Package 'BiGGR'

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Type Package

Title Creates an interface to BiGG database, provides a framework for simulation and produces flux graphs

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Depends R (>= 2.10.0),LIM,igraph,Rgraphviz,minet,graph,rsbml,limSolve,diagram,hyperdraw

Description This package provides an interface to simulate metabolic reconstruction from the BiGG database(http://bigg.ucsd.edu/).
The package aids in performing flux balance analysis (FBA) on the similar lines of the COBRA toolbox(http://systemsbiology.ucsd.edu/Downloads/Cobra_Toolbox)
but with the added value of vizualizing the results in the form of a metabolic network using the graphviz framework.

License GPL (>= 2)

URL http://www.r-project.org, http://www.bioinformatics.nl

LazyLoad yes

Repository CRAN

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R topics documented:

`addReact2StoM` *adds a user defined reaction to stoichiometric matrix*

Description

Adds a user defined reaction to stoichiometric matrix which is not found in the BiGG Database

Usage

```
addReact2StoM(sm,reactID,react)
```

Arguments

`sm`	is of type incidence matrix representing reconstructions in the database.
`reactID`	is of type character string representing the enzyme which catalyzes the reaction.
`react`	is of type character string representing the actual reaction with co-efficients for e.g. `glucose + ATP -> glucose 6-phosphate + ADP`.

Details

This function should be used only when a reaction is not found in the reconstructions from BiGG

Value

`sm`	returns a matrix of the entire reconstruction for an organizm(s) available from the BiGG Database with user defined reaction(s)

Warning

to be used only when a reaction is not found in the reconstructions

Author(s)

Anand K. Gavai <anand.gavai@bioinformatics.nl>

See Also

getAdjMfromStoM,

Examples

```
data("Glycolysis")
sm<-getSMfromModel(Glycolysis,"R_HEX1")
sm
reactID<-"R_ABC"
react<-"A+B->C+D"
sm<-addReact2StoM(sm,reactID,react)
sm
```

---

attachMetAbbre *Attaches abbreviation prefix "M_" for the metabolite identifiers*

Description

Attaches abbreviation prefix "M_" (Reactions)

Usage

```
attachMetAbbre(Metabolites)
```

Arguments

Metabolites	This file is exported from database of metabolic reconstructions (BiGG) at http://bigg.ucsd.edu/bigg/main.pl

Value

A character vector with reaction names from reaction file Reactions with a prefix "R_" attached

Author(s)

Anand K. Gavai <anand.gavai@bioinformatics.nl>

References

http://bigg.ucsd.edu/

Examples

```
## Not run:
## The function is used to get abbreviation for the
## reaction names from the reactions file
abbre<- attachMetAbbre("/examples/Metabolites.txt")
abbre

## End(Not run)
```

`attachReactAbbre` *Attaches abbreviation prefix "R_" for the reaction identifiers*

Description

Attaches abbreviation prefix "R_" (Reactions)

Usage

```
attachReactAbbre(Reactions)
```

Arguments

`Reactions`	This file is exported from database of metabolic reconstructions (BiGG) at http://bigg.ucsd.edu/bigg/main.pl

Value

A character vector with reaction names from reaction file `Reactions` with a prefix "R_" attached

Author(s)

Anand K. Gavai <anand.gavai@bioinformatics.nl>

References

http://bigg.ucsd.edu/

Examples

```
## Not run:
## The function is used to get abbreviation for the
## reaction names from the reactions file
abbre<- attachReactAbbre("/examples/Metabolites.txt")
abbre

## End(Not run)
```

createBiggModel *createBiggModel*

Description

creates a model file to be run for simulations of metabolic fluxes

Usage

```
createBiggModel(metabolites_file,reactions_file,maximize,
equation_var,equation_value,constraint,externals)
```

Arguments

metabolites_file	is a dataframe of metabolites participating in a reaction. This file is exported from database of metabolic reconstructions (BiGG) at http://bigg.ucsd.edu/bigg/searchMet.pl
reactions_file	is a dataframe of reactions participating in a metabolic pathway. This file can be exported from database of metabolic reconstructions (BiGG) at http://bigg.ucsd.edu/bigg/main.pl
maximize	is a character vector consisting the tag of the reaction(s) to be maximized or minimized
equation_var	is a character vector specifying the name for the reaction to be maximized or minimized
equation_value	is a numeric value for the reactions specified in equation_var
constraint	is a character vector specifying the minimum and maximum values(boundary) under which the solution for the maximize reaction should fall
externals	a character vector of metabolites as provided by the user for speficific pathways for which FBA (flux balance analysis needs to be performed)

Value

A model file with with extension ".lim" is created

Note

none

Author(s)

Anand K. Gavai <anand.gavai@bioinformatics.nl>

References

Soetaert K, van Oevelen D (2009). LIM: Linear Inverse Model examples and solution methods. R package version 1.3

Examples

```
## The function is currently defined as

## Not run:
metabolites_file<-"glycolysis_M.csv" # download from the BiGG database
reactions_file<-"glycolysis_R.csv"   # download from the BiGG database
maximize<-"R_PYK"
equation_var<-"R_HEX1"
equation_value<-1
constraint<-"[0,1000]"
externals<-c("glcD","pyr")
model.lim<-createBiggModel(metabolites_file,reactions_file,maximize,equation_var,equation_value,constraint,ext


## End(Not run)
```

`E.coli_iAF1260` *Ecoli dataset with ORFs and thermodynamic information*

Description

A genome-scale metabolic reconstruction for Escherichia coli K-12 MG1655 that accounts for 1260 ORFs and thermodynamic information

Usage

```
E.coli_iAF1260
```

Format

An sbml object of class rsbml

Source

Molecular Systems Biology, 3:121(2007)

References

Feist, A.M., Henry, C.S., Reed, J.L., Krummenacker, M., Joyce, A.R., Karp, P.D., Broadbelt, L.J., Hatzimanikatis, V., Palsson, B.O., *A genome-scale metabolic reconstruction for Escherichia coli K-12 MG1655 that accounts for 1260 ORFs and thermodynamic information*, olecular Systems Biology, 3:121 (2007)

E.coli_iJR904 *Ecoli genome-scale model*

Description

An expanded genome-scale model of Escherichia coli K-12 (iJR904 GSM/GPR)

Usage

```
E.coli_iJR904
```

Format

An sbml object of class rsbml

Source

Genome Biology, 4(9): R54.1-R54.12 (2003)

References

Reed, J.L., Vo, T.D., Schilling, C.H., and Palsson, B.O., *An expanded genome-scale model of Escherichia coli K-12 (iJR904 GSM/GPR)*, Genome Biology, 4(9): R54.1-R54.12 (2003).

getAdjMfromStoM *getAdjMfromStoM*

Description

constructs an adjacency matrix from a stoichiometric matrix

Usage

```
getAdjMfromStoM(sm, react_name, minimal)
```

Arguments

sm	is a stoichiometric matrix (or incidence matrix) for the entire metabolic reconstruction for a given organism, as provided in the datasets of this package see `getStoichiometricMatrix`
react_name	is a character vector provided by the `reactions` file as exported from (BiGG) at http://bigg.ucsd.edu/bigg/main.pl for a specific pathways of interest.
minimal	logical if set to TRUE would leave out common biproducts of reactions for example: atp,adp,nadh,nadh2 etc. from the visualization

Value

adjM	returns an object of class matrix for the selected reactions

Author(s)

Anand K. Gavai <anand.gavai@bioinformatics.nl>

See Also

getStoichiometricMatrix

Examples

```
## Not run:
data("Glycolysis")
uptake<-"R_HEX1"
sm<-getSMfromModel(Glycolysis,uptake)
sm
react_name<- attachReactAbbre("/examples/Reactions.txt") #attach abbreviations
adjM<- getAdjMfromStoM(sm,react_name,"TRUE")
adjM #adjacency matrix or incidence matrix for the selected pathway

## End(Not run)
```

---

getEdgeWidths *getEdgeWidths*

Description

gets the descritized value for rates (fluxes) of reactioins to be displayed on the graph object

Usage

```
getEdgeWidths(rates, levels)
```

Arguments

rates	is a one dimentional numeric vector with values representing fluxes as computed from the LIM package from the model file
levels	a numeric value representing the levels at which the fluxes need to be descritized

Value

dz_rates	a one dimentional numeric vector of descritized rates for individual reactions

Author(s)

Anand K. Gavai <anand.gavai@bioinformatics.nl>

See Also

getRates,createBiggModel

Examples

```
data("Glycolysis")
levels<-7
rates<-getRates(Glycolysis)
dz_rates<-getEdgeWidths(rates,levels)
dz_rates
```

---

getFluxGraph *Gets graphical representation of a flux distribution*

Description

Displays graphical representation of flux distribution using the Hypergraph package

Usage

```
getFluxGraph(gnel, rates,levels, layout)
```

Arguments

gnel	A graphNEL object
rates	a numeric vector representing descritized rates of fluxes as estimated from the LIM package
levels	A numeric value giving the levels of descritization to be performed
layout	A character striing representing layout from standard Graphviz library for e.g "dot","neato","circo","fdp","sfdp","twopi"

Value

gnel	returns an object of class RagraphBPH with values of fluxes attached to edges, to be used to be displayed by hypergraph

Author(s)

Anand K. Gavai <anand.gavai@bioinformatics.nl>

See Also

getRates,getEdgeWidths,getAdjMfromStoM,getStoichiometricMatrix

Examples

```
## Not run:
data("gnel")
data("Glycolysis")
rates<-getRates(gnel)
levels<-7
layout<-"dot"
ragnel<-getFluxGraph(gnel,rates,levels,layout)
ragnel

## End(Not run)
```

`getRates` *Get Optimized Rates*

Description

getRates takes the model file as the argument and based on the description of the model file generates flux values for "minimum" or "maximum" reaction rates

Usage

```
getRates(modelFile)
```

Arguments

`modelFile`	A model file as generated from the createBiggModel function

Value

The value returned is one dimentional numeric vector of flux rates for each reaction

Author(s)

Anand K. Gavai <anand.gavai@bioinformatics.nl>

See Also

`getEdgeWidths`

Examples

```
data("Glycolysis")
rates<-getRates(Glycolysis)
rates
```

`getSMfromModel` *Get stochiometric matrix from the model file*

Description

`getSMfromModel` takes the model file as the argument and returns the stochiometric matrix from the model file

Usage

```
getSMfromModel(modelFile,uptake)
```

Arguments

`modelFile`	A character string giving the name of model file as generated from the createBiggModel or pruneBiggModel function.
`uptake`	A character string giving the name of the name of the uptake substrate.

Value

The value returned is a two dimentional matrix representing the stochiometric matrix

Author(s)

Anand K. Gavai <anand.gavai@bioinformatics.nl>

See Also

getStoichiometricMatrix

Examples

```
data("Glycolysis")
sm<-getSMfromModel(Glycolysis,"R_HEX1")
sm
```

`getStoichiometricMatrix` *Get entire stoichiometric matrix from the metabolic reconstruction for a specific organism exported in SBML format*

Description

get stoichiometric matrix from the model(sbmlobj), where sbmlobj is of type `SBML`

Usage

```
getStoichiometricMatrix(sbmlobj)
```

Arguments

sbmlobj	is of class SBML.

Value

sm returns a matrix of the entire reconstruction for an organizm(s) available from the BiGG Database

Author(s)

Anand K. Gavai <anand.gavai@bioinformatics.nl>

See Also

getAdjMfromStoM

Examples

```
data(H.sapiens_Recon_1)
sm<-getStoichiometricMatrix(model(H.sapiens_Recon_1))
sm
```

Glycolysis *Metabolic reconstruction of Glycolysis pathway*

Description

Model of Glycolysis pathway

Usage

```
Glycolysis
```

Format

A model file created as an example

References

Gavai et al, *BiGGR: An open source initiative for constraint-based modeling in R using the BiGG database*.

gnel — *Example graphnel object of Glycolysis pathway*

Description

"Glycolysis"

Usage

```
gnel
```

Format

A graphnel object file created as an example

References

Gavai et al, "BiGGR: An open source initiative for constraint-based modeling in R using the BiGG database".

H.pylori_ilT341 — *H.pylori in silico genome-scale characterization of single and double deletion mutants*

Description

An Expanded Metabolic Reconstruction of Helicobacter pylori (iIT341 GSM/GPR): An in silico genome-scale characterization of single and double deletion mutants

Usage

```
H.pylori_ilT341
```

Format

An sbml object of class rsbml

Source

Journal of Bacteriology, 187(16): 5818-5830 (2005)

References

Thiele, I., Vo, T.D., Price, N.D. and Palsson, B., *An Expanded Metabolic Reconstruction of Helicobacter pylori* (iIT341 GSM/GPR): An in silico genome-scale characterization of single and double deletion mutants", Journal of Bacteriology, 187(16): 5818-5830 (2005)

H.sapiens_Recon_1 *Human metabolic reconstruction*

Description

"Global reconstruction of the human metabolic network based on genomic and bibliomic data"

Usage

```
H.sapiens_Recon_1
```

Format

An sbml object of class rsbml

Source

Proc. Natl Acad. Sci. 104(6):1777-82 (2007)

References

Duarte, N.D., Becker, S. A., Jamshidi, N., Thiele, I., Mo, M. L., Vo, T. D., Srivas, R., Palsson, B. O., "Global reconstruction of the human metabolic network based on genomic and bibliomic data", Proc. Nat Acad. Sci. 104(6):1777-82 (2007)

M.barkeri_iAF692 *Metabolic reconstruction of M.barkeri*

Description

"Modeling methanogenesis with a genome-scale metabolic reconstruction of Methanosarcina barkeri"

Usage

```
M.barkeri_iAF692
```

Format

An sbml object of class rsbml

Source

Molecular Systems Biology, 2(1):msb4100046-E1-E14 (2006)

References

Feist, A.M., Scholten, J.C.M., Palsson, B.O., Brockman, F.J., and Ideker, T., "Modeling methanogenesis with a genome-scale metabolic reconstruction of Methanosarcina barkeri", Molecular Systems Biology, 2(1):msb4100046-E1-E14 (2006)

`model2hyperdraw` *Draws a hypergraph representation from a model file*

Description

Convert a model file to a `hypergraph` representation

Usage

```
model2hyperdraw(modelFile,uptake,minimal,levels,layout)
```

Arguments

`modelFile`	is a file created from `createModel` or `pruneModel`
`uptake`	is a character vector representing the substrate uptake of in a metabolic process
`minimal`	is a logical value TRUE or FALSE to visualize externals on a graph
`levels`	is a numeric value to determine the levels of thickness of edges
`layout`	is a character string representing the layout engine to be used for visualization for example "dot", "twopi","neato","fdp","sfdp" and "circo"

Value

`graphNEL object`
returns an `graphNEL` object representation.

Author(s)

Anand K. Gavai <anand.gavai@bioinformatics.nl>

See Also

graphBPH

Examples

```
data("Glycolysis")
uptake<-"glcD"
minimal<-"TRUE"
levels<-7
layout<-"neato"
gnel<-model2hyperdraw(Glycolysis,"glcD",TRUE,levels,layout)
gnel
```

possibleExternals *possibleExternals*

Description

Finds the possible externals from an object of type liminput

Usage

```
possibleExternals(liminput)
```

Arguments

liminput	is an object of type liminput

Note

none

Author(s)

Anand K. Gavai <anand.gavai@bioinformatics.nl>

References

Soetaert K, van Oevelen D (2009). LIM: Linear Inverse Model examples and solution methods. R package version 1.3

Examples

```
  ## Not run:
data("Glycolysis")
liminput<-Read(Glycolysis)
ext<-possibleExternals(liminput)
ext

## End(Not run)
```

pruneBiggModel *pruneBiggModel*

Description

prunes the model file which is already created from the createBiggModel function

Usage

```
pruneBiggModel(modelFile,metabolites,reactions,maximize,equation_var,equation_value,constraint,exte
```

Arguments

modelFile	is a file as created from the createModel function.
metabolites	is a dataframe of metabolites participating in a reaction. This file is exported from database of metabolic reconstructions(BiGG)at http://bigg.ucsd.edu/bigg/searchMet.pl.
reactions	is a dataframe of reactions participating in a metabolic pathway. This file can be exported from database of metabolic reconstructions (BiGG) at http://bigg.ucsd.edu/bigg/main.pl.
maximize	is a character vector consisting the tag of the reaction(s) to be maximized or minimized.
equation_var	is a character vector specifying the name for the reaction to be maximized or minimized.
equation_value	is a numeric value for the reactions specified in reaction_init_flux.
constraint	is a character vector specifying the minimum and maximum values(boundary) under which the solution for the maximize reaction should fall.
externals	a character vector of metabolites as provided by the user for speficific pathways for which FBA (flux balance analysis needs to be performed)

Value

A model file with with extension ".lim" is created

Note

none

Author(s)

Anand K. Gavai <anand.gavai@bioinformatics.nl>

References

Soetaert K, van Oevelen D (2009). LIM: Linear Inverse Model examples and solution methods. R package version 1.3

Examples

```
## Not run:
## The function is currently defined as
metabolites_file<-"glycolysis_M.csv" # metabolites as exported from Bigg database
reactions_file<-"glycolysis_R.csv"   # reactions as exported from Bigg database
maximize<-"R_PYK"
equation_var<-"R_HEX1"
equation_value<-1
constraints<-"[0,1000]"
externals<-c("glcD","pyr")
Model.LIM<-createModel(metabolites_file,reactions_file,maximize,
     equation_var,equation_value,constraints,externals)
prunedModel.LIM<-pruneBiggModel(Model.LIM,metabolites_file,reactions_file,
     maximize,equation_var,equation_value,constraints,externals)

## End(Not run)
```

`rmvReactFromStoM` *removes a reaction from the stoichiometric matrix*

Description

Removes an existing reaction from the stoichiometric matrix

Usage

```
rmvReactFromStoM(sm,reactID)
```

Arguments

`sm`	is of type incidence matrix representing reactions.
`reactID`	is of type character string representing the enzyme which catalyzes the reaction found in the stochiometric matrix.

Details

This function should be used only when a reaction needs to be removed from the stochiometric matrix

Value

`sm`	returns a stoichiometric matrix with selected reaction removed.

Warning

to be used only when a reaction is not found in the reconstructions

Author(s)

Anand K. Gavai <anand.gavai@bioinformatics.nl>

See Also

addReact2StoM

Examples

```
data("Glycolysis")
sm<-getSMfromModel(Glycolysis,"R_HEX1")
sm
reactID <- "R_PYK"
csm<-sm
csm[10,1]<-0
csm
sm<-rmvReactFromStoM(sm,reactID)
sm
```

S.aureus_iSB619 *Metabolic reconstruction of S.aureus*

Description

"Genome-scale reconstruction of the metabolic network in Staphylococcus aureus N315: an initial draft to the two-dimensional annotation"

Usage

```
S.aureus_iSB619
```

Format

An sbml object of class rsbml

Source

BMC Microbiology, 5(1):8 (2005)

References

Becker, S.A. and Palsson, B.O., "Genome-scale reconstruction of the metabolic network in Staphylococcus aureus N315: an initial draft to the two-dimensional annotation", BMC Microbiology, 5(1):8 (2005)

S.cerevisiae_iND750 *Metabolic reconstruction of S.cerevisiae*

Description

"Reconstruction and Validation of Saccharomyces cerevisiae iND750, a Fully Compartmentalized Genome-scale Metabolic Model"

Usage

```
S.cerevisiae_iND750
```

Format

An sbml object of class rsbml

Source

Genome Research, 14: 1298-1309 (2004)

References

Duarte, N.C., Herrgard, M.J., and Palsson, B.O., " Reconstruction and Validation of Saccharomyces cerevisiae iND750, a Fully Compartmentalized Genome-scale Metabolic Model", Genome Research, 14: 1298-1309 (2004)

Index