# Package 'SpaTalk'

June 9, 2022

**Title** Infer Cell-Cell Communication for Spatial Transcriptomics

**Version** 1.0

**Depends** R (>= 4.0.0), ggalluvial, doParallel

**Description** This package can infer cell-cell communication for spatial transcriptomics.

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.2

**Imports** Seurat (>= 3.0.0),
   methods,
   reshape2,
   Matrix,
   NNLM,
   stringr,
   progress,
   stats,
   ggplot2,
   ggExtra,
   crayon,
   ggpubr,
   grDevices,
   scales,
   scatterpie,
   pheatmap,
   corrplot,
   circlize,
   ggraph,
   ggrepel,
   igraph,
   foreach,
   parallel,
   iterators

**Suggests** rmarkdown,
   knitr,
   prettydoc

**VignetteBuilder** knitr

# R topics documented:

createSpaTalk          *SpaTalk object*

## Description

create SpaTalk object using spatial transcriptomics data.

## Usage

```
createSpaTalk(
  st_data,
  st_meta,
  species,
  if_st_is_sc,
  spot_max_cell,
  celltype = NULL
)
```

## Arguments

| | |
|---|---|
| st_data | A data.frame or matrix or dgCMatrix containing counts of spatial transcriptomics, each column representing a spot or a cell, each row representing a gene. |
| st_meta | A data.frame containing coordinate of spatial transcriptomics with three columns, namely 'spot', 'x', 'y' for spot-based spatial transcriptomics data or 'cell', 'x', 'y' for single-cell spatial transcriptomics data. |
| species | A character meaning species of the spatial transcriptomics data. 'Human' or 'Mouse'. |
| if_st_is_sc | A logical meaning if it is single-cell spatial transcriptomics data. TRUE is FALSE. |
| spot_max_cell | A integer meaning max cell number for each plot to predict. If if_st_sc is FALSE, please determine the spot_max_cell. For 10X (55um), we recommend 30. For Slide-seq, we recommend 1. |
| celltype | A character containing the cell type of ST data. To skip the deconvolution step and directly infer cell-cell communication, please define the cell type. Default is NULL. |

## Value

SpaTalk object

---

| dec_cci | *Decomposing cell-cell communications for spatial transciptomics data* |
|---|---|

---

## Description

Identify the cell-cell communications for single-cell or spot-based spatial transciptomics data with proximal ligand-receptor-target interactions.

## Usage

```
dec_cci(
  object,
  celltype_sender,
  celltype_receiver,
  n_neighbor = 10,
  min_pairs = 5,
  min_pairs_ratio = 0,
  per_num = 1000,
```

```
  pvalue = 0.05,
  co_exp_ratio = 0.1,
  if_doParallel = T,
  use_n_cores = NULL
)
```

### Arguments

| | |
|---|---|
| object | SpaTalk object after [find_lr_path](#). |
| celltype_sender | |
| | Name of celltype_sender. |
| celltype_receiver | |
| | Name of celltype_receiver. |
| n_neighbor | Number of neighbor cells to select as the proximal cell-cell pair. Default is `10`. |
| min_pairs | Min proximal cell-cell pairs between for sending and receiving cell types. Default is 5. |
| min_pairs_ratio | |
| | Min proximal cell-cell pairs ratio between for sending and receiving cell types. Default is `0`. |
| per_num | Number of repeat times for permutation test. Default is `1000`. |
| pvalue | Include the significantly proximal LR pairs with this cutoff of p value from permutation test. Default is `0.05`. |
| co_exp_ratio | Min cell ratio in receiving cells with co-expressed source and target genes for predicting the downstream pathway activity. |
| if_doParallel | Use doParallel. Default is TRUE. |
| use_n_cores | Number of CPU cores to use. Default is all cores - 2. |

### Value

SpaTalk object containing the inferred LR pairs and pathways.

---

| dec_cci_all | *Decomposing cell-cell communications for spatial transciptomics data* |
|---|---|

---

### Description

Identify the all cell-cell communications for single-cell or spot-based spatial transciptomics data with proximal ligand-receptor-target interactions.

### Usage

```
dec_cci_all(
  object,
  n_neighbor = 10,
  min_pairs = 5,
  min_pairs_ratio = 0,
  per_num = 1000,
  pvalue = 0.05,
```

```
  co_exp_ratio = 0.1,
  if_doParallel = T,
  use_n_cores = NULL
)
```

## Arguments

| | |
|---|---|
| object | SpaTalk object after [find_lr_path](#). |
| n_neighbor | Number of neighbor cells to select as the proximal cell-cell pair. Default is `10`. |
| min_pairs | Min proximal cell-cell pairs between for sending and receiving cell types. Default is 5. |
| min_pairs_ratio | |
| | Min proximal cell-cell pairs ratio between for sending and receiving cell types. Default is `0`. |
| per_num | Number of repeat times for permutation test. Default is `1000`. |
| pvalue | Include the significantly proximal LR pairs with this cutoff of p value from permutation test. Default is `0.05`. |
| co_exp_ratio | Min cell ratio in receiving cells with co-expressed source and target genes for predicting the downstream pathway activity. |
| if_doParallel | Use doParallel. Default is TRUE. |
| use_n_cores | Number of CPU cores to use. Default is all cores - 2. |

## Value

SpaTalk object containing the inferred LR pairs and pathways.

---

| dec_celltype | *Decomposing cell type for spatial transcriptomics data* |
|---|---|

---

## Description

Identify the cellular composition for single-cell or spot-based spatial transcriptomics data with non-negative regression.

## Usage

```
dec_celltype(
  object,
  sc_data,
  sc_celltype,
  min_percent = 0.5,
  min_nFeatures = 10,
  if_use_normalize_data = T,
  if_use_hvg = F,
  if_doParallel = T,
  use_n_cores = NULL,
  iter_num = 1000,
  method = 1,
  env = "base",
  anaconda_path = "~/anaconda3",
  dec_result = NULL
)
```

## Arguments

| | |
|---|---|
| object | SpaTalk object generated from createSpaTalk. |
| sc_data | A A data.frame or matrix or dgCMatrix containing counts of single-cell RNA-seq data as the reference, each column representing a cell, each row representing a gene. |
| sc_celltype | A character containing the cell type of the reference single-cell RNA-seq data. |
| min_percent | Min percent to predict new cell type for single-cell st_data or predict new cell for spot-based st_data. Default is 0.5. |
| min_nFeatures | Min number of expressed features/genes for each spot/cell in st_data. Default is 10. |
| if_use_normalize_data | |
| | Whether to use normalized st_data and sc_data with Seurat normalization. Default is TRUE. set it FALSE when the st_data and sc_data are already normalized matrix with other methods. |
| if_use_hvg | Whether to use highly variable genes for non-negative regression. Default is FALSE. |
| if_doParallel | Use doParallel. Default is TRUE. |
| use_n_cores | Number of CPU cores to use. Default is all cores - 2. |
| iter_num | Number of iteration to generate the single-cell data for spot-based data. Default is 1000. |
| method | 1 means using the SpaTalk deconvolution method, 2 means using RCTD, 3 means using Seurat, 4 means using SPOTlight, 5 means using deconvSeq, 6 means using stereoscope, 7 means using cell2location |
| env | When method set to 6, namely use stereoscope python package to deconvolute, please define the python environment of installed stereoscope. Default is the 'base' environment. Anaconda is recommended. |
| anaconda_path | When use python package, please define the path to anaconda, default is ~/anaconda3 |
| dec_result | A matrix of deconvolution result from other upcoming methods, row represents spots or cells, column represents cell types of scRNA-seq reference. See demo_dec_result |

## Value

SpaTalk object containing the decomposing results.

---

demo_dec_result            *Demo data of dec_result*

---

## Description

Demo data of dec_result

## Usage

```
demo_dec_result()
```

## Details

dec_result used in [dec_celltype](#) must be a matrix object, each row representing a spot, each column representing a cell type.

## Value

A matrix.

## Examples

```
dec_result_demo <- demo_dec_result()
```

---

demo_geneinfo                    *Demo data of geneinfo*

---

## Description

Demo data of geneinfo

## Usage

```
demo_geneinfo()
```

## Details

geneinfo used in [dec_celltype](#) 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 used in [dec_cci](#) must be a data.frame object with three columns, namely 'ligand', 'receptor', 'species'.

## Value

A data.frame.

### Examples

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

---

demo_pathways　　　　　　*Demo data of pathways*

---

### Description

Demo data of pathways

### Usage

```
demo_pathways()
```

### Details

pathways used in `dec_cci` must be a data.frame object with seven columns, namely `'src'`, `'dest'`, `'pathway'`, `'source'`, `'type'`, `'src_tf'`, `'dest_tf'`, `'species'`.

### Value

A data.frame.

### 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 used in `dec_celltype` must be a matrix object, each column representing a cell, each row representing a gene.

### Value

A matrix.

### Examples

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

---

demo_st_data                     *Demo data of st_data*

---

### Description

Demo data of st_data.

### Usage

```
demo_st_data()
```

### Details

st_data used in [dec_celltype](#) must be a `matrix` object, each column representing a spot, each row representing a gene.

### Value

A matrix.

### Examples

```
st_data_demo <- demo_st_data()
```

---

demo_st_meta                     *Demo data of st_meta*

---

### Description

Demo data of st_meta

### Usage

```
demo_st_meta()
```

### Details

st_meta used in [dec_celltype](#) must be a `data.frame` object with three columns, namely `'spot'`, `'x'`, `'y'` for spot-based spatial transcriptomics data.

### Value

A data.frame.

### Examples

```
st_meta_demo <- demo_st_meta()
```

---

demo_st_sc_data                    *Demo data of single-cell st_data*

---

### Description

Demo data of single-cell st_data.

### Usage

```
demo_st_sc_data()
```

### Details

st_data used in [dec_celltype](#) must be a matrix object, each column representing a cell, each row representing a gene.

### Value

A matrix.

### Examples

```
st_data_demo <- demo_st_sc_data()
```

---

demo_st_sc_meta                    *Demo data of st_sc_meta*

---

### Description

Demo data of st_sc_meta

### Usage

```
demo_st_sc_meta()
```

### Details

st_sc_meta used in [dec_celltype](#) must be a data.frame object with three columns, namely 'cell', 'x', 'y' for single-cell spatial transcriptomics data.

### Value

A data.frame.

### Examples

```
st_sc_meta_demo <- demo_st_sc_meta()
```

---

find_lr_path *Find lrpairs and pathways*

---

### Description

Find `lrpairs` and `pathways` with receptors having downstream targets and transcriptional factors.

### Usage

```
find_lr_path(
  object,
  lrpairs,
  pathways,
  max_hop = NULL,
  if_doParallel = T,
  use_n_cores = NULL
)
```

### Arguments

| | |
|---|---|
| `object` | SpaTalk object generated from [dec_celltype](). |
| `lrpairs` | A data.frame of the system data containing ligand-receptor pairs of `'Human'` and `'Mouse'` from CellTalkDB. |
| `pathways` | A data.frame of the system data containing gene-gene interactions and pathways from KEGG and Reactome as well as the information of transcriptional factors. |
| `max_hop` | Max hop from the receptor to the downstream target transcriptional factor to find for receiving cells. Default is 3 for human and 4 for mouse. |
| `if_doParallel` | Use doParallel. Default is TRUE. |
| `use_n_cores` | Number of CPU cores to use. Default is all cores - 2. |

### Value

SpaTalk object containing the filtered lrpairs and pathways.

---

geneinfo *geneinfo*

---

### Description

Gene symbols of `'Human'` and `'Mouse'` updated on June 30, 2021 for revising count matrix.

### Usage

```
geneinfo
```

### Format

An object of class `data.frame` with 250934 rows and 3 columns.

**Source**

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

---

generate_spot | *Generate pseudo spot st_data*

---

**Description**

Generate pseudo spot st_data with single-cell st_data

**Usage**

```
generate_spot(st_data, st_meta, x_min, x_res, x_max, y_min, y_res, y_max)
```

**Arguments**

| | |
|---|---|
| st_data | A data.frame or matrix or dgCMatrix containing counts of spatial transcriptomics, each column representing a cell, each row representing a gene. |
| st_meta | A data.frame containing coordinate of spatial transcriptomics with three columns, `'cell'`, `'x'`, `'y'`, and `celltype`. |
| x_min | Min value of x axis. |
| x_res | Resolution of x coordinate. |
| x_max | Max value of x axis. |
| y_min | Min value of y axis. |
| y_res | Resolution of y coordinate. |
| y_max | Max value of y axis. |

**Value**

A list of spot st_data and st_meta

---

get_lr_path | *Get LR and downstream pathways*

---

**Description**

Get LR and downstream pathways and get p value of receptor-related pathways with LR-target genes by the Fisher-exact test.

**Usage**

```
get_lr_path(
  object,
  celltype_sender,
  celltype_receiver,
  ligand,
  receptor,
  min_gene_num = 5
)
```

## Arguments

| | |
|---|---|
| `object` | SpaTalk object generated from [`dec_cci`](#). |
| `celltype_sender` | |
| | Name of celltype_sender. |
| `celltype_receiver` | |
| | Name of celltype_receiver. |
| `ligand` | Name of ligand from celltype_sender. |
| `receptor` | Name of receptor from celltype_receiver. |
| `min_gene_num` | Min genes number for each pathway. |

## Value

A list containing two data.frame. One is LR and downstream pathways, another is the p value of receptor-related pathways with LR-target genes.

---

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

---

## Description

Ligand-receptor pairs of `'Human'` and `'Mouse'` containing 3398 human and 2033 mouse pairs.

## Usage

```
lrpairs
```

## Format

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

## Source

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

---

| `pathways` | *pathways* |
|---|---|

---

## Description

KEGG pathways and Reactomes of `'Human'` and `'Mouse'` for intra-cellular genes and transcription factors.

## Usage

```
pathways
```

## Format

An object of class `data.frame` with 669197 rows and 8 columns.

## Source

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

<https://reactome.org/>

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

---

plot_ccdist                        *Plot cell-cell distribution*

---

## Description

Point plot with spatial distribution of celltype_sender and celltype_receiver

## Usage

```
plot_ccdist(
  object,
  celltype_sender,
  celltype_receiver,
  color = NULL,
  size = 1,
  if_plot_others = T,
  if_plot_density = T,
  if_plot_edge = T,
  if_show_arrow = T,
  arrow_length = 0.05,
  plot_cells = NULL
)
```

## Arguments

| | |
|---|---|
| object | SpaTalk object generated from [dec_celltype](). |
| celltype_sender | |
| | Name of celltype_sender. |
| celltype_receiver | |
| | Name of celltype_receiver. |
| color | Color for celltype_sender, celltype_receiver, and others. Three values. |
| size | Point size. Default is 1. |
| if_plot_others | Whether to plot others. Default is TRUE. |
| if_plot_density | |
| | Whether to plot marginal density plots. Default is TRUE. |
| if_plot_edge | Whether to plot edge between neighbors. Default is TRUE. |
| if_show_arrow | Whether to show the arrow of the plotted edge. Default is TRUE. |
| arrow_length | Arrow length. |
| plot_cells | Which cells to plot. Default is all cells. Input a character vector of cell names to plot. |

plot_cci_lrpairs            *Plot LR pairs*

## Description

Heatmap with LR pairs of celltype_sender and celltype_receiver

## Usage

```
plot_cci_lrpairs(
  object,
  celltype_sender,
  celltype_receiver,
  top_lrpairs = 20,
  color = NULL,
  border_color = "black",
  type = "sig",
  fontsize_number = 5,
  number_color = "black",
  color_low = NULL,
  color_high = NULL
)
```

## Arguments

| | |
|---|---|
| object | SpaTalk object generated from [dec_cci](). |
| celltype_sender | |
| | Name of celltype_sender. |
| celltype_receiver | |
| | Name of celltype_receiver. |
| top_lrpairs | Number of top lrpairs for plotting. Default is 20. |
| color | Color for the cells in heatmap. |
| border_color | color of cell borders on heatmap, use NA if no border should be drawn. |
| type | Set 'sig' to plot significant LR pairs or set 'number' to plot the number of spatial LR interactions. |
| fontsize_number | |
| | fontsize of the numbers displayed in cells. |
| number_color | color of the text. |
| color_low | For 'number' type, define the color for the lowest value. |
| color_high | For 'number' type, define the color for the highest value. |

| plot_lrpair | *Plot LR pair* |
|---|---|

### Description

Point plot with LR pair from celltype_sender to celltype_receiver

### Usage

```
plot_lrpair(
  object,
  celltype_sender,
  celltype_receiver,
  ligand,
  receptor,
  color = NULL,
  size = 1,
  if_plot_density = T,
  if_plot_edge = T,
  if_show_arrow = T,
  arrow_length = 0.05,
  plot_cells = NULL
)
```

### Arguments

| | |
|---|---|
| object | SpaTalk object generated from [dec_celltype](dec_celltype). |
| celltype_sender | |
| | Name of celltype_sender. |
| celltype_receiver | |
| | Name of celltype_receiver. |
| ligand | Name of ligand from celltype_sender. |
| receptor | Name of receptor from celltype_receiver. |
| color | Color for ligand, receptor, and others. Three values. |
| size | Point size. Default is 1. |
| if_plot_density | |
| | Whether to plot marginal density plots. Default is TRUE. |
| if_plot_edge | Whether to plot edge between neighbors. Default is TRUE. |
| if_show_arrow | Whether to show the arrow of the plotted edge. Default is TRUE. |
| arrow_length | Arrow length. |
| plot_cells | Which cells to plot. Default is all cells. Input a character vector of cell names to plot. |

---

plot_lrpair_vln *Plot spatial distance of LR pair with vlnplot*

---

### Description

Violin plot spatial distance of LR pair between expressed senders and receivers and between expressed cell-cell pairs.

### Usage

```
plot_lrpair_vln(
  object,
  celltype_sender,
  celltype_receiver,
  ligand,
  receptor,
  vln_color = NULL,
  if_plot_boxplot = T,
  box_width = 0.2
)
```

### Arguments

| | |
|---|---|
| object | SpaTalk object generated from [dec_celltype](#). |
| celltype_sender | |
| | Name of celltype_sender. |
| celltype_receiver | |
| | Name of celltype_receiver. |
| ligand | Name of ligand from celltype_sender. |
| receptor | Name of receptor from celltype_receiver. |
| vln_color | Color for violins. Two values. |
| if_plot_boxplot | |
| | Whether to plot boxplot. Default is TRUE. |
| box_width | Box width. Default is 0.2. |

---

plot_lr_path *Plot LR and downstream pathways*

---

### Description

Plot network with LR and downstream pathways

**Usage**

```
plot_lr_path(
  object,
  celltype_sender,
  celltype_receiver,
  ligand,
  receptor,
  color = NULL,
  size = 5,
  arrow_length = 0.1
)
```

**Arguments**

| | |
|---|---|
| object | SpaTalk object generated from [dec_cci](#). |
| celltype_sender | |
| | Name of celltype_sender. |
| celltype_receiver | |
| | Name of celltype_receiver. |
| ligand | Name of ligand from celltype_sender. |
| receptor | Name of receptor from celltype_receiver. |
| color | Color for points Two values. |
| size | Size of points. |
| arrow_length | Arrow length. |

---

| plot_path2gene | *River plot of significantly activated pathways and related downstream genes of receptors.* |
|---|---|

---

**Description**

River plot of significantly activated pathways and related downstream genes of receptors.

**Usage**

```
plot_path2gene(
  object,
  celltype_sender,
  celltype_receiver,
  ligand,
  receptor,
  min_gene_num = 5,
  pvalue = 0.5,
  color = NULL,
  color_flow = "blue"
)
```

## Arguments

| | |
|---|---|
| `object` | SpaTalk object generated from [`dec_cci`](#). |
| `celltype_sender` | |
| | Name of celltype_sender. |
| `celltype_receiver` | |
| | Name of celltype_receiver. |
| `ligand` | Name of ligand from celltype_sender. |
| `receptor` | Name of receptor from celltype_receiver. |
| `min_gene_num` | Min genes number for each pathway. |
| `pvalue` | P value of the Fisher-exact test. |
| `color` | Color of pathways and genes. Two values. |
| `color_flow` | Color of the flow. |

---

`plot_st_celltype`  *Plot spatial distribution of a single cell type*

---

## Description

Ponit plot with spatial distribution of a single predicted cell type for transcriptomics data

## Usage

```
plot_st_celltype(
  object,
  celltype,
  size = 1,
  color_celltype = "blue",
  color_others = "grey"
)
```

## Arguments

| | |
|---|---|
| `object` | SpaTalk object generated from [`dec_celltype`](#). |
| `celltype` | Name of cell type in the `sc_celltype`. |
| `size` | Point size. Default is 1. |
| `color_celltype` | Color for the celltype of interest. |
| `color_others` | Color for the others. |

---

plot_st_celltype_all    *Plot spatial distribution of all cell types*

---

### Description

Plot spatial distribution of all predicted cell types for transcriptomics data

### Usage

```
plot_st_celltype_all(object, size = 1, color = NULL)
```

### Arguments

| | |
|---|---|
| object | SpaTalk object generated from [dec_celltype](). |
| size | Point size. Default is 1. |
| color | Color for all predicted cell types. |

---

plot_st_celltype_density

*Plot spatial density of a single cell type*

---

### Description

Plot spatial density of a single predicted cell type for transcriptomics data

### Usage

```
plot_st_celltype_density(
  object,
  celltype,
  type,
  if_plot_point = T,
  point_color = NULL,
  point_size = 1,
  color_low = "grey",
  color_mid = NULL,
  color_high = "blue",
  color_midpoint = NULL,
  size = 1
)
```

### Arguments

| | |
|---|---|
| object | SpaTalk object generated from [dec_celltype](). |
| celltype | Name of cell type in the sc_celltype. |
| type | Select 'contour' or 'raster'. |
| if_plot_point | Whether to plot points when type is 'contour'. |
| point_color | Point color. |

| | |
|---|---|
| point_size | Point size. Default is 1. |
| color_low | Color for the lowest value. |
| color_mid | Color for the middle value for using scale_color_gradient2. Default is NULL. |
| color_high | Color for the highest value. |
| color_midpoint | Value for the middle scale. Default is NULL. |
| size | Line size when type is 'contour'. Default is 1. |

---

plot_st_celltype_percent

*Plot spatial distribution of a single cell type percent*

---

### Description

Plot spatial distribution of a single predicted cell type percent for transcriptomics data

### Usage

```
plot_st_celltype_percent(
  object,
  celltype,
  size = 1,
  color_low = NULL,
  color_mid = NULL,
  color_high = NULL,
  color_midpoint = NULL
)
```

### Arguments

| | |
|---|---|
| object | SpaTalk object generated from [dec_celltype](). |
| celltype | Name of cell type in the sc_celltype. |
| size | Point size. Default is 1. |
| color_low | Color for the lowest value. |
| color_mid | Color for the middle value for using scale_color_gradient2. Default is NULL. |
| color_high | Color for the highest value. |
| color_midpoint | Value for the middle scale. Default is NULL. |

---

plot_st_cor_heatmap         *Plot heatpmap of correlation between marker genes and cell types*

---

### Description

Plot heatpmap of correlation between the expression of marker genes and the predicted score of cell types among all spatial cells or spots.

### Usage

```
plot_st_cor_heatmap(
  object,
  marker_genes,
  celltypes,
  color_low = NULL,
  color_mid = NULL,
  color_high = NULL,
  scale = "none",
  if_show_top = T,
  top_direction = "row",
  border_color = NA
)
```

### Arguments

| | |
|---|---|
| object | SpaTalk object generated from [dec_celltype](). |
| marker_genes | A character containing the known marker genes to plot, provide at least two marker genes of interest. |
| celltypes | A character containing name of cell type in the sc_celltype. Default is to plot all cell types. |
| color_low | Color for the lowest value. |
| color_mid | Color for the middle value for using scale_color_gradient2. Default is NULL. |
| color_high | Color for the highest value. |
| scale | Character indicating if the values should be centered and scaled in either the row direction or the column direction, or none. Corresponding values are 'row', 'column' and 'none'. |
| if_show_top | Whether to plot a symbol to the highest value across rows or columns. Default is TRUE. |
| top_direction | Direction to identify the highest value, select 'row' or 'column'. |
| border_color | Color of the cell border. Default is 'NA'. |

---

plot_st_gene              *Plot spatial distribution of gene*

---

### Description

Point plot with spatial distribution of a gene for transcriptomics data

### Usage

```
plot_st_gene(
  object,
  gene,
  size = 1,
  color_low = "grey",
  color_mid = NULL,
  color_high = "blue",
  color_midpoint = NULL,
  if_use_newmeta = T,
  celltype = NULL,
  if_plot_others = T
)
```

### Arguments

| | |
|---|---|
| object | SpaTalk object generated from `dec_celltype`. |
| gene | Symbol of gene, e.g., 'AKT1'. |
| size | Point size. Default is 1. |
| color_low | Color for the lowest value. |
| color_mid | Color for the middle value for using `scale_color_gradient2`. Default is NULL. |
| color_high | Color for the highest value. |
| color_midpoint | Value for the middle scale. Default is NULL. |
| if_use_newmeta | Whether to use newmeta o plot the spatial distribution of gene after `dec_celltype` for spot-based data. Default is TRUE. |
| celltype | gene in which celltype to plot. Default is NULL. Set N`if_use_newmeta` TRUE when using this parameter. |
| if_plot_others | Whether to plot other cells when to use defined `celltype`. |

### Details

Please set `if_use_newmeta` as FALSE to plot the spatial distribution of gene before `dec_celltype` for spot-based data.

---

plot_st_pie *Plot spatial transcriptomics data*

---

### Description

Plot scatterpie for spatial transcriptomics data

### Usage

```
plot_st_pie(object, pie_scale = 1, xy_ratio = 1, color = NULL)
```

### Arguments

| | |
|---|---|
| object | SpaTalk object generated from `dec_celltype`. |
| pie_scale | Scale of each pie to plot. Default is 1. |
| xy_ratio | Ratio of y and x coordinates. Default is 1. |
| color | Filled of colors for pie plot, length of `color` must be equal to the number of unique cell types in `sc_celltype`. |

---

plot_st_pie_generate *Plot spatial transcriptomics data*

---

### Description

Plot scatterpie for spot-based ST data

### Usage

```
plot_st_pie_generate(st_meta, pie_scale = 1, xy_ratio = 1, color = NULL)
```

### Arguments

| | |
|---|---|
| st_meta | st_meta generated from `generate_spot` |
| pie_scale | Scale of each pie to plot. Default is 1. |
| xy_ratio | Ratio of y and x coordinates. Default is 1. |
| color | Filled of colors for pie plot, length of `color` must be equal to the number of unique cell types in `sc_celltype`. |

---

rev_gene  *Pre-processing step: revising gene symbols*

---

## Description

Revise genes according to NCBI Gene symbols updated in June 30, 2021 for count matrix, user-custom lrpairs data.frame, and user-custom pathways data.frame.

## Usage

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

## Arguments

| | |
|---|---|
| data | A data.frame or matrix or dgCMatrix containing count data each column representing a spot or a cell, each row representing a gene; Or a data.frame containing ligand-receptor pairs; Or a data.frame containing gene-gene interactions and pathways from KEGG and Reactome as well as the information of transcriptional factors. |
| data_type | A character to define the type of data, select 'count' for the data matrix, 'lrpairs' for the data.frame containing lrpairs, 'pathways' for the data.frame containing pathways. |
| species | Species of the data.'Human' or 'Mouse'. |
| geneinfo | A data.frame of the system data containing gene symbols of 'Human' and 'Mouse' updated on June 30, 2021 for revising count matrix. |

## Value

A new matrix or data.frame.

---

set_expected_cell  *Set the expected cell*

---

## Description

Set the expected cell in SpaTalk object

## Usage

```
set_expected_cell(object, value)
```

## Arguments

| | |
|---|---|
| object | SpaTalk object |
| value | Th number of expected cell for each spot, must be equal to the spot number. |

## Value

SpaTalk object

| SpaTalk | *Definition of 'SpaTalk' class* |
|---|---|

**Description**

An S4 class containing the data, meta, and results of inferred cell type compositions, LR pairs, and pathways.

**Slots**

data A list containing the raw and normalized data.

meta A list containing the raw and new meta data.

para A list containing the parameters.

coef A matrix containing the results of deconvolution.

cellpair A list containing the cell-cell pairs based on the spatial distance.

dist A matrix containing the Euclidean distance among cells.

lrpair A data frame containing the inferred LR pairs.

tf A data frame containing the TFs of receptors.

lr_path A list containing the lrpairs and pathways.

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