Package ‘IntramiRExploreR’

January 12, 2024

Title Predicting Targets for Drosophila Intragenic miRNAs
Version 1.24.0
Author Surajit Bhattacharya and Daniel Cox
Maintainer Surajit Bhattacharya <sbhattach2@childrensnational.org>
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
Encoding UTF-8
LazyData true
RoxygenNote 7.1.2
URL https://github.com/VilainLab/IntramiRExploreR
BugReports https://github.com/VilainLab/IntramiRExploreR
git_url https://git.bioconductor.org/packages/IntramiRExploreR
git_branch RELEASE_3_18
git_last_commit 72598bd
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 microRNAs 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 microRNAs 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

Description

A precomputed dataset containing the targets, scores and other attributes of 83 intragenic microRNAs 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
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

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

```r
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

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

Examples

```r
## Not run:
miR = "dme-miR-12"
ax <- Visualisation(miR, mRNA_type = c("GeneSymbol"), method = c("Both"),
  platform = c("Affy1"), thresh = 100)
genex <- ax$Target_GeneSymbol
GetGOS_ALL(genex, 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**
```r
## 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**

```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/
miRTargets_Summary

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**: Response, in boolean
- **Intergenic**: Response, in boolean
- **Gene**: miRNA name, miRNA symbol
- **Type_of_HostGene.mRNA_IncRNA**: Type of Hostgene
- **Notes**: Comments about the miRNA

miRTargets_Stat

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".
- outputPath: 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

```r
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

```r
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'.
Visualisation

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

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