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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)

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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.
genesiset_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

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)")
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**

```r
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**

```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**

```r
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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