Package 'enrichViewNet'

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Type Package

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Title From functional enrichment results to biological networks

Description This package enables the visualization of functional enrichment results as network graphs. First the package enables the visualization of enrichment results, in a format corresponding to the one generated by gprofiler2, as a customizable Cytoscape network. In those networks, both gene datasets (GO terms/pathways/protein complexes) and genes associated to the datasets are represented as nodes. While the edges connect each gene to its dataset(s). The package also provides the option to create enrichment maps from functional enrichment results. Enrichment maps enable the visualization of enriched terms into a network with edges connecting overlapping genes.

Encoding UTF-8

License Artistic-2.0

Depends R (>= 4.2.0)

Imports gprofiler2, strex, RCy3, jsonlite, stringr, enrichplot, methods

Suggests BiocStyle, knitr, rmarkdown, testthat

biocViews BiologicalQuestion, Software, Network, NetworkEnrichment, GO

VignetteBuilder knitr

URL https://github.com/adeschen/enrichViewNet, https://adeschen.github.io/enrichViewNet/

BugReports https://github.com/adeschen/enrichViewNet/issues

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R topics documented:

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enrichViewNet-package   *From functional enrichment results to biological networks*

Description

The `enrichViewNet` package enables the visualization of enrichment results, in a format corresponding to the one generated by gprofiler2 (<https://cran.r-project.org/web/packages/gprofiler2/index.html>) under the form of Cytoscape network (<https://cytoscape.org/>).

Details

In those networks, both gene datasets (GO terms/pathways/protein complexes) and genes are represented as nodes. A edge connect a gene to its datasets. In the current version, only genes present in at least one gene dataset are retained.

Author(s)

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See Also

- [createNetwork](#) for transforming functional enrichment results from gprofiler2 into a Cytoscape network

---

createBasicEmap *Create a basic enrichment map*

Description

The function creates a basic enrichment map using functional enrichment results.

Usage

```
createBasicEmap(
  gostResults,
  backgroundGenes,
  showCategory,
  groupCategory,
  categoryLabel,
  categoryNode,
  significantMethod
)
```

Arguments

gostResults   a data.frame containing the enrichment results to be plot.

backgroundGenes

                 a vector of character string representing the name of the genes present in the request.

showCategory   a positive integer or a vector of characters representing terms. If a integer, the first n terms will be displayed. If vector of terms, the selected terms will be displayed.

groupCategory   a logical indicating if the categories should be grouped.

categoryLabel   a positive numeric representing the amount by which plotting category nodes label size should be scaled relative to the default (1).

categoryNode   a positive `numeric` representing the amount by which plotting category nodes
                    should be scaled relative to the default (1).

significantMethod

                    a `character` string representing the name of the multiple testing correction
                    method used on the results.

Value

a `ggplot` object representing the enrichment map.

Author(s)

Astrid Deschênes

Examples

```
## Load the result of an enrichment analysis done with gprofiler2
data(parentalNapaVsDMSOEnrichment)

## Only retain the results section
gostResults <- as.data.frame(parentalNapaVsDMSOEnrichment$result)

## Limit the results to Wikipathways
## and remove the root term
gostResults <- gostResults[which(gostResults$source == "WP"),]
gostResults <- gostResults[which(gostResults$term_id != "WIKIPATHWAYS"),]

## Extract meta data information
meta <- parentalNapaVsDMSOEnrichment$meta

## Get all background genes
backgroundGenes <- meta$query_metadata$queries[["parental_napa_vs_DMSO"]]

## Get significant method
significantMethod <- meta$query_metadata$significance_threshold_method

## Create basic enrichment map using Wikipathways terms
enrichViewNet:::createBasicEmap(gostResults=gostResults,
    backgroundGenes=backgroundGenes, showCategory=30L,
    groupCategory=FALSE, categoryLabel=1, categoryNode=1,
    significantMethod=significantMethod)
```

---

createCytoscapeCXJSON   *Create CX JSON text representing the network*

Description

Create a CX JSON text that represent the network which includes information about nodes and
edges present in the network.

Usage

```
createCytoscapeCXJSON(gostResults, gostObject, title)
```

Arguments

gostResults   a data.frame containing the terms retained for the creation of the network.

gostObject   a list created by gprofiler2 that contains the results from an enrichment analysis.

title   a character string representing the name assigned to the network.

Value

character string that represent the network in a CX JSON format.

Author(s)

Astrid Deschênes

Examples

```
## Loading dataset containing result from an enrichment analysis done with
## gprofiler2
data(demoGOST)

## Only retained the WikiPathways results
results <- demoGOST$result[demoGOST$result$source == "WP", ]

jsonFormat <- enrichViewNet:::createCytoscapeCXJSON(
                gostResults = results, gostObject = demoGOST,
                title = "WikiPathways")
```

---

createCytoscapeNetwork

Create network and load it into Cytoscape

Description

Create network from gprofiler2 results and load it into Cytoscape

Usage

```
createCytoscapeNetwork(gostResults, gostObject, title, collection)
```

Arguments

gostResults	a data.frame containing the terms retained for the creation of the network.
gostObject	a list created by gprofiler2 that contains the results from an enrichment analysis.
title	a character string representing the name assigned to the network.
collection	a character string representing the collection name assigned to the network.

Value

TRUE

Author(s)

Astrid Deschênes

Examples

```
## Loading dataset containing result from an enrichment analysis done with
## gprofiler2
data(demoGOST)

## Only retained the WikiPathways results
results <- demoGOST$result[demoGOST$result$source == "WP", ]

## The creation of the network can only be done when Cytoscape
## is up and running
## A network using GO - Molecular Function enriched terms will be
## generated and loaded into Cytoscape
if (enrichViewNet:::isCytoscapeRunning()) {
    enrichViewNet:::createCytoscapeNetwork(gostResults=results,
        gostObject=demoGOST, title="Test", collection="New Collection")
}
```

---

createEnrichMap	*Using functional enrichment results in gprofiler2 format to create an enrichment map*

Description

User selected enrichment terms are used to create an enrichment map. The selection of the term can by specifying by the source of the terms (GO:MF, REAC, TF, etc...) or by listing the selected term IDs. The map is only generated when there is at least on significant term to graph.

Usage

```
createEnrichMap(
  gostObject,
  query,
 source = c("TERM_ID", "GO:MF", "GO:CC", "GO:BP", "KEGG", "REAC", "TF", "MIRNA", "HPA",
    "CORUM", "HP", "WP"),
  termIDs = NULL,
  removeRoot = TRUE,
  showCategory = 30L,
  groupCategory = FALSE,
  categoryLabel = 1,
  categoryNode = 1
)
```

Arguments

gostObject   a list corresponding to gprofiler2 enrichment output that contains and that con-
               tains the results from an enrichment analysis.

query   a character string representing the name of the query that is going to be used
               to generate the graph. The query must exist in the gostObject object.

source   a character string representing the selected source that will be used to gen-
               erate the network. To hand-pick the terms to be used, "TERM_ID" should be
               used and the list of selected term IDs should be passed through the termIDs
               parameter. The possible sources are "GO:BP" for Gene Ontology Biological
               Process, "GO:CC" for Gene Ontology Cellular Component, "GO:MF" for Gene
               Ontology Molecular Function, "KEGG" for Kegg, "REAC" for Reactome, "TF"
               for TRANSFAC, "MIRNA" for miRTarBase, "CORUM" for CORUM database,
               "HP" for Human phenotype ontology and "WP" for WikiPathways. Default:
               "TERM_ID".

termIDs   a vector of character strings that contains the term IDS retained for the cre-
               ation of the network. Default: NULL.

removeRoot   a logical that specified if the root terms of the selected source should be re-
               moved (when present). Default: TRUE.

showCategory   a positive integer or a vector of characters representing terms. If a integer,
               the first n terms will be displayed. If vector of terms, the selected terms will be
               displayed. Default: 30L.

groupCategory a logical indicating if the categories should be grouped. Default: FALSE.

categoryLabel a positive numeric representing the amount by which plotting category nodes
               label size should be scaled relative to the default (1). Default: 1.s

categoryNode   a positive numeric representing the amount by which plotting category nodes
               should be scaled relative to the default (1). Default: 1.

Value

a ggplot object which is the enrichment map for enrichment results.

Author(s)

Astrid Deschênes

Examples

```
## Loading dataset containing result from an enrichment analysis done with
## gprofiler2
data(parentalNapaVsDMSOEnrichment)

## Extract query information (only one in this dataset)
query <- unique(parentalNapaVsDMSOEnrichment$result$query)

## Create graph for Gene Ontology - Cellular Component related results
createEnrichMap(gostObject=parentalNapaVsDMSOEnrichment,
    query=query, source="GO:CC", removeRoot=TRUE)
```

---

createMetaDataSectionCXJSON

Create meta data section for the CX JSON file

Description

Create meta data section for the CX JSON file that contains the network information

Usage

```
createMetaDataSectionCXJSON()
```

Value

a JSON object that contains the meta data section related to the network

Author(s)

Astrid Deschênes

Examples

```
## Create the JSON object that contains the meta data information
enrichViewNet:::createMetaDataSectionCXJSON()
```

---

createNetwork	*Using functional enrichment results from gprofiler2 to create a Cytoscape network*

Description

User selected enrichment terms are used to create a Cytoscape network where the selected terms and the genes that where part of the enrichment analysis are all represented as nodes. Edges are linking the genes to their terms. The selection of the term can by specifying the source of the terms (GO:MF, REAC, TF, etc...) or by listing the selected term IDs. The network is only generated when there is at least on significant term to graph.

Usage

```
createNetwork(
  gostObject,
  source = c("TERM_ID", "GO:MF", "GO:CC", "GO:BP", "KEGG", "REAC", "TF", "MIRNA", "HPA",
     "CORUM", "HP", "WP"),
  termIDs = NULL,
  removeRoot = TRUE,
  title = "gprofiler network",
  collection = "enrichment results",
  fileName = "gprofilerNetwork.cx"
)
```

Arguments

gostObject	a list created by gprofiler2 that contains the results from an enrichment analysis.
source	a character string representing the selected source that will be used to generate the network. To hand-pick the terms to be used, "TERM_ID" should be used and the list of selected term IDs should be passed through the termIDs parameter. The possible sources are "GO:BP" for Gene Ontology Biological Process, "GO:CC" for Gene Ontology Cellular Component, "GO:MF" for Gene Ontology Molecular Function, "KEGG" for Kegg, "REAC" for Reactome, "TF" for TRANSFAC, "MIRNA" for miRTarBase, "CORUM" for CORUM database, "HP" for Human phenotype ontology and "WP" for WikiPathways. Default: "TERM_ID".
termIDs	a vector of character strings that contains the term IDS retained for the creation of the network. Default: NULL.
removeRoot	a logical that specified if the root terms of the selected source should be removed (when present). Default: TRUE.
title	a character string representing the name assigned to the network. Default: "gprofiler network".
collection	a character string representing the collection name assigned to the network. Default: "enrichment results".

fileName	a `character` string representing the name of the CX JSON file that is created when Cytoscape is not running. The name must have a '.cx' extension. Default: "gprofilerNetwork_01.cx".

Value

TRUE

Author(s)

Astrid Deschênes

Examples

```
## Loading dataset containing result from an enrichment analysis done with
## gprofiler2
data(demoGOST)

## Create network for Gene Ontology - Molecular Function related results
## in Cytoscape (when the application is opened)
## Otherwise, create a CX file in the temporary directory
## The file can be opened in Cytoscape
createNetwork(gostObject=demoGOST, source="GO:MF", removeRoot=FALSE,
    title="GO Molecular Function Graph",
    fileName=file.path(tempdir(), "GO_MF_demo.cx"))
```

---

demoGOST	*The result of a functional enrichment analysis done with* gprofiler2 *(*<https://cran.r-project.org/web/packages/gprofiler2/vignettes/gprofiler2.html>*).*

Description

The object is a `list` with 2 entries. It contains the results of the enrichment analysis as well as the metadata related to the analysis.

Usage

```
data(demoGOST)
```

Format

The `list` contains two entries. The `result` entry contains a `data.frame` with the significant results obtained by an enrichment analysis done with `gprofiler2`. The `meta` entry contains a named list with all the metadata for the query.

Details

This dataset can be used to test the [createNetwork](#) function.

Value

A list containing two entries. The result entry contains a data.frame with the significant results obtained by an enrichment analysis done with gprofiler2. The meta entry contains a named list with all the metadata for the query.

See Also

- [createNetwork](#) for transforming functional enrichment results from gprofiler2 into a Cytoscape network

Examples

```
## Loading dataset containing result from an enrichment analysis done with
## gprofiler2
data(demoGOST)

## Create network for WikiPathways results
## in Cytoscape (if the application is open)
## Otherwise, create a CX file in the temporary directory
## The file can be opened in Cytoscape
createNetwork(gostObject=demoGOST, source="WP", title="Wikipathways",
    fileName=file.path(tempdir(), "Wikipathways_Demo.cx"))
```

---

extractNodesAndEdgesInfoForCXJSON

Extract information about nodes and edges

Description

Extract information about nodes and edges that is necessary to create the CX JSON text representing the network

Usage

```
extractNodesAndEdgesInfoForCXJSON(gostResults, gostObject)
```

Arguments

gostResults   a data.frame containing the terms retained for the creation of the network.

gostObject   a list created by gprofiler2 that contains the results from an enrichment analysis.

Value

a `list` containing 4 entries:

- "nodes"a `data.frame` containing the information about the nodes present in the network.
- "edges"a `data.frame` containing the information about the edges present in the network.
- "nodeAttributes"a `data.frame` containing the attributes associated to the nodes present in the network.
- "edgesAttributes"a `data.frame` containing the attributes associated to the edges present in the network

Author(s)

Astrid Deschênes

Examples

```
## Loading dataset containing result from an enrichment analysis done with
## gprofiler2
data(demoGOST)

## Only retained the WikiPathways results
results <- demoGOST$result[demoGOST$result$source == "WP", ]

information <- enrichViewNet:::extractNodesAndEdgesInfoForCXJSON(
                gostResults=results, gostObject=demoGOST)
```

---

extractNodesAndEdgesWhenIntersection

Extract node and edge information to be used to create Cytoscape network

---

Description

Create a list containing all node and edge information needed to create the Cytoscape network

Usage

```
extractNodesAndEdgesWhenIntersection(gostResults, gostObject)
```

Arguments

gostResults   a `data.frame` containing the terms retained for the creation of the network. The `data.frame` does not contain a column called "intersection".

gostObject   a `list` created by gprofiler2 that contains the results from an enrichment analysis.

Value

`list` containing 2 entries:

- "nodes" a `data.frame` containing the information about the nodes present in the network.
- "edges" a `data.frame` containing the information about the edges present in the network.

Author(s)

Astrid Deschênes

Examples

```
## Loading dataset containing result from an enrichment analysis done with
## gprofiler2
data(parentalNapaVsDMSOEnrichment)

## Only retained the GO Molecular Function results
results <- parentalNapaVsDMSOEnrichment$result[
        parentalNapaVsDMSOEnrichment$result$source == "GO:MF", ]

information <-
    enrichViewNet:::extractNodesAndEdgesWhenIntersection(
        gostResults=results, gostObject=parentalNapaVsDMSOEnrichment)
```

---

extractNodesAndEdgesWhenNoIntersection
Extract node and edge information to be used to create Cytoscape network

---

Description

Create a list containing all node and edge information needed to create the Cytoscape network

Usage

```
extractNodesAndEdgesWhenNoIntersection(gostResults, gostObject)
```

Arguments

gostResults	a `data.frame` containing the terms retained for the creation of the network.
gostObject	a `list` created by gprofiler2 that contains the results from an enrichment analysis.

Value

`list` containing 2 entries:

- "nodes" a `data.frame` containing the information about the nodes present in the network.
- "edges" a `data.frame` containing the information about the edges present in the network.

Author(s)

Astrid Deschênes

Examples

```
## Loading dataset containing result from an enrichment analysis done with
## gprofiler2
data(demoGOST)

## Only retained the GO Molecular Function results
results <- demoGOST$result[demoGOST$result$source == "GO:MF", ]

information <-
    enrichViewNet:::extractNodesAndEdgesWhenNoIntersection(
                gostResults=results, gostObject=demoGOST)
```

---

isCytoscapeRunning   *Verifying that Cytoscape is running*

Description

Verifying that Cytoscape is running

Usage

```
isCytoscapeRunning()
```

Value

a `logical` indicating if Cytoscape is running.

Author(s)

Astrid Deschênes

Examples

```
## Test if Cytoscape is running
enrichViewNet:::isCytoscapeRunning()
```

---

parentalNapaVsDMSODEG *The result of a differential expression analysis done between napabu-casin treated and DMSO control parental MiaPaCa2 cells. The cells were treated for 2 hour with 0.5 uM napabucasin. The protocol to generate the RNA-seq is described in Froeling F.E.M. et al 2019.*

Description

The object is a `data.frame` with 24184 rows and 4 columns. Each row correspond to a tested gene.

Usage

```
data(parentalNapaVsDMSODEG)
```

Format

a `data.frame` containing the results of a differential expression analysis between napabucasin treated and DMSO control parental MiaPaCa2 cells for all 24184 genes tested. The 4 columns are:

- EnsemblID a `character` string representing the unique Ensembl identifier for the tested gene
- EnsemblID a `numeric` representing the expression difference (in log2FoldChange) between the napabucasin treatment and the DMSO control for the tested gene
- padj a `numeric` representing the adjusted p-value associated to the difference in expression for the tested gene; NA when the adjusted p-value as not been calculated (equivalent to not significant)
- GeneName a `character` string representing the name of the tested gene

Details

The differentially expressed genes between napabucasin-treated cells (0.5 uM) and DMSO as vehicle control are reprinted from Clinical Cancer Research, 2019, 25 (23), 7162–7174, Fieke E.M. Froeling, Manojit Mosur Swamynathan, Astrid Deschênes, Iok In Christine Chio, Erin Brosnan, Melissa A. Yao, Priya Alagesan, Matthew Lucito, Juying Li, An-Yun Chang, Lloyd C. Trotman, Pascal Belleau, Youngkyu Park, Harry A. Rogoff, James D. Watson, David A. Tuveson, Bioactivation of napabucasin triggers reactive oxygen species–mediated cancer cell death, with permission from AACR.

Value

a `data.frame` containing the results of a differential expression analysis between napabucasin treated and DMSO control parental MiaPaCa2 cells for all 24184 genes tested. The 4 columns are:

- EnsemblID a `character` string representing the unique Ensembl identifier for the tested gene
- EnsemblID a `numeric` representing the expression difference (in log2FoldChange) between the napabucasin treatment and the DMSO control for the tested gene

- padj a `numeric` representing the adjusted p-value associated to the difference in expression for the tested gene; NA when the adjusted p-value as not been calculated (equivalent to not significant)
- GeneName a `character` string representing the name of the tested gene

Source

The original RNA-sequencing data is available at the Gene Expression Omnibus (GEO) under the accession number GSE135352.

See Also

- [createNetwork](#) for transforming functional enrichment results from gprofiler2 into a Cytoscape network

Examples

```
## Required library
library(gprofiler2)

## Loading data set containing the results of a differentially expressed
## analysis between 2-hour treatment with 0.5 uM napabucasin and
## DMSO vehicle control parental MiaPaCa2 cells
data(parentalNapaVsDMSODEG)

allGenes <- unique(parentalNapaVsDMSODEG$EnsemblID)

## Select the significantly differentially expressed genes
selection <- which(abs(parentalNapaVsDMSODEG$log2FoldChange) > 1 &
                        parentalNapaVsDMSODEG$padj < 0.05)

selectedGenes <- unique(parentalNapaVsDMSODEG$EnsemblID[selection])

## Run an enrichment analysis using WikiPathways dataset
gostres <- gost(query = list(parental_napa_vs_DMSO=selectedGenes),
    organism="hsapiens",
    correction_method = "g_SCS",
    sources=c("WP"), significant=TRUE, evcodes=TRUE,
    custom_bg=allGenes, exclude_iea=TRUE)
```

---

parentalNapaVsDMSOEnrichment

> *The result of an enrichment analysis has been done using the significantly differentially expressed genes between napabucasin treated and DMSO control parental MiaPaCa2 cells. The cells were treated for 2 hour with 0.5 uM napabucasin. The protocol to generate the RNA-seq is described in Froeling F.E.M. et al 2019.*

Description

The enrichment analysis was done with gprofile2 package (Kolberg L et al 2020) with database version 'e109_eg56_p17_1d3191d' and g:SCS multiple testing correction method applying significance threshold of 0.05 (Raudvere U et al 2019). All tested genes were used as background.

Usage

```
data(parentalNapaVsDMSOEnrichment)
```

Format

a `list` containing 2 entries:

- result a `data.frame` with the significantly enriched terms
- meta a TODO

Details

The object is a named `list` with 2 entries. The 'result' entry contains a `data.frame` with the enrichment analysis results and the 'meta' entry contains metadata information.

The dataset used for the enrichment analysis is associated to this publication:

Froeling F.E.M. et al.Bioactivation of Napabucasin Triggers Reactive Oxygen Species–Mediated Cancer Cell Death. Clin Cancer Res 1 December 2019; 25 (23): 7162–7174

The enrichment analysis has been done with gprofile2 package (Kolberg L et al 2020) with database version 'e109_eg56_p17_1d3191d' and g:SCS multiple testing correction method applying significance threshold of 0.05 (Raudvere U et al 2019). All tested genes were used as background.

Value

a `list` containing 2 entries:

- result a `data.frame` with the significantly enriched terms
- meta a TODO

Source

The original RNA-sequencing data is available at the Gene Expression Omnibus (GEO) under the accession number GSE135352.

See Also

- [createNetwork](#) for transforming functional enrichment results from gprofiler2 into a Cytoscape network

Examples

```
## Required library
library(gprofiler2)

## Loading dataset containing the results of a differentially expressed
## analysis between 2-hour treatment with 0.5 uM napabucasin and
## DMSO vehicle control parental MiaPaCa2 cells
data(parentalNapaVsDMSOEnrichment)

## TODO
```

---

removeRootTerm   *Remove root term if present in the list of selected terms*

Description

Remove root term if present in the list of selected terms

Usage

```
removeRootTerm(gostResult)
```

Arguments

gostResults   a data.frame containing the terms retained for the creation of the network.

Value

a data.frame of selected terms without the root term.

Author(s)

Astrid Deschênes

Examples

```
## Loading dataset containing result from an enrichment analysis done with
## gprofiler2
data(demoGOST)

## Only retained the GO - Molecular Function results
results <- demoGOST$result[demoGOST$result$source == "WP", ]

## Remove WIKIPATHWAYS root term
enrichViewNet:::removeRootTerm(gostResult=results)
```

rosaNapaVsDMSODEG	*The result of a differential expression analysis done between napabucasin treated and DMSO control MiaPaCa2 cells stably expressing the Rosa26 control vector. The cells were treated for 2 hour with 0.5 uM napabucasin. The protocol to generate the RNA-seq is described in Froeling F.E.M. et al 2019.*

Description

The object is a `data.frame` with 23542 rows and 4 columns. Each row correspond to a tested gene.

Usage

```
data(rosaNapaVsDMSODEG)
```

Format

a `data.frame` containing the results of a differential expression analysis between napabucasin treated and DMSO control MiaPaCa2 cells stably expressing the Rosa26 control vector for all 23542 genes tested. The 4 columns are:

- EnsemblID a `character` string representing the unique Ensembl identifier for the tested gene
- EnsemblID a `numeric` representing the expression difference (in log2FoldChange) between the napabucasin treatment and the DMSO control for the tested gene
- padj a `numeric` representing the adjusted p-value associated to the difference in expression for the tested gene
- GeneName a `character` string representing the name of the tested gene

Details

The differentially expressed genes between napabucasin-treated cells (0.5 uM) and DMSO as vehicle control are reprinted from Clinical Cancer Research, 2019, 25 (23), 7162–7174, Fieke E.M. Froeling, Manojit Mosur Swamynathan, Astrid Deschênes, Iok In Christine Chio, Erin Brosnan, Melissa A. Yao, Priya Alagesan, Matthew Lucito, Juying Li, An-Yun Chang, Lloyd C. Trotman, Pascal Belleau, Youngkyu Park, Harry A. Rogoff, James D. Watson, David A. Tuveson, Bioactivation of napabucasin triggers reactive oxygen species–mediated cancer cell death, with permission from AACR.

Value

a `data.frame` containing the results of a differential expression analysis between napabucasin treated and DMSO control MiaPaCa2 cells stably expressing the Rosa26 control vector for all 23542 genes tested. The 4 columns are:

- EnsemblID a `character` string representing the unique Ensembl identifier for the tested gene
- log2FoldChange a `numeric` representing the expression difference (in log2FoldChange) between the napabucasin treatment and the DMSO control for the tested gene

- padj a numeric representing the adjusted p-value associated to the difference in expression for
  the tested gene

- GeneName a character string representing the name of the tested gene

Source

The original RNA-sequencing data is available at the Gene Expression Omnibus (GEO) under the
accession number GSE135352.

See Also

- createNetwork for transforming functional enrichment results from gprofiler2 into a Cy-
  toscape network

Examples

```
## Required library
library(gprofiler2)

## Loading dataset containing the results of a differentially expressed
## analysis between 2-hour treatment with 0.5 uM napabucasin and
## DMSO vehicle control MiaPaCa2 cells stably expressing the
## Rosa26 control vector
data(rosaNapaVsDMSODEG)

allGenes <- unique(rosaNapaVsDMSODEG$EnsemblID)

## Select the significantly differentially expressed genes
selection <- which(abs(rosaNapaVsDMSODEG$log2FoldChange) > 1 &
                            rosaNapaVsDMSODEG$padj < 0.05)

selectedGenes <- unique(rosaNapaVsDMSODEG$EnsemblID[selection])

## Run an enrichment analysis using Transfac dataset (transcription factor)
gostres <- gost(query = list(rosa_napa_vs_DMSO=selectedGenes),
    organism="hsapiens",
    correction_method = "g_SCS",
    sources=c("TF"), significant=TRUE, evcodes=TRUE,
    custom_bg=allGenes, exclude_iea=TRUE)
```

rosaNapaVsDMSOEnrichment

> *The result of an enrichment analysis has been done using the significantly differentially expressed genes between napabucasin treated and DMSO control MiaPaCa2 cells stably expressing the Rosa26 control vector. The cells were treated for 2 hour with 0.5 uM napabucasin. The protocol to generate the RNA-seq is described in Froeling F.E.M. et al 2019.*

Description

The enrichment analysis was done with gprofile2 package (Kolberg L et al 2020) with database version 'e109_eg56_p17_1d3191d' and g:SCS multiple testing correction method applying significance threshold of 0.05 (Raudvere U et al 2019). All tested genes were used as background.

Usage

```
data(rosaNapaVsDMSOEnrichment)
```

Format

a `list` containing 2 entries:

- result a `data.frame` with the significantly enriched terms
- meta a TODO

Details

The object is a named `list` with 2 entries. The 'result' entry contains a `data.frame` with the enrichment analysis results and the 'meta' entry contains metadata information.

The dataset used for the enrichment analysis is associated to this publication:

Froeling F.E.M. et al.Bioactivation of Napabucasin Triggers Reactive Oxygen Species–Mediated Cancer Cell Death. Clin Cancer Res 1 December 2019; 25 (23): 7162–7174

The enrichment analysis has been done with gprofile2 package (Kolberg L et al 2020) with database version 'e109_eg56_p17_1d3191d' and g:SCS multiple testing correction method applying significance threshold of 0.05 (Raudvere U et al 2019). All tested genes were used as background.

Value

a `list` containing 2 entries:

- result a `data.frame` with the significantly enriched terms
- meta a TODO

Source

The original RNA-sequencing data is available at the Gene Expression Omnibus (GEO) under the accession number GSE135352.

See Also

- [createNetwork](#) for transforming functional enrichment results from gprofiler2 into a Cytoscape network

Examples

```
## Required library
library(gprofiler2)

## Loading dataset containing the results of a differentially expressed
## analysis between 2-hour treatment with 0.5 uM napabucasin and
## DMSO control MiaPaCa2 cells stably expressing the Rosa26 control vector
data(rosaNapaVsDMSOEnrichment)

## TODO
```

---

validateCreateEnrichMapArguments
                    Validate arguments passed to creatNetwork() function

---

Description

Validate the arguments passed to creatNetwork() function. First, the object containing the enrichment results must correspond to a object created by gprofiler2 software. Second, the selected source must at least have one enriched term in the results. Then, if the source is 'TERM_ID', the listed terms must be present in the enrichment results.

Usage

```
validateCreateEnrichMapArguments(
  gostObject,
  query,
  source,
  termIDs,
  removeRoot,
  showCategory,
  groupCategory,
  categoryLabel,
  categoryNode
)
```

Arguments

gostObject   a list created by gprofiler2 that contains the results from an enrichment analysis.

query   a `character` string representing the name of the query that is going to be used
                     to generate the graph. The query must exist in the `gostObject` object.

source   a `character` string representing the selected source that will be used to gen-
                     erate the network. To hand-pick the terms to be used, "TERM_ID" should be
                     used and the list of selected term IDs should be passed through the `termIDs`
                     parameter. The possible sources are "GO:BP" for Gene Ontology Biological
                     Process, "GO:CC" for Gene Ontology Cellular Component, "GO:MF" for Gene
                     Ontology Molecular Function, "KEGG" for Kegg, "REAC" for Reactome, "TF"
                     for TRANSFAC, "MIRNA" for miRTarBase, "CORUM" for CORUM database,
                     "HP" for Human phenotype ontology and "WP" for WikiPathways.

termIDs   a vector of `character` strings that contains the term IDs retained for the cre-
                     ation of the network. This parameter is only used when `source` is set to "TERM_ID".

removeRoot   a `logical` that specified if the root terms of the selected source should be re-
                     moved (when present).

showCategory   a positive `integer` or a `vector` of `characters` representing terms. If a `integer`,
                     the first n terms will be displayed. If `vector` of terms, the selected terms will be
                     displayed.

groupCategory   a `logical` indicating if the categories should be grouped.

categoryLabel   a positive `numeric` representing the amount by which plotting category nodes
                     label size should be scaled relative to the default (1).

categoryNode   a positive `numeric` representing he amount by which plotting category nodes
                     should be scaled relative to the default (1).

Value

TRUE when all arguments are valid

Author(s)

Astrid Deschênes

Examples

```
## Load the result of an enrichment analysis done with gprofiler2
data(demoGOST)

## Check that all arguments are valid
enrichViewNet:::validateCreateEnrichMapArguments(gostObject=demoGOST,
    query="query_1", source="GO:BP", termIDs=NULL, removeRoot=FALSE,
    showCategory=20, groupCategory=FALSE,
    categoryLabel=1.1, categoryNode=1)
```

validateCreateNetworkArguments

Validate arguments passed to creatNetwork() function

Description

Validate the arguments passed to creatNetwork() function. First, the object containing the enrichment results must correspond to a object created by gprofiler2 software. Second, the selected source must at least have one enriched term in the results. Then, if the source is 'TERM_ID', the listed terms must be present in the enrichment results.

Usage

```
validateCreateNetworkArguments(
  gostObject,
  source,
  termIDs,
  removeRoot,
  fileName
)
```

Arguments

gostObject	a list created by gprofiler2 that contains the results from an enrichment analysis.
source	a character string representing the selected source that will be used to generate the network. To hand-pick the terms to be used, "TERM_ID" should be used and the list of selected term IDs should be passed through the termIDs parameter. The possible sources are "GO:BP" for Gene Ontology Biological Process, "GO:CC" for Gene Ontology Cellular Component, "GO:MF" for Gene Ontology Molecular Function, "KEGG" for Kegg, "REAC" for Reactome, "TF" for TRANSFAC, "MIRNA" for miRTarBase, "CORUM" for CORUM database, "HP" for Human phenotype ontology and "WP" for WikiPathways.
termIDs	a vector of character strings that contains the term IDs retained for the creation of the network. This parameter is only used when source is set to "TERM_ID".
removeRoot	a logical that specified if the root terms of the selected source should be removed (when present).
fileName	a character string representing the name of the CX JSON file that is created when Cytoscape is not running. The name must have a '.cx' extension.

Value

TRUE when all arguments are valid

Author(s)

Astrid Deschênes

Examples

```
## Load the result of an enrichment analysis done with gprofiler2
data(demoGOST)

## Check that all arguments are valid
enrichViewNet:::validateCreateNetworkArguments(gostObject=demoGOST,
    source="GO:BP", termIDs=NULL, removeRoot=FALSE, fileName="test.cx")
```

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