

# Package ‘IntramiRExploreR’

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**Title** Predicting Targets for Drosophila Intragenic miRNAs

**Version** 1.28.0

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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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**LazyData** true

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**BugReports** <https://github.com/VilainLab/IntramiRExploreR>

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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 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

---

Affy2\_Pearson\_Final     *Targets for the microRNA analyzed from Affy2 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

```
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 'BothIntersect'

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**

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

---

|                    |   |
|--------------------|---|
| Gene_Visualisation | <i>Visualises the targetGene:miRNA network using Cytoscape and igraph</i> |
|--------------------|---|

---

**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', 'FBGN' 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**

```
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 output 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 | <i>IntramiRExploreR: Prediction of targets for Intragenic miRNA in Drosophila.</i> |
|------------------|--|

---

### 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 | <i>Contains the miRNA function information from Flybase database.</i> |
|----------------------|---|

---

### 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 | <i>Contains the summary for the intragenic miRNA.</i> |
|------------------|---|

---

**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 | <i>Extracting miRNAs that target a query gene.</i> |
|-----------------|--|

---

**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 "BothIntersect"         |
| 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)
```

---

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        | 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='GeneSymbol',method='Pearson'),  
platform='Affy1',visualisation='igraph',layout='kamadakawai',  
path=tempdir())
```

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