

Package ‘PFP’

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Type Package

Title Pathway Fingerprint Framework in R

Version 1.2.0

biocViews Software, Pathways, RNASeq

Description An implementation of the pathway fingerprint framework that introduced in paper “Pathway Fingerprint: a novel pathway knowledge and topology based method for biomarker discovery and characterization”.

This method provides a systematic comparisons between a gene set (such as a list of differentially expressed genes) and well-studied “basic pathway networks” (KEGG pathways), measuring the importance of pathways and genes for the gene set.

The package is helpful for researchers to find the biomarkers and its function.

Depends R (>= 4.0)

Imports graph, igraph, KEGGgraph, clusterProfiler, ggplot2, plyr, tidy, magrittr, stats, methods, utils

Suggests knitr, testthat, rmarkdown, org.Hs.eg.db

License GPL-2

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calc_PFP_score	<i>Get the pathway fingerprint of a gene_list</i>
----------------	---

Description

It can evaluate the performance of a gene list in the pathway networks.

Usage

```
calc_PFP_score(  
  genes,  
  PFPRefnet,  
  lambda = 0.5,  
  coeff1 = 1,  
  coeff2 = 0.1,  
  statistic = TRUE,  
  bg_genelist = NULL,  
  adjust_method = "BH"  
)
```

Arguments

genes,	a vector of characters
PFPRefnet,	A PFPRefnet class
lambda,	a numeric, the coefficient for keeping balance between the node_score and edge_score in PFP model
coeff1,	a numeric, the weight coefficient for directly connected score in PFP model
coeff2,	a numeric, the weight coefficient for indirectly connected score in PFP model
statistic,	a logical, whether to do the statistical test
bg_genelist,	a vector of characters, background gene set for the statistical test
adjust_method,	statistic test method for adjust the p_value. It could be "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".

Details

The main part of pathway fingerprint. PFP is used to evaluate the performance of a gene_list in some pathway networks by considering the genes' topological location in a pathway. Then we can get every gene's score and the pathway score is caculated by sum all genes' score. All pathways' scores combine the pathway fingerprint.

Value

The score of PFP

Examples

```
data(gene_list_hsa)
data(PFPRefnet_hsa)
PFP <- calc_PFP_score(gene_list_hsa,PFPRefnet_hsa)
```

data_std	<i>A matrix of counts A dataset of gene expression profile, a large matrix with 21 rows and 2603 columns.</i>
----------	---

Description

A matrix of counts A dataset of gene expression profile, a large matrix with 21 rows and 2603 columns.

Format

Gene list obtained by differential gene analysis

Examples

```
data(data_std)
```

genes_score-methods	<i>The score of genes in PFP class</i>
---------------------	--

Description

This function extract the detail scores of every gene in the gene_list by specific condition.

Usage

```
genes_score(
  object,
  index = NULL,
  index_type = c("pathway_id", "pathway_name", "slice")
)

## S4 method for signature 'PFP'
genes_score(
  object,
  index = NULL,
  index_type = c("pathway_id", "pathway_name", "slice")
)
```

Arguments

object, PFP class
index, character, indicating the groups to subset.
index_type, "pathway_id", "pathway_name", "slice"

Value

a named vector of numeric scores

See Also

[PFP-class](#)

Examples

```
data(PFP_test1)  
genes_score <- genes_score(PFP_test1)
```

gene_list_hsa	<i>A gene list of human gene_list_hsa is a array of 40 genetic ENTREZID.</i>
---------------	--

Description

A gene list of human gene_list_hsa is a array of 40 genetic ENTREZID.

Format

Gene list obtained by differential gene analysis

Examples

```
data(gene_list_hsa)
```

get_asso_net *merge the edges_coexp and edges_kegg*

Description

This function will remove the co-expressed edges in edges_coexp which also emerge in edges_kegg.

Usage

```
get_asso_net(
  edges_coexp,
  edges_kegg,
  file_dir = NULL,
  if_symbol = TRUE,
  trans_fun = trans_edges_id,
  from_type = "ENTREZID",
  to_type = "SYMBOL",
  gene_info_db = NULL
)
```

Arguments

edges_coexp,	a data.frame whose colnames is "source", "target", "weight", "pathway", "edge_type".
edges_kegg,	a data.frame whose colnames is "source", "target", "weight", "pathway", "edge_type".
file_dir,	a character, the root to save the result of nodes & edges.
if_symbol,	a logical, whether to translate the gene id type. Default is TRUE.
trans_fun,	a function, when if_symbol is <i>TRUE</i> , it will use the trans_fun function to translate the gene ids. Default is trans_edges_id.
from_type,	a character, the parameter in trans_fun. It is the type of gene ID, "ENSEMBL", "GO", "SYMBOL" and so on.
to_type,	a character, the parameter in trans_fun. It is the type of gene ID, "ENSEMBL", "GO", "SYMBOL" and so on.
gene_info_db,	an AnnotationDb-object for gene annotation, such as "org.Hs.eg.db".

Details

This function will remove the co-expressed edges in edges_coexp which also emerge in edges_kegg. It will return a list contains two data.frames. One is the merged data. Another is the nodes information of the edges.

Value

the nodes information of the edges.

Examples

```
data(PFPRefnet_hsa)
data(data_std)
data(PFP_test1)
rank1 <- rank_PFP(object = PFP_test1, total_rank = TRUE)
pathway_select <- refnet_info(rank1)[1, "id"]
gene_test <- pathways_score(rank1)$genes_score[[pathway_select]]$ENTREZID
edges_coexp <- get_exp_cor_edges(gene_test, data_std)
gene_list2 <- unique(c(edges_coexp$source, edges_coexp$target))
edges_kegg <- get_bg_related_kegg(gene_list2,
                                 PFPRefnet=PFPRefnet_hsa,
                                 rm_duplicated = TRUE)
```

get_bg_related_kegg *get_bg_related_kegg*

Description

This function will select all genes in all kegg pathways which are directly connected with the genes in `gene_list`

Usage

```
get_bg_related_kegg(gene_list, PFPRefnet, rm_duplicated = FALSE)
```

Arguments

`gene_list`, a vector of characters, refers to genes ids
`PFPRefnet`, an object of PFPRefnet class, it contains all kegg pathways.
`rm_duplicated`, a logical, whether to remove the duplicated kegg edges in different pathways.
 Default is *FALSE*

Details

It will return a data.frame which can be translated a graph or network. In the data.frame, `source` refers to the genes in `gene_list`, `target` refers to the directly connected genes in kegg, `weight` is 0.5, no real means, `pathway` refers to the pathway which the edge emerge and `edge_type` is "kegg". Note, if `rm_duplicated` is *FALSE*, it may return many duplicated edges, which will be complex when plotting a network. If `rm_duplicated` is *TRUE*, it will retain the first pathway which contains the duplicated edge.

Value

the related kegg network.

Examples

```
data(PFPRefnet_hsa)
data(gene_list_hsa)
edges_kegg <- get_bg_related_kegg(gene_list_hsa,
                                  PFPRefnet=PFPRefnet_hsa,
                                  rm_duplicated = TRUE)
```

```
get_exp_cor_edges      get co-expression genes
```

Description

compute the correlation coefficient of gene expression data, return the most related genes

Usage

```
get_exp_cor_edges(
  gene_list,
  data_std,
  method = "spearman",
  num = 5,
  cor_threshold = NULL
)
```

Arguments

gene_list,	a vector of characters
data_std,	a matrix of data, such as gene expression data, whose rownames are gene names or ids and colnames are sample names
method,	a character, which method to compare the correlation of gene expression data it could be "pearson", "kendall", "spearman", "spearman" is default
num,	an integer, the top number of co-expressed genes to choose, 5 is default
cor_threshold,	a numeric, the threshold of the correlation coefficient to choose, default is <i>NULL</i>

Details

This function computes the correlation coefficient of gene expression data between `gene_list` and `data_std`, it will return a `data.frame` which can be translated a graph or network. In the `data.frame`, `source` refers to the genes in `gene_list`, `target` refers to the top coexpressed genes, `weight` refers to the correlated coefficient of genes in `source` and `target`, `pathway` is "uncertain" and `edge_type` is "coexp". Note, when choosing the top co-expressed genes, we will use the `num` param if the `cor_threshold` param is *NULL*. If not, we will choose the `cor_threshold` param.

Value

the coexp of edges.

Examples

```
data(data_std)
data(PFP_test1)
rank1 <- rank_PFP(object = PFP_test1, total_rank = TRUE)
pathway_select <- refnet_info(rank1)[1, "id"]
gene_test <- pathways_score(rank1)$genes_score[[pathway_select]]$ENTREZID
edges_coexp <- get_exp_cor_edges(gene_test, data_std)
```

`get_pathway_info` *get pathway info of a species in KEGG*

Description

This function helps get pathway info of a species in KEGG.

Usage

```
get_pathway_info(spec)
```

Arguments

`spec`, a character, refers to the species in KEGG. hsa, mmu...

Details

, get pathway info of a species in KEGG. It will return a data.frame.

Value

a data.frame whose colnames contains "index", "id", "name" and "group"

Examples

```
pathway_info <- get_pathway_info("hsa")
```

get_PFPRefnet	<i>get a PFPRefnet for a species</i>
---------------	--------------------------------------

Description

This function helps update the latest PFPRefnet object for a species

Usage

```
get_PFPRefnet(spec, file_root = ".", test_mode = FALSE)
```

Arguments

spec,	a character, refers to the species in KEGG. hsa, mmu...
file_root,	a character, file dir to download the kgml files.
test_mode,	please set whether to test this function.

Details

, gupdate the latest PFPRefnet object for a species in KEGG. It will return a PFPRefnet object.

Value

a PFPRefnet object.

Examples

```
PFPRefnet1 <- get_PFPRefnet("hsa", ".", test_mode=TRUE)
```

group-methods	<i>group information of PFPRefnet</i>
---------------	---------------------------------------

Description

This function contains names of basic groups of the networks and group number, as well as the size of each group

Usage

```
group(object)

## S4 method for signature 'PFPRefnet'
group(object)
```

Arguments

object, PFPRefnet class

Value

a list contains names of basic groups of the networks and group number, as well as the size of each group

See Also

[PFPRefnet-class](#)

Examples

```
data(PFPRefnet_hsa)
group <- group(PFPRefnet_hsa)
```

kegg_download	<i>download kegg KGML files</i>
---------------	---------------------------------

Description

This function will download all kegg KGML files assigned by spec.

Usage

```
kegg_download(spec, file_root = ".", test_mode = FALSE)
```

Arguments

spec, a character, refers to the species names in kegg, such as "hsa", "mmu"...

file_root, a character, refers to the root you want to save kegg pathway kgml files in.

test_mode, please set whether to test this function.

Details

Downloading all kegg KGML files assigned by spec from <https://www.kegg.jp/kegg/xml/>, which may take tens of minutes.

Value

the kegg KGML files

Examples

```
kegg_download(spec, file_root=".", test_mode=TRUE)
```

network-methods

Basic pathway networks of PFPreRefnet class

Description

This function extract the basic networks of PFPreRefnet class.

Usage

```
network(object)
```

```
## S4 method for signature 'PFPreRefnet'  
network(object)
```

Arguments

object, PFPreRefnet class

Value

a graphNEL list of all basic networks

See Also

[PFPreRefnet-class](#)

Examples

```
data(PFPreRefnet_hsa)  
network <- network(PFPreRefnet_hsa)
```

net_info-methods

Basic pathway networks information of PFPreRefnet class

Description

This function extract the basic networks information of PFPreRefnet class.

Usage

```
net_info(object)
```

```
## S4 method for signature 'PFPreRefnet'  
net_info(object)
```

Arguments

object, PFPRefnet class

Value

a dataframe contains basic networks' information

See Also

[PFPRefnet-class](#)

Examples

```
data(PFPRefnet_hsa)
net_info <- net_info(PFPRefnet_hsa)
```

net_names-methods *Names of basic networks*

Description

This function extract the network names of PFPRefnet.

Usage

```
net_names(object)

## S4 method for signature 'PFPRefnet'
net_names(object)
```

Arguments

object, PFPRefnet class

Value

a vector contains pathway names

See Also

[PFPRefnet-class](#)

Examples

```
data(PFPRefnet_hsa)
net_names <- net_names(PFPRefnet_hsa)
```

pathways_score-methods

Basic pathway networks scores of PFP class

Description

This function can extract the details in pathway fingerprint scores.

Usage

```
pathways_score(object)
```

```
## S4 method for signature 'PFP'  
pathways_score(object)
```

Arguments

object, PFP class

Value

as list, details in pathway fingerprint scores.

See Also

[PFP-class](#)

Examples

```
data(PFP_test1)  
pathways_score <- pathways_score(PFP_test1)
```

pathway_info

pathway_info pathway_info is dataframe of the information of pathway, 539rows, 4columns.

Description

pathway_info pathway_info is dataframe of the information of pathway, 539rows, 4columns.

Format

a list

Examples

```
data(pathway_info)
```

pathway_info_hsa	<i>pathway_info pathway_info is dataframe of the information of pathway, 539rows, 4columns.</i>
------------------	---

Description

pathway_info pathway_info is dataframe of the information of pathway, 539rows, 4columns.

Format

a list pathway_info_hsa pathway_info_hsa is dataframe of the information of pathway, 539rows, 4columns. The main data is about human.

Examples

```
data(pathway_info_hsa)
```

PFP	<i>The NFP package</i>
-----	------------------------

Description

This package implementation the applications of network finger print method.

PFP-class	PFP-class
-----------	-----------

Description

An S4 object for storing pathway fingerprint scores information.

Slots

pathways_score, a list contains PFP_score, stats_test, genes_score. PFP_score is a numeric score indicating the performance of a gene_list in some pathways.stats_test is a statistic test for the PFP_score. genes_score is the detail scores of every gene in the gene_list.

refnet_info, a data.frame, which contains the specific information of pathway networks. Just be the same as [net_info](#) in [PFPRefnet-class](#), including the index, id, name, group and species.

method

- `pathways_score`, signature(object = "PFP"): extract the pathways score
- `refnet_info`, signature(object = "PFP"): extract the pathway networks information
- `PFP_score`, signature(object = "PFP"): extract the PFP score
- `stats_test`, signature(object = "PFP"): extract p_value & p_adj_value
- `genes_score`, signature(object = "PFP", index=NULL, index_type = c("pathway_id", "pathway_name", "slice")): extract the genes score
- `refnet_names`, signature(object = "PFP"): extract the refnet names
- `sub_PFP`, signature(object = "PFP", group_name = NULL, index = NULL, index_type = c("slice", "pathway_id")): subset of PFP object
- `show_PFP`, signature(object = "PFP"): display methods for S4 classes PFP
- `plot_PFP`, signature(object, type = "character", p_size = "numeric", l_size = 'numeric'): plot the Pathway Fingerprint.
- `rank_PFP` signature(object = "PFP", total_rank = FALSE, decreasing=TRUE) sort the PFP score.

See Also

[pathways_score-methods](#), [refnet_info-methods](#), [PFP_score-methods](#), [stats_test-methods](#), [genes_score-methods](#), [refnet_names-methods](#), [sub_PFP-methods](#), [show_PFP-methods](#), [plot_PFP-methods](#), [rank_PFP-methods](#),

Examples

```
data(PFP_test1)
PFP_test1
```

PFPrefnets-class

PFPrefnets-class

Description

An S4 object for storing PFP reference network information.

Value

a object of PFPrefnets class

Slots

`network`, object of graphNEL list represents the basic networks.

`net_info`, a dataframe which contains the index, id, name, group and species. It contains the information of the pathway networks, whose row number is the same with `network`.

#' @section method:

- `network`, signature(object = "PFPreRefnet"): extract networks of PFPreRefnet
- `net_info`, signature(object = "PFPreRefnet"): extract net information of PFPreRefnet
- `group`, signature(object = "PFPreRefnet"): extract group information
- `net_names`, signature(object = "PFPreRefnet"): the names of basic networks
- `subnet`, signature(object = "PFPreRefnet"): subset basic networks, e.g. a group of a networks or some networks of some given groups
- `show_net`, signature(object = "PFPreRefnet"): display methods for S4 classes PFPreRefnet, see also [show_net](#)

See Also

[network-methods](#), [net_info-methods](#), [group-methods](#), [net_names-methods](#), [subnet-methods](#), [show_net-methods](#),

Examples

```
data(PFPreRefnet_hsa)
PFPreRefnet_hsa
```

PFPreRefnet_hsa

Pathway fingerprint data of human

Description

A dataset containing the pathway maps of KEGG PFPreRefnet_hsa is a PFPreRefnet class with `network` (a list of length 338), `net_info`

Format

A PFPreRefnet object, more details see [PFPreRefnet-class](#)

See Also

[PFPreRefnet-class](#)

Examples

```
data(PFPreRefnet_hsa)
```

PFPRefnet_mmu	<i>Pathway fingerprint data of mouse</i>
---------------	--

Description

A dataset containing the pathway maps of KEGG PFPRefnet_mmu a PFPRefnet class with network(a list of length 334), net_info (a dataframe, 334rows and 5 columns), the main data is about mouse.

Format

A PFPRefnet object, more details see [PFPRefnet-class](#)

See Also

[PFPRefnet-class](#)

Examples

```
data(PFPRefnet_mmu)
```

PFP_score-methods	<i>The score of PFP</i>
-------------------	-------------------------

Description

This function can extract the PFP_score of PFP.

Usage

```
PFP_score(object)  
  
## S4 method for signature 'PFP'  
PFP_score(object)
```

Arguments

object, PFP class

Value

the PFP_score

See Also

[PFP-class](#)

Examples

```
data(PFP_test1)
PFP_score <- PFP_score(PFP_test1)
```

PFP_test1	<i>PFP_test1</i>
-----------	------------------

Description

A dataset of PFP class a PFP class with pathways_score(a list of length 3), refnet_info (a dataframe, 338rows and 3 columns), the main data is about human.

Format

A PFPRefnet object,

See Also

[PFP-class](#)

Examples

```
data(PFP_test1)
```

PFP_test2	<i>PFP_test2</i>
-----------	------------------

Description

A dataset of PFP class

Format

A PFPRefnet object,

Details

a PFP class with pathways_score(a list of length 3), refnet_info (a dataframe, 338rows and 3 columns), the main data is about human.

See Also

[PFP-class](#)

Examples

```
data(PFP_test2)
```

plot_PFP-methods *Plot PFP results*

Description

Function for visualization PFP results.

Usage

```
plot_PFP(  
  object,  
  type = c("matchstick", "line", "point"),  
  p_size = 1,  
  l_size = 0.5  
)  
  
## S4 method for signature 'PFP'  
plot_PFP(  
  object,  
  type = c("matchstick", "line", "point"),  
  p_size = 1,  
  l_size = 0.5  
)
```

Arguments

object,	PFP class
type,	types of the visaulization of <i>PFP</i> object, 'matchstick', 'line', 'point'. Default is 'matchstick'.
p_size,	point size of plot, default is 1.
l_size,	line size of plot, default is 0.5.

Value

a plot of PFP

See Also

[PFP-class](#)

Examples

```
data(PFP_test1)  
plot_PFP(PFP_test1,'line', p_size = 1, l_size = 0.5)
```

plot_PFPlist	<i>Plot multiple PFPs.</i>
--------------	----------------------------

Description

Function for visualization multiple PFPs.

Usage

```
plot_PFPlist(object, l_size = 0.5)
```

Arguments

object,	PFP a list of PFP.
l_size,	line size of plot, default is 0.5.

Value

plot the PFP list

See Also

[PFP-class](#)

Examples

```
data(PFP_test1)
pfp_list <- list(a=PFP_test1)
plot_PFPlist(pfp_list)
```

rank_PFP-methods	<i>rank PFPscore</i>
------------------	----------------------

Description

rank the PFP object by the value of PFP_score.

Usage

```
rank_PFP(  
  object,  
  total_rank = FALSE,  
  decreasing = TRUE,  
  thresh_slot = "p_adj_value",  
  thresh_value = 0.05  
)
```

```
## S4 method for signature 'PFP'  
rank_PFP(  
  object,  
  total_rank = FALSE,  
  decreasing = TRUE,  
  thresh_slot = "p_adj_value",  
  thresh_value = 0.05  
)
```

Arguments

object,	PFP class
total_rank,	a logical, whether to rank in total range,the default is <i>TRUE</i>
decreasing,	a logical, Sorting method, the default is <i>TRUE</i>
thresh_slot,	a character, it could be 'p_value' or 'p_adj_value', it means the threshold slot to choose for select the significant pathway. Default is 'p_adj_value'.It also could be <i>NULL</i> ,it means that you don't want to select the significant pathway and you will select all pathways.
thresh_value,	a numeric, threshold value of 'p_value' or 'p_adjust_value' for pathway selection

Value

a ranked PFP object.

See Also

[PFP-class](#)

Examples

```
data(PFP_test1)  
rank_PFP(PFP_test1,  
  total_rank=FALSE,  
  decreasing=TRUE,  
  thresh_slot="p_adj_value",  
  thresh_value = 0.05)
```

refnet_info-methods *Basic network information of PFP class*

Description

This function extract the detail information of reference pathway networks.

Usage

```
refnet_info(object)

## S4 method for signature 'PFP'
refnet_info(object)
```

Arguments

object, PFP class

Value

detail information of reference pathway networks

See Also

[PFP-class](#)

Examples

```
data(PFP_test1)
refnet_info <- refnet_info(PFP_test1)
```

refnet_names-methods *Names of basic networks*

Description

This function extract the reference pathway network names of PFP.

Usage

```
refnet_names(object)

## S4 method for signature 'PFP'
refnet_names(object)
```

Arguments

object, PFPRefnet class

Value

a vector contains pathway names

Examples

```
data(PFP_test1)
refnet_names <- refnet_names(PFP_test1)
```

result_PFP-methods *result of the PFP object.*

Description

get the result of the PFP object.

Usage

```
result_PFP(object, thresh_slot = NULL, thresh_value = 0.05)
```

```
## S4 method for signature 'PFP'
```

```
result_PFP(object, thresh_slot = NULL, thresh_value = 0.05)
```

Arguments

object, PFP class

thresh_slot, a character, it could be 'p_value' or 'p_adj_value', it means the threshold slot to choose for select the significant pathway. Default is *NULL*, it means that you don't want to select the significant pathway and you will select all pathways.

thresh_value, a numeric, threshold value of 'p_value' or 'p_adjust_value' for pathway selection, Default is 0.05.

Value

the scores and the information of PFP object.

See Also

[PFP-class](#)

Examples

```
data(PFP_test1)
result_PFP(PFP_test1,
           thresh_slot="p_adj_value",
           thresh_value = 0.05)
```

show_net	<i>Show an Object</i>
----------	-----------------------

Description

show method short for PFPretnet object

Usage

```
show_net(object)
```

```
## S4 method for signature 'PFPretnet'  
show_net(object)
```

Arguments

object, PFPretnet object

Value

show the network

See Also

[PFPretnet-class](#)

Examples

```
data(PFPretnet_hsa)  
show_net(PFPretnet_hsa)
```

show_PFP	<i>The show_PFP generic function</i>
----------	--------------------------------------

Description

Show a short summary for PFP object.

Usage

```
show_PFP(object)
```

```
## S4 method for signature 'PFP'  
show_PFP(object)
```

Arguments

object, PFP object

Value

show the PFP

Examples

```
data(PFP_test1)
show_PFP(PFP_test1)
```

stats_test-methods *The P value of PFP*

Description

This function can extract the result of statistical analysis

Usage

```
stats_test(object)

## S4 method for signature 'PFP'
stats_test(object)
```

Arguments

object, PFP class

Value

Statistical test result of each pathway score

See Also

[PFP-class](#)

Examples

```
data(PFP_test1)
stats_test <- stats_test(PFP_test1)
```

`subnet-methods`*Subset the basic networks*

Description

Extract or Replace parts of the PFPRefnet.

Usage

```
subnet(  
  object,  
  group_name = NULL,  
  index = NULL,  
  index_type = c("slice", "pathway_id", "pathway_name")  
)  
  
## S4 method for signature 'PFPRefnet'  
subnet(  
  object,  
  group_name = NULL,  
  index = NULL,  
  index_type = c("slice", "pathway_id", "pathway_name")  
)
```

Arguments

<code>object</code> ,	PFPRefnet class.
<code>group_name</code> ,	character, indicating the groups to subset.
<code>index</code> ,	NULL or a list contains slice/numeric, character, specifying elements to extract. This parameter' length must be the same as <code>group_name</code> . Default is <i>NULL</i> , indicating extract all the networks of a group. See <i>details</i> for more information.
<code>index_type</code> ,	character, the type pf index, which could be "slice","id","name".

Details

This function help users to extract the specific networks for customized analysis, which could be of entire group networks or some part of a specific group networks.

Note, the `index` argument is only worked while the `group_name` argument is consideration, which means `group_name` is not *NULL*. And the length must be the same as `group_name`. Default is *NULL*, indicating extract the entire group basic networks.

Value

sub the network

See Also

[PFPretnet-class](#)

Examples

```
data(PFPretnet_hsa)
subnet <- subnet(PFPretnet_hsa)
```

sub_PFP-methods *subset of PFP object*

Description

This function extract the subsets of PFP-class.

Usage

```
sub_PFP(
  object,
  group_name = NULL,
  index = NULL,
  index_type = c("slice", "pathway_id", "pathway_name")
)

## S4 method for signature 'PFP'
sub_PFP(
  object,
  group_name = NULL,
  index = NULL,
  index_type = c("slice", "pathway_id", "pathway_name")
)
```

Arguments

object,	PFP class
group_name,	the group name in kegg
index,	the index of pathway, NULL or a list contains slice/numeric, character, specifying elements to extract. This parameter' length must be the same as group_name. Default is <i>NULL</i> , indicating extract all the networks of a group. See <i>details</i> for more information.
index_type,	the index type,such as "slice","pathway_id","pathway_name"

Details

This function help users to extract the specific networks PFPscores for customized analysis, which could be of entire group PFP or some part of a specific group PFP.

Note, the index argument is only worked while the group_name argument is consideration, which means group_name is not *NULL*. And the length must be the same as group_name. Default is *NULL*, indicating extract the entire PFP.

Value

a PFP object contains just the selected elements.

See Also

[PFP-class](#)

Examples

```
data(PFP_test1)
PFP_test1
```

trans_edges_id	<i>trans_edges_id</i>
----------------	-----------------------

Description

translate the id name in edges_data

Usage

```
trans_edges_id(
  edges_data,
  from_type = "ENTREZID",
  to_type = "SYMBOL",
  gene_info_db = NULL
)
```

Arguments

edges_data,	the edges_data to translate, it can be the data.frame got from get_exp_cor_edges or get_asso_net , or a data.frame contains the same colnames with them.
from_type,	a character,the type of gene ID, "ENSEMBL","GO","SYMBOL" and so on.
to_type,	a character,the type of gene ID, "ENSEMBL","GO","SYMBOL" and so on.
gene_info_db,	a gene

Details

Translate the id name in edges_data. Note, the from_type must be consistent with the genes id type in edges_data. The gene_info_db must be consistent with the species in edges_data

Value

the id of the edges.

Examples

```
data(PFPretnet_hsa)
data(gene_list_hsa)
edges_kegg <- get_bg_related_kegg(gene_list_hsa,
                                  PFPretnet=PFPretnet_hsa,
                                  rm_duplicated = TRUE)
```

trans_graph2PFPretnet *translate graph_list to PFPretnet class*

Description

This function will translate all graphs in graph_list to a [PFPretnet-class](#) object.

Usage

```
trans_graph2PFPretnet(graph_list, pathway_info)
```

Arguments

graph_list, a list of [graphNEL](#).
pathway_info, a data.frame, which contains all kegg pathways "index", "id", "name", "group", "species"

Details

translating all graphs in graph_list to a [PFPretnet-class](#) object. The pathway_info can be designed by yourself, but the colnames must be "index", "id", "name", "group" and "species".

Value

a PFPretnet

Examples

```
data(PFPretnet_hsa)
PFPretnet_hsa
```

trans_xml2graph	<i>translate kgml files to graphNEL</i>
-----------------	---

Description

This function will translate all kegg KGML files in path `file_dir`.

Usage

```
trans_xml2graph(file_dir, test_mode = FALSE)
```

Arguments

`file_dir`, a character, refers to the `file_path` where kegg KGML files are stored.
`test_mode`, please set whether to test this function.

Details

transform all KEGG KGML files downloaded by the function `kegg_download()` in path `file_dir` to the graphNEL object

Value

a list of graphNEL

Examples

```
trans_xml2graph(file_dir, test=TRUE)
```

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