Package ‘graphite’
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HumanCyc, KEGG, NCI, Panther, Reactome and SPIKE databases.
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as.list.DeprecatedPathwayList

Conversion of DeprecatedPathwayLists into lists.

Description

Converts a DeprecatedPathwayList into a list of Pathways.

Usage

```r
## S3 method for class ' DeprecatedPathwayList'
as.list(x, ...)
```

Arguments

- `x` a DeprecatedPathwayList object
- `...` extra arguments to as.list

Value

A list of pathways.

Author(s)

Gabriele Sales

See Also

DeprecatedPathwayList

Examples

```r
as.list(reactome)
```
as.list.PathwayList

Conversion of PathwayLists into lists.

Description

Converts a PathwayList into a list of Pathways.

Usage

```r
## 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

```r
as.list(kegg)
```

biocarta

BioCarta pathways

Description

BioCarta pathways.

Direct access to this object is deprecated. Call `pathways(species, "biocarta")` instead.
Pathway topology conversion

BioCarta pathways were retrieved in BioPax format from the PDI database web page.

We define a pathway for each BioPax tag “pathway”. Pathway nodes often correspond to multiple gene products. These can be divided into protein complexes (proteins linked by protein-protein interactions) and groups made of alternative members (genes with similar biochemical functions). Thus, when considering signal propagation these groups are considered differently. The first kind (hereafter group AND) should be expanded into a clique (all proteins connected to the others), while the second (hereafter group OR) should be expanded without connection among them. In the BioPax format only one type of group is allowed: protein complexes (group AND) with the tag 'complex'. However, it often happens that the 'protein' tag contains multiple 'xref' pointing to alternative elements of the process (group OR).

Compound mediated interactions are interactions for which a compound acts as a bridge between two elements. Since chemical compounds are not usually measured with high-throughput technology, they should be removed from the network to analyse gene signals. However, the trivial elimination of the compounds, without signal propagation, will strongly bias the topology interrupting the signals that pass through them. If element ‘A’ is linked to compound ‘c’ and compound ‘c’ is linked to element ‘B’, element ‘A’ should be linked to element ‘B’. Not all compounds are considered for the propagation because some of them (for example: H2O, ATP, ADP) are highly frequent in map descriptions and the signal propagation through them would lead to chains too long. Compounds not considered for propagation are not characteristic of a specific reaction, but act as secondary substrates/products widely shared among different processes.

graphite allows the user to see the single/multiple relation types that characterized an edge. The type of edges have been kept as much as possible similar to those annotated in the original data format. Some new types have been introduced due to topological conversion needs.

See Also
PathwayList

---

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, edges, species, database, identifier, timestamp=NULL)

Arguments

- **id** the pathway identifier.
- **title** the title of the pathway.
- **edges** a data.frame of pathway edges. Must have the following columns: src, dest, direction and type. Direction must be one of the two strings: "directed" or "undirected".
- **species** the species the pathway belongs to.
**database**  
the name of the database the pathway derives from.

**identifier**  
the type of identifier used to label the pathway nodes.

**timestamp**  
when the pathway was annotated, by default the time `buildPathway` is called.

See Also  

**Pathway-class**

Examples  

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

---

**convertIdentifiers**  
*Convert the node identifiers of a pathway.*

Description  

Converts the node identifiers of pathways.

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. It can be 3 (the default) or 2.

Details
Requires the RCytoscape package.

See Also
Pathway
pathwayGraph

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

DeprecatedPathwayList-class

Class "DeprecatedPathwayList"

Description
Represents deprecated objects for accessing pathway databases.

Extends
Class "Pathways", directly.
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$\text{title}^\wedge$ Access one of the 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.

runDEGraph(l, expr, classes, maxNodes=150, ...) Runs a DEGraph 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

PathwayList

Description

HumanCyc pathways.

Direct access to this object is deprecated. Call pathways(species, "humancyc") instead.


Pathway topology conversion

HumanCyc pathways were retrieved in the BioPax format downloaded by the Pathway Commons web page http://www.pathwaycommons.org.

We define a pathway for each BioPax tag “pathway”. Pathway nodes often correspond to multiple gene products. These can be divided into protein complexes (proteins linked by protein-protein interactions) and groups made of alternative members (genes with similar biochemical functions). Thus, when considering signal propagation these groups are considered differently. The first kind (hereafter group AND) should be expanded into a clique (all proteins connected to the others), while the second (hereafter group OR) should be expanded without connection among them. In
the BioPax format only one type of group is allowed: protein complexes (group AND) with the tag 'complex'. However, it often happens that the 'protein' tag contains multiple 'xref' pointing to alternative elements of the process (group OR).

Compound mediated interactions are interactions for which a compound acts as a bridge between two elements. Since chemical compounds are not usually measured with high-throughput technology, they should be removed from the network to analyse gene signals. However, the trivial elimination of the compounds, without signal propagation, will strongly bias the topology interrupting the signals that pass through them. If element 'A' is linked to compound 'c' and compound 'c' is linked to element 'B', element 'A' should be linked to element 'B'. Not all compounds are considered for the propagation because some of them (for example: H2O, ATP, ADP) are highly frequent in map descriptions and the signal propagation through them would lead to chains too long. Compounds not considered for propagation are not characteristic of a specific reaction, but act as secondary substrates/products widely shared among different processes.

graphite allows the user to see the single/multiple relation types that characterized an edge. The type of edges have been kept as much as possible similar to those annotated in the original data format. Some new types have been introduced due to topological conversion needs.

See Also

PathwayList

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**Description**

**KEGG pathways.**

Direct access to this object is deprecated. Call pathways(species, "kegg") instead.


**Pathway topology conversion**

KEGG pathway were retrieved in KGML format from the KEGG ftp site.

KEGG database provides separate xml files, one for each pathway. A pathway is therefore define by all the reactions described within each file.

Pathway nodes often correspond to multiple gene products. These can be divided into protein complexes (proteins linked by protein-protein interactions) and groups made of alternative members (genes with similar biochemical functions). Thus, when considering signal propagation these groups are considered differently. The first kind (hereafter group AND) should be expanded into a clique (all proteins connected to the others), while the second (hereafter group OR) should be expanded without connection among them. In the KGML format there are two ways of defining nodes with multiple elements: protein complexes (group AND defined by entry type="group") and groups with alternative members (group OR defined by entry type="gene").

Compound mediated interactions are interactions for which a compound acts as a bridge between two elements. Since chemical compounds are not usually measured with high-throughput technology, they should be removed from the network to analyse gene signals. However, the trivial elimination of the compounds, without signal propagation, will strongly bias the topology interrupting the signals that pass through them. If element 'A' is linked to compound 'c' and compound
'c' is linked to element 'B', element 'A' should be linked to element 'B'. Within the KGML format there are two different ways of describing a compound mediated interaction: i) direct interaction type="PPrel" ('A' interacts with 'B' through compound 'c') and ii) indirect one type="PCrel" ('A' interacts to compound 'c' and 'c' interacts with 'B').

Not all compounds are considered for the propagation because some of them (for example: H2O, ATP, ADP) are highly frequent in map descriptions and the signal propagation through them would lead to chains too long. Compounds not considered for propagation are not characteristic of a specific reaction, but act as secondary substrates/products widely shared among different processes.

graphite allows the user to see the single/multiple relation types that characterized an edge. The type of edges have been kept as much as possible similar to those annotated in the original data format. Some new types have been introduced due to topological conversion needs.

See Also
PathwayList
See Also

PathwayList

Panther pathways

Description

PANTHER pathways.

Direct access to this object is deprecated. Call pathways(species, "panther") instead.


Pathway topology conversion

Panther pathways were retrieved in the BioPax format downloaded by the Pathway Commons web page http://www.pathwaycommons.org.

We define a pathway for each BioPax tag “pathway”. Pathway nodes often correspond to multiple gene products. These can be divided into protein complexes (proteins linked by protein-protein interactions) and groups made of alternative members (genes with similar biochemical functions). Thus, when considering signal propagation these groups are considered differently. The first kind (hereafter group AND) should be expanded into a clique (all proteins connected to the others), while the second (hereafter group OR) should be expanded without connection among them. In the BioPax format only one type of group is allowed: protein complexes (group AND) with the tag ‘complex’. However, it often happens that the ‘protein’ tag contains multiple ‘xref’ pointing to alternative elements of the process (group OR).

Compound mediated interactions are interactions for which a compound acts as a bridge between two elements. Since chemical compounds are not usually measured with high-throughput technology, they should be removed from the network to analyse gene signals. However, the trivial elimination of the compounds, without signal propagation, will strongly bias the topology interrupting the signals that pass through them. If element ‘A’ is linked to compound ‘c’ and compound ‘c’ is linked to element ‘B’, element ‘A’ should be linked to element ‘B’. Not all compounds are considered for the propagation because some of them (for example: H2O, ATP, ADP) are highly frequent in map descriptions and the signal propagation through them would lead to chains too long. Compounds not considered for propagation are not characteristic of a specific reaction, but act as secondary substrates/products widely shared among different processes.

graphite allows the user to see the single/multiple relation types that characterized an edge. The type of edges have been kept as much as possible similar to those annotated in the original data format. Some new types have been introduced due to topological conversion needs.

See Also

PathwayList
Pathway-class

Pathway-class  Class "Pathway"

Description

A biological pathway.

Slots

- id: the native ID of the pathway.
- title: the title of the pathway.
- edges: a data.frame describing the edges of this pathway.
- database: the name of the database the pathway was derived from.
- species: the name of the species in which the pathway was annotated.
- identifier: the type of node identifier used by this pathway.
- timestamp: the date in which the pathway data was retrieved.

Methods

- convertIdentifiers(p, to) Returns a new pathway using a different type of node identifiers.
- edges(p) Returns a data.frame describing the edges of this pathway.
- nodes(p) Return the names of the nodes belonging to this pathway.
- plot(p) Shows the pathway topology in Cytoscape.
- runClipper(p, expr, classes, method, ...) Runs a clipper analysis over the pathway.
- runDEGraph(p, expr, classes, ...) Runs a DEGraph analysis over the pathway.
- runTopologyGSA(p, test, exp1, exp2, alpha, ...) Runs a topologyGSA analysis over the pathway.

Author(s)

Gabriele Sales

See Also

pathways
### 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**

```r
pathwayGraph(pathway, edge.types=NULL)
```

**Arguments**

- `pathway`: a `Pathway` object.
- `edge.types`: keep only the edges matching the type names in this vector.

**Value**

A `graphNEL` object.

**See Also**

`Pathway`

`graphNEL`
Examples

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

Description

A collection of pathways from a single database.

Extends

Class "Pathways", directly.

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(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.
rudDEGraph(l, expr, classes, maxNodes=150, ...) Runs a DEGraph analysis over all the pathways in the list.
rudTopographyGSA(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
pathways  

Retrieves a list of pathways.

Description

This function retrieves a list of pathways from a database for a given species.

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

Examples

pathways("hsapiens", "reactome")

Pathways-class  

Class "Pathways"

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

reactome
Reactome pathways

Description
Reactome pathways.
Direct access to this object is deprecated. Call pathways(species, “reactome”) instead.
Pathway topology conversion

Reactome pathways were retrieved in the BioPax format from the Reactome database web page. We define a pathway for each BioPax tag "pathway". Pathway nodes often correspond to multiple gene products. These can be divided into protein complexes (proteins linked by protein-protein interactions) and groups made of alternative members (genes with similar biochemical functions). Thus, when considering signal propagation these groups are considered differently. The first kind (hereafter group AND) should be expanded into a clique (all proteins connected to the others), while the second (hereafter group OR) should be expanded without connection among them. In the BioPax format only one type of group is allowed: protein complexes (group AND) with the tag 'complex'. However, it often happens that the 'protein' tag contains multiple 'xref' pointing to alternative elements of the process (group OR).

Compound mediated interactions are interactions for which a compound acts as a bridge between two elements. Since chemical compounds are not usually measured with high-throughput technology, they should be removed from the network to analyse gene signals. However, the trivial elimination of the compounds, without signal propagation, will strongly bias the topology interrupting the signals that pass through them. If element 'A' is linked to compound 'c' and compound 'c' is linked to element 'B', element 'A' should be linked to element 'B'. Not all compounds are considered for the propagation because some of them (for example: H2O, ATP, ADP) are highly frequent in map descriptions and the signal propagation through them would lead to chains too long. Compounds not considered for propagation are not characteristic of a specific reaction, but act as secondary substrates/products widely shared among different processes.

graphite allows the user to see the single/multiple relation types that characterized an edge. The type of edges have been kept as much as possible similar to those annotated in the original data format. Some new types have been introduced due to topological conversion needs.

See Also

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.

Usage

runClipper(x, expr, classes, method, ...)

Arguments

x a PathwayList, a list of Pathways or a single Pathway object.
expr a matrix (size: number p of genes x number n of samples) of gene expression.
runClipperMulti

Run a topological analysis on an expression dataset using clipper.

Description

This function is deprecated and will be removed in a future release. You can use runClipper instead.

Usage

runClipperMulti(pathways, expr, classes, method, maxNodes=150, ...)

Arguments

- pathways: a PathwayList object.
- expr: a matrix (size: number p of genes x number n 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".
- maxNodes: ignore a pathway when it has more than this number of nodes.
- ...: Additional options; see for details easyClip.

Details

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

References


See Also

clipper

Examples

```r
if (require(clipper) & require(ALL)){
  k <- pathways("hsapiens", "kegg")
  path <- convertIdentifiers(k$'Chronic myeloid leukemia', "entrez")
  genes <- nodes(path)
  data(ALL)
  all <- as.matrix(exprs(ALL[1:length(genes),1:20]))
  classes <- c(rep(1,10), rep(2,10))
  rownames(all) <- genes
  runClipper(path, all, classes, "mean", pathThr=0.1)
}
```
runDEGraph

Details

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

Value

A list with two elements:

- results: a list with one entry for each successfully analyzed pathway;
- errors: a vector containing the error messages of failed analyses.

References


See Also

clipper

Examples

```r
if (require(clipper) & require(ALL)){
  k <- pathways("hsapiens", "kegg")
  paths <- convertIdentifiers(k[1:5], "entrez")
  genes <- unlist(lapply(paths, nodes))
  data(ALL)
  all <- as.matrix(exprs(ALL[1:length(genes),1:20]))
  classes <- c(rep(1,10), rep(2,10))
  rownames(all) <- genes
  runClipperMulti(paths, all, classes, "mean", pathThr=0.1)
}
```

---

runDEGraph  
**Run a topological analysis on an expression dataset using DEGraph package.**

Description

DEGraph implements recent hypothesis testing methods which directly assess whether a particular gene network is differentially expressed between two conditions.

Usage

```r
runDEGraph(x, expr, classes, ...)
```

Arguments

- **x**  
a `PathwayList`, a list of `Pathways` or a single `Pathway` object.
- **expr**  
a matrix (size: number p of genes x number n of samples) of gene expression.
- **classes**  
a vector (length: n) of class assignments.
- **...**  
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.
runDEGraphMulti

Run a topological analysis on an expression dataset using DEGraph package.

Description

This function is deprecated and will be removed in a future release. You can use runDEGraph instead.

Usage

runDEGraphMulti(pathways, expr, classes, maxNodes=150)

Arguments

- **pathways**: a `PathwayList` object.
- **expr**: A matrix (size: number p of genes x number n of samples) of gene expression.
- **classes**: A vector (length: n) of class assignments.
- **maxNodes**: Ignore pathways with more than "maxNodes" nodes. Set to NULL to disable the filter.

Details

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

Value

A list with two elements:

- **results**: a list with one entry for each successfully analyzed pathway;
- **errors**: a vector containing the error messages of failed analyses.

Details

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

References


Examples

```r
if (require(DEGraph)) {
  data("Loi2008.DEGraphVignette"

  b <- pathways("hsapiens", "biocarta")
  p <- convertIdentifiers(b["actions of nitric oxide in the heart"], "entrez")
  runDEGraph(p, exprLoi2008, classLoi2008)
}
```
runSPIA

References


See Also
testOneGraph

Examples

if (require(DEGraph)) {
  data("Loi2008_DEGraphVignette")

  b <- pathways("hsapiens", "biocarta")
  ps <- convertIdentifiers(b[1:3], "entrez")
  runDEGraphMulti(ps, exprLoi2008, classLoi2008)
}

runSPIA 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 A list of pathways like kegg, nci or reactome.

... Additional options to pass to spia.

Details

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

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

Examples

if (require(SPIA) && require(hgu133plus2.db)) {
  data(colorectalcancer)
  
  x <- hgu133plus2ENTREZ
  top$ENTREZ <- unlist(as.list(x[top$ID]))
  top <- top[!is.na(top$ENTREZ), ]
  top <- top[!duplicated(top$ENTREZ), ]
  tg1 <- top[top$adj.P.Val < 0.05, ]

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

  b <- pathways("hsapiens", "biocarta")
  prepareSPIA(b[1:20], "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.
Usage

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.

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

---

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

Description

This function is deprecated and will be removed in a future release. You can use `runTopologyGSA` instead.

Usage

`runTopologyGSAMulti(pathways, test, exp1, exp2, alpha, maxNodes=150, ...)"
Arguments

- **pathways**: A `PathwayList` 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.
- **maxNodes**: Ignore pathways with more than "maxNodes" nodes. Set to "NULL" to disable the filter.
- **...**: Additional parameters for topologyGSA.

Details

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

Value

A list with two elements:

- results: a list with one entry for each successfully analyzed pathway;
- errors: a vector containing the error messages of failed analyses.

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)
  k <- pathways("hsapiens", "kegg")
  ps <- convertIdentifiers(
    k[c("Acute myeloid leukemia", "Fc epsilon RI signaling pathway")],
    "symbol")
  runTopologyGSAMulti(ps, "var", y1, y2, 0.05)
}
```
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