

Package: scGenePanel (via r-universe)

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Title Multi-panel visualization for single cell expression data

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Description scGenePanel creates coordinated, gene-centric multi-panel visualizations for single-cell RNA-seq data stored in Seurat or SingleCellExperiment objects. It combines group-stratified UMAP embeddings, cell-type-specific expression distributions, and quantitative cell-frequency and expression summaries in a single figure. An accompanying Shiny application supports interactive exploration using the same workflow.

Depends R (>= 4.0.0)

Imports methods, stats, Seurat (>= 4.1.1), SingleCellExperiment, SummarizedExperiment, dplyr, magrittr, ggplot2, ggpubr, ggforce, ggthemes, ggsci, cowplot, patchwork, grid, gridExtra, flextable, RColorBrewer, scales, scCustomize, shiny, shinydashboard, shinyjs, shinyWidgets

Suggests knitr, rmarkdown, BiocManager, testthat (>= 3.0.0), BiocStyle

biocViews Software, GeneExpression, SingleCell, Visualization, DimensionReduction, Transcriptomics

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VignetteBuilder knitr

BugReports <https://github.com/vandydata/scGenePanel/issues>

URL <https://github.com/vandydata/scGenePanel>

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Repository <https://biocstaging.r-universe.dev>

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.check_if_dim_red_exists	
	<i>Check if dimension reduction embedding exists</i>

Description

Check if the specified dimension reduction embedding exists in the Seurat object

Usage

.check_if_dim_red_exists(seurat_obj, dim_red)

Arguments

- seurat_obj A Seurat object
- dim_red The name of the dimension reduction embedding to check

Value

returns an error message if the specified dimension reduction does not exist #' @noRd

discrete_col_palette	<i>Discrete color palettes from multiple packages (varibow, Rcolorbrewer, ggtheme)</i>
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Description

Discrete color palettes from multiple packages (varibow, Rcolorbrewer, ggtheme)

Usage

```
discrete_col_palette(num_colors, hex_cols = NULL, palette = NULL)
```

Arguments

num_colors	Number of colors to be generated.
hex_cols	hex code of the colors to be selected for violin plot
palette	Options are "Tableau" or RColorBrewer qualitative variables like "Dark2", "Paired", "Set1", "Set2", "Set3", "Accent" etc. if empty, the function will use based on the entered n.

Value

A color palette for plotting violin plot

scGenePanel	<i>scGenePanel - A method for generating scRNAseq multi-panel gene expression visuals that are focused on one gene, all cell types, and a chosen metadata attribute of interest.</i>
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Description

scGenePanel exports a multi-panel scRNAseq gene expression plots of UMAP clusters highlighted with user defined cell types and split view on user defined sample groups, violin plot with user defined sample groups along with tabular cell counts, ratios and expression values per sample group, in one visual

Usage

```
scGenePanel(
  object,
  gene,
  meta_group,
  cell_type_name,
  cell_type_colname,
  dim_red = "umap",
  col_palette = "Tableau",
```

```

    group_order = NULL,
    output_dir = tempdir()
  )

```

Arguments

<code>object</code>	A Seurat or SingleCellExperiment object. Seurat objects will be automatically updated to the current package version if needed
<code>gene</code>	Name of gene to explore gene expression in UMAP, violin plot, and cell frequency table
<code>meta_group</code>	The metadata column name of the variable to split the UMAP, violinplot and cell frequency table by. for example, to split by disease condition
<code>cell_type_name</code>	The cell type identity to highlight in UMAP
<code>cell_type_colname</code>	The metadata column name that contains the cell identity annotations
<code>dim_red</code>	Dimension reduction embedding to use
<code>col_palette</code>	Color palettes to choose for violinplot panel. Options are "Tableau" or RColorBrewer qualitative variables like "Dark2", "Paired", "Set1", "Set2", "Set3", "Accent" etc.
<code>group_order</code>	User defined order of the meta_groups to be displayed
<code>output_dir</code>	Output directory where the image will be saved

Value

A ggplot object containing a multi-panel visualization with UMAP plots, violin plots, and cell frequency statistics for the specified gene and cell type

Examples

```

# Load example pancreatic islet data from package
example_file <- system.file(
  "extdata",
  "human_panc_islets.Rds",
  package = "scGenePanel")
human_panc_islets <- readRDS(example_file)

# Basic usage - create gene panel for insulin expression in beta cells
panel <- scGenePanel(
  object = human_panc_islets,
  gene = "INS", # Insulin gene
  meta_group = "Age", # Group by age (14y, 39y, 50y, 59y, 66y)
  cell_type_name = "Beta", # Highlight beta cells
  cell_type_colname = "CellTypes" # Cell type column
)

# Advanced usage with custom colors and ordering
panel_advanced <- scGenePanel(

```

```

    object = human_panc_islets,
    gene = "GCG",                      # Glucagon for alpha cells
    meta_group = "Sex",                 # Group by sex (F/M)
    cell_type_name = "Alpha",           # Highlight alpha cells
    cell_type_colname = "CellTypes",
    col_palette = "Set2",               # Custom color palette
    group_order = c("F", "M"),         # Custom group order
    output_dir = tempdir()              # Save to temp directory
  )

# Example with different cell type and gene
somatostatin_panel <- scGenePanel(
  object = human_panc_islets,
  gene = "SST",                       # Somatostatin for delta cells
  meta_group = "Batch",               # Group by batch
  cell_type_name = "Delta",           # Highlight delta cells
  cell_type_colname = "CellTypes"
)

```

scGenePanelShiny

Launch Interactive Gene Panel Shiny Application

Description

scGenePanelShiny launches a Shiny web application for interactive exploration of single-cell gene expression data with dynamic parameter selection.

Usage

```
scGenePanelShiny(object = NULL)
```

Arguments

object A Seurat or SingleCellExperiment object. If NULL, loads example data

Value

Invisibly returns NULL. Function is called for its side effect of launching the Shiny application.

Examples

```

# Example 1: Launch with example data
if (interactive()){
  scGenePanelShiny()
}

# Example 2: Launch with seurat object
data <- readRDS(system.file("extdata", "human_panc_islets.Rds", package = "scGenePanel"))
if (interactive()){

```

```
    scGenePanelShiny(data)  
  }
```

```
# Example 3: Launch with SCE object  
data <- readRDS(system.file("extdata", "sce_object.Rds", package = "scGenePanel"))  
if (interactive()){  
  scGenePanelShiny(data)  
}
```

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