

# RmiR

February 8, 2012

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RmiR

*Coupling miRNA and Gene expression results*

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## 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="probes", verbose=FALSE)
read.mir(mirna=NULL, genes=NULL, annotation=NULL, id="probes", dbname=c("targetscan", "pictar"), org="Hs", id="probes", verbose=FALSE)
```

## Arguments

<code>mirna</code>	A data.frame with two columns, the first with the microRNA names, the second with the expression values.
<code>genes</code>	A data.frame with two columns, the first with gene ID (probes, symbols, ensembl, entrez...), the second with the expression values.
<code>annotation</code>	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.
<code>dbname</code>	A selected database of miRNA target. See <code>RmiR.hsa_dbconn</code> , default is "targetscan". If using <code>read.mir</code> it can be a vector of databases, default are "targetscan" and "pictar".
<code>id</code>	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.
<code>id.out</code>	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 <code>id</code> is "probes" or "gene" to leave just the entrez gene annotation.
<code>at.least</code>	Minimum number of databases that should yield the result, when the search is performed in multiple databases with <code>read.mir</code> . If it is 1 it is basically an union between databases. Default is 2.
<code>org</code>	Define the targets database package of the desired organism. Default is "Hs"
<code>verbose</code>	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 coefficient 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

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

```

**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 retrieve 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 up or down regulated.

### Value

<code>couples</code>	The couples of <code>mature_miRNA</code> and targets in <code>entrez gene</code> annotation.
<code>mirExpr</code>	A matrix with the expression of miRNA in order by <code>timeline</code> .
<code>geneExpr</code>	A matrix with the expression of miRNA in order by <code>timeline</code> .
<code>mirCV</code>	A matrix with the coefficients of variation of the miRNAs from <code>RmiR</code> or <code>read.mir</code> .
<code>geneCV</code>	A matrix with the coefficients of variation of the genes resulting from <code>RmiR</code> or <code>read.mir</code> .
<code>correlation</code>	A vector with the correlation value between miRNAs and gene targets.
<code>reps</code>	With <code>readRmiRtc</code> 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
```

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RmiRdata

*Simple demonstration data for the RmiR package*

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### 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)
```

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plotRmiRtc	<i>Plot object from read.mir or a selected gene and respective miRNAs from a miRtcList object</i>
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### Description

Plotting 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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