Package 'STDistance'

July 22, 2025

Title Spatial Transcriptomics Distance Calculation and Visualization

Version 0.6.6

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.

License GPL (>= 3)

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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Contents

`calculate_correlations` *Perform correlation analysis between spatial features and distance metrics with visualization*

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

`spatial_data`	A data frame containing spatial coordinates and cell type info
`reference_type`	The reference cell type to calculate distances from
`target_types`	Vector of target cell types to calculate distances to
`x_col`	Column name for x-coordinates
`y_col`	Column name for y-coordinates
`id_col`	Column name for cell identifiers
`type_col`	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_ABCDepi")
```

`distance_results` *distance_results*

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` *Metadata*

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` *Normalize spatial coordinates*

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` *Visualize Nearest Neighbor Distances with Boxplot and Mean ± SEM*

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")
```

`posi` *posi*

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_ABCDepi` 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` *tissue_posi*

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

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

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

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

Value

A ggplot object showing the spatial relationships

Examples

```
visualize_spatial_network(posi, sample="SP8", reference_type="Macrophage",
                          target_type="Epithelial_cells_A",
                          x_col = "pxl_row_in_fullres",
                          y_col = "pxl_col_in_fullres",
                          type_col = "celltype_ABCDepi",
                          color_palette = c("Macrophage" = "#90ee90",
                         "Epithelial_cells_A" = "#377EB8"))
```

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