Package ‘pcxn’

April 6, 2018

Type Package

Version 2.0.0

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>

License MIT + file LICENSE

biocViews ExperimentData, ExpressionData, MicroarrayData, GEO, Homo_sapiens_Data, OneChannelData, PathwayInteractionDatabase

NeedsCompilation no

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

Imports methods, grDevices, utils, pheatmap

Depends R (>= 3.4), pcxnData

Encoding UTF-8

RoxygenNote 6.0.1

R topics documented:

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

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

Package: pcxn
Type: Package
Version: 2.0.0
Date: 2018-4-1
License: MIT

Author(s)

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

References


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/gene set 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

cxn_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

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

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:

```r
ctxn_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:

```r
ctxn_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:

```r
ctxn_analyze("MSigDB_H",c("HALLMARK_COAGULATION","HALLMARK_UV_RESPONSE_UP")
```

# If specific parameters are desired we can use the full list of arguments:

```r
ctxn_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

# 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

**Value**

a pheatmap object

**Author(s)**

Sokratis Kariotis

**See Also**

`pcxn_network`

**Examples**

```r
# 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**

*Create a network of a pcxn object*

**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

*Topic **package**
  pcxn, 2

Introduction to pcxn (pcxn), 2

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