Package ‘PanomiR’

May 3, 2024

Title Detection of miRNAs that regulate interacting groups of pathways

Version 1.8.0

Description PanomiR is a package to detect miRNAs that target groups of pathways from gene expression data. This package provides functionality for generating pathway activity profiles, determining differentially activated pathways between user-specified conditions, determining clusters of pathways via the PCxN package, and generating miRNAs targeting clusters of pathways. These function can be used separately or sequentially to analyze RNA-Seq data.

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Encoding UTF-8

RoxygenNote 7.1.2

Suggests testthat (>= 3.0.0), BiocStyle, knitr, rmarkdown

Config/testthat/edition 3

biocViews GeneExpression, GeneSetEnrichment, GeneTarget, miRNA, Pathways

Imports clusterProfiler, dplyr, forcats, GSEABase, igraph, limma, metap, org.Hs.eg.db, parallel, preprocessCore, RColorBrewer, rlang, tibble, withr, utils

Depends R (>= 4.2.0)

URL https://github.com/pouryany/PanomiR

BugReports https://github.com/pouryany/PanomiR/issues

VignetteBuilder knitr

git_url https://git.bioconductor.org/packages/PanomiR

git_branch RELEASE_3_19

git_last_commit fd5ac15

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-02
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aggInvCoverFn

Internal function for modification of prioritization.

Description
Internal function for modification of prioritization.

Usage
aggInvCoverFn(selector, coverName)

Arguments
- selector: a prioritization table
- coverName: a new column name

Value
an updated scoring of miRNAs in a cluster of pathways

aggInvFn

The function calculate targeting score of miRNA w.r.t to a cluster of pathways via inverse normal method

Description
The function calculate targeting score of miRNA w.r.t to a cluster of pathways via inverse normal method

Usage
aggInvFn(enriches, pathways, isSelector = TRUE, thresh = NULL)

Arguments
- enriches: a table of miRNA pathway enrichments. Universe
- pathways: queried pathways. e.g. cluster pathways
- isSelector: internal argument
- thresh: internal argument

Value
a scoring of miRNAs in a cluster of pathways
aggLogCoverFn  
Internal function for modification of prioritization.

Description
Internal function for modification of prioritization.

Usage
aggLogCoverFn(selector, coverName)

Arguments
- selector: a prioritization table
- coverName: a new column name

Value
an updated scoring of miRNAs in a cluster of pathways

aggLogFn  
The function calculate targeting score of miRNA w.r.t to a cluster of pathways via log aggregation method.

Description
The function calculate targeting score of miRNA w.r.t to a cluster of pathways via log aggregation method.

Usage
aggLogFn(enriches, pathways, isSelector, thresh = 0)

Arguments
- enriches: a table of miRNA pathway enrichments. Universe
- pathways: queried pathways. e.g. cluster pathways
- isSelector: internal argument
- thresh: internal argument

Value
a scoring of miRNAs in a cluster of pathways
alignToUniverse

**Description**

function to align a list of sets and a reference universe

**Usage**

`alignToUniverse(pathwaySets, universe)`

**Arguments**

- `pathwaySets`: a list of sets
- `universe`: all set elements must be a subset of universe

**Value**

a list of sets, aligned to universe

---

clusterPlot

*Plots clusters of pathways with associated directionality.*

**Description**

Plots clusters of pathways with associated directionality.

**Usage**

`clusterPlot(
    subNet,
    subplot = FALSE,
    topClusters = 2,
    prefix = "",
    outDir = ".",
    plotSave = TRUE
)`

**Arguments**

- `subNet`: pathways network (edge list of pathways)
- `subplot`: if TRUE, store individual clusters plots and connected plots in Figures directory of plots
- `topClusters`: plot figures for top x clusters
- `prefix`: add prefix to plots
- `outDir`: output directory
- `plotSave`: saves the plot if set true. Otherwise display
differentialPathwayAnalysis

**Value**

a set of plots for DE-PCXN and subclusters

**Examples**

```r
data(miniTestsPanomiR)
clusterPlot(miniTestsPanomiR$miniPathClusts$DE_PCXN, plotSave = FALSE)
```

---

differentialPathwayAnalysis

* Differential Expression Analysis For Pathways

**Description**

Performs differential expression analysis for pathways using LIMMA package with gene counts

**Usage**

```r
differentialPathwayAnalysis(
  geneCounts,
  pathways,
  covariates,
  condition,
  adjustCovars = NULL,
  covariateCorrection = FALSE,
  quantileNorm = FALSE,
  outDir = ".",
  saveOutName = NULL,
  id = "ENSEMBL",
  deGenes = NULL,
  minPathSize = 10,
  method = "x2",
  trim = 0.025,
  geneCountsLog = TRUE,
  contrastConds = NA
)
```

**Arguments**

- **geneCounts**: Gene counts, rows refer to genes and columns to samples.
- **pathways**: Pathways table, containing pathway names and genes with id specified.
- **covariates**: Covariates/metadata file; rows matches the columns of geneCounts.
- **condition**: Condition to be examined (tumor vs normal etc); must exist in covariates column.
- **adjustCovars**: Adjustment covariates like batch; if NULL, no adjustments performed.
enrichAllPairs

- **covariateCorrection**
  If TRUE, performs covariates detection and correction; requires `adjustCovars`; (limma).
- **quantileNorm**
  If TRUE, performs quantile normalization on pathway summary statistics; from *preprocess* package.
- **outDir**
  Output directory.
- **saveOutName**
  If not NULL, saves output as RDS using save name, if NULL, does not save output.
- **id**
  ID matching genes to pathways; rownames of geneCounts.
- **deGenes**
  If not NULL, add t-scores to pathways summary statistics; filter by genes t-scores.
- **minPathSize**
  Minimum pathway size.
- **method**
  Define method to use for pathway summary statistics; specifications in documentation.
- **trim**
  Filter pathways with mean less than trim threshold in pathway summary statistics.
- **geneCountsLog**
  If TRUE, log(geneCounts).
- **contrastConds**
  Provide a contrast expression to be used in Limma comparison. This is necessary if you have more than two levels in the condition covariate.

**Value**
List containing differentially expressed pathways as DEP and pathway summary statistics as pathwaySummaryStats.

**Examples**
```r
data("path_gene_table")
data("miniTestsPanomiR")
differentialPathwayAnalysis(geneCounts = miniTestsPanomiR$mini_LIHC_Exp,
pathways = path_gene_table,
covariates = miniTestsPanomiR$mini_LIHC_Cov,
condition = 'shortLetterCode')
```

---

enrichAllPairs  
*Pairwise enrichment analysis between two given lists of sets*

**Description**
Pairwise enrichment analysis between two given lists of sets

**Usage**
enrichAllPairs(mirSets, pathwaySets, pathsRef, numCores)
getDesignMatrix

**Arguments**

- mirSets: a list of targets of miRNAs
- pathwaySets: a list of pathways
- pathsRef: universe of genes.
- numCores: number of cores to calculate the results.

**Value**

enrichment analysis results

---

**getDesignMatrix**

*Obtain Design Matrix*

**Description**

Modified from covariates pipeline of Menachem Former. Imported from [https://github.com/th1vairam/CovariateAnalysis](https://github.com/th1vairam/CovariateAnalysis)

**Usage**

```r
getDesignMatrix(covariatesDataFrame, intercept = TRUE, reLevels = list())
```

**Arguments**

- covariatesDataFrame: Dataframe of covariates.
- intercept: intercept in the linear model.
- reLevels: TBA.

**Value**

List containing a design matrix.

**Examples**

```r
data(iris)
getDesignMatrix(iris)
```
getDiffExpTable

**Description**

function to get a DE table

**Usage**

```r
getDiffExpTable(expMat, designMat, contrastsName)
```

**Arguments**

- `expMat`: an expression matrix
- `designMat`: a design Matrix
- `contrastsName`: the contrast to perform

**Value**

a table of differential expression

---

getResidual

**Description**

function to get residuals with respect to a set of covariates

**Usage**

```r
getResidual(covariates, adjustCovars, pathSumStats)
```

**Arguments**

- `covariates`: a covariate dataframe.
- `adjustCovars`: covariates to adjust for
- `pathSumStats`: an expression matrix

**Value**

a matrix of adjusted expression
gscExample  
Example genesets from MSigDB

Description
Example genesets from MSigDB

Usage
data(gscExample)

Format
A GeneSet Collection object containing two genesets.

Source
http://www.gsea-msigdb.org/gsea/index.jsp

Examples
data(gscExample)

jackKnifeBase  
Outputs a table with col x (miRNA), probability of observing k (depending on methodology) against a random distribution with jack-knifing of the pathway cluster (removing a pathway at a time)

Description
Outputs a table with col x (miRNA), probability of observing k (depending on methodology) against a random distribution with jack-knifing of the pathway cluster (removing a pathway at a time)

Usage
jackKnifeBase(
  selector,
  pathways,
  enrichNull,
  fn,
  jackKnifeData,
  m,
  numCores = 1
)
linColumnFinder

Arguments

- selector: Table with x(miRNA) in pathway cluster and observed k (depending on methodology).
- pathways: Pathways in pathway cluster.
- enrichNull: Enrichment dataset with x (miRNA), y (pathway) and pval (probability of observing x in pathway cluster).
- fn: Methodology function.
- jackKnifeData: Random distribution data with jack-knifing (i.e. one less pathway)
- m: method name
- numCores: number of cores

Value

Outputs a new selector table with col x, pval_jk

Usage

linColumnFinder(mat)

Arguments

- mat: an input design matrix.

Value

- a list of independent columns

Examples

data("iris")
designMat <- getDesignMatrix(iris)
linColumnFinder(designMat$design)
mappingPathwaysClusters

Outputs a table with pathways and their respective clusters

Description
Outputs a table with pathways and their respective clusters

Usage

mappingPathwaysClusters(
    pcxn,
    dePathways,
    clusteringFunction = NULL,
    edgeFDR = 0.05,
    correlationCutOff = 0.316,
    pathwayFDR = 0.05,
    topPathways = 200,
    plotOut = TRUE,
    subplot = TRUE,
    topClusters = 2,
    prefix = "",
    outDir = "",
    saveNameCSV = NULL,
    weighted = FALSE
)

Arguments

pcxn            pathways network (edge list of pathways)
dePathways      differential expressed pathways, obtained from *DifferentialPathwayAnalysis*
clusteringFunction    clustering algorithm
defDR            FDR threshold for pathway-pathway adjusted p-values; filter edges with adjusted p-values less than given threshold
correlationCutOff  cut-off threshold for pathway-pathway correlation; filter pathways with correlation less than given threshold
pathwayFDR      FDR threshold for DE pathways adjusted p-values; filter pathways with adjusted p-values less than given threshold
topPathways     use only top x paths; if NULL, use all paths
plotOut         if TRUE, store graph plot in Figures directory of plots
subplot         if TRUE, store individual clusters plots and connected plots in Figures directory of plots
methodProbBase

- **topClusters**: plot figures for top x clusters
- **prefix**: add prefix to plots
- **outDir**: output directory
- **saveNameCSV**: if not NULL, saves output as csv using save name
- **weighted**: True if you wish to include correlation weights in clustering

**Value**

A list where the first item is a table with each row containing a pathway and its respective cluster. The second item is an igraph object.

**Examples**

```r
data("miniTestsPanomiR")

mappingPathwaysClusters(pcxn = miniTestsPanomiR$miniPCXN,
                        dePathways = miniTestsPanomiR$miniDEP,
                        topPathways = 200,
                        outDir=".",
                        plot = FALSE,
                        subplot = FALSE,
                        prefix=''
                        clusteringFunction = "cluster_louvain",
                        correlationCutOff = 0.1)
```

**methodProbBase**

Outputs a table with col x, miRNA, probability of observing k against a random distribution of the cover of methodology

**Description**

Outputs a table with col x, miRNA, probability of observing k against a random distribution of the cover of methodology

**Usage**

```r
methodProbBase(samplingData, selector, m, nPaths = 100, coverFn = NULL)
```

**Arguments**

- **samplingData**: Random distribution data.
- **selector**: Table with x(miRNA) in pathway cluster and observed k (depending on methodology).
- **m**: Method name.
- **nPaths**: Number of pathways used to generate the samplingData at each iteration. Default is set at 100.
- **coverFn**: Cover of methodology function.
miniTestsPanomiR

**Value**

Outputs a new selector table with col x, pval and cover.

---

**miniTestsPanomiR**  
*Readouts and datasets for minimal reproducible examples of the PanomiR.*

---

**Description**

The item miniEnrich is a reduced representation of the TargetScan. For full table use miRNAPathwayEnrichment function in the package along with msigdb_c2 and targetScan_03 datasets.

**Usage**

data(miniTestsPanomiR)

**Format**

A list of 5:

- **mini_LIHC_Exp**  a reduced expression dataset from TCGA LIHC data
- **mini_LIHC_Cov**  a reduced covariates dataset from TCGA LIHC data
- **miniEnrich**  a reduced table of miRNA-pathway enrichment, TargetScan.
- **miniDEP**  Differentially activated pathways from reduced TCGA LIHC
- **miniPCXN**  reduced representation of PCXN network
- **miniPathClusts**  miniDEP mapped to miniPCXN

**Details**

These datasets include reduced representation of TCGA LIHC data for reproducing the pipeline.  
doi: 10.1016/j.cell.2017.05.046

A reduced representation of PCxN is provided. For full dataset and method please refer to pcxn.org or https://doi.org/10.1371/journal.pcbi.1006042

**Examples**

data(miniTestsPanomiR)
miRNAPathwayEnrichment

Enrichment Probability Of miRNAs

Description

Outputs enrichment probability of miRNAs based on pathway clusters.

Usage

miRNAPathwayEnrichment(
  mirSets,
  pathwaySets,
  geneSelection = NULL,
  mirSelection = NULL,
  fromID = "ENSGMB",
  toID = "ENTREZID",
  minPathSize = 9,
  numCores = 1,
  outDir = ".",
  saveOutName = NULL
)

Arguments

- **mirSets**: Table of miRNAs and a list of their interactions with genes in ENTREZ ID.
- **pathwaySets**: Table of pathways and a list of their interactions with genes in ENTREZ ID.
- **geneSelection**: Table of genes with dtype; if not NULL, select only genes from a given table.
- **mirSelection**: Table of miRNA names; if not NULL, select only miRNAs from given table.
- **fromID**: ID of genes in geneSelection.
- **toID**: ID of genes used in pcxn and pathways set.
- **minPathSize**: Filter out pathways with sets less than given value.
- **numCores**: Number of CPU cores to use, must be at least one.
- **outDir**: Output directory.
- **saveOutName**: If not NULL, saves output as RDS using save name.

Value

Table of enrichment, each row contains mirna-pathway and its enrichment p-values.

Examples

data(msigdb_c2)
data(targetScan_03)
miRNAPathwayEnrichment(targetScan_03[1:20],msigdb_c2[1:20])
Description

Canonical pathways from Molecular Signatures Database, MsigDb V6.2

Usage

data(msigdb_c2)

Format

A list of 1143 pathways

Source

http://www.gsea-msigdb.org/gsea/index.jsp

Examples

data(msigdb_c2)

---

Description

Generates a table of pathways and genes associations.

Usage

pathwayGeneTab(
    pathAdress = NA,
    pathwayList = NA,
    fromType = "ENTREZID",
    toType = "ENSEMBL",
    outDir = NA
)
**pathwaySummary**

**Pathway Summary Statistics**

**Description**

Generates a table of pathway activity profiles per sample.

**Usage**

```r
pathwaySummary(
  exprsMat,
  pathwayRef,
  id = "ENSEMBL",
  zNormalize = FALSE,
  method = FALSE,
  deGenes = NULL,
  trim = 0,
  tScores = NULL
)
```
Arguments

- **exprsMat**: Gene expression matrix with row names as genes and samples as columns.
- **pathwayRef**: Table of pathway-gene associations. Created from `pathwayGeneTab` function.
- **id**: Gene annotation type in the row name of gene expression data.
- **zNormalize**: Normalization of pathway summary score.
- **method**: Choice of how to summarize gene ranks into pathway statistics.
- **deGenes**: List of differentially expressed genes along with t-scores. Only necessary if working on Top 50% summary method.
- **trim**: Percentage of top and bottom ranked genes to be excluded from pathway summary statistics.
- **tScores**: Argument for Top-50-percent-genes method.

Value

- **pathExp**: Table of pathway activity profiles per sample.

Examples

```r
pathTab <- tibble::tribble(
  ~Pathway, ~ENTREZID, ~ENSEMBL,
  "Path1", "125", "ENSG00000196616",
  "Path1", "3099", "ENSG00000159399",
  "Path2", "5230", "ENSG00000102144",
  "Path2", "5162", "ENSG00000168291"
)

exprsMat <- matrix(2 * (seq_len(12)), 4, 3)
rownames(exprsMat) <- pathTab$ENSEMBL
colnames(exprsMat) <- LETTERS[seq_len(3)]
pathwaySummary(exprsMat, pathTab, method = "x2")
```

---

**path_gene_table**

_A table of gene-pathway association. based on the pathways of MSigDB._

---

Description

A table of gene-pathway association. based on the pathways of MSigDB.

Usage

```r
data(path_gene_table)
```
**Format**

A matrix with 3 columns and 76926 rows:

- **Pathway** An MSigDB annotated pathway
- **ENTREZID** The ENTREZID of a gene belonging to the pathway
- **ENSEMBL** The ENSEMBL of a gene belonging to the pathway

**Examples**

```r
data(path_gene_table)
```

---

**pCutCoverFn**

Internal function for modification of prioritization.

**Description**

Internal function for modification of prioritization.

**Usage**

```r
pCutCoverFn(selector, coverName)
```

**Arguments**

- `selector` a prioritization table
- `coverName` a new column name

**Value**

an updated scoring of miRNAs in a cluster of pathways

---

**pCutFn**

Score miRNAs In a Cluster Of Pathways

**Description**

The function to count the number of enriched pathways for each miRNA.

**Usage**

```r
pCutFn(enriches, pathways, isSelector, thresh = 0.05)
```
Arguments

- enriches: Table of miRNA pathway enrichments.
- pathways: Queried pathways, e.g. cluster pathways.
- isSelector: Internal argument.
- thresh: Threshold from p-value cut-off.

Value

P-value based scoring of miRNAs in a cluster of pathways.

---

**pcxnToNet**  
*Creates a network out of pcxn table*

Description

Creates a network out of pcxn table

Usage

pcxnToNet(pcxn, edgeFDR, correlationCutOff, weighted)

Arguments

- pcxn: pathways network edge list of pathways
- edgeFDR: FDR threshold for pathway-pathway adjusted p-values; filter edges with adjusted p-values less than given threshold
- correlationCutOff: cut-off threshold for pathway-pathway correlation; filter pathways with correlation less than given threshold
- weighted: True if you wish to include correlation weights in clustering

Value

enrichment analysis results
prioritizeMicroRNA

**Description**

Outputs a table of miRNA ordered with respective p-values derived from method for prioritization

**Usage**

```r
prioritizeMicroRNA(
  enriches0,
  pathClust,
  method = "AggInv",
  methodThresh = NULL,
  enrichmentFDR = 0.25,
  topClust = 2,
  sampRate = 1000,
  outDir = ".",
  dataDir = ".",
  saveSampling = TRUE,
  runJackKnife = TRUE,
  saveJackKnife = FALSE,
  numCores = 1,
  saveCSV = TRUE,
  prefix = "",
  autoSeed = TRUE
)
```

**Arguments**

- `enriches0`: miRNA-pathway enrichment dataset obtained from miRNAPathwayEnrichment.
- `pathClust`: Pathway clusters, obtained from MappingPathwaysClusters.
- `methodThresh`: Vector of methods threshold for each method in method, if NULL use default thresh values in method.
- `enrichmentFDR`: FDR cut-off calculating miRNA-pathway hits in the input cluster based on significant enrichment readouts.
- `topClust`: Top x clusters to perform miRNA prioritization on.
- `sampRate`: Sampling rate for CLT.
- `outDir`: Output directory.
- `dataDir`: Data directory.
- `saveSampling`: If TRUE, saves sampling data as RDS for each cluster in topClust in dataDir.
- `runJackKnife`: If TRUE, jacknifing will be performed.
**saveJackKnife**  If TRUE, saves jack-knifed sampling data as RDS for each cluster in topClust in dataDir.

**numCores**  Number of CPU cores to use, must be at least one.

**saveCSV**  If TRUE, saves CSV file for each cluster in topClust in outDir.

**prefix**  Prefix for all saved data.

**autoSeed**  random permutations are generated based on predetermined seeds. TRUE will give identical results in different runs.

**Value**
Table of miRNA and p-values, each row contains a miRNA and its associated p-values from the methods.

**Examples**
```r
data("miniTestsPanomiR")

prioritizeMicroRNA(enriches0 = miniTestsPanomiR$miniEnrich,
                   pathClust = miniTestsPanomiR$miniPathClusts$Clustering,
                   topClust = 1,
                   sampRate = 50,
                   method = c("aggInv"),
                   saveSampling = FALSE,
                   runJackKnife = FALSE,
                   numCores = 1,
                   saveCSV = FALSE)
```

---

**reportEnrichment**  *Publication-ready miRNA-Pathway Enrichment table*

**Description**
This function summarizes the outputs

**Usage**
```r
reportEnrichment(enrichmentTable)
```

**Arguments**

enrichmentTable

  Outputs from [miRNAPathwayEnrichment()] function

**Value**
A summarized miRNA-Pathway enrichment table
samplingDataBase

Examples

data(msigdb_c2)
data(targetScan_03)
eTab <- miRNAPathwayEnrichment(targetScan_03[1:20],msigdb_c2[1:20])

repTab <- reportEnrichment(eTab)

| samplingDataBase | Outputs a table of sampling data(rows are miRNA and cols are samples) |

Description

Outputs a table of sampling data(rows are miRNA and cols are samples)

Usage

samplingDataBase(
  enrichNull,
  selector,
  sampRate,
  fn,
  nPaths,
  samplingDataFile,
  jackKnife = FALSE,
  saveSampling,
  numCores = 1,
  autoSeed = TRUE
)

Arguments

enrichNull  Enrichment dataset with x (miRNA), y (pathway) and pval (probability of observing x in pathway cluster).
selector  Table with x(miRNA) in pathway cluster.
sampRate  Sampling rate.
fn  Methodology function.
nPaths  Number of pathways in pathway cluster.
samplingDataFile  If file exists, load. Else, perform random sampling
jackKnife  If TRUE, conduct sampling with one less pathway, used for jack knifing
saveSampling  If TRUE, data is saved.
numCores  number of cores used
autoSeed  random permutations are generated based on predetermined seeds. TRUE will give identical results in different runs.
sumlogFn

Value

Outputs of sampling data.

sumlogCoverFn

Internal function for modification of prioritization.

Description

Internal function for modification of prioritization.

Usage

sumlogCoverFn(selector, coverName)

Arguments

selector  a prioritization table  
coverName  a new column name

Value

an updated scoring of miRNAs in a cluster of pathways

sumlogFn

The function calculate targeting score of miRNA w.r.t to a cluster of pathways via sumlog aggregation method.

Description

The function calculate targeting score of miRNA w.r.t to a cluster of pathways via sumlog aggregation method.

Usage

sumlogFn(enriches, pathways, isSelector, thresh = NULL)

Arguments

enriches  a table of miRNA pathway enrichments. Universe  
pathways  queried pathways. e.g. cluster pathways  
isSelector  internal argument  
thresh  internal argument

Value

a scoring of miRNAs in a cluster of pathways
### sumzCoverFn

**Description**

Internal function for modification of prioritization.

**Usage**

```r
sumzCoverFn(selector, coverName)
```

**Arguments**

- `selector`: a prioritization table
- `coverName`: a new column name

**Value**

an updated scoring of miRNAs in a cluster of pathways

### sumzFn

**Description**

The function calculate targeting score of miRNA w.r.t to a cluster of pathways via sumz aggregation method.

**Usage**

```r
sumzFn(enriches, pathways, isSelector, thresh = NULL)
```

**Arguments**

- `enriches`: a table of miRNA pathway enrichments. Universe
- `pathways`: queried pathways. e.g. cluster pathways
- `isSelector`: internal argument
- `thresh`: internal argument

**Value**

a scoring of miRNAs in a cluster of pathways
### tableFromGSC

**Pathway-Gene Associations from GeneSet collections**

**Description**
This function enables to utilize MSigDB packages and GSEABase objects to incorporate customized genesets into PanomiR.

**Usage**

```
tableFromGSC(gsCollection, fromType = "ENTREZID", toType = "ENSEMBL")
```

**Arguments**
- `gsCollection`: An GSEABase gene set collection object
- `fromType`: gene annotation type used in your input data
- `toType`: gene annotation type to be produced in the output

**Value**
A table of pathway-gene associations

**Examples**

```
data(gscExample)
tableFromGSC(gscExample)
```

### targetScan_03

*A processed list of miRNA target gene sets from the TargetScan dataset. Each list item is a list of genes targeted by the respective miRNA family*

**Description**
The interactions are filtered to only human interactions.

**Usage**

```
data(targetScan_03)
```

**Format**
A list of 439 items

**Details**
The interactions are filtered to have a Cumulative weighted context++ score of < -0.3
targetScan_03

Source

http://www.targetscan.org/vert_72/

Examples

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