

# Package ‘miRTalk’

June 9, 2023

**Type** Package

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

**Depends** R (> 4.1.0), 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** 7.1.2

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

**Suggests** rmarkdown,  
knitr,  
prettydoc

**VignetteBuilder** knitr

**R topics documented:**

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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, if_normalize = TRUE)
```

**Arguments**

sc_data	A data.frame or matrix or dgCMatrix 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
species	A character meaning species of the single-cell transcriptomics data. 'Human', 'Mouse' or 'Rat'
if_normalize	Normalize sc_data with Seurat LogNormalize. Set it FALSE when sc_data has been normalized.

**Value**

miRTalk object

---

demo_gene2go	<i>Demo data of gene2go</i>
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---

**Description**

Demo data of gene2go

**Usage**

```
demo_gene2go()
```

**Details**

gene2go must be a data.frame object with three columns, namely 'symbol', 'GO\_term', 'species'.

**Examples**

```
gene2go_demo <- demo_gene2go()
```

---

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>
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---

**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_pathways`*Demo data of pathways*

---

**Description**

Demo data of pathways

**Usage**

```
demo_pathways()
```

**Details**

pathways must be a `data.frame` object with four columns, namely 'src', 'dest', 'pathway', 'species'

**Examples**

```
pathways_demo <- demo_pathways()
```

---

`demo_sc_data`*Demo data of sc\_data*

---

**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()
```

---

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

---

**Description**

Find highly variable target genes by excluding the cell-type-specific potential marker genes

**Usage**

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

**Arguments**

object	miRTalk object after <a href="#">find_miRNA</a>
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	<i>Find expressed miRNAs</i>
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---

**Description**

Find expressed miRNAs among all cells

**Usage**

```
find_miRNA(object, mir_info)
```

**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>

**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,
  mir2tar,
  min_cell_num = 10,
  pvalue = 0.05,
  resolution = "mature",
  min_percent = 0.05,
  if_doParallel = TRUE,
  use_n_cores = 4
)
```

**Arguments**

object	miRTalk object after <a href="#">create_miRTalk</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_cell_num	Min cell number for each cell type and expressed miRNA. Default is 10
pvalue	Cutoff of p value. Default is 0.05
resolution	Correct to precursor or mature miRNAs. Use 'precursor' or 'mature'. Default is 'mature'
min_percent	Min percent of expressed cells for target genes of miRNA. Default is 0.05
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

---

gene2go	<i>gene2go</i>
---------	----------------

---

**Description**

A data.frame containing GO terms, i.e., process, function, and component, of "Human", "Mouse", and "Rat" updated on Jan, 02, 2022 for revising count matrix.

**Usage**

```
gene2go
```

**Format**

An object of class `data.frame` with 1190681 rows and 7 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_gene2go	<i>Get GO terms</i>
-------------	---------------------

---

**Description**

Get GO terms for target genes

**Usage**

```
get_gene2go(target_genes, gene2go, species)
```

**Arguments**

target_genes	Character of one or more target genes
gene2go	A <code>data.frame</code> of the system data containing GO terms for 'Human', 'Mouse' or 'Rat'. see <a href="#">demo_gene2go</a>
species	A character meaning species of the target genes. 'Human', 'Mouse' or 'Rat'

**Value**

GO terms for one or more target genes



---

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

---

**Description**

Get all miRNAs' activity for a given sender cell type

**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_pathways	<i>Get pathways</i>
--------------	---------------------

---

**Description**

Get pathways for target genes

**Usage**

```
get_pathways(target_genes, pathways, species)
```

**Arguments**

target_genes	Character of one or more target genes
pathways	A data.frame of the system data containing gene-gene interactions and pathways from KEGG and Reactome for 'Human', 'Mouse' or 'Rat'. see <a href="#">demo_pathways</a>
species	A character meaning species of the target genes. 'Human', 'Mouse' or 'Rat'

**Value**

Pathways for one or more target genes

---

 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 544329 rows and 8 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.

`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 5 columns.

**Source**

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

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

---

`pathways`*pathways*

---

**Description**

KEGG pathways of "Human", "Mouse", and "Rat".

**Usage**

```
pathways
```

**Format**

An object of class data.frame with 222355 rows and 5 columns.

**Source**

<https://www.genome.jp/kegg/pathway.html>

---

plot\_miR2tar\_chord      *Chord plot of EV-derived miRNAs and target genes*

---

### Description

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

### Usage

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

### Arguments

object	miRTalk object after <a href="#">find_miRTalk</a>
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
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>
show_type	which type of miRNAs to show, "prob" or "score" for inferred miRNAs-target interactions. Default is "prob"
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

### Value

Chord plot of EV-derived miRNAs and target genes

---

plot\_miR2tar\_circle     *Circle plot of EV-derived miRNAs and target genes*

---

### Description

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

### Usage

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

### Arguments

object	miRTalk object after <a href="#">find_miRTalk</a>
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
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

### 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.

**Usage**

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

**Arguments**

object	miRTalk object after <a href="#">find_miRTalk</a>
celltype_sender	Name of celltype_sender
celltype_receiver	Name of celltype_receiver
miRNA	which miRNAs to use. Default is to plot all inferred miRNAs
show_type	which type of miRNAs to show, "prob" or "score" for inferred miRNAs-target interactions. Default is "prob"
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     *Chord plot of cell-cell communications*

---

**Description**

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

**Usage**

```
plot_miRTalk_chord(
  object,
  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>
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
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", "activity", or "score" for sum of inferred miRNAs number and activity, respectively, or "prob" for max probability. 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, activity, score, or the max probability

### Usage

```

plot_miRTalk_circle(
  object,
  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>
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
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", "activity", or "score" for sum of inferred miRNAs number and activity, respectively, or "prob" for max probability. 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, activity, score, or the max probability by retaining all cell type nodes

### Usage

```

plot_miRTalk_circle_simple(
  object,
  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>
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
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", "activity", or "score" for sum of inferred miRNAs number and activity, respectively, or "prob" for max probability. 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, activity, score, or the max probability

### Usage

```

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

```

**Arguments**

object	miRTalk object after <code>find_miRTalk</code>
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
show_type	which type of miRNAs to show, "number", "activity", or "score" for sum of inferred miRNAs number and activity, respectively, or "prob" for max probability. Default is "number"
text_size	Size of text labels. Default is 10
viridis_option	option in <code>scale_color_viridis</code> , can be "A", "B", "C", "D", "E", "F", "G", "H". Default is "D".
...	parameters pass to <code>heatmaply</code> , e.g., <code>grid_color</code> , <code>grid_width</code>

**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, activity, score, or the max probability

**Usage**

```
plot_miRTalk_sankey(
  object,
  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 <code>find_miRTalk</code>
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
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", "activity", or "score" for sum of inferred miRNAs number and activity, respectively, or "prob" for max probability. 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 top receivers. Rows for cell pairs, and columns for miRNAs by default.

**Usage**

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

**Arguments**

object	miRTalk object after <a href="#">find_miRTalk</a>
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
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,
  celltype = NULL,
  miRNA = NULL,
  text_size = 10,
  if_horizontal = TRUE,
  viridis_option = "D",
  ...
)
```

### Arguments

object	miRTalk object after <a href="#">find_miRTalk</a>
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
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

---

rev_gene	<i>Pre-processing step: revising gene symbols</i>
----------	---

---

### 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.

---

show,miRTalk-method    *Show miRTalk object*

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**Description**

Show miRTalk object

**Usage**

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

**Arguments**

object	miRTalk object
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**Value**

miRTalk object

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