Package ‘graphite’

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**Description**

Converts a `PathwayList` into a list of `Pathways`.

**Usage**

```r
def 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**

```r
as.list(pathways("hsapiens", "kegg"))```
Description

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

Usage

```r
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.

Value

A new `Pathway` instance.

Examples

```r
data <- data.frame(src_type = "ENTREZID", src = "672",
deriv_type = "ENTREZID", deriv = "7157",
direction = "undirected", type = "binding")
pathway <- buildPathway("#1", "example", "hsapiens", "database", data)
```

# Example with metabolites:
```
data <- data.frame(src_type = "ENTREZID", src = "672",
deriv_type = "ENTREZID", deriv = "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$`mTORC1-mediated 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:

- graph: the `graphNEL` object sent to Cytoscape.
- suid: the RCy3 network SUID.

See Also

- `Pathway`
- `pathwayGraph`

Examples

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

# End(Not run)
```
Pathway-class  

Class "Pathway"

Description
A biological pathway.

Variants
A Pathway instance actually stores multiple variants of the same biological data.

This is the list of included variants:

- proteins: includes only interactions among proteins;
- metabolites: includes only interactions among metabolites;
- mixed: includes all available interactions.

Methods

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

```r
reactome <- pathways("hsapiens", "reactome")
pathway <- reactome[[1]]

pathwayTitle(pathway)
pathwaySpecies(pathway)
nodes(pathway)
edges(pathway)
```

---

**pathwayDatabases**

List the available pathway databases.

Description

Obtains the list of pathway databases available through graphite.

Usage

```r
pathwayDatabases()
```

Value

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

Author(s)

Gabriele Sales

See Also

`pathways`

Examples

```r
pathwayDatabases()
```
pathwayGraph

*Graph representing the topology of a pathway*

**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$'mTORC1-mediated signalling', edge.types="Binding")
```

---

**PathwayList-class**  
*Class* "PathwayList"

**Description**

A collection of pathways from a single database.

**Extends**

Class "Pathways", directly.
**Methods**

- `l[i]` returns a selection of the pathways contained in the pathway list.
- `l[[i]]` gives access to one of the pathways contained in the pathway list.
- `l$title` loads a pathways by its title.
- `convertIdentifiers(l, to)` returns a new list of pathways using a different type of node identifiers.
- `length(l)` returns the number of pathways contained in the list.
- `names(l)` 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:

- KEGG
- PANTHER
- PathBank
- PharmGKB
- Reactome
- SMPDB
- WikiPathways

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

pathways("hsapiens", "reactome")
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.

Value

This function has no return value.

References


See Also

runSPIA
spia
PathwayList
**Description**

Run a topological analysis on an expression dataset using SPIA.

**Usage**

```r
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**


runTopologyGSA

See Also

spia

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

  kegg <- pathways("hsapiens", "kegg")[1:20]
  kegg <- convertIdentifiers(kegg, "ENTREZID")
  prepareSPIA(kegg, "keggEx")
  runSPIA(de = DE_Colorectal, all = ALL_Colorectal, "keggEx")

  unlink("keggExSPIA.RData")
}
```

**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.
runTopologyGSA

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.

Value
See documentation of pathway.var.test and pathway.mean.test.

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

Examples
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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