

# Package ‘enrichViewNet’

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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.

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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. An edge connects 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
- [createEnrichMap](#) for transforming functional enrichment results from gprofiler2 into an enrichment map

---

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,  
  line,  
  ...  
)
```

## Arguments

|                              |   |
|------------------------------|---|
| <code>gostResults</code>     | a <code>data.frame</code> containing the enrichment results to be plot.   |
| <code>backgroundGenes</code> | a vector of character string representing the name of the genes present in the request.   |
| <code>showCategory</code>    | 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. |
| <code>groupCategory</code>   | a logical indicating if the categories should be grouped.   |
| <code>categoryLabel</code>   | 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.

line a non-negative numeric representing the scale of line width.

... additional arguments that will be pass to the [emapplot](#) function.

**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, line=1)
```

---

```
createCXJSONForCytoscape
```

*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**

```
createCXJSONForCytoscape(nodeEdgeInfo, title)
```

**Arguments**

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

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(parentalNapaVsDMSOEnrichment)

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

## Extract node and edge information
information <- enrichViewNet::extractInformationWhenIntersection(
  gostResults=results)

jsonFormat <- enrichViewNet::createCXJSONForCytoscape(
  nodeEdgeInfo=information, title="WikiPathways")
```

---

|                 |   |
|-----------------|---|
| createEnrichMap | <i>Using functional enrichment results in gprofiler2 format to create an enrichment map</i> |
|-----------------|---|

---

**Description**

User selected enrichment terms are used to create an enrichment map. The selection of the term can be specified 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 one 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,
line = 1,
...
)

```

### Arguments

|               |   |
|---------------|---|
| gostObject    | a list corresponding to gprofiler2 enrichment output that contains and 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 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.  |
| 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.   |
| line          | a non-negative numeric representing the scale of line width. Default: 1.  |
| ...           | additional arguments that will be pass to the <a href="#">emapplot</a> function.  |

### 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)
```

---

```
createEnrichMapMultiBasic
```

*Using functional enrichment results in gprofiler2 format to create an enrichment map with multiple groups from different enrichment analyses*

---

**Description**

User selected enrichment terms are used to create an enrichment map. The selection of the term can be specified 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 one significant term to graph.

**Usage**

```
createEnrichMapMultiBasic(
  gostObjectList,
  queryList,
  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,
  line = 1,
  ...
)
```

**Arguments**

**gostObjectList** a list of gprofiler2 objects that contain the results from an enrichment analysis. The list must contain at least 2 entries. The number of entries must correspond to the number of entries for the queryList parameter.

**queryList** a list of character strings representing the names of the queries that are going to be used to generate the graph. The query names must exist in the associated gostObjectList objects and follow the same order. The number of entries must correspond to the number of entries for the gostObjectList parameter.

|               |   |
|---------------|---|
| 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.  |
| 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.  |
| categoryNode  | a positive numeric representing the amount by which plotting category nodes should be scaled relative to the default (1). Default: 1.   |
| line          | a non-negative numeric representing the scale of line width. Default: 1.  |
| ...           | additional arguments that will be pass to the <a href="#">emapplot</a> function.  |

**Value**

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

**Author(s)**

Astrid Deschênes

**Examples**

```
## Loading dataset containing results from 2 enrichment analyses done with
## gprofiler2
data(parentalNapaVsDMSOEnrichment)
data(rosaNapaVsDMSOEnrichment)

## Extract query information (only one in each dataset)
query1 <- unique(parentalNapaVsDMSOEnrichment$result$query)[1]
query2 <- unique(rosaNapaVsDMSOEnrichment$result$query)[1]

## Create graph for KEGG related results from
## 2 enrichment analyses
createEnrichMapMultiBasic(gostObjectList=list(parentalNapaVsDMSOEnrichment,
  rosaNapaVsDMSOEnrichment),
  queryList=list(query1, query2), source="KEGG", removeRoot=TRUE)
```



---

```
createEnrichMapMultiComplex
```

*Using functional enrichment results in gprofiler2 format to create an enrichment map with multiple groups from same or different enrichment analyses*

---

## Description

User selected enrichment terms are used to create an enrichment map. The selection of the term can be specified 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 one significant term to graph.

## Usage

```
createEnrichMapMultiComplex(
  gostObjectList,
  queryInfo,
  showCategory = 30L,
  groupCategory = FALSE,
  categoryLabel = 1,
  categoryNode = 1,
  line = 1,
  ...
)
```

## Arguments

- |                             |  |
|-----------------------------|--|
| <code>gostObjectList</code> | a list of gprofiler2 objects that contain the results from an enrichment analysis. The list must contain at least 2 entries. The number of entries must correspond to the number of entries for the <code>queryList</code> parameter.  |
| <code>queryInfo</code>      | a data.frame contains one row per group being displayed. The number of rows must correspond to the number of entries for the <code>gostObjectList</code> parameter. The mandatory columns are: <ul style="list-style-type: none"> <li>• <code>queryName</code>: a character string representing the name of the query retained for this group). The query names must exist in the associated <code>gostObjectList</code> objects and follow the same order.</li> <li>• <code>source</code>: 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 <code>termIDs</code> 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".</li> <li>• <code>removeRoot</code>: a logical that specified if the root terms of the selected source should be removed (when present).</li> <li>• <code>termIDs</code>: a character strings that contains the term IDs retained for the creation of the network separated by a comma ',' when the "TERM_ID" source is selected. Otherwise, it should be an empty string ("").</li> </ul> |

- groupName: a character strings that contains the name of the group to be shown in the legend. Each group has to have a unique name.

|               |   |
|---------------|---|
| 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.  |
| categoryNode  | a positive numeric representing the amount by which plotting category nodes should be scaled relative to the default (1). Default: 1.   |
| line          | a non-negative numeric representing the scale of line width. Default: 1.  |
| ...           | additional arguments that will be pass to the <a href="#">emapplot</a> function.  |

**Value**

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

**Author(s)**

Astrid Deschênes

**Examples**

```
## Loading dataset containing results from 2 enrichment analyses done with
## gprofiler2
data(parentalNapaVsDMSOEnrichment)
data(rosaNapaVsDMSOEnrichment)

## TODO
gostObjectList=list(parentalNapaVsDMSOEnrichment,
  parentalNapaVsDMSOEnrichment, rosaNapaVsDMSOEnrichment,
  rosaNapaVsDMSOEnrichment)

## Create data frame containing required information enabling the
## selection of the retained enriched terms for each enrichment analysis.
## One line per enrichment analyses present in the gostObjectList parameter
## With this data frame, the enrichment results will be split in 4 groups:
## 1) KEGG significant terms from parental napa vs DMSO (no root term)
## 2) REACTOME significant terms from parental napa vs DMSO (no root term)
## 3) KEGG significant terms from rosa napa vs DMSO (no root term)
## 4) REACTOME significant terms from rosa napa vs DMSO (no root term)
queryDataFrame <- data.frame(queryName=c("parental_napa_vs_DMSO",
  "parental_napa_vs_DMSO", "rosa_napa_vs_DMSO", "rosa_napa_vs_DMSO"),
  source=c("KEGG", "REAC", "KEGG", "REAC"),
  removeRoot=c(TRUE, TRUE, TRUE, TRUE), termIDs=c("", "", "", ""),
  groupName=c("parental - KEGG", "parental - Reactome",
    "rosa - KEGG", "rosa - Reactome"), stringsAsFactors=FALSE)

## Create graph for KEGG and REACTOME significant results from
## 2 enrichment analyses
createEnrichMapMultiComplex(gostObjectList=gostObjectList,
  queryInfo=queryDataFrame, line=1.5)
```

---

`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()
```

---

`createMultiEmap`*Create a basic enrichment map*

---

**Description**

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

**Usage**

```
createMultiEmap(  
  gostResultsList,  
  queryList,  
  showCategory,  
  groupCategory,  
  categoryLabel,  
  categoryNode,  
  line,  
  ...  
)
```

**Arguments**

|                 |  |
|-----------------|--|
| gostResultsList | a list of data.frame containing the enrichment results to be plot with different group identification.   |
| queryList       | a list of character string representing the name of query retained for each enrichment results present in the gostResultsList parameter. The query should be present in its associated enrichment results. |
| 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).  |
| line            | a non-negative numeric representing the scale of line width.   |
| ...             | additional arguments that will be pass to the <a href="#">emapplot</a> function.   |

**Value**

a ggplot object representing the enrichment map with different colors for each group of enrichment results.

**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 subsection of REACTOME and KEGG
gostResultsREAC <- gostResults[which(gostResults$source == "REAC"),]
gostResultsREAC <- gostResultsREAC[1:13, ]
gostResultsKEGG <- gostResults[which(gostResults$source == "KEGG"),]

## Extract meta data information
queryList <- list("parental - REACTOME", "parental - KEGG")

## Create basic enrichment map using Wikipathways terms
enrichViewNet::createMultiEmap(gostResultsList=list(gostResultsREAC,
  gostResultsKEGG), queryList=queryList, showCategory=30L,
  groupCategory=FALSE, categoryLabel=1, categoryNode=1, line=1.4)
```

---

|               |  |
|---------------|--|
| createNetwork | <i>Using functional enrichment results from gprofiler2 to create a Cytoscape network</i> |
|---------------|--|

---

## Description

User selected enrichment terms are used to create a Cytoscape network where the selected terms and the genes that were part of the enrichment analysis are all represented as nodes. Edges are linking the genes to their terms. The selection of the term can be 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 one significant term to graph. When the enrichment analysis contains more than one query, only one query can be selected to generate the network.

## 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,
  query = NULL,
  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.  |
| query      | a character string that specified the retained query to generate the network. When NULL, the query present in the result is retained; NULL cannot be used when more than one query is present. Default: NULL.   |
| 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(parentalNapaVsDMSOEnrichment)

## Some of the enrichment results present in the dataset
head(parentalNapaVsDMSOEnrichment$result)

## 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=parentalNapaVsDMSOEnrichment, source="KEGG",
              removeRoot=FALSE, title="KEGG Graph",
              fileName=file.path(tempdir(), "KEGG_demo.cx"))
```

---

```
createNetworkForCytoscape
```

*Create network and load it into Cytoscape*

---

**Description**

Create network from gprofiler2 results and load it into Cytoscape

**Usage**

```
createNetworkForCytoscape(nodeEdgeInfo, title, collection)
```

**Arguments**

nodeEdgeInfo a TODO

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(parentalNapaVsDMSOEnrichment)

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

## Extract node and edge information
information <- enrichViewNet::extractInformationWhenIntersection(
  gostResults=results)

## 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::createNetworkForCytoscape(nodeEdgeInfo=information,
    title="Test", collection="New Collection")
}
```

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
- [createEnrichMap](#) for transforming functional enrichment results from `gprofiler2` into an enrichment map

**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"))
```

---

`extractInformationWhenIntersection`

*Extract node and edge information to be used to create network when interaction column is present*

---

**Description**

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

**Usage**

```
extractInformationWhenIntersection(gostResults)
```

**Arguments**

`gostResults` a `data.frame` containing the terms retained for the creation of the network. The `data.frame` must contain a column called "intersection".

**Value**

list containing 2 entries:

- "geneNodes": a `data.frame` containing the information about the nodes present in the network. The nodes are genes.



- "termNodes": a data.frame containing the information about the nodes present in the network. The nodes are terms.
- "edges": a data.frame containing the information about the edges present in the network. The edges connect one gene to one term.

**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", ]

## Extract node and edge information
information <-
  enrichViewNet::extractInformationWhenIntersection(
    gostResults=results)
```

---

extractInformationWhenNoIntersection

*Extract information about nodes and edges to be used to create network when interaction column is missing*

---

**Description**

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

**Usage**

```
extractInformationWhenNoIntersection(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 and meta-data from an enrichment analysis.

**Value**

list containing 2 entries:

- "geneNodes": a data.frame containing the information about the nodes present in the network. The nodes are genes.
- "termNodes": a data.frame containing the information about the nodes present in the network. The nodes are terms.

- "edges": a data.frame containing the information about the edges present in the network. The edges connect one gene to one term.

**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::extractInformationWhenNoIntersection(
  gostResults=results, gostObject=demoGOST)
```

---

extractNodesAndEdgesInformation

*Extract node and edge information from the enrichment results*

---

**Description**

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

**Usage**

```
extractNodesAndEdgesInformation(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:

- "geneNodes": a data.frame containing the information about the nodes present in the network. The nodes are genes.
- "termNodes": a data.frame containing the information about the nodes present in the network. The nodes are terms.
- "edges": a data.frame containing the information about the edges present in the network. The edges connect one gene to one term.

**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", ]

## Extract node and edge information
information <-
  enrichViewNet::extractNodesAndEdgesInformation(
    gostResults=results, gostObject=parentalNapaVsDMSOEnrichment)
```

---

|               |   |
|---------------|---|
| filterResults | <i>Filter the results to retain only the selected terms</i> |
|---------------|---|

---

**Description**

Filter the enrichment results to retain only the selected terms and remove root term if requested.

**Usage**

```
filterResults(gostResults, source, termIDs, removeRoot)
```

**Arguments**

|             |   |
|-------------|---|
| gostResults | a data.frame containing the enriched terms that should be filtered.   |
| 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 or NULL.  |
| removeRoot  | a logical that specified if the root terms of the selected source should be removed (when present).   |

**Value**

a data.frame of filtered terms with or 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

## Remove WIKIPATHWAYS root term
selected <- enrichViewNet:::filterResults(gostResults=results, source="WP",
    termIDs=NULL, removeRoot=TRUE)
```

---

formatInformationForCXJSON

*Transform the node and edge information into a format easy to process to create a CX JSON text file*

---

## Description

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

## Usage

```
formatInformationForCXJSON(results)
```

## Arguments

**results** a list containing the information about the nodes and edges present in the network. TODOS

## 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(parentalNapaVsDMSOEnrichment)

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

## Extract node and edge information
info <- enrichViewNet::extractNodesAndEdgesInformation(gostResults=results,
  gostObject=parentalNapaVsDMSOEnrichment)

## Format node and edge information
information <- enrichViewNet::formatInformationForCXJSON(result=info)
```

---

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()
```

---

```
manageNameDuplicationInEmap
```

*Change name description in data frame when more than one term as the same name*

---

### Description

The function adds the ID of the term at the name of the name description when terms with different ID share the same name. For example, "MAPK pathway" would become "MAPK pathway (KEGG:04010)".

### Usage

```
manageNameDuplicationInEmap(clProfDF)
```

### Arguments

`clProfDF` a data.frame containing the enrichment terms that are going to be graphed as an enrichment map. The data.frame must contain at least one case of duplicated name descriptions for different term IDs.

### Value

a data.frame with the name descriptions modified for terms with duplicated name descriptions but different term IDs.

### Author(s)

Astrid Deschênes

### Examples

```
## Data frame with duplicated name descriptions for different IDs
clustData <- data.frame(Cluster=c("group 1", "group 1", "group 2"),
  ID=c("WP:WP4925", "WP:WP382", "KEGG:04010"),
  Description=c("Unfolded protein response",
    rep("MAPK signaling pathway", 2)),
  GeneRatio=c("4/157", "3/157", "3/157"),
  BgRatio=c("4/24022", "3/24022", "3/24022"),
  pvalues=c(1.55e-4, 8.13e-8, 4.33e-5),
  p.adjust=c(1e-3, 1e-3, 1.4e-3), qvalue=c(1e-3, 1e-3, 1.4e-3),
  geneID=c("ENSG000107968/ENSG000120129/ENSG000123358/ENSG000158050",
    "ENSG000107968/ENSG000120129/ENSG000158050",
    "ENSG000107968/ENSG000120129/ENSG000158050"),
  Count=c(4, 3, 3))

## Change the name descriptions for the duplicated terms
enrichViewNet::manageNameDuplicationInEmap(clProfDF=clustData)
```

---

 manageQueryDuplicationInEmap

*Change query name when more than one queries have the same name*


---

### Description

The function adds an unique ID at the name of the query when more than one query have the same name.

### Usage

```
manageQueryDuplicationInEmap(queryList)
```

### Arguments

queryList      a list containing the query names.

### Value

a list with the query names modified for queries with duplicated names.

### Author(s)

Astrid Deschênes

### Examples

```
## List of query names with duplicated names
queryList <- list("parental_vs_DMSO", "rosa_vs_DMSO", "parental_vs_DMSO",
  "rosa_vs_DMSO", "parental_vs_Control", "rosa_vs_DMSO")

## Change the query names for the duplicated names
enrichViewNet:::manageQueryDuplicationInEmap(queryList=queryList)
```

---

parentalNapaVsDMSODEG *The result of a differential expression analysis done between napabucasin treated and DMSO control parental MiaPaCa2 cells. The cells were treated for 2 hours 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
- "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

**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
- "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 Cytoscape network
- [createEnrichMap](#) for transforming functional enrichment results from gprofiler2 into an enrichment map



## 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 created by gprofiler2 that contains the results from the enrichment analysis:

- "result": a data.frame with the significantly enriched terms
- "meta": a list with the meta-data information

**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 list with the meta-data information

**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
- [createEnrichMap](#) for transforming functional enrichment results from gprofiler2 into an enrichment map

**Examples**

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

## Create an enrichment map for the GO:CC terms
createEnrichMap(gostObject=parentalNapaVsDMSOEnrichment,
  query="parental_napa_vs_DMSO", source="GO:CC")
```

---

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**

`gostResult` 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 WikiPathways results
results <- demoGOST$result[demoGOST$result$source == "WP", ]

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

---

|                   |  |
|-------------------|--|
| rosaNapaVsDMSODEG | <i>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 hours with 0.5 uM napabucasin. The protocol to generate the RNA-seq is described in Froeling F.E.M. et al 2019.</i> |
|-------------------|--|

---

**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
- "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

## 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 Cytoscape network
- [createEnrichMap](#) for transforming functional enrichment results from gprofiler2 into an enrichment map

## 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 that 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 created by gprofiler2 that contains the results from the enrichment analysis:

- "result": a data.frame with the significantly enriched terms
- "meta": a list with the meta-data information

## 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 created by gprofiler2 that contains the results from the enrichment analysis:

- "result": a data.frame with the significantly enriched terms
- "meta": a list with the meta-data information

**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
- [createEnrichMap](#) for transforming functional enrichment results from gprofiler2 into an enrichment map

**Examples**

```
## Loading dataset containing the enrichment analysis done on the
## 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)

## Create an enrichment map for the KEGG terms
createEnrichMap(gostObject=rosaNapaVsDMSOEnrichment,
  query="rosa_napa_vs_DMSO", source="KEGG")
```

---

validateCreateEnrichMapArguments

*Validate arguments passed to createEnrichMap() function*

---

**Description**

Validate the arguments passed to createEnrichMap() 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,
    line
)

```

### 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 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).   |
| 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).   |
| line          | a non-negative numeric representing the scale of line width.  |

### 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, line=1.2)

```

---

 validateCreateEnrichMapMultiArguments

*Validate arguments passed to createEnrichMapMultiBasic() function*


---

### Description

Validate the arguments passed to createEnrichMapMultiBasic() 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

```
validateCreateEnrichMapMultiArguments(
  gostObjectList,
  queryList,
  source,
  termIDs,
  removeRoot,
  showCategory,
  groupCategory,
  categoryLabel,
  categoryNode,
  line
)
```

### Arguments

|                |   |
|----------------|---|
| gostObjectList | a list of gprofiler2 objects that contain the results from an enrichment analysis. The list must contain at least 2 entries. The number of entries must correspond to the number of entries for the queryList parameter.  |
| queryList      | a list of character strings representing the names of the queries that are going to be used to generate the graph. The query names must exist in the associated gostObjectList objects and follow the same order. The number of entries must correspond to the number of entries for the gostObjectList parameter.  |
| 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).   |
| 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).            |
| line          | a non-negative numeric representing the scale of line width.   |

**Value**

TRUE when all arguments are valid

**Author(s)**

Astrid Deschênes

**Examples**

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

## Check that all arguments are valid
enrichViewNet::validateCreateEnrichMapMultiArguments(
  gostObjectList=list(parentalNapaVsDMSOEnrichment,
                      rosaNapaVsDMSOEnrichment),
  queryList=list("parental_napa_vs_DMSO", "rosa_napa_vs_DMSO"),
  source="GO:BP", termIDs=NULL, removeRoot=FALSE,
  showCategory=20, groupCategory=FALSE,
  categoryLabel=1.1, categoryNode=1, line=1.2)
```

---

```
validateCreateEnrichMapMultiComplexArg
```

*Validate arguments passed to validateCreateEnrichMapMultiComplex() function*

---

**Description**

Validate the arguments passed to validateCreateEnrichMapMultiComplex() 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**

```
validateCreateEnrichMapMultiComplexArg(
  gostObjectList,
  queryInfo,
  showCategory,
  groupCategory,
  categoryLabel,
  categoryNode,
  line
)
```

**Arguments**

|                             |  |
|-----------------------------|--|
| <code>gostObjectList</code> | a list of <code>gprofiler2</code> objects that contain the results from an enrichment analysis. The list must contain at least 2 entries. The number of entries must correspond to the number of entries for the <code>queryList</code> parameter.   |
| <code>queryInfo</code>      | a <code>data.frame</code> contains one row per group being displayed. The number of rows must correspond to the number of entries for the <code>gostObjectList</code> parameter. The mandatory columns are: <ul style="list-style-type: none"> <li><code>queryName</code>: a character string representing the name of the query retained for this group). The query names must exist in the associated <code>gostObjectList</code> objects and follow the same order.</li> <li><code>source</code>: 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 <code>termIDs</code> 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".</li> <li><code>removeRoot</code>: a logical that specified if the root terms of the selected source should be removed (when present).</li> <li><code>termIDs</code>: a character strings that contains the term IDS retained for the creation of the network separated by a comma ',' when the "TERM_ID" source is selected. Otherwise, it should be a empty string ("").</li> <li><code>groupName</code>: a character strings that contains the name of the group to be shown in the legend. Each group has to have a unique name.</li> </ul> |
| <code>showCategory</code>   | 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.  |
| <code>groupCategory</code>  | a logical indicating if the categories should be grouped.  |
| <code>categoryLabel</code>  | a positive numeric representing the amount by which plotting category nodes label size should be scaled relative to the default (1).   |
| <code>categoryNode</code>   | a positive numeric representing he amount by which plotting category nodes should be scaled relative to the default (1).   |
| <code>line</code>           | a non-negative numeric representing the scale of line width.   |

**Value**

TRUE when all arguments are valid

**Author(s)**

Astrid Deschênes

**Examples**

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

```

queryDataFrame <- data.frame(queryName=c("parental_napa_vs_DMSO",
  "rosa_napa_vs_DMSO"), source=c("KEGG", "WP"), removeRoot=c(TRUE, TRUE),
  termIDs=c("", ""), groupName=c("parental - KEGG", "rosa - WP"),
  stringsAsFactors=FALSE)

## Check that all arguments are valid
enrichViewNet::validateCreateEnrichMapMultiComplexArg(
  gostObjectList=list(parentalNapaVsDMSOEnrichment,
    rosaNapaVsDMSOEnrichment),
  queryInfo=queryDataFrame,
  showCategory=20, groupCategory=FALSE,
  categoryLabel=1.1, categoryNode=1, line=1.2)

```

---

```
validateCreateEnrichMapSubSectionArguments
```

*Validate common arguments passed to createEnrichMap() and createEnrichMapMultiBasic() functions*

---

## Description

Validate the common arguments passed to createEnrichMap() and createEnrichMapMultiBasic() functions.

## Usage

```

validateCreateEnrichMapSubSectionArguments(
  showCategory,
  groupCategory,
  categoryLabel,
  categoryNode,
  line
)

```

## Arguments

|               |   |
|---------------|---|
| 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).   |
| line          | a non-negative numeric representing the scale of line width.  |

## Value

TRUE when all arguments are valid

**Author(s)**

Astrid Deschênes

**Examples**

```
## Check that all arguments are valid
enrichViewNet::validateCreateEnrichMapSubSectionArguments(
  showCategory=20, groupCategory=FALSE, categoryLabel=1.1, categoryNode=1,
  line=0.5)
```

---

```
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,
  query,
  title,
  collection,
  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).   |

|            |   |
|------------|---|
| query      | a character string that specified the retained query to generate the network or NULL.   |
| title      | a character string representing the name assigned to the network.   |
| collection | a character string representing the collection name assigned to the network.  |
| 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, query=NULL,
  title="Network graph Test",
  collection="test collection", fileName="test.cx")
```

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