

Package ‘pcxn’

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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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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)

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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 | <i>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.</i> |
|------------|--|

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 | <i>Discover correlated pathway/gene sets of a single pathway/gene set or correlation relationships among multiple pathways/gene sets.</i> |
|----------------------|---|

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

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 | <i>Draw a heatmap of a pcxn object</i> |
|--------------|--|

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 <code>pcxn_explore</code> or <code>pcxn_analyze</code> functions |
| cluster_method | clustering method drawn from: "ward.D", "ward.D2", "single", "complete", "average", "mcquitty", "median", "centroid" |

Value

a heatmap 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> |
|--------------|--|

Description

Create a network of a pcxn object

Usage

```
pcxn_network(object)
```

Arguments

| | |
|--------|---|
| object | pcxn object created by <code>explore</code> or <code>analyze</code> 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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