RmiR

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`RmiR` *Coupling miRNA and Gene expression results*

Description

Coupling miRNA and Gene expression results for a selected target database.

Usage

```
  RmiR(mirna=NULL,genes=NULL,annotation=NULL,dbname="targetscan",org="Hs",id="pr

read.mir(mirna=NULL,genes=NULL,annotation=NULL,id="probes",dbname=c("targetscan"
```

Arguments

`mirna`	A data.frame with two columns, the first with the microRNA names, the second with the expression values.
`genes`	A data.frame with two columns, the first with gene ID (probes, symbols, ensembl, entrez...), the second with the expression values.
`annotation`	The annotation package to annotate the genes file with entrez gene ID, eg: Agilent 44k annotation="hgug4112a.db" or annotation="org.Hs.eg.db" for human not using microarrays probes.
`dbname`	A selected database of miRNA target. See `RmiR.hsa_dbconn`, default is "targetscan". If using `read.mir` it can be a vector of databases, default are "targetscan" and "pictar".
`id`	The type of annotation of the genes input file. An accepted value is one of: "genes" for entrez gene id, "probes" for microarray probes id, "ensembl" for ensembl gene id, "unigene" for unigene gene id and "alias" for official gene symbols and aliases.
`id.out`	The annotation of the genes in the output. The default it is "symbol", to have the HGNC symbols, it can be also "probes" if the input `id` is "probes" or "gene" to leave just the entrez gene annotation.
`at.least`	Minimum number of databases that should yeld the result, when the search is performed in multiple databases with `read.mir`. If it is 1 it is basically an union between databases. Default is 2.
`org`	Define the targets database package of the desired organism. Default is "Hs"
`verbose`	If it is desired or not to have some verbose output while analysing the data. Default is FALSE

Details

RmiR couples the gene expression and microRNA expression. It uses the AnnotationDbi package to annotate the gene expression file. We intend to put already filtered and significant values in the input file, so in case of duplicate probes or different sequences identifying the same gene or more than one values for a miRNA, the function will take just the mean of the different results and give the corresponding coefficent of variation. Each input file must have two columns. The first one for annotation, the second for expression value. The name of the columns does not matter.

read.mir uses RmiR but performs the search in one or more databases and returns only the object present in at.least databases. If at.least is equal to 1 we basically do an union between the results from the databases of choice, if we specify just a database in dbname it is exactly the same of the RmiR function.

Value

mature_miRNA	The resulting miRNAs present in the input file with at least one target in the selected database.
gene_id	The resulting entrez gene ids present in the input file that are also targets in the selected database.
mirExpr	microRNA expression value
geneExpr	Gene expression Value
mirCV	miRNA expression coefficent of variation in case of duplication otherwise is NA
geneCV	Gene expression coefficent of variation in case of duplication otherwise is NA
symbol	If the id.out is "symbol".
probe_id	If the id.out is "probes".

See Also

RmiR.hsa_dbconn,

Examples

```
## Merge gene expression and mirna expression for agilent IDs

genes <- data.frame(genes=c("A_23_P171258", "A_23_P150053", "A_23_P150053",
    "A_23_P150053", "A_23_P202435", "A_24_P90097",
    "A_23_P127948"))
genes$expr <- c(1.21, -1.50, -1.34, -1.45, -2.41, -2.32, -3.03)

mirna <- data.frame(mirna=c("hsa-miR-148b", "hsa-miR-27b", "hsa-miR-25",
    "hsa-miR-181a", "hsa-miR-27a", "hsa-miR-7",
    "hsa-miR-32", "hsa-miR-32", "hsa-miR-7"))
mirna$expr <- c(1.23, 3.52, -2.42, 5.2, 2.2, -1.42, -1.23, -1.20, -1.37)

RmiR(genes=genes, mirna=mirna, annotation="hgug4112a.db", id="probes")

## Search in pictar

RmiR(genes=genes, mirna=mirna, annotation="hgug4112a.db", id="probes",
     dbname="pictar")
## or

read.mir(genes=genes, mirna=mirna, annotation="hgug4112a.db", id="probes",
```

```
          dbname="pictar", at.least=1)

## Search in miranda, pictar and targetscan, present in each database:

read.mir(genes=genes, mirna=mirna, annotation="hgug4112a.db", id="probes",
 dbname=c("miranda", "pictar", "targetscan"), at.least=3)

## Search in miranda, pictar and targetscan, present in at least 2 database:

read.mir(genes=genes, mirna=mirna, annotation="hgug4112a.db", id="probes",
 dbname=c("miranda", "pictar", "targetscan"), at.least=2)
```

RmiRtc *Time Course relationship between microRNA and Genes*

Description

Given a timeline of experiments resulting from RmiR or read.mir, it calculates the correlation between the trend of miRNA and corresponding gene targets.

Usage

```
RmiRtc(timeline = NULL, timevalue = NULL, method = "pearson")
readRmiRtc(miRtcObj, correlation = -0.75, exprLev = 1, annotation= NULL, fileNam
```

Arguments

timeline	A vector with the names of the experiments resulting from RmiR or read.mir, in chronological order.
timevalue	A vector of numbers with the unity of time correspondig to timeline.
method	Method to use to calculate the correlation between miRNA and gene expression, default is "pearson". For other see cor from stats package.
miRtcObj	An object resulting from RmiRtc.
annotation	The annotation package to retrive the corresponding symbol given the gene_id . eg: Agilent 44k annotation="hgug4112a.db" or annotation="org.Hs.eg.db".
correlation	The correlation level desired to filter the miRtcList object created with the RmiRtc function.
exprLev	The absolute value of gene expression as cut-off to filter the miRtcList object created with the RmiRtc function.
fileName	The file name to print the file with the gene targets with the number of miRNAs matching the correlation criteria. If nothing is specified, no file will be created.

Details

RmiRtc creates an miRtcList wich includes all the information of the time course experiment: couples of miRNA and gene target, expression of gene and miRNA in the time, the correlation between the miRNA and the gene expression trends.

readRmiRtc subsets the miRtcList created with RmiRtc. We can select a correlation level, if positive we select the correlated genes and miRNas, if negative the anti-correlated couples. Also we can decrease the data by setting a log ratio cut off for the gene expression, to select only the case which the a gene is op or down regulated.

Value

couples	The couples of mature_miRNA and targets in entrez gene annotation.
mirExpr	A matrix with the expression of miRNA in order by timeline.
geneExpr	A matrix with the expression of miRNA in order by timeline.
mirCV	A matrix with the coefficents of variation of the miRNAs from RmiR or read.mir.
geneCV	A matrix with the coefficents of variation of the genes resulting from RmiR or read.mir.
correlation	A vector with the correlation value between miRNAs and gene targets.
reps	With readRmiRtc we list all the gene targets ordered by the number of miRNAs matching the correlation criteria.

See Also

RmiR, read.mir, plotRmiRtc

Examples

```
##An example without the data
data(RmiR)
res1 <- read.mir(genes=gene1, mirna=mir1, annotation="hgug4112a.db")
res2 <- read.mir(genes=gene2, mirna=mir2, annotation="hgug4112a.db")
res3 <- read.mir(genes=gene3, mirna=mir3, annotation="hgug4112a.db")

res_tc <- RmiRtc(timeline=c("res1", "res2", "res3"),
 timevalue=c(12,48,72))
res <- readRmiRtc(res_tc, correlation=-0.9, exprLev=1,
  annotation="hgug4112a.db")
res$reps
```

RmiRdata *Simple demostration data for the RmiR package*

Description

Gene expression and microRNA expression data from the same RNA in a time course experiment

Usage

```
data(RmiR)
```

See Also

RmiR_dbconn,RmiR

Examples

```
data(RmiR)
```

plotRmiRtc *Plot object from read.mir or a selected gene and respective miRNAs from a miRtcList object*

Description

Ploting function for object coming from read.mir or a selected gene and respective miRNAs from a miRtcList object

Usage

```
plotRmiRtc(miRtcObj,gene_id=NULL,timeunit="Time",legend.x=NULL,legend.y=NULL,s
```

Arguments

miRtcObj	A data.frame resulting from read.mir or RmiR functions or a miRtcList-class object.
gene_id	Selected gene_id contained in a miRtcList-class object.
timeunit	Name for the abscissae axes, normally a time unit like "Hours", "PD" etc.
legend.x	Position of the legend in the x-axes.
legend.y	Position of the legend in the y-axes.
svgTips	TRUE if you want to use the RSVGTipsDevice, default is FALSE.
svgname	Name for the SVG image output.
height	Height of the graphs.
width	Width of the graphs.

Details

The function plots the trends of a gene target with the specified gene_id and respective miRNA contained in a miRtcList-class object.

If the miRtcObj argument is a dataframe coming from read.mir function, the resulting plot will be a point graph in SVG format. Each couple miRNA/Target is a point, the x value is the gene target expression value and the y value is the microRNA expression value. To decrease the size of the graph is possible to select just the desired miRNAs or gene targets in the data.frame

See Also

readRmiRtc,miRtcList

Examples

```
        data(RmiR)
        res1 <- read.mir(genes=gene1, mirna=mir1, annotation="hgug4112a.db")
        res2 <- read.mir(genes=gene2, mirna=mir2, annotation="hgug4112a.db")
        res3 <- read.mir(genes=gene3, mirna=mir3, annotation="hgug4112a.db")

        res_tc <- RmiRtc(timeline=c("res1", "res2", "res3"),
timevalue=c(12, 48, 72))
```

```
        res <- readRmiRtc(res_tc, correlation=-0.9, exprLev=1,
  annotation="hgug4112a.db")

## List of genes with anti-correlated miRNAs:

res$reps

## Plot of the first gene of the list:
plotRmiRtc (res, gene_id=351, timeunit="Hours")

## Setting the position of the legend:

plotRmiRtc (res,gene_id=351, legend.x=50, legend.y=0, timeunit="Hours")

## Plot with RSVGTipsDevice:

plotRmiRtc (res,gene_id=351, legend.x=50, legend.y=0, timeunit="Hours",
    svgTips=TRUE)

## Plot of a read.mir results:

plotRmiRtc (res1, svgname="gene1.svg", svgTips=TRUE)
```

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