

# Package ‘miRTalk’

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**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,  
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crayon, utils, correlation, scales, ggraph, igraph, circlize,  
heatmaply, networkD3, viridis

**Suggests** rmarkdown, knitr, prettydoc

**VignetteBuilder** knitr

**NeedsCompilation** no

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

### Description

create miRTalk object using single-cell transcriptomics data

### Usage

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

### Arguments

sc_data	A data.frame or matrix or dgCMatrx containing raw counts of single-cell RNA-seq data. see <a href="#">demo_sc_data</a>
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".

**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	<i>Find highly variable target genes</i>
-----------	--

---

**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**

<code>object</code>	miRTalk object after <a href="#">find_miRNA</a>
<code>pvalue</code>	Cutoff of p value. Default is 0.05
<code>log2fc</code>	log2 fold change for identifying the highly expressed genes in each cell type. Default is 0.5
<code>min_cell_num</code>	Min cell number for each cell type. Default is 10
<code>nfeatures</code>	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 <a href="#">create_miRTalk</a>
mir_info	A data.frame of the system data containing information of EV-derived miRNA of 'Human', 'Mouse' or 'Rat'. see <a href="#">demo_mir_info</a>
mir2tar	A data.frame of the system data containing relationship of miRNA and its target genes for 'Human', 'Mouse' or 'Rat'. see <a href="#">demo_mir2tar</a>
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 <a href="https://doi.org/10.1038/s41586-021-04234-3">https://doi.org/10.1038/s41586-021-04234-3</a>
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_consider_condition = TRUE,
  if_doParallel = TRUE,
  use_n_cores = 4
)
```

**Arguments**

object	miRTalk object after <a href="#">create_miRTalk</a>
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_consider_condition	Whether to infer for each condition. Default is TRUE
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,
  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 <a href="#">demo_mir_info</a>
mir2tar	A data.frame of the system data containing relationship of miRNA and its target genes for 'Human', 'Mouse' or 'Rat'. see <a href="#">demo_mir2tar</a>
if_normalize	Normalize sc_data with Seurat LogNormalize. Set it FLASE 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".
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 $\geq 0$ ) 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 288559 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 <a href="#">find_miRTalk</a>
simple	Whether to show the simple results. Default is TRUE

**Value**

A data.frame containing all miRNA-target interactions.

---

```
get_miRTalk_circulating_score
```

*Get circulating score of inferred miRNAs*

---

**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      Get overlapped pathways
```

---

**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`*mir2path*

---

**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`*mir2tar*

---

**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

*Definition of 'miRTalk' class***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

*mir\_info***Description**

A data.frame containing information 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 <a href="#">find_miRTalk</a>
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 <a href="#">chordDiagram</a>
text_size	Size of text labels. Default is 0.5
y_scale	y_scale to adjust the text. Default is 1
...	parameters pass to <a href="#">chordDiagram</a> , e.g., link.arr.width, link.arr.length, link.arr.col
show_type	which type of miRNAs to show, "prob" or "score" for inferred miRNAs-target interactions. Default is "prob"

## 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 <a href="#">find_miRTalk</a>
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 <a href="#">find_miRTalk</a>
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 <a href="#">scale_color_viridis</a> , can be "A", "B", "C", "D", "E", "F", "G", "H". Default is "D".
...	parameters pass to <a href="#">heatmaply</a> , 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 <a href="#">find_miRTalk</a>
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 <a href="#">chordDiagram</a>
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 <a href="#">chordDiagram</a> , 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     *Circle plot of cell-cell communications*

---

### 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 <a href="#">find_miRTalk</a>
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 <a href="#">find_miRTalk</a>
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 <a href="#">find_miRTalk</a>
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 <a href="#">scale_color_viridis</a> , can be "A", "B", "C", "D", "E", "F", "G", "H". Default is "D".
...	parameters pass to <a href="#">heatmaply</a> , 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 <a href="#">find_miRTalk</a>
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 <a href="#">sankeyNetwork</a>

**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 to 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 <a href="#">find_miRTalk</a>
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 <a href="#">scale_color_viridis</a> , 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 <a href="#">find_miRTalk</a>
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 <a href="#">scale_color_viridis</a> , can be "A", "B", "C", "D", "E", "F", "G", "H". Default is "D".
...	parameters pass to <a href="#">heatmaply</a> , 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 <a href="#">find_miRTalk</a>
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 <a href="#">heatmaply</a> , 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 <a href="#">scale_color_viridis</a> , can be "A", "B", "C", "D", "E", "F", "G", "H". Default is "D".
...	parameters pass to <a href="#">heatmaply</a> , 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**

<code>data</code>	A data.frame or matrix or dgCMatrix
<code>data_type</code>	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
<code>species</code>	Species of the data. 'Human', 'Mouse' or 'Rat'
<code>geneinfo</code>	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.

---

<code>risc</code>	<i>risc</i>
-------------------	-------------

---

**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>

---

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

---

**Description**

Show miRTalk object

**Usage**

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

**Arguments**

<code>object</code>	miRTalk object
---------------------	----------------

**Value**

miRTalk object

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