

# Package ‘PanomiR’

June 27, 2025

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

**Version** 1.13.0

**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

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**Depends** R (>= 4.2.0)

**URL** <https://github.com/pouryany/PanomiR>

**BugReports** <https://github.com/pouryany/PanomiR/issues>

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**Author** Pourya Naderi [aut, cre],  
Yue Yang (Alan) Teo [aut],  
Ilya Sytchev [aut],  
Winston Hide [aut]

**Maintainer** Pourya Naderi <pouryany@gmail.com>

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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 | <i>function to align a list of sets and a reference universe</i> |
|-----------------|------------------------------------------------------------------|

---

**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 | <i>Plots clusters of pathways with associated directionality.</i> |
|-------------|-------------------------------------------------------------------|

---

### 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 | <i>Differential Expression Analysis For Pathways</i> |
|-----------------------------|------------------------------------------------------|

---

### 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 | <i>Pairwise enrichment analysis between two given lists of sets</i> |
|----------------|---------------------------------------------------------------------|

---

**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 Forman. 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 | <i>function to get a DE table</i> |
|-----------------|-----------------------------------|

---

**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 | <i>function to get residuals with respect to a set of covariates</i> |
|-------------|----------------------------------------------------------------------|

---

**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 | <i>Example genesets from MSigDB</i> |
|------------|-------------------------------------|

---

**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 | <i>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)</i> |
|---------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

---

**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

*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

**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**

|               |                                                                               |
|---------------|-------------------------------------------------------------------------------|
| 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])
```

---

|           |                                                                           |
|-----------|---------------------------------------------------------------------------|
| 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

### Source

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

*targetScan\_03*

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### **Examples**

```
data(targetScan_03)
```

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