# Package ‘mirTarRnaSeq’

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**Type** Package

**Title** mirTarRnaSeq

**Version** 1.17.0

**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 expriments. These experiments can be time point experiments, and or condition expriments.

**License** MIT + file LICENSE

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**Author** Mercedeh Movassagh [aut, cre] (ORCID:
<`https://orcid.org/0000-0001-7690-0230`>),
Sarah Morton [aut],
Rafael Irizarry [aut],
Jeffrey Bailey [aut],
Joseph N Paulson [aut]

**Maintainer** Mercedeh Movassagh <`mercedeh@ds.dfci.harvard.edu`>

# Contents

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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 transforemed diff expression file (genrated using TZtranz) |
| `miRNA` | Matrix or data frame miRNA from transforemed diff file (genrated 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` *This is data is the mRNA FC and miRNA FC correlation data. This data set is used in documentation examples.*

### Description

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

---

## `downloadMirandaFile` *downloadMirandaFile Read internal Miranda file*

### 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` *drawCorPlot correlation plots for mRNA and miRNA regression results*

---

### 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` *drawInterPlots for finInterResult miRNA and mRNA Interrelation real data*

---

### 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 *fdrSig Ruturns FDR significant miRNA/mRNA predictions*

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

### Description

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

---

## `finInterResult` *finInterResult miRNA and mRNA interrelation in two-time points results in a dataframe.*

---

### 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 interelation dataframe

### Examples

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

---

## `geneVari` *geneVari Makes a list of gene names to be used in the runModels function*

---

### 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` | *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.* |

## 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` | *Return Miranda data for a given species.* |

## Description

Reads Miranda file for a given speicies 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` *Model functions for GLM with Gaussian model.*

---

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

---

## 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 standardaized 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` *Model functions for zero inflated model using either Poisson or Negative Binomial distributions.*

### Description

Implements standardaized 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` *alias for glm_zeroinfl("negbin")*

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

---

### Description

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

---

## `makeFormulaRightSide` *makeFormulaRightSide makes right hand side of formula for model variables: vector of indep. variables*

---

### 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` *miRanComp comparison of mRNAs present with miRanda file targets*

---

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

---

### Description

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

---

## `miRandaIntersect` *miRandaIntersect Looks for Intersection of Significant output results with miRanda Results from getInputSpeciesDF function*

---

### 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` *mirandaIntersectInter Looks for Intersection of Significant output results with miRanda Results from getInputSpeciesDF function*

### Description

Compares and looks for intersection if significant output results with miRanda Results from getInputSpeciesDF and outputs a final filterd ourput 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` *This is data is the results file from mouse miRanda getInputSpecies function. This data set is used in documentation examples.*

---

### Description

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

---

`miranda_sponge_predict` *Transform miRanda data for relevant mRNA and miRNA to matrix form compatible with sponge*

---

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

---

### Description

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

---

| | |
|---|---|
| `miRNA0_2` | *This is data is the miRNA0_2 FC for 0-2 time point. This data set is used in documentation examples.* |

## Description

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

---

| | |
|---|---|
| `miRNA0_5` | *This is data is the miRNA0_5 FC for 0-5 time point. This data set is used in documentation examples.* |

## Description

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

---

| | |
|---|---|
| `miRNA2_5` | *This is data is the miRNA2_5 FC for 2-5 time point. This data set is used in documentation examples.* |

## Description

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

---

| | |
|---|---|
| `miRNA_fc` | *This is data is the combined miRNA FC for all time points. This data set is used in documentation examples.* |

## Description

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

---

| | |
|---|---|
| `miRNA_fc2` | *This data is the miRNA fold change data set for difference or interrelation section. This data set is used in documentation examples.* |

## Description

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

---

## `mirRnaDensityCor` *mirRnaDensityCor for miRTarRNASeq miRNA and mRNA correlation real data versus sampled data*

---

### 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` *mirRnaDensityInter for mirTarRnaSeq miRNA and mRNA Interrelation real data versus sampled data*

---

### 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` *mirRnaHeatmap pheatmap for miRTarRNASeq miRNA and mRNA correlation*

### 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` *mirRnaHeatmapDiff heatmap for miRTarRNASeq miRNA and mRNA correlation*

### 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$corrs, 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` *Obtain model input data*

### 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` *Obtain model name*

### Description

Obtain model name

### Usage

```
modelModelName(x)
```

### Arguments

| | |
|---|---|
| `x` | fitted model |

### Value

model name

### Examples

```
modelModelName(some_model)
```

---

## `modelModelPvalue` *Obtain model p-value*

### Description

Obtain model p-value

### Usage

```
modelModelPvalue(x)
```

### Arguments

| | |
|---|---|
| `x` | fitted model |

### Value

Pvalue for the model

### Examples

```
modelModelPvalue(some_model)
```

---

## `modelsFilter` *modelsFilter Filter a list of models based on logical expression*

---

### 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 elemenets, such as returned by `runModelsZInf()` |
| `expr` | expresion that yields a logical vector (evaluated in the environmnet of `model`) |
| `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` *Obtain p-values for terms in model formula*

---

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

---

### Description

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

---

## `mRNA0_2` *This is data is the mRNA0_2 FC for 0-2 time point. This data set is used in documentation examples.*

---

### 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` *Sparse Partial Correlations On mRNA/miRNA Expression We make mirTarRnaSeq compatible to SPONGE package in order to estimate sparse matrix correlation (using elstic 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.*

---

## Description

Sparse Partial Correlations On mRNA/miRNA Expression We make mirTarRnaSeq compatible to SPONGE package in order to estimate sparse matrix correlation (using elstic 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` *one2OneRnaMiRNA correlation for miRNA and mRNA using differntial expression fold change and if/when available p-value*

---

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

---

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

---

### Description

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

---

## `plotFit` *Plot model*

---

### 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` *Plot residuals*

---

### 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` *plotTerms*

## 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` *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.*

## 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,
  DiffExpmRNA,
  DiffExpmiRNA,
  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. |
| `DiffExpmRNA` | deferentially/expressed mRNAs expression file. |
| `DiffExpmiRNA` | deferentially/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` *runModels runs miRNA mrna model model for various miRNA-mRNA data distributions*

## 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-vlaues, annova, and significance for each gene and the miRNA/s of interest

### Examples

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

---

## `sampCorRnaMirna` *sampCorRnaMirna 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` | *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.* |

## 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` | *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.* |

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

## Description

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

---

## `threshSig` *threshSig Using shuffling threshold finds appropriate significant miRNA-mRNA correlation*

---

### 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` *threshSigInter Using shuffling threshold finds appropriate significant miRNA-mRNA correlation*

---

### Description

This function uses the sampCorRnaMirna shuffled output to determine an appropriate thershold 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` *twoTimePoint miRNA and mRNA interrelation in two timepoints*

### 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` *twoTimePointSamp miRNA and mRNA interrelation in two timepoints sampling*

### 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` *tzTransTranspose and z-score transformation*

### 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)
```

# Index