

Package ‘STDistance’

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Title Spatial Transcriptomics Distance Calculation and Visualization

Version 0.6.4

Description Analysis of spatial relationships between cell types in spatial transcriptomics data. Spatial proximity is a critical factor in cell-cell communication. The package calculates nearest neighbor distances between specified cell types and provides visualization tools to explore spatial patterns. Applications include studying cell-cell interactions, immune microenvironment characterization, and spatial organization of tissues.

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Encoding UTF-8

RoxygenNote 7.3.2

Depends R (>= 4.0.0)

Imports dplyr, ggplot2, Hmisc, scales, stats, RColorBrewer, tidyr,

Suggests testthat, knitr, rmarkdown

LazyData true

VignetteBuilder knitr

NeedsCompilation no

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calculate_correlations	
	<i>Perform correlation analysis between spatial features and distance metrics with visualization</i>

Description

Perform correlation analysis between spatial features and distance metrics with visualization

Usage

```
calculate_correlations(  
  spatial_data,  
  distance_results,  
  spatial_feature,  
  distance_metric,  
  method = "pearson",  
  plot = TRUE,  
  plot_title = NULL  
)
```

Arguments

- spatial_data Spatial data containing feature columns and Newbarcode identifier
- distance_results Distance results containing distance metrics and Newbarcode identifier
- spatial_feature Column name from spatial_data to use for correlation (e.g., "gen2_SPLIz_numeric")
- distance_metric Column name from distance_results to use for correlation (e.g., "Epithelial_cells_A")
- method Correlation method ("pearson", "spearman", "kendall")
- plot Logical, whether to generate a scatter plot
- plot_title Title for the scatter plot (optional)

Value

A list containing correlation results and ggplot object (if plot=TRUE)

Examples

```
calculate_correlations(spatial_data = posi,
                      distance_results = distance_results,
                      spatial_feature = "gen2_SPLIz_numeric",
                      distance_metric = "Epithelial_cells_A",
                      method = "pearson",
                      plot = TRUE,
                      plot_title = "Correlation between Gene Expression and Distance")
```

```
calculate_nearest_distances
```

Calculate nearest distances between cell types

Description

Calculate nearest distances between cell types

Usage

```
calculate_nearest_distances(
  spatial_data,
  reference_type,
  target_types,
  x_col = "pxl_row_in_fullres",
  y_col = "pxl_col_in_fullres",
  id_col = "barcode",
  type_col = "Epi_strom"
)
```

Arguments

<code>spatial_data</code>	A data frame containing spatial coordinates and cell type info
<code>reference_type</code>	The reference cell type to calculate distances from
<code>target_types</code>	Vector of target cell types to calculate distances to
<code>x_col</code>	Column name for x-coordinates
<code>y_col</code>	Column name for y-coordinates
<code>id_col</code>	Column name for cell identifiers
<code>type_col</code>	Column name for cell type information

Value

A data frame with nearest distances for each reference cell

Examples

```
calculate_nearest_distances(posi, reference_type="Macrophage",
                           target_types=c("Epithelial_cells_A", "Epithelial_cells_B",
                                           "Epithelial_cells_C", "Epithelial_cells_D"),
                           id_col = "Newbarcode",
                           type_col = "celltype_ABCDipi")
```

distance_results	<i>distance_results</i>
------------------	-------------------------

Description

A data frame with nearest distances for each reference cell

Usage

```
data("distance_results")
```

Format

A data frame with 18 observations on the following 5 variables.

Newbarcode a character vector

Epithelial_cells_A a numeric vector

Epithelial_cells_B a numeric vector

Epithelial_cells_C a numeric vector

Epithelial_cells_D a numeric vector

Details

A data frame with nearest distances for each reference cell.

Source

This study.

References

Wang, Z., Yang, L., Yang, S., Li, G., Xu, M., Kong, B., Shao, C., & Liu, Z. (2025). Isoform switch of CD47 provokes macrophage-mediated pyroptosis in ovarian cancer. bioRxiv, 2025.2004.2017.649282. <https://doi.org/10.1101/2025.04.17.649282>

Examples

```
data(distance_results)
## maybe str(distance_results) ; plot(distance_results) ...
```

metadata	<i>Metadata</i>
----------	-----------------

Description

Metadata of a Seurat Object.

Usage

```
data("metadata")
```

Format

A data frame with 293 observations on the following 9 variables.

- orig.ident a character vector
- nCount_Spatial a numeric vector
- nFeature_Spatial a numeric vector
- nCount_SCT a numeric vector
- nFeature_SCT a numeric vector
- integrated_snn_res.0.8 a numeric vector
- seurat_clusters a numeric vector
- celltype_ABCDepi a character vector
- gen2_SPLIz_numeric a numeric vector

Details

Metadata dataframe can be exported from Seurat Object as follows. The Seurat Object should be fully annotated and the metadata dataframe should included: orig.ident, celltype, the target gene expression, splicing index (SpliZ), etc.

Source

This study.

References

Wang, Z., Yang, L., Yang, S., Li, G., Xu, M., Kong, B., Shao, C., & Liu, Z. (2025). Isoform switch of CD47 provokes macrophage-mediated pyroptosis in ovarian cancer. bioRxiv, 2025.2004.2017.649282. <https://doi.org/10.1101/2025.04.17.649282>

Examples

```
data(metadata)
## maybe str(metadata) ; plot(metadata) ...
```

normalize_spatial	<i>Normalize spatial coordinates</i>
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Description

Normalize spatial coordinates

Usage

```
normalize_spatial(  
  data,  
  sample_col = "Sample",  
  x_col = "pxl_row_in_fullres",  
  y_col = "pxl_col_in_fullres",  
  min_value = 1,  
  max_value = 10000  
)
```

Arguments

data	A data frame containing spatial coordinates
sample_col	Column name specifying sample IDs
x_col	Column name for x-coordinates
y_col	Column name for y-coordinates
min_value	Minimum value for normalization range
max_value	Maximum value for normalization range

Value

A data frame with normalized coordinates

Examples

```
tissue_posi_normalized<-normalize_spatial(tissue_posi)
```

plot_distance_boxplot	<i>Visualize Nearest Neighbor Distances with Boxplot and Mean ± SEM</i>
-----------------------	---

Description

Creates a boxplot visualization of distance metrics with overlaid mean points and SEM error bars. Suitable for comparing multiple groups with potentially skewed distributions.

Usage

```
plot_distance_boxplot(
  distance_result,
  id_col = "barcode",
  show_points = FALSE,
  y_scale = c("original", "log10"),
  palette = "Set2"
)
```

Arguments

distance_result	A data.frame generated by calculate_nearest_distances(), containing distance measurements with columns: id_col + target_types.
id_col	Name of the column containing cell IDs (default: "barcode").
show_points	Logical, whether to overlay individual data points (default: FALSE).
y_scale	Method for y-axis scaling: "original" or "log10" (default: "original").
palette	Color palette name from RColorBrewer (default: "Set2").

Value

A ggplot2 object. Additional customization can be done using ggplot2 functions.

Examples

```
plot_distance_boxplot(distance_results, id_col = "Newbarcode")
```

plot_radial_distance *Radial Distance Visualization with Collision Avoidance*

Description

Creates a radial plot with automatic label placement to prevent overlaps between nodes and text labels.

Usage

```
plot_radial_distance(
  distance_result,
  reference_type,
  id_col = "barcode",
  scale_radius = 1,
  show_labels = TRUE,
  palette = "Set2",
  label_padding = 0.15,
  center_label_expansion = 1.5
)
```

Arguments

- `distance_result` Data.frame from `calculate_nearest_distances()`
- `reference_type` Name of the reference cell type (center node)
- `id_col` Name of ID column (default: "barcode")
- `scale_radius` Scaling factor for layout (default: 1)
- `show_labels` Whether to show distance labels (default: TRUE)
- `palette` Color palette name (default: "Set2")
- `label_padding` Radial padding for labels (default: 0.15)
- `center_label_expansion` Center expansion for labels (default: 1.5)

Value

A `ggplot2` object

Examples

```
plot_radial_distance(distance_results,id_col = "Newbarcode",
                      reference_type = "Macrophages",label_padding = 0.3,
                      show_labels = TRUE,palette = "Dark2")
```

<i>posi</i>	<i>posi</i>
-------------	-------------

Description

Merged spatial location and metadata information.

Usage

```
data("posi")
```

Format

A data frame with 293 observations on the following 18 variables.

`Newbarcode` a character vector

`barcode` a character vector

`in_tissue` a numeric vector

`array_row` a numeric vector

`array_col` a numeric vector

`pxl_row_in_fullres` a numeric vector

`pxl_col_in_fullres` a numeric vector

Sample a character vector
Sampleid a numeric vector
orig.ident a character vector
nCount_Spatial a numeric vector
nFeature_Spatial a numeric vector
nCount_SCT a numeric vector
nFeature_SCT a numeric vector
integrated_snn_res.0.8 a numeric vector
seurat_clusters a numeric vector
celltype_ABCDipi a character vector
gen2_SPLIz_numeric a numeric vector

Details

Merged spatial location and metadata information.

Source

This study.

References

Wang, Z., Yang, L., Yang, S., Li, G., Xu, M., Kong, B., Shao, C., & Liu, Z. (2025). Isoform switch of CD47 provokes macrophage-mediated pyroptosis in ovarian cancer. bioRxiv, 2025.2004.2017.649282. <https://doi.org/10.1101/2025.04.17.649282>

Examples

```
data(posi)
## maybe str(posi) ; plot(posi) ...
```

tissue_posi	<i>tissue_posi</i>
-------------	--------------------

Description

Position of the spots from spatial transcriptome data.

Usage

```
data("tissue_posi")
```

Format

A data frame with 9984 observations on the following 9 variables.

barcode a character vector
 in_tissue a numeric vector
 array_row a numeric vector
 array_col a numeric vector
 pxl_row_in_fullres a numeric vector
 pxl_col_in_fullres a numeric vector
 Sample a character vector
 Sampleid a numeric vector
 Newbarcode a character vector

Details

Please find the tissue_positions.csv from the spaceranger output files: ./out/spatial/tissue_positions.csv
 Multiple samples should be merged together, adding "samples" and "Newbarcode" columns.

Source

This study.

References

Wang, Z., Yang, L., Yang, S., Li, G., Xu, M., Kong, B., Shao, C., & Liu, Z. (2025). Isoform switch of CD47 provokes macrophage-mediated pyroptosis in ovarian cancer. bioRxiv, 2025.2004.2017.649282. <https://doi.org/10.1101/2025.04.17.649282>

Examples

```
data(tissue_posi)
## maybe str(tissue_posi) ; plot(tissue_posi) ...
```

```
tissue_posi_normalized
```

tissue_posi_normalized

Description

Normalized tissue spots position.

Usage

```
data("tissue_posi_normalized")
```

Format

A data frame with 9984 observations on the following 9 variables.

barcode a character vector
in_tissue a numeric vector
array_row a numeric vector
array_col a numeric vector
pxl_row_in_fullres a numeric vector
pxl_col_in_fullres a numeric vector
Sample a character vector
Sampleid a numeric vector
Newbarcode a character vector

Details

Normalized tissue spots position.

Source

This study.

References

Wang, Z., Yang, L., Yang, S., Li, G., Xu, M., Kong, B., Shao, C., & Liu, Z. (2025). Isoform switch of CD47 provokes macrophage-mediated pyroptosis in ovarian cancer. *bioRxiv*, 2025.2004.2017.649282. <https://doi.org/10.1101/2025.04.17.649282>

Examples

```
data(tissue_posi_normalized)
## maybe str(tissue_posi_normalized) ; plot(tissue_posi_normalized) ...
```

visualize_spatial_gradient

Visualize spatial network with expression gradient

Description

Visualize spatial network with expression gradient

Usage

```

visualize_spatial_gradient(
  spatial_data,
  sample,
  gradient_type,
  fixed_type,
  expression_col = "gen2_SPLIz_numeric",
  x_col = "pxl_row_in_fullres",
  y_col = "pxl_col_in_fullres",
  type_col = "Epi_strom",
  fixed_color = "#A9C6D9",
  line_color = "#666666",
  gradient_palette = "C",
  point_size = 1,
  point_alpha = 0.8,
  line_width = 0.3,
  line_alpha = 0.6,
  show_legend = TRUE,
  legend_title = "Expression",
  grid_major_color = "gray90",
  grid_minor_color = "gray95",
  border_color = "black",
  background_color = "white"
)

```

Arguments

<code>spatial_data</code>	Spatial coordinates data frame containing cell types and expression values
<code>sample</code>	Sample name in the spatial transcriptome data
<code>gradient_type</code>	Cell type to show with expression gradient coloring
<code>fixed_type</code>	Cell type to show in fixed color (default gray)
<code>expression_col</code>	Column name containing expression values (default "gen2_SPLIz_numeric")
<code>x_col</code>	Column name for x-coordinates (default "pxl_row_in_fullres")
<code>y_col</code>	Column name for y-coordinates (default "pxl_col_in_fullres")
<code>type_col</code>	Column name for cell type information (default "Epi_strom")
<code>fixed_color</code>	Color for the fixed cell type (default "#A9C6D9" - light gray-blue)
<code>line_color</code>	Color for connection lines (default "#666666" - dark gray)
<code>gradient_palette</code>	Color palette for expression gradient (default viridis option "C")
<code>point_size</code>	Size of points (default 1)
<code>point_alpha</code>	Transparency of points (default 0.8)
<code>line_width</code>	Width of connection lines (default 0.3)
<code>line_alpha</code>	Transparency of connection lines (default 0.6)
<code>show_legend</code>	Logical whether to show legend (default TRUE)

legend_title	Title for the legend (default "Expression")
grid_major_color	
	Color for major grid lines (default "gray90")
grid_minor_color	
	Color for minor grid lines (default "gray95")
border_color	Color for plot border (default "black")
background_color	
	Color for plot background (default "white")

Value

A ggplot object showing the spatial relationships with expression gradient

Examples

```
visualize_spatial_gradient(spatial_data = posi,
                           sample="SP8",
                           gradient_type = "Epithelial_cells_A",
                           fixed_type = "Macrophage",
                           expression_col = "gen2_SPLIz_numeric",
                           type_col = "celltype_ABCDipi",
                           legend_title = "Expression",
                           background_color = "white")
```

```
visualize_spatial_multinetwork
```

Visualize spatial relationships between multiple cell types

Description

Visualize spatial relationships between multiple cell types

Usage

```
visualize_spatial_multinetwork(
  spatial_data,
  sample,
  reference_type,
  target_types,
  x_col = "pxl_row_in_fullres",
  y_col = "pxl_col_in_fullres",
  type_col = "Epi_strom",
  color_palette = NULL,
  point_alpha = 0.7,
  line_alpha = 0.5,
  point_size = 1.5,
  line_width = 0.3,
  show_legend = TRUE
)
```

Arguments

<code>spatial_data</code>	Spatial coordinates data frame
<code>sample</code>	Sample name in the spatial transcriptome data
<code>reference_type</code>	Reference cell type (character vector of length 1)
<code>target_types</code>	Target cell type(s) (character vector of 1 or more)
<code>x_col</code>	Column name for x-coordinates
<code>y_col</code>	Column name for y-coordinates
<code>type_col</code>	Column name for cell type information
<code>color_palette</code>	Named vector of colors for cell types
<code>point_alpha</code>	Transparency level for points
<code>line_alpha</code>	Transparency level for connection lines
<code>point_size</code>	Size of points in plot
<code>line_width</code>	Width of connection lines
<code>show_legend</code>	Logical, whether to show legend

Value

A ggplot object showing the spatial relationships

Examples

```
visualize_spatial_multinetwork(posi, sample="SP8", reference_type="Macrophage",
                               target_type=c("Epithelial_cells_A", "Epithelial_cells_B"),
                               type_col = "celltype_ABCDepi")
```

```
visualize_spatial_network
```

Visualize spatial relationships between cell types

Description

Visualize spatial relationships between cell types

Usage

```
visualize_spatial_network(
  spatial_data,
  sample,
  reference_type,
  target_type,
  x_col = "pxl_row_in_fullres",
  y_col = "pxl_col_in_fullres",
  type_col = "Epi_strom",
  color_palette = c(Macrophage = "#90ee90", Epithelial_cells_A = "#377EB8"),
  alpha = 0.7
)
```

Arguments

<code>spatial_data</code>	Spatial coordinates data frame
<code>sample</code>	Sample name in the spatial transcriptome data
<code>reference_type</code>	Reference cell type
<code>target_type</code>	Target cell type
<code>x_col</code>	Column name for x-coordinates
<code>y_col</code>	Column name for y-coordinates
<code>type_col</code>	Column name for cell type information
<code>color_palette</code>	Named vector of colors for cell types
<code>alpha</code>	Transparency level for points and lines

Value

A ggplot object showing the spatial relationships

Examples

[illegible]

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