Package 'SingleCellComplexHeatMap'

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Type Package

Title Complex Heatmaps for Single Cell Expression Data with Dual
Information Display

Version 0.1.2

Maintainer XueCheng Fang <xuecheng328@gmail.com>

Description Creates complex heatmaps for single cell RNA-seq data that simultaneously
display gene expression levels (as color intensity) and expression percentages
(as circle sizes). Supports gene grouping, cell type annotations, and time point
comparisons. Built on top of 'ComplexHeatmap' and integrates with 'Seurat' objects.
For more details see Gu (2022) <doi:10.1002/imt2.43> and Hao (2024) <doi:10.1038/s41587-
023-01767-y>.

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Encoding UTF-8

RoxygenNote 7.3.2

Depends R (>= 4.0.0)

Imports ComplexHeatmap (>= 2.10.0), Seurat (>= 4.0.0), dplyr (>=
1.0.0), tidyr (>= 1.0.0), RColorBrewer, circlize (>= 0.4.0),
grid, grDevices, stats, magrittr

Suggests testthat (>= 3.0.0), knitr, rmarkdown, viridis, devtools,
BiocManager, ggsci, SeuratObject

URL https://github.com/FanXuRong/SingleCellComplexHeatMap

BugReports https://github.com/FanXuRong/SingleCellComplexHeatMap/issues

VignetteBuilder knitr

NeedsCompilation no

Author XueCheng Fang [aut, cre]

Repository CRAN

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Contents

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create_cell_annotations

Create Cell Type and Time Point Annotations for Heatmap Columns

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Description

Parses column names to extract time points and cell types, creates annotations and reorders matrices.

Usage

```
create_cell_annotations(
  exp_mat,
  percent_mat,
  split_pattern = "_",
  time_position = 1,
  celltype_start = 2,
  time_points_order = NULL,
  cell_types_order = NULL,
  time_color_palette = "Accent",
  celltype_color_palette = "Dark2",
  show_time_annotation = TRUE,
  show_celltype_annotation = TRUE,
  time_point_title = "Time Point",
  cell_type_title = "Cell Type"
)
```

Arguments

`exp_mat`	Expression matrix with samples as columns
`percent_mat`	Percentage matrix with samples as columns
`split_pattern`	Character string used to split column names (default: "_")
`time_position`	Integer indicating position of time point in split names (default: 1)
`celltype_start`	Integer indicating starting position of cell type in split names (default: 2)
`time_points_order`	
	Character vector specifying order of time points (default: NULL for automatic)
`cell_types_order`	
	Character vector specifying order of cell types (default: NULL for automatic)

time_color_palette

> Character string specifying palette name OR character vector of colors for time points (default: "Accent")

celltype_color_palette

> Character string specifying palette name OR character vector of colors for cell types (default: "Dark2")

show_time_annotation

> Logical indicating whether to show time point annotation (default: TRUE)

show_celltype_annotation

> Logical indicating whether to show cell type annotation (default: TRUE)

time_point_title

> Character string for time point annotation title (default: "Time Point")

cell_type_title

> Character string for cell type annotation title (default: "Cell Type")

Value

A list containing exp_mat_ordered (reordered expression matrix), percent_mat_ordered (reordered percentage matrix), col_annotation (ComplexHeatmap column annotation object), col_split_factor (factor for column splitting based on time points), and annotation_df (data frame with column annotations).

See Also

create_single_cell_complex_heatmap, prepare_expression_matrices

Examples

```
# Load a small example Seurat object
data("pbmc_small", package = "SeuratObject")
pbmc_small$timepoint <- sample(c("0h", "6h"), ncol(pbmc_small), replace = TRUE)
pbmc_small$timepoint_celltype <- paste(pbmc_small$timepoint, pbmc_small$RNA_snn_res.0.8, sep = "_")
features <- c("CD3D", "CD79A", "MS4A1")

# Prepare expression matrices first
matrices <- prepare_expression_matrices(pbmc_small, features, group_by = "timepoint_celltype")

# Create cell annotations with custom ordering
col_annotations <- create_cell_annotations(
  exp_mat = matrices$exp_mat,
  percent_mat = matrices$percent_mat,
  split_pattern = "_",
  time_points_order = c("0h", "6h"),
  cell_types_order = levels(pbmc_small$RNA_snn_res.0.8)
)

# Access results
ordered_exp_mat <- col_annotations$exp_mat_ordered
```

---

create_gene_annotations

Create Gene Group Annotations for Heatmap Rows

Description

Creates gene grouping annotations and reorders expression matrices based on gene classifications.

Usage

```
create_gene_annotations(
  exp_mat,
  percent_mat,
  gene_classification,
  color_palette = "Set1",
  sort_within_groups = TRUE,
  annotation_title = "Gene Group"
)
```

Arguments

exp_mat	Expression matrix with genes as rows
percent_mat	Percentage matrix with genes as rows
gene_classification	
	Named list where names are group labels and values are character vectors of gene names
color_palette	Character string specifying palette name OR character vector of colors (default: "Set1")
sort_within_groups	
	Logical indicating whether to sort genes within each group (default: TRUE)
annotation_title	
	Character string for annotation title (default: "Gene Group")

Value

A list containing exp_mat_ordered (reordered expression matrix), percent_mat_ordered (reordered percentage matrix), row_annotation (ComplexHeatmap row annotation object), row_split_factor (factor for row splitting), and annotation_df (data frame with gene annotations).

See Also

[create_single_cell_complex_heatmap](), [prepare_expression_matrices]()

Examples

```
# Load a small example Seurat object
data("pbmc_small", package = "SeuratObject")
features <- c("CD3D", "CD79A", "MS4A1", "GZMK", "CCL5")

# Prepare expression matrices first
matrices <- prepare_expression_matrices(pbmc_small, features, group_by = "RNA_snn_res.0.8")

# Define gene groups
gene_groups <- list(
  "T-cell Markers" = c("CD3D", "GZMK", "CCL5"),
  "B-cell Markers" = c("CD79A", "MS4A1")
)

# Create gene annotations
annotations <- create_gene_annotations(
  exp_mat = matrices$exp_mat,
  percent_mat = matrices$percent_mat,
  gene_classification = gene_groups,
  color_palette = "Set1"
)

# Access results
ordered_exp_mat <- annotations$exp_mat_ordered
```

```
create_single_cell_complex_heatmap
```
Create Complex Heatmap for Single Cell Expression Data

Description

Creates a complex heatmap that displays both gene expression levels (as color intensity) and expression percentages (as circle sizes) for single cell RNA-seq data. This function provides extensive customization options while maintaining ease of use.

Usage

```
create_single_cell_complex_heatmap(
  seurat_object,
  features,
  gene_classification = NULL,
  group_by = "seurat_clusters",
  idents = NULL,
  time_points_order = NULL,
  cell_types_order = NULL,
  color_range = c(-1, 0, 2),
  color_palette = NULL,
```

```
    max_circle_size = 2,
    row_fontsize = 8,
    col_fontsize = 9,
    col_name_rotation = 90,
    row_title_fontsize = 10,
    col_title_fontsize = 10,
    show_heatmap_legend = TRUE,
    show_percentage_legend = TRUE,
    legend_side = "right",
    cell_border_color = "grey80",
    split_pattern = "_",
    gene_color_palette = "Set1",
    time_color_palette = "Accent",
    celltype_color_palette = "Dark2",
    show_gene_grouping = NULL,
    show_time_annotation = TRUE,
    show_celltype_annotation = TRUE,
    split_by = "time",
    merge_legends = TRUE,
    percentage_legend_title = "Expression %",
    percentage_legend_labels = c("0%", "25%", "50%", "75%", "100%"),
    percentage_breaks = NULL,
    return_data = FALSE,
    save_plot = NULL,
    plot_width = 10,
    plot_height = 8,
    plot_dpi = 300,
    assay = NULL,
    slot = "scale.data",
    cluster_cells = TRUE,
    cluster_features = TRUE,
    clustering_distance_rows = "euclidean",
    clustering_distance_cols = "euclidean",
    clustering_method_rows = "complete",
    clustering_method_cols = "complete",
    color_palette_main = c("blue", "white", "red"),
    annotation_colors = NULL,
    show_feature_names = TRUE,
    feature_names_gp = NULL,
    legend_title = "Expression",
    gene_group_title = "Gene Group",
    time_point_title = "Time Point",
    cell_type_title = "Cell Type",
    show_cell_borders = TRUE,
    show_column_annotation = TRUE,
    gene_name_mapping = NULL,
    ...
  )
```

Arguments

`seurat_object`	A Seurat object containing single cell data
`features`	Character vector of gene names to plot
`gene_classification`	
	Named list where names are group labels and values are character vectors of gene names (default: NULL for no gene grouping)
`group_by`	Character string specifying the metadata column to group by (default: "seurat_clusters")
`idents`	Numeric or character vector specifying which cell groups to include (default: NULL for all)
`time_points_order`	
	Character vector specifying order of time points. Only affects display order, not data filtering (default: NULL for automatic)
`cell_types_order`	
	Character vector specifying order of cell types. Only affects display order, not data filtering (default: NULL for automatic)
`color_range`	Numeric vector specifying color mapping break points for expression values. Its length must match color_palette if color_palette is a vector. (default: c(-1, 0, 2))
`color_palette`	Character vector specifying colors for expression heatmap. Its length must match color_range. If NULL, a default palette (viridis or color_palette_main) is generated to match color_range length (default: NULL)
`max_circle_size`	
	Numeric specifying maximum circle radius in mm. This applies to the highest percentage value in percentage_breaks (default: 2)
`row_fontsize`	Numeric specifying row name font size (default: 8)
`col_fontsize`	Numeric specifying column name font size (default: 9)
`col_name_rotation`	
	Numeric specifying column name rotation angle (default: 90)
`row_title_fontsize`	
	Numeric specifying row title font size (default: 10)
`col_title_fontsize`	
	Numeric specifying column title font size (default: 10)
`show_heatmap_legend`	
	Logical indicating whether to show heatmap legend (default: TRUE)
`show_percentage_legend`	
	Logical indicating whether to show percentage legend (default: TRUE)
`legend_side`	Character string specifying legend position (default: "right")
`cell_border_color`	
	Character string specifying cell border color (default: "grey80")
`split_pattern`	Character string used to split column names for parsing (default: "_")
`gene_color_palette`	
	Character string specifying palette name OR character vector of colors for gene groups (default: "Set1")

time_color_palette

    Character string specifying palette name OR character vector of colors for time points (default: "Accent")

celltype_color_palette

    Character string specifying palette name OR character vector of colors for cell types (default: "Dark2")

show_gene_grouping

    Logical indicating whether to show gene grouping (default: TRUE if gene_classification provided)

show_time_annotation

    Logical indicating whether to show time point annotation (default: TRUE)

show_celltype_annotation

    Logical indicating whether to show cell type annotation (default: TRUE)

split_by   Character string specifying how to split columns: "time", "celltype", or "none" (default: "time")

merge_legends Logical indicating whether to merge legends (default: TRUE)

percentage_legend_title

    Character string for percentage legend title (default: "Expression %")

percentage_legend_labels

    Character vector for percentage legend labels

percentage_breaks

    Numeric vector specifying actual percentage values corresponding to labels

return_data Logical; if TRUE, return underlying data instead of drawing only

save_plot   File path to save the drawn heatmap (PNG)

plot_width   Numeric; width in inches for saving

plot_height   Numeric; height in inches for saving

plot_dpi   Numeric; resolution (DPI) for saved plot

assay   Seurat assay name to extract data from

slot   Seurat slot name within assay (e.g., "scale.data", "data")

cluster_cells Logical; whether to cluster columns (cells)

cluster_features

    Logical; whether to cluster rows (features)

clustering_distance_rows

    Distance metric for row clustering

clustering_distance_cols

    Distance metric for column clustering

clustering_method_rows

    Clustering method for rows

clustering_method_cols

    Clustering method for columns

color_palette_main

    Fallback color palette when viridis unavailable

annotation_colors

                  Named list of custom annotation colors

show_feature_names

                  Logical; whether to show feature (row) names

feature_names_gp

                  gpar object controlling feature name appearance

legend_title   Character; title for main heatmap legend

gene_group_title

                  Character string for gene group annotation title (default: "Gene Group")

time_point_title

                  Character string for time point annotation title (default: "Time Point")

cell_type_title

                  Character string for cell type annotation title (default: "Cell Type")

show_cell_borders

                  Logical indicating whether to show cell border lines (default: TRUE)

show_column_annotation

                  Logical indicating whether to show column annotations (default: TRUE)

gene_name_mapping

                  Named character vector for mapping gene names, where names are original gene names and values are display names (default: NULL)

...   Additional arguments passed to ComplexHeatmap::Heatmap()

Value

A ComplexHeatmap object. If return_data is TRUE, returns a list containing the heatmap object and underlying data matrices.

---

prepare_expression_matrices

                Prepare Expression and Percentage Matrices from Seurat DotPlot

---

Description

Extracts and reshapes expression data from a Seurat DotPlot object into matrices suitable for complex heatmap visualization.

Usage

```
prepare_expression_matrices(
  seurat_object,
  features,
  group_by = "seurat_clusters",
  idents = NULL,
  split_pattern = "_",
  time_position = 1,
  celltype_start = 2
)
```

Arguments

`seurat_object`	A Seurat object containing single cell data
`features`	Character vector of gene names to plot
`group_by`	Character string specifying the metadata column to group by (default: "seurat_clusters")
`idents`	Numeric or character vector specifying which cell groups to include (default: NULL for all)
`split_pattern`	Character string used to split column names for parsing (default: "_")
`time_position`	Integer indicating position of time point in split names (default: 1)
`celltype_start`	Integer indicating starting position of cell type in split names (default: 2)

Value

A list containing exp_mat (matrix of scaled expression values), percent_mat (matrix of expression percentages), and dotplot_data (original DotPlot data frame).

See Also

create_single_cell_complex_heatmap

Examples

```
# Load a small example Seurat object
data("pbmc_small", package = "SeuratObject")
features <- c("CD3D", "CD79A", "MS4A1")

# Basic usage
matrices <- prepare_expression_matrices(
  seurat_object = pbmc_small,
  features = features,
  group_by = "RNA_snn_res.0.8"
)

# Access the results
expression_matrix <- matrices$exp_mat
percentage_matrix <- matrices$percent_mat
```

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