

# About pcdnData

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

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## 1 Description

The pcdnData 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

## 2 Using pcdnData with pcdn package

The data in this package are primarily used by the pcdn package. For the following examples to work, the pcdn package needs to be installed. For further explanations of some of the functions mentioned in the examples please refer to pcdn.

```
> # Use the pcdn library
> library(pcdn)
> library(pcdnData)
> # 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_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")
> data(list = ds)
> # Explore the static extendable network by focusing on single pathways and their
> # 10 most correlated neighbours in the pathprint collection
> pcdn.obj <- pcdn_explore(collection = "pathprint",
+                          query_geneset = "Alzheimer's disease (KEGG)",
+                          adj_overlap = FALSE,
+                          top = 10,
+                          min_abs_corr = 0.05,
+                          max_pval = 0.05)
[1] "Successful exploring: Based on Alzheimer's disease (KEGG) and 10 top correlated geneset"
```

```

> # Analyse relationships between groups of pathways shown to be enriched in the
> # collection by gene set enrichment
> 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 )
[1] "Successful analyzing: Based on phenotype 0 [ABC transporters (KEGG), ACE Inhibitor Path
> # Generate the heatmap for any pcxn object generated by the
> # explore or analyze function
> hm <- pcxn_heatmap(pcxn.obj , cluster_method = "complete")
> # Get the gene members (Entrez Ids and symbols) of any pathway/geneset in the
> # data
> gene_members <- pcxn_gene_members(pathway_name = "Alzheimer's disease (KEGG)")
>

```