# Package 'scCrossTalk'

April 14, 2023

**Title** Infer and visualize cell-cell communication for single-cell RNA-seq data

**Version** 1.0

**Depends** R (>= 4.0.0)

**Description**
This package can infer and visualize cell-cell communication for single-cell RNA-seq data.

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.2

**Imports** Seurat,
Matrix,
graphics,
ggplot2,
ggrepel,
methods,
pheatmap,
progress,
reshape2,
crayon,
utils,
scales,
ggraph,
igraph,
circlize,
heatmaply,
networkD3,
viridis

**Suggests** rmarkdown,
knitr,
prettydoc

**VignetteBuilder** knitr

## R topics documented:

---

create_scCrossTalk          *Create scCrossTalk object*

---

### Description

create scCrossTalk object using single-cell transcriptomics data

### Usage

```
create_scCrossTalk(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 demo_sc_data |
| 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' or 'Mouse'. |
| if_normalize | Normalize sc_data with Seurat LogNormalize. Set it FLASE when sc_data has been normalized. |

### Value

scCrossTalk object

---

demo_geneinfo *Demo data of geneinfo*

---

### 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_lrpairs *Demo data of lrpairs*

---

### Description

Demo data of lrpairs

### Usage

```
demo_lrpairs()
```

### Details

lrpairs must be a data.frame object with three columns, namely 'ligand', 'receptor', 'species'.

### Value

A data.frame.

### Examples

```
lrpairs_demo <- demo_lrpairs()
```

---

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 dgCMatrix object, each column representing a cell, each row representing a gene.

### Value

A dgCMatrix object.

### Examples

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

---

find_lrpairs                    *Find highly expressed ligand-receptor pairs*

---

### Description

Find highly expressed ligands and receptors between pairwise cell types using Z score

### Usage

```
find_lrpairs(
  object,
  lrpairs,
  min_cell_num = 10,
  cell_min_pct = 0.1,
  p_value = 0.05
)
```

### Arguments

| | |
|---|---|
| object | scCrossTalk object after create_scCrossTalk |
| lrpairs | A data.frame of the system data containing ligand-receptor pairs of 'Human' and 'Mouse'. see demo_lrpairs |
| min_cell_num | Min cell number for each cell type. Default is 10 |
| cell_min_pct | Include the ligand and receptor gene detected in at least this many cells in each cluster. Default is 0.1 |
| p_value | Include the significantly highly expressed ligands and receptors with this cutoff of p value from Z score. Default is 0.05 |

## Value

scCrossTalk object containing the enriched ligand-receptor pairs and cell-cell communications

---

geneinfo                    *geneinfo*

---

## Description

A data.frame containing gene symbols of "Human" and "Mouse" updated on June 19, 2022 for revising gene symbols.

## Usage

```
geneinfo
```

## Format

An object of class data.frame with 288559 rows and 3 columns.

## Source

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

---

get_top_lrpairs           *Get top n LR-pairs*

---

## Description

Get top n LR-pairs for each cell pairs

## Usage

```
get_top_lrpairs(object, top_n = 10)
```

## Arguments

| | |
|---|---|
| object | scCrossTalk object after create_scCrossTalk |
| top_n | Number of top LR-pairs. Default is 10 |

## Value

A data.frame containing the top n LR-pairs for each cell pairs

| lrpairs | *lrpairs* |
|---------|-----------|

## Description

A data.frame containing ligand-receptor interactions for "Human" and "Mouse" from CellTalkDB.

## Usage

```
lrpairs
```

## Format

An object of class data.frame with 5427 rows and 3 columns.

## Source

<http://tcm.zju.edu.cn/celltalkdb/>

| plot_cci_chord | *Chord plot of cell-cell communications* |
|----------------|------------------------------------------|

## Description

Chord plot of cell-cell communications from senders to receivers with the sum of inferred number
or score of ligand-receptor interactions

## Usage

```
plot_cci_chord(
  object,
  celltype = NULL,
  celltype_color = NULL,
  ligand = NULL,
  receptor = 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` | scCrossTalk object after [find_lrpairs](#) |
| `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` |
| `ligand` | which ligand to use. Default is to plot all inferred ligands |
| `receptor` | which receptor to use. Default is to plot all inferred receptors |
| `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 to show, `"number"` and `"score"` for sum of inferred LR number and 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 ligand-receptor interactions

---

| `plot_cci_circle` | *Circle plot of cell-cell communications* |
|---|---|

---

## Description

Circle plot of cell-cell communications from senders to receivers with the sum of inferred number or score of ligand-receptor interactions

## Usage

```
plot_cci_circle(
  object,
  celltype = NULL,
  ligand = NULL,
  receptor = 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` | scCrossTalk object after [`find_lrpairs`](#) |
| `celltype` | which cell types to plot. Default is to plot all cell types |
| `ligand` | which ligand to use. Default is to plot all inferred ligands |
| `receptor` | which receptor to use. Default is to plot all inferred receptors |
| `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 to show, `"number"` and `"score"` for sum of inferred LR number and 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

Circle plot of cell-cell communications mediated by ligand-receptor interactions

---

plot_cci_heatmap    *Heatmap plot of cell-cell communications*

---

## Description

Heatmap plot of cell-cell communications from senders to receivers with the sum of inferred number or score of ligand-receptor interactions

## Usage

```
plot_cci_heatmap(
  object,
  celltype = NULL,
  ligand = NULL,
  receptor = NULL,
  show_type = "number",
  text_size = 10,
  viridis_option = "D",
  ...
)
```

## Arguments

| | |
|---|---|
| object | scCrossTalk object after [find_lrpairs](#) |
| celltype | which cell types to plot by order. Default is to plot all cell types |
| ligand | which ligand to use. Default is to plot all inferred ligands |
| receptor | which receptor to use. Default is to plot all inferred receptors |
| show_type | which type to show, `"number"` and `"score"` for sum of inferred LR number and 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 |

## Value

Heatmap plot of cell-cell communications mediated by ligand-receptor interactions

---

plot_cci_lrpairs_bubble

*Bubble plot of inferred ligand-receptor pairs*

---

## Description

Bubble plot of inferred ligand-receptor pairs from senders top receivers. Rows for cell pairs, and columns for LR pairs by default.

## Usage

```
plot_cci_lrpairs_bubble(
  object,
  celltype = NULL,
  ligand = NULL,
  receptor = NULL,
  if_show_autocrine = FALSE,
  if_horizontal = TRUE,
  size = 2,
  viridis_option = "D"
)
```

## Arguments

| | |
|---|---|
| object | scCrossTalk object after [find_lrpairs](#) |
| celltype | which cell types to plot. Default is to plot all cell types |
| ligand | which ligand to use. Default is to plot all inferred ligands |
| receptor | which receptor to use. Default is to plot all inferred receptors |
| if_show_autocrine | |
| | Whether to show autocrine. Default is `FALSE` |
| if_horizontal | Whether to plot with the horizontal direction. Default is `TRUE` |
| size | Size of the bubble. Default is 2 |
| viridis_option | option in [scale_color_viridis](#), can be "A", "B", "C", "D", "E", "F", "G", "H". Default is "D". |

**Value**

Bubble plot of inferred ligand-receptor pairs

---

plot_cci_lrpairs_heatmap

*Heatmap plot of all lrpairs among cell pairs*

---

**Description**

heatmap plot of inferred lrpairs. Rows for cell pairs, and columns for LR pairs by default.

**Usage**

```
plot_cci_lrpairs_heatmap(
  object,
  celltype = NULL,
  ligand = NULL,
  receptor = NULL,
  if_show_autocrine = FALSE,
  if_horizontal = TRUE,
  text_size = 10,
  viridis_option = "D",
  ...
)
```

**Arguments**

| | |
|---|---|
| object | scCrossTalk object after [find_lrpairs](#) |
| celltype | which cell types to plot. Default is to plot all cell types |
| ligand | which ligand to use. Default is to plot all inferred ligands |
| receptor | which receptor to use. Default is to plot all inferred receptors |
| if_show_autocrine | |
| | Whether to show autocrine. Default is `FALSE` |
| if_horizontal | Whether to plot with the horizontal direction. Default is `TRUE` |
| 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 |

**Value**

Heatmap plot of all lrpairs among cell pairs

plot_cci_sankey *Sankey plot of cell-cell communications*

### Description

Sankey plot of cell-cell communications from senders to receivers with the sum of inferred number or score of ligand-receptor interactions

### Usage

```
plot_cci_sankey(
  object,
  celltype = NULL,
  ligand = NULL,
  receptor = 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 | scCrossTalk object after [find_lrpairs](#) |
| celltype | which cell types to plot. Default is to plot all cell types |
| ligand | which ligand to use. Default is to plot all inferred ligands |
| receptor | which receptor to use. Default is to plot all inferred receptors |
| 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 to show, `"number"` and `"score"` for sum of inferred LR number and 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 ligand-receptor interactions

plot_lrpairs_chord          *Chord plot of ligand-receptor pairs*

## Description

Chord plot of ligand-receptor pairs from senders to receivers.

## Usage

```
plot_lrpairs_chord(
  object,
  celltype_sender,
  celltype_receiver,
  celltype_color = NULL,
  ligand = NULL,
  receptor = NULL,
  edge_color = NULL,
  edge_type = "circle",
  text_size = 0.5,
  y_scale = 1,
  ...
)
```

## Arguments

| | |
|---|---|
| object | scCrossTalk object after [find_lrpairs](#) |
| 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 |
| ligand | which ligand to use. Default is to plot all inferred ligands |
| receptor | which receptor to use. Default is to plot all inferred receptors |
| 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 ligand-receptor pairs from senders to receivers

plot_lrpairs_heatmap        *Heatmap plot of ligand-receptor pairs*

### Description

Heatmap plot of ligand-receptor pairs from senders to receivers.

### Usage

```
plot_lrpairs_heatmap(
  object,
  celltype_sender,
  celltype_receiver,
  ligand = NULL,
  receptor = NULL,
  text_size = 5,
  if_horizontal = TRUE,
  viridis_option = "D",
  ...
)
```

### Arguments

| | |
|---|---|
| object | scCrossTalk object after [find_lrpairs](#) |
| celltype_sender | |
| | Name of celltype_sender. One or more cell types |
| celltype_receiver | |
| | Name of celltype_receiver. One or more cell types |
| ligand | which ligand to use. Default is to plot all inferred ligands |
| receptor | which receptor to use. Default is to plot all inferred receptors |
| 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 ligand-receptor pairs

rev_gene                        *Pre-processing step: revising gene symbols*

### Description

Revise genes according to NCBI Gene symbols updated in June 19, 2022 for count matrix and user-custom lrpairs 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, 'lrpairs' for the lrpairs data.frame |
| species | Species of the data.'Human' or 'Mouse' |
| geneinfo | A data.frame of the system data containing gene symbols of 'Human' or 'Mouse' updated on June 19, 2022 for revising gene symbols |

### Value

A new data.frame, matrix, or dgCMatrix.

scCrossTalk                     *Definition of 'scCrossTalk' class*

### Description

An S4 class containing the data, meta, and results of inferred cell-cell communications mediated by ligand-receptor interactions.

### Slots

data A list containing the data.

meta A data.frame containing the meta data.

species A character containing the species.

lrdb A data.frame containing expressed ligand and receptor genes.

cci A data.frame containing enriched ligand-receptor interactions.

show,scCrossTalk-method
*Show scCrossTalk object*

## Description

Show scCrossTalk object

## Usage

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

## Arguments

object          scCrossTalk object after `create_scCrossTalk`

## Value

scCrossTalk object

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