

Package ‘miRTalk’

December 24, 2024

Type Package

Title Infer cell-cell communications mediated by EV-derived miRNAs

Depends R (>= 3.5.0), doParallel

Version 1.0

Description This package is to infer cell-cell communications mediated by EV-derived miRNAs.

License GPL (>= 3)

Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

Imports Seurat, Matrix, foreach, ggplot2, ggrepel, methods, parallel,
pheatmap, progress, RColorBrewer, grDevices, reshape2, stringr,
crayon, utils, correlation, scales, ggraph, igraph, circlize,
heatmaply, networkD3, viridis

Suggests rmarkdown, knitr, prettydoc

VignetteBuilder knitr

RemoteType github

RemoteHost api.github.com

RemoteRepo miRTalk

RemoteUsername multitalk

RemoteRef HEAD

RemoteSha 96e5dd8fb8a05866108678bc53ec106e6bf95b50

GithubRepo miRTalk

GithubUsername multitalk

GithubRef HEAD

GithubSHA1 96e5dd8fb8a05866108678bc53ec106e6bf95b50

NeedsCompilation no

Author Xin Shao [aut, cre] (<<https://orcid.org/0000-0002-1928-3878>>)

Maintainer Xin Shao <xin_shao@zju.edu.cn>

Contents

create_miRTalk	2
demo_geneinfo	3
demo_mir2tar	4
demo_mir_info	4
demo_sc_data	5
evbiog	5
find_hvtg	6
find_miRNA	6
find_miRTalk	7
find_miRTalk_bulk	8
gene2path	10
geneinfo	10
get_miRTalk_cci	11
get_miRTalk_circulating_score	11
get_miRTalk_pathway	12
mir2path	12
mir2tar	13
miRTalk	13
mir_info	14
plot_miR2tar_chord	14
plot_miR2tar_circle	15
plot_miR2tar_heatmap	16
plot_miRTalk_chord	17
plot_miRTalk_circle	18
plot_miRTalk_circle_simple	19
plot_miRTalk_heatmap	20
plot_miRTalk_sankey	21
plot_miR_bubble	22
plot_miR_heatmap	23
plot_target_heatmap	24
rev_gene	25
risc	25
ritac	26
show_miRTalk-method	26

Index	27
--------------	-----------

create_miRTalk	<i>Create miRTalk object</i>
----------------	------------------------------

Description

create miRTalk object using single-cell transcriptomics data

Usage

```
create_miRTalk(  
  sc_data,  
  sc_celltype,  
  species,  
  condition,  
  if_normalize = TRUE,  
  evbiog,  
  risc,  
  ritac  
)
```

Arguments

sc_data	A data.frame or matrix or dgCMatrix containing raw counts of single-cell RNA-seq data. see demo_sc_data
sc_celltype	A character containing the cell type of the single-cell RNA-seq data with the same length as the number of cells.
species	A character meaning species of the single-cell transcriptomics data. 'Human', 'Mouse' or 'Rat'
condition	A character with the same length as the number of cells, e.g., control/disease/treatment, phase 1/2/3, men/women.
if_normalize	Normalize sc_data with Seurat LogNormalize. Set it FALSE when sc_data has been normalized.
evbiog	A data.frame of the system data containing extracellular vesicle biogenesis genes of "Human", "Mouse", and "Rat".
risc	A data.frame of the system data containing RNA-induced silencing complex related genes of "Human", "Mouse", and "Rat".
ritac	A data.frame of the system data containing RNA-induced transcriptional activation complex related genes of "Human", "Mouse", and "Rat".

Value

miRTalk object

demo_geneinfo	<i>Demo data of geneinfo</i>
---------------	------------------------------

Description

Demo data of geneinfo

Usage

```
demo_geneinfo()
```

Details

geneinfo must be a data.frame object with three columns, namely 'symbol', 'synonyms', 'species'.

Examples

```
geneinfo_demo <- demo_geneinfo()
```

demo_mir2tar	<i>Demo data of mir2tar</i>
--------------	-----------------------------

Description

Demo data of mir2tar

Usage

```
demo_mir2tar()
```

Details

mir2tar must be a `data.frame` object with four columns, namely 'miRNA', 'miRNA_mature', 'target_gene', 'species'

Examples

```
mir2tar_demo <- demo_mir2tar()
```

demo_mir_info	<i>Demo data of mir_info</i>
---------------	------------------------------

Description

Demo data of mir_info

Usage

```
demo_mir_info()
```

Details

mir_info must be a `data.frame` object with four columns, namely 'miRNA', 'miRNA_mature', 'gene', 'species'

Examples

```
mir_info_demo <- demo_mir_info()
```

demo_sc_data	<i>Demo data of sc_data</i>
--------------	-----------------------------

Description

Demo data of sc_data.

Usage

```
demo_sc_data()
```

Details

sc_data can be a data.frame, matrix, or dgCMatrx object, each column representing a cell, each row representing a gene.

Value

A dgCMatrx object.

Examples

```
sc_data_demo <- demo_sc_data()
```

evbiog	<i>evbiog</i>
--------	---------------

Description

Extracellular vesicle biogenesis genes of "Human", "Mouse", and "Rat".

Usage

```
evbiog
```

Format

An object of class data.frame with 75 rows and 2 columns.

Source

<https://www.gsea-msigdb.org/gsea/msigdb>

find_hvtg

Find highly variable target genes

Description

Find highly variable target genes with DEGs and HVGs

Usage

```
find_hvtg(
  object,
  pvalue = 0.05,
  log2fc = 0.5,
  min_cell_num = 10,
  nfeatures = 3000
)
```

Arguments

object	miRTalk object after find_miRNA
pvalue	Cutoff of p value. Default is 0.05
log2fc	log2 fold change for identifying the highly expressed genes in each cell type. Default is 0.5
min_cell_num	Min cell number for each cell type. Default is 10
nfeatures	Number of features to select as top variable features. Default is 3000

Value

miRTalk object containing highly variable target genes without the cell-type-specific potential marker genes

find_miRNA

Find expressed miRNAs

Description

Find expressed miRNAs among all cells and generate background distribution for permutation test

Usage

```
find_miRNA(
  object,
  mir_info,
  mir2tar,
  min_percent = 0.05,
  database = "miRTarBase",
  resolution = "mature",
  regulation = "negative",
)
```

```

    EXOmotif = NULL,
    if_use_human_data = FALSE,
    if_combine = TRUE,
    gene2gene = NULL,
    per_num = 1000
)

```

Arguments

object	miRTalk object after create_miRTalk
mir_info	A data.frame of the system data containing information of EV-derived miRNA of 'Human', 'Mouse' or 'Rat'. see demo_mir_info
mir2tar	A data.frame of the system data containing miRNA-target interactions for 'Human', 'Mouse' or 'Rat'. see demo_mir2tar
min_percent	Min percent of expressed cells for target genes of miRNA. Default is 0.05
database	Which database of miRNA-target interactions to use, "miRTarBase" and/or "TarBase". Default is the "miRTarBase". It can also be "TarBase" or c("miRTarBase", "TarBase")
resolution	Correct to precursor or mature miRNAs. Use 'precursor' or 'mature'. Default is 'mature'
regulation	Inference of negative or positive regulation. Default is "negative". Set it as "positive" and set database as "TarBase" for inferring positive regulation.
EXOmotif	A sequence called EXOmotif to help miRNA secretion in EVs such as "CAUG", "CGGGAG". Please refer to https://doi.org/10.1038/s41586-021-04234-3
if_use_human_data	Whether to use homologous human data in mir_info and mir2tar for mouse or rat scRNA-seq data. For human scRNA-seq data, no need to do it. For mouse or rat data, you can set it TRUE.
if_combine	Whether to use combined homologous mir_info and mir2tar when if_use_human_data is TRUE. Default is TRUE.
gene2gene	A data.frame of the system data containing the gene orthologs among human, mouse, and rat. If if_use_human_data is TRUE, please provide it, like "gene2gene = gene2gene"
per_num	Number of permutation test. Default is 1000

Value

miRTalk object containing the expressed miRNAs

find_miRTalk	<i>Infer cell-cell communications mediated by EV-derived miRNAs</i>
--------------	---

Description

Infer cell-cell communications mediated by exosomal miRNAs from senders to receivers

Usage

```
find_miRTalk(
  object,
  min_cell_num = 10,
  min_percent = 0.05,
  pvalue = 0.05,
  per_num = 1000,
  if_filter_miRNA = FALSE,
  if_doParallel = TRUE,
  use_n_cores = 4
)
```

Arguments

object	miRTalk object after create_miRTalk
min_cell_num	Min cell number for each cell type and expressed miRNA. Default is 10
min_percent	Min percent of expressed cells for target genes of miRNA. Default is 0.05
pvalue	Cutoff of p value. Default is 0.05
if_filter_miRNA	Whether to filter the significantly highly expressed miRNAs. Default is FALSE
if_doParallel	Use doParallel. Default is TRUE
use_n_cores	Number of CPU cores to use. Default is 4

Value

miRTalk object containing the inferred cell-cell communications mediated by EV-derived miRNAs

find_miRTalk_bulk	<i>Infer EV-derived miR-target interactions for bulk data</i>
-------------------	---

Description

Infer EV-derived miR-target interactions for paired bulk RNA-seq and miRNA-seq data

Usage

```
find_miRTalk_bulk(
  rna_data,
  mirna_data,
  type,
  resolution = "mature",
  species,
  mir_info,
  mir2tar,
  if_normalize = TRUE,
  if_use_evbiog_risc = TRUE,
  evbiog = NULL,
  risc = NULL,
  ritac = NULL,
```



```

    score_scale_method = "1",
    target_scale_method = "1",
    database = "miRTarBase",
    regulation = "negative",
    if_use_human_data = FALSE,
    if_combine = TRUE,
    gene2gene = NULL
)

```

Arguments

rna_data	RNA-seq data with rows containing genes and columns containing samples.
mirna_data	miRNA-seq data with rows containing miRNA and columns containing samples.
type	Which types of mirna_data, miRNA genes, precursor or mature miRNAs. Use 'gene', 'precursor' or 'mature'.
resolution	Correct to precursor or mature miRNAs. Use 'precursor' or 'mature'. Default is 'mature'
species	A character meaning species of the single-cell transcriptomics data. 'Human', 'Mouse' or 'Rat'
mir_info	A data.frame of the system data containing information of EV-derived miRNA of 'Human', 'Mouse' or 'Rat'. see demo_mir_info
mir2tar	A data.frame of the system data containing relationship of miRNA and its target genes for 'Human', 'Mouse' or 'Rat'. see demo_mir2tar
if_normalize	Normalize sc_data with Seurat LogNormalize. Set it FALSE when rna_data and mirna_data have been normalized.
if_use_evbiog_risc	if considering module score of extracellular vesicle biogenesis genes and RNA-induced silencing complex related genes. Default is TRUE. Consider set it FALSE for the comparison of scores between various conditions.
evbiog	A data.frame of the system data containing extracellular vesicle biogenesis genes of "Human", "Mouse", and "Rat".
risc	A data.frame of the system data containing RNA-induced silencing complex related genes of "Human", "Mouse", and "Rat".
ritac	A data.frame of the system data containing RNA-induced transcriptional activation complex related genes of "Human", "Mouse", and "Rat".
score_scale_method	Methods for scale the Seurat scores of evbiog and risc signatures, "1" for min max scale used in scRNA-seq data by default, and "2" for rank scale. For small sample size, set it to "2" to reduce the zero scores.
target_scale_method	Methods for scale the target gene expression, "1" for rank scale used in scRNA-seq data by default, "2" for the scale with values divided by the max value for each sample, "3" for min max scale. For bulk RNA-seq, consider set it to "2" (all values >= 0) or "3" to reduce the significant heterogeneity of samples, especially human samples.
database	Which database of miRNA-target interactions to use, "miRTarBase" and/or "TarBase". Default is the "miRTarBase". It can also be "TarBase" or c("miRTarBase", "TarBase")

regulation	Inference of negative or positive regulation. Default is "negative". Set it as "positive" and set database as "TarBase" for inferring positive regulation.
if_use_human_data	Whether to use homologous human data in mir_info and mir2tar for mouse or rat scRNA-seq data. For human scRNA-seq data, no need to do it. For mouse or rat data, you can set it TRUE.
if_combine	Whether to use combined homologous mir_info and mir2tar when if_use_human_data is TRUE. Default is TRUE.
gene2gene	A data.frame of the system data containing the gene orthologs among human, mouse, and rat. If if_use_human_data is TRUE, please provide it, like "gene2gene = gene2gene"

Value

A data.frame containing score for each miRNA-target interaction across samples

gene2path	<i>gene2path</i>
-----------	------------------

Description

A data.frame containing relationship of genes and related pathways, i.e., KEGG, GO_BP, REACTOME, WIKIPATHWAYS of "Human", "Mouse", and "Rat" updated on Jan, 02, 2022 for revising count matrix.

Usage

```
gene2path
```

Format

An object of class `data.frame` with 2817311 rows and 5 columns.

Source

<https://www.ncbi.nlm.nih.gov/gene>

geneinfo	<i>geneinfo</i>
----------	-----------------

Description

A data.frame containing gene symbols of "Human", "Mouse", and "Rat" updated on Jan, 02, 2022 for revising count matrix.

Usage

```
geneinfo
```

Format

An object of class `data.frame` with 288563 rows and 3 columns.

Source

<https://www.ncbi.nlm.nih.gov/gene>

get_miRTalk_cci	<i>Get miRNA-target interactions</i>
-----------------	--------------------------------------

Description

Get simple results of miRNA-target interactions and specificity.

Usage

```
get_miRTalk_cci(object, simple = TRUE)
```

Arguments

object	miRTalk object after find_miRTalk
simple	Whether to show the simple results. Default is TRUE

Value

A `data.frame` containing all miRNA-target interactions.

get_miRTalk_circulating_score	<i>Get circulating score of inferred miRNAs</i>
-------------------------------	---

Description

Get circulating score of inferred miRNAs.

Usage

```
get_miRTalk_circulating_score(object)
```

Arguments

object	miRTalk object after find_miRTalk
--------	---

Value

A `data.frame` containing all potential circulating miRNAs.

get_miRTalk_pathway	<i>Get overlapped pathways</i>
---------------------	--------------------------------

Description

Get overlapped pathways between miRNA and target gene related pathways

Usage

```
get_miRTalk_pathway(
  object,
  gene2path,
  mir2path,
  miRNA = NULL,
  targetgenes = NULL
)
```

Arguments

object	miRTalk object after find_miRTalk
gene2path	A data.frame of the system data containing gene-related pathways from KEGG, Reactome, GO_BP, Wikipathways for 'Human', 'Mouse' or 'Rat'.
mir2path	A data.frame of the system data containing miRNA-related pathways from KEGG, Reactome, GO_BP, Wikipathways for 'Human', 'Mouse' or 'Rat'.
miRNA	which miRNAs to analyze. Default is all inferred miRNAs in senders.
targetgenes	which targetgenes to analyze. Default is all inferred target genes in receivers.

Value

A list of pathways for miRNAs and target genes.

mir2path	<i>mir2path</i>
----------	-----------------

Description

A data.frame containing relationship of miRNAs and related pathways, i.e., KEGG, GO_BP, REACTOME, WIKIPATHWAYS of "Human", "Mouse", and "Rat" updated on Jan, 02, 2022 for revising count matrix.

Usage

```
mir2path
```

Format

An object of class data.frame with 130339 rows and 4 columns.

Source

<https://mirtarbase.cuhk.edu.cn/>

mir2tar	<i>mir2tar</i>
---------	----------------

Description

A data.frame containing relationship of miRNA and its target genes for "Human", "Mouse", and "Rat".

Usage

```
mir2tar
```

Format

An object of class `data.frame` with 6212276 rows and 9 columns.

Source

<https://mirtarbase.cuhk.edu.cn/>

miRTalk	<i>Definition of 'miRTalk' class</i>
---------	--------------------------------------

Description

An S4 class containing the data, meta, and results of inferred cell-cell communications mediated by EV-derived miRNAs.

Slots

`data` A list containing the data and variable genes.

`meta` A data.frame containing the meta data.

`species` A character containing the species.

`miR` A data.frame containing expressed miRNA genes.

`miR2tar` A data.frame containing expressed miRNAs and their target genes.

`type` A character containing the type of miRNA.

`per_test_list` Generated background distribution for permutation test.

`cci` A data.frame containing the significantly enriched EV-derived miRNAs and their target genes.

mir_info	<i>mir_info</i>
----------	-----------------

Description

A data.frame containing infomation of exosomal miRNA of "Human", "Mouse", and "Rat".

Usage

mir_info

Format

An object of class data.frame with 3934 rows and 10 columns.

Source

<http://bioinfo.life.hust.edu.cn/EVmiRNA#!/>
<https://mirtarbase.cuhk.edu.cn/>

plot_miR2tar_chord	<i>Chord plot of EV-derived miRNAs and target genes</i>
--------------------	---

Description

Chord plot of EV-derived miRNAs and target genes from senders to receivers with communication score

Usage

```
plot_miR2tar_chord(  
  object,  
  condition = NULL,  
  celltype_sender,  
  celltype_receiver,  
  celltype_color = NULL,  
  miRNA = NULL,  
  edge_color = NULL,  
  edge_type = "circle",  
  text_size = 0.5,  
  y_scale = 1,  
  ...  
)
```

Arguments

object	miRTalk object after find_miRTalk
condition	which conditions to plot. Default is plot all conditions.
celltype_sender	Name of celltype_sender. One or more cell types
celltype_receiver	Name of celltype_receiver. One or more cell types
celltype_color	Colors for the celltype_sender nodes and celltype_receiver nodes, or use "NO" to make it simple
miRNA	which miRNAs to use. Default is to plot all inferred miRNAs in senders.
edge_color	Colors for the edges from the sender cell type
edge_type	Types for the edges from the sender cell type. Default is "circle". "big.arrow" for big arrow, "triangle" for triangle, "ellipse" for ellipse, "curved" for curved. Details see chordDiagram
text_size	Size of text labels. Default is 0.5
y_scale	y_scale to adjust the text. Default is 1
...	parameters pass to chordDiagram , e.g., link.arr.width, link.arr.length, link.arr.col

Value

Chord plot of EV-derived miRNAs and target genes

plot_miR2tar_circle	<i>Circle plot of EV-derived miRNAs and target genes</i>
---------------------	--

Description

Chord plot of EV-derived miRNAs and target genes from senders to receivers.

Usage

```
plot_miR2tar_circle(
  object,
  condition = NULL,
  celltype_sender,
  celltype_receiver,
  celltype_color = NULL,
  miRNA = NULL,
  node_size = 3,
  edge_color = NULL,
  edge_width = 0.5,
  text_size = 3,
  if_show_legend = F
)
```

Arguments

object	miRTalk object after <code>find_miRTalk</code>
condition	which conditions to plot. Default is plot all conditions.
celltype_sender	Name of celltype_sender. One cell type
celltype_receiver	Name of celltype_receiver. One cell type
celltype_color	Colors for the celltype_sender nodes and celltype_receiver nodes, or use "NO" to make it simple
miRNA	which miRNAs to use. Default is to plot all inferred miRNAs in senders.
node_size	Size of node. Default is 3
edge_color	Colors for the edges from the sender cell type
edge_width	Width of edge. Default is 0.5
text_size	Size of text labels. Default is 3
if_show_legend	Whether to show legends. Default is FALSE

Value

ggplot2 object for Circle plot of EV-derived miRNAs and target genes

`plot_miR2tar_heatmap` *Heatmap plot of EV-derived miRNAs and target genes*

Description

Heatmap plot of EV-derived miRNAs and target genes from senders to receivers with communication score displayed

Usage

```
plot_miR2tar_heatmap(
  object,
  condition = NULL,
  celltype_sender,
  celltype_receiver,
  miRNA = NULL,
  text_size = 5,
  if_horizontal = TRUE,
  viridis_option = "D",
  ...
)
```


Arguments

object	miRTalk object after find_miRTalk
condition	which conditions to plot. Default is plot all conditions.
celltype_sender	Name of celltype_sender
celltype_receiver	Name of celltype_receiver
miRNA	which miRNAs to use. Default is to plot all inferred miRNAs in senders.
text_size	Size of text labels. Default is 3
if_horizontal	Whether to plot with the horizontal direction. Default is TRUE
viridis_option	option in scale_color_viridis , can be "A", "B", "C", "D", "E", "F", "G", "H". Default is "D".
...	parameters pass to heatmaply , e.g., grid_color

Value

Heatmap plot of EV-derived miRNAs and target genes

plot_miRTalk_chord	<i>Chord plot of cell-cell communications</i>
--------------------	---

Description

Chord plot of cell-cell communications from senders to receivers with the sum of inferred miRNAs number, EVmiR_score, or score

Usage

```
plot_miRTalk_chord(
  object,
  condition = NULL,
  celltype = NULL,
  celltype_color = NULL,
  miRNA = NULL,
  edge_color = NULL,
  edge_type = "big.arrow",
  show_type = "number",
  if_show_autocrine = FALSE,
  text_size = 1.5,
  y_scale = 0.1,
  ...
)
```

Arguments

object	miRTalk object after find_miRTalk
condition	which conditions to plot. Default is plot all conditions.
celltype	which cell types to plot by order. Default is to plot all cell types.
celltype_color	Colors for the cell types, whose length must be equal to celltype
miRNA	which miRNAs to use. Default is to plot all inferred miRNAs in senders.
edge_color	Colors for the edges from the sender cell type, whose length must be equal to celltype
edge_type	Types for the edges from the sender cell type. Default is "big.arrow". "ellipse" for ellipse, "triangle" for triangle, "curved" for curved. Details see chordDiagram
show_type	which type of miRNAs to show, "number", "EVmiR_score", or "score" for sum of inferred miRNAs number, EVmiR_score, and MiTI_score, respectively. Default is "number"
if_show_autocrine	Whether to show autocrine. Default is FALSE
text_size	Size of text labels. Default is 1.5
y_scale	y_scale to adjust the text. Default is 0.1
...	parameters pass to chordDiagram , e.g., link.arr.width, link.arr.length, link.arr.col

Value

Chord plot of cell-cell communications mediated by EV-derived miRNA

plot_miRTalk_circle	<i>Circle plot of cell-cell communications</i>
---------------------	--

Description

Circle plot of cell-cell communications from senders to receivers with the sum of inferred miRNAs number, EVmiR_score, or score

Usage

```
plot_miRTalk_circle(
  object,
  condition = NULL,
  celltype = NULL,
  miRNA = NULL,
  celltype_color = NULL,
  edge_color = NULL,
  edge_type = "fan",
  show_type = "number",
  if_show_autocrine = FALSE,
  edge_alpha = 0.5,
  node_size = 10,
  text_size = 5
)
```

Arguments

object	miRTalk object after <code>find_miRTalk</code>
condition	which conditions to plot. Default is plot all conditions.
celltype	which cell types to plot. Default is to plot all cell types.
miRNA	which miRNAs to use. Default is to plot all inferred miRNAs in senders.
celltype_color	Colors for the cell types, whose length must be equal to celltype
edge_color	Colors for the edges from the sender cell type, whose length must be equal to celltype
edge_type	Types for the edges. "fan" by default, "link", "hive"
show_type	which type of miRNAs to show, "number", "EVmiR_score", or "score" for sum of inferred miRNAs number, EVmiR_score, and MiTI_score, respectively. Default is "number"
if_show_autocrine	Whether to show autocrine. Default is FALSE
edge_alpha	Transparency of edge. Default is 0.5
node_size	Size of node. Default is 10
text_size	Size of text. Default is 5

Value

ggplot2 object for Circle plot of cell-cell communications mediated by EV-derived miRNA

plot_miRTalk_circle_simple

Circle plot of cell-cell communications by retaining all cell type nodes

Description

Circle plot of cell-cell communications from senders to receivers with the sum of inferred miRNAs number, EVmiR_score, or score by retaining all cell type nodes

Usage

```
plot_miRTalk_circle_simple(
  object,
  condition = NULL,
  celltype,
  celltype_dir = "sender",
  miRNA = NULL,
  celltype_color = NULL,
  edge_color = NULL,
  edge_type = "fan",
  show_type = "number",
  if_show_autocrine = FALSE,
  edge_alpha = 0.5,
  node_size = 10,
  text_size = 5
)
```

Arguments

object	miRTalk object after <code>find_miRTalk</code>
condition	which conditions to plot. Default is plot all conditions.
celltype	which cell types to plot. one or more cell types
celltype_dir	which direction to plot, "sender" or "receiver". Default is as "sender".
miRNA	which miRNAs to use. Default is to plot all inferred miRNAs in senders.
celltype_color	Colors for the cell types, whose length must be equal to celltype
edge_color	Colors for the edges from the sender cell type, whose length must be equal to celltype
edge_type	Types for the edges. "fan" by default, "link", "hive"
show_type	which type of miRNAs to show, "number", "EVmiR_score", or "score" for sum of inferred miRNAs number, EVmiR_score, and MiTI_score, respectively. Default is "number"
if_show_autocrine	Whether to show autocrine. Default is FALSE
edge_alpha	Transparency of edge. Default is 0.5
node_size	Size of node. Default is 10
text_size	Size of text. Default is 5

Value

ggplot2 object for Circle plot of cell-cell communications mediated by EV-derived miRNA

plot_miRTalk_heatmap *Heatmap plot of cell-cell communications*

Description

Heatmap plot of cell-cell communications from senders to receivers with the sum of inferred miRNAs number, EVmiR_score, or score

Usage

```
plot_miRTalk_heatmap(
  object,
  condition = NULL,
  celltype = NULL,
  miRNA = NULL,
  show_type = "number",
  text_size = 10,
  viridis_option = "D",
  ...
)
```

Arguments

object	miRTalk object after find_miRTalk
condition	which conditions to plot. Default is plot all conditions.
celltype	which cell types to plot by order. Default is to plot all cell types
miRNA	which miRNAs to use. Default is to plot all inferred miRNAs in senders.
show_type	which type of miRNAs to show, "number", "EVmiR_score", or "score" for sum of inferred miRNAs number, EVmiR_score, and MiTI_score, respectively. Default is "number"
text_size	Size of text labels. Default is 10
viridis_option	option in scale_color_viridis , can be "A", "B", "C", "D", "E", "F", "G", "H". Default is "D".
...	parameters pass to heatmaply , e.g., grid_color, grid_width

Value

Heatmap plot of cell-cell communications mediated by EV-derived miRNA

plot_miRTalk_sankey *Sankey plot of cell-cell communications*

Description

Sankey plot of cell-cell communications from senders to receivers with the sum of inferred miRNAs number, EVmiR_score, or score

Usage

```
plot_miRTalk_sankey(
  object,
  condition = NULL,
  celltype = NULL,
  miRNA = NULL,
  celltype_color = NULL,
  edge_color = NULL,
  show_type = "number",
  if_show_autocrine = FALSE,
  edge_alpha = 0.5,
  node_size = 40,
  text_size = 15,
  node_pad = 20,
  ...
)
```

Arguments

object	miRTalk object after find_miRTalk
condition	which conditions to plot. Default is plot all conditions.
celltype	which cell types to plot. Default is to plot all cell types
miRNA	which miRNAs to use. Default is to plot all inferred miRNAs in senders.
celltype_color	Colors for the cell types, whose length must be equal to celltype
edge_color	Colors for the edges from the sender cell type, whose length must be equal to celltype, Or use "NO" to cancel it
show_type	which type of miRNAs to show, "number", "EVmiR_score", or "score" for sum of inferred miRNAs number, EVmiR_score, and MiTI_score, respectively. Default is "number"
if_show_autocrine	Whether to show autocrine. Default is FALSE
edge_alpha	Transparency of edge. Default is 0.5
node_size	Size of node. Default is 40
text_size	Size of text. Default is 15
node_pad	Size of node padding. Numeric essentially influences the width height. Default is 20
...	parameters pass to sankeyNetwork

Value

Sankey plot of cell-cell communications mediated by EV-derived miRNA

plot_miR_bubble	<i>Bubble plot of inferred miRNA</i>
-----------------	--------------------------------------

Description

Bubble plot of inferred miRNA from senders top receivers. Rows for cell pairs, and columns for miRNAs by default.

Usage

```
plot_miR_bubble(
  object,
  condition = NULL,
  celltype = NULL,
  miRNA = NULL,
  if_show_autocrine = FALSE,
  if_horizontal = TRUE,
  viridis_option = "D"
)
```

Arguments

object	miRTalk object after find_miRTalk
condition	which conditions to plot. Default is plot all conditions.
celltype	which cell types to plot. Default is to plot all cell types
miRNA	which miRNAs to plot. Default is to plot all inferred miRNAs in senders.
if_show_autocrine	Whether to show autocrine. Default is FALSE
if_horizontal	Whether to plot with the horizontal direction. Default is TRUE
viridis_option	option in scale_color_viridis , can be "A", "B", "C", "D", "E", "F", "G", "H". Default is "D".

Value

ggplot2 object for Bubble plot of inferred miRNA

plot_miR_heatmap	<i>Heatmap plot of inferred miRNA</i>
------------------	---------------------------------------

Description

heatmap plot of inferred miRNA for each sender. Rows for cell types, and columns for miRNAs by default

Usage

```
plot_miR_heatmap(
  object,
  condition = NULL,
  celltype = NULL,
  miRNA = NULL,
  text_size = 10,
  if_horizontal = TRUE,
  viridis_option = "D",
  ...
)
```

Arguments

object	miRTalk object after find_miRTalk
condition	which conditions to plot. Default is plot all conditions.
celltype	which cell types to plot. Default is to plot all cell types
miRNA	which miRNAs to plot. Default is to plot all inferred miRNAs in senders.
text_size	Size of text labels. Default is 10
if_horizontal	Whether to plot with the horizontal direction. Default is TRUE
viridis_option	option in scale_color_viridis , can be "A", "B", "C", "D", "E", "F", "G", "H". Default is "D".
...	parameters pass to heatmaply , e.g., grid_color, grid_width

Value

Heatmap plot of inferred miRNA

plot_target_heatmap	<i>Heatmap plot of inferred targets in receivers</i>
---------------------	--

Description

heatmap plot of inferred targets in receivers. Rows for cell-type-specific miRNAs, and columns for targets in receivers by default

Usage

```
plot_target_heatmap(
  object,
  condition = NULL,
  celltype,
  targetgenes = NULL,
  limits = c(0, 1),
  text_size = 10,
  if_horizontal = TRUE,
  viridis_option = "D",
  ...
)
```

Arguments

object	miRTalk object after find_miRTalk
condition	which conditions to plot. Default is plot all conditions.
celltype	which cell types as receivers to plot, one or more cell types.
targetgenes	which targetgenes to plot. Default is to plot all inferred target genes in receivers.
limits	A parameter heatmaply , a two dimensional numeric vector specifying the data range for the scale. Default is 0-1
text_size	Size of text labels. Default is 10
if_horizontal	Whether to plot with the horizontal direction. Default is TRUE
viridis_option	option in scale_color_viridis , can be "A", "B", "C", "D", "E", "F", "G", "H". Default is "D".
...	parameters pass to heatmaply , e.g., grid_color, grid_width

Value

Heatmap plot of inferred targets

rev_gene

*Pre-processing step: revising gene symbols***Description**

Revise genes according to NCBI Gene symbols updated in June 19, 2022 for count matrix, user-custom mir_info data.frame, and mir2tar data.frame

Usage

```
rev_gene(data = NULL, data_type = NULL, species = NULL, geneinfo = NULL)
```

Arguments

data	A data.frame or matrix or dgCMatrix
data_type	A character to define the type of data, select 'count' for the data matrix, 'mir_info' for the mir_info data.frame, 'mir2tar' for the mir2tar data.frame, 'pathways' for the pathways data.frame, 'GO_BP' for the GO_BP data.frame
species	Species of the data. 'Human', 'Mouse' or 'Rat'
geneinfo	A data.frame of the system data containing gene symbols of 'Human', 'Mouse' and 'Rat' updated on June 19, 2022 for revising gene symbols

Value

A new data.frame, matrix, or dgCMatrix.

risc

*risc***Description**

RNA-induced silencing complex related genes of "Human", "Mouse", and "Rat".

Usage

```
risc
```

Format

An object of class data.frame with 36 rows and 2 columns.

Source

<https://doi.org/10.1016/j.molcel.2021.11.026>

ritac	<i>ritac</i>
-------	--------------

Description

RNA-induced transcriptional activation complex related genes of "Human", "Mouse", and "Rat".

Usage

```
ritac
```

Format

An object of class `data.frame` with 45 rows and 2 columns.

Source

<https://doi.org/10.1038/cr.2016.22>

show,miRTalk-method	<i>Show miRTalk object</i>
---------------------	----------------------------

Description

Show miRTalk object

Usage

```
## S4 method for signature 'miRTalk'  
show(object)
```

Arguments

object	miRTalk object
--------	----------------

Value

miRTalk object

Index

* datasets

- evbiog, [5](#)
- gene2path, [10](#)
- geneinfo, [10](#)
- mir2path, [12](#)
- mir2tar, [13](#)
- mir_info, [14](#)
- risc, [25](#)
- ritac, [26](#)

- chordDiagram, [15](#), [18](#)
- create_miRTalk, [2](#), [7](#), [8](#)

- demo_geneinfo, [3](#)
- demo_mir2tar, [4](#), [7](#), [9](#)
- demo_mir_info, [4](#), [7](#), [9](#)
- demo_sc_data, [3](#), [5](#)

- evbiog, [5](#)

- find_hvtg, [6](#)
- find_miRNA, [6](#), [6](#)
- find_miRTalk, [7](#), [11](#), [12](#), [15–24](#)
- find_miRTalk_bulk, [8](#)

- gene2path, [10](#)
- geneinfo, [10](#)
- get_miRTalk_cci, [11](#)
- get_miRTalk_circulating_score, [11](#)
- get_miRTalk_pathway, [12](#)

- heatmaply, [17](#), [21](#), [23](#), [24](#)

- mir2path, [12](#)
- mir2tar, [13](#)
- mir_info, [14](#)
- miRTalk, [13](#)
- miRTalk-class (miRTalk), [13](#)

- plot_miR2tar_chord, [14](#)
- plot_miR2tar_circle, [15](#)
- plot_miR2tar_heatmap, [16](#)
- plot_miR_bubble, [22](#)
- plot_miR_heatmap, [23](#)
- plot_miRTalk_chord, [17](#)

- plot_miRTalk_circle, [18](#)
- plot_miRTalk_circle_simple, [19](#)
- plot_miRTalk_heatmap, [20](#)
- plot_miRTalk_sankey, [21](#)
- plot_target_heatmap, [24](#)

- rev_gene, [25](#)
- risc, [25](#)
- ritac, [26](#)

- sankeyNetwork, [22](#)
- scale_color_viridis, [17](#), [21](#), [23](#), [24](#)
- show_miRTalk-method, [26](#)