

# Package ‘miRSM’

September 24, 2025

**Type** Package

**Title** Inferring miRNA sponge modules in heterogeneous data

**Version** 2.5.4

**Description** The package aims to identify miRNA sponge or ceRNA modules in heterogeneous data. It provides several functions to study miRNA sponge modules at single-sample and multi-sample levels, including popular methods for inferring gene modules (candidate miRNA sponge or ceRNA modules), and two functions to identify miRNA sponge modules at single-sample and multi-sample levels, as well as several functions to conduct modular analysis of miRNA sponge modules.

**Depends** R (>= 4.4.0)

**License** GPL-3

**URL** <https://github.com/zhangjunpeng411/miRSM>

**Encoding** UTF-8

**biocViews** GeneExpression, BiomedicalInformatics, Clustering,  
GeneSetEnrichment, Microarray, Software, GeneRegulation,  
GeneTarget

**RoxygenNote** 7.3.2

**Imports** WGCNA, flashClust, dynamicTreeCut, GFA, igraph, RColorBrewer,  
grid, MCL, fabia, NMF, biclust, iBBiG, BicARE, isa2, methods,  
rJava, BiBitR, rqubic, Biobase, PMA, stats, dbscan, mclust,  
SOMbrero, ppclust, Rcpp, utils, SummarizedExperiment, GSEABase,  
org.Hs.eg.db, clusterProfiler, ReactomePA, DOSE,  
MatrixCorrelation, energy

**Suggests** BiocStyle, knitr, rmarkdown, testthat

**VignetteBuilder** knitr

**BugReports** <https://github.com/zhangjunpeng411/miRSM/issues>

**git\_url** <https://git.bioconductor.org/packages/miRSM>

**git\_branch** devel

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|            |                   |
|------------|-------------------|
| BRCA_genes | <i>BRCA genes</i> |
|------------|-------------------|

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Description

BRCA genes

Format

BRCA\_genes: A SummarizedExperiment object with 4819 BRCA related genes (including lncRNAs and mRNAs).

Details

The BRCA related lncRNAs are from LncRNADisease v2.0, Lnc2Cancer v2.0 and MNDR v2.0. The BRCA related mRNAs are from DisGeNET v5.0 and COSMIC v86.

## References

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- Cui T, Zhang L, Huang Y, Yi Y, Tan P, Zhao Y, Hu Y, Xu L, Li E, Wang D. (2018) "MNDR v2.0: an updated resource of ncRNA-disease associations in mammals". *Nucleic Acids Res.*, 46, D371-D374.
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- Pinero J, Bravo A, Queralt-Rosinach N, Gutierrez-Sacristan A, Deu-Pons J, Centeno E, Garcia-Garcia J, Sanz F, Furlong LI. (2017) "DisGeNET: a comprehensive platform integrating information on human disease-associated genes and variants". *Nucleic Acids Res.*, 45, D833-D839.

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ceRExp

*ceRNA expression data*


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## Description

ceRNA expression data

## Format

ceRExp: A SummarizedExperiment object with 72 BRCA and 72 normal samples (rows) and 305 lncRNAs (columns).

## Details

The matched breast invasive carcinoma (BRCA) miRNA, lncRNA and mRNA expression data is obtained from TCGA (<http://cancergenome.nih.gov/>). lncRNA expression data is regarded as ceRNA expression data. The data focuses on 72 individuals for which the complete sets of tumor and matched normal (i.e., normal tissue taken from the same patient) profiles are available. A lncRNA which has missing values in more than 10 are imputed using the k-nearest neighbours (KNN) algorithm from the impute R package. We use the limma R package to infer differentially expressed lncRNAs between tumour and normal samples. After the analysis, we select top 305 lncRNAs which are differentially expressed at a significant level (adjusted p-value < 1E-02, adjusted by Benjamini & Hochberg method).

---

cor\_binary

cor\_binary

---

## Description

Generation of positively correlated binary matrix between ceRNAs, or ceRNAs and mRNAs

## Usage

```
cor_binary(
  ceRExp,
  mRExp = NULL,
  cor.method = "pearson",
  pos.p.value.cutoff = 0.01
)
```

## Arguments

|                    |                                                                                                                |
|--------------------|----------------------------------------------------------------------------------------------------------------|
| ceRExp             | A SummarizedExperiment object. ceRNA expression data: rows are samples and columns are ceRNAs.                 |
| mRExp              | NULL (default) or a SummarizedExperiment object. mRNA expression data: rows are samples and columns are mRNAs. |
| cor.method         | The method of calculating correlation selected, including 'pearson' (default), 'kendall', 'spearman'.          |
| pos.p.value.cutoff | The significant p-value cutoff of positive correlation.                                                        |

## Value

A binary matrix.

## Author(s)

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

## References

Langfelder P, Horvath S. WGCNA: an R package for weighted correlation network analysis. BMC Bioinformatics. 2008, 9:559.

## Examples

```
data(BRCASampleData)
cor_binary_matrix <- cor_binary(ceRExp, mRExp)
```

---

|             |                    |
|-------------|--------------------|
| diff_module | <i>diff_module</i> |
|-------------|--------------------|

---

## Description

Inferring differential modules between two list of module groups

## Usage

```
diff_module(  
  Module.group1,  
  Module.group2,  
  sim.cutoff = 0.8,  
  sim.method = "Simpson"  
)
```

## Arguments

|               |                                                                                                                                            |
|---------------|--------------------------------------------------------------------------------------------------------------------------------------------|
| Module.group1 | List object, the first list of module group.                                                                                               |
| Module.group2 | List object, the second list of module group.                                                                                              |
| sim.cutoff    | Similarity cutoff between modules, the interval is [0 1].                                                                                  |
| sim.method    | Methods for calculating similarity between two modules, select one of three methods (Simpson, Jaccard and Lin). Default method is Simpson. |

## Value

A list of differential modules

## Author(s)

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

## Examples

```
library(GSEABase)  
data(BRCASampleData)  
modulegenes_WGCNA_all <- module_WGCNA(ceRExp, mRExp)  
modulegenes_WGCNA_1 <- module_WGCNA(ceRExp[-1, ], mRExp[-1, ])  
Differential_module <- diff_module(geneIds(modulegenes_WGCNA_all), geneIds(modulegenes_WGCNA_1))
```

---

|        |                              |
|--------|------------------------------|
| miRExp | <i>miRNA expression data</i> |
|--------|------------------------------|

---

### Description

miRNA expression data

### Format

miRExp: A SummarizedExperiment object with 72 BRCA and 72 normal samples (rows) and 226 miRNAs (columns).

### Details

The matched breast invasive carcinoma (BRCA) miRNA, lncRNA and mRNA expression data is obtained from TCGA (<http://cancergenome.nih.gov/>). The data focuses on 72 individuals for which the complete sets of tumor and matched normal (i.e., normal tissue taken from the same patient) profiles are available. A miRNA which has missing values in more than 10 are imputed using the k-nearest neighbours (KNN) algorithm from the impute R package. We use the limma R package to infer differentially expressed miRNAs, ceRNAs and mRNAs between tumour and normal samples. After the analysis, we select top 226 miRNAs which are differentially expressed at a significant level (adjusted p-value < 1E-02, adjusted by Benjamini & Hochberg method).

---

|       |              |
|-------|--------------|
| miRSM | <i>miRSM</i> |
|-------|--------------|

---

### Description

Identify miRNA sponge modules using sensitivity canonical correlation (SCC), sensitivity distance correlation (SDC), sensitivity RV coefficient (SRVC), sensitivity similarity index (SSI), sensitivity generalized coefficient of determination (SGCD), sensitivity Coxhead's or Rozeboom's coefficient (SCRC), and sponge module (SM) methods.

### Usage

```
miRSM(
  miRExp = NULL,
  ceRExp,
  mRExp = NULL,
  miRTarget,
  CandidateModulegenes,
  typex = "standard",
  typez = "standard",
  nperms = 100,
  method = c("SCC", "SDC", "SRVC", "SM", "SSI", "SGCD", "SCRC"),
  num_shared_miRNAs = 3,
  pvalue.cutoff = 0.05,
  MC.cutoff = 0.8,
  SMC.cutoff = 0.1,
```

```
RV_method = c("RV", "RV2", "RVadjMaye", "RVadjGhaziri"),
BCmethod = "BCPlaid",
CRC_method = c("Coxhead", "Rozeboom")
)
```

### Arguments

|                      |                                                                                                                                                                                                                                     |
|----------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| miRExp               | NULL (default) or a SummarizedExperiment object. miRNA expression data: rows are samples and columns are miRNAs.                                                                                                                    |
| ceRExp               | A SummarizedExperiment object. ceRNA expression data: rows are samples and columns are ceRNAs.                                                                                                                                      |
| mRExp                | NULL (default) or a SummarizedExperiment object. mRNA expression data: rows are samples and columns are mRNAs.                                                                                                                      |
| miRTarget            | A SummarizedExperiment object. Putative miRNA-target binding information.                                                                                                                                                           |
| CandidateModulegenes | List object: a list of candidate miRNA sponge modules. Only for the SCC, SDC, SRVC, SSI, SGCD and SCRC methods.                                                                                                                     |
| typex                | The columns of x unordered (type='standard') or ordered (type='ordered'). Only for the SCC method.                                                                                                                                  |
| typez                | The columns of z unordered (type='standard') or ordered (type='ordered'). Only for the SCC method.                                                                                                                                  |
| nperms               | The number of permutations. Only for the SCC method.                                                                                                                                                                                |
| method               | The method selected to identify miRNA sponge modules, including 'SCC', 'SDC', 'SRVC', 'SM', 'SSI', 'SGCD' and 'SCRC'.                                                                                                               |
| num_shared_miRNAs    | The number of common miRNAs shared by a group of ceRNAs and mRNAs. Only for the SCC, SDC, SRVC, SSI, SGCD and SCRC methods.                                                                                                         |
| pvalue.cutoff        | The p-value cutoff of significant sharing of common miRNAs by a group of ceRNAs and mRNAs or significant correlation.                                                                                                               |
| MC.cutoff            | The cutoff of matrix correlation (canonical correlation, distance correlation and RV coefficient). Only for the SCC, SDC, SRVC, SSI, SGCD and SCRC methods.                                                                         |
| SMC.cutoff           | The cutoff of sensitivity matrix correlation (sensitivity canonical correlation, sensitivity distance correlation and sensitivity RV coefficient). Only for the SCC, SDC, SRVC, SSI, SGCD and SCRC methods when miRExp is not NULL. |
| RV_method            | the method of calculating RV coefficients. Select one of 'RV', 'RV2', 'RVadj-Maye' and 'RVadjGhaziri' methods. Only for the SRVC method.                                                                                            |
| BCmethod             | Specification of the biclustering method, including 'BCBimax', 'BCCC', 'BC-Plaid' (default), 'BCQuest', 'BCSpectral', 'BCXmotifs'. Only for the SM method.                                                                          |
| CRC_method           | the method of calculating matrix correlation. Select one of 'Coxhead' and 'Rozeboom' methods. Only for the SCRC method.                                                                                                             |

### Value

List object: Group competition of miRNA sponge modules, and miRNA sponge modules.

### Author(s)

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

## References

- Witten DM, Tibshirani R, Hastie T. A penalized matrix decomposition, with applications to sparse principal components and canonical correlation analysis. *Biostatistics*. 2009, 10(3):515-34.
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- Robert P, Escoufier Y. A unifying tool for linear multivariate statistical methods: the RV-Coefficient. *Applied Statistics*, 1976, 25(3):257-265.
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- Coxhead P. Measuring the relationship between two sets of variables. *British journal of mathematical and statistical psychology*, 1974, 27(2): 205-212.
- Rozeboom WW. Linear correlations between sets of variables. *Psychometrika*, 1965, 30(1): 57-71.

## Examples

```
data(BRCASampleData)
modulegenes_igraph <- module_igraph(ceRExp[, seq_len(10)],
  mRExp[, seq_len(10)])
# Identify miRNA sponge modules using sensitivity RV coefficient (SRVC)
miRSM_igraph_SRVC <- miRSM(miRExp, ceRExp, mRExp, miRTarget,
  modulegenes_igraph, method = "SRVC",
  SMC.cutoff = 0.01, RV_method = "RV")
```

---

miRSM\_SS

---

*miRSM\_SS*


---

## Description

Inferring sample-specific miRNA sponge modules

## Usage

```
miRSM_SS(
  Modulelist.all,
  Modulelist.exceptk,
  sim.cutoff = 0.8,
  sim.method = "Simpson"
)
```

**Arguments**

`Modulelist.all` List object, modules using all of samples.

`Modulelist.exceptk` List object, modules using all of samples excepting sample k.

`sim.cutoff` Similarity cutoff between modules, the interval is [0 1].

`sim.method` Methods for calculating similarity between two modules, select one of three methods (Simpson, Jaccard and Lin). Default method is Simpson.

**Value**

A list of sample-specific miRNA sponge modules

**Author(s)**

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

**Examples**

```
data(BRCASampleData)
nsamples <- 3
modulegenes_all <- module_igraph(ceExp[, 151:300], mExp[, 151:300])
modulegenes_exceptk <- lapply(seq(nsamples), function(i)
  module_WGCNA(ceExp[-i, seq(150)],
    mExp[-i, seq(150)]))

miRSM_SRVC_all <- miRSM(miExp, ceExp[, 151:300], mExp[, 151:300],
  miRTarget, modulegenes_all,
  method = "SRVC", SMC.cutoff = 0.01,
  RV_method = "RV")
miRSM_SRVC_exceptk <- lapply(seq(nsamples), function(i) miRSM(miExp[-i, ],
  ceExp[-i, seq(150)], mExp[-i, seq(150)],
  miRTarget, modulegenes_exceptk[[i]],
  method = "SRVC",
  SMC.cutoff = 0.01, RV_method = "RV"))

Modulegenes_all <- miRSM_SRVC_all[[2]]
Modulegenes_exceptk <- lapply(seq(nsamples), function(i)
  miRSM_SRVC_exceptk[[i]][[2]])

Modules_SS <- miRSM_SS(Modulegenes_all, Modulegenes_exceptk)
```

---

miRTarget

*miRNA-target interactions*


---

**Description**

miRNA-target interactions

**Format**

miRTarget: A SummarizedExperiment object with 29901 miRNA-target interactions.

## Details

The miRNA-target binding information is from miRTarBase v8.0 (<http://mirtarbase.mbc.nctu.edu.tw/php/index.php>), and LncBase v2.0 ([http://carolina.imis.athena-innovation.gr/diana\\_tools/web/index.php?r=lncbasev2/index](http://carolina.imis.athena-innovation.gr/diana_tools/web/index.php?r=lncbasev2/index)). Among 226 miRNAs, 305 lncRNAs and 500 mRNAs which are differentially expressed, we obtain 29901 miRNA-target interactions (including miRNA-lncRNA and miRNA-mRNA interactions).

## References

Hastie T, Tibshirani R, Narasimhan B, Chu G. impute: Imputation for microarray data. R package version 1.54.0. doi: 10.18129/B9.bioc.impute.

Ritchie ME, Phipson B, Wu D, Hu Y, Law CW, Shi W, et al. limma powers differential expression analyses for RNA-sequencing and microarray studies. Nucleic Acids Res. 2015; 43(7):e47.

---

|                |                       |
|----------------|-----------------------|
| module_biclust | <i>module_biclust</i> |
|----------------|-----------------------|

---

## Description

Identification of gene modules from matched ceRNA and mRNA expression data or single gene expression data using a series of biclustering packages, including biclust, iBBiG, fabia, BicARE, isa2, s4vd, BiBitR and rqubic

## Usage

```
module_biclust(
  ceRExp,
  mRExp = NULL,
  BCmethod = "fabia",
  num.modules = 10,
  num.ModuleceRs = 2,
  num.ModulemRs = 2
)
```

## Arguments

|                |                                                                                                                                                                                                                                                                           |
|----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ceRExp         | A SummarizedExperiment object. ceRNA expression data: rows are samples and columns are ceRNAs.                                                                                                                                                                            |
| mRExp          | NULL (default) or a SummarizedExperiment object. mRNA expression data: rows are samples and columns are mRNAs.                                                                                                                                                            |
| BCmethod       | Specification of the biclustering method, including 'BCBimax', 'BCCC', 'BC-Plaid' (default), 'BCQuest', 'BCSpectral', 'BCXmotifs', iBBiG, 'fabia', 'fabiap', 'fabias', 'mfsc', 'nmfdiv', 'nmfeu', 'nmfsc', 'FLOC', 'isa', 'BCs4vd', 'BC-ssvd', 'bibit' and 'quBicluster'. |
| num.modules    | The number of modules to be identified. For the 'BCPlaid', 'BCSpectral', 'isa' and 'bibit' methods, no need to set the parameter. For the 'quBicluster' method, the parameter is used to set the number of biclusters that should be reported.                            |
| num.ModuleceRs | The minimum number of ceRNAs in each module.                                                                                                                                                                                                                              |
| num.ModulemRs  | The minimum number of mRNAs in each module.                                                                                                                                                                                                                               |

**Value**

GeneSetCollection object: a list of module genes.

**Author(s)**

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

**References**

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- Kluger Y, Basri R, Chang JT, Gerstein M. Spectral biclustering of microarray data: coclustering genes and conditions. *Genome Res*. 2003, 13(4):703-16.
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- Lee M, Shen H, Huang JZ, Marron JS. Biclustering via sparse singular value decomposition. *Biometrics*. 2010, 66(4):1087-95.
- Rodriguez-Baena DS, Perez-Pulido AJ, Aguilar-Ruiz JS. A biclustering algorithm for extracting bit-patterns from binary datasets. *Bioinformatics*. 2011, 27(19):2738-45.
- Li G, Ma Q, Tang H, Paterson AH, Xu Y. QUBIC: a qualitative biclustering algorithm for analyses of gene expression data. *Nucleic Acids Res*. 2009, 37(15):e101.

**Examples**

```
data(BRCASampleData)
modulegenes_biclust <- module_biclust(ceRExp[, seq_len(30)],
  mRExp[, seq_len(30)])
```



module\_clust

*module\_clust***Description**

Identification of gene modules from matched ceRNA and mRNA expression data or single gene expression data using a series of clustering packages, including stats, flashClust, dbscan, subspace, mclust, SOMbrero and ppclust packages.

**Usage**

```
module_clust(
  ceRExp,
  mRExp = NULL,
  cluster.method = "kmeans",
  num.modules = 10,
  num.ModuleceRs = 2,
  num.ModulemRs = 2
)
```

**Arguments**

|                |                                                                                                                                                                                                                                          |
|----------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ceRExp         | A SummarizedExperiment object. ceRNA expression data: rows are samples and columns are ceRNAs.                                                                                                                                           |
| mRExp          | NULL (default) or a SummarizedExperiment object. mRNA expression data: rows are samples and columns are mRNAs.                                                                                                                           |
| cluster.method | Specification of the clustering method, including 'kmeans'(default), 'hclust', 'dbscan', 'clique', 'gmm', 'som' and 'fcm'.                                                                                                               |
| num.modules    | Parameter of the number of modules to be identified for the 'kmeans', 'hclust', 'gmm' and 'fcm' methods. Parameter of the number of intervals for the 'clique' method. For the 'dbscan' and 'som' methods, no need to set the parameter. |
| num.ModuleceRs | The minimum number of ceRNAs in each module.                                                                                                                                                                                             |
| num.ModulemRs  | The minimum number of mRNAs in each module.                                                                                                                                                                                              |

**Value**

GeneSetCollection object: a list of module genes.

**Author(s)**

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

**References**

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Langfelder P, Horvath S. Fast R Functions for Robust Correlations and Hierarchical Clustering. Journal of Statistical Software. 2012, 46(11):1-17.

Ester M, Kriegel HP, Sander J, Xu X. A density-based algorithm for discovering clusters in large spatial databases with noise, Proceedings of 2nd International Conference on Knowledge Discovery and Data Mining (KDD-96), 1996, 96(34): 226-231.

Campello RJGB, Moulavi D, Sander J. Density-based clustering based on hierarchical density estimates, Pacific-Asia conference on knowledge discovery and data mining. Springer, Berlin, Heidelberg, 2013: 160-172.

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Dunn JC. A fuzzy relative of the ISODATA process and its use in detecting compact well-separated clusters. Journal of Cybernetics, 1973, 3(3):32-57.

Bezdek JC. Cluster validity with fuzzy sets. Journal of Cybernetics, 1974, 3: 58-73.

Bezdek JC. Pattern recognition with fuzzy objective function algorithms. Plenum, NY, 1981.

## Examples

```
data(BRCASampleData)
modulegenes_clust <- module_clust(ceRExp[, seq_len(30)],
  mRExp[, seq_len(30)])
```

---

module\_Coexpress

*module\_Coexpress*

---

## Description

Co-expression analysis of each miRNA sponge module and its corresponding random miRNA sponge modules

## Usage

```
module_Coexpress(
  ceRExp,
  mRExp = NULL,
  Modulelist,
  resample = 1000,
  method = c("mean", "median"),
  test.method = c("t.test", "wilcox.test")
)
```

**Arguments**

|             |                                                                                                                                                                                                                                                                                       |
|-------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ceRExp      | A SummarizedExperiment object. ceRNA expression data: rows are samples and columns are ceRNAs.                                                                                                                                                                                        |
| mRExp       | NULL (default) or a SummarizedExperiment object. mRNA expression data: rows are samples and columns are mRNAs.                                                                                                                                                                        |
| Moduleelist | List object: a list of the identified miRNA sponge modules.                                                                                                                                                                                                                           |
| resample    | The number of random miRNA sponge modules generated, and 1000 times in default.                                                                                                                                                                                                       |
| method      | The method used to evaluate the co-expression level of each miRNA sponge module. Users can select "mean" or "median" to calculate co-expression value of each miRNA sponge module and its corresponding random miRNA sponge module.                                                   |
| test.method | The method used to evaluate statistical significance p-value of co-expression level higher than random miRNA sponge modules. Users can select "t.test" or "wilcox.test" to calculate statistical significance p-value of co-expression level higher than random miRNA sponge modules. |

**Value**

List object: co-expression values of miRNA sponge modules and their corresponding random miRNA sponge modules, and statistical significance p-value of co-expression level higher than random miRNA sponge modules.

**Author(s)**

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

**Examples**

```
data(BRCASampleData)
modulegenes_WGCNA <- module_WGCNA(ceRExp, mRExp)
# Identify miRNA sponge modules using sensitivity RV coefficient (SRVC)
miRSM_WGCNA_SRVC <- miRSM(miRExp, ceRExp, mRExp, miRTarget,
                          modulegenes_WGCNA, method = "SRVC",
                          SMC.cutoff = 0.01, RV_method = "RV")
miRSM_WGCNA_SRVC_genes <- miRSM_WGCNA_SRVC[[2]]
miRSM_WGCNA_Coexpress <- module_Coexpress(ceRExp, mRExp,
                                          miRSM_WGCNA_SRVC_genes,
                                          resample = 10, method = "mean",
                                          test.method = "t.test")
```

---

module\_FA

*module\_FA*


---

**Description**

Functional analysis of miRNA sponge modules, including functional enrichment and disease enrichment analysis

**Usage**

```
module_FA(
  Modulelist,
  GOont = "BP",
  KEGGorganism = "hsa",
  Reactomeorganism = "human",
  OrgDb = "org.Hs.eg.db",
  padjustvaluecutoff = 0.05,
  padjustedmethod = "BH",
  Analysis.type = c("FEA", "DEA")
)
```

**Arguments**

|                    |                                                                                                                                                        |
|--------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|
| Modulelist         | List object: a list of miRNA sponge modules.                                                                                                           |
| GOont              | One of 'MF', 'BP', and 'CC' subontologies.                                                                                                             |
| KEGGorganism       | Organism, supported organism listed in <a href="http://www.genome.jp/kegg/catalog/org_list.html">http://www.genome.jp/kegg/catalog/org_list.html</a> . |
| Reactomeorganism   | Organism, one of 'human', 'rat', 'mouse', 'celegans', 'yeast', 'zebrafish', 'fly'.                                                                     |
| OrgDb              | OrgDb                                                                                                                                                  |
| padjustvaluecutoff | A cutoff value of adjusted p-values.                                                                                                                   |
| padjustedmethod    | Adjusted method of p-values, can select one of 'holm', 'hochberg', 'hommel', 'bonferroni', 'BH', 'BY', 'fdr', 'none'.                                  |
| Analysis.type      | The type of functional analysis selected, including 'FEA' (functional enrichment analysis) and 'DEA' (disease enrichment analysis).                    |

**Value**

List object: a list of enrichment analysis results.

**Author(s)**

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

**References**

Zhang J, Liu L, Xu T, Xie Y, Zhao C, Li J, Le TD (2019). "miRspongeR: an R/Bioconductor package for the identification and analysis of miRNA sponge interaction networks and modules." BMC Bioinformatics, 20, 235.

Zhang J, Liu L, Zhang W, Li X, Zhao C, Li S, Li J, Le TD. miRspongeR 2.0: an enhanced R package for exploring miRNA sponge regulation. Bioinform Adv. 2022 Sep 2;2(1):vbac063.

Yu G, Wang L, Han Y, He Q (2012). "clusterProfiler: an R package for comparing biological themes among gene clusters." OMICS: A Journal of Integrative Biology, 16(5), 284-287.

## Examples

```
## Not run:
data(BRCASampleData)
modulegenes_WGCNA <- module_WGCNA(ceRExp, mRExp)
# Identify miRNA sponge modules using sensitivity RV coefficient (SRVC)
miRSM_WGCNA_SRVC <- miRSM(miRExp, ceRExp, mRExp, miRTarget,
                           modulegenes_WGCNA, method = "SRVC",
                           SMC.cutoff = 0.01, RV_method = "RV")
miRSM_WGCNA_SRVC_genes <- miRSM_WGCNA_SRVC[[2]]
miRSM_WGCNA_SRVC_FEA <- module_FA(miRSM_WGCNA_SRVC_genes, Analysis.type = 'FEA')
miRSM_WGCNA_SRVC_DEA <- module_FA(miRSM_WGCNA_SRVC_genes, Analysis.type = 'DEA')

## End(Not run)
```

---

module\_GFA

*module\_GFA*


---

## Description

Identification of gene modules from matched ceRNA and mRNA expression data or single gene expression data using GFA package

## Usage

```
module_GFA(
  ceRExp,
  mRExp = NULL,
  StrengthCut = 0.9,
  iter.max = 5000,
  num.ModuleceRs = 2,
  num.ModulemRs = 2
)
```

## Arguments

|                |                                                                                                                |
|----------------|----------------------------------------------------------------------------------------------------------------|
| ceRExp         | A SummarizedExperiment object. ceRNA expression data: rows are samples and columns are ceRNAs.                 |
| mRExp          | NULL (default) or a SummarizedExperiment object. mRNA expression data: rows are samples and columns are mRNAs. |
| StrengthCut    | Desired minimum strength (absolute value of association with interval [0 1]) for each bicluster.               |
| iter.max       | The total number of Gibbs sampling steps (default 1000).                                                       |
| num.ModuleceRs | The minimum number of ceRNAs in each module.                                                                   |
| num.ModulemRs  | The minimum number of mRNAs in each module.                                                                    |

## Value

GeneSetCollection object: a list of module genes.

**Author(s)**

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

**References**

Bunte K, Leppäaho E, Saarinen I, Kaski S. Sparse group factor analysis for biclustering of multiple data sources. *Bioinformatics*. 2016, 32(16):2457-63.

Leppäaho E, Ammad-ud-din M, Kaski S. GFA: exploratory analysis of multiple data sources with group factor analysis. *J Mach Learn Res*. 2017, 18(39):1-5.

**Examples**

```
data(BRCASampleData)
modulegenes_GFA <- module_GFA(ceRExp[seq_len(20), seq_len(15)],
  mRExp[seq_len(20), seq_len(15)], iter.max = 3000)
```

---

|                  |                         |
|------------------|-------------------------|
| module_group_sim | <i>module_group_sim</i> |
|------------------|-------------------------|

---

**Description**

Calculating similarity between two list of module groups

**Usage**

```
module_group_sim(Module.group1, Module.group2, sim.method = "Simpson")
```

**Arguments**

|               |                                                                                                                                            |
|---------------|--------------------------------------------------------------------------------------------------------------------------------------------|
| Module.group1 | List object, the first list of module group.                                                                                               |
| Module.group2 | List object, the second list of module group.                                                                                              |
| sim.method    | Methods for calculating similarity between two modules, select one of three methods (Simpson, Jaccard and Lin). Default method is Simpson. |

**Value**

Similarity between two list of module groups

**Author(s)**

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

**References**

Simpson E H. Measurement of diversity. *Nature*, 1949, 163(4148): 688-688.

Jaccard P. The distribution of the flora in the alpine zone. 1. *New phytologist*, 1912, 11(2): 37-50.

Lin D. An information-theoretic definition of similarity. in: *ICML*. 1998, 98(1998): 296-304.

## Examples

```
library(GSEABase)
data(BRCASampleData)
modulegenes_WGCNA <- module_WGCNA(ceRExp, mRExp)
modulegenes_igraph <- module_igraph (ceRExp, mRExp)
Sim <- module_group_sim(geneIds(modulegenes_WGCNA), geneIds(modulegenes_igraph))
```

---

|               |                      |
|---------------|----------------------|
| module_igraph | <i>module_igraph</i> |
|---------------|----------------------|

---

## Description

Identification of gene modules from matched ceRNA and mRNA expression data or single gene expression data using igraph package

## Usage

```
module_igraph(
  ceRExp,
  mRExp = NULL,
  cor.method = "pearson",
  pos.p.value.cutoff = 0.01,
  cluster.method = "greedy",
  num.ModuleceRs = 2,
  num.ModulemRs = 2
)
```

## Arguments

|                    |                                                                                                                                                          |
|--------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|
| ceRExp             | A SummarizedExperiment object. ceRNA expression data: rows are samples and columns are ceRNAs.                                                           |
| mRExp              | NULL (default) or a SummarizedExperiment object. mRNA expression data: rows are samples and columns are mRNAs.                                           |
| cor.method         | The method of calculating correlation selected, including 'pearson' (default), 'kendall', 'spearman'.                                                    |
| pos.p.value.cutoff | The significant p-value cutoff of positive correlation.                                                                                                  |
| cluster.method     | The clustering method selected in <b>igraph</b> package, including 'betweenness', 'greedy' (default), 'infomap', 'prop', 'eigen', 'louvain', 'walktrap'. |
| num.ModuleceRs     | The minimum number of ceRNAs in each module.                                                                                                             |
| num.ModulemRs      | The minimum number of mRNAs in each module.                                                                                                              |

## Value

GeneSetCollection object: a list of module genes.

## Author(s)

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

## References

Csardi G, Nepusz T. The igraph software package for complex network research, InterJournal, Complex Systems. 2006:1695.

## Examples

```
data(BRCASampleData)
modulegenes_igraph <- module_igraph(ceRExp[, seq_len(10)],
  mRExp[, seq_len(10)])
```

---

module\_miRdistribute    *module\_miRdistribute*

---

## Description

miRNA distribution analysis of sharing miRNAs by the identified miRNA sponge modules

## Usage

```
module_miRdistribute(share_miRs)
```

## Arguments

share\_miRs      List object: a list of common miRNAs of each miRNA sponge module generated by share\_miRs function.

## Value

Matrix object: miRNA distribution in each miRNA sponge module.

## Author(s)

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

## Examples

```
data(BRCASampleData)
modulegenes_WGCNA <- module_WGCNA(ceRExp, mRExp)
# Identify miRNA sponge modules using sensitivity RV coefficient (SRVC)
miRSM_WGCNA_SRVC <- miRSM(miRExp, ceRExp, mRExp, miRTarget,
  modulegenes_WGCNA, method = "SRVC",
  SMC.cutoff = 0.01, RV_method = "RV")
miRSM_WGCNA_SRVC_genes <- miRSM_WGCNA_SRVC[[2]]
miRSM_WGCNA_share_miRs <- share_miRs(miRExp, miRTarget, miRSM_WGCNA_SRVC_genes)
miRSM_WGCNA_miRdistribute <- module_miRdistribute(miRSM_WGCNA_share_miRs)
```

---

|                   |                          |
|-------------------|--------------------------|
| module_miR sponge | <i>module_miR sponge</i> |
|-------------------|--------------------------|

---

**Description**

Extract miRNA sponge interactions of each miRNA sponge module

**Usage**

```
module_miR sponge(Moduleelist)
```

**Arguments**

Moduleelist      List object: a list of the identified miRNA sponge modules.

**Value**

List object: miRNA sponge interactions of each miRNA sponge module.

**Author(s)**

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

**Examples**

```
data(BRCASampleData)
modulegenes_WGCNA <- module_WGCNA(ceRExp, mRExp)
# Identify miRNA sponge modules using sensitivity RV coefficient (SRVC)
miRSM_WGCNA_SRVC <- miRSM(miRExp, ceRExp, mRExp, miRTarget,
                          modulegenes_WGCNA, method = "SRVC",
                          SMC.cutoff = 0.01, RV_method = "RV")
miRSM_WGCNA_SRVC_genes <- miRSM_WGCNA_SRVC[[2]]
miRSM_WGCNA_miR sponge <- module_miR sponge(miRSM_WGCNA_SRVC_genes)
```

---

|                   |                          |
|-------------------|--------------------------|
| module_miR target | <i>module_miR target</i> |
|-------------------|--------------------------|

---

**Description**

Extract miRNA-target interactions of each miRNA sponge module

**Usage**

```
module_miR target(share_miRs, Moduleelist)
```

**Arguments**

share\_miRs      List object: a list of common miRNAs of each miRNA sponge module generated by share\_miRs function.

Moduleelist      List object: a list of the identified miRNA sponge modules.

**Value**

List object: miRNA-target interactions of each miRNA sponge module.

**Author(s)**

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

**Examples**

```
data(BRCASampleData)
modulegenes_WGCNA <- module_WGCNA(ceExp, mRExp)
# Identify miRNA sponge modules using sensitivity RV coefficient (SRVC)
miRSM_WGCNA_SRVC <- miRSM(miRExp, ceExp, mRExp, miRTarget,
                          modulegenes_WGCNA, method = "SRVC",
                          SMC.cutoff = 0.01, RV_method = "RV")
miRSM_WGCNA_SRVC_genes <- miRSM_WGCNA_SRVC[[2]]
miRSM_WGCNA_share_miRs <- share_miRs(miRExp, miRTarget, miRSM_WGCNA_SRVC_genes)
miRSM_WGCNA_miRtarget <- module_miRtarget(miRSM_WGCNA_share_miRs,
                                           miRSM_WGCNA_SRVC_genes)
```

---

module\_NMF

*module\_NMF*

---

**Description**

Identification of gene modules from matched ceRNA and mRNA expression data or single gene expression data using NMF package

**Usage**

```
module_NMF(
  ceExp,
  mRExp = NULL,
  NMF.algorithm = "brunet",
  num.modules = 10,
  num.ModuleceRs = 2,
  num.ModulemRs = 2
)
```

**Arguments**

|                |                                                                                                                                             |
|----------------|---------------------------------------------------------------------------------------------------------------------------------------------|
| ceExp          | A SummarizedExperiment object. ceRNA expression data: rows are samples and columns are ceRNAs.                                              |
| mRExp          | NULL (default) or a SummarizedExperiment object. mRNA expression data: rows are samples and columns are mRNAs.                              |
| NMF.algorithm  | Specification of the NMF algorithm, including 'brunet' (default), 'Frobenius', 'KL', 'lee', 'nsNMF', 'offset', 'siNMF', 'snmf/l', 'snmf/r'. |
| num.modules    | The number of modules to be identified.                                                                                                     |
| num.ModuleceRs | The minimum number of ceRNAs in each module.                                                                                                |
| num.ModulemRs  | The minimum number of mRNAs in each module.                                                                                                 |

**Value**

GeneSetCollection object: a list of module genes.

**Author(s)**

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

**References**

Gaujoux R, Seoighe C. A flexible R package for nonnegative matrix factorization. BMC Bioinformatics. 2010, 11:367.

**Examples**

```
data(BRCASampleData)
# Reimport NMF package to avoid conflicts with DelayedArray package
library(NMF)
modulegenes_NMF <- module_NMF(ceExp[, seq_len(10)],
  mRExp[, seq_len(10)])
```

---

module\_ProNet

*module\_ProNet*


---

**Description**

Identification of gene modules from matched ceRNA and mRNA expression data or single gene expression data using ProNet package

**Usage**

```
module_ProNet(
  ceExp,
  mRExp = NULL,
  cor.method = "pearson",
  pos.p.value.cutoff = 0.01,
  cluster.method = "MCL",
  num.ModuleceRs = 2,
  num.ModulemRs = 2
)
```

**Arguments**

|                    |                                                                                                                |
|--------------------|----------------------------------------------------------------------------------------------------------------|
| ceExp              | A SummarizedExperiment object. ceRNA expression data: rows are samples and columns are ceRNAs.                 |
| mRExp              | NULL (default) or a SummarizedExperiment object. mRNA expression data: rows are samples and columns are mRNAs. |
| cor.method         | The method of calculating correlation selected, including 'pearson' (default), 'kendall', 'spearman'.          |
| pos.p.value.cutoff | The significant p-value cutoff of positive correlation                                                         |

cluster.method The clustering method selected in **ProNet** package, including 'FN', 'MCL' (default), 'LINKCOMM', 'MCODE'.

num.ModuleceRs The minimum number of ceRNAs in each module.

num.ModulemRs The minimum number of mRNAs in each module.

**Value**

GeneSetCollection object: a list of module genes.

**Author(s)**

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

**References**

Clauset A, Newman ME, Moore C. Finding community structure in very large networks. Phys Rev E Stat Nonlin Soft Matter Phys., 2004, 70(6 Pt 2):066111.

Enright AJ, Van Dongen S, Ouzounis CA. An efficient algorithm for large-scale detection of protein families. Nucleic Acids Res., 2002, 30(7):1575-84.

Kalinka AT, Tomancak P. linkcomm: an R package for the generation, visualization, and analysis of link communities in networks of arbitrary size and type. Bioinformatics, 2011, 27(14):2011-2.

Bader GD, Hogue CW. An automated method for finding molecular complexes in large protein interaction networks. BMC Bioinformatics, 2003, 4:2.

**Examples**

```
data(BRCASampleData)
modulegenes_ProNet <- module_ProNet(ceRExp[, seq_len(10)],
  mRExp[, seq_len(10)])
```

---

module\_Validate

*module\_Validate*


---

**Description**

Validation of miRNA sponge interactions in each miRNA sponge module

**Usage**

```
module_Validate(Modulelist, Groundtruth)
```

**Arguments**

Modulelist List object: a list of the identified miRNA sponge modules.

Groundtruth Matrix object: a list of experimentally validated miRNA sponge interactions.

**Value**

List object: a list of validated miRNA sponge interactions in each miRNA sponge module

**Author(s)**

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

**Examples**

```
data(BRCASampleData)
modulegenes_WGCNA <- module_WGCNA(ceRExp, mRExp)
# Identify miRNA sponge modules using sensitivity RV coefficient (SRVC)
miRSM_WGCNA_SRVC <- miRSM(miRExp, ceRExp, mRExp, miRTarget,
                           modulegenes_WGCNA, method = "SRVC",
                           SMC.cutoff = 0.01, RV_method = "RV")
miRSM_WGCNA_SRVC_genes <- miRSM_WGCNA_SRVC[[2]]
Groundtruthcsv <- system.file("extdata", "Groundtruth_high.csv", package="miRSM")
Groundtruth <- read.csv(Groundtruthcsv, header=TRUE, sep=",")
miRSM.Validate <- module_Validate(miRSM_WGCNA_SRVC_genes, Groundtruth)
```

---

module\_WGCNA

*module\_WGCNA*


---

**Description**

Identification of co-expressed gene modules from matched ceRNA and mRNA expression data or single gene expression data using WGCNA package

**Usage**

```
module_WGCNA(
  ceRExp,
  mRExp = NULL,
  RsquaredCut = 0.9,
  num.ModuleceRs = 2,
  num.ModulemRs = 2
)
```

**Arguments**

|                |                                                                                                                |
|----------------|----------------------------------------------------------------------------------------------------------------|
| ceRExp         | A SummarizedExperiment object. ceRNA expression data: rows are samples and columns are ceRNAs.                 |
| mRExp          | NULL (default) or a SummarizedExperiment object. mRNA expression data: rows are samples and columns are mRNAs. |
| RsquaredCut    | Desired minimum scale free topology fitting index $R^2$ with interval [0 1].                                   |
| num.ModuleceRs | The minimum number of ceRNAs in each module.                                                                   |
| num.ModulemRs  | The minimum number of mRNAs in each module.                                                                    |

**Value**

GeneSetCollection object: a list of module genes.

**Author(s)**

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

## References

Langfelder P, Horvath S. WGCNA: an R package for weighted correlation network analysis. BMC Bioinformatics. 2008, 9:559.#'

## Examples

```
data(BRCASampleData)
modulegenes_WGCNA <- module_WGCNA(ceRExp[, seq_len(80)],
  mRExp[, seq_len(80)])
```

---

|       |                             |
|-------|-----------------------------|
| mRExp | <i>mRNA expression data</i> |
|-------|-----------------------------|

---

## Description

mRNA expression data

## Format

mRExp: A SummarizedExperiment object with 72 BRCA and 72 normal samples (rows) and 226 miRNAs (columns).

## Details

The matched breast invasive carcinoma (BRCA) miRNA, lncRNA and mRNA expression data is obtained from TCGA (<http://cancergenome.nih.gov/>). The data focuses on 72 individuals for which the complete sets of tumor and matched normal (i.e., normal tissue taken from the same patient) profiles are available. A mRNA which has missing values in more than 10 are imputed using the k-nearest neighbours (KNN) algorithm from the impute R package. We use the limma R package to infer differentially expressed mRNAs between tumour and normal samples. After the analysis, we select top 500 mRNAs which are differentially expressed at a significant level (adjusted p-value < 1E-02, adjusted by Benjamini & Hochberg method).

---

|            |                   |
|------------|-------------------|
| share_miRs | <i>share_miRs</i> |
|------------|-------------------|

---

## Description

Extract common miRNAs of each miRNA sponge module

## Usage

```
share_miRs(miRExp = NULL, miRTarget, Modulelist)
```

## Arguments

|            |                                                                                                                  |
|------------|------------------------------------------------------------------------------------------------------------------|
| miRExp     | NULL (default) or a SummarizedExperiment object. miRNA expression data: rows are samples and columns are miRNAs. |
| miRTarget  | A SummarizedExperiment object. Putative miRNA-target binding information.                                        |
| Modulelist | List object: a list of the identified miRNA sponge modules.                                                      |

**Value**

List object: a list of common miRNAs of each miRNA sponge module.

**Author(s)**

Junpeng Zhang (<https://www.researchgate.net/profile/Junpeng-Zhang-2>)

**Examples**

```
data(BRCASampleData)
modulegenes_WGCNA <- module_WGCNA(ceRExp, mRExp)
# Identify miRNA sponge modules using sensitivity RV coefficient (SRVC)
miRSM_WGCNA_SRVC <- miRSM(miRExp, ceRExp, mRExp, miRTarget,
                          modulegenes_WGCNA, method = "SRVC",
                          SMC.cutoff = 0.01, RV_method = "RV")
miRSM_WGCNA_SRVC_genes <- miRSM_WGCNA_SRVC[[2]]
miRSM_WGCNA_share_miRs <- share_miRs(miRExp, miRTarget, miRSM_WGCNA_SRVC_genes)
```

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