Package ‘mirTarRnaSeq’

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Type Package
Title mirTarRnaSeq
Version 1.10.0
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 expriments.
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Decifer a 'model parameter' and run appropriate glm_. . . function.

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 TZ-tranz)

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**  
*corMirnaRna correlation for miRNA and mRNA*

**Description**

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

**Usage**

```r
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**

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

corMirnaRnaMiranda

**corMirnaRnaMiranda**  
*corMirnaRnaMiranda correlation for miRNA and mRNA*

**Description**

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

**Usage**

```r
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".

**Examples**

```r
x <- corMirnaRnaMiranda(mRNA, miRNA, CorVal, getInputSpeciesDF, method = "spearman")
```
Value

Correlation dataframe

Examples

```r
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**

```r
downloadMirandaFile(urlf)
```

**Arguments**

- `urlf` URL of the specific chosen file

**Value**

data.frame containing downloaded miRanda file

**Examples**

```r
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

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

---

**fdrSig**

*fdrSig Returns FDR significant miRNA/mRNA predictions*

---

**Description**

This function performs FDR correction on the p_values generated by the runModels function list.

**Usage**

```r
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 values, annova, and significance for each gene and the miRNA/s of interest

**Examples**

```r
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 interrelation dataframe

**Examples**

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

---

**geneVari**

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

**Description**

This function defines the boundaries 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

```r
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 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

```r
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
glm_gaussian

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
 glm_poisson

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

Model functions for zero inflated model using either Poisson or Negative Binomial distributions.

Description

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

Usage

```r
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

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

---

glm_zeroinfl_negbin

alias for glm_zeroinfl("negbin")

Description

alias for glm_zeroinfl("negbin")

Usage

```r
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

```r
x <- glm_zeroinfl_negbin()
```
importMirandaFile

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")
**Description**

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

**Usage**

```r
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**

```r
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)

Description

This 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

```r
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 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

```r
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

```r
miranda_sponge_predict(mirna_exp, diff_exp, miranda_data)
```
## Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>mirna_exp</td>
<td>miRNA expression data.frame with miRNA for rows and samples for columns</td>
</tr>
<tr>
<td>diff_exp</td>
<td>mRNA expression data.frame with mRNA for rows and samples for columns</td>
</tr>
<tr>
<td>miranda_data</td>
<td>miRanda data.frame with the first two columns having miRNA and mRNA names</td>
</tr>
</tbody>
</table>

## Value

matrix adjacency matrix with column names miRNA and row names mRNA

<table>
<thead>
<tr>
<th>miRNA</th>
<th>This is data is the miRNA expression file. This data set is used in documentation examples.</th>
</tr>
</thead>
</table>

### Description

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

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

### Description

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

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

### Description

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

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>miRNA2_5</td>
<td>This is data is the miRNA2_5 FC for 2-5 time point. This data set is used in documentation examples.</td>
</tr>
<tr>
<td>miRNA_fc</td>
<td>This is data is the combined miRNA FC for all time points. This data set is used in documentation examples.</td>
</tr>
<tr>
<td>miRNA_fc2</td>
<td>This data is the miRNA fold change data set for difference or interrelation section. This data set is used in documentation examples.</td>
</tr>
<tr>
<td>mirRnaDensityCor</td>
<td>mirRnaDensityCor for miRTarRNASeq miRNA and mRNA correlation real data versus sampled data</td>
</tr>
</tbody>
</table>

**Description**

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

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

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

**Usage**

```r
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**

```r
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**

```r
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**

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

**Description**

This function draws heatmaps for miRNA and mRNA correlation while using default and heatmap 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 heatmap
- `upper_bound`: is the upper_bound of the correlation heatmap scale default is zero user can set to values based on output of correlation result (value)
- `main`: is the title of the heatmap
- `color`: default inferno(50) from the library viridis R base, R colorbrewer and viridis compatible
- `fontsize`: default is 7 user adjustable

**Value**

heatmap Obj

**Examples**

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

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

**Usage**

```r
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**

```r
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**

```r
modelData(x)
```

**Arguments**

- `x` fitted model

**Value**
Input data for the fitted model

**Examples**

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

---

### modelModelName

**Obtain model name**

**Description**
Obtain model name

**Usage**

```r
modelModelName(x)
```

**Arguments**

- `x` fitted model

**Value**
model name

**Examples**

```r
modelModelName(some_model)
```
modelModelPvalue

Description
Obtain model p-value

Usage
modelModelPvalue(x)

Arguments
x fitted model

Value
Pvalue for the model

Examples
modelModelPvalue(some_model)

modelsFilter

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 environment 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.
**modelTermPvalues**

*Obtain p-values for terms in model formula*

**Examples**

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

**Description**

Obtain p-values for terms in model formula

**Usage**

```r
modelTermPvalues(x)
```

**Arguments**

- `x`: fitted model

**Value**

P-value for the terms in the fitted model

**Examples**

```r
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.
<table>
<thead>
<tr>
<th>mRNA0_5</th>
<th>This is data is the mRNA0_5 FC for 0-5 time point. This data set is used in documentation examples.</th>
</tr>
</thead>
</table>

**Description**

This is data is the mRNA0_5 FC for 0-5 time point. This data set is used in documentation examples.

<table>
<thead>
<tr>
<th>mRNA2_5</th>
<th>This is data is the mRNA2_5 FC for 2-5 time point. This data set is used in documentation examples.</th>
</tr>
</thead>
</table>

**Description**

This is data is the mRNA2_5 FC for 2-5 time point. This data set is used in documentation examples.

<table>
<thead>
<tr>
<th>mRNA_fc</th>
<th>This is data is the combined mRNA FC for all time points. This data set is used in documentation examples.</th>
</tr>
</thead>
</table>

**Description**

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

<table>
<thead>
<tr>
<th>mRNA_fc2</th>
<th>This data is the mRNA fold change data set for difference or interrelation section. This data set is used in documentation examples.</th>
</tr>
</thead>
</table>

**Description**

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

```r
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 differential 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

```r
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 column 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

```r
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.

outs2

This is data is the output file resulted from time point/conditions background difference/interrelation 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.

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**

*Plot model*

**Description**
Plot 2D description

**Usage**
plotFit(model)

**Arguments**
- model linear model

**Value**
does not return value

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

```r
r
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.
- `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.
runModel

Value

List of run models

Examples

```r
mirnas <- c("ebv-mir-bart9-5p", "ebv-mir-bart6-3p")
x <- runAllMirnaModels(mirnas, mRNA, miRNA, miRandan, 
  prob = 0.90, fdr_cutoff = 0.1, method = "fdr", 
  all_coef = 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

```r
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")
Description

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

Usage

```r
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

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

Description

This 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.
The function `threshSig` in the `InterR` package is used to determine an appropriate threshold for significant mRNA and miRNA relationship of the dataset and shows all those with significant relationships.

### 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

```r
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 correlations.
Examples

\[ x \leftarrow \text{mirRnaHeatmap}(\text{outs}, \text{corr}_0) \]

---

**threshSigInter**

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

---

**Description**

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

**Usage**

\[ \text{threshSigInter}(\text{corr0}, \text{corrS}, \text{pvalue} = 0.05) \]

**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**

\[ x \leftarrow \text{threshSigInter}(\text{corr}_0, \text{outs}, \text{pvalue} = 0.05) \]

---

**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**

\[ \text{twoTimePoint}(\text{mRNA}, \text{miRNA}) \]
twoTimePointSamp

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)
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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