Package 'IntramiRExploreR'

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Title Predicting Targets for Drosophila Intragenic miRNAs

Version 0.99.3

Author Surajit Bhattacharya and Daniel Cox

Maintainer Surajit Bhattacharya <sbhattacharya3@student.gsu.edu>

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 (>= 3.1.2)

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

Suggests RDAVIDWebService,
gProfileR,
topGO,
KEGGprofile,
org.Dm.eg.db,
testthat

VignetteBuilder knitr

License GPL-2

biocViews Software, Microarray, GeneTarget, StatisticalMethod

Encoding UTF-8

LazyData true

RoxygenNote 5.0.1

URL https://github.com/sbhattacharya3/IntramiRExploreR/

BugReports https://github.com/sbhattacharya3/IntramiRExploreR/issues

R topics documented:

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 microR-NAs 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 microR-
NAs 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 microR-
NAs 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 microR-NAs 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

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chipbase   *Transcription factors binding to miRNA upstream.*

Description

A dataset containing the transcription factor that binds upstream of a given miRNA.

Usage

```
chipbase
```

Format

A data frame with 1711 rows and 6 variables:

name location,in Chromosomal Location

tfName Transcription Factor,in Gene Symbol

up5kbNum Region of binding, in Kilo Bases

down1kbNum Region of binding, in Kilo Bases

tssPos Region of binding, Exact position

miRNAs miRNA name, miRNA symbol

Source

http://rna.sysu.edu.cn/chipbase/

---

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)
```

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.

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"), path,
   layout = c("kamadakawai", "reingold.tilford", "fruchterman.reingold",
   "interactive"))
```

Arguments

mRNA	A String or vector containing the miRNA name.
mRNA_type	A String depicting the mRNA type to be displayed. The choices are "GeneSymbol","FBID" and "CGID".
method	A String depicting the chosen method. Choices are "Pearson","Distance","Both"
platform	A String depicting the chosen platform. Choices are "Affy1","Affy2".
visualisation	A String depicting the chosen visualisation. Choices are "igraph","Cytoscape" and "text".
path	String. The path where the network images are stored.
layout	String depicting the network layout chosen. Choices are "kamadakawai","reingold.tilford","fruchterm 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"))
```

GetGOS_ALL	*Gene ontology for Target Genes.*

Description

Gene ontology for Target Genes.

Usage

```
GetGOS_ALL(gene, GO = c("DAVID", "topGO"), term = c("GOTERM_BP_ALL",
  "GOTERM_MF_ALL", "GOTERM_CC_ALL"), geneIdType = "ALIAS", email, path,
  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. Choices are "David" and "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"
email	Email Id to connect to David.
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:
gene=c("wdb","Ank2")
GetGOS_ALL(gene,GO=c("topGO"),term=c("GO_BP"),
          path="C://",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.
Text	logical . To choose between storing the data as text file. Default is FALSE.

Value

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)
```

MiR_ChipBase   *Extracting Transcription factors that bind to query miRNA.*

Description

Extracting Transcription factors that bind to query miRNA.

Usage

```
MiR_ChipBase(m)
```

Arguments

m   character or character vector. miRNA name.

Value

dataframe. Containing the Transcription factor and miRNA.

Examples

```
m="dme-miR-12"
a <- MiR_ChipBase(m)
```

TF_ChipBase   *Extracting microRNAs that a particular transcription factor bind to.*

Description

Extracting microRNAs that a particular transcription factor bind to.

Usage

```
TF_ChipBase(trf)
```

Arguments

trf   character or character vector. Transcription factor name. factor name.

Value

dataframe. Containing the Transcription factor and miRNA.

Examples

```
trf="CBP"
a <- TF_ChipBase(trf)
```

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

Description

Visualises the miRNA:targetGene 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"),
  path = tempdir(), layout = c("kamadakawai", "reingold.tilford",
  "fruchterman.reingold", "interactive"))
```

Arguments

miRNA	A String or vector containing the miRNA name.
mRNA_type	A String depicting the mRNA type to be displayed. The choices are "GeneSymbol","FBID" and "CGID".
method	A String depicting the chosen method. Choices are "Pearson","Distance","Both"
platform	A String depicting the chosen platform. Choices are "Affy1","Affy2".
thresh	An Integer. The number of results to ouput for a given input.
visualisation	A String depicting the chosen visualisation. Choices are "igraph","Cytoscape" and "text".
path	String. The path where the network images are stored.
layout	String depicting the network layout chosen. Choices are "kamadakawai","reingold.tilford", "fruchterman.reingold" and "interactive".

Value

Depending upon the ouput choice network image or dataframe containing miRNA targets 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="C://")
```

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