Package ‘mirIntegrator’

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Type Package
Title Integrating microRNA expression into signaling pathways for pathway analysis
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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

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augmented_pathways

Signaling pathways augmented with miRNA.

Description

Human signaling KEGG pathways augmented with validated miRNA-target interactions from mir-TarBase 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


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

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

References

Examples
data(GSE43592_miRNA)
head(GSE43592_miRNA)

GSE43592_mRNA

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

Usage
data(GSE43592_mRNA)
integrate_mir

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

Source

References

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.
**kegg_pathways**

**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)**

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**Examples**

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

**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**

```r
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**


Examples

```r
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

```r
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](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/](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

Examples

data(mirTarBase)
head(mirTarBase)

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

names_pathways

List of KEGG signaling pathways’ names.

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

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

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)

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Examples

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

```r
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

```r
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**

```r
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**

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

Get the smallest pathway

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

`smaallest_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)
smaallest_pathway(augmented_pathways)
smaallest_pathway
```
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