Package 'miRspongeR'

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Type Package

Title Identification and analysis of miRNA sponge regulation

Version 2.16.2

Description This package provides several functions to explore miRNA sponge (also called ceRNA or miRNA decoy) regulation from putative miRNA-target interactions or/and transcriptomics data (including bulk, single-cell and spatial gene expression data). It provides eight popular methods for identifying miRNA sponge interactions, and an integrative method to integrate miRNA sponge interactions from different methods, as well as the functions to validate miRNA sponge interactions, and infer miRNA sponge modules, conduct enrichment analysis of miRNA sponge modules, and conduct survival analysis of miRNA sponge modules. By using a sample control variable strategy, it provides a function to infer sample-specific miRNA sponge interactions. In terms of sample-specific miRNA sponge interactions, it implements three similarity methods to construct sample-sample correlation network.

Depends R (>= 4.4.0)

License GPL-3

URL <https://github.com/zhangjunpeng411/miRspongeR>

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`integrateMethod` *Integrate method for identifying miRNA sponge interactions by integrating different methods*

Description

Integrate method for identifying miRNA sponge interactions by integrating different methods.

Usage

```
integrateMethod(Interlist, Intersect_num)
```

Arguments

`Interlist`	List object, a list of miRNA sponge interactions from different methods.
`Intersect_num`	The least number of different methods intersected for integration. The value of 1 means the union of miRNA sponge interactions from different methods.

Value

A list of integrated miRNA sponge interactions.

Author(s)

Junpeng Zhang (https://www.researchgate.net/profile/Junpeng_Zhang3)

Examples

```
# Obtain expression data file "ExpData.csv" in csv format
ExpDatacsv <- system.file("extdata","ExpData.csv",package="miRspongeR")
ExpData <- read.csv(ExpDatacsv, header=TRUE, sep=",")

# Obtain miRNA-target interaction data file "miR2Target.csv" in csv format
miR2Target <- system.file("extdata", "miR2Target.csv", package="miRspongeR")
miRTarget <- read.csv(miR2Target, header=TRUE, sep=",")
miRHomologyceRInt <- spongeMethod(miRTarget, method = "miRHomology")
pcceRInt <- spongeMethod(miRTarget, ExpData, method = "pc")
sppcceRInt <- spongeMethod(miRTarget, ExpData, method = "sppc")
Interlist <- list(miRHomologyceRInt[, 1:2], pcceRInt[, 1:2], sppcceRInt[, 1:2])
IntegrateceRInt <- integrateMethod(Interlist, 2)
```

`moduleDEA` *Disease enrichment analysis of modules*

Description

Disease enrichment analysis of modules. The disease ontology databases have three types including DO: Disease Ontology database (http://disease-ontology.org/), and NCG: Network of Cancer Genes database (http://ncg.kcl.ac.uk/).

Usage

```
moduleDEA(Modulelist, OrgDb = "org.Hs.eg.db",
padjustvaluecutoff = 0.05, padjustedmethod = "BH")
```

Arguments

`Modulelist`	A list of miRNA sponge modules.
`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".

Value

A list of disease enrichment analysis results.

Author(s)

Junpeng Zhang (https://www.researchgate.net/profile/Junpeng_Zhang3)

References

Yu G, Wang L, Yan G, et al. DOSE: an R/Bioconductor package for Disease Ontology Semantic and Enrichment analysis. Bioinformatics, 2015, 31(4):608-609.

Examples

```
# Obtain miRNA-target interaction data file "miR2Target.csv" in csv format
## Not run:
miR2Target <- system.file("extdata", "miR2Target.csv", package="miRspongeR")
miRTarget <- read.csv(miR2Target, header=TRUE, sep=",")
miRHomologyceRInt <- spongeMethod(miRTarget, method = "miRHomology")
spongenetwork_Cluster <- netModule(miRHomologyceRInt[, 1:2])
sponge_Module_DEA <- moduleDEA(spongenetwork_Cluster)

## End(Not run)
```

`moduleFEA` *Functional GO, KEGG and Reactome enrichment analysis of modules*

Description

Functional GO, KEGG and Reactome enrichment analysis of modules. GO: Gene Ontology database (http://www.geneontology.org/), KEGG: Kyoto Encyclopedia of Genes and Genomes Pathway Database (http://www.genome.jp/kegg/) and Reactome: Reactome Pathway Database (http://reactome.org/).

Usage

```
moduleFEA(Modulelist, ont = "BP", KEGGorganism = "hsa",
Reactomeorganism = "human", OrgDb = "org.Hs.eg.db",
padjustvaluecutoff = 0.05, padjustedmethod = "BH")
```

Arguments

`Modulelist`	A list of miRNA sponge modules.
`ont`	One of "MF", "BP", and "CC" subontologies.
`KEGGorganism`	Organism, supported organism listed in http://www.genome.jp/kegg/catalog/org_list.html
`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".

Value

A list of functional GO, KEGG and Reactome enrichment analysis results.

Author(s)

Junpeng Zhang (https://www.researchgate.net/profile/Junpeng_Zhang3)

References

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

2. Yu G and He Q. ReactomePA: an R/Bioconductor package for reactome pathway analysis and visualization. Molecular BioSystems, 2016, 12(12), pp. 477-479.

Examples

```
## Not run:
# Obtain expression data file "ExpData.csv" in csv format
ExpDatacsv <- system.file("extdata","ExpData.csv",package="miRspongeR")
ExpData <- read.csv(ExpDatacsv, header=TRUE, sep=",")

# Obtain miRNA-target interaction data file "miR2Target.csv" in csv format
miR2Target <- system.file("extdata", "miR2Target.csv", package="miRspongeR")
miRTarget <- read.csv(miR2Target, header=TRUE, sep=",")
pcceRInt <- spongeMethod(miRTarget, ExpData, method = "pc")
spongenetwork_Cluster <- netModule(pcceRInt[, 1:2])
sponge_Module_FEA <- moduleFEA(spongenetwork_Cluster)

## End(Not run)
```

---

moduleSurvival *Survival analysis of modules*

Description

Survival analysis of modules.

Usage

```
moduleSurvival(Modulelist, ExpData, SurvData,
devidePercentage=.5, plot = FALSE)
```

Arguments

Modulelist	A list of miRNA sponge modules.
ExpData	An input expression data, the columns are genes and the rows are samples.
SurvData	An input survival data, three columns contain the information of sample, time (Months) and status, respectively.
devidePercentage	A percentage value, the percentage of high risk group.
plot	A logical value, plot or not.

Value

Survival analysis result of modules.

Author(s)

Junpeng Zhang (https://www.researchgate.net/profile/Junpeng_Zhang3)

References

Terry M. Therneau and Patricia M. Grambsch. Modeling Survival Data: Extending the Cox Model. Springer, New York. ISBN 0-387-98784-3, 2000.

Examples

```
# Obtain expression data file "ExpData.csv" in csv format
ExpDatacsv <- system.file("extdata","ExpData.csv",package="miRspongeR")
ExpData <- read.csv(ExpDatacsv, header=TRUE, sep=",")

# Obtain miRNA-target interaction data file "miR2Target.csv" in csv format
miR2Target <- system.file("extdata", "miR2Target.csv", package="miRspongeR")
miRTarget <- read.csv(miR2Target, header=TRUE, sep=",")

# Obtain survival data file "SurvData.csv" in csv format
SurvDatacsv <- system.file("extdata", "SurvData.csv", package="miRspongeR")
SurvData <- read.csv(SurvDatacsv, header=TRUE, sep=",")
pcceRInt <- spongeMethod(miRTarget, ExpData, method = "pc")
spongenetwork_Cluster <- netModule(pcceRInt[, 1:2])
sponge_Module_Survival <- moduleSurvival(spongenetwork_Cluster,
ExpData, SurvData)
```

---

netModule *Identifying miRNA sponge modules from network*

Description

Identifying miRNA sponge modules from network. Possible methods include FN, MCL, LINKCOMM, MCODE, betweenness, infomap, prop, eigen, louvain, walktrap.

Usage

```
netModule(spongenetwork, method = "MCL", directed = FALSE, modulesize = 3, save = FALSE)
```

Arguments

spongenetwork	Input miRNA sponge interaction network.
method	Cluster method, can select one of FN, MCL, LINKCOMM, MCODE, betweenness, infomap, prop, eigen, louvain, walktrap.
directed	A logical value, the network is directed or not.
modulesize	The size cutoff of the identified modules.
save	A logical value, save the identified modules or not.

Value

A list of miRNA sponge modules.

Author(s)

Junpeng Zhang (https://www.researchgate.net/profile/Junpeng_Zhang3)

References

1. 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.

2. 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.

3. 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.

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

5. Newman ME, Girvan M. Finding and evaluating community structure in networks. Phys Rev E Stat Nonlin Soft Matter Phys. 2004;69(2 Pt 2):026113.

6. Rosvall M, Bergstrom CT. Maps of random walks on complex networks reveal community structure. Proc Natl Acad Sci U S A. 2008;105(4):1118-1123.

7. Raghavan UN, Albert R, Kumara S. Near linear time algorithm to detect community structures in large-scale networks. Phys Rev E Stat Nonlin Soft Matter Phys. 2007;76(3 Pt 2):036106.

8. Newman ME. Finding community structure in networks using the eigenvectors of matrices. Phys Rev E Stat Nonlin Soft Matter Phys. 2006;74(3 Pt 2):036104.

9. Blondel VD, Guillaume JL, Lambiotte R, Lefebvre E. Fast unfolding of communities in large networks. Journal of statistical mechanics: theory and experiment, 2008, 2008(10): P10008.

10. Pons P, Latapy M. Computing communities in large networks using random walks. Graph Algorithms Appl. 2006.

Examples

```
# Obtain miRNA-target interaction data file "miR2Target.csv" in csv format
miR2Target <- system.file("extdata", "miR2Target.csv", package="miRspongeR")
miRTarget <- read.csv(miR2Target, header=TRUE, sep=",")
miRHomologyceRInt <- spongeMethod(miRTarget, method = "miRHomology")
spongenetwork_Cluster <- netModule(miRHomologyceRInt[, 1:2])
```

---

precomputed_null_model

A null model for testing purposes in SPONGE R package

Description

A null model for testing purposes in SPONGE R package

Usage

```
precomputed_null_model
```

Format

A list (different gene-gene correlations k) of lists (different number of miRNAs m) of sampled mscor values (100 each, computed from 144 samples)

---

querymiRTargetbinding

Query miRNA-target interactions by combining expression data and putative miRNA-target interactions

---

Description

Query miRNA-target interactions by combining expression data and putative miRNA-target interactions.

Usage

```
querymiRTargetbinding(ExpData, miRTarget, type = c("all", "miRNA", "target"))
```

Arguments

ExpData	An input gene expression data frame, the rows are samples and the columns are genes.
miRTarget	An input miRNA-target interaction data frame, the first column is miRNA with name "mir" and the second column is target with name "gene".
type	The type of queried miRNA-target interactions, type "all" for querying both miRNAs and targets in gene expression data, type "miRNA" for querying only miRNAs in gene expression data, and type "target" for querying only targets in gene expression data.

Value

A list of queried miRNA-target interactions

Author(s)

Junpeng Zhang (https://www.researchgate.net/profile/Junpeng_Zhang3)

Examples

```
# Obtain expression data file "ExpData.csv" in csv format
ExpDatacsv <- system.file("extdata","ExpData.csv",package="miRspongeR")
ExpData <- read.csv(ExpDatacsv, header=TRUE, sep=",")

# Obtain miRNA-target interaction data file "miR2Target.csv" in csv format
miR2Target <- system.file("extdata", "miR2Target.csv", package="miRspongeR")
miRTarget <- read.csv(miR2Target, header=TRUE, sep=",")
miR2Target_queried <- querymiRTargetbinding(ExpData, miRTarget, type = "all")
```

---

sample_cor_network *Identifying sample-sample correlation network*

Description

Identifying sample-sample correlation network in terms of sample-specific miRNA sponge networks.

Usage

```
sample_cor_network(ceRNet, genes_num, method = "Simpson",
simcutoff = 0.5, padjustvaluecutoff = 0.01,
padjustmethod = "BH", num.cores = 2)
```

Arguments

ceRNet	List object, input sample-specific miRNA sponge networks.
genes_num	Number of possible miRNA sponges.
method	Methods for calculating similatiry between two sample-specific miRNA sponge networks, select one of three methods (Simpson, Jaccard and Lin). Default method is Simpson.
simcutoff	A cutoff value of asimilatiry.
padjustvaluecutoff	A cutoff value of adjusted p-values.
padjustmethod	Adjusted method of p-values, can select one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none".
num.cores	The number of CPU cores to be selected.

Value

A list of sample-sample correlations.

Author(s)

Junpeng Zhang (https://www.researchgate.net/profile/Junpeng_Zhang3)

References

1. Tucker CM, Cadotte MW, Carvalho SB, et al. A guide to phylogenetic metrics for conservation, community ecology and macroecology. Biol Rev Camb Philos Soc. 2017;92(2):698-715.

2. Jaccard P. The Distribution of the Flora in the Alpine Zone. The New Phytologist 11, no. 2 (1912): 37–50.

3. Lin D, et al. An information-theoretic definition of similarity. In: Icml, vol. 98. 1998. p. 296–304.

Examples

```
# Obtain expression data file "ExpData.csv" in csv format
ExpDatacsv <- system.file("extdata","ExpData.csv",package="miRspongeR")
ExpData <- read.csv(ExpDatacsv, header=TRUE, sep=",")

# Obtain miRNA-target interaction data file "miR2Target.csv" in csv format
miR2Target <- system.file("extdata", "miR2Target.csv", package="miRspongeR")
miRTarget <- read.csv(miR2Target, header=TRUE, sep=",")

# Identifying sample-specific miRNA sponge interactions, the sppc method
# is used to identify miRNA sponge interactions
sponge_sample_specific_net <- sponge_sample_specific(miRTarget, ExpData, senscorcutoff = 0.1, method = "sppc")

sample_cor_network_res <- sample_cor_network(sponge_sample_specific_net,
genes_num = 31, padjustvaluecutoff = 0.05)
```

---

spongeMethod *Identifying miRNA sponge interactions*

Description

We implement eight popular methods (miRHomology, pc, sppc, ppc, hermes, muTaME, cernia, and SPONGE) to identify miRNA sponge interactions. The parallel methods ("miRHomology_parallel", "pc_parallel", "sppc_parallel", "ppc_parallel", "hermes_parallel", "muTaME_parallel", "cernia_parallel") are the parallel versions of the original methods ("miRHomology", "pc", "sppc", "ppc", "hermes", "muTaME", "cernia").

Usage

```
spongeMethod(miRTarget, ExpData = NULL, mres = NULL,
consider.miR.expr = "TRUE", minSharedmiR = 3,
poscorcutoff = 0, num_perm = 100,
padjustvaluecutoff = 0.01,
padjustmethod = "BH", senscorcutoff = 0.3,
scorecutoff = 0.5, null_model,
method = c("miRHomology", "miRHomology_parallel", "pc",
"pc_parallel", "sppc", "sppc_parallel", "ppc", "ppc_parallel", "hermes", "hermes_parallel",
"muTaME", "muTaME_parallel", "cernia",
"cernia_parallel", "sponge_parallel"),
num.cores = 2)
```

Arguments

miRTarget	Putative miRNA-target interactions. Required option for method "miRHomology", "miRHomology_parallel", "pc", "pc_parallel", "sppc", "sppc_parallel", "ppc", "ppc_parallel", "hermes", "hermes_parallel", "muTaME", "muTaME_parallel", "cernia", "cernia_parallel", and "sponge_parallel".
ExpData	An input expression data frame, the columns are genes and the rows are samples. Required option for method "pc", "pc_parallel", "sppc", "sppc_parallel", "ppc", "ppc_parallel", "hermes" "hermes_parallel", "cernia", "cernia_parallel", and "sponge_parallel".
mres	Putative MiRNA Response Elements (mres) data frame, each row contains five elements: Mirna, Target, energy, gap_l, gap_r. Required option for method "muTaME", "muTaME_parallel", "cernia", and "cernia_parallel".
consider.miR.expr	Logical value, TRUE for considering miRNA expression data and FALSE for ignoring miRNA expression data
minSharedmiR	The minimum number of shared miRNAs between targets. Required option for method "miRHomology", "miRHomology_parallel", "pc", "pc_parallel", "sppc", "sppc_parallel", "ppc", "ppc_parallel", "hermes", "hermes_parallel", "muTaME", "muTaME_parallel", "cernia", "cernia_parallel", and "sponge_parallel".
poscorcutoff	A cutoff value of positive correlation. Required option for method "pc", "pc_parallel", "sppc", "sppc_parallel", "cernia", "cernia_parallel", and "sponge_parallel".
num_perm	The number of permutations. Required option for method "ppc", "ppc_parallel", "hermes", "hermes_parallel".
padjustvaluecutoff	A cutoff value of adjusted p-values. Required option for method "miRHomology", "miRHomology_parallel", "pc", "pc_parallel", "sppc", "sppc_parallel", "ppc", "ppc_parallel", "hermes", "hermes_parallel", "muTaME", "muTaME_parallel", "cernia", "cernia_parallel", and "sponge_parallel".
padjustmethod	Adjusted method of p-values, can select one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". Required option for method "miRHomology", "miRHomology_parallel", "pc", "pc_parallel", "sppc", "sppc_parallel", "ppc", "ppc_parallel", "hermes", "hermes_parallel", "muTaME", "muTaME_parallel", "cernia", "cernia_parallel", and "sponge_parallel".

`senscorcutoff` A cutoff value of sensitivity partial pearson correlation. Required option for method "sppc", "sppc_parallel", and "sponge_parallel".

`scorecutoff` A cutoff value of normalized score (range from 0 to 1). Required option for method "muTaME", "muTaME_parallel", "cernia", and "cernia_parallel".

`null_model` Optional, pre-computed null model. Users can also build null model using "sponge_build_null_model" function in SPONGE R package. Required option for method "sponge_parallel".

`method` Select a method for identifying miRNA sponge interactions, can select one of "miRHomology", "miRHomology_parallel", "pc", "pc_parallel", "sppc", "sppc_parallel", "ppc", "ppc_parallel", "hermes", "hermes_parallel", "muTaME", "muTaME_parallel", "cernia", "cernia_parallel", "sponge_parallel". The seven methods ("miRHomology_parallel", "pc_parallel", "sppc_parallel", "ppc_parallel", "hermes_parallel", "muTaME_parallel", "cernia_parallel") are the parallel versions of the seven original methods ("miRHomology", "pc", "sppc", "ppc", "hermes", "muTaME", "cernia").

`num.cores` The number of CPU cores to be selected. Required option for method "miRHomology_parallel", "pc_parallel", "sppc_parallel", "ppc_parallel", "hermes_parallel", "muTaME_parallel", "cernia_parallel", and "sponge_parallel".

Value

A list of identified miRNA sponge interactions.

Author(s)

Junpeng Zhang (https://www.researchgate.net/profile/Junpeng_Zhang3)

References

1. Le TD, Zhang J, Liu L, et al. Computational methods for identifying miRNA sponge interactions. Brief Bioinform., 2017, 18(4):577-590.

2. Li JH, Liu S, Zhou H, et al. starBase v2.0: decoding miRNA-ceRNA, miRNA-ncRNA and protein-RNA interaction networks from large-scale CLIP-Seq data. Nucleic Acids Res., 2014, 42(Database issue):D92-7.

3. Sarver AL, Subramanian S. Competing endogenous RNA database. Bioinformation, 2012, 8(15):731-3.

4. Zhou X, Liu J, Wang W, Construction and investigation of breast-cancer-specific ceRNA network based on the mRNA and miRNA expression data. IET Syst Biol., 2014, 8(3):96-103.

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6. Paci P, Colombo T, Farina L, Computational analysis identifies a sponge interaction network between long non-coding RNAs and messenger RNAs in human breast cancer. BMC Syst Biol., 2014, 8:83.

7. Sumazin P, Yang X, Chiu HS, et al. An extensive microRNA-mediated network of RNA-RNA interactions regulates established oncogenic pathways in glioblastoma. Cell, 2011, 147(2):370-81.

8. Tay Y, Kats L, Salmena L, et al. Coding-independent regulation of the tumor suppressor PTEN by competing endogenous mRNAs. Cell, 2011, 147(2):344-57.

9. Sardina DS, Alaimo S, Ferro A, Pulvirenti A, Giugno R. A novel computational method for inferring competing endogenous interactions. Brief Bioinform. 2017;18(6):1071-1081.

10. List M, Dehghani Amirabad A, Kostka D, Schulz MH. Large-scale inference of competing endogenous RNA networks with sparse partial correlation. Bioinformatics. 2019;35(14):i596-i604.

Examples

```
# Obtain expression data file "ExpData.csv" in csv format
ExpDatacsv <- system.file("extdata","ExpData.csv",package="miRspongeR")
ExpData <- read.csv(ExpDatacsv, header=TRUE, sep=",")

# Obtain miRNA-target interaction data file "miR2Target.csv" in csv format
miR2Target <- system.file("extdata", "miR2Target.csv", package="miRspongeR")
miRTarget <- read.csv(miR2Target, header=TRUE, sep=",")

# miRHomology method
miRHomologyceRInt <- spongeMethod(miRTarget, method = "miRHomology")

# pc method
pcceRInt <- spongeMethod(miRTarget, ExpData, method = "pc")

# sppc method
sppcceRInt <- spongeMethod(miRTarget, ExpData, senscorcutoff = 0.1, method = "sppc")
```

`spongeValidate` *Validation of computationally predicted miRNA sponge interactions*

Description

Validation of computationally predicted miRNA sponge interactions. The built-in groundtruth of miRNA sponge interactions are from miRSponge (<http://bio-bigdata.hrbmu.edu.cn/miRSponge/>), lncACTdb (<http://bio-bigdata.hrbmu.edu.cn/LncACTdb/>), LncCeRBase (<http://www.insect-genome.com/LncCeRBase/fi

Usage

```
spongeValidate(spongenetwork, directed = FALSE, Groundtruth)
```

Arguments

`spongenetwork`	Input miRNA sponge interaction network.
`directed`	A logical value, the network is directed or not.
`Groundtruth`	The groundtruth of miRNA sponge interactions.

Value

A list of experimentally validated miRNA sponge interactions.

Author(s)

Junpeng Zhang (https://www.researchgate.net/profile/Junpeng_Zhang3)

Examples

```
# Obtain miRNA-target interaction data file "miR2Target.csv" in csv format
miR2Target <- system.file("extdata", "miR2Target.csv", package="miRspongeR")
miRTarget <- read.csv(miR2Target, header=TRUE, sep=",")

# Obtain experimentally validated miRNA sponge interaction data file "Groundtruth.csv" in csv format
Groundtruthcsv <- system.file("extdata", "Groundtruth.csv", package="miRspongeR")
Groundtruth <- read.csv(Groundtruthcsv, header=TRUE, sep=",")
miRHomologyceRInt <- spongeMethod(miRTarget, method = "miRHomology")
spongenetwork_validated <- spongeValidate(miRHomologyceRInt[, 1:2], directed = FALSE, Groundtruth)
```

---

sponge_sample_specific

Identifying sample-specific miRNA sponge interactions

Description

A sample control variable strategy is used to identify sample-specific miRNA sponge interactions. In the strategy, seven popular methods (pc, sppc, ppc, hermes, muTaME, cernia, and SPONGE) to identify miRNA sponge interactions.

Usage

```
sponge_sample_specific(miRTarget, ExpData = NULL, mres = NULL,
consider.miR.expr = "TRUE", minSharedmiR = 3, poscorcutoff = 0,
num_perm = 100, padjustvaluecutoff = 0.01, padjustmethod = "BH",
senscorcutoff = 0.3, scorecutoff = 0.5, null_model,
method = c("pc", "pc_parallel", "sppc", "sppc_parallel",
"ppc", "ppc_parallel", "hermes", "hermes_parallel", "cernia",
"cernia_parallel", "sponge_parallel"), num.cores = 2)
```

Arguments

miRTarget	Putative miRNA-target interactions. Required option for method "pc", "pc_parallel", "sppc", "sppc_parallel", "ppc", "ppc_parallel", "hermes", "hermes_parallel", "muTaME", "muTaME_parallel", "cernia", "cernia_parallel", and "sponge_parallel".
ExpData	An input expression data frame, the columns are genes and the rows are samples. Required option for method "pc", "pc_parallel", "sppc", "sppc_parallel", "ppc", "ppc_parallel", "hermes" "hermes_parallel", "cernia", "cernia_parallel", and "sponge_parallel".
mres	Putative MiRNA Response Elements (mres) data frame, each row contains five elements: Mirna, Target, energy, gap_l, gap_r. Required option for method "muTaME", "muTaME_parallel", "cernia", and "cernia_parallel".

`consider.miR.expr`
: Logical value, TRUE for considering miRNA expression data and FALSE for ignoring miRNA expression data

`minSharedmiR`
: The minimum number of shared miRNAs between targets. Required option for method "pc", "pc_parallel", "sppc", "sppc_parallel", "ppc", "ppc_parallel", "hermes", "hermes_parallel", "muTaME", "muTaME_parallel", "cernia", "cernia_parallel", and "sponge_parallel".

`poscorcutoff`
: A cutoff value of positive correlation. Required option for method "pc", "pc_parallel", "sppc", "sppc_parallel", "cernia", "cernia_parallel", and "sponge_parallel".

`num_perm`
: The number of permutations. Required option for method "ppc", "ppc_parallel", "hermes", "hermes_parallel".

`padjustvaluecutoff`
: A cutoff value of adjusted p-values. Required option for method "pc", "pc_parallel", "sppc", "sppc_parallel", "ppc", "ppc_parallel", "hermes", "hermes_parallel", "muTaME", "muTaME_parallel", "cernia", "cernia_parallel", and "sponge_parallel".

`padjustmethod`
: Adjusted method of p-values, can select one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". Required option for method "miRHomology", "miRHomology_parallel", "pc", "pc_parallel", "sppc", "sppc_parallel", "ppc", "ppc_parallel", "hermes", "hermes_parallel", "muTaME", "muTaME_parallel", "cernia", "cernia_parallel", and "sponge_parallel".

`senscorcutoff`
: A cutoff value of sensitivity partial pearson correlation. Required option for method "sppc", "sppc_parallel", and "sponge_parallel".

`scorecutoff`
: A cutoff value of normalized score (range from 0 to 1). Required option for method "muTaME", "muTaME_parallel", "cernia", and "cernia_parallel".

`null_model`
: Optional, pre-computed null model. Users can also build null model using "sponge_build_null_model" function in SPONGE R package. Required option for method "sponge_parallel".

`method`
: Select a method for identifying miRNA sponge interactions, can select one of "pc", "pc_parallel", "sppc", "sppc_parallel", "ppc", "ppc_parallel", "hermes", "hermes_parallel", "muTaME", "muTaME_parallel", "cernia", "cernia_parallel", "sponge_parallel". The seven methods ("miRHomology_parallel", "pc_parallel", "sppc_parallel", "ppc_parallel", "hermes_parallel", "muTaME_parallel", "cernia_parallel") are the parallel versions of the seven original methods ("miRHomology", "pc", "sppc", "ppc", "hermes", "muTaME", "cernia").

`num.cores`
: The number of CPU cores to be selected. Required option for method "pc_parallel", "sppc_parallel", "ppc_parallel", "hermes_parallel", "muTaME_parallel", "cernia_parallel", and "sponge_parallel".

Value

A list of sample-specific miRNA sponge interactions.

Author(s)

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Examples

```
# Obtain expression data file "ExpData.csv" in csv format
ExpDatacsv <- system.file("extdata","ExpData.csv",package="miRspongeR")
ExpData <- read.csv(ExpDatacsv, header=TRUE, sep=",")

# Obtain miRNA-target interaction data file "miR2Target.csv" in csv format
miR2Target <- system.file("extdata", "miR2Target.csv", package="miRspongeR")
miRTarget <- read.csv(miR2Target, header=TRUE, sep=",")

# Identifying sample-specific miRNA sponge interactions,
# the sppc method is used to identify miRNA sponge interactions
sponge_sample_specific_net <- sponge_sample_specific(miRTarget, ExpData, senscorcutoff = 0.1, method = "sppc")
```

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