

Package ‘pcxn’

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Type Package

Version 2.25.0

Title Exploring, analyzing and visualizing functions utilizing the pcxnData package

Description Discover the correlated pathways/gene sets of a single pathway/gene set or discover correlation relationships among multiple pathways/gene sets. Draw a heatmap or create a network of your query and extract members of each pathway/gene set found in the available collections (MSigDB H hallmark, MSigDB C2 Canonical pathways, MSigDB C5 GO BP and Pathprint).

Author Sokratis Kariotis, Yered Pita-Juarez, Winston Hide, Wenbin Wei

Maintainer Sokratis Kariotis <s.kariotis@sheffield.ac.uk>

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pcxn	<i>Exploring, analyzing and visualizing functions utilizing the pcxnData package</i>
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Description

Discover the correlated pathways/gene sets of a single pathway/gene set or discover correlation relationships among multiple pathways/gene sets. Draw a heatmap or create a network of your query and extract members of each pathway/gene set found in the available collections (MSigDB H hallmark, MSigDB C2 Canonical pathways, MSigDB C5 GO BP and Pathprint).

Details

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Author(s)

Sokratis Kariotis, Yered Pita-Juarez, Winston Hide, Wenbin Wei
 Maintainer: Sokratis Kariotis <s.kariotis@sheffield.ac.uk>

References

Pita-Juarez Y., Altschuler G., Kariotis S., Wei W., Koler K., Tanzi R. and W. A. Hide (2018). "The Pathway Coexpression Network: Revealing Pathway Relationships."

Examples

```
library(pcxnData)

# load the data
ds = c("cp_gs_v5.1", "gobp_gs_v5.1", "h_gs_v5.1", "pathprint.Hs.gs",
      "pathCor_CPv5.1_dframe",
      "pathCor_CPv5.1_unadjusted_dframe",
      "pathCor_GOBpv5.1_dframe",
      "pathCor_GOBpv5.1_unadjusted_dframe",
      "pathCor_Hv5.1_dframe",
      "pathCor_Hv5.1_unadjusted_dframe",
      "pathCor_pathprint_v1.2.3_dframe",
      "pathCor_pathprint_v1.2.3_unadjusted_dframe")

data(list = ds)

# Explore the static extendable network (correlation coefficients are adjusted
# for gene overlap) by focusing on single pathways and their 10 most correlated
# neighbours in the pathprint collection
pcxn.obj <- pcxn_explore(collection = "pathprint",
                        query_geneset = "Alzheimer's disease (KEGG)",
                        adj_overlap = TRUE,
                        top = 10,
                        min_abs_corr = 0.05,
                        max_pval = 0.05)

# Explore the static extendable network (correlation coefficients are not
# adjusted for gene overlap) by focusing on single pathways and their
# 10 most correlated neighbours in the pathprint collection
pcxn.obj <- pcxn_explore(collection = "pathprint",
                        query_geneset = "Alzheimer's disease (KEGG)",
                        adj_overlap = FALSE,
                        top = 10,
                        min_abs_corr = 0.05,
                        max_pval = 0.05)

# Analyse relationships between groups of pathways shown to be enriched in the
# collection by gene set enrichment (correlation coefficients are adjusted
# for gene overlap)
pcxn.obj <- pcxn_analyze(collection = "pathprint",
                        phenotype_0_genesets = c("ABC transporters (KEGG)",
                                                "ACE Inhibitor Pathway (Wikipathways)",
                                                "AR down reg. targets (Netpath)"),
                        phenotype_1_genesets = c("DNA Repair (Reactome)"),
                        adj_overlap = TRUE,
                        top = 10,
                        min_abs_corr = 0.05,
                        max_pval = 0.05 )

# Analyse relationships between groups of pathways shown to be enriched in the
# collection by gene set enrichment (correlation coefficients are not adjusted
# for gene overlap)
```

```
pcxn.obj <- pcxn_analyze(collection = "pathprint",
  phenotype_0_genesets = c("ABC transporters (KEGG)",
    "ACE Inhibitor Pathway (Wikipathways)",
    "AR down reg. targets (Netpath)"),
  phenotype_1_genesets = c("DNA Repair (Reactome)"),
  adj_overlap = FALSE,
  top = 10,
  min_abs_corr = 0.05,
  max_pval = 0.05 )

# Generate the heatmap for any pcxn object generated by the pcxn_explore() or
# pcxn_analyze() function
hm <- pcxn_heatmap(pcxn.obj , cluster_method = "complete")

# Get the gene members (Entrez Ids and names) of any pathway/geneset in the
# available collections
genesets_list <- pcxn_gene_members(pathway_name = "Alzheimer's disease (KEGG)")

# Create a network for any pcxn object generated by the pcxn_explore() or
# pcxn_analyze() function
# network <- pcxn_network(pcxn.obj)
```

pcxn-class

A pcxn object produced by pcxn_explore() or pcxn_analyze(). It holds the corresponding analysis, the data produced by the analysis and the geneset groups involved.

Description

A pcxn object produced by pcxn_explore() or pcxn_analyze(). It holds the corresponding analysis, the data produced by the analysis and the geneset groups involved.

Value

pcxn object with a type, data and geneset_groups field

Slots

type character.
 data matrix.
 geneset_groups list.

Examples

```
# Create and show a pcxn object
pcxn <- pcxn_explore("pathprint", "Alzheimer's disease (KEGG)", 10,
  0.05, 0.05)
```

```
pcxn
```

pcxn_explore_analyze *Discover correlated pathway/gene sets of a single pathway/gene set or correlation relationships among multiple pathways/gene sets.*

Description

Using `pcxn_explore`, select a single pathway/gene set from one of the four collections (MSigDB H hallmark gene sets, MSigDB C2 Canonical pathways, MSigDB C5 GO BP gene sets, and Pathprint) and discover its correlated pathway/gene sets within the same collection.

Using `pcxn_analyze`, discover correlation relationships among multiple pathways/gene sets identified by GSEA (gene set enrichment analysis). All the input pathways/gene sets should come from the same collection. MSigDB H hallmark gene sets, MSigDB C2 Canonical pathways, MSigDB C5 GO BP gene sets, and Pathprint are treated as four separate collections.

Usage

```
pcxn_explore(collection = c("pathprint", "MSigDB_H", "MSigDB_C2_CP",
                           "MSigDB_C5_GO_BP"),
             query_geneset,
             adj_overlap = FALSE,
             top = 10,
             min_abs_corr = 0.05,
             max_pval = 0.05)

pcxn_analyze(collection = c("pathprint", "MSigDB_H", "MSigDB_C2_CP",
                           "MSigDB_C5_GO_BP"),
             phenotype_0_genesets,
             phenotype_1_genesets,
             adj_overlap = FALSE,
             top = 10,
             min_abs_corr = 0.05,
             max_pval = 0.05)
```

Arguments

<code>collection</code>	pathways' collection chosen among: "pathprint", "MSigDB_H", "MSigDB_C2_CP", "MSigDB_C5_GO_BP"
<code>query_geneset</code>	the single pathway of interest
<code>phenotype_0_genesets</code>	genesets/pathways of the first group of pathways
<code>phenotype_1_genesets</code>	genesets/pathways of the second group of pathways
<code>adj_overlap</code>	whether the correlation coefficients are adjusted for gene overlap
<code>top</code>	most correlated genesets/pathways
<code>min_abs_corr</code>	minimum absolute correlation
<code>max_pval</code>	maximum p-value

Value

a pcxn object

Author(s)

Sokratis Kariotis

References

Pita-Juarez Y., Altschuler G., Kariotis S., Wei W., Koler K., Tanzi R. and W. A. Hide (2018). "The Pathway Coexpression Network: Revealing Pathway Relationships."

Examples

```
# pcxn_explore function can be used with the default parameters:
pcxn_explore("pathprint", "Alzheimer's disease (KEGG)")

# If specific parameters are desired we can use the full list of arguments:
pcxn_explore("pathprint", "Alzheimer's disease (KEGG)", FALSE,
             100, 0.02, 0.045)

# pcxn_analyze can be used with two gene sets and the default parameters:
pcxn_analyze("pathprint", c("ABC transporters (KEGG)",
                             "ACE Inhibitor Pathway (Wikipathways)",
                             "AR down reg. targets (Netpath)"),
             c("DNA Repair (Reactome)"))

# Alternatively, you can use only one gene set:
pcxn_analyze("MSigDB_H", c("HALLMARK_COAGULATION", "HALLMARK_UV_RESPONSE_UP"))

# If specific parameters are desired we can use the full list of arguments:
pcxn_analyze("pathprint", c("ABC transporters (KEGG)",
                             "ACE Inhibitor Pathway (Wikipathways)",
                             "AR down reg. targets (Netpath)"),
             c("DNA Repair (Reactome)"),
             FALSE,
             top = 100,
             min_abs_corr = 0.025,
             max_pval = 0.03)
```

pcxn_gene_members

Acquire the gene members of a pathway from the pcxnData package

Description

Acquire the gene members of one of the available pathways that belong to MSigDB H hallmark pathways, MSigDB C2 Canonical pathways, MSigDB C5 GO BP gene sets or Pathprint genesets

Usage

```
pcxn_gene_members(pathway_name = "Alzheimer's disease (KEGG)")
```

Arguments

pathway_name the pathway whose members we want

Value

a matrix of Entrez IDs and gene symbols

Author(s)

Sokratis Kariotis

Examples

```
# Get the members of a single pathway
pcxn_gene_members("Alzheimer's disease (KEGG)")
```

pcxn_heatmap *Draw a heatmap of a pcxn object*

Description

Draw a heatmap of a pcxn object where color represents correlation coefficients.

Usage

```
pcxn_heatmap(object, cluster_method = "complete")
```

Arguments

object pcxn object created by pcxn_explore or pcxn_analyze functions
cluster_method clustering method drawn from: "ward.D", "ward.D2", "single", "complete", "average", "mcquitty", "median", "centroid"

Value

a pheatmap object

Author(s)

Sokratis Kariotis

See Also

[pcxn_network](#)

Examples

```
# Draw a heatmap of a pcxn object with a specific clustering method
object <- pcxn_explore("pathprint", "Alzheimer's disease (KEGG)", 10, 0.05, 0.05)

pcxn_heatmap(object, "complete")
```

pcxn_network	<i>Create a network of a pcxn object</i>
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Description

Create a network of a pcxn object

Usage

```
pcxn_network(object)
```

Arguments

object pcxn object created by explore or analyze functions

Value

draws a tkplot object and saves a graph object representing the network

Examples

```
# Create a network of a pcxn object
object <- pcxn_explore("pathprint", "Alzheimer's disease (KEGG)",
  10, 0.05, 0.05)

# network <- pcxn_network(object)
```


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