

# Package ‘mirIntegrator’

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**Type** Package

**Title** Integrating microRNA expression into signaling pathways for pathway analysis

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**Depends** R (>= 3.3)

**Imports** graph, ROntoTools, ggplot2, org.Hs.eg.db, AnnotationDbi, Rgraphviz

**Suggests** RUnit, BiocGenerics

**Description** Tools for augmenting signaling pathways to perform pathway analysis of microRNA and mRNA expression levels.

**License** GPL (>=3)

**URL** <http://datad.github.io/mirIntegrator/>

**biocViews** Network, Microarray, GraphAndNetwork, Pathways, KEGG

**NeedsCompilation** no

**git\_url** <https://git.bioconductor.org/packages/mirIntegrator>

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|                    |   |
|--------------------|---|
| augmented_pathways | <i>Signaling pathways augmented with miRNA.</i> |
|--------------------|---|

---

**Description**

Human signaling KEGG pathways augmented with validated miRNA-target interactions from mirTarBase using the mirIntegrator package. These interactions represent the biological miRNA repression over its target genes and are included in the model as negative links.

**Usage**

```
data("augmented_pathways")
```

**Value**

A list of graphNEL objects where each graph is a pathway that were augmented with miRNA-target interactions. The name of each pathway is its KEGG pathway identifier.

**Source**

Generated using the mirIntegrator package. A script that constructs the augmented\_pathways object may be found in 'inst/scripts/get\_augmented\_pathways.R', see the example.

**References**

M. Kanehisa and S. Goto, *KEGG: Kyoto Encyclopedia of Genes and Genomes*, Nucleic Acids Research, vol. 28, pp. 27-30, January 2000.

S.-D. Hsu, Y.-T. Tseng, S. Shrestha, Y.-L. Lin, A. Khaleel, C.-H. Chou, C.-F. Chu, H.-Y. Huang, C.-M. Lin, S.-Y. Ho, T.-Y. Jian, F.-M. Lin, T.-H. Chang, S.-L. Weng, K.-W. Liao, I.-E. Liao, C.-C. Liu, and H.-D. Huang, *miRTarBase update 2014: an information resource for experimentally validated miRNA-target interactions*, Nucleic Acids Research, vol. 42, pp. D78 - D85, Jan. 2014.

**See Also**

[mirTarBase](#) and [kegg\\_pathways](#)

**Examples**

```
data(augmented_pathways)
head(augmented_pathways)

script <- system.file("scripts", "get_augmented_pathways.R",
                      package = "mirIntegrator")

script
readLines(script)
```

---

|                |   |
|----------------|---|
| GSE43592_miRNA | <i>Top table of preprocessed miRNA of GSE43592 dataset.</i> |
|----------------|---|

---

**Description**

A data.frame with the Log fold change and p-value of preprocessed miRNA expression of GSE43592 dataset.

**Usage**

```
data(GSE43592_miRNA)
```

**Value**

A data frame with 881 miRNAs with the following 8 variables: entre, ID, logFC, AveExpr, t, P.Value, adj.P.Val, B.

**Source**

Raw data obtained from <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE43592> and preprocessed with the limma package version 3.24.0.

**References**

M. Jernas, C. Malmstrom, M. Axelsson, I. Nookaew, H. Wadenvik, J. Lycke, and B. Olsson, *MicroRNA regulate immune pathways in t-cells in multiple sclerosis (MS)*, BMC immunology, vol. 14, p. 32, 2013.

Ritchie ME, Phipson B, Wu D, Hu Y, Law CW, Shi W and Smyth GK (2015). *limma powers differential expression analyses for RNA-sequencing and microarray studies*. Nucleic Acids Research, 43(7), pp. e47.

**Examples**

```
data(GSE43592_miRNA)
head(GSE43592_miRNA)
```

---

GSE43592\_mRNA

*Top table of preprocessed mRNA of GSE43592 dataset.*


---

### Description

A data.frame with the Log fold change and p-value of preprocessed mRNA expression of GSE43592 dataset.

### Usage

```
data(GSE43592_mRNA)
```

### Value

A data frame with 19611 mRNAs with the following 8 variables: entre, ID, logFC, AveExpr, t, P.Value, adj.P.Val, B.

### Source

Raw data obtained from <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE43592> and preprocessed with the limma package version 3.24.0.

### References

M. Jernas, C. Malmstrom, M. Axelsson, I. Nookaew, H. Wadenvik, J. Lycke, and B. Olsson, *MicroRNA regulate immune pathways in t-cells in multiple sclerosis (MS)*, BMC immunology, vol. 14, p. 32, 2013.

Ritchie ME, Phipson B, Wu D, Hu Y, Law CW, Shi W and Smyth GK (2015). *limma powers differential expression analyses for RNA-sequencing and microarray studies*. Nucleic Acids Research, 43(7), pp. e47.

### Examples

```
data(GSE43592_mRNA)
head(GSE43592_mRNA)
```

---

integrate\_mir

*Produce augmented pathways*


---

### Description

This function takes each pathway of the input list of signaling pathways and adds the miRNAs that are related to it.

**Usage**

```
integrate_mir(original_pathways, targets_db)
```

**Arguments**

**original\_pathways**

A list of `graph::graphNEL` objects where each of the nodes is named with '`<gene_ID>`'. Gene IDs used to identify the nodes must be the same gene IDs used to identify the genes on the miRNA-target interactions data.frame, `targets_db`. i.e. If the genes are identified by Entrez ID on the `original_pathways` `graph::graphNEL` list, then the `targets_db` data.frame must identify the genes by Entrez ID as well. Nodes of each `graph::graphNEL` represent the genes involved in the pathway and edges represent the biological interactions (activation or repression) among those genes (activation or repression).

**targets\_db**

A data.frame with columns: '`miRNA`' which names the miRNAs and '`Target.ID`' which gives the gene ID of the target gene. The Gene IDs used to identify the "`Target.ID`" column must be the same gene IDs used on the nodes of the `original_pathways`. i.e. If the genes are identified by Entrez ID on the `original_pathways` `graph::graphNEL` list, then the `targets_db` data.frame must identify the genes by Entrez ID as well.

**Value**

Gene signaling pathways augmented with miRNA interactions. This is a list of `graph::graphNEL` objects where each of the nodes is named with '`<gene_ID>`'. Nodes of each `graph::graphNEL` represent genes and miRNAs involved in the pathway and edges represent the biological interactions (activation or repression) among them.

**Author(s)**

Diana Diaz <dmd at wayne dot edu>

**Examples**

```
data(kegg_pathways)
data(mirTarBase)
kegg_pathways <- kegg_pathways[1:5] #delete this for augmenting all pathways.
augmented_pathways <- integrate_mir(kegg_pathways, mirTarBase)
```

---

kegg\_pathways

*List of KEGG signaling pathways of human.*

---

**Description**

This dataset contains 149 KEGG signaling pathways of human. The original pathways were parsed to a list of `graphNEL` objects using the `ROntoTools` package. The original KEGG pathways were published by Kanehisa Laboratories, release 73.0+/01-03, Jan 2015.

**Usage**

```
data("kegg_pathways")
```

**Value**

A list of graphNEL objects where each graph represents one KEGG signaling pathway. The name of each pathway is its KEGG pathway identifier.

**Source**

Obtained using the ROntoTools package Version 1.2.0 with KEGG database release 73.0+/01-03, Jan 2015. A script that constructs the kegg\_pathways object may be found in 'inst/scripts/get\_kegg\_pathways.R', see the example.

**References**

M. Kanehisa and S. Goto, *KEGG: Kyoto Encyclopedia of Genes and Genomes*, Nucleic Acids Research, vol. 28, pp. 27-30, January 2000.

C. Voichita, M. Donato, and S. Draghici, *Incorporating gene significance in the impact analysis of signaling pathways*, in 2012 11th International Conference on Machine Learning and Applications (ICMLA), vol. 1, pp. 126-131, Dec. 2012.

**Examples**

```
data(kegg_pathways)
head(kegg_pathways)

script <- system.file("scripts", "get_kegg_pathways.R",
                      package = "mirIntegrator")
script
readLines(script)
```

---

mirTarBase

---

*MicroRNA-target interactions in human.*


---

**Description**

Dataset of miRNA-target interactions in human obtained from mirTarBase release 4.5: Nov. 1, 2013.

**Usage**

```
data(mirTarBase)
```

**Format**

A data.frame with 39083 interactions and 9 variables. The columns needed for this package are:

- miRNA: which contains the miRNA ID,
- Target.ID: contains the entrez ID of the gene targeted by the miRNA

**Details**

This dataset is licensed by its authors (Hsu et al.), see <http://mirtarbase.mbc.nctu.edu.tw/cache/download/LICENSE>.

**Value**

A data.frame with human miRNA-targets interactions

**Source**

Downloaded from <http://mirtarbase.mbc.nctu.edu.tw/> on 4/1/2015. A script which downloads the file and constructs the mirTarBase object may be found in 'inst/scripts/get\_mirTarBase.R', see the example.

**References**

S.-D. Hsu, Y.-T. Tseng, S. Shrestha, Y.-L. Lin, A. Khaleel, C.-H. Chou, C.-F. Chu, H.-Y. Huang, C.-M. Lin, S.-Y. Ho, T.-Y. Jian, F.-M. Lin, T.-H. Chang, S.-L. Weng, K.-W. Liao, I.-E. Liao, C.-C. Liu, and H.-D. Huang, *miRTarBase update 2014: an information resource for experimentally validated miRNA-target interactions*, Nucleic Acids Research, vol. 42, pp. D78 - D85, Jan. 2014.

**Examples**

```
data(mirTarBase)
head(mirTarBase)

script <- system.file("scripts", "get_mirTarBase.R",
                      package = "mirIntegrator")
script
readLines(script)
```

---

|                |  |
|----------------|--|
| names_pathways | <i>List of KEGG signaling pathways' names.</i> |
|----------------|--|

---

**Description**

Names of the KEGG signaling pathways in human obtained with the ROntoTools package. The original KEGG pathways were published by Kanehisa Laboratories, release 73.0+/01-03, Jan 2015.

**Usage**

```
data("names_pathways")
```

**Value**

A list of KEGG signaling pathways' names.

**Source**

Obtained using the ROntoTools package Version 1.2.0 with KEGG database release 73.0+/01-03, Jan 2015. A script that constructs the names\_pathways object may be found in 'inst/scripts/get\_names\_pathways.R', see the example.

**References**

M. Kanehisa and S. Goto, *KEGG: Kyoto Encyclopedia of Genes and Genomes*, Nucleic Acids Research, vol. 28, pp. 27-30, January 2000.

C. Voichita, M. Donato, and S. Draghici, *Incorporating gene significance in the impact analysis of signaling pathways*, in 2012 11th International Conference on Machine Learning and Applications (ICMLA), vol. 1, pp. 126-131, Dec. 2012.

**Examples**

```
data(names_pathways)
head(names_pathways)

script <- system.file("scripts", "get_names_pathways.R",
                      package = "mirIntegrator")
script
readLines(script)
```

---

pathways2pdf

*Export augmented pathways to pdf*

---

**Description**

This function creates a pdf file with plottings of a list of augmented pathways.

**Usage**

```
pathways2pdf(original_pathways, augmented_pathways, pathway_names, file)
```

**Arguments**

original\_pathways

A list of graph::graphNEL objects where each of the nodes is named with '<gene\_ID>'. Nodes of each graph::graphNEL represent the genes involved in the pathway and edges represent the biological interactions (activation or repression) among those genes (activation or repression).



**augmented\_pathways** A list of `graph::graphNEL` objects where each of the nodes is named with '`<gene_ID>`'. Nodes of each `graph::graphNEL` represent genes and miRNAs involved in the pathway and edges represent the biological interactions (activation or repression) among them.

**pathway\_names** A list of names of the pathways named by '`<pathway_ID>`'.

**file** The name of the file where the plots will be saved.

**Value**

A pdf file with the plottings of the augmented pathways.

**Author(s)**

Diana Diaz <dmd at wayne dot edu>

**Examples**

```
data(augmented_pathways)
data(kegg_pathways)
data(names_pathways)
#The following instruction writes a pfd with three pathways
pathways2pdf(kegg_pathways[18:20],augmented_pathways[18:20],
             names_pathways[18:20], "three_pathways.pdf")
#The following instruction writes a pfd with all the pathways:
#NOTE: It may take time.
# pathways2pdf(kegg_pathways,augmented_pathways,
#             names_pathways, "all_pathways.pdf")
```

---

plot\_augmented\_pathway

*Plotting of augmented pathway*


---

**Description**

Functions for plotting a particular augmented pathway. In the plot, miRNAs that were added to the original pathway are differentiated from proteins that were originally in the pathway. Blue boxes represent the proteins that were part of the original pathway, and black boxes represent the miRNAs that were added during augmentation.

**Usage**

```
plot_augmented_pathway(original_pathway, augmented_pathway,
  pathway_name = " ", ...)
```

**Arguments**

- `original_pathway` A `graph::graphNEL` object where each of the nodes is named with '`<gene_ID>`'. Nodes of each `graph::graphNEL` represent the genes involved in the pathway and edges represent the biological interactions (activation or repression) among those genes.
- `augmented_pathway` A `graph::graphNEL` object where each of the nodes is named with '`<gene_ID>`'. Nodes of each `graph::graphNEL` represent genes and miRNAs involved in the pathway and edges represent the biological interactions (activation or repression) among them.
- `pathway_name` The name of the pathway.
- `...` Other arguments for the '`<plotPathway2Colors>`' function.

**Value**

A plot of one augmented pathway with the new nodes highlighted in black.

**Author(s)**

Diana Diaz <dmd at wayne dot edu>

**Examples**

```
data(augmented_pathways)
data(kegg_pathways)
data(names_pathways)

plot_augmented_pathway(kegg_pathways[[18]], augmented_pathways[[18]],
  pathway_name = names_pathways[[18]])
```

---

plot\_change

---

*Plotting the change in pathways order*


---

**Description**

Function for plotting a lines plot of the difference in pathways' order. The resultant plot shows the comparison between the order of the original pathways and the order of the augmented pathways. It also contains a line with the order difference (order of the augmented pathways minus order of the original pathways). The order of a biological pathway is the number of genes that are involved in it.

**Usage**

```
plot_change(original_pathways, augmented_pathways, pathway_names, ...)
```

**Arguments**

- `original_pathways` A list of `graph::graphNEL` objects where each of the nodes is named with '`<gene_ID>`'. Nodes of each `graph::graphNEL` represent the genes involved in the pathway and edges represent the biological interactions (activation or repression) among those genes (activation or repression).
- `augmented_pathways` A list of `graph::graphNEL` objects where each of the nodes is named with '`<gene_ID>`'. Nodes of each `graph::graphNEL` represent genes and miRNAs involved in the pathway and edges represent the biological interactions (activation or repression) among them.
- `pathway_names` A list of names of the pathways named by '`<pathway_ID>`'.
- `...` Other arguments for the '`<plotLines>`' function.

**Value**

A lines plot of the comparison of pathways order.

**Author(s)**

Diana Diaz <dmd at wayne dot edu>

**Examples**

```
data(augmented_pathways)
data(kegg_pathways)
data(names_pathways)
plot_change(kegg_pathways, augmented_pathways, names_pathways)
```

---

|                               |                                 |
|-------------------------------|---------------------------------|
| <code>smallest_pathway</code> | <i>Get the smallest pathway</i> |
|-------------------------------|---------------------------------|

---

**Description**

Find the pathway with the fewer number of nodes among a list of pathways. This simple function is an example of how to navigate the genes on a list of pathways.

**Usage**

```
smallest_pathway(pathways)
```

**Arguments**

- `pathways` A list of `graph::graphNEL` objects.

**Value**

The index of the pathway with fewer number of nodes.

**Author(s)**

Diana Diaz <dmd at wayne dot edu>

**Examples**

```
data(augmented_pathways)
smallest_pathway(augmented_pathways)
smallest_pathway
```

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