

Package ‘miRmapper’

July 20, 2017

Title A package for the S4 miRmapper class

Version 0.0.0.9000

Description This package allows for the implementation of the S4 class called 'miRmapper'.
miRmapper constructs a miRmapper object that, through its methods, can be used for analyzing the predicted impact that micro RNAs have on the post transcriptional regulation of mRNAs. The user will provide the list of miRNAs of interest and the predicted target genes for each, as well as a list of the differentially expressed genes from the sequencing experiment. The various methods of the miRmapper class will generate metrics and plots of the interactions.

Depends R (>= 3.4.0)

Imports gplots,
ggplot2,
reshape2,
ggdendro,
plyr

License GPL-2

Encoding UTF-8

LazyData true

Collate 'miRmapper.R'
'adjMat.R'
'barPlot.R'
'dendrogram.R'
'getAdjmat.R'
'getDEgenes.R'
'getImpact.R'
'getInteractions.R'
'identityPlot.R'
'initialize.R'
'runAnalysis.R'
'setDEgenes.R'
'setInteractions.R'

RoxygenNote 6.0.1

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adjMat	<i>adjMat</i>
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Description

This generic is for use on the miRmapper class to generate an adjacency matrix of the interaction network. The matrix has a column for each miRNA and a row for each gene. 0 indicates no interaction, while a 1 indicates an interaction.

Usage

```
adjMat(object)

## S4 method for signature 'miRmapper'
adjMat(object)
```

Arguments

object a 'miRmapper' object

Value

a matrix object of the interaction network

Examples

```
adjMat(Object)
```

barPlot	<i>barPlot</i>
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Description

This generic is for use on the 'miRmapper' class, used to generate a bar plot that depicts the impact of each miRNA of the set of gene targets.

Usage

```
barPlot(object)

## S4 method for signature 'miRmapper'
barPlot(object)
```

Arguments

object a 'miRmapper' object

Value

plot bar graph of the impact percentages for the miRNAs

Examples

```
barPlot(Object)
```

dendrogram	<i>dendrogram</i>
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Description

This generic is for use on the miRmapper class, used to generate a dendrogram for miRNA clustering based on shared targets

Usage

```
dendrogram(object)

## S4 method for signature 'miRmapper'
dendrogram(object)
```

Arguments

object a 'miRmapper' object

Value

plot dendrogram figure of miRNAs

Examples

```
dendrogram(Object)
```

```
getAdjmat
```

```
getAdjmat
```

Description

This generic is for use on the 'miRmapper' class that returns the adjacency matrix generated from the interactions.

Usage

```
getAdjmat(object)
```

```
## S4 method for signature 'miRmapper'
getAdjmat(object)
```

Arguments

object a 'miRmapper' object

Value

Adjacency matrix of the interactions

Examples

```
getAdjmat(Object)
```

```
getDEgenes
```

```
getDEgenes
```

Description

This generic is for use on the miRmapper class that returns the 'DEgenes' slot of the 'miRmapper' object.

Usage

```
getDEgenes(object)
```

```
## S4 method for signature 'miRmapper'
getDEgenes(object)
```

Arguments

object a 'miRmapper' object

Value

a list of differentially expressed genes

Examples

```
getDEgenes(Object)
```

getImpact	<i>getImpact</i>
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Description

This generic is for use on the miRmapper class to generate metrics that measure the predicted impact each miRNA has on the differentially expression genes.

Usage

```
getImpact(object)  
  
## S4 method for signature 'miRmapper'  
getImpact(object)
```

Arguments

object a 'miRmapper' object

Value

a dataframe object of impact metrics for each miRNA

Examples

```
getImpact(Object)
```

getInteractions	<i>getInteractions</i>
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Description

This generic is for use on the miRmapper class that returns the 'interactions' slot of a miRmapper object.

Usage

```
getInteractions(object)  
  
## S4 method for signature 'miRmapper'  
getInteractions(object)
```

Arguments

object a 'miRmapper' object

Value

a dataframe of miRNA to gene interactions

Examples

```
getInteractions(Object)
```

identityPlot

identityPlot

Description

This generic is for use on the miRmapper class, used to generate a heatmap representing an identity plot that represents the similarity between miRNAs. A darker colors indicate a cluster where interactions are shared.

Usage

```
identityPlot(object)
```

```
## S4 method for signature 'miRmapper'  
identityPlot(object)
```

Arguments

object a 'miRmapper' object

Value

plot a heatmap of the miRNAs

Examples

```
identityPlot(Object)
```

miRmapper-class	<i>An S4 class to represent miRNA to gene interactions</i>
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Description

An S4 class to represent miRNA to gene interactions

Usage

```
miRmapper(interactions = list(), DEgenes = list())
```

Slots

interactions a list of miRNA to gene interactions (2 columns)

DEgenes a list of differentially expressed genes from a sequencing experiment

adjmat a matrix object generated from the 'setAdjMat' method

runAnalysis	<i>runAnalysis</i>
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Description

This generic is for use on the miRmapper class to perform the the entire miRmapper analysis and export all outputs into a directory named 'miRmapper-Output' that is placed in the users working directory.

Usage

```
runAnalysis(object)
```

```
## S4 method for signature 'miRmapper'
runAnalysis(object)
```

Arguments

object a 'miRmapper' object

Value

5 output files into a directory named "miRmapper-Output". The files consist of a table indicating the total predicted gene targets for each miRNA and its percentage of impact, a table of the adjacency matrix that details the miRNA-target network, a bar plot of the the miRNA impact percentages, a dedrogram depicting miRNA clusters, and an identity heatmap depicting miRNA clustering.

Examples

```
runAnalysis(Object)
```

setDEgenes	<i>setDEgenes</i>
------------	-------------------

Description

This generic is for use on the miRmapper class, used to set the 'DEgenes' slot of a 'miRmapper' object.

Usage

```
setDEgenes(object, genes)

## S4 method for signature 'ANY'
setDEgenes(object, genes)
```

Arguments

object	a 'miRmapper' object
genes	a 'list' object containing one column of gene symbols

Value

None

Examples

```
setDEgenes(Object, genes)
```

setInteractions	<i>setInteractions</i>
-----------------	------------------------

Description

This generic is for use on the miRmapper class, used to set the 'interactions' slot of a 'miRmapper' object.

Usage

```
setInteractions(object, interactions.list)

## S4 method for signature 'ANY'
setInteractions(object, interactions.list)
```

Arguments

object	a 'miRmapper' object
interactions.list	a 'list' object containing two columns with each row representing a miRNA to gene interaction.

Value

None

Examples

```
setInteractions(Object, interactions.list)
```

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