Package ‘IntramiRExploreR’

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Title Predicting Targets for Drosophila Intragenic miRNAs
Version 1.24.0
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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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RoxygenNote 7.1.2
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Affy1_Distance_Final

Targets for the microRNA analyzed from Affy1 platform using Distance.

Description
A precomputed dataset containing the targets, scores and other attributes of 83 intragenic microRNAs using Distance Correlation for platform 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 platform using Pearson.

**Description**
A precomputed dataset containing the targets, scores and other attributes of 83 intragenic microRNA-NAs using Pearson Correlation for platform 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 platform using Distance.

**Description**
A precomputed dataset containing the targets, scores and other attributes of 83 intragenic microRNA-NAs using Distance Correlation for platform 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

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**Description**

A precomputed dataset containing the targets, scores and other attributes of 83 intragenic microRNA-NAs using Pearson Correlation for platform 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**
```r
evaluate_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**
```r
miRNA="dme-miR-12"
evaluate_HostGene(miRNA)
```

---

extract_intragenic_miR

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

**Description**
Extract Intragenic miRNA for a given Host gene.

**Usage**
```r
evaluate_intragenic_miR(gene)
```

**Arguments**

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

**Examples**
```r
gene="Gmap"
evaluate_intragenic_miR(gene)
```
genes_Stat

Extracting miRNAs that target a query gene.

Description

Extracting miRNAs that target a query gene.

Usage

```r
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 output choice data is stored in the path specified. Default option prints output to the console.

Examples

```r
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 output choice network image or dataframe containing miRNAs that target the query gene are output.

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

```r
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

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

Description

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

Examples

## Not run:
```r
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

```r
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/](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

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

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 output 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)

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.
miRNA_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** integer. 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 output choice network image or dataframe containing miRNAs that target the query gene are output.

**Examples**

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

* datasets
  Affy1_Distance_Final, 2
  Affy1_Pearson_Final, 3
  Affy2_Distance_Final, 3
  Affy2_Pearson_Final, 4
  miRNA_ID_to_Function, 9
  miRNA_summary_DB, 10

Affy1_Distance_Final, 2
Affy1_Pearson_Final, 3
Affy2_Distance_Final, 3
Affy2_Pearson_Final, 4

extract_HostGene, 5
extract_intragenic_miR, 5

Gene_Visualisation, 7
genes_Stat, 6
GetGOS_ALL, 8

IntramiRExploreR, 9

miRNA_ID_to_Function, 9
miRNA_summary_DB, 10
miRTargets_Stat, 10

Visualisation, 11