Package ‘IDMIR’

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Type Package

Title Identification of Dysregulated MiRNAs Based on MiRNA-MiRNA Interaction Network

Version 0.1.0

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Description A systematic biology tool was developed to identify dysregulated miRNAs via a miRNA-miRNA interaction network. 'IDMIR' first constructed a weighted miRNA interaction network through integrating miRNA-target interaction information, molecular function data from Gene Ontology (GO) database and gene transcriptomic data in specific-disease context, and then, it used a network propagation algorithm on the network to identify significantly dysregulated miRNAs.

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Encoding UTF-8

LazyData true

Imports egg, fastmatch, forestplot, ggplot2, grDevices, grid, igraph, pheatmap, survival, survminer

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NeedsCompilation no

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R topics documented:

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GetData_Mirna

**Description**

Get the example data

**Usage**

GetData_Mirna(Data)

**Arguments**

- **Data**: A character should be one of "survival", "GEP", "MF_Target", "MiRNA_Target", "matrix_mirna_go_inter", "matrix_mirna_go_jaccard"

**Value**

data

GetGDEscore

**Description**

Function "GetGDEscore" is used to calculate gene differential expression levels.

**Usage**

GetGDEscore(ExpData, Label)
**IdentifyMiRNA**

**Arguments**

- **ExpData**: A gene expression profile of interest (rows are genes, columns are samples).
- **Label**: A character vector consists of "0" and "1" which represent sample class in the gene expression profile. "0" means normal sample and "1" means disease sample.

**Value**

A matrix with one column of GDEscore.

**Examples**

```r
# Obtain the example data
GEP<-GetData_Mirna("GEP")
label<-GetData_Mirna("label")
# Run the function
GDEscore<-GetGDEscore(GEP,label)
MiRNAScore<-IdentifyMiRNA(GDEscore,nperm=5, damping=0.90)
```

**Description**

The function "IdentifyMiRNA" is used to identify significantly dysregulated miRNAs by calculating the eigenvector centrality of miRNAs.

**Usage**

```r
IdentifyMiRNA(GDEscore.table,nperm=1000,damping=0.90)
```

**Arguments**

- **GDEscore.table**: A matrix with one column of GDEscore.
- **nperm**: The Number of random permutations (default: 100).
- **damping**: Restart the probability of the random-walk algorithm (default: 0.9).

**Value**

A data frame with seven columns those are "MiRNA", "Target", "Number" (number of targets), "Score" (Centrality score), "P-value", and "FDR".

**Examples**

```r
# Obtain the example data
GEP<-GetData_Mirna("GEP")
label<-GetData_Mirna("label")
# Run the function
GDEscore<-GetGDEscore(GEP,label)
MiRNAScore<-IdentifyMiRNA(GDEscore,nperm=5, damping=0.90)
```
MirnaData

An environment variable that includes some example data

Description
An environment variable that includes some example data. matrix_mirna_go_inter: A matrix of Jaccard score between MiRNAs and GOMF. matrix_mirna_go_jaccard: A matrix consisting of genes shared by MiRNAs targets and GOMF. MiRNAScore: a ranked list of strong and weak associations with cancer. MF_Target: GOMF and corresponding targets. MiRNA_Target: MiRNAs and corresponding targets. zscore_BRCA: An example gene expression profile. label: A vector representing the label of the sample of BRCA, where "1" is the disease sample and "0" is the normal sample. survival: A dataframe including three columns which are sample, status, and time.

Usage
MirnaData

Format
An environment variable

MutiMiRNA_CRModel

Description
Function "MutiMiRNA_CRModel" can build a multivariate Cox model through integrating the models constructed separately based on different mirna targets.

Usage
MutiMiRNA_CRModel(ExpData, MiRNAs, SurvivalData, cutoff.point=NULL)

Arguments
ExpData A gene expression profile of interest (rows are genes, columns are samples).
MiRNAs An interest miRNA vector.
SurvivalData Survival data (the column names are: "sample", "status", and "time") corresponding to the samples in gene expression profile of interest.
cutoff.point A numeric value used to divide high-risk and low-risk groups.

Value
A list includes a data frame with seven parts those are "sample", "status", "time", "target gene expression", "risk score", "group", and a data frame with five columns those are "Gene", "HR", "HR.95L", "HR.95H", "beta", and "P-value".
Examples

# Obtain the example data
GEP<-GetData_Mirna("GEP")
survival<-GetData_Mirna("survival")
MiRNAs<-c("hsa-miR-21-5p","hsa-miR-26a-5p","hsa-miR-369-5p","hsa-miR-1238-3p","hsa-miR-10b-5p")
# Run the function
MutiMiRNA_CRData<-MutiMiRNA_CRModel(GEP, MiRNAs,survival,cutoff.point=NULL)

Description

Function "PlotForest" can visualize the result of Cox regression analysis through forest plot.

Usage

PlotForest(MiRNA_CRData,g.pos = 2,b.size = 3,col = c("#FE0101", 
#1C61B6", 
"#A4A4A4"),
lwd.zero = 2,lwd.ci = 3,x.lab = "Hazard Ratio Plot")

Arguments

MiRNA_CRData  A list includes a data frame with seven parts those are "sample", "status", "time", "target genes expression", "risk score", "group", and a data frame with five columns those are "Gene", "HR", "HR.95L", "HR.95H", "beta", and "P-value".

g.pos  The position of the graph element within the table of text. The position can be 1-(ncol(labeltext) + 1). You can also choose set the position to "left" or "right".

b.size  Override the default box size based on precision.

col  Set the colors for all the elements in the plot.

lwd.zero  lwd for the vertical line that gives the no-effect line, see gpar.

lwd.ci  lwd for the confidence bands, see gpar.

x.lab  x-axis label.

Value

Forest maps associated with the Cox risk model.

Examples

# Obtain the example data
GEP<-GetData_Mirna("GEP")
survival<-GetData_Mirna("survival")
MiRNAs<-c("hsa-miR-21-5p","hsa-miR-26a-5p","hsa-miR-369-5p","hsa-miR-1238-3p","hsa-miR-10b-5p")
# Run the function
SingleMiRNA_CRData<-SingleMiRNA_CRModel(GEP,
The function "PlotHeatmap" is used to plot a heat map of miRNA targets expression.

**Usage**

```r
PlotHeatmap(MiRNA_CRData, yaxis=c(-2,2), scale="row", cluster.rows=FALSE, cluster.cols=FALSE, show.colnames=FALSE, ann_colors=c("#ef6d6d","#5470c6"), col=c("#ef6d6d","#5470c6"))
```

**Arguments**

- **MiRNA_CRData**: A list includes a data frame with seven parts those are "sample", "status", "time", "target genes expression", "risk score", "group", and a data frame with five columns those are "Gene", "HR", "HR.95L", "HR.95H", "beta", and "P-value".
- **yaxis**: The upper and lower limits of this heat map.
- **scale**: character indicating if the values should be centered and scaled in either the row direction or the column direction, or none. Corresponding values are "row", "column" and "none".
- **cluster.rows**: A logical value that represents whether row clustering is used.
- **cluster.cols**: A logical value that represents whether col clustering is used.
- **show.colnames**: This parameter controls whether column names are displayed.
- **ann_colors**: Vector of colors used to define groups.
- **col**: Vector of colors used in the heatmap.

**Value**

A heat map of miRNA targets expression.

**Examples**

```r
# Obtain the example data
GEP<-GetData_Mirna("GEP")
survival<-GetData_Mirna("survival")
MiRNAs<-c("hsa-miR-21-5p","hsa-miR-26a-5p","hsa-miR-369-5p","hsa-miR-1238-3p","hsa-miR-10b-5p")
# Run the function
SingleMiRNA_CRData<-SingleMiRNA_CRModel(GEP,
"hsa-miR-21-5p",survival,cutoff.point=NULL)
PlotForest(SingleMiRNA_CRData)
MutiMiRNA_CRData<-MutiMiRNA_CRModel(GEP,
MiRNAs,survival,cutoff.point=NULL)
PlotForest(MutiMiRNA_CRData)
```
```
"hsa-miR-21-5p",survival,cutoff.point=NULL)
PlotHeatmap(SingleMiRNA_CRData)
MutiMiRNA_CRData<-MutiMiRNA_CRModel(GEP,
MiRNAs,survival,cutoff.point=NULL)
PlotHeatmap(MutiMiRNA_CRData)
```

---

**Description**

Function "PlotScatter" is used to plot a scatter diagram.

**Usage**

```r
PlotScatter(MiRNA_CRData,status.0='Alive',status.1='Dead',
TitleYlab_A='Risk Score',TitleYlab_B='Survival Time',TitleXlab='Rank',
TitleLegend_A='Risk Group',TitleLegend_B='Status',
color.A=c(low='blue',high='red'),color.B=c(status.0='blue',status.1='red'))
```

**Arguments**

- **MiRNA_CRData**
  A list includes a data frame with seven parts those are "sample", "status", "time", "target genes expression", "risk score", "group", and a data frame with five columns those are "Gene", "HR", "HR.95L", "HR.95H", "beta", and "P-value".

- **status.0**
  string. Code for event 0. Default is 'Alive'

- **status.1**
  string. Code for event 1. Default is 'Dead'

- **TitleYlab_A**
  string, y-lab title for figure A. Default is 'Riskscore'

- **TitleYlab_B**
  string, y-lab title for figure B. Default is 'Survival Time'

- **TitleXlab**
  string, x-lab title for figure B. Default is 'Rank'

- **TitleLegend_A**
  string, legend title for figure A. Default is 'Risk Group'

- **TitleLegend_B**
  string, legend title for figure B. Default is 'Status'

- **color.A**
  color for figure A. Default is low = 'blue', high = 'red'

- **color.B**
  color for figure B. Default is status.0 = 'blue', status.1 = 'red'

**Value**

A riskscore picture
Examples

# Obtain the example data
GEP<-GetData_Mirna("GEP")
survival<-GetData_Mirna("survival")
MiRNAs<-c("hsa-miR-21-5p","hsa-miR-26a-5p","hsa-miR-369-5p","hsa-miR-1238-3p","hsa-miR-10b-5p")
# Run the function
SingleMiRNA_CRData<-SingleMiRNA_CRModel(GEP,
  "hsa-miR-21-5p",survival,cutoff.point=NULL)
PlotScatter(SingleMiRNA_CRData)
MutiMiRNA_CRData<-MutiMiRNA_CRModel(GEP,
  MiRNAs,survival,cutoff.point=NULL)
PlotScatter(MutiMiRNA_CRData)

Description

Function "PlotSurvival" is used to draw a Kaplan-Meier curve.

Usage

PlotSurvival(MiRNA_CRData,colors=c("#ef6d6d","#5470c6"))

Arguments

MiRNA_CRData A list includes a data frame with seven parts those are "sample", "status", "time", "target genes expression", "risk score", "group", and a data frame with five columns those are "Gene", "HR", "HR.95L", "HR.95H", "beta", and "P-value".

colors Vector of colors used to define groups.

Value

A survival curve of a data set.

Examples

# Obtain the example data
GEP<-GetData_Mirna("GEP")
survival<-GetData_Mirna("survival")
MiRNAs<-c("hsa-miR-21-5p","hsa-miR-26a-5p","hsa-miR-369-5p","hsa-miR-1238-3p","hsa-miR-10b-5p")
# Run the function
SingleMiRNA_CRData<-SingleMiRNA_CRModel(GEP,
  "hsa-miR-21-5p",survival,cutoff.point=NULL)
PlotSurvival(SingleMiRNA_CRData)
MutiMiRNA_CRData<-MutiMiRNA_CRModel(GEP,
  MiRNAs,survival,cutoff.point=NULL)
PlotSurvival(MutiMiRNA_CRData)
Description

Function "SingleMiRNA_CRModel" uses survival data to build a multivariate Cox model using the targets of a single miRNA.

Usage

SingleMiRNA_CRModel(ExpData,MiRNA,cutoff.point=NULL,SurvivalData)

Arguments

- **ExpData**: A gene expression profile of interest (rows are genes, columns are samples).
- **MiRNA**: A miRNA ID.
- **cutoff.point**: A numeric value is used to divide high-risk and low-risk groups.
- **SurvivalData**: Survival data (the column names are: "sample", "status", "time") corresponding to samples in the gene expression profile of interest.

Value

A list includes a data frame with seven parts those are "sample", "status", "time", "target genes expression", "risk score", "group", and a dataframe with five columns those are "Gene", "HR", "HR.95L", "HR.95H", "beta", and "P-value".

Examples

```r
# Obtain the example data
GEP<-GetData_Mirna("GEP")
survival<-GetData_Mirna("survival")
# Run the function
SingleMiRNA_CRData<-SingleMiRNA_CRModel(GEP,
"hsa-miR-21-5p",cutoff.point=NULL,survival)
```
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