

# Package ‘pcxnData’

February 22, 2024

**Version** 2.24.0

**Title** Correlation coefficients and p values between pre-defined pathway/gene sets

**Description** PCxN database contains correlation coefficients and p values between pre-defined gene sets within MSigDB H hallmark gene sets, MSigDB C2 CP (Canonical pathways), MSigDB C5 GO BP gene sets and Pathprint respectively, as well as adjusted pathway correlations to account for the shared genes between pathway pairs.

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**License** MIT + file LICENSE

**biocViews** ExperimentData, ExpressionData, MicroarrayData, GEO, Homo\_sapiens\_Data, OneChannelData, PathwayInteractionDatabase

**NeedsCompilation** no

**Suggests** pcxn

**Depends** R (>= 3.4)

**Encoding** UTF-8

**RoxygenNote** 6.0.1

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pcxnData	<i>Correlation coefficients and p values between pre-defined pathway/gene sets</i>
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## Description

The pcxnData package contains correlation coefficients and p values between pre-defined gene sets within MSigDB H hallmark gene sets, MSigDB C2 CP (Canonical pathways), MSigDB C5 GO BP gene sets and Pathprint respectively. In addition to the unadjusted pathway correlations, this package provides those that were adjusted to account for the shared genes between pathway pairs.

## Usage

```
data(list = c("cp_gs_v5.1", "gobp_gs_v5.1", "h_gs_v5.1", "pathprint.Hs.gs",
  "pathCor_CPv5.1_dframe", "pathCor_GOBPv5.1_dframe", "pathCor_Hv5.1_dframe",
  "pathCor_pathprint_v1.2.3_dframe", "pathCor_CPv5.1_unadjusted_dframe",
  "pathCor_GOBPv5.1_unadjusted_dframe", "pathCor_Hv5.1_unadjusted_dframe",
  "pathCor_pathprint_v1.2.3_unadjusted_dframe"))
```

## Format

A data frame contains the following columns.

Pathway.A / Pathway.B Columns that hold a pathway/gene set name

PathCor Correlation between two pathways

p.value P-value of the correlation

Overlap.Coefficient The overlap coefficient between two gene sets is the size of the intersection divided by the size of the smaller of the two sets. If one of the sets is a subset of the other, the overlap coefficient is 1.

p.Adjust The adjusted p-value of the correlation

## Details

```
Package: pcxnData
Type: Package
Version: 2.0.0
Date: 2018-2-1
License: MIT
```

**Value**

Includes dataframes containing adjusted and unadjusted correlation between two pathways drawn from one of four collections: MSigDB H hallmark gene sets, MSigDB C2 CP (Canonical pathways), MSigDB C5 GO BP gene sets and Pathprint. For each of the above collections the package includes a list that holds the members of each pathway/gene set.

**Author(s)**

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**References**

Pita-Juarez Y., Altschuler G., Kariotis S., Wei W., Koler K., Tanzi R. and W. A. Hide (2017). "The Pathway Coexpression Network: Revealing Pathway Relationships."

**Examples**

```
# Load all data
data(list = c("cp_gs_v5.1", "gobp_gs_v5.1", "h_gs_v5.1", "pathprint.Hs.gs",
             "pathCor_CPv5.1_dframe", "pathCor_GOBPv5.1_dframe", "pathCor_Hv5.1_dframe",
             "pathCor_pathprint_v1.2.3_dframe", "pathCor_CPv5.1_unadjusted_dframe",
             "pathCor_GOBPv5.1_unadjusted_dframe", "pathCor_Hv5.1_unadjusted_dframe",
             "pathCor_pathprint_v1.2.3_unadjusted_dframe"))

# Load an object containing correlation coefficients, p values, overlap
# coefficients and adjusted p values and the corresponding unadjusted one
data("pathCor_pathprint_v1.2.3_dframe")
data("pathCor_pathprint_v1.2.3_unadjusted_dframe")

# Load an object containing the gene members of each gene set in a collection
data("cp_gs_v5.1")

# Objects in environment
objects()

# Object types are data.frame or list
class(pathCor_pathprint_v1.2.3_dframe)
class(cp_gs_v5.1)

# Get the first parts of the objects
head(pathCor_pathprint_v1.2.3_dframe)
head(cp_gs_v5.1)

# Get dimensions of an object
dim(pathCor_pathprint_v1.2.3_dframe)
```

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