

# Package ‘pcxn’

April 10, 2023

**Type** Package

**Version** 2.20.0

**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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**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

**git\_url** <https://git.bioconductor.org/packages/pcxn>

**git\_branch** RELEASE\_3\_16

**git\_last\_commit** 46bb6ad

**git\_last\_commit\_date** 2022-11-01

**Date/Publication** 2023-04-10

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pcxn	<i>Exploring, analyzing and visualizing functions utilizing the pcxnData package</i>
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## 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)

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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)
```

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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>
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### 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

<code>collection</code>	pathways' collection chosen among: "pathprint", "MSigDB_H", "MSigDB_C2_CP", "MSigDB_C5_GO_BP"
<code>query_geneset</code>	the single pathway of interest
<code>phenotype_0_genesets</code>	genesets/pathways of the first group of pathways
<code>phenotype_1_genesets</code>	genesets/pathways of the second group of pathways
<code>adj_overlap</code>	whether the correlation coefficients are adjusted for gene overlap
<code>top</code>	most correlated genesets/pathways
<code>min_abs_corr</code>	minimum absolute correlation
<code>max_pval</code>	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)
```

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pcxn\_gene\_members

*Acquire the gene members of a pathway from the pcxnData package*

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**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")
```

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pcxn_network	<i>Create a network of a pcxn object</i>
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**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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