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).

Author Sokratis Kariotis, Yered Pita-Juarez, Winston Hide, Wenbin Wei

Maintainer Sokratis Kariotis <s.kariotis@sheffield.ac.uk>

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

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

Imports methods, grDevices, utils, pheatmap

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Contents

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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)

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

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` *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 *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

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 *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
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

```
# 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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