Package ‘graphite’

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databases.
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as.list.PathwayList  Conversion of PathwayLists into lists.

Description

Converts a PathwayList into a list of Pathways.

Usage

## S3 method for class 'PathwayList'
as.list(x, ...)

Arguments

x  a PathwayList object

...  extra arguments to as.list

Value

A list of pathways.

Author(s)

Gabriele Sales

See Also

PathwayList

Examples

as.list(pathways("hsapiens", "kegg"))
buildPathway

Build a Pathway object.

Description

This function creates a new object of type Pathway given a data frame describing its edges.

Usage

buildPathway(id, title, species, database, proteinEdges,
metaboliteEdges = NULL, mixedEdges = NULL,
timestamp = NULL)

Arguments

id the pathway identifier.
title the title of the pathway.
species the species the pathway belongs to.
database the name of the database the pathway derives from.
proteinEdges a data.frame of edges between proteins (or genes).
Must have the following columns: src_type, src, dest_type, dest, direction and type.
Direction must be one of the two strings: "directed" or "undirected".
metaboliteEdges interactions between metabolites.
Can be NULL. Otherwise, it must have the same structure as proteinEdges.
mixedEdges interactions between metabolites and proteins.
Can be NULL. Otherwise, it must have the same structure as proteinEdges.
timestamp when the pathway was annotated, by default the time buildPathway is called.

See Also

Pathway-class

Examples

edges <- data.frame(src_type = "ENTREZID", src="672",
dest_type = "ENTREZID", dest="7157",
direction="undirected", type="binding")
pathway <- buildPathway("#1", "example", "hsapiens", "database", edges)

# Example with metabolites:
edges <- data.frame(src_type = "ENTREZID", src="672",
dest_type = "ENTREZID", dest="7157",
direction="undirected", type="binding")
mixed <- data.frame(src_type = "CHEBI", src="77750",
dest_type = "ENTREZID", dest="7157",
direction="undirected", type="binding")
pathway <- buildPathway("#1", "example", "hsapiens", "database",
edges, mixedEdges = mixed)
**convertIdentifiers**  
*Convert the node identifiers of a pathway.*

**Description**
Converts the node identifiers of pathways.
If the option Ncpus is set to a value larger than 1 and the package parallel is installed, the conversion procedure will automatically use multiple cores.

**Usage**
convertIdentifiers(x, to)

**Arguments**
x can be a list of pathways or a single pathway
to a string describing the type of the identifier. Can assume the values "entrez", "symbol" or the name of one of the columns provided by an Annotation package (for example, "UNIPROT").

**Value**
A Pathway object.

**See Also**
Pathway

**Examples**
r <- pathways("hsapiens", "reactome")
convertIdentifiers(r$`mTOR signalling", "symbol")

---

**cytoscapePlot**  
*Plot a pathway graph in Cytoscape*

**Description**
Renders the topology of a pathway as a Cytoscape graph.

**Usage**
cytoscapePlot(pathway, ..., cy.ver = 3)

**Arguments**
pathway a Pathway object.
... optional arguments forwarded to pathwayGraph.
cy.ver select a Cytoscape version. Only version 3 is supported in this release.
Details

Requires the RCy3 package.

Value

An invisible list with two items:

- \texttt{graph}: the \texttt{graphNEL} object sent to Cytoscape.
- \texttt{suid}: the RCy3 network SUID.

See Also

- \texttt{Pathway}
- \texttt{pathwayGraph}

Examples

```r
## Not run:
r <- pathways()
cytoscapePlot(convertIdentifiers(reactome$`Unwinding of DNA`, "symbol"))
## End(Not run)
```

---

### Description

A biological pathway.

### Variants

A \texttt{Pathway} instance actually stores multiple variants of the same biological data. This is the list of included variants:

- \texttt{proteins}: includes only interactions among proteins;
- \texttt{metabolites}: includes only interactions among metabolites;
- \texttt{mixed}: includes all available interactions.

### Methods

- \texttt{pathwayId(p)}: Returns the native ID of the pathway.
- \texttt{pathwayTitle(p)}: Returns the title of the pathway.
- \texttt{pathwayDatabase(p)}: Returns the name of the database the pathway was derived from.
- \texttt{pathwaySpecies(p)}: Returns the name of the species in which the pathway was annotated.
- \texttt{pathwayTimestamp(p)}: Returns the date of pathway data retrieval.
- \texttt{pathwayURL(p)}: Returns the URL of the pathway in its original database, if available.
- \texttt{convertIdentifiers(p, to)}: Returns a new pathway using a different type of node identifiers.
pathwayDatabases

edges(p, which = c("proteins", "metabolites", "mixed"), stringsAsFactors = TRUE):
  Returns a data.frame describing the edges of this pathway.
  The option which selects the desired pathway variant (see section "Variants" above).
  If stringsAsFactors is TRUE, strings are converted to factors.

nodes(p, which = c("proteins", "metabolites", "mixed")): Returns the names of the nodes
  belonging to this pathway.
  The option which selects the desired pathway variant (see section "Variants" above).

plot(p): Shows the pathway topology in Cytoscape.

runClipper(p, expr, classes, method, ...): Runs a clipper analysis over the pathway.
runTopologyGSA(p, test, exp1, exp2, alpha, ...): Runs a topologyGSA analysis over the
  pathway.

Author(s)
  Gabriele Sales

See Also
  pathways

Description
  Obtains the list of pathway databases available through graphite.

Usage
  pathwayDatabases()

Value
  Returns a data.frame with two columns: species and database.

Author(s)
  Gabriele Sales

See Also
  pathways

Examples
  pathwayDatabases()
Description

Builds a graphNEL object representing the topology of a pathway.

Usage

```
pathwayGraph(pathway, which = "proteins", edge.types = NULL)
```

Arguments

- **pathway**: a `Pathway` object.
- **which**: the pathway variant you want. See `Pathway` documentation for a list of the supported variants.
- **edge.types**: keep only the edges matching the type names in this vector.

Value

A graphNEL object.

See Also

- `Pathway`
- `graphNEL`

Examples

```
r <- pathways("hsapiens", "reactome")
pathwayGraph(r$"mTOR signalling", edge.types="Binding")
```

PathwayList-class

A collection of pathways from a single database.

Class "PathwayList"
Methods

1[i]: Returns a selection of the pathways contained in the pathway list.
1[[i]]: Access one of the pathways contained in the pathway list.
1$\"title\$: Access one of the pathways by its title.

convertIdentifiers(1, to) Returns a new list of pathways using a different type of node identifiers.

length(1) Returns the number of pathways contained in the list.

names(1) Returns the titles of the pathways contained in the list.

prepareSPIA(l, pathwaySetName, print.names=FALSE) Prepares the pathways for a SPIA analysis.

runClipper(l, expr, classes, method, maxNodes=150, ...) Runs a clipper analysis over all the pathways in the list.

runTopologyGSA(l, test, exp1, exp2, alpha, maxNodes=150, ...) Runs a topologyGSA analysis over all the pathways in the list.

Author(s)

Gabriele Sales

See Also

pathways

Description

Retrieve a list of pathways from a database for a given species.

graphite currently supports the following databases:

- BioCarta
- HumanCyc
- KEGG
- NCI-Nature Pathway Interaction Database
- PANTHER
- PharmGKB
- Reactome
- SMPDB

Call the pathwayDatabase function for more details.

Usage

pathways(species, database)
Arguments

- **species**: one of the supported species
- **database**: the name of the pathway database

Value

A PathwayList object.

See Also

PathwayList, pathwayDatabases

Examples

```r
pathways("hsapiens", "reactome")
```

Description

A virtual class acting as a common parent to all other classes representing pathway databases.

Objects from the Class

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

Methods

No methods defined with class "Pathways" in the signature.

Author(s)

Gabriele Sales

See Also

PathwayList
prepareSPIA  

Prepare pathway dataset needed by runSPIA.

Description

Prepare pathway dataset needed by runSPIA. See runSPIA and spia for more details.

Usage

prepareSPIA(db, pathwaySetName, print.names = FALSE)

Arguments

db a PathwayList object or a list of Pathways.
pathwaySetName name of the output pathway set.
print.names print pathway names as the conversion advances.

References


See Also

runSPIA
spia
PathwayList

runClipper  

Run a topological analysis on an expression dataset using clipper.

Description

clipper is a package for topological gene set analysis. It implements a two-step empirical approach based on the exploitation of graph decomposition into a junction tree to reconstruct the most relevant signal path. In the first step clipper selects significant pathways according to statistical tests on the means and the concentration matrices of the graphs derived from pathway topologies. Then, it "clips" the whole pathway identifying the signal paths having the greatest association with a specific phenotype.

If the option Ncpus is set to a value larger than 1 and the package parallel is installed, the conversion procedure will automatically use multiple cores.
runClipper

Usage

runClipper(x, expr, classes, method, which = "proteins", seed = NULL, ...)

Arguments

x  a PathwayList, a list of Pathways or a single Pathway object.
expr a matrix (size: number of genes x number of samples) of gene expression.
classes a vector (length: n) of class assignments.
method the kind of test to perform on the cliques. It could be either "mean" or "variance".
which the pathway variant you want.
See Pathway documentation for a list of the supported variants.
seed if not NULL, set the seed for the random number generator used by clipper.
... additional options: see for details easyClip.

When invoked on a PathwayList, you can use the named option maxNodes to limit the analysis to those pathways with at most a given number of nodes.

Details

The expression data and the pathway have to be annotated in the same set of identifiers.

References


See Also

caller

easyClip

Examples

if (require(clipper) & require(ALL) & require(a4Preproc)) {
  data(ALL)
  pheno <- as(phenoData(ALL), "data.frame")
  samples <- unlist(lapply(c("NEG", "BCR/ABL"), function(t) {
    which(grepl("B\d*", pheno$BT) & (pheno$mol.biol == t))[1:10]
  }))
  classes <- c(rep(1,10), rep(2,10))
  expr <- exprs(ALL)[,samples]
  rownames(expr) <- paste("ENTREZID", featureData(addGeneInfo(ALL))$ENTREZID, sep = ":\n"")
  k <- as.list(pathways("hsapiens", "kegg"))
  selected <- k[c("Bladder cancer", "Hippo signaling pathway - multiple species")]
  runClipper(selected, expr, classes, "mean", pathThr = 0.1)
}
Run SPIA analysis

Description
Run a topological analysis on an expression dataset using SPIA.

Usage
runSPIA(de, all, pathwaySetName, ...)

Arguments
- **de**: A named vector containing log2 fold-changes of the differentially expressed genes. The names of this numeric vector are Entrez gene IDs.
- **all**: A vector with the Entrez IDs in the reference set. If the data was obtained from a microarray experiment, this set will contain all genes present on the specific array used for the experiment. This vector should contain all names of the 'de' argument.
- **pathwaySetName**: The name of a pathway set created with prepareSPIA.
- **...**: Additional options to pass to spia.

Details
The spia option "organism" is internally used. It is an error use it in the additional options.

Value
The same of spia, without KEGG links. A data frame containing the ranked pathways and various statistics: pSize is the number of genes on the pathway; NDE is the number of DE genes per pathway; tA is the observed total perturbation accumulation in the pathway; pNDE is the probability to observe at least NDE genes on the pathway using a hypergeometric model; pPERT is the probability to observe a total accumulation more extreme than tA only by chance; pG is the p-value obtained by combining pNDE and pPERT; pGfdr and pGFWER are the False Discovery Rate and respectively Bonferroni adjusted global p-values; and the Status gives the direction in which the pathway is perturbed (activated or inhibited).

References


See Also
spia
runTopologyGSA

Examples

```r
if (require(SPIA) && require(hgu133plus2.db)) {
  data(colorectalCancer)

  top$ENTREZ <- mapIds(hgu133plus2.db, top$ID, "ENTREZID", "PROBEID", multiVals = "first")
  top <- top[!is.na(top$ENTREZ) & !duplicated(top$ENTREZ), ]
  top$ENTREZ <- paste("ENTREZID", top$ENTREZ, sep = ":")
  tg1 <- top[top$adj.P.Val < 0.05, ]

  DE_Colorectal = tg1$logFC
  names(DE_Colorectal) <- tg1$ENTREZ
  ALL_Colorectal <- top$ENTREZ

  biocarta <- pathways("hsapiens", "biocarta")[1:20]
  biocarta <- convertIdentifiers(biocarta, "ENTREZID")
  prepareSPIA(biocarta, "biocartaEx")
  runSPIA(de = DE_Colorectal, all = ALL_Colorectal, "biocartaEx")
}
```

runTopologyGSA Run a topological analysis on an expression dataset using topologyGSA.

Description

Use graphical models to test the pathway components highlighting those involved in its deregulation.

If the option Ncpus is set to a value larger than 1 and the package parallel is installed, the conversion procedure will automatically use multiple cores.

Usage

```r
runTopologyGSA(x, test, exp1, exp2, alpha, ...)
```

Arguments

- **x** a `PathwayList`, a list of `Pathways` or a single `Pathway` object.
- **test** Either "var" and "mean". Determine the type of test used by topologyGSA.
- **exp1** Experiment matrix of the first class, genes in columns.
- **exp2** Experiment matrix of the second class, genes in columns.
- **alpha** Significance level of the test.
- **...** Additional parameters forwarded to `topologyGSA`.

When invoked on a `PathwayList`, can use the named option "maxNodes" to limit the analysis to those pathways having up to this given number of nodes.

Details

This function produces a warning and returns NULL when the number of genes in common between the expression matrices and the pathway is less than 3.
References

Massa MS, Chiogna M, Romualdi C. Gene set analysis exploiting the topology of a pathway. BMC System Biol. 2010 Sep 1;4:121.

See Also

`pathway.var.test` `pathway.mean.test`

Examples

```r
if (require(topologyGSA)) {
  data(examples)
  colnames(y1) <- paste("SYMBOL", colnames(y1), sep = ":")
  colnames(y2) <- paste("SYMBOL", colnames(y2), sep = ":")

  k <- pathways("hsapiens", "kegg")
  p <- convertIdentifiers(k[["Fc epsilon RI signaling pathway"]], "SYMBOL")
  runTopologyGSA(p, "var", y1, y2, 0.05)
}
```
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