

# Package ‘PanomiR’

November 28, 2023

**Title** Detection of miRNAs that regulate interacting groups of pathways

**Version** 1.7.0

**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** devel

**git\_last\_commit** 938892f

**git\_last\_commit\_date** 2023-10-24

**Repository** Bioconductor 3.19

**Date/Publication** 2023-11-27

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aggInvCoverFn	<i>Internal function for modification of prioritization.</i>
---------------	--

---

**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	<i>The function calculate targeting score of miRNA w.r.t to a cluster of pathways via inverse normal method</i>
----------	---

---

**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	<i>Internal function for modification of prioritization.</i>
---------------	--

---

**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	<i>The function calculate targeting score of miRNA w.r.t to a cluster of pathways via log aggregation method.</i>
----------	---

---

**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

**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.

covariateCorrection	If TRUE, performs covariates detection and correction; requires <b>adjustCovars</b> ; (limma).
quantileNorm	If TRUE, performs quantile normalization on pathway summary statistics; from <b>preprocess</b> 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 documentations.
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**

```
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)
```

**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	<i>Obtain Design Matrix</i>
-----------------	-----------------------------

---

**Description**

Modified from covariates pipeline of Menachem Former. Imported from <https://github.com/th1vairam/CovariateAnalysis>

**Usage**

```
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**

```
data(iris)
getDesignMatrix(iris)
```



---

getDiffExpTable      *function to get a DE table*

---

**Description**

function to get a DE table

**Usage**

```
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**

```
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
)
```

**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

---

linColumnFinder	<i>Function imported from <a href="https://github.com/th1vairam/CovariateAnalysis">https://github.com/th1vairam/CovariateAnalysis</a> Modified from <a href="http://stackoverflow.com/questions/13088770/">http://stackoverflow.com/questions/13088770/</a> Function to find linearly dependednt columns of a matrix</i>
-----------------	--

---

**Description**

Function imported from <https://github.com/th1vairam/CovariateAnalysis> Modified from <http://stackoverflow.com/questions/13088770/>  
Function to find linearly dependednt 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 <i>*DifferentialPathwayAnalysis*</i>
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

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**

```
data("miniTestsPanomiR")

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

---

methodProbBase	<i>Outputs a table with col x, miRNA, probability of observing k against a random distribution of the cover of methodology</i>
----------------	--

---

**Description**

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

**Usage**

```
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	<i>Readouts and datasets for minimal reproducible examples of the PanomiR.</i>
------------------	--

---

**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

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

**Arguments**

<code>mirSets</code>	Table of miRNAs and a list of their interactions with genes in ENTREZ ID.
<code>pathwaySets</code>	Table of pathways and a list of their interactions with genes in ENTREZ ID.
<code>geneSelection</code>	Table of genes with dtype; if not NULL, select only genes from a given table.
<code>mirSelection</code>	Table of miRNA names; if not NULL, select only miRNAs from given table.
<code>fromID</code>	ID of genes in <code>geneSelection</code> .
<code>toID</code>	ID of genes used in <code>pcxn</code> and <code>pathways</code> set.
<code>minPathSize</code>	Filter out pathways with sets less than given value.
<code>numCores</code>	Number of CPU cores to use, must be at least one.
<code>outDir</code>	Output directory.
<code>saveOutName</code>	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])
```

---

msigdb_c2	<i>Canonical pathways from Molecular Signatures Database, MsigDb V6.2</i>
-----------	---

---

**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	<i>Pathway-Gene Associations</i>
----------------	----------------------------------

---

**Description**

Generates a table of pathways and genes associations.

**Usage**

```
pathwayGeneTab(  
  pathAddress = NA,  
  pathwayList = NA,  
  fromType = "ENTREZID",  
  toType = "ENSEMBL",  
  outDir = NA  
)
```



**Arguments**

pathAddress	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**

```
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**

```
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 <a href="#">pathwayGeneTab</a> 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**

```
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	<i>A table of gene-pathway association. based on the pathways of MSigDB.</i>
-----------------	--

---

**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**

```
data(path_gene_table)
```

---

pCutCoverFn	<i>Internal function for modification of prioritization.</i>
-------------	--

---

**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	<i>Score miRNAs In a Cluster Of Pathways</i>
--------	--

---

**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.

---

pcxnToNet	<i>Creates a network out of pcxn table</i>
-----------	--

---

**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      *Prioritize miRNA*

---

## Description

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

## Usage

```
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.
method	Vector of methods pCut, AggInv, AggLog, sumz, sumlog.
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, jackknifing 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$miniEnrich,
  pathClust = miniTestsPanomiR$miniPathClusters$Clustering,
  topClust = 1,
  sampRate = 50,
  method = c("aggInv"),
  saveSampling = FALSE,
  runJackKnife = FALSE,
  numCores = 1,
  saveCSV = FALSE)
```

---

reportEnrichment	<i>Publication-ready miRNA-Pathway Enrichment table</i>
------------------	---

---

**Description**

This function summarizes the outputs

**Usage**

```
reportEnrichment(enrichmentTable)
```

**Arguments**

```
enrichmentTable
  Outputs from [miRNAPathwayEnrichment()] function
```

**Value**

A summarized miRNA-Pathway enrichment table

**Examples**

```

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

repTab <- reportEnrichment(eTab)

```

---

samplingDataBase	<i>Outputs a table of sampling data(rows are miRNA and cols are samples)</i>
------------------	--

---

**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.

**Value**

Outputs of sampling data.

---

sumlogCoverFn	<i>Internal function for modification of prioritization.</i>
---------------	--

---

**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	<i>The function calculate targeting score of miRNA w.r.t to a cluster of pathways via sumlog aggregation method.</i>
----------	--

---

**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	<i>Internal function for modification of prioritization.</i>
-------------	--

---

**Description**

Internal function for modification of prioritization.

**Usage**

```
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	<i>The function calculate targeting score of miRNA w.r.t to a cluster of pathways via sumz aggregation method.</i>
--------	--

---

**Description**

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

**Usage**

```
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	<i>Pathway-Gene Associations from GeneSet collections</i>
--------------	---

---

**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	<i>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</i>
---------------	--

---

**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*

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**Source**

[http://www.targetscan.org/vert\\_72/](http://www.targetscan.org/vert_72/)

**Examples**

```
data(targetScan_03)
```

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