Package ‘pcxn’

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Type Package

Version 2.24.0

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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Suggests igraph, annotate, org.Hs.eg.db

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R topics documented:

pcxn ................................................................. 2
pcxn-class ......................................................... 4
pcxn_explore_analyze ................................. 5
pcxn_gene_members ........................................ 6
pcxn_heatmap ..................................................... 7
pcxn_network ..................................................... 8

Index 9

pcxn  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).

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

library(pcxnData)

dl = 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)

description

cxn-class

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

Value

cxn object with a type, data and geneset_groups field

Slots

type character.
da matrix.
genset_groups list.

Examples

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

pcxn
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**

```r
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**

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

Value

a pcxn object

Author(s)

Sokratis Kariotis

References


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

```r
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

```r
# 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**

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

**Arguments**

- `object`: pcxn object created by pcxn_explore or pcxn_analyze functions

**Value**

a pheatmap object

**Author(s)**

Sokratis Kariotis

**See Also**

- pcxn_network
### pcxn_network

#### 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)
```
Index

* package
  pcxn, 2

Introduction to pcxn (pcxn), 2

pcxn, 2
pcxn-class, 4
pcxn_analyze (pcxn_explore_analyze), 5
pcxn_explore (pcxn_explore_analyze), 5
pcxn_explore_analyze, 5
pcxn_gene_members, 6
pcxn_heatmap, 7
pcxn_network, 7, 8