Package ‘pcxn’

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Type Package

Version 2.26.0

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).

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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

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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
types 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)

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References

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

**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**

```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**

```r
# 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)
```

**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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>pcxn object created by pcxn_explore or pcxn_analyze functions</td>
</tr>
<tr>
<td>cluster_method</td>
<td>clustering method drawn from: &quot;ward.D&quot;, &quot;ward.D2&quot;, &quot;single&quot;, &quot;complete&quot;, &quot;average&quot;, &quot;mcquitty&quot;, &quot;median&quot;, &quot;centroid&quot;</td>
</tr>
</tbody>
</table>

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

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)
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