Package 'mirTarRnaSeq'

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Type Package

Title mirTarRnaSeq

Version 1.0.0

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.

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R topics documented:

`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.

---

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.

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)
```

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