

# Package ‘mirTarRnaSeq’

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**Type** Package

**Title** mirTarRnaSeq

**Version** 1.13.0

**Description** mirTarRnaSeq R package can be used for interactive mRNA miRNA sequencing statistical analysis. This package utilizes expression or differential expression mRNA and miRNA sequencing results and performs interactive correlation and various GLMs (Regular GLM, Multivariate GLM, and Interaction GLMs ) analysis between mRNA and miRNA experiments. These experiments can be time point experiments, and or condition experiments.

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---

canonicalModel\_      *Decifer a 'model parameter' and run appropriate glm\_... function.*

---

**Description**

Return canonical model from model type string, function of object. Returns a model as returned by `glm_gaussian()` and others, based on a string, function or model type object (i.e. "glm\_gaussian", `glm_gaussian` or `glm_gaussian()`).

**Usage**

```
canonicalModel_(model)
```

**Arguments**

model                    string, function or object representing a model type.

**Value**

model type object

---

Combine                    *This is data is the mRNA expression across samples and miRNA expression data which is to be investigated in one file. This data set is used in documentation examples.*

---

**Description**

This is data is the mRNA expression across samples and miRNA expression data which is to be investigated in one file. This data set is used in documentation examples.

---

combiner                    *combiner combines the miRNA and mRNA files*

---

**Description**

This function makes and intersection dataframe for mRNA and miRNA/s of interest to be tested.

**Usage**

```
combiner(mRNA, miRNA, miRNA_select)
```

**Arguments**

mRNA                    Matrix or data.frame mRNA/RNA from transformed diff expression file (generated using TZtranz)

miRNA                    Matrix or data frame miRNA from transformed diff file (generated using TZtranz)

miRNA\_select            A vector of character's for miRNAs which the user is interested in investigating if glm is use 1 miRNA should be input. If multivariate several miRNAs should be imported, same goes for interaction determination for miRNAs. Note we do not recommend more than 3-4 miRNAs at a time for the latter cases.

**Value**

A dataframe which includes only mRNAs and miRNA intersection for the next estimation geneVari output.

**Examples**

```
miRNA_select <- c("ebv-mir-bart9-5p")
x <- combiner(mRNA, miRNA, miRNA_select)
```

---

corMirnaRna                      *corMirnaRna correlation for miRNA and mRNA*

---

### Description

This function uses the output of one2OneRnaMiRNA and returns the correlation dataframe

### Usage

```
corMirnaRna(mRNA, miRNA, method = "pearson")
```

### Arguments

mRNA	mRNA file generated from foldchanges (FC) obj of the one2OneRnaMiRNA
miRNA	miRNA file generated from foldchanges (FC) obj of the one2OneRnaMiRNA
method	Default is "pearson" else use "kendall" or "spearman"

### Value

Correlation data.frame

### Examples

```
x <- corMirnaRna(mRNA_fc, miRNA_fc, method = "spearman")
```

---

corMirnaRnaMiranda                      *corMirnaRnaMiranda correlation for miRNA and mRNA*

---

### Description

This function uses the output of one2OneRnaMiRNA and returns the correlation dataframe.

### Usage

```
corMirnaRnaMiranda(mRNA, miRNA, CorVal, getInputSpeciesDF, method = "pearson")
```

### Arguments

mRNA	mRNA file generated from foldchanges (FC) obj of the one2OneRnaMiRNA.
miRNA	miRNA file generated from foldchanges (FC) obj of the one2OneRnaMiRNA
CorVal	Correlation cut off.Example: If correlation -0.2 it would only return correlations with smaller than this value correlation for miRNA and mRNA at various time points.
getInputSpeciesDF	The dataframe generated from the getInputSpecies function.
method	Default is "pearson" else use "kendall" or "spearman".

**Value**

Correlation dataframe

**Examples**

```
x <- corMirnaRnaMiranda(mRNA_fc, miRNA_fc, Cor = -0.9, miRandaM)
```

---

corr_0	<i>This is data is the mRNA FC and miRNA FC correlation data. This data set is used in documentation examples.</i>
--------	--

---

**Description**

This is data is the mRNA FC and miRNA FC correlation data. This data set is used in documentation examples.

---

downloadMirandaFile	<i>downloadMirandaFile Read internal Miranda file</i>
---------------------	---

---

**Description**

Reads internal Miranda file from extdata and returns it as a data.frame

**Usage**

```
downloadMirandaFile(urlf)
```

**Arguments**

urlf                      URL of the specific chosen file

**Value**

data.frame containing downloaded miRanda file

**Examples**

```
x <- downloadMirandaFile(
  "https://zenodo.org/record/4615670/files/Mouse_miRanda.txt.gz"
)
```

---

drawCorPlot	<i>drawCorPlot correlation plots for mRNA and miRNA regression results</i>
-------------	--

---

### Description

This function plots correlations for mRNA and miRNAs regression results (negative correlation for multi and individual interactions and positive and negative for interactions)

### Usage

```
drawCorPlot(corMatrix, ...)
```

### Arguments

corMatrix	Significant correlation matrix
...	parameters form the corrplot package

### Value

miRNA mRNA target correlation plot

### Examples

```
x <- drawCorPlot(corMatrix)
```

---

drawInterPlots	<i>drawInterPlots for finInterResult miRNA and mRNA Interrelation real data</i>
----------------	---

---

### Description

This function draws miRNA, mRNA density plots for miRNA and mRNA Interrelation while comparing in addition to overall FC\_miRNA and FC\_mRNA plots from the finInterResult dataframe function.

### Usage

```
drawInterPlots(mrna, mirna, final_results)
```

### Arguments

mrna	mRNA results of twoTimePoint function.
mirna	miRNA results of twoTimePoint function.
final_results	finInterResult miRNA and mRNA interrelation in two timepoints results in a dataframe.

**Value**

par plots

**Examples**

```
x <- drawInterPlots(mRNA_fc2, miRNA_fc2, final_results)
```

---

fdrSig	<i>fdrSig Returns FDR significant miRNA/mRNA predictions</i>
--------	--

---

**Description**

This function performs FDR correction on the p\_values generated by the runModels function list.

**Usage**

```
fdrSig(RMobj, value = 0.05, method = "fdr")
```

**Arguments**

RMobj	The output of runModels
value	The FDR value default is 0.1
method	The p-value adjustment method default is fdr. It could be either of the following "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", or "fdr".

**Value**

A list of FDR corrected p vlaues, annova, and significance for each gene and the miRNA/s of interest

**Examples**

```
models <- runModels(Combine, geneVariant, "ebv-mir-bart9-5p")
x <- fdrSig(models, value = 0.1, method = "fdr")
```

---

final_results	<i>This is data is the mRNA FC and miRNA FC correlation/interaction data results after filtration. This data set is used in documentation examples.</i>
---------------	---

---

**Description**

This is data is the mRNA FC and miRNA FC correlation/interaction data results after filtration. This data set is used in documentation examples.



---

finInterResult	<i>finInterResult miRNA and mRNA interrelation in two-time points results in a dataframe.</i>
----------------	---

---

**Description**

This function uses the output of one2OneRnaMiRNA and returns a sampled from orig file interrelation dataframe depending on user sampling selection.

**Usage**

```
finInterResult(results)
```

**Arguments**

results	Results from mirandaIntersectInter
---------	------------------------------------

**Value**

miRNA mRNA interrelation dataframe

**Examples**

```
x <- finInterResult(results)
```

---

geneVari	<i>geneVari Makes a list of gene names to be used in the runModels function</i>
----------	---

---

**Description**

This function defines the boudnaries of mRNA vs miRNAs of interest to be analysed by the runModels function

**Usage**

```
geneVari(Combined, miRNA_select)
```

**Arguments**

Combined	the combined file for mRNA and selected miRNAs output of combiner function
miRNA_select	The vector of selected miRNA/s

**Value**

A vector of characters with defined mRNA dimensions

**Examples**

```
x <- geneVari(Combine, "ebv-mir-bart9-5p")
```

---

geneVariant	<i>This is data is the mRNA expression across samples and miRNA expression data which is to be investigated giving directions on which data is miRNA and which is mRNA. This data set is used in documentation examples.</i>
-------------	--

---

**Description**

This is data is the mRNA expression across samples and miRNA expression data which is to be investigated giving directions on which data is miRNA and which is mRNA. This data set is used in documentation examples.

---

getInputSpecies	<i>Return Miranda data for a given species.</i>
-----------------	---

---

**Description**

Reads Miranda file for a given species and returns it as a data.frame, thresholded by percent identity. Header options are Score (threshold), Energy-Kcal/Mol(energy), Subject-IdentityPercent(targetIden), Query-IdentityPercent (mirnaIden)

**Usage**

```
getInputSpecies(  
  selection,  
  threshold = 60,  
  energy = NULL,  
  targetIden = NULL,  
  mirnaIden = NULL  
)
```

**Arguments**

selection	Species (species selection are either for mature miRNA species "Human1", "Mouse", "C.elegans", "Epstein_Barr", "Epstein_Barr_Human", "Drosophila", "Kaposi_Sarcoma", "KSHV_Human", "Cytomegalovirus", "CMV_Human")
threshold	miRanda score threshold default 60
energy	miRanda folding energy threshold default NULL
targetIden	miRanda target identity score default NULL
mirnaIden	miRanda mirna identity score default NULL

**Value**

data.frame with Miranda data.

**Examples**

```
x <- getInputSpecies("Epstein_Barr", threshold = 60) # Default is threshold 60
```

---

glm_gaussian	<i>Model functions for GLM with Gaussian model.</i>
--------------	---

---

**Description**

Implements standardized functions to fit the glm with Gaussian family and to obtain coefficients, pvalues, etc.

**Usage**

```
glm_gaussian()
```

**Value**

structure containing functions fit, coefficients, aic, data, pterm, pmodel, and a character string "glm\_gaussian" in model.

**Examples**

```
x <- glm_gaussian()
```

---

glm_multi	<i>Model functions for GLM with negative binomial family.</i>
-----------	---

---

**Description**

Runs models 'glm\_gaussian', 'glm\_nb', 'glm\_poisson', 'glm\_zeroinfl(poisson)', 'glm\_zeroinfl(negbin)' and returns mode with lowest AIC.

**Usage**

```
glm_multi(
  models = c(glm_gaussian, glm_nb, glm_poisson, glm_zeroinfl_poisson,
             glm_zeroinfl_negbin)
)
```

**Arguments**

models            Model type, one or more of glm\_gaussian, glm\_nb, glm\_poisson, glm\_zeroinfl\_poisson or glm\_zeroinfl\_negbin

**Value**

structure containing functions `fit`, `coefficients`, `aic`, `data`, `pterm`, `pmodel`, and a character string "glm\_multi" in `model`.

**Examples**

```
x <- glm_multi()
```

---

`glm_nb`*Model functions for GLM with negative binomial family.*

---

**Description**

Implements standardized functions to fit the negative binomial GLM and to obtain coefficients, pvalues, etc.

**Usage**

```
glm_nb()
```

**Value**

structure containing functions `fit`, `coefficients`, `aic`, `data`, `pterm`, `pmodel`, and a character string "glm\_nb" in `model`.

**Examples**

```
x <- glm_nb()
```

---

`glm_poisson`*Model functions for GLM with Poisson model.*

---

**Description**

Implements standardized functions to fit the glm with Poisson family and to obtain coefficients, pvalues, etc.

**Usage**

```
glm_poisson()
```

**Value**

structure containing functions `fit`, `coefficients`, `aic`, `data`, `pterm`, `pmodel`, and a character string "glm\_poisson" in `model`.

**Examples**

```
x <- glm_poisson()
```

---

glm_zeroinfl	<i>Model functions for zero inflated model using either Poisson or Negative Binomial distributions.</i>
--------------	---

---

**Description**

Implements standardized functions to fit the zero inflated model with Poisson or Negative Binomial distribution, and to obtain coefficients, pvalues, etc.

**Usage**

```
glm_zeroinfl(dist = "poisson")
```

**Arguments**

dist            either 'poisson' or 'negbin'

**Value**

structure containing functions fit, coefficients, aic, data, pterm, pmodel, and a character string "glm\_zeroinfl" in model.

**Examples**

```
x <- glm_zeroinfl("negbin")
```

---

glm_zeroinfl_negbin	<i>alias for glm_zeroinfl("negbin")</i>
---------------------	---

---

**Description**

alias for glm\_zeroinfl("negbin")

**Usage**

```
glm_zeroinfl_negbin(...)
```

**Arguments**

...            passed to glm\_zeroinfl

**Value**

structure containing functions fit, coefficients, aic, data, pterm, pmodel, and a character string "glm\_zeroinfl" in model.

**Examples**

```
x <- glm_zeroinfl_negbin()
```

---

```
glm_zeroinfl_poisson  alias for glm_zeroinfl("poisson")
```

---

**Description**

alias for `glm_zeroinfl("poisson")`

**Usage**

```
glm_zeroinfl_poisson(...)
```

**Arguments**

... passed to `glm_zeroinfl`

**Value**

structure containing functions `fit`, `coefficients`, `aic`, `data`, `pterm`, `pmodel`, and a character string `"glm_zeroinfl"` in `model`.

**Examples**

```
x <- glm_zeroinfl_poisson()
```

---

```
importMirandaFile  importMirandaFile Read internal Miranda file
```

---

**Description**

Reads internal Miranda file from `extdata` and returns it as a `data.frame`

**Usage**

```
importMirandaFile(fn)
```

**Arguments**

`fn` filename

**Value**

`data.frame` containing Miranda data

**Examples**

```
x <- importMirandaFile("Mouse_miRanda.txt")
```

---

inter0	<i>This is data is the mRNA FC and miRNA FC correlation/interaction original data. This data set is used in documentation examples.</i>
--------	---

---

### Description

This is data is the mRNA FC and miRNA FC correlation/interaction original data. This data set is used in documentation examples.

---

makeFormulaRightSide	<i>makeFormulaRightSide makes right hand side of formula for model variables: vector of indep. variables</i>
----------------------	--

---

### Description

This function make right hand side of formula for model variables: vector of indep. variables (i.e. miRNAs) mode: 'multi' for simple, 'inter' for model with interactions returns a string in the form "~ a + b", or "~ a + b + a \* b"

### Usage

```
makeFormulaRightSide(variables, mode = "multi")
```

### Arguments

variables	The vector created by miRNA_select
mode	One of "multi", "inter" or NULL

### Value

data.frame containing Miranda data

### Examples

```
x <- makeFormulaRightSide(variables, mode = "multi")
```

---

miRanComp	<i>miRanComp comparison of mRNAs present with miRanda file targets</i>
-----------	--

---

**Description**

This function generates a dataframe consisting of mRNA or miRNAs present in miRanda generated file using the `miRTarRNASeq:::getInputSpecies()` function

**Usage**

```
miRanComp(miRNA, miRanda)
```

**Arguments**

miRNA	Matrix or data.frame miRNA/RNA file or transformed diff expression file (generated using TZtranz)
miRanda	A dataframe of miRanda file with miRNA\$V1 and miRNA targets miRNA\$V2

**Value**

An miRNA expression dataframe which includes only Genes/Targets present in miRanda file

**Examples**

```
x <- miRanComp(miRNA, miRanda)
```

---

miRanda	<i>This is data is the results file from EBV miRanda getInputSpecies function. This data set is used in documentation examples.</i>
---------	---

---

**Description**

This is data is the results file from EBV miRanda getInputSpecies function. This data set is used in documentation examples.



---

miRandaIntersect	<i>miRandaIntersect Looks for Intersection of Significant output results with miRanda Results from getInputSpeciesDF function</i>
------------------	---

---

**Description**

Compares and looks for intersection if significant output results with miRanda Results from getInputSpeciesDF and outputs a final filtered output for only those pairs of miRNA and mRNA which have actually been predicted to be targets in miRanda file function

**Usage**

```
miRandaIntersect(sig_corrs, corrS, mRNA, miRNA, getInputSpeciesDF)
```

**Arguments**

sig_corrs	correlation matrix, produced by threshSig.
corrS	vector of correlations/differences, from the sampCorRnaMirna function.
mRNA	mRNA FC matrix.
miRNA	miRNA FC matrix.
getInputSpeciesDF	miranda data, produced by getInputSpecies.

**Value**

An object containing data.frames of significant mRNA, miRNA and correlation matrix filtered by miRanda input.

**Examples**

```
x <- miRandaIntersect(sig_InterR, outs2, mRNA_fc, miRNA_fc, miRandaM)
```

---

mirandaIntersectInter	<i>mirandaIntersectInter Looks for Intersection of Significant output results with miRanda Results from getInputSpeciesDF function</i>
-----------------------	--

---

**Description**

Compares and looks for intersection if significant output results with miRanda Results from getInputSpeciesDF and outputs a final filtered output for only those pairs of miRNA and mRNA which have actually been predicted to be targets in miRanda file function

**Usage**

```
mirandaIntersectInter(sig_corrs, corrS, mRNA, miRNA, getInputSpeciesDF)
```

**Arguments**

sig_corrs	correlation matrix, produced by threshSig
corrS	vector of Differences/Correlations, from the sampCorRnaMirna function.
mRNA	mRNA FC matrix.
miRNA	miRNA FC matrix.
getInputSpeciesDF	miranda data, produced by getInputSpecies.

**Value**

An object containing data.frames of significant mRNA, miRNA and correlation matrix filtered by miranda input.

**Examples**

```
x <- mirandaIntersectInter(sig_InterR, outs2, mRNA_fc2, miRNA_fc2, miRandaM)
```

---

miRandaM	<i>This is data is the results file from mouse miRanda getInputSpecies function. This data set is used in documentation examples.</i>
----------	---

---

**Description**

This is data is the results file from mouse miRanda getInputSpecies function. This data set is used in documentation examples.

---

miranda_sponge_predict	<i>Transform miRanda data for relevant mRNA and miRNA to matrix form compatible with sponge</i>
------------------------	---

---

**Description**

Transforms miRanda data into adjacency matrix, with 1 indicating presence of a relationship between a mRNA and miRNA, and 0 otherwise. miRanda input is filtered by miRNA and mRNA present in 'mirna\_exp' and 'diff\_expr' row names, respectively.

**Usage**

```
miranda_sponge_predict(mirna_exp, diff_exp, miranda_data)
```

**Arguments**

mirna_exp	miRna expression data.frame with miRNA for rows and samples for columns
diff_exp	mRNA expression data.frame with mRNA for rows and samples for columns
miranda_data	miRanda data.frame with the first two columns having miRNA and mRNA names

**Value**

matrix adjacency matrix with column names miRNA and row names mRNA

---

miRNA	<i>This is data is the miRNA expression file. This data set is used in documentation examples.</i>
-------	--

---

**Description**

This is data is the miRNA expression file. This data set is used in documentation examples.

---

miRNA0_2	<i>This is data is the miRNA0_2 FC for 0-2 time point. This data set is used in documentation examples.</i>
----------	---

---

**Description**

This is data is the miRNA0\_2 FC for 0-2 time point. This data set is used in documentation examples.

---

miRNA0_5	<i>This is data is the miRNA0_5 FC for 0-5 time point. This data set is used in documentation examples.</i>
----------	---

---

**Description**

This is data is the miRNA0\_5 FC for 0-5 time point. This data set is used in documentation examples.

---

miRNA2_5	<i>This is data is the miRNA2_5 FC for 2-5 time point. This data set is used in documentation examples.</i>
----------	---

---

**Description**

This is data is the miRNA2\_5 FC for 2-5 time point. This data set is used in documentation examples.

---

miRNA_fc	<i>This is data is the combined miRNA FC for all time points. This data set is used in documentation examples.</i>
----------	--

---

**Description**

This is data is the combined miRNA FC for all time points. This data set is used in documentation examples.

---

miRNA_fc2	<i>This data is the miRNA fold change data set for difference or interrelation section. This data set is used in documentation examples.</i>
-----------	--

---

**Description**

This data is the miRNA fold change data set for difference or interrelation section. This data set is used in documentation examples.

---

mirRnaDensityCor	<i>mirRnaDensityCor for miRTarRNASeq miRNA and mRNA correlation real data versus sampled data</i>
------------------	---

---

**Description**

This function draws density plots for miRNA and mRNA correlation while comparing real data vs sampled data. It mainly illustrates the where the lower relationships lie.

**Usage**

```
mirRnaDensityCor(corr0, corrS, pvalue = 0.05)
```

**Arguments**

corr0	data.frame results of corMirnaRna function.
corrS	data.frame results from the sampCorRnaMirna function.
pvalue	The p value threshold to be used on the data density plot default is 0.05.

**Value**

Density plot

**Examples**

```
x <- mirRnaDensityCor(corr_0, outs, pvalue = 0.05)
```

---

mirRnaDensityInter	<i>mirRnaDensityInter for mirTarRnaSeq miRNA and mRNA Interrelation real data versus sampled data</i>
--------------------	---

---

**Description**

This function draws density plots for miRNA and mRNA Interrelation while comparing real data vs sampled data. It mainly illustrates the where the lower relationships lie.

**Usage**

```
mirRnaDensityInter(Inter0, OUTS, pvalue = 0.05)
```

**Arguments**

Inter0	data.frame results of twoTimePoint function.
OUTS	data.frame results from the twoTimePointSamp function.
pvalue	The p value threshold to be used on the data density plot default is 0.05.

**Value**

Density plot

**Examples**

```
x <- mirRnaDensityInter(Inter0, OUTS, pvalue = 0.05)
```

---

mirRnaHeatmap	<i>mirRnaHeatmap pheatmap for miRTarRNASeq miRNA and mRNA correlation</i>
---------------	---

---

## Description

This function draws pheatmaps for miRNA and mRNA correlation while using default and pheatmap for all other parameters

## Usage

```
mirRnaHeatmap(  
  finalF,  
  ...,  
  upper_bound = 0,  
  main = "Default mRNA miRNA heatmap",  
  color = c(viridis::inferno(50), "grey90"),  
  fontsize = 7  
)
```

## Arguments

finalF	data.frame results of corMirnaRnaMiranda or corMirnaRna function
...	arguments passed onto pheatmap
upper_bound	is the upper_bound of the correlation pheatmap scale default is zero user can set to values based on output of correlation result (value)
main	is the title of the pheatmap
color	default inferno(50) from the library viridis R base, R colorbrewer and viridis compatible
fontsize	default is 7 user adjustable

## Value

pheatmap Obj

## Examples

```
x <- mirRnaHeatmap(corr_0)
```

---

mirRnaHeatmapDiff	<i>mirRnaHeatmapDiff heatmap for miRTarRNASeq miRNA and mRNA correlation</i>
-------------------	--

---

## Description

This function draws heatmaps (pheatmaps) for miRNA and mRNA correlation while using default and heatmap for all other parameters

## Usage

```
mirRnaHeatmapDiff(  
  finalF,  
  ...,  
  upper_bound = 0,  
  main = "Default mRNA miRNA heatmap",  
  color = c("grey90", viridis::inferno(50)),  
  fontsize = 7  
)
```

## Arguments

finalF	data.frame results of corMirnaRnaMiranda or corMirnaRna function
...	arguments passed onto pheatmap
upper_bound	is the upper_bound of the correlation pheatmap scale default is zero user can set to values based on output of correlation result (value)
main	is the title of the pheatmap
color	default inferno(50) from the library viridis R base, R colorbrewer and viridis compatible
fontsize	default is 7 user adjustable

## Value

pheatmap Obj

## Examples

```
x <- mirRnaHeatmapDiff(results$corr, upper_bound = -0.1, color = rainbow(50), fontsize = 10)
```

`modelAIC`*Obtain model AIC*

---

**Description**

Obtain model AIC

**Usage**

```
modelAIC(x)
```

**Arguments**

x                    fitted model

**Value**

AIC for model

**Examples**

```
modelAIC(some_model)
```

---

`modelCoefficients`*Obtain coefficients*

---

**Description**

Obtain coefficients

**Usage**

```
modelCoefficients(x)
```

**Arguments**

x                    fitted model

**Value**

fitted model coefficients

**Examples**

```
modelCoefficients(some_model)
```



---

modelData	<i>Obtain model input data</i>
-----------	--------------------------------

---

**Description**

Obtain model input data

**Usage**

```
modelData(x)
```

**Arguments**

x                    fitted model

**Value**

Input data for the fitted model

**Examples**

```
x <- modelData(some_model)
```

---

modelModelName	<i>Obtain model name</i>
----------------	--------------------------

---

**Description**

Obtain model name

**Usage**

```
modelModelName(x)
```

**Arguments**

x                    fitted model

**Value**

model name

**Examples**

```
modelModelName(some_model)
```

---

modelModelPvalue	<i>Obtain model p-value</i>
------------------	-----------------------------

---

**Description**

Obtain model p-value

**Usage**

```
modelModelPvalue(x)
```

**Arguments**

x	fitted model
---	--------------

**Value**

Pvalue for the model

**Examples**

```
modelModelPvalue(some_model)
```

---

modelsFilter	<i>modelsFilter Filter a list of models based on logical expression</i>
--------------	---

---

**Description**

This function can be used to filter a list of models (such as returned by `runModelsZInf()`) based on a logical expression.

**Usage**

```
modelsFilter(models, expr, quiet = FALSE)
```

**Arguments**

models	list of models and related elements, such as returned by <code>runModelsZInf()</code>
expr	expression that yields a logical vector (evaluated in the environment of <code>model</code> )
quiet	suppress warnings

**Value**

models but with all elements filtered by logical expression `expr`. Elements for which filter could not be applied (e.g. length mismatch between element and condition) are set to `NA`.

**Examples**

```
x <- modelsFilter(models, pvalues < 0.05)
x <- modelsFilter(models, is_significant)
x <- modelsFilter(models, is_significant == FALSE)
```

---

modelTermPvalues	<i>Obtain p-values for terms in model formula</i>
------------------	---

---

**Description**

Obtain p-values for terms in model formula

**Usage**

```
modelTermPvalues(x)
```

**Arguments**

x	fitted model
---	--------------

**Value**

Pvalue for the terms in the fitted model

**Examples**

```
modelTermPvalues(some_model)
```

---

mRNA	<i>This is data is the mRNA expression file. This data set is used in documentation examples.</i>
------	---

---

**Description**

This is data is the mRNA expression file. This data set is used in documentation examples.

---

mRNA0_2	<i>This is data is the mRNA0_2 FC for 0-2 time point. This data set is used in documentation examples.</i>
---------	--

---

**Description**

This is data is the mRNA0\_2 FC for 0-2 time point. This data set is used in documentation examples.

---

mRNA0\_5

*This is data is the mRNA0\_5 FC for 0-5 time point. This data set is used in documentation examples.*

---

**Description**

This is data is the mRNA0\_5 FC for 0-5 time point. This data set is used in documentation examples.

---

mRNA2\_5

*This is data is the mRNA2\_5 FC for 2-5 time point. This data set is used in documentation examples.*

---

**Description**

This is data is the mRNA2\_5 FC for 2-5 time point. This data set is used in documentation examples.

---

mRNA\_fc

*This is data is the combined mRNA FC for all time points. This data set is used in documentation examples.*

---

**Description**

This is data is the combined mRNA FC for all time points. This data set is used in documentation examples.

---

mRNA\_fc2

*This data is the mRNA fold change data set for difference or interrelation section. This data set is used in documentation examples.*

---

**Description**

This data is the mRNA fold change data set for difference or interrelation section. This data set is used in documentation examples.

---

one2manySponge	<i>Sparse Partial Correlations On mRNA/miRNA Expression We make mirTarRnaSeq compatible to SPONGE package in order to estimate sparse matrix correlation (using elastic net) for prediction potential miRNA-mRNA interaction. Note this function/method is suggested for miRNA/mRNA interactions in many samples with a notable variance of mRNA/miRNA expression. This model also only reports negative sparse partial correlation predictions.</i>
----------------	--

---

**Description**

Sparse Partial Correlations On mRNA/miRNA Expression We make mirTarRnaSeq compatible to SPONGE package in order to estimate sparse matrix correlation (using elastic net) for prediction potential miRNA-mRNA interaction. Note this function/method is suggested for miRNA/mRNA interactions in many samples with a notable variance of mRNA/miRNA expression. This model also only reports negative sparse partial correlation predictions.

**Usage**

```
one2manySponge(mirna_exp, diff_exp, miranda_sponge_predict, non_null = TRUE)
```

**Arguments**

mirna_exp	miRNA expression data.frame with miRNA for rows and samples for columns
diff_exp	mRNA expression data.frame with mRNA for rows and samples for columns
miranda_sponge_predict	miRanda sponge compatible matrix produced by miranda_sponge_predict function
non_null	The default for this parameter is TRUE, hence it returns only non-null estimated if FALSE it would return all NULL and TRUE estimates.

**Value**

matrix adjacency matrix with column names miRNA and row names mRNA

---

one2OneRnaMiRNA	<i>one2OneRnaMiRNA correlation for miRNA and mRNA using differential expression fold change and if/when available p-value</i>
-----------------	---

---

**Description**

This function inputs accept a list of dataframes and returns an obj with two dataframes called FC and p-value. FC with rownames == genes and columns are FC1, 2, 3, ... (with fold-changes) - P-value with rownames == genes and columns are P1, 2, 3, ... (with p-values) both data.frames have the same order dimensions.

**Usage**

```
one2OneRnaMiRNA(
  files,
  gene_colname = "Gene",
  fc_colname = "FC",
  pval_colname = "pvalue",
  pthreshold = NULL
)
```

**Arguments**

files	a list of dataframes either miRNAs or mRNAs from various time points.
gene_colname	Default is a vector character of length 1 "Gene" user can alter if they choose This column contains the gene names.
fc_colname	Default "FC" is coloumn name for fold changes user can alter if they choose.
pval_colname	Default is "pvalue" column name for p-values (in input).
pthreshold	P-value threshold.

**Value**

Correlation dataframe

**Examples**

```
x <- one2OneRnaMiRNA(files)
```

---

outs	<i>This is data is the output file resulted from time point/conditions background correlation model. This data set is used in documentation examples.</i>
------	---

---

**Description**

This is data is the output file resulted from time point/conditions background correlation model.  
This data set is used in documentation examples.

---

outs2	<i>This is data is the output file resulted from time point/conditions background difference/interrelation model. This data set is used in documentation examples.</i>
-------	--

---

**Description**

This is data is the output file resulted from time point/conditions background difference/interrelation model. This data set is used in documentation examples.

---

plotFit	<i>Plot model</i>
---------	-------------------

---

**Description**

Plot 2D description

**Usage**

```
plotFit(model)
```

**Arguments**

model            linear model

**Value**

does not return value

**Examples**

```
plotFit(lm(x ~ y, data = data.frame(x = runif(10), y = runif(10))))
```

---

plotResiduals	<i>Plot residuals</i>
---------------	-----------------------

---

**Description**

Plot residuals description

**Usage**

```
plotResiduals(model)
```

**Arguments**

model            linear model

**Value**

does not return value

**Examples**

```
plotResiduals(lm(x ~ y, data = data.frame(x = runif(10), y = runif(10))))
```

---

plotTerms	<i>plotTerms</i>
-----------	------------------

---

**Description**

Plot terms description

**Usage**

```
plotTerms(model)
```

**Arguments**

model            linear model

**Value**

does not return value

**Examples**

```
plotTerms(lm(x ~ y, data = data.frame(x = runif(10), y = runif(10))))
```

---

results	<i>This is data is the output file resulted from time point or conditions or correlation or interrelation model. This data set is used in documentation examples.</i>
---------	---

---

**Description**

This is data is the output file resulted from time point or conditions or correlation or interrelation model. This data set is used in documentation examples.



---

runAllMirnaModels      *runAllMirnaModels runModel for all miRNAs*

---

### Description

This function runs the "runModel" function for all miRNAs and mRNA combinations of two and returns a list with significant genes and FDR models

### Usage

```
runAllMirnaModels(
  mirnas,
  DiffExp mRNA,
  DiffExp miRNA,
  miranda_data,
  prob = 0.75,
  fdr_cutoff = 0.1,
  method = "fdr",
  cutoff = 0.05,
  all_coeff = FALSE,
  mode = NULL,
  family = glm_poisson(),
  scale = 1
)
```

### Arguments

mirnas	vector of unique miRNAs under investigation.
DiffExp mRNA	differentially/expressed mRNAs expression file.
DiffExp miRNA	differentially/expressed miRNAs expression file.
miranda_data	getInputSpecies output file ( use low filters).
prob	user defined ratio for miRanda distribution for miRanda score selection default is 0.75.
fdr_cutoff	cutoff for FDR selection default is 0.1.
method	finInterResult miRNA and mRNA interrelation in two time points results in a dataframe.
cutoff	P-value cutoff of the model.
all_coeff	if true only models with all negative coefficients will be selected if false at least one negative coefficient should be in the model; default is TRUE.
mode	model mode, default is Null, can be changed to "multi" and "inter".
family	Default is glm_poisson(), for zero inflated negative binomial NB option use glm_zeroinfl(dist="negbin").
scale	if normalized data (FPKM,RPKM,TPM,CPM), scale to 10 etc., however the higher you go on #scale the less accuracy your p-value estimate will be.

**Value**

List of run models

**Examples**

```
mirnas <- c("ebv-mir-bart9-5p", "ebv-mir-bart6-3p")
x <- runAllMirnaModels(mirnas, mRNA, miRNA, miRanda,
  prob = 0.90, fdr_cutoff = 0.1, method = "fdr",
  all_coeff = TRUE, mode = "multi",
  family = glm_poisson(), scale = 100
)
```

---

runModel

*Run a model of a specific kind*

---

**Description**

Run a model of a specific kind

**Usage**

```
runModel(x, data, ..., model = glm_gaussian())
```

**Arguments**

x	model formula
data	data.frame to run the model on
...	passed on to fit()
model	model type

**Value**

fitted model

---

runModels	<i>runModels runs miRNA mrna model model for various miRNA-mRNA data distributions</i>
-----------	--

---

### Description

This function defines the boundaries of mRNA vs miRNAs of interest to be analysed by the runModels function

### Usage

```
runModels(
  combination,
  select_mRNA,
  select_miRNA,
  mode = NULL,
  family = glm_poisson(),
  scale = 1,
  cutoff = 0.05,
  all_coeff = NULL
)
```

### Arguments

combination	the combined file for mRNA and selected miRNAs output of combiner function
select_mRNA	the output of gene_variant function.
select_miRNA	The vector of miRNA/s to be investigated.
mode	the mode of analysis if more than one miRNA is being investigated multivariate "multi" or co-variate/interaction analysis "inter" is being used
family	gaussian or poisson
scale	factor to scale input data (for genes) by, prior to rounding and model fitting. (scale must be greater than zero).
cutoff	p-value cut off to call significance
all_coeff	if true only models with all negative coefficients will be selected if false at least one

### Value

A list of p-values, annova, and significance for each gene and the miRNA/s of interest

### Examples

```
x <- runModels(Combine, geneVariant, "ebv-mir-bart9-5p")
```

---

sampCorRnaMirna	<i>sampCorRnaMirna</i> sampling for correlation for miRNA and mRNA
-----------------	--

---

### Description

This function uses the output of one2OneRnaMiRNA and returns a sampled from original file correlation dataframe depending on user sampling selection.

### Usage

```
sampCorRnaMirna(
  mRNA,
  miRNA,
  method = "pearson",
  Shrounds = 100,
  Srounds = 1000
)
```

### Arguments

mRNA	mRNA file generated from fold changes (FC) obj of the one2OneRnaMiRNA.
miRNA	miRNA file generated from fold changes (FC) obj of the one2OneRnaMiRNA.
method	Default is "pearson" else use "kendall" or "spearman".
Shrounds	number of shuffling over the FC data, default is 100.
Srounds	number of sampling from the shuffled data, default is 1000.

### Value

Correlation data frame

### Examples

```
x <- sampCorRnaMirna(mRNA_fc, miRNA_fc, method = "pearson", Shrounds = 10, Srounds = 10)
```

---

sig_corrs	<i>This is data is the output file resulted from time point or conditions experiment for correlation model after filtering and threshold modification. This data set is used in documentation examples.</i>
-----------	---

---

### Description

This is data is the output file resulted from time point or conditions experiment for correlation model after filtering and threshold modification. This data set is used in documentation examples.

---

sig_InterR	<i>This is data is the output file resulted from time point or conditions experiment for interrelation model after filtering and threshold modification. This data set is used in documentation examples.</i>
------------	---

---

**Description**

This is data is the output file resulted from time point or conditions experiment for interrelation model after filtering and threshold modification. This data set is used in documentation examples.

---

some_model	<i>This is data is the results file from regression analysis and its estimates. This data set is used in documentation examples.</i>
------------	--

---

**Description**

This is data is the results file from regression analysis and its estimates. This data set is used in documentation examples.

---

threshSig	<i>threshSig Using shuffling threshold finds appropriate significant miRNA-mRNA correlation</i>
-----------	---

---

**Description**

This function uses the sampCorRnaMirna shuffled output to determine an appropriate threshold for significant mRNA and miRNA relationship of the dataset and shows all those with significant relationships.

**Usage**

```
threshSig(corr0, corrS, pvalue = 0.05)
```

**Arguments**

corr0	data.frame results of corMirnaRna function.
corrS	vector of correlations, from the sampCorRnaMirna function.
pvalue	The p value threshold to be used on the sampled data.

**Value**

A dataframe of Significant mRNA and miRNA

**Examples**

```
x <- mirRnaHeatmap(outs, corr_0)
```

---

threshSigInter	<i>threshSigInter Using shuffling threshold finds appropriate significant miRNA-mRNA correlation</i>
----------------	--

---

**Description**

This function uses the sampCorRnaMirna shuffled output to determine an appropriate threshold for significant mRNA and miRNA relationship of the dataset and shows all those with significant relationships.

**Usage**

```
threshSigInter(corr0, corrS, pvalue = 0.05)
```

**Arguments**

corr0	data.frame results of corMirnaRna function.
corrS	vector of correlations, from the sampCorRnaMirna function.
pvalue	The p value threshold to be used on the sampled data.

**Value**

A dataframe of Significant mRNA and miRNA

**Examples**

```
x <- threshSigInter(corr_0, outs, pvalue = 0.05)
```

---

twoTimePoint	<i>twoTimePoint miRNA and mRNA interrelation in two timepoints</i>
--------------	--

---

**Description**

This function uses the output of one2OneRnaMiRNA and returns a sampled from original file interrelation dataframe depending on user sampling selection.

**Usage**

```
twoTimePoint(mRNA, miRNA)
```

**Arguments**

mRNA mRNA file generated from fold changes (FC) obj of the one2OneRnaMiRNA.  
 miRNA miRNA file generated from fold changes (FC) obj of the one2OneRnaMiRNA.

**Value**

miRNA mRNA interrelation dataframe

**Examples**

```
x <- twoTimePoint(mRNA_fc2, miRNA_fc2)
```

---

twoTimePointSamp	<i>twoTimePointSamp miRNA and mRNA interrelation in two timepoints sampling</i>
------------------	---

---

**Description**

This function uses the output of one2OneRnaMiRNA and returns a sampled from orig file interrelation dataframe depending on user sampling selection.

**Usage**

```
twoTimePointSamp(mRNA, miRNA, Shrounds = 100, Srounds = 1000)
```

**Arguments**

mRNA mRNA file generated from fold changes (FC) obj of the one2OneRnaMiRNA.  
 miRNA miRNA file generated from fold changes (FC) obj of the one2OneRnaMiRNA.  
 Shrounds number of shuffling over the FC data, default is 100.  
 Srounds number of sampling from the shuffled data, default is 1000.

**Value**

miRNA mRNA interrelation dataframe

**Examples**

```
x <- twoTimePointSamp(mRNA, miRNA, Shrounds = 10, Srounds = 10)
```

---

tzTrans	<i>tzTransTranspose and z-score transformation</i>
---------	--

---

**Description**

Transposes and z-score transforms a matrix or data.frame.

**Usage**

```
tzTrans(x)
```

**Arguments**

x                    matrix of miRNA or mRNA or the data frame to be transformed

**Value**

transposed and transformed version of x as a matrix.

**Examples**

```
x <- tzTrans(miRNA)
```



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