problem object to file (e.g. in lp format).

Usage

```
## S4 method for signature 'optObj_clpAPI,character'
writeProb(lp, fname, ff = "lp")

## S4 method for signature 'optObj_cplexAPI,character'
writeProb(lp, fname, ff = "lp")

## S4 method for signature 'optObj_glpkAPI,character'
writeProb(lp, fname, ff = "lp", ...)

## S4 method for signature 'optObj_lpSolveAPI,character'
writeProb(lp, fname, ff = "lp", ...)
```

Arguments

lp	An object extending class optObj.
fname	A single character string giving the file name to write to.
ff	A single character string giving the file format to use, see Details. Default: "lp".
...	Further arguments passed to the corresponding API routine.

Details

Argument "ff" is unused with **clpAPI**. Valid values for **cplexAPI** and lpSolveAPI are available in their documentations. For **glpkAPI**, argument "ff" can be "lp" for LP file format, "mps" for MPS file format or "glpk" for GLPK file format.

Methods

signature(lp = "optObj_clpAPI", fname = "character") method to use with package **optObj_clpAPI**. Argument ff is not used here.

signature(lp = "optObj_cplexAPI", fname = "character") method to use with package **optObj_cplexAPI**.

signature(lp = "optObj_glpkAPI", fname = "character") method to use with package **optObj_glpkAPI**.

signature(lp = "optObj_lpSolveAPI", fname = "character") method to use with package **optObj_lpSolveAPI**.

Author(s)

Gabriel Gelius-Dietrich

See Also

Superclass optObj and constructor function optObj.

---

ypd *In Sillico YPD Medium*

Description

Apply in sillico medium to bakers yeast metabolic network model iND750 by Duarte et al. 2004.

Usage

```
ypd(model, def_bnd = SYBIL_SETTINGS("MAXIMUM"), ver = "harrison2007")
```

Arguments

model	An object of class modelorg.
def_bnd	A single numeric value. Absolute value for uppper and lower bounds for reaction bounds. Default: SYBIL_SETTINGS("MAXIMUM").
ver	A single character string giving the version of the YPD medium. Can be set to harrison2007 or bilu2006 (see Details below). Default: harrison2007.

Details

The function ypd identifies exchange reactions via the function findExchReact. The lower bounds of all exchange fluxes is set to zero (not allowing any flux into the network) and the upper bounds are set to the value of def_bnd (default: output is unbounded). The lower bound input of the input fluxes is set like in the table below.

Two different versions of YPD medium are available: Harrison et al. 2007 and Bilu et al. 2006.

Harrison et al 2007:

EX_ala_L(e)	-0.5
EX_arg_L(e)	-0.5
EX_asn_L(e)	-0.5
EX_asp_L(e)	-0.5
EX_chol(e)	-0.5
EX_cys_L(e)	-0.5
EX_dcyt(e)	-0.5
EX_ergst(e)	-0.5
EX_glc(e)	-20

EX_glu_L(e)	-0.5
EX_gly(e)	-0.5
EX_gua(e)	-0.5
EX_h(e)	def_bnd * -1
EX_hdca(e)	-0.5
EX_his_L(e)	-0.5
EX_leu_L(e)	-0.5
EX_lys_L(e)	-0.5
EX_met_L(e)	-0.5
EX_nh4(e)	def_bnd * -1
EX_o2(e)	-2
EX_ocdca(e)	-0.5
EX_pi(e)	def_bnd * -1
EX_pro_L(e)	-0.5
EX_ser_L(e)	-0.5
EX_so4(e)	def_bnd * -1
EX_thr_L(e)	-0.5
EX_thymd(e)	-0.5
EX_trp_L(e)	-0.5
EX_ttdca(e)	-0.5
EX_tyr_L(e)	-0.5
EX_ura(e)	-0.5

Bilu et al 2006:

EX_nh4(e)	def_bnd * -1
EX_pi(e)	def_bnd * -1
EX_so4(e)	def_bnd * -1
EX_glc(e)	-20
EX_o2(e)	-2
EX_ala_L(e)	-0.5
EX_arg_L(e)	-0.5
EX_asn_L(e)	-0.5
EX_asp_L(e)	-0.5
EX_cys_L(e)	-0.5
EX_his_L(e)	-0.5
EX_leu_L(e)	-0.5
EX_lys_L(e)	-0.5
EX_met_L(e)	-0.5
EX_pro_L(e)	-0.5
EX_ser_L(e)	-0.5
EX_thr_L(e)	-0.5
EX_trp_L(e)	-0.5
EX_tyr_L(e)	-0.5
EX_dcyt(e)	-0.5
EX_gly(e)	-0.5
EX_gua(e)	-0.5

EX_thymd(e)	−0.5
EX_h2o(e)	def_bnd * -1
EX_na1(e)	def_bnd * -1
EX_k(e)	def_bnd * -1
EX_co2(e)	def_bnd * -1
EX_ade(e)	−0.5
EX_gln_L(e)	−0.5
EX_ile_L(e)	−0.5
EX_phe_L(e)	−0.5
EX_val_L(e)	−0.5

Value

An instance of class modelorg with input fluxes set corresponding to the desired YPD medium.

Author(s)

Gabriel Gelius-Dietrich

References

Harrison, R., Papp, B., Pal, C., Oliver, S. G. and Delnert, D. (2007) Plasticity of genetic interactions in metabolic networks of yeast. *PNAS* **104**, 2307–2312.

Bilu, Y., Shlomi, T., Barkai, N. and Ruppin, E. (2006) Conservation of expression and sequence of metabolic genes is reflected by activity across metabolic states. *PLoS Comput Biol* **2**, 932–938.

See Also

modelorg, findExchReact and SYBIL_SETTINGS

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