

Package ‘SpaTalk’

May 26, 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:

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| | |
|---------------|-----------------------|
| createSpaTalk | <i>SpaTalk object</i> |
|---------------|-----------------------|

Description

create SpaTalk object using spatial transcriptomics data.

Usage

```
createSpaTalk(st_data, st_meta, species, if_st_is_sc, spot_max_cell)
```

Arguments

| | |
|---------------|---|
| st_data | A data.frame or matrix or dgCMatrx 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. |

Value

SpaTalk object

| | |
|---------|--|
| dec_cci | <i>Decomposing cell-cell communications for spatial transcriptomics data</i> |
|---------|--|

Description

Identify the cell-cell communications for single-cell or spot-based spatial transcriptomics 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 | <i>Decomposing cell-cell communications for spatial transcriptomics data</i> |
|-------------|--|

Description

Identify the all cell-cell communications for single-cell or spot-based spatial transcriptomics 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 | <i>Decomposing cell type for spatial transcriptomics data</i> |
|--------------|---|

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 dgCMatix 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 | <i>Demo data of dec_result</i> |
|-----------------|--------------------------------|

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

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 | <i>Demo data of lrpairs</i> |
|--------------|-----------------------------|

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 | <i>Demo data of pathways</i> |
|---------------|------------------------------|

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

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 | <i>Demo data of st_data</i> |
|--------------|-----------------------------|

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 | <i>Demo data of st_meta</i> |
|--------------|-----------------------------|

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 | <i>Demo data of single-cell st_data</i> |
|-----------------|---|

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 | <i>Demo data of st_sc_meta</i> |
|-----------------|--------------------------------|

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 | <i>Find lrpairs and pathways</i> |
|--------------|----------------------------------|

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

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 | <i>Generate pseudo spot st_data</i> |
|---------------|-------------------------------------|

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 dgCMatix 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 | <i>Get LR and downstream pathways</i> |
|-------------|---------------------------------------|

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 | <i>lrpairs</i> |
|---------|----------------|

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 | <i>pathways</i> |
|----------|-----------------|

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 | <i>Plot cell-cell distribution</i> |
|-------------|------------------------------------|

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 | <i>Plot LR pairs</i> |
|------------------|----------------------|

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 = NULL,
  fontsize_number = 1,
  number_color = "black"
)
```

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. |

| | |
|-------------|---------------------|
| plot_lrpair | <i>Plot LR pair</i> |
|-------------|---------------------|

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 . |
| 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 | <i>Plot LR and downstream pathways</i> |
|--------------|--|

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 | <i>River plot of significantly activated pathways and related downstream genes of receptors.</i> |
|----------------|--|

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 | <i>Plot spatial distribution of a single cell type</i> |
|------------------|--|

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 | <i>Plot spatial distribution of all cell types</i> |
|----------------------|--|

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 heatmap of correlation between marker genes and cell types

Description

Plot heatmap 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 | <i>Plot spatial distribution of gene</i> |
|--------------|--|

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 <code>scale_color_gradient2</code> . 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 <code>Nif_use_newmeta</code> 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 | <i>Plot spatial transcriptomics data</i> |
|-------------|--|

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 <code>sc_celltype</code> . |

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 matrix 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 | <i>Set the expected cell</i> |
|-------------------|------------------------------|

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 | <i>Definition of 'SpaTalk' class</i> |
|---------|--------------------------------------|

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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