Package ‘PanomiR’

April 4, 2024

Title Detection of miRNAs that regulate interacting groups of pathways

Version 1.6.0

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)

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

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R topics documented:

aggInvCoverFn .................................................. 3
aggInvFn ......................................................... 3
aggLogCoverFn .................................................... 4
aggLogFn .......................................................... 4
alignToUniverse ................................................... 5
clusterPlot ......................................................... 5
differentialPathwayAnalysis ..................................... 6
enrichAllPairs ..................................................... 7
getDesignMatrix .................................................... 8
getDiffExpTable ................................................... 9
getResidual ......................................................... 9
gscExample ......................................................... 10
jackKnifeBase ..................................................... 10
linColumnFinder ................................................... 11
mappingPathwaysClusters ........................................ 12
methodProbBase ................................................... 13
miniTestsPanomiR .................................................. 14
miRNAPathwayEnrichment ......................................... 15
msigdb_c2 ........................................................ 16
pathwayGeneTab .................................................... 16
pathwaySummary .................................................... 17
path_gene_table ..................................................... 18
pCutCoverFn ......................................................... 19
pCutFn .............................................................. 19
pcxnToNet .......................................................... 20
prioritizeMicroRNA ................................................ 21
reportEnrichment ................................................... 22
samplingDataBase .................................................. 23
sumlogCoverFn ...................................................... 24
sumlogFn ........................................................... 24
sumzCoverFn ......................................................... 25
sumzFn .............................................................. 25
tableFromGSC ........................................................ 26
targetScan_03 ......................................................... 26

Index  28
**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
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

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  

function to align a list of sets and a reference universe

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**

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**

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**

**Description**

Pairwise enrichment analysis between two given lists of sets

**Usage**

enrichAllPairs(mirSets, pathwaySets, pathsRef, numCores)

**Parameters**

- `mirSets` (vector): List of mir sets.
- `pathwaySets` (vector): List of pathway sets.
- `pathsRef` (vector): Reference sets for pathways.
- `numCores` (integer): Number of cores to use for parallel processing.

**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')
```
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/thlvairam/CovariateAnalysis](https://github.com/thlvairam/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

**Function to get a DE table**

### 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

**Function to get residuals with respect to a set of covariates**

### 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

Description

Function imported from https://github.com/th1vairam/CovariateAnalysis
Modified from http://stackoverflow.com/questions/13088770/
Function to find linearly dependent columns of a matrix

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
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
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

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>topClusters</td>
<td>plot figures for top x clusters</td>
</tr>
<tr>
<td>prefix</td>
<td>add prefix to plots</td>
</tr>
<tr>
<td>outDir</td>
<td>output directory</td>
</tr>
<tr>
<td>saveNameCSV</td>
<td>if not NULL, saves output as csv using save name</td>
</tr>
<tr>
<td>weighted</td>
<td>True if you wish to include correlation weights in clustering</td>
</tr>
</tbody>
</table>

**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)
```

**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.
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

```r
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

```r
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 = "ENSEMBL",
toID = "ENTREZID",
minPathSize = 9,
numCores = 1,
outDir = ".",
saveOutName = NULL
)

Arguments

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

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])
msigdb_c2  Canonical pathways from Molecular Signatures Database, MsigDb V6.2

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)

pathwayGeneTab  Pathway-Gene Associations

Description
Generates a table of pathways and genes associations.

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

- **pathAdress**: Address to an RDS file containing list of pathways where each element is a list of genes similar to GMT format.
- **pathwayList**: If you wish to use a list of pathways instead of a file use this argument instead. The list must contain no NA values.
- **fromType**: gene annotation type used in your input data.
- **toType**: gene annotation type to be produced in the output.
- **outDir**: Address to save an RDS for a table of pathway-gene association

**Value**

- `pathExpTab` Table of pathway-gene association.

**Examples**

```r
pathway1 <- c("125", "3099", "126")
pathway2 <- c("5232", "5230", "5162")
pathList <- list("Path1" = pathway1, "Path2" = pathway2)
res <- pathwayGeneTab(pathwayList = pathList)

data(msigdb_c2)
pathwayGeneTab(pathwayList = msigdb_c2[1:2])
```

---

**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
)
```
path_gene_table

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
data(path_gene_table)

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")
```

Description

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

Usage

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**
```
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**
```
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.

---

```r
pcxnToNet

Creates a network out of pcxn table
```

**Description**

Creates a network out of pcxn table

**Usage**

```r
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

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

reportEnrichment(enrichmentTable)

Arguments

enrichmentTable

Outputs from [miRNAPathwayEnrichment()] function

Value

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

**Examples**

```r
data(msigdb_c2)
data(targetScan_03)
eTab <- miRNAPathwayEnrichment(targetScan_03[1:20],msigdb_c2[1:20])
repTab <- reportEnrichment(eTab)
```

**Description**

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

**Usage**

```r
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

data(targetScan_03)
Index

* datasets
   gscExample, 10
   miniTestsPanomiR, 14
   msigdb_c2, 16
   path_gene_table, 18
   targetScan_03, 26

* internal
   aggInvCoverFn, 3
   aggInvFn, 3
   aggLogCoverFn, 4
   aggLogFn, 4
   pCutCoverFn, 19
   pCutFn, 19
   sumlogCoverFn, 24
   sumlogFn, 24
   sumzCoverFn, 25
   sumzFn, 25

   aggInvCoverFn, 3
   aggInvFn, 3
   aggLogCoverFn, 4
   aggLogFn, 4
   alignToUniverse, 5

   clusterPlot, 5

   differentialPathwayAnalysis, 6

   enrichAllPairs, 7

   getDesignMatrix, 8
   getDiffExpTable, 9
   getResidual, 9
   gscExample, 10

   jackKnifeBase, 10

   linColumnFinder, 11

   mappingPathwaysClusters, 12

   methodProbBase, 13

   miniTestsPanomiR, 14
   miRNAPathwayEnrichment, 15
   msigdb_c2, 16

   path_gene_table, 18
   pathwayGeneTab, 16, 18
   pathwaySummary, 17
   pCutCoverFn, 19
   pCutFn, 19
   pcxnToNet, 20
   prioritizeMicroRNA, 21

   reportEnrichment, 22

   samplingDataBase, 23
   sumlogCoverFn, 24
   sumlogFn, 24
   sumzCoverFn, 25
   sumzFn, 25

   tableFromGSC, 26

   targetScan_03, 26