

# Package ‘IntramiRExploreR’

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**Title** Predicting Targets for Drosophila Intragenic miRNAs

**Version** 1.26.0

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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

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.2

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

**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

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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

<code>gene</code>	character. gene Identifier.
<code>geneIDType</code>	character. GeneIDType choices are 'GeneSymbol', 'FBGN', 'CGID'
<code>method</code>	character. Choices are 'Pearson', 'Distance', 'Both' and 'BothIntersected'
<code>Platform</code>	character. Choices are 'Affy1', 'Affy2'.
<code>Text</code>	logical . To choose between storing the data as text file. Default is FALSE.
<code>outpath</code>	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      *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

```
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)
```



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

**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>
------------------	---

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### 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

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

### 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 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)
```

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Visualisation	<i>Visualises the targetGene:miRNA network using Cytoscape and igraph</i>
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**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=c('GeneSymbol'),method=c('Pearson'),  
platform=c('Affy1'),visualisation=c('igraph'),layout=c('kamadakawai'),  
path=tempdir())
```

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