Package: SpaTalk (via r-universe)

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Title Spatially Resolved Cell-Cell Communication Inference for Spatial Transcriptomics

Version 2.0.0

Depends R (>= 4.0.0), ggalluvial, doParallel

Description Infers spatially resolved cell-cell communications from spatial transcriptomics data using graph network and knowledge graph approaches. Supports both single-cell resolution and spot-based spatial transcriptomics platforms. Provides cell type deconvolution, ligand-receptor interaction analysis, and downstream pathway inference.

URL https://zaoqu-liu.github.io/SpaTalk/, https://github.com/Zaoqu-Liu/SpaTalk

BugReports https://github.com/Zaoqu-Liu/SpaTalk/issues

License GPL (>= 3)

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Use Rcpp for fast permutation if available

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Description

Use Rcpp for fast random walk if available

Usage

```
.use_cpp_random_walk()
```

cpp_batch_coexp *Calculate co-expression for multiple gene pairs*

Description

Calculate co-expression for multiple gene pairs

Usage

```
cpp_batch_coexp(st_data_mat, src_genes, dest_genes, cell_indices)
```

Arguments

st_data_mat	Expression matrix
src_genes	Source gene indices (1-based)
dest_genes	Destination gene indices (1-based)
cell_indices	Cell indices to use (1-based)

Value

Co-expression ratios

cpp_batch_cor *Calculate correlation between a vector and matrix columns*

Description

Calculate correlation between a vector and matrix columns

Usage

```
cpp_batch_cor(vec1, mat)
```

Arguments

vec1	Reference vector
mat	Matrix where each column is compared to vec1

Value

Pearson correlation coefficients

cpp_coexp_fast *Calculate co-expression ratios*

Description

Calculate co-expression ratios

Usage

```
cpp_coexp_fast(ligand_expr, receptor_expr)
```

Arguments

ligand_expr	Ligand expression matrix (n_genes x n_cells)
receptor_expr	Receptor expression matrix (n_genes x n_cells)

Value

Co-expression ratios

cpp_fast_dist *Calculate Euclidean distance matrix*

Description

Calculate Euclidean distance matrix

Usage

```
cpp_fast_dist(x, y)
```

Arguments

x	X coordinates
y	Y coordinates

Value

Distance matrix

cpp_fast_sampling *Sample cells to reconstruct spot expression*

Description

Sample cells to reconstruct spot expression

Usage

```
cpp_fast_sampling(
  spot_ndata,
  sc_ndata_mat,
  cell_indices_by_type,
  spot_celltypes,
  iter_num = 200L,
  tolerance = 0.001,
  seed = 123L
)
```

Arguments

spot_ndata	Spot expression vector
sc_ndata_mat	Single-cell expression matrix
cell_indices_by_type	List of cell indices for each cell type
spot_celltypes	Cell types to sample for this spot
iter_num	Maximum number of iterations
tolerance	Convergence tolerance (unused, kept for API compatibility)
seed	Random seed for reproducibility

Value

Best cell combination and correlation

cpp_knn *Find K nearest neighbors*

Description

Find K nearest neighbors

Usage

```
cpp_knn(dist_mat, query_idx, k)
```

Arguments

dist_mat	Distance matrix
query_idx	Query index (0-based)
k	Number of neighbors

Value

Neighbor indices (0-based)

---

cpp_permutation_test *Permutation test for LR co-expression significance*

Description

Permutation test for LR co-expression significance

Usage

```
cpp_permutation_test(
  st_data_mat,
  ligand_genes,
  receptor_genes,
  sender_cells,
  receiver_cells,
  per_num = 1000L,
  seed = 123L
)
```

Arguments

st_data_mat	Expression matrix
ligand_genes	Ligand gene indices (1-based R indexing)
receptor_genes	Receptor gene indices (1-based R indexing)
sender_cells	Sender cell indices (1-based)
receiver_cells	Receiver cell indices (1-based)
per_num	Number of permutations
seed	Random seed for reproducibility

Value

List with real_ratios and pvalues

cpp_random_walk *Random walk on gene-gene interaction network*

Description

Random walk on gene-gene interaction network

Usage

```
cpp_random_walk(
  ggi_src,
  ggi_dest,
  receptor_name,
  tf_names,
  n_walks = 10000L,
  max_hop = 10L,
  seed = 123L
)
```

Arguments

ggi_src	Source gene names
ggi_dest	Destination gene names
receptor_name	Starting receptor name
tf_names	TF names to score
n_walks	Number of random walks
max_hop	Maximum number of hops per walk
seed	Random seed for reproducibility

Value

TF visit frequency scores

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_retain_other_genes = 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_retain_other_genes	Whether to retain other genes which are not overlapped between sc_data and st_data when reconstructing the single-cell ST data. Default is FALSE. Set it TRUE to obtain the constructed single-cell ST data with genes consistent with that in sc_data.
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. When method set to 7, namely use cell2location python package to deconvolute, please install cell2location to "base" environment.
anaconda_path	When using stereoscope, please define the env parameter as well as 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 LRI pairs or set 'number' to plot the number of spatial LRI pairs.
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_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_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.
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_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 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

show,SpaTalk-method *Show SpaTalk object*

Description

Show SpaTalk object

Usage

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

Arguments

object	A SpaTalk object

Value

Invisible NULL, prints summary information

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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