Package 'IntramiRExploreR'

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Title Predicting Targets for Drosophila Intragenic miRNAs

Version 1.34.0

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Description Intra-miR-ExploreR, an integrative miRNA target prediction bioinformatics tool, identifies targets combining expression and biophysical interactions of a given microRNA (miR). Using the tool, we have identified targets for 92 intragenic miRs in D. melanogaster, using available microarray expression data, from Affymetrix 1 and Affymetrix2 microarray array platforms, providing a global perspective of intragenic miR targets in Drosophila. Predicted targets are grouped according to biological functions using the DAVID Gene Ontology tool and are ranked based on a biologically relevant scoring system, enabling the user to identify functionally relevant targets for a given miR.

Depends R (>= 3.4)

Imports igraph (>= 1.0.1), FGNet (>= 3.0.7), knitr (>= 1.12.3), stats, utils, grDevices, graphics

Suggests gProfileR, topGO, org.Dm.eg.db, rmarkdown, testthat

VignetteBuilder knitr

License GPL-2

biocViews Software, Microarray, GeneTarget, StatisticalMethod, GeneExpression, GenePrediction

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`Affy1_Distance_Final` *Targets for the microRNA analyzed from Affy1 plaform using Distance.*

Description

A precomputed dataset containing the targets, scores and other attributes of 83 intragenic microRNAs using Distance Correlation for plaform Affymetrix 1.

Usage

```
Affy1_Distance_Final
```

Format

A data frame with 53399 rows and 8 variables:

miRNA miRNA name, miRNA symbol

GeneSymbol Gene name, in Gene Symbol

FBGN Gene name, in FlybaseID

CGID Gene name, in CGID

Score Computed Score, in float

GeneFunction Gene Functions, from Flybase

experiments Experiments, from ArrayExpress

TargetDatabases Target Database Name, from TargetDatabases

Affy1_Pearson_Final *Targets for the microRNA analyzed from Affy1 plaform using Pearson.*

Description

A precomputed dataset containing the targets, scores and other attributes of 83 intragenic microRNAs using Pearson Correlation for plaform Affymetrix 1.

Usage

```
Affy1_Pearson_Final
```

Format

A data frame with 41845 rows and 8 variables:

miRNA miRNA name, miRNA symbol

GeneSymbol Gene name, in Gene Symbol

FBGN Gene name, in FlybaseID

CGID Gene name, in CGID

Score Computed Score, in float

GeneFunction Gene Functions, from Flybase

experiments Experiments, from ArrayExpress

TargetDatabases Target Database Name, from TargetDatabases

Affy2_Distance_Final *Targets for the microRNA analyzed from Affy2 plaform using Distance.*

Description

A precomputed dataset containing the targets, scores and other attributes of 83 intragenic microRNAs using Distance Correlation for plaform Affymetrix 1.

Usage

```
Affy2_Distance_Final
```

Format

A data frame with 73374 rows and 8 variables:

miRNA miRNA name, miRNA symbol

GeneSymbol Gene name, in Gene Symbol

FBGN Gene name, in FlybaseID

CGID Gene name, in CGID

Score Computed Score, in float

GeneFunction Gene Functions, from Flybase

experiments Experiments, from ArrayExpress

TargetDatabases Target Database Name, from TargetDatabases

`Affy2_Pearson_Final` *Targets for the microRNA analyzed from Affy2 plaform using Pearson.*

Description

A precomputed dataset containing the targets, scores and other attributes of 83 intragenic microRNAs using Pearson Correlation for plaform Affymetrix 1.

Usage

```
Affy2_Pearson_Final
```

Format

A data frame with 52913 rows and 8 variables:

miRNA miRNA name, miRNA symbol

GeneSymbol Gene name, in Gene Symbol

FBGN Gene name, in FlybaseID

CGID Gene name, in CGID

Score Computed Score, in float

GeneFunction Gene Functions, from Flybase

experiments Experiments, from ArrayExpress

TargetDatabases Target Database Name, from TargetDatabases

`extract_HostGene` *Extract Host Gene for a given Intragenic miRNA.*

Description

Extract Host Gene for a given Intragenic miRNA.

Usage

```
extract_HostGene(miRNA)
```

Arguments

`miRNA`	A String containing the miRNA name.

Value

genf, a character string or vector containing Host gene for the Intragenic miRNA.

Examples

```
miRNA="dme-miR-12"
extract_HostGene(miRNA)
```

`extract_intragenic_miR` *Extract Intragenic miRNA for a given Host gene.*

Description

Extract Intragenic miRNA for a given Host gene.

Usage

```
extract_intragenic_miR(gene)
```

Arguments

`gene`	character. Gene Symbol.

Value

miRf, a character string or vector containing Intragenic miRNA for the Host Gene.

Examples

```
gene="Gmap"
extract_intragenic_miR(gene)
```

genes_Stat *Extracting miRNAs that target a query gene.*

Description

Extracting miRNAs that target a query gene.

Usage

```
genes_Stat(
  gene,
  geneIDType = c("GeneSymbol", "FBGN", "CGID"),
  method = c("Pearson", "Distance", "Both", "BothIntersect"),
  Platform = c("Affy1", "Affy2"),
  Text = FALSE,
  outpath = tempdir()
)
```

Arguments

gene	character. gene Identifier.
geneIDType	character. GeneIDtype choices are 'GeneSymbol', 'FBGN', 'CGID'
method	character. Choices are 'Pearson','Distance','Both' and 'BothIntersected'
Platform	character. Choices are 'Affy1','Affy2'.
Text	logical . To choose between storing the data as text file. Default is FALSE.
outpath	character. The path where the data is stored if TEXT=TRUE. Default is

Value

Outputs the miRNA information, Target Prediction Score, miRNA miRNA function and Target Database that predicts the interaction in a dataframe. Depending upon the ouput choice data is stored in the path specified. Default option prints output to the console.

Examples

```
gene="Syb"
genes_Stat(gene,geneIDType="GeneSymbol",method=c("Pearson"),
           Platform=c("Affy1"),Text=FALSE)
```

Gene_Visualisation *Visualises the targetGene:miRNA network using Cytoscape and igraph*
.

Description

Visualises the targetGene:miRNA network using Cytoscape and igraph .

Usage

```
Gene_Visualisation(
  mRNA,
  mRNA_type = c("GeneSymbol", "FBGN", "CGID"),
  method = c("Pearson", "Distance", "Both"),
  platform = c("Affy1", "Affy2"),
  visualisation = c("igraph", "Cytoscape", "text", "console"),
  path = tempdir(),
 layout = c("kamadakawai", "reingold.tilford", "fruchterman.reingold", "interactive")
)
```

Arguments

mRNA	character. gene Identifier.
mRNA_type	character. mRNA id type. The choices are 'GeneSymbol','FBID' and 'CGID'.
method	character. Statistical Methods. Choices are 'Pearson','Distance','Both'
platform	character. Affymetrix Platforms. Choices are 'Affy1','Affy2'.
visualisation	character.Visualisation type. Choices are 'igraph','Cytoscape','text'and "console"
path	character. Path where data.frame is saved when visualisation is text. Default is tempdir().
layout	character. Network choices. Choices are 'kamadakawai','reingold.tilford','fruchterman.reingold' and 'interactive'.

Value

Depending upon the ouput choice network image or dataframe containg miRNAs that target the query gene are ouput.

Examples

```
mRNA='Syb'
Gene_Visualisation(mRNA,mRNA_type=c('GeneSymbol'),method=c('Pearson'),
                   platform=c('Affy1'), visualisation = "console")
```

GetGOS_ALL *Gene ontology for Target Genes.*

Description

Gene ontology for Target Genes.

Usage

```
GetGOS_ALL(
  gene,
  GO = c("topGO"),
  term = c("GOTERM_BP_ALL", "GOTERM_MF_ALL", "GOTERM_CC_ALL"),
  geneIdType = "ALIAS",
  path = tempdir(),
  ontology = c("GO_BP", "GO_MF", "GO_CC"),
  filename
)
```

Arguments

gene	List A String or vector containing the Gene names.
GO	A String depicting the chosen GO tool. Choice is "topGO"
term	A String depicting the chosen term. Choices are "GOTERM_BP_ALL","GOTERM_MF_ALL", "GOTERM_CC_ALL".
geneIdType	Type of gene Id given as input. Default "ALIAS"
path	String. The path where the data is stored if TEXT=TRUE.
ontology	Ontology selection for topGO. Choices are "GO_BP","GO_MF","GO_CC".
filename	Name of the file to store Gene Ontology.

Value

Depending upon the ouput choice data is stored in the path specified. Default option prints output to the console.

Examples

```
## Not run:
miR="dme-miR-12"
a<-Visualisation(miR,mRNA_type=c("GeneSymbol"),method=c("Both"),
   platform=c("Affy1"),thresh=100)
genes<-a$Target_GeneSymbol
GetGOS_ALL(genes,GO=c("topGO"),term=c("GO_BP"),path=tempdir(),
     filename="test")

## End(Not run)
```

IntramiRExploreR — *IntramiRExploreR:Prediction of targets for Intragenic miRNA in Drosophila.*

Description

Prediction of targets for Drosophila Intragenic microRNAs and Integrated approach using Gene Ontology and Networking tools.

Examples

```
## Not run:
gene='Gmap'
extract_intragenic_miR(gene)

## End(Not run)
```

miRNA_ID_to_Function — *Contains the miRNA function information from Flybase database.*

Description

A dataset containing the function for the intragenic miRNA.

Usage

```
miRNA_ID_to_Function
```

Format

A data frame with 66 rows and 4 variables:

miRNA miRNA name, miRNA symbol

FBGN target gene name, gene symbol

miRNAFunction miRNA function, from Flybase

Source

http://flybase.org/

miRNA_summary_DB *Contains the summary for the intragenic miRNA.*

Description

A dataset containing the summary for the intragenic miRNA.

Usage

```
miRNA_summary_DB
```

Format

A data frame with 257 rows and 6 variables:

miRNA miRNA name, miRNA symbol

Intragenic Responsee, in boolean

Intergenic Responsee, in boolean

Gene miRNA name, miRNA symbol

Type.of.HostGene.mRNA.lncRNA. Type of Hostgene

Notes Comments about the miRNA

miRTargets_Stat *Extracting miRNAs that target a query gene.*

Description

Extracting miRNAs that target a query gene.

Usage

```
miRTargets_Stat(
  miR,
  method = c("Pearson", "Distance", "Both", "BothIntersect"),
  Platform = c("Affy1", "Affy2"),
  outpath = tempdir(),
  Text = FALSE
)
```

Arguments

miR	character. miRNA symbol.
method	character. Choices are "Pearson", "Distance","Both" and "BothIntersected"
Platform	character. Choices are "Affy1","Affy2".
outpath	character. The path where the data is stored if TEXT=TRUE. Default is tempdir().
Text	logical . To choose between storing the data as text file. Default is FALSE.

Value

Outputs the target information, Target Prediction Score, miRNA target function and Target Database that predicts the interaction in a dataframe. Depending upon the ouput choice data is stored in the path specified. Default option prints output to the console.

Examples

```
miRNA="dme-miR-12"
miRTargets_Stat (miRNA,method=c ("Pearson"),Platform=c ("Affy1"),Text=FALSE)
```

Visualisation *Visualises the targetGene:miRNA network using Cytoscape and igraph .*

Description

Visualises the targetGene:miRNA network using Cytoscape and igraph .

Usage

```
Visualisation(
  miRNA,
  mRNA_type = c("GeneSymbol", "FBID", "CGID"),
  method = c("Pearson", "Distance", "Both"),
  platform = c("Affy1", "Affy2"),
  thresh = 50,
  visualisation = c("igraph", "Cytoscape", "Text", "console"),
  path = tempdir(),
 layout = c("kamadakawai", "reingold.tilford", "fruchterman.reingold", "interactive")
)
```

Arguments

miRNA	character. miRNA Identifier.
mRNA_type	character. mRNA id type. The choices are 'GeneSymbol','FBID' and 'CGID'.
method	character. Statistical Methods. Choices are 'Pearson','Distance','Both'

platform	character. Affymetrix Platforms. Choices are 'Affy1','Affy2'.
thresh	integar. Threshold depicting number of rows to show.
visualisation	character.Visualisation type. Choices are 'igraph','Cytoscape','text' and 'console'.
path	character. Path where data.frame is saved when visualisation is text. Default is tempdir().
layout	character. Network choices. Choices are 'kamadakawai','reingold.tilford','fruchterman.reingold' and 'interactive'.

Value

Depending upon the ouput choice network image or dataframe containg miRNAs that target the query gene are ouput.

Examples

```
miRNA='dme-miR-12'
Visualisation(miRNA,mRNA_type=c('GeneSymbol'),method=c('Pearson'),
platform=c('Affy1'),visualisation=c('igraph'),layout=c('kamadakawai'),
          path=tempdir())
```

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