

Package ‘SCpubr’

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Type Package

Title Generate Publication Ready Visualizations of Single Cell
Transcriptomics Data

Version 2.0.1

Description A system that provides a streamlined way of generating publication ready plots for known Single-Cell transcriptomics data in a “publication ready” format. This is, the goal is to automatically generate plots with the highest quality possible, that can be used right away or with minimal modifications for a research article.

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URL <https://github.com/enblacar/SCpubr/>,
<https://enblacar.github.io/SCpubr-book/>

BugReports <https://github.com/enblacar/SCpubr/issues/>

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do_AlluvialPlot	<i>Generate Alluvial plots.</i>
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Description

This function is based on the **ggalluvial** package. It allows you to generate alluvial plots from a given Seurat object.

Usage

```
do_AlluvialPlot(  
  sample,  
  first_group,  
  last_group,  
  middle_groups = NULL,  
  colors.use = NULL,  
  plot.title = NULL,  
  plot.subtitle = NULL,  
  plot.caption = NULL,  
  font.size = 14,  
  font.type = "sans",  
  xlab = NULL,  
  ylab = "Number of cells",  
  repel = FALSE,  
  fill.by = last_group,  
  use_labels = FALSE,  
  stratum.color = "black",  
  stratum.fill = "white",  
  stratum.width = 1/3,  
  stratum.fill.conditional = FALSE,  
  use_geom_flow = FALSE,  
  alluvium.color = "white",  
  flow.color = "white",  
  flip = FALSE,  
  label.color = "black",  
  curve_type = "sigmoid",  
  use_viridis = FALSE,  
  viridis.palette = "G",  
  viridis.direction = -1,  
  sequential.palette = "YlGnBu",  
  sequential.direction = 1,  
  plot.grid = FALSE,  
  grid.color = "grey75",  
  grid.type = "dashed",  
  na.value = "white",  
  legend.position = "right",  
  legend.title = NULL,  
)
```

```

plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
first_group	character Categorical metadata variable. First group of nodes of the alluvial plot.
last_group	character Categorical metadata variable. Last group of nodes of the alluvial plot.
middle_groups	character Categorical metadata variable. Vector of groups of nodes of the alluvial plot.
colors.use	character Named list of colors corresponding to the unique values in fill.by (which defaults to last_group).
plot.title, plot.subtitle, plot.caption	character Title, subtitle or caption to use in the plot.
font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
xlab, ylab	character Titles for the X and Y axis.
repel	logical Whether to repel the text labels.
fill.by	character One of first_group, middle_groups (one of the values, if multiple mid_groups) or last_group. These values will be used to color the alluvium/flow.
use_labels	logical Whether to use labels instead of text for the stratum.
stratum.color, alluvium.color, flow.color	character Color for the border of the alluvium (and flow) and stratum.
stratum.fill	character Color to fill the stratum.
stratum.width	logical Width of the stratum.
stratum.fill.conditional	logical Whether to fill the stratum with the same colors as the alluvium/flow.
use_geom_flow	logical Whether to use geom_flow instead of geom_alluvium . Visual results might differ.
flip	logical Whether to invert the axis of the displayed plot.
label.color	character Color for the text labels.

curve_type	<p>character Type of curve used in <code>geom_alluvium</code>. One of:</p> <ul style="list-style-type: none"> • linear. • cubic. • quintic. • sine. • arctangent. • sigmoid. • xspline.
use_viridis	logical Whether to use viridis color scales.
viridis.palette	character A capital letter from A to H or the scale name as in <code>scale_fill_viridis</code> .
viridis.direction	numeric Either 1 or -1. Controls how the gradient of viridis scale is formed.
sequential.palette	character Type of sequential color palette to use. Out of the sequential palettes defined in <code>brewer.pal</code> .
sequential.direction	numeric Direction of the sequential color scale. Either 1 or -1.
plot.grid	logical Whether to plot grid lines.
grid.color	character Color of the grid in the plot. In heatmaps, color of the border of the cells.
grid.type	<p>character One of the possible linetype options:</p> <ul style="list-style-type: none"> • blank. • solid. • dashed. • dotted. • dotdash. • longdash. • twodash.
na.value	character Color value for NA.
legend.position	<p>character Position of the legend in the plot. One of:</p> <ul style="list-style-type: none"> • top: Top of the figure. • bottom: Bottom of the figure. • left: Left of the figure. • right: Right of the figure. • none: No legend is displayed.
legend.title	character Title for the legend.
plot.title.face, plot.subtitle.face, plot.caption.face, axis.title.face, axis.text.face, legend.title	<p>character Controls the style of the font for the corresponding theme element.</p> <p>One of:</p> <ul style="list-style-type: none"> • plain: For normal text. • italic: For text in italic. • bold: For text in bold. • bold.italic: For text both in italic and bold.

Value

A ggplot2 object.

Examples

```
# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_AlluvialPlot", passive = TRUE)
message(value)
if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your Seurat object.
sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))

  # Compute basic sankey plot.
p <- SCpubr::do_AlluvialPlot(sample = sample,
                             first_group = "orig.ident",
                             last_group = "seurat_clusters")

} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`.")
}
```

do_BarPlot

Create Bar Plots.

Description

Create Bar Plots.

Usage

```
do_BarPlot(
  sample,
  group.by,
  order = FALSE,
  add.n = FALSE,
  add.n.face = "bold",
  add.n.expand = c(0, 1.15),
  add.n.size = 4,
  order.by = NULL,
  split.by = NULL,
  facet.by = NULL,
  position = "stack",
  font.size = 14,
```

```

font.type = "sans",
legend.position = "bottom",
legend.title = NULL,
legend.ncol = NULL,
legend.nrow = NULL,
legend.byrow = FALSE,
axis.text.x.angle = 45,
xlab = NULL,
ylab = NULL,
colors.use = NULL,
flip = FALSE,
plot.title = NULL,
plot.subtitle = NULL,
plot.caption = NULL,
plot.grid = FALSE,
grid.color = "grey75",
grid.type = "dashed",
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain",
strip.text.face = "bold",
return_data = FALSE
)

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
group.by	character Metadata column to compute the counts of. Has to be either a character or factor column.
order	logical Whether to order the results in descending order of counts.
add.n	logical Whether to add the total counts on top of each bar.
add.n.face	character Font face of the labels added by add.n.
add.n.expand	numeric Vector of two numerics representing the start and end of the scale. Minimum should be 0 and max should be above 1. This basically expands the Y axis so that the labels fit when flip = TRUE. <ul style="list-style-type: none"> • <code>stack</code>: Set the bars side by side, displaying the total number of counts. Uses position_stack. • <code>fill</code>: Set the bars on top of each other, displaying the proportion of counts from the total that each group represents. Uses position_fill.
add.n.size	numeric Size of the labels
order.by	character When <code>split.by</code> is used, value of <code>group.by</code> to reorder the columns based on its value.

split.by	character Metadata column to split the values of group.by by. If not used, defaults to the active idents.
facet.by	character Metadata column to gather the columns by. This is useful if you have other overarching metadata.
position	character Position function from ggplot2 . Either stack or fill.
font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
legend.position	character Position of the legend in the plot. One of: <ul style="list-style-type: none"> • top: Top of the figure. • bottom: Bottom of the figure. • left: Left of the figure. • right: Right of the figure. • none: No legend is displayed.
legend.title	character Title for the legend.
legend.ncol	numeric Number of columns in the legend.
legend.nrow	numeric Number of rows in the legend.
legend.byrow	logical Whether the legend is filled by row or not.
axis.text.x.angle	numeric Degree to rotate the X labels. One of: 0, 45, 90.
xlab, ylab	character Titles for the X and Y axis.
colors.use	named_vector Named vector of valid color representations (either name of HEX codes) with as many named colors as unique values of group.by. If group.by is not provided, defaults to the unique values of Idents . If not provided, a color scale will be set by default.
flip	logical Whether to invert the axis of the displayed plot.
plot.title, plot.subtitle, plot.caption	character Title, subtitle or caption to use in the plot.
plot.grid	logical Whether to plot grid lines.
grid.color	character Color of the grid in the plot. In heatmaps, color of the border of the cells.
grid.type	character One of the possible linetype options: <ul style="list-style-type: none"> • blank. • solid. • dashed. • dotted. • dotdash.


```

        plot.title = "Number of cells per cluster in each sample",
        position = "stack")

} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`.")
}

```

do_BeeSwarmPlot	<i>BeeSwarm plot.</i>
-----------------	-----------------------

Description

BeeSwarm plot.

Usage

```

do_BeeSwarmPlot(
  sample,
  feature_to_rank,
  group.by = NULL,
  assay = NULL,
  reduction = NULL,
  slot = NULL,
  continuous_feature = FALSE,
  order = FALSE,
  colors.use = NULL,
  legend.title = NULL,
  legend.type = "colorbar",
  legend.position = if (isTRUE(continuous_feature)) {
    "bottom"
  } else {
    "none"
  },
  legend.framewidth = 0.5,
  legend.tickwidth = 0.5,
  legend.length = 20,
  legend.width = 1,
  legend.framecolor = "grey50",
  legend.tickcolor = "white",
  legend.ncol = NULL,
  legend.icon.size = 4,
  plot.title = NULL,
  plot.subtitle = NULL,
  plot.caption = NULL,

```

```

xlab = NULL,
ylab = NULL,
font.size = 14,
font.type = "sans",
remove_x_axis = FALSE,
remove_y_axis = FALSE,
flip = FALSE,
use_viridis = TRUE,
viridis.palette = "G",
viridis.direction = 1,
sequential.palette = "YlGnBu",
sequential.direction = -1,
verbose = TRUE,
raster = FALSE,
raster.dpi = 300,
plot_cell_borders = TRUE,
border.size = 1.5,
border.color = "black",
pt.size = 2,
min.cutoff = NA,
max.cutoff = NA,
na.value = "grey75",
number.breaks = 5,
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
feature_to_rank	character Feature for which the cells are going to be ranked. Ideal case is that this feature is stored as a metadata column.
group.by	character Metadata variable to group the output by. Has to be a character of factor column.
assay	character Assay to use. Defaults to the current assay.
reduction	character Reduction to use. Can be the canonical ones such as "umap", "pca", or any custom ones, such as "diffusion". If you are unsure about which reductions you have, use <code>Seurat::Reductions(sample)</code> . Defaults to "umap" if present or to the last computed reduction if the argument is not provided.
slot	character Data slot to use. Only one of: counts, data, scale.data. Defaults to "data".

`continuous_feature` [logical](#) | Is the feature to rank and color for continuous? I.e: an enrichment score.

`order` [logical](#) | Whether to reorder the groups based on the median of the ranking.

`colors.use` [named_vector](#) | Named vector of valid color representations (either name of HEX codes) with as many named colors as unique values of `group.by`. If `group.by` is not provided, defaults to the unique values of `Idents`. If not provided, a color scale will be set by default.

`legend.title` [character](#) | Title for the legend.

`legend.type` [character](#) | Type of legend to display. One of:

- `normal`: Default legend displayed by **ggplot2**.
- `colorbar`: Redefined colorbar legend, using [guide_colorbar](#).

`legend.position` [character](#) | Position of the legend in the plot. One of:

- `top`: Top of the figure.
- `bottom`: Bottom of the figure.
- `left`: Left of the figure.
- `right`: Right of the figure.
- `none`: No legend is displayed.

`legend.framewidth`, `legend.tickwidth` [numeric](#) | Width of the lines of the box in the legend.

`legend.length`, `legend.width` [numeric](#) | Length and width of the legend. Will adjust automatically depending on legend side.

`legend.framecolor` [character](#) | Color of the lines of the box in the legend.

`legend.tickcolor` [character](#) | Color of the ticks of the box in the legend.

`legend.ncol` [numeric](#) | Number of columns in the legend.

`legend.icon.size` [numeric](#) | Size of the icons in legend.

`plot.title`, `plot.subtitle`, `plot.caption` [character](#) | Title, subtitle or caption to use in the plot.

`xlab`, `ylab` [character](#) | Titles for the X and Y axis.

`font.size` [numeric](#) | Overall font size of the plot. All plot elements will have a size relationship with this font size.

`font.type` [character](#) | Base font family for the plot. One of:

- `mono`: Mono spaced font.
- `serif`: Serif font family.
- `sans`: Default font family.

`remove_x_axis`, `remove_y_axis` [logical](#) | Remove X axis labels and ticks from the plot.

<code>flip</code>	logical Whether to invert the axis of the displayed plot.
<code>use_viridis</code>	logical Whether to use viridis color scales.
<code>viridis.palette</code>	character A capital letter from A to H or the scale name as in <code>scale_fill_viridis</code> .
<code>viridis.direction</code>	numeric Either 1 or -1. Controls how the gradient of viridis scale is formed.
<code>sequential.palette</code>	character Type of sequential color palette to use. Out of the sequential palettes defined in <code>brewer.pal</code> .
<code>sequential.direction</code>	numeric Direction of the sequential color scale. Either 1 or -1.
<code>verbose</code>	logical Whether to show extra comments, warnings, etc.
<code>raster</code>	logical Whether to raster the resulting plot. This is recommendable if plotting a lot of cells.
<code>raster.dpi</code>	numeric Pixel resolution for rasterized plots. Defaults to 1024. Only activates on Seurat versions higher or equal than 4.1.0.
<code>plot_cell_borders</code>	logical Whether to plot border around cells.
<code>border.size</code>	numeric Width of the border of the cells.
<code>border.color</code>	character Color for the border of the heatmap body.
<code>pt.size</code>	numeric Size of the dots.
<code>min.cutoff, max.cutoff</code>	numeric Set the min/max ends of the color scale. Any cell/group with a value lower than <code>min.cutoff</code> will turn into <code>min.cutoff</code> and any cell with a value higher than <code>max.cutoff</code> will turn into <code>max.cutoff</code> . In <code>FeaturePlots</code> , provide as many values as features. Use NAs to skip a feature.
<code>na.value</code>	character Color value for NA.
<code>number.breaks</code>	numeric Controls the number of breaks in continuous color scales of <code>ggplot2</code> -based plots.
<code>plot.title.face, plot.subtitle.face, plot.caption.face, axis.title.face, axis.text.face, legend.title</code>	character Controls the style of the font for the corresponding theme element. One of: <ul style="list-style-type: none"> • <code>plain</code>: For normal text. • <code>italic</code>: For text in italic. • <code>bold</code>: For text in bold. • <code>bold.italic</code>: For text both in italic and bold.

Value

A `ggplot2` object containing a Bee Swarm plot.

Examples

```

# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_BeeSwarmPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your Seurat object.
sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))

  # Basic Bee Swarm plot - categorical coloring.
  # This will color based on the unique values of seurat_clusters.
  p <- SCpubr::do_BeeSwarmPlot(sample = sample,
                               feature_to_rank = "PC_1",
                               group.by = "seurat_clusters",
                               continuous_feature = FALSE)

  # Basic Bee Swarm plot - continuous coloring.
  # This will color based on the PC_1 values.
  p <- SCpubr::do_BeeSwarmPlot(sample = sample,
                               feature_to_rank = "PC_1",
                               group.by = "seurat_clusters",
                               continuous_feature = TRUE)
} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`".)
}

```

do_BoxPlot

*Generate Box Plots.***Description**

Generate Box Plots.

Usage

```

do_BoxPlot(
  sample,
  feature,
  group.by = NULL,
  split.by = NULL,
  assay = NULL,
  slot = "data",
  font.size = 14,
  font.type = "sans",

```

```

axis.text.x.angle = 45,
colors.use = NULL,
na.value = "grey75",
plot.title = NULL,
plot.subtitle = NULL,
plot.caption = NULL,
xlab = NULL,
ylab = NULL,
legend.title = NULL,
legend.title.position = "top",
legend.position = NULL,
boxplot.line.color = "black",
outlier.color = "black",
outlier.alpha = 0.5,
boxplot.linewidth = 0.5,
boxplot.width = NULL,
plot.grid = TRUE,
grid.color = "grey75",
grid.type = "dashed",
flip = FALSE,
order = FALSE,
use_silhouette = FALSE,
use_test = FALSE,
comparisons = NULL,
test = "wilcox.test",
map_signif_level = TRUE,
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
feature	character Feature to represent.
group.by	character Metadata variable to group the output by. Has to be a character of factor column.
split.by	character Secondary metadata variable to further group (split) the output by. Has to be a character of factor column.
assay	character Assay to use. Defaults to the current assay.
slot	character Data slot to use. Only one of: counts, data, scale.data. Defaults to "data".
font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.

font.type	character Base font family for the plot. One of: <ul style="list-style-type: none">• mono: Mono spaced font.• serif: Serif font family.• sans: Default font family.
axis.text.x.angle	numeric Degree to rotate the X labels. One of: 0, 45, 90.
colors.use	named_vector Named vector of valid color representations (either name of HEX codes) with as many named colors as unique values of group.by. If group.by is not provided, defaults to the unique values of Idents . If not provided, a color scale will be set by default.
na.value	character Color value for NA.
plot.title, plot.subtitle, plot.caption	character Title, subtitle or caption to use in the plot.
xlab, ylab	character Titles for the X and Y axis.
legend.title	character Title for the legend.
legend.title.position	character Position for the title of the legend. One of: <ul style="list-style-type: none">• top: Top of the legend.• bottom: Bottom of the legend.• left: Left of the legend.• right: Right of the legend.
legend.position	character Position of the legend in the plot. One of: <ul style="list-style-type: none">• top: Top of the figure.• bottom: Bottom of the figure.• left: Left of the figure.• right: Right of the figure.• none: No legend is displayed.
boxplot.line.color	character Color of the borders of the boxplots if use_silhouette is FALSE.
outlier.color	character Color of the outlier dots.
outlier.alpha	numeric Alpha applied to the outliers.
boxplot.linewidth	numeric Width of the lines in the boxplots. Also controls the lines of the tests applied if use_test is set to true.
boxplot.width	numeric Width of the boxplots.
plot.grid	logical Whether to plot grid lines.
grid.color	character Color of the grid in the plot. In heatmaps, color of the border of the cells.
grid.type	character One of the possible linetype options: <ul style="list-style-type: none">• blank.• solid.

	<ul style="list-style-type: none"> • dashed. • dotted. • dotdash. • longdash. • twodash.
flip	logical Whether to invert the axis of the displayed plot.
order	logical Whether to order the boxplots by average values. Can not be used alongside split.by.
use_silhouette	logical Whether to color the borders of the boxplots instead of the inside area.
use_test	logical Whether to apply a statistical test to a given pair of elements. Can not be used alongside split.by.
comparisons	A list of length-2 vectors. The entries in the vector are either the names of 2 values on the x-axis or the 2 integers that correspond to the index of the columns of interest.
test	the name of the statistical test that is applied to the values of the 2 columns (e.g. t.test, wilcox.test etc.). If you implement a custom test make sure that it returns a list that has an entry called p.value.
map_signif_level	Boolean value, if the p-value are directly written as annotation or asterisks are used instead. Alternatively one can provide a named numeric vector to create custom mappings from p-values to annotation: For example: c("***=0.001, "**=0.01, "*=0.05). Alternatively, one can provide a function that takes a numeric argument (the p-value) and returns a string.
plot.title.face, plot.subtitle.face, plot.caption.face, axis.title.face, axis.text.face, legend.title	character Controls the style of the font for the corresponding theme element. One of: <ul style="list-style-type: none"> • plain: For normal text. • italic: For text in italic. • bold: For text in bold. • bold.italic: For text both in italic and bold.

Value

A ggplot2 object.

Examples

```
# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_BoxPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your Seurat object.
  sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))
```

```

# Basic box plot.
p <- SCpubr::do_BoxPlot(sample = sample,
                        feature = "nCount_RNA")
p

# Use silhouette style.
p <- SCpubr::do_BoxPlot(sample = sample,
                        feature = "nCount_RNA",
                        use_silhouette = TRUE)
p

# Order by mean values.
p <- SCpubr::do_BoxPlot(sample = sample,
                        feature = "nCount_RNA",
                        order = TRUE)
p

# Apply second grouping.
sample$orig.ident <- ifelse(sample$seurat_clusters %in% c("0", "1", "2", "3"), "A", "B")
p <- SCpubr::do_BoxPlot(sample = sample,
                        feature = "nCount_RNA",
                        split.by = "orig.ident")
p

# Apply statistical tests.
p <- SCpubr::do_BoxPlot(sample = sample,
                        feature = "nCount_RNA",
                        group.by = "orig.ident",
                        use_test = TRUE,
                        comparisons = list(c("A", "B")))
p

} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies`.")
}

```

do_CellularStatesPlot *Cellular States plot.*

Description

This plot aims to show the relationships between distinct enrichment scores. If 3 variables are provided, the relationship is between the Y axis and the dual X axis. If 4 variables are provided, each corner of the plot represents how enriched the cells are in that given list. How to interpret this? In a 3-variable plot, the Y axis just means one variable. The higher the cells are in the Y axis the more enriched they are in that given variable. The X axis is a dual parameter one. Cells falling into each extreme of the axis are highly enriched for either x1 or x2, while cells falling in between are

not enriched for any of the two. In a 4-variable plot, each corner shows the enrichment for one of the 4 given features. Cells will tend to locate in either of the four corners, but there will be cases of cells locating mid-way between two given corners (enriched in both features) or in the middle of the plot (not enriched for any).

Usage

```
do_CellularStatesPlot(  
  sample,  
  input_gene_list,  
  x1,  
  y1,  
  x2 = NULL,  
  y2 = NULL,  
  group.by = NULL,  
  colors.use = NULL,  
  legend.position = "bottom",  
  legend.icon.size = 4,  
  legend.ncol = NULL,  
  legend.nrow = NULL,  
  legend.byrow = FALSE,  
  plot.title = NULL,  
  plot.subtitle = NULL,  
  plot.caption = NULL,  
  font.size = 14,  
  font.type = "sans",  
  xlab = NULL,  
  ylab = NULL,  
  axis.ticks = TRUE,  
  axis.text = TRUE,  
  verbose = FALSE,  
  enforce_symmetry = FALSE,  
  plot_marginal_distributions = FALSE,  
  marginal.type = "density",  
  marginal.size = 5,  
  marginal.group = TRUE,  
  plot_cell_borders = TRUE,  
  plot_enrichment_scores = FALSE,  
  border.size = 2,  
  border.color = "black",  
  pt.size = 2,  
  raster = FALSE,  
  raster.dpi = 1024,  
  plot_features = FALSE,  
  features = NULL,  
  use_viridis = TRUE,  
  viridis.palette = "G",  
  viridis.direction = 1,  
  sequential.palette = "YlGnBu",
```

```

sequential.direction = -1,
nbin = 24,
ctrl = 100,
number.breaks = 5,
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample [Seurat](#) | A Seurat object, generated by [CreateSeuratObject](#).

input_gene_list [named_list](#) | Named list of lists of genes to be used as input.

x1 [character](#) | A name of a list from `input_gene_list`. First feature in the X axis. Will go on the right side of the X axis if `y2` is not provided and top-right quadrant if provided.

y1 [character](#) | A name of a list from `input_gene_list`. First feature on the Y axis. Will become the Y axis if `y2` is not provided and bottom-right quadrant if provided.

x2 [character](#) | A name of a list from `input_gene_list`. Second feature on the X axis. Will go on the left side of the X axis if `y2` is not provided and top-left quadrant if provided.

y2 [character](#) | A name of a list from `input_gene_list`. Second feature on the Y axis. Will become the bottom-left quadrant if provided.

group.by [character](#) | Metadata variable to group the output by. Has to be a character of factor column.

colors.use [named_vector](#) | Named vector of valid color representations (either name of HEX codes) with as many named colors as unique values of `group.by`. If `group.by` is not provided, defaults to the unique values of [Idents](#). If not provided, a color scale will be set by default.

legend.position [character](#) | Position of the legend in the plot. One of:

- `top`: Top of the figure.
- `bottom`: Bottom of the figure.
- `left`: Left of the figure.
- `right`: Right of the figure.
- `none`: No legend is displayed.

legend.icon.size [numeric](#) | Size of the icons in legend.

legend.ncol [numeric](#) | Number of columns in the legend.

legend.nrow	numeric Number of rows in the legend.
legend.byrow	logical Whether the legend is filled by row or not.
plot.title, plot.subtitle, plot.caption	character Title, subtitle or caption to use in the plot.
font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
xlab, ylab	character Titles for the X and Y axis.
axis.ticks	logical Whether to show axis ticks.
axis.text	logical Whether to show axis text.
verbose	logical Whether to show extra comments, warnings, etc.
enforce_symmetry	logical Whether to enforce the plot to follow a symmetry (3 variables, the X axis has 0 as center, 4 variables, all axis have the same range and the plot is squared).
plot_marginal_distributions	logical Whether to plot marginal distributions on the figure or not.
marginal.type	character One of: <ul style="list-style-type: none"> • density: Compute density plots on the margins. • histogram: Compute histograms on the margins. • boxplot: Compute boxplot on the margins. • violin: Compute violin plots on the margins. • densigram: Compute densigram plots on the margins.
marginal.size	numeric Size ratio between the main and marginal plots. A value of 5 means that the main plot is 5 times bigger than the marginal plots.
marginal.group	logical Whether to group the marginal distribution by group.by or current identities.
plot_cell_borders	logical Whether to plot border around cells.
plot_enrichment_scores	logical Whether to report enrichment scores for the input lists as plots.
border.size	numeric Width of the border of the cells.
border.color	character Color for the border of the heatmap body.
pt.size	numeric Size of the dots.
raster	logical Whether to raster the resulting plot. This is recommendable if plotting a lot of cells.
raster.dpi	numeric Pixel resolution for rasterized plots. Defaults to 1024. Only activates on Seurat versions higher or equal than 4.1.0.

`plot_features` **logical** | Whether to also report any other feature onto the primary plot.
`features` **character** | Additional features to plot.
`use_viridis` **logical** | Whether to use viridis color scales.
`viridis.palette` **character** | A capital letter from A to H or the scale name as in `scale_fill_viridis`.
`viridis.direction` **numeric** | Either 1 or -1. Controls how the gradient of viridis scale is formed.
`sequential.palette` **character** | Type of sequential color palette to use. Out of the sequential palettes defined in `brewer.pal`.
`sequential.direction` **numeric** | Direction of the sequential color scale. Either 1 or -1.
`nbin` **numeric** | Number of bins to use in `AddModuleScore`.
`ctrl` **numeric** | Number of genes in the control set to use in `AddModuleScore`.
`number.breaks` **numeric** | Controls the number of breaks in continuous color scales of ggplot2-based plots.
`plot.title.face`, `plot.subtitle.face`, `plot.caption.face`, `axis.title.face`, `axis.text.face`, `legend.title` **character** | Controls the style of the font for the corresponding theme element.
One of:

- `plain`: For normal text.
- `italic`: For text in italic.
- `bold`: For text in bold.
- `bold.italic`: For text both in italic and bold.

Details

This plots are based on the following publications:

- Neftel, C. *et al.* An Integrative Model of Cellular States, Plasticity, and Genetics for Glioblastoma. *Cell* 178, 835-849.e21 (2019). doi:10.1016/j.cell.2019.06.024
- Tirosh, I., Venteicher, A., Hebert, C. *et al.* Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. *Nature* 539, 309–313 (2016). doi:10.1038/nature20123

Value

A ggplot2 object containing a butterfly plot.

Examples

```

# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_CellularStatesPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

```

```

# Define your Seurat object.
sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))

# Define some gene sets to query. It has to be a named list.
gene_set <- list("A" = rownames(sample)[1:10],
                "B" = rownames(sample)[11:20],
                "C" = rownames(sample)[21:30],
                "D" = rownames(sample)[31:40])

# Using two variables: A scatter plot X vs Y.
p <- SCpubr::do_CellularStatesPlot(sample = sample,
                                  input_gene_list = gene_set,
                                  x1 = "A",
                                  y1 = "B",
                                  nbin = 1,
                                  ctrl = 10)

p

# Using three variables. Figure from: https://www.nature.com/articles/nature20123.
p <- SCpubr::do_CellularStatesPlot(sample = sample,
                                  input_gene_list = gene_set,
                                  x1 = "A",
                                  y1 = "B",
                                  x2 = "C",
                                  nbin = 1,
                                  ctrl = 10)

p

# Using four variables. Figure from: https://pubmed.ncbi.nlm.nih.gov/31327527/
p <- SCpubr::do_CellularStatesPlot(sample = sample,
                                  input_gene_list = gene_set,
                                  x1 = "A",
                                  y1 = "C",
                                  x2 = "B",
                                  y2 = "D",
                                  nbin = 1,
                                  ctrl = 10)

p
} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`".)
}

```

Description

Generate a Chord diagram.

Usage

```
do_ChordDiagramPlot(
  sample = NULL,
  from = NULL,
  to = NULL,
  colors.from = NULL,
  colors.to = NULL,
  big.gap = 10,
  small.gap = 1,
  link.border.color = NA,
  link.border.width = 1,
  highlight_group = NULL,
  alpha.highlight = 25,
  link.sort = NULL,
  link.decreasing = TRUE,
  z_index = FALSE,
  self.link = 1,
  symmetric = FALSE,
  directional = 1,
  direction.type = c("diffHeight", "arrows"),
  link.arr.type = "big.arrow",
  scale = FALSE,
  alignment = "default",
  annotationTrack = c("grid", "axis"),
  padding_labels = 4,
  ...
)
```

Arguments

`sample` [Seurat](#) | A Seurat object, generated by [CreateSeuratObject](#).

`from`, `to` [character](#) | Categorical metadata variable to be used as origin and end points of the interactions.

`colors.from`, `colors.to` [named_vector](#) | Named vector of colors corresponding to the unique values of "from" and "to".

`big.gap` [numeric](#) | Space between the groups in "from" and "to".

`small.gap` [numeric](#) | Space within the groups.

`link.border.color` [character](#) | Color for the border of the links. NA = no color.

`link.border.width` [numeric](#) | Width of the border line of the links.

highlight_group	character A value from from that will be used to highlight only the links coming from it.
alpha.highlight	numeric A value between 00 (double digits) and 99 to depict the alpha of the highlighted links. No transparency needs "FF"
link.sort	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
link.decreasing	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
z_index	logical Whether to bring the bigger links to the top.
self.link	numeric Behavior of the links. One of: <ul style="list-style-type: none"> • 1: Prevents self linking. • 2: Allows self linking.
symmetric	pass to chordDiagramFromMatrix
directional	numeric Set the direction of the links. One of: <ul style="list-style-type: none"> • 0: Non-directional data. • 1: Links go from "from" to "to". • -1: Links go from "to" to "from". • 2: Links go in both directions.
direction.type	character How to display the directions. One of: <ul style="list-style-type: none"> • diffHeight: Sets a line at the origin of the group showing to how many groups and in which proportion this group is linked to. • arrows: Sets the connection as arrows. • both: Sets up both behaviors. Use as: <code>c("diffHeight", "arrows")</code>.
link.arr.type	character Sets the appearance of the arrows. One of: <ul style="list-style-type: none"> • triangle: Arrow with a triangle tip at the end displayed on top of the link. • big.arrow: The link itself ends in a triangle shape.
scale	logical Whether to put all nodes the same width.
alignment	character How to align the diagram. One of: <ul style="list-style-type: none"> • default: Allows circlize to set up the plot as it sees fit. • horizontal: Sets the break between "from" and "to" groups on the horizontal axis. • vertical: Sets the break between "from" and "to" groups on the vertical axis.
annotationTrack	pass to chordDiagramFromMatrix or chordDiagramFromDataFrame
padding_labels	numeric Number of extra padding (white spaces) of the labels so that they do not overlap with the scales.
...	For internal use only.

Value

A circlize plot.

Examples

```
# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_ChordDiagramPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your Seurat object.
  sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))

  # Basic chord diagram.
  sample$assignment <- ifelse(sample$seurat_clusters %in% c("0", "4", "7"), "A", "B")
  sample$assignment[sample$seurat_clusters %in% c("1", "2")] <- "C"
  sample$assignment[sample$seurat_clusters %in% c("10", "5")] <- "D"
  sample$assignment[sample$seurat_clusters %in% c("8", "9")] <- "E"

  p <- SCpubr::do_ChordDiagramPlot(sample = sample,
                                   from = "seurat_clusters",
                                   to = "assignment")

  p

} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`.")
}
```

do_ColorPalette

Generate color scales based on a value.

Description

This function is an adaptation of `colortools` package. As the package was removed from CRAN on 23-06-2022, this utility function came to existence in order to cover the gap. It is, on its basis, an adaptation of the package into a single function. Original code, developed by Gaston Sanchez, can be found in: <https://github.com/gastonstat/colortools>

Usage

```
do_ColorPalette(
  colors.use,
  n = 12,
  opposite = FALSE,
  adjacent = FALSE,
  triadic = FALSE,
  split_complementary = FALSE,
```

```

    tetradic = FALSE,
    square = FALSE,
    complete_output = FALSE,
    plot = FALSE,
    font.size = 14,
    font.type = "sans"
  )

```

Arguments

colors.use	character One color upon which generate the color scale. Can be a name or a HEX code.
n	numeric Number of colors to include in the color wheel. Use it when all other options are FALSE, otherwise, it becomes 12.
opposite	logical Return the opposing color to the one provided.
adjacent	logical Return the adjacent colors to the one provided.
triadic	logical Return the triadic combination of colors to the one provided.
split_complementary	logical Return the split complementary combination of colors to the one provided.
tetradic	logical Return the tetradic combination of colors to the one provided.
square	logical Return the square combination of colors to the one provided.
complete_output	logical Runs all the previous options and returns all the outputs as a list that contains all color vectors, all plots and a combined plot with everything.
plot	logical Whether to also return a plot displaying the values instead of a vector with the color.
font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.

Value

A character vector with the desired color scale.

Examples

```

# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_ColorPalette", passive = TRUE)

if (isTRUE(value)){
  # Generate a color wheel based on a single value.

```

```

colors <- SCpubr::do_ColorPalette(colors.use = "steelblue")
p <- SCpubr::do_ColorPalette(colors.use = "steelblue",
                             plot = TRUE)

# Generate a pair of opposite colors based on a given one.
colors <- SCpubr::do_ColorPalette(colors.use = "steelblue",
                                 opposite = TRUE)
p <- SCpubr::do_ColorPalette(colors.use = "steelblue",
                             opposite = TRUE,
                             plot = TRUE)

# Generate a trio of adjacent colors based on a given one.
colors <- SCpubr::do_ColorPalette(colors.use = "steelblue",
                                 adjacent = TRUE)
p <- SCpubr::do_ColorPalette(colors.use = "steelblue",
                             adjacent = TRUE,
                             plot = TRUE)

# Generate a trio of triadic colors based on a given one.
colors <- SCpubr::do_ColorPalette(colors.use = "steelblue",
                                 triadic = TRUE)
p <- SCpubr::do_ColorPalette(colors.use = "steelblue",
                             triadic = TRUE,
                             plot = TRUE)

# Generate a trio of split complementary colors based on a given one.
colors <- SCpubr::do_ColorPalette(colors.use = "steelblue",
                                 split_complementary = TRUE)
p <- SCpubr::do_ColorPalette(colors.use = "steelblue",
                             split_complementary = TRUE,
                             plot = TRUE)

# Generate a group of tetradic colors based on a given one.
colors <- SCpubr::do_ColorPalette(colors.use = "steelblue",
                                 tetradic = TRUE)
p <- SCpubr::do_ColorPalette(colors.use = "steelblue",
                             tetradic = TRUE,
                             plot = TRUE)

# Generate a group of square colors based on a given one.
colors <- SCpubr::do_ColorPalette(colors.use = "steelblue",
                                 square = TRUE)
p <- SCpubr::do_ColorPalette(colors.use = "steelblue",
                             square = TRUE,
                             plot = TRUE)

# Retrieve the output of all options.
out <- SCpubr::do_ColorPalette(colors.use = "steelblue",
                              complete_output = TRUE)

## Retrieve the colors.
colors <- out$colors
## Retrieve the plots.
plots <- out$plots

```

```
## Retrieve a combined plot with all the options.
p <- out$combined_plot

} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`.")
}
```

do_CopyNumberVariantPlot

Display CNV scores from inferCNV as Feature Plots.

Description

Display CNV scores from inferCNV as Feature Plots.

Usage

```
do_CopyNumberVariantPlot(
  sample,
  infercnv_object,
  chromosome_locations,
  group.by = NULL,
  using_metacells = FALSE,
  metacell_mapping = NULL,
  legend.type = "colorbar",
  legend.position = "bottom",
  legend.length = 20,
  legend.width = 1,
  legend.framewidth = 0.5,
  legend.tickwidth = 0.5,
  legend.framecolor = "grey50",
  legend.tickcolor = "white",
  font.size = 14,
  pt.size = 1,
  font.type = "sans",
  axis.text.x.angle = 45,
  enforce_symmetry = TRUE,
  legend.title = NULL,
  na.value = "grey75",
  viridis.palette = "G",
  viridis.direction = 1,
  verbose = FALSE,
  min.cutoff = NA,
  max.cutoff = NA,
  number.breaks = 5,
```

```

diverging.palette = "RdBu",
diverging.direction = -1,
sequential.palette = "YlGnBu",
sequential.direction = -1,
use_viridis = TRUE,
return_object = FALSE,
grid.color = "white",
border.color = "black",
flip = FALSE,
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample [Seurat](#) | A Seurat object, generated by [CreateSeuratObject](#).

infercnv_object [infercnv](#) | Output inferCNV object run on the same Seurat object.

chromosome_locations [tibble](#) | Tibble containing the chromosome regions to use. Can be obtained using `utils::data("human_chr_locations", package = "SCpubr")`.

group.by [character](#) | Metadata variable to group the output by. Has to be a character of factor column.

using_metacells [logical](#) | Whether inferCNV was run using metacells or not.

metacell_mapping [named_vector](#) | Vector or cell - metacell mapping.

legend.type [character](#) | Type of legend to display. One of:

- `normal`: Default legend displayed by **ggplot2**.
- `colorbar`: Redefined colorbar legend, using [guide_colorbar](#).

legend.position [character](#) | Position of the legend in the plot. One of:

- `top`: Top of the figure.
- `bottom`: Bottom of the figure.
- `left`: Left of the figure.
- `right`: Right of the figure.
- `none`: No legend is displayed.

legend.length, **legend.width** [numeric](#) | Length and width of the legend. Will adjust automatically depending on legend side.

legend.framewidth, legend.tickwidth
 numeric | Width of the lines of the box in the legend.

legend.framecolor
 character | Color of the lines of the box in the legend.

legend.tickcolor
 character | Color of the ticks of the box in the legend.

font.size
 numeric | Overall font size of the plot. All plot elements will have a size relationship with this font size.

pt.size
 numeric | Size of the dots.

font.type
 character | Base font family for the plot. One of:

- mono: Mono spaced font.
- serif: Serif font family.
- sans: Default font family.

axis.text.x.angle
 numeric | Degree to rotate the X labels. One of: 0, 45, 90.

enforce_symmetry
 logical | Return a symmetrical plot axes-wise or continuous color scale-wise, when applicable.

legend.title
 character | Title for the legend.

na.value
 character | Color value for NA.

viridis.palette
 character | A capital letter from A to H or the scale name as in [scale_fill_viridis](#).

viridis.direction
 numeric | Either 1 or -1. Controls how the gradient of viridis scale is formed.

verbose
 logical | Whether to show extra comments, warnings, etc.

min.cutoff, max.cutoff
 numeric | Set the min/max ends of the color scale. Any cell/group with a value lower than min.cutoff will turn into min.cutoff and any cell with a value higher than max.cutoff will turn into max.cutoff. In FeaturePlots, provide as many values as features. Use NAs to skip a feature.

number.breaks
 numeric | Controls the number of breaks in continuous color scales of ggplot2-based plots.

diverging.palette
 character | Type of symmetrical color palette to use. Out of the diverging palettes defined in [brewer.pal](#).

diverging.direction
 numeric | Either 1 or -1. Direction of the diverging palette. This basically flips the two ends.

sequential.palette
 character | Type of sequential color palette to use. Out of the sequential palettes defined in [brewer.pal](#).

sequential.direction
 numeric | Direction of the sequential color scale. Either 1 or -1.

use_viridis
 logical | Whether to use viridis color scales.

return_object `logical` | Returns the Seurat object with the modifications performed in the function. Normally, this contains a new assay with the data that can then be used for any other visualization desired.

grid.color `character` | Color of the grid in the plot. In heatmaps, color of the border of the cells.

border.color `character` | Color for the border of the heatmap body.

flip `logical` | Whether to invert the axis of the displayed plot.

plot.title.face, plot.subtitle.face, plot.caption.face, axis.title.face, axis.text.face, legend.title `character` | Controls the style of the font for the corresponding theme element. One of:

- `plain`: For normal text.
- `italic`: For text in italic.
- `bold`: For text in bold.
- `bold.italic`: For text both in italic and bold.

Value

A list containing Feature Plots for different chromosome regions and corresponding dot plots by groups..

Examples

```

# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_CopyNumberVariantPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # This function expects that you have run inferCNV on your
  # own and you have access to the output object.

  # Define your Seurat object.
  sample <- readRDS(system.file("extdata/seurat_dataset_example.rds",
                                package = "SCpubr"))

  # Define your inferCNV object.
  infercnv_object <- readRDS(system.file("extdata/infercnv_object_example.rds",
                                         package = "SCpubr"))

  # Get human chromosome locations.
  chromosome_locations = SCpubr::human_chr_locations

  # Compute for a all chromosomes.
  p <- SCpubr::do_CopyNumberVariantPlot(sample = sample,
                                         infercnv_object = infercnv_object,
                                         using_metacells = FALSE,
                                         chromosome_locations = chromosome_locations)

```



```
} else if (base::isFALSE(value)){  
  message("This function can not be used without its suggested packages.")  
  message("Check out which ones are needed using `SCpubr::state_dependencies()`".)  
}
```

do_CorrelationPlot *Create correlation matrix heatmaps.*

Description

Create correlation matrix heatmaps.

Usage

```
do_CorrelationPlot(  
  sample = NULL,  
  input_gene_list = NULL,  
  cluster = TRUE,  
  remove.diagonal = TRUE,  
  mode = "hvg",  
  assay = NULL,  
  group.by = NULL,  
  legend.title = "Pearson coef.",  
  enforce_symmetry = ifelse(mode == "hvg", TRUE, FALSE),  
  font.size = 14,  
  font.type = "sans",  
  na.value = "grey75",  
  legend.width = 1,  
  legend.length = 20,  
  legend.framewidth = 0.5,  
  legend.tickwidth = 0.5,  
  legend.framecolor = "grey50",  
  legend.tickcolor = "white",  
  legend.type = "colorbar",  
  legend.position = "bottom",  
  min.cutoff = NA,  
  max.cutoff = NA,  
  number.breaks = 5,  
  plot.title = NULL,  
  plot.subtitle = NULL,  
  plot.caption = NULL,  
  diverging.palette = "RdBu",  
  diverging.direction = -1,  
  use_viridis = FALSE,  
  viridis.palette = "G",  
  viridis.direction = -1,
```

```

sequential.palette = "YlGnBu",
sequential.direction = 1,
axis.text.x.angle = 45,
grid.color = "white",
border.color = "black",
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

`sample` [Seurat](#) | A Seurat object, generated by [CreateSeuratObject](#).

`input_gene_list` [named_list](#) | Named list of lists of genes to be used as input.

`cluster` [logical](#) | Whether to cluster the elements in the heatmap or not.

`remove.diagonal` [logical](#) | Whether to convert diagonal to NA. Normally this value would be 1, heavily shifting the color scale.

`mode` [character](#) | Different types of correlation matrices can be computed. Right now, the only possible value is "hvg", standing for Highly Variable Genes. The sample is subset for the HVG and the data is re-scaled. Scale data is used for the correlation.

`assay` [character](#) | Assay to use. Defaults to the current assay.

`group.by` [character](#) | Metadata variable to group the output by. Has to be a character of factor column.

`legend.title` [character](#) | Title for the legend.

`enforce_symmetry` [logical](#) | Return a symmetrical plot axes-wise or continuous color scale-wise, when applicable.

`font.size` [numeric](#) | Overall font size of the plot. All plot elements will have a size relationship with this font size.

`font.type` [character](#) | Base font family for the plot. One of:

- `mono`: Mono spaced font.
- `serif`: Serif font family.
- `sans`: Default font family.

`na.value` [character](#) | Color value for NA.

`legend.length`, `legend.width` [numeric](#) | Length and width of the legend. Will adjust automatically depending on legend side.

`legend.framewidth, legend.tickwidth`
 numeric | Width of the lines of the box in the legend.

`legend.framecolor`
 character | Color of the lines of the box in the legend.

`legend.tickcolor`
 character | Color of the ticks of the box in the legend.

`legend.type` **character** | Type of legend to display. One of:

- normal: Default legend displayed by **ggplot2**.
- colorbar: Redefined colorbar legend, using `guide_colorbar`.

`legend.position`
 character | Position of the legend in the plot. One of:

- top: Top of the figure.
- bottom: Bottom of the figure.
- left: Left of the figure.
- right: Right of the figure.
- none: No legend is displayed.

`min.cutoff, max.cutoff`
 numeric | Set the min/max ends of the color scale. Any cell/group with a value lower than `min.cutoff` will turn into `min.cutoff` and any cell with a value higher than `max.cutoff` will turn into `max.cutoff`. In FeaturePlots, provide as many values as features. Use NAs to skip a feature.

`number.breaks` **numeric** | Controls the number of breaks in continuous color scales of `ggplot2`-based plots.

`plot.title, plot.subtitle, plot.caption`
 character | Title, subtitle or caption to use in the plot.

`diverging.palette`
 character | Type of symmetrical color palette to use. Out of the diverging palettes defined in `brewer.pal`.

`diverging.direction`
 numeric | Either 1 or -1. Direction of the diverging palette. This basically flips the two ends.

`use_viridis` **logical** | Whether to use viridis color scales.

`viridis.palette`
 character | A capital letter from A to H or the scale name as in `scale_fill_viridis`.

`viridis.direction`
 numeric | Either 1 or -1. Controls how the gradient of viridis scale is formed.

`sequential.palette`
 character | Type of sequential color palette to use. Out of the sequential palettes defined in `brewer.pal`.

`sequential.direction`
 numeric | Direction of the sequential color scale. Either 1 or -1.

`axis.text.x.angle`
 numeric | Degree to rotate the X labels. One of: 0, 45, 90.

grid.color **character** | Color of the grid in the plot. In heatmaps, color of the border of the cells.

border.color **character** | Color for the border of the heatmap body.

plot.title.face, plot.subtitle.face, plot.caption.face, axis.title.face, axis.text.face, legend.title **character** | Controls the style of the font for the corresponding theme element.
One of:

- plain: For normal text.
- italic: For text in italic.
- bold: For text in bold.
- bold.italic: For text both in italic and bold.

Value

A ggplot2 object.

Examples

```
# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_CorrelationPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your Seurat object.
  sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))

  # Default values.
  p <- SCpubr::do_CorrelationPlot(sample = sample)
  p
} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies`.")
}
```

do_DimPlot

Wrapper for [DimPlot](#).

Description

Wrapper for [DimPlot](#).

Usage

```
do_DimPlot(  
  sample,  
  reduction = NULL,  
  group.by = NULL,  
  split.by = NULL,  
  colors.use = NULL,  
  shuffle = TRUE,  
  order = NULL,  
  raster = FALSE,  
  pt.size = 1,  
  label = FALSE,  
  label.color = "black",  
  label.fill = "white",  
  label.size = 4,  
  label.box = TRUE,  
  repel = FALSE,  
  cells.highlight = NULL,  
  idents.highlight = NULL,  
  idents.keep = NULL,  
  sizes.highlight = 1,  
  ncol = NULL,  
  plot.title = NULL,  
  plot.subtitle = NULL,  
  plot.caption = NULL,  
  legend.title = NULL,  
  legend.position = "bottom",  
  legend.title.position = "top",  
  legend.ncol = NULL,  
  legend.nrow = NULL,  
  legend.icon.size = 4,  
  legend.byrow = FALSE,  
  raster.dpi = 2048,  
  dims = c(1, 2),  
  font.size = 14,  
  font.type = "sans",  
  na.value = "grey75",  
  plot_cell_borders = TRUE,  
  border.size = 2,  
  border.color = "black",  
  border.density = 1,  
  plot_marginal_distributions = FALSE,  
  marginal.type = "density",  
  marginal.size = 5,  
  marginal.group = TRUE,  
  plot.axes = FALSE,  
  plot_density_contour = FALSE,  
  contour.position = "bottom",
```

```

contour.color = "grey90",
contour.lineend = "butt",
contour.linejoin = "round",
contour.expand_axes = 0.25,
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
reduction	character Reduction to use. Can be the canonical ones such as "umap", "pca", or any custom ones, such as "diffusion". If you are unsure about which reductions you have, use <code>Seurat::Reductions(sample)</code> . Defaults to "umap" if present or to the last computed reduction if the argument is not provided.
group.by	character Metadata variable to group the output by. Has to be a character of factor column.
split.by	character Secondary metadata variable to further group (split) the output by. Has to be a character of factor column.
colors.use	named_vector Named vector of valid color representations (either name of HEX codes) with as many named colors as unique values of group.by. If group.by is not provided, defaults to the unique values of Idents . If not provided, a color scale will be set by default.
shuffle	logical Whether to shuffle the cells or not, so that they are not plotted cluster-wise. Recommended.
order	character Vector of identities to be plotted. Either one with all identities or just some, which will be plotted last.
raster	logical Whether to raster the resulting plot. This is recommendable if plotting a lot of cells.
pt.size	numeric Size of the dots.
label	logical Whether to plot the cluster labels in the UMAP. The cluster labels will have the same color as the cluster colors.
label.color	character Color of the labels in the plot.
label.fill	character Color to fill the labels. Has to be a single color, that will be used for all labels. If NULL, the colors of the clusters will be used instead.
label.size	numeric Size of the labels in the plot.
label.box	logical Whether to plot the plot labels as geom_text (FALSE) or geom_label (TRUE).
repel	logical Whether to repel the text labels.

<code>cells.highlight</code> , <code>idents.highlight</code>	<code>character</code> Vector of cells/identities to focus into. The identities have to match those in <code>Seurat::Idents(sample)</code> . The rest of the cells will be grayed out. Both parameters can be used at the same time.
<code>idents.keep</code>	<code>character</code> Vector of identities to keep. This will effectively set the rest of the cells that do not match the identities provided to NA, therefore coloring them according to <code>na.value</code> parameter.
<code>sizes.highlight</code>	<code>numeric</code> Point size of highlighted cells using <code>cells.highlight</code> parameter.
<code>ncol</code>	<code>numeric</code> Number of columns used in the arrangement of the output plot using "split.by" parameter.
<code>plot.title</code> , <code>plot.subtitle</code> , <code>plot.caption</code>	<code>character</code> Title, subtitle or caption to use in the plot.
<code>legend.title</code>	<code>character</code> Title for the legend.
<code>legend.position</code>	<code>character</code> Position of the legend in the plot. One of: <ul style="list-style-type: none">• top: Top of the figure.• bottom: Bottom of the figure.• left: Left of the figure.• right: Right of the figure.• none: No legend is displayed.
<code>legend.title.position</code>	<code>character</code> Position for the title of the legend. One of: <ul style="list-style-type: none">• top: Top of the legend.• bottom: Bottom of the legend.• left: Left of the legend.• right: Right of the legend.
<code>legend.ncol</code>	<code>numeric</code> Number of columns in the legend.
<code>legend.nrow</code>	<code>numeric</code> Number of rows in the legend.
<code>legend.icon.size</code>	<code>numeric</code> Size of the icons in legend.
<code>legend.byrow</code>	<code>logical</code> Whether the legend is filled by row or not.
<code>raster.dpi</code>	<code>numeric</code> Pixel resolution for rasterized plots. Defaults to 1024. Only activates on Seurat versions higher or equal than 4.1.0.
<code>dims</code>	<code>numeric</code> Vector of 2 numerics indicating the dimensions to plot out of the selected reduction. Defaults to <code>c(1, 2)</code> if not specified.
<code>font.size</code>	<code>numeric</code> Overall font size of the plot. All plot elements will have a size relationship with this font size.
<code>font.type</code>	<code>character</code> Base font family for the plot. One of: <ul style="list-style-type: none">• mono: Mono spaced font.• serif: Serif font family.• sans: Default font family.

`na.value` **character** | Color value for NA.
`plot_cell_borders` **logical** | Whether to plot border around cells.
`border.size` **numeric** | Width of the border of the cells.
`border.color` **character** | Color for the border of the heatmap body.
`border.density` **numeric** | Controls the number of cells used when `plot_cell_borders = TRUE`. Value between 0 and 1. It computes a 2D kernel density and based on this cells that have a density below the specified quantile will be used to generate the cluster contour. The lower this number, the less cells will be selected, thus reducing the overall size of the plot but also potentially preventing all the contours to be properly drawn.
`plot_marginal_distributions` **logical** | Whether to plot marginal distributions on the figure or not.
`marginal.type` **character** | One of:

- `density`: Compute density plots on the margins.
- `histogram`: Compute histograms on the margins.
- `boxplot`: Compute boxplot on the margins.
- `violin`: Compute violin plots on the margins.
- `densigram`: Compute densigram plots on the margins.

`marginal.size` **numeric** | Size ratio between the main and marginal plots. A value of 5 means that the main plot is 5 times bigger than the marginal plots.
`marginal.group` **logical** | Whether to group the marginal distribution by `group.by` or current identities.
`plot.axes` **logical** | Whether to plot axes or not.
`plot_density_contour` **logical** | Whether to plot density contours in the UMAP.
`contour.position` **character** | Whether to plot density contours on top or at the bottom of the visualization layers, thus overlapping the clusters/cells or not.
`contour.color` **character** | Color of the density lines.
`contour.lineend` **character** | Line end style (round, butt, square).
`contour.linejoin` **character** | Line join style (round, mitre, bevel).
`contour_expand_axes` **numeric** | To make the contours fit the plot, the limits of the X and Y axis are expanding a given percentage from the min and max values for each axis. This controls such percentage.
`plot.title.face`, `plot.subtitle.face`, `plot.caption.face`, `axis.title.face`, `axis.text.face`, `legend.title` **character** | Controls the style of the font for the corresponding theme element. One of:

- `plain`: For normal text.
- `italic`: For text in italic.
- `bold`: For text in bold.
- `bold.italic`: For text both in italic and bold.

Value

A ggplot2 object containing a DimPlot.

Examples

```
# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_DimPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your Seurat object.
  sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))

  # Basic DimPlot.
  p <- SCpubr::do_DimPlot(sample = sample)

  # Restrict the amount of identities displayed.
  p <- SCpubr::do_DimPlot(sample = sample,
                          idents.keep = c("1", "3", "5"))

  # Group by another variable rather than `Seurat::Idents(sample)`
  p <- SCpubr::do_DimPlot(sample = sample,
                          group.by = "seurat_clusters")

  # Split the output in as many plots as unique identities.
  p <- SCpubr::do_DimPlot(sample = sample,
                          split.by = "seurat_clusters")

  # Highlight given identities
  p <- SCpubr::do_DimPlot(sample,
                          idents.highlight = c("1", "3"))
} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies`.`")
}
```

do_DotPlot

This function is a wrapper for [DotPlot](#). It provides most of its functionalities while adding extra. You can

Description

This function is a wrapper for [DotPlot](#). It provides most of its functionalities while adding extra. You can

Usage

```
do_DotPlot(  
  sample,  
  features,  
  assay = NULL,  
  group.by = NULL,  
  scale = FALSE,  
  legend.title = NULL,  
  legend.type = "colorbar",  
  legend.position = "bottom",  
  legend.framewidth = 0.5,  
  legend.tickwidth = 0.5,  
  legend.length = 20,  
  legend.width = 1,  
  legend.framecolor = "grey50",  
  legend.tickcolor = "white",  
  colors.use = NULL,  
  dot.scale = 6,  
  plot.title = NULL,  
  plot.subtitle = NULL,  
  plot.caption = NULL,  
  xlab = NULL,  
  ylab = NULL,  
  font.size = 14,  
  font.type = "sans",  
  cluster = FALSE,  
  flip = FALSE,  
  axis.text.x.angle = 45,  
  scale.by = "size",  
  use_viridis = FALSE,  
  viridis.palette = "G",  
  viridis.direction = -1,  
  sequential.palette = "YlGnBu",  
  sequential.direction = 1,  
  na.value = "grey75",  
  dot_border = TRUE,  
  plot.grid = TRUE,  
  grid.color = "grey75",  
  grid.type = "dashed",  
  number.breaks = 5,  
  plot.title.face = "bold",  
  plot.subtitle.face = "plain",  
  plot.caption.face = "italic",
```

```

axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample [Seurat](#) | A Seurat object, generated by [CreateSeuratObject](#).

features [character](#) | Features to represent.

assay [character](#) | Assay to use. Defaults to the current assay.

group.by [character](#) | Metadata variable to group the output by. Has to be a character of factor column.

scale [logical](#) | Whether the data should be scaled or not. Non-scaled data allows for comparison across genes. Scaled data allows for an easier comparison along the same gene.

legend.title [character](#) | Title for the legend.

legend.type [character](#) | Type of legend to display. One of:

- normal: Default legend displayed by **ggplot2**.
- colorbar: Redefined colorbar legend, using [guide_colorbar](#).

legend.position [character](#) | Position of the legend in the plot. One of:

- top: Top of the figure.
- bottom: Bottom of the figure.
- left: Left of the figure.
- right: Right of the figure.
- none: No legend is displayed.

legend.framewidth, legend.tickwidth [numeric](#) | Width of the lines of the box in the legend.

legend.length, legend.width [numeric](#) | Length and width of the legend. Will adjust automatically depending on legend side.

legend.framecolor [character](#) | Color of the lines of the box in the legend.

legend.tickcolor [character](#) | Color of the ticks of the box in the legend.

colors.use [named_vector](#) | Named vector of valid color representations (either name of HEX codes) with as many named colors as unique values of group.by. If group.by is not provided, defaults to the unique values of [Idents](#). If not provided, a color scale will be set by default.

dot.scale [numeric](#) | Scale the size of the dots.

plot.title, plot.subtitle, plot.caption [character](#) | Title, subtitle or caption to use in the plot.

xlab, ylab [character](#) | Titles for the X and Y axis.

font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
cluster	logical Whether to cluster the identities based on the expression of the features.
flip	logical Whether to invert the axis of the displayed plot.
axis.text.x.angle	numeric Degree to rotate the X labels. One of: 0, 45, 90.
scale.by	character How to scale the size of the dots. One of: <ul style="list-style-type: none"> • radius: use radius aesthetic. • size: use size aesthetic.
use_viridis	logical Whether to use viridis color scales.
viridis.palette	character A capital letter from A to H or the scale name as in scale_fill_viridis .
viridis.direction	numeric Either 1 or -1. Controls how the gradient of viridis scale is formed.
sequential.palette	character Type of sequential color palette to use. Out of the sequential palettes defined in brewer.pal .
sequential.direction	numeric Direction of the sequential color scale. Either 1 or -1.
na.value	character Color value for NA.
dot_border	logical Whether to plot a border around dots.
plot.grid	logical Whether to plot grid lines.
grid.color	character Color of the grid in the plot. In heatmaps, color of the border of the cells.
grid.type	character One of the possible linetype options: <ul style="list-style-type: none"> • blank. • solid. • dashed. • dotted. • dotdash. • longdash. • twodash.
number.breaks	numeric Controls the number of breaks in continuous color scales of <code>ggplot2</code> -based plots.
plot.title.face, plot.subtitle.face, plot.caption.face, axis.title.face, axis.text.face, legend.title	character Controls the style of the font for the corresponding theme element. One of:

- plain: For normal text.
- italic: For text in italic.
- bold: For text in bold.
- bold.italic: For text both in italic and bold.

Value

A ggplot2 object containing a Dot Plot.

Examples

```
# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_DotPlot", passive = TRUE)

if (isTRUE(value)){
  # Define your Seurat object.
  sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))

  # Basic Dot plot.
  p <- SCpubr::do_DotPlot(sample = sample,
                          features = "EPC1")

  # Querying multiple features.
  genes <- rownames(sample)[1:14]
  p <- SCpubr::do_DotPlot(sample = sample,
                          features = genes)

  # Inverting the axes.
  p <- SCpubr::do_DotPlot(sample = sample,
                          features = genes,
                          cluster = TRUE,
                          plot.title = "Clustered",
                          flip = TRUE)

  # Modifying default colors.
  # Two colors to generate a gradient.
  p <- SCpubr::do_DotPlot(sample = sample,
                          features = genes,
                          colors.use = c("#001219", "#e9d8a6"))

  # Querying multiple features as a named list - splitting by each item in list.
  # Genes have to be unique.
  genes <- list("Naive CD4+ T" = rownames(sample)[1:2],
               "EPC1+ Mono" = rownames(sample)[3:4],
               "Memory CD4+" = rownames(sample)[5],
               "B" = rownames(sample)[6],
               "CD8+ T" = rownames(sample)[7],
               "FCGR3A+ Mono" = rownames(sample)[8:9],
               "NK" = rownames(sample)[10:11],
               "DC" = rownames(sample)[12:13],
               "Platelet" = rownames(sample)[14])
}
```

```

p <- SCpubr::do_DotPlot(sample = sample,
                        features = genes)

# Clustering the identities.
p <- SCpubr::do_DotPlot(sample = sample,
                        features = genes,
                        cluster = TRUE,
                        plot.title = "Clustered")
} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`.")
}

```

do_EnrichmentHeatmap *Create enrichment scores heatmaps.*

Description

This function computes the enrichment scores for the cells using [AddModuleScore](#) and then aggregates the scores by the metadata variables provided by the user and displays it as a heatmap, computed by [Heatmap](#).

Usage

```

do_EnrichmentHeatmap(
  sample,
  input_gene_list,
  features.order = NULL,
  groups.order = NULL,
  cluster = TRUE,
  scale_scores = TRUE,
  assay = NULL,
  slot = NULL,
  reduction = NULL,
  group.by = NULL,
  verbose = FALSE,
  na.value = "grey75",
  legend.position = "bottom",
  use_viridis = FALSE,
  viridis.palette = "G",
  viridis.direction = 1,
  legend.framewidth = 0.5,
  legend.tickwidth = 0.5,
  legend.length = 20,
  legend.width = 1,
  legend.framecolor = "grey50",

```

```

legend.tickcolor = "white",
legend.type = "colorbar",
font.size = 14,
font.type = "sans",
axis.text.x.angle = 45,
enforce_symmetry = FALSE,
nbin = 24,
ctrl = 100,
flavor = "Seurat",
legend.title = NULL,
ncores = 1,
storeRanks = TRUE,
min.cutoff = NA,
max.cutoff = NA,
pt.size = 1,
plot_cell_borders = TRUE,
border.size = 2,
return_object = FALSE,
number.breaks = 5,
sequential.palette = "YlGnBu",
diverging.palette = "RdBu",
diverging.direction = -1,
sequential.direction = 1,
flip = FALSE,
grid.color = "white",
border.color = "black",
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
input_gene_list	named_list Named list of lists of genes to be used as input.
features.order	character Should the gene sets be ordered in a specific way? Provide it as a vector of characters with the same names as the names of the gene sets.
groups.order	named_list Should the groups in the heatmaps be ordered in a specific way? Provide it as a named list (as many lists as values in group.by) with the order for each of the elements in the groups.
cluster	logical Whether to perform clustering of rows and columns.
scale_scores	logical Whether to transform the scores to a range of 0-1 for plotting.

assay	character Assay to use. Defaults to the current assay.
slot	character Data slot to use. Only one of: counts, data, scale.data. Defaults to "data".
reduction	character Reduction to use. Can be the canonical ones such as "umap", "pca", or any custom ones, such as "diffusion". If you are unsure about which reductions you have, use <code>Seurat::Reductions(sample)</code> . Defaults to "umap" if present or to the last computed reduction if the argument is not provided.
group.by	character Metadata variable to group the output by. Has to be a character of factor column.
verbose	logical Whether to show extra comments, warnings, etc.
na.value	character Color value for NA.
legend.position	character Position of the legend in the plot. One of: <ul style="list-style-type: none"> • top: Top of the figure. • bottom: Bottom of the figure. • left: Left of the figure. • right: Right of the figure. • none: No legend is displayed.
use_viridis	logical Whether to use viridis color scales.
viridis.palette	character A capital letter from A to H or the scale name as in scale_fill_viridis .
viridis.direction	numeric Either 1 or -1. Controls how the gradient of viridis scale is formed.
legend.framewidth, legend.tickwidth	numeric Width of the lines of the box in the legend.
legend.length, legend.width	numeric Length and width of the legend. Will adjust automatically depending on legend side.
legend.framecolor	character Color of the lines of the box in the legend.
legend.tickcolor	character Color of the ticks of the box in the legend.
legend.type	character Type of legend to display. One of: <ul style="list-style-type: none"> • normal: Default legend displayed by ggplot2. • colorbar: Redefined colorbar legend, using guide_colorbar.
font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
axis.text.x.angle	numeric Degree to rotate the X labels. One of: 0, 45, 90.

enforce_symmetry	logical Whether the geysers and feature plot has a symmetrical color scale.
nbin	numeric Number of bins to use in AddModuleScore .
ctrl	numeric Number of genes in the control set to use in AddModuleScore .
flavor	character One of: Seurat, UCell. Compute the enrichment scores using AddModuleScore or AddModuleScore_UCell .
legend.title	character Title for the legend.
ncores	numeric Number of cores used to run UCell scoring.
storeRanks	logical Whether to store the ranks for faster UCell scoring computations. Might require large amounts of RAM.
min.cutoff, max.cutoff	numeric Set the min/max ends of the color scale. Any cell/group with a value lower than min.cutoff will turn into min.cutoff and any cell with a value higher than max.cutoff will turn into max.cutoff. In FeaturePlots, provide as many values as features. Use NAs to skip a feature.
pt.size	numeric Size of the dots.
plot_cell_borders	logical Whether to plot border around cells.
border.size	numeric Width of the border of the cells.
return_object	logical Return the Seurat object with the enrichment scores stored.
number.breaks	numeric Controls the number of breaks in continuous color scales of ggplot2-based plots.
sequential.palette	character Type of sequential color palette to use. Out of the sequential palettes defined in brewer.pal .
diverging.palette	character Type of symmetrical color palette to use. Out of the diverging palettes defined in brewer.pal .
diverging.direction	numeric Either 1 or -1. Direction of the diverging palette. This basically flips the two ends.
sequential.direction	numeric Direction of the sequential color scale. Either 1 or -1.
flip	logical Whether to invert the axis of the displayed plot.
grid.color	character Color of the grid in the plot. In heatmaps, color of the border of the cells.
border.color	character Color for the border of the heatmap body.
plot.title.face, plot.subtitle.face, plot.caption.face, axis.title.face, axis.text.face, legend.title	character Controls the style of the font for the corresponding theme element. One of: <ul style="list-style-type: none"> • plain: For normal text. • italic: For text in italic. • bold: For text in bold. • bold.italic: For text both in italic and bold.

Value

A ggplot2 object.

Examples

```
# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_EnrichmentHeatmap", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your Seurat object.
  sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))

  # Genes have to be unique.
  genes <- list("A" = rownames(sample)[1:5],
               "B" = rownames(sample)[6:10],
               "C" = rownames(sample)[11:15])

  # Default parameters.
  p <- SCpubr::do_EnrichmentHeatmap(sample = sample,
                                   input_gene_list = genes,
                                   nbin = 1,
                                   ctrl = 10)

  p

} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies`.`")
}
```

do_ExpressionHeatmap *Create heatmaps of averaged expression by groups.*

Description

This function generates a heatmap with averaged expression values by the unique groups of the metadata variables provided by the user.

Usage

```
do_ExpressionHeatmap(
  sample,
  features,
  group.by = NULL,
  assay = NULL,
  cluster = TRUE,
```

```

features.order = NULL,
groups.order = NULL,
slot = "data",
legend.title = "Avg. Expression",
na.value = "grey75",
legend.position = "bottom",
legend.width = 1,
legend.length = 20,
legend.framewidth = 0.5,
legend.tickwidth = 0.5,
legend.framecolor = "grey50",
legend.tickcolor = "white",
legend.type = "colorbar",
font.size = 14,
font.type = "sans",
axis.text.x.angle = 45,
enforce_symmetry = FALSE,
min.cutoff = NA,
max.cutoff = NA,
diverging.palette = "RdBu",
diverging.direction = -1,
sequential.palette = "YlGnBu",
sequential.direction = 1,
number.breaks = 5,
use_viridis = FALSE,
viridis.palette = "G",
viridis.direction = -1,
flip = FALSE,
grid.color = "white",
border.color = "black",
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
features	character Features to represent.
group.by	character Metadata variable to group the output by. Has to be a character of factor column.
assay	character Assay to use. Defaults to the current assay.
cluster	logical Whether to perform clustering of rows and columns.

features.order	character Should the gene sets be ordered in a specific way? Provide it as a vector of characters with the same names as the names of the gene sets.
groups.order	named_list Should the groups in the heatmaps be ordered in a specific way? Provide it as a named list (as many lists as values in group.by) with the order for each of the elements in the groups.
slot	character Data slot to use. Only one of: counts, data, scale.data. Defaults to "data".
legend.title	character Title for the legend.
na.value	character Color value for NA.
legend.position	character Position of the legend in the plot. One of: <ul style="list-style-type: none"> • top: Top of the figure. • bottom: Bottom of the figure. • left: Left of the figure. • right: Right of the figure. • none: No legend is displayed.
legend.length, legend.width	numeric Length and width of the legend. Will adjust automatically depending on legend side.
legend.framewidth, legend.tickwidth	numeric Width of the lines of the box in the legend.
legend.framecolor	character Color of the lines of the box in the legend.
legend.tickcolor	character Color of the ticks of the box in the legend.
legend.type	character Type of legend to display. One of: <ul style="list-style-type: none"> • normal: Default legend displayed by ggplot2. • colorbar: Redefined colorbar legend, using guide_colorbar.
font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
axis.text.x.angle	numeric Degree to rotate the X labels. One of: 0, 45, 90.
enforce_symmetry	logical Return a symmetrical plot axes-wise or continuous color scale-wise, when applicable.
min.cutoff, max.cutoff	numeric Set the min/max ends of the color scale. Any cell/group with a value lower than min.cutoff will turn into min.cutoff and any cell with a value higher than max.cutoff will turn into max.cutoff. In FeaturePlots, provide as many values as features. Use NAs to skip a feature.

`diverging.palette` **character** | Type of symmetrical color palette to use. Out of the diverging palettes defined in `brewer.pal`.

`diverging.direction` **numeric** | Either 1 or -1. Direction of the diverging palette. This basically flips the two ends.

`sequential.palette` **character** | Type of sequential color palette to use. Out of the sequential palettes defined in `brewer.pal`.

`sequential.direction` **numeric** | Direction of the sequential color scale. Either 1 or -1.

`number.breaks` **numeric** | Controls the number of breaks in continuous color scales of ggplot2-based plots.

`use_viridis` **logical** | Whether to use viridis color scales.

`viridis.palette` **character** | A capital letter from A to H or the scale name as in `scale_fill_viridis`.

`viridis.direction` **numeric** | Either 1 or -1. Controls how the gradient of viridis scale is formed.

`flip` **logical** | Whether to invert the axis of the displayed plot.

`grid.color` **character** | Color of the grid in the plot. In heatmaps, color of the border of the cells.

`border.color` **character** | Color for the border of the heatmap body.

`plot.title.face`, `plot.subtitle.face`, `plot.caption.face`, `axis.title.face`, `axis.text.face`, `legend.title` **character** | Controls the style of the font for the corresponding theme element. One of:

- `plain`: For normal text.
- `italic`: For text in italic.
- `bold`: For text in bold.
- `bold.italic`: For text both in italic and bold.

Value

A ggplot2 object.

Examples

```
# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_ExpressionHeatmap", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your Seurat object.
  sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))

  # Define list of genes.
```

```

genes <- rownames(sample)[1:10]

# Default parameters.
p <- SCpubr::do_ExpressionHeatmap(sample = sample,
                                 features = genes,
                                 viridis.direction = -1)

p
} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`.")
}

```

do_FeaturePlot

Wrapper for [FeaturePlot](#).

Description

Wrapper for [FeaturePlot](#).

Usage

```

do_FeaturePlot(
  sample,
  features,
  assay = NULL,
  reduction = NULL,
  slot = NULL,
  order = FALSE,
  group.by = NULL,
  group.by.colors.use = NULL,
  group.by.legend = NULL,
  group.by.show.dots = TRUE,
  group.by.dot.size = 8,
  group.by.cell_borders = FALSE,
  group.by.cell_borders.alpha = 0.1,
  split.by = NULL,
  idents.keep = NULL,
  cells.highlight = NULL,
  idents.highlight = NULL,
  dims = c(1, 2),
  enforce_symmetry = FALSE,
  pt.size = 1,
  font.size = 14,
  font.type = "sans",
  legend.title = NULL,
  legend.type = "colorbar",

```

```
legend.position = "bottom",
legend.framewidth = 0.5,
legend.tickwidth = 0.5,
legend.length = 20,
legend.width = 1,
legend.framecolor = "grey50",
legend.tickcolor = "white",
legend.ncol = NULL,
legend.nrow = NULL,
legend.byrow = FALSE,
plot.title = NULL,
plot.subtitle = NULL,
plot.caption = NULL,
individual.titles = NULL,
individual.subtitles = NULL,
individual.captions = NULL,
ncol = NULL,
use_viridis = FALSE,
viridis.palette = "G",
viridis.direction = 1,
raster = FALSE,
raster.dpi = 1024,
plot_cell_borders = TRUE,
border.size = 2,
border.color = "black",
border.density = 1,
na.value = "grey75",
verbose = TRUE,
plot.axes = FALSE,
min.cutoff = rep(NA, length(features)),
max.cutoff = rep(NA, length(features)),
plot_density_contour = FALSE,
contour.position = "bottom",
contour.color = "grey90",
contour.lineend = "butt",
contour.linejoin = "round",
contour_expand_axes = 0.25,
label = FALSE,
label.color = "black",
label.size = 4,
number.breaks = 5,
diverging.palette = "RdBu",
diverging.direction = -1,
sequential.palette = "YlGnBu",
sequential.direction = 1,
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
```

```

axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
features	character Features to represent.
assay	character Assay to use. Defaults to the current assay.
reduction	character Reduction to use. Can be the canonical ones such as "umap", "pca", or any custom ones, such as "diffusion". If you are unsure about which reductions you have, use <code>Seurat::Reductions(sample)</code> . Defaults to "umap" if present or to the last computed reduction if the argument is not provided.
slot	character Data slot to use. Only one of: counts, data, scale.data. Defaults to "data".
order	logical Whether to order the cells based on expression.
group.by	character Metadata variable based on which cells are grouped. This will effectively introduce a big dot in the center of each cluster, colored using a categorical color scale or with the values provided by the user in <code>group.by.colors.use</code> . It will also displays a legend.
group.by.colors.use	character Colors to use for the group dots.
group.by.legend	character Title for the legend when <code>group.by</code> is used. Use NA to disable it and NULL to use the default column title provided in <code>group.by</code> .
group.by.show.dots	logical Controls whether to place in the middle of the groups.
group.by.dot.size	numeric Size of the dots placed in the middle of the groups.
group.by.cell_borders	logical Plots another border around the cells displaying the same color code of the dots displayed with <code>group.by</code> . Legend is shown always with <code>alpha = 1</code> regardless of the alpha settings.
group.by.cell_borders.alpha	numeric Controls the transparency of the new borders drawn by <code>group.by.cell_borders</code> .
split.by	character Secondary metadata variable to further group (split) the output by. Has to be a character of factor column.
idents.keep	character Vector of identities to plot. The gradient scale will also be subset to only the values of such identities.
cells.highlight, idents.highlight	character Vector of cells/identities to focus into. The identities have to much those in <code>Seurat::Idents(sample)</code> The rest of the cells will be grayed out. Both parameters can be used at the same time.

<code>dims</code>	numeric Vector of 2 numerics indicating the dimensions to plot out of the selected reduction. Defaults to <code>c(1, 2)</code> if not specified.
<code>enforce_symmetry</code>	logical Return a symmetrical plot axes-wise or continuous color scale-wise, when applicable.
<code>pt.size</code>	numeric Size of the dots.
<code>font.size</code>	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
<code>font.type</code>	character Base font family for the plot. One of: <ul style="list-style-type: none"> • <code>mono</code>: Mono spaced font. • <code>serif</code>: Serif font family. • <code>sans</code>: Default font family.
<code>legend.title</code>	character Title for the legend.
<code>legend.type</code>	character Type of legend to display. One of: <ul style="list-style-type: none"> • <code>normal</code>: Default legend displayed by ggplot2. • <code>colorbar</code>: Redefined colorbar legend, using <code>guide_colorbar</code>.
<code>legend.position</code>	character Position of the legend in the plot. One of: <ul style="list-style-type: none"> • <code>top</code>: Top of the figure. • <code>bottom</code>: Bottom of the figure. • <code>left</code>: Left of the figure. • <code>right</code>: Right of the figure. • <code>none</code>: No legend is displayed.
<code>legend.framewidth</code> , <code>legend.tickwidth</code>	numeric Width of the lines of the box in the legend.
<code>legend.length</code> , <code>legend.width</code>	numeric Length and width of the legend. Will adjust automatically depending on legend side.
<code>legend.framecolor</code>	character Color of the lines of the box in the legend.
<code>legend.tickcolor</code>	character Color of the ticks of the box in the legend.
<code>legend.ncol</code>	numeric Number of columns in the legend.
<code>legend.nrow</code>	numeric Number of rows in the legend.
<code>legend.byrow</code>	logical Whether the legend is filled by row or not.
<code>plot.title</code> , <code>plot.subtitle</code> , <code>plot.caption</code>	character Title, subtitle or caption to use in the plot.
<code>individual.titles</code> , <code>individual.subtitles</code> , <code>individual.captions</code>	character Titles or subtitles. for each feature if needed. Either <code>NULL</code> or a vector of equal length of features.
<code>ncol</code>	numeric Number of columns used in the arrangement of the output plot using <code>"split.by"</code> parameter.

`use_viridis` **logical** | Whether to use viridis color scales.
`viridis.palette` **character** | A capital letter from A to H or the scale name as in [scale_fill_viridis](#).
`viridis.direction` **numeric** | Either 1 or -1. Controls how the gradient of viridis scale is formed.
`raster` **logical** | Whether to raster the resulting plot. This is recommendable if plotting a lot of cells.
`raster.dpi` **numeric** | Pixel resolution for rasterized plots. Defaults to 1024. Only activates on Seurat versions higher or equal than 4.1.0.
`plot_cell_borders` **logical** | Whether to plot border around cells.
`border.size` **numeric** | Width of the border of the cells.
`border.color` **character** | Color for the border of the heatmap body.
`border.density` **numeric** | Controls the number of cells used when `plot_cell_borders = TRUE`. Value between 0 and 1. It computes a 2D kernel density and based on this cells that have a density below the specified quantile will be used to generate the cluster contour. The lower this number, the less cells will be selected, thus reducing the overall size of the plot but also potentially preventing all the contours to be properly drawn.
`na.value` **character** | Color value for NA.
`verbose` **logical** | Whether to show extra comments, warnings, etc.
`plot.axes` **logical** | Whether to plot axes or not.
`min.cutoff, max.cutoff` **numeric** | Set the min/max ends of the color scale. Any cell/group with a value lower than `min.cutoff` will turn into `min.cutoff` and any cell with a value higher than `max.cutoff` will turn into `max.cutoff`. In FeaturePlots, provide as many values as features. Use NAs to skip a feature.
`plot_density_contour` **logical** | Whether to plot density contours in the UMAP.
`contour.position` **character** | Whether to plot density contours on top or at the bottom of the visualization layers, thus overlapping the clusters/cells or not.
`contour.color` **character** | Color of the density lines.
`contour.lineend` **character** | Line end style (round, butt, square).
`contour.linejoin` **character** | Line join style (round, mitre, bevel).
`contour_expand_axes` **numeric** | To make the contours fit the plot, the limits of the X and Y axis are expanding a given percentage from the min and max values for each axis. This controls such percentage.
`label` **logical** | Whether to plot the cluster labels in the UMAP. The cluster labels will have the same color as the cluster colors.


```

        features = c("EPC1"))

# Splitting the FeaturePlot by a variable and
# maintaining the color scale and the UMAP shape.
p <- SCpubr::do_FeaturePlot(sample = sample,
                           features = "EPC1",
                           split.by = "seurat_clusters")

} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies`'")
}

```

do_FunctionalAnnotationPlot

Compute functional annotation plots using GO or KEGG ontologies

Description

Compute functional annotation plots using GO or KEGG ontologies

Usage

```

do_FunctionalAnnotationPlot(
  genes,
  org.db,
  organism = "hsa",
  database = "GO",
  GO_ontology = "BP",
  min.overlap = NULL,
  p.adjust.cutoff = 0.05,
  pAdjustMethod = "BH",
  minGSSize = 10,
  maxGSSize = 500,
  font.size = 10,
  font.type = "sans",
  axis.text.x.angle = 45,
  xlab = NULL,
  ylab = NULL,
  plot.title = NULL,
  plot.subtitle = NULL,
  plot.caption = NULL,
  legend.type = "colorbar",
  legend.position = "bottom",
  legend.framewidth = 0.5,
  legend.tickwidth = 0.5,
  legend.length = 10,

```

```

legend.width = 1,
legend.framecolor = "grey50",
legend.tickcolor = "white",
number.breaks = 5,
return_matrix = FALSE,
grid.color = "white",
border.color = "black",
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

genes	character Vector of gene symbols to query for functional annotation.
org.db	OrgDB Database object to use for the query.
organism	character Supported KEGG organism.
database	character Database to run the analysis on. One of: <ul style="list-style-type: none"> • GO. • KEGG.
GO_ontology	character GO ontology to use. One of: <ul style="list-style-type: none"> • BP: For Biological Process. • MF: For Molecular Function. • CC: For Cellular Component.
min.overlap	numeric Filter the output result to the terms which are supported by this many genes.
p.adjust.cutoff	numeric Significance cutoff used to filter non-significant terms.
pAdjustMethod	character Method to adjust for multiple testing. One of: <ul style="list-style-type: none"> • holm. • hochberg. • hommel. • bonferroni. • BH. • BY. • fdr. • none.
minGSSize	numeric Minimal size of genes annotated by Ontology term for testing.
maxGSSize	numeric Maximal size of genes annotated for testing.

font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
axis.text.x.angle	numeric Degree to rotate the X labels. One of: 0, 45, 90.
xlab, ylab	character Titles for the X and Y axis.
plot.title, plot.subtitle, plot.caption	character Title, subtitle or caption to use in the plot.
legend.type	character Type of legend to display. One of: <ul style="list-style-type: none"> • normal: Default legend displayed by ggplot2. • colorbar: Redefined colorbar legend, using guide_colorbar.
legend.position	character Position of the legend in the plot. One of: <ul style="list-style-type: none"> • top: Top of the figure. • bottom: Bottom of the figure. • left: Left of the figure. • right: Right of the figure. • none: No legend is displayed.
legend.framewidth, legend.tickwidth	numeric Width of the lines of the box in the legend.
legend.length, legend.width	numeric Length and width of the legend. Will adjust automatically depending on legend side.
legend.framecolor	character Color of the lines of the box in the legend.
legend.tickcolor	character Color of the ticks of the box in the legend.
number.breaks	numeric Controls the number of breaks in continuous color scales of ggplot2-based plots.
return_matrix	logical Returns the matrices with the enriched Terms for further use.
grid.color	character Color of the grid in the plot. In heatmaps, color of the border of the cells.
border.color	character Color for the border of the heatmap body.
plot.title.face, plot.subtitle.face, plot.caption.face, axis.title.face, axis.text.face, legend.title	character Controls the style of the font for the corresponding theme element. One of: <ul style="list-style-type: none"> • plain: For normal text. • italic: For text in italic. • bold: For text in bold. • bold.italic: For text both in italic and bold.

Value

A list containing a heatmap of the presence/absence of the genes in the enriched term, as well as a bar plot, dot plot and tree plot of the enriched terms.

Examples

```
# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_FunctionalAnnotationPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Need to load this library or equivalent.
  suppressMessages(library("org.Hs.eg.db"))

  # Define list of genes to query.
  genes.use <- c("CCR7", "CD14", "LYZ",
                "S100A4", "MS4A1",
                "MS4A7", "GNLY", "NKG7", "FCER1A",
                "CST3", "PPBP")

  # Compute the grouped GO terms.
  out <- SCpubr::do_FunctionalAnnotationPlot(genes = genes.use,
                                             org.db = org.Hs.eg.db)

} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`.")
}
```

do_GeyserPlot

Generate a Geyser plot.

Description

A Geyser plot is a custom plot in which we plot continuous values on the Y axis grouped by a categorical value in the X. This is plotted as a dot plot, jittered so that the dots span all the way to the other groups. On top of this, the mean and .66 and .95 of the data is plotted, depicting the overall distribution of the dots. The cells can, then, be colored by a continuous variable (same as Y axis or different) or a categorical one (same as X axis or different).

Usage

```
do_GeyserPlot(
  sample,
  features,
  assay = NULL,
```

```
slot = "data",
group.by = NULL,
split.by = NULL,
enforce_symmetry = FALSE,
scale_type = "continuous",
order = TRUE,
plot_cell_borders = TRUE,
jitter = 0.45,
pt.size = 1,
border.size = 2,
border.color = "black",
legend.position = "bottom",
legend.width = 1,
legend.length = 20,
legend.framewidth = 0.5,
legend.tickwidth = 0.5,
legend.framecolor = "grey50",
legend.tickcolor = "white",
legend.type = "colorbar",
font.size = 14,
font.type = "sans",
axis.text.x.angle = 45,
viridis.palette = "G",
viridis.direction = 1,
colors.use = NULL,
na.value = "grey75",
legend.ncol = NULL,
legend.nrow = NULL,
legend.icon.size = 4,
legend.byrow = FALSE,
legend.title = NULL,
plot.title = NULL,
plot.subtitle = NULL,
plot.caption = NULL,
xlab = "Groups",
ylab = feature,
flip = FALSE,
min.cutoff = rep(NA, length(features)),
max.cutoff = rep(NA, length(features)),
number.breaks = 5,
diverging.palette = "RdBu",
diverging.direction = -1,
sequential.palette = "YlGnBu",
sequential.direction = -1,
use_viridis = TRUE,
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
```



```

axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

`sample` [Seurat](#) | A Seurat object, generated by [CreateSeuratObject](#).

`features` [character](#) | Features to represent.

`assay` [character](#) | Assay to use. Defaults to the current assay.

`slot` [character](#) | Data slot to use. Only one of: counts, data, scale.data. Defaults to "data".

`group.by` [character](#) | Metadata variable to group the output by. Has to be a character of factor column.

`split.by` [character](#) | Secondary metadata variable to further group (split) the output by. Has to be a character of factor column.

`enforce_symmetry` [logical](#) | Return a symmetrical plot axes-wise or continuous color scale-wise, when applicable.

`scale_type` [character](#) | Type of color scale to use. One of:

- `categorical`: Use a categorical color scale based on the values of "group.by".
- `continuous`: Use a continuous color scale based on the values of "feature".

`order` [logical](#) | Whether to order the groups by the median of the data (highest to lowest).

`plot_cell_borders` [logical](#) | Whether to plot border around cells.

`jitter` [numeric](#) | Amount of jitter in the plot along the X axis. The lower the value, the more compacted the dots are.

`pt.size` [numeric](#) | Size of the dots.

`border.size` [numeric](#) | Width of the border of the cells.

`border.color` [character](#) | Color for the border of the heatmap body.

`legend.position` [character](#) | Position of the legend in the plot. One of:

- `top`: Top of the figure.
- `bottom`: Bottom of the figure.
- `left`: Left of the figure.
- `right`: Right of the figure.
- `none`: No legend is displayed.

`legend.length`, `legend.width` [numeric](#) | Length and width of the legend. Will adjust automatically depending on legend side.

`legend.framewidth`, `legend.tickwidth` [numeric](#) | Width of the lines of the box in the legend.

legend.framecolor	character Color of the lines of the box in the legend.
legend.tickcolor	character Color of the ticks of the box in the legend.
legend.type	character Type of legend to display. One of: <ul style="list-style-type: none"> • normal: Default legend displayed by ggplot2. • colorbar: Redefined colorbar legend, using guide_colorbar.
font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
axis.text.x.angle	numeric Degree to rotate the X labels. One of: 0, 45, 90.
viridis.palette	character A capital letter from A to H or the scale name as in scale_fill_viridis .
viridis.direction	numeric Either 1 or -1. Controls how the gradient of viridis scale is formed.
colors.use	character Named vector of colors to use. Has to match the unique values of group.by when scale_type is set to categorical.
na.value	character Color value for NA.
legend.ncol	numeric Number of columns in the legend.
legend.nrow	numeric Number of rows in the legend.
legend.icon.size	numeric Size of the icons in legend.
legend.byrow	logical Whether the legend is filled by row or not.
legend.title	character Title for the legend.
plot.title, plot.subtitle, plot.caption	character Title, subtitle or caption to use in the plot.
xlab, ylab	character Titles for the X and Y axis.
flip	logical Whether to invert the axis of the displayed plot.
min.cutoff, max.cutoff	numeric Set the min/max ends of the color scale. Any cell/group with a value lower than min.cutoff will turn into min.cutoff and any cell with a value higher than max.cutoff will turn into max.cutoff. In FeaturePlots, provide as many values as features. Use NAs to skip a feature.
number.breaks	numeric Controls the number of breaks in continuous color scales of ggplot2-based plots.
diverging.palette	character Type of symmetrical color palette to use. Out of the diverging palettes defined in brewer.pal .


```
} else if (base::isFALSE(value)){  
  message("This function can not be used without its suggested packages.")  
  message("Check out which ones are needed using `SCpubr::state_dependencies()`".)  
}
```

do_GroupedGOTermPlot *Compute an overview of the GO terms associated with the input list of genes.*

Description

Compute an overview of the GO terms associated with the input list of genes.

Usage

```
do_GroupedGOTermPlot(  
  genes,  
  org.db,  
  levels.use = NULL,  
  GO_ontology = "BP",  
  min.overlap = 3,  
  flip = TRUE,  
  colors.use = c(Present = "#1e3d59", Absent = "#bccbcd"),  
  legend.position = "bottom",  
  reverse.levels = TRUE,  
  axis.text.x.angle = 45,  
  font.size = 10,  
  font.type = "sans",  
  plot.title = paste0("GO | ", GO_ontology),  
  plot.subtitle = NULL,  
  plot.caption = NULL,  
  verbose = FALSE,  
  return_matrices = FALSE,  
  grid.color = "white",  
  border.color = "black",  
  plot.title.face = "bold",  
  plot.subtitle.face = "plain",  
  plot.caption.face = "italic",  
  axis.title.face = "bold",  
  axis.text.face = "plain",  
  legend.title.face = "bold",  
  legend.text.face = "plain"  
)
```

Arguments

genes	character Vector of gene symbols to query for functional annotation.
org.db	OrgDB Database object to use for the query.
levels.use	numeric Vector of numerics corresponding to the GO ontology levels to plot. If NULL will compute all recursively until there are no results.
GO_ontology	character GO ontology to use. One of: <ul style="list-style-type: none"> • BP: For Biological Process. • MF: For Molecular Function. • CC: For Cellular Component.
min.overlap	numeric Filter the output result to the terms which are supported by this many genes.
flip	logical Whether to invert the axis of the displayed plot.
colors.use	character Named vector with two colors assigned to the names Present and Absent.
legend.position	character Position of the legend in the plot. One of: <ul style="list-style-type: none"> • top: Top of the figure. • bottom: Bottom of the figure. • left: Left of the figure. • right: Right of the figure. • none: No legend is displayed.
reverse.levels	logical Whether to place the higher levels first when computing the joint heatmap.
axis.text.x.angle	numeric Degree to rotate the X labels. One of: 0, 45, 90.
font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
plot.title, plot.subtitle, plot.caption	character Title, subtitle or caption to use in the plot.
verbose	logical Whether to show extra comments, warnings, etc.
return_matrices	logical Returns the matrices of grouped GO terms.
grid.color	character Color of the grid in the plot. In heatmaps, color of the border of the cells.
border.color	character Color for the border of the heatmap body.
plot.title.face, plot.subtitle.face, plot.caption.face, axis.title.face, axis.text.face, legend.title	character Controls the style of the font for the corresponding theme element. One of:

- plain: For normal text.
- italic: For text in italic.
- bold: For text in bold.
- bold.italic: For text both in italic and bold.

Value

A list containing all the matrices for the respective GO levels and all the individual and combined heatmaps.

Examples

```
# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_GroupedGOTermPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Need to load this library or equivalent.
  suppressMessages(library("org.Hs.eg.db"))

  # Define list of genes to query.
  genes.use <- c("CCR7", "CD14", "LYZ",
                "S100A4", "MS4A1",
                "MS4A7", "GNLY", "NKG7", "FCER1A",
                "CST3", "PPBP")

  # Compute the grouped GO terms.
  out <- SCpubr::do_GroupedGOTermPlot(genes = genes.use,
                                     org.db = org.Hs.eg.db)
} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`.")
}
```

do_GroupwiseDEPlot *Compute a heatmap with the results of a group-wise DE analysis.*

Description

Compute a heatmap with the results of a group-wise DE analysis.

Usage

```
do_GroupwiseDEPlot(
  sample,
  de_genes,
```

```

group.by = NULL,
number.breaks = 5,
top_genes = 5,
use_viridis = FALSE,
viridis.direction = -1,
viridis.palette.pvalue = "C",
viridis.palette.logfc = "E",
viridis.palette.expression = "G",
sequential.direction = 1,
sequential.palette.pvalue = "YlGn",
sequential.palette.logfc = "YlOrRd",
sequential.palette.expression = "YlGnBu",
assay = NULL,
slot = "data",
legend.position = "bottom",
legend.width = 1,
legend.length = 20,
legend.framewidth = 0.5,
legend.tickwidth = 0.5,
legend.framecolor = "grey50",
legend.tickcolor = "white",
legend.type = "colorbar",
font.size = 14,
font.type = "sans",
axis.text.x.angle = 45,
min.cutoff = NA,
max.cutoff = NA,
na.value = "grey75",
grid.color = "white",
border.color = "black",
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
de_genes	tibble DE genes matrix resulting of running <code>Seurat::FindAllMarkers()</code> .
group.by	character Metadata variable to group the output by. Has to be a character of factor column.
number.breaks	numeric Controls the number of breaks in continuous color scales of ggplot2-based plots.
top_genes	numeric Top N differentially expressed (DE) genes by group to retrieve.

`use_viridis` **logical** | Whether to use viridis color scales.
`viridis.direction` **numeric** | Either 1 or -1. Controls how the gradient of viridis scale is formed.
`viridis.palette.pvalue`, `viridis.palette.logfc`, `viridis.palette.expression` **character** | Viridis color palettes for the p-value, logfc and expression heatmaps. A capital letter from A to H or the scale name as in `scale_fill_viridis`.
`sequential.direction` **numeric** | Direction of the sequential color scale. Either 1 or -1.
`sequential.palette.pvalue`, `sequential.palette.expression`, `sequential.palette.logfc` **character** | Sequential palettes for p-value, logfc and expression heatmaps. Type of sequential color palette to use. Out of the sequential palettes defined in `brewer.pal`.
`assay` **character** | Assay to use. Defaults to the current assay.
`slot` **character** | Data slot to use. Only one of: counts, data, scale.data. Defaults to "data".
`legend.position` **character** | Position of the legend in the plot. One of:

- top: Top of the figure.
- bottom: Bottom of the figure.
- left: Left of the figure.
- right: Right of the figure.
- none: No legend is displayed.

`legend.length`, `legend.width` **numeric** | Length and width of the legend. Will adjust automatically depending on legend side.
`legend.framewidth`, `legend.tickwidth` **numeric** | Width of the lines of the box in the legend.
`legend.framecolor` **character** | Color of the lines of the box in the legend.
`legend.tickcolor` **character** | Color of the ticks of the box in the legend.
`legend.type` **character** | Type of legend to display. One of:

- normal: Default legend displayed by **ggplot2**.
- colorbar: Redefined colorbar legend, using `guide_colorbar`.

`font.size` **numeric** | Overall font size of the plot. All plot elements will have a size relationship with this font size.
`font.type` **character** | Base font family for the plot. One of:

- mono: Mono spaced font.
- serif: Serif font family.
- sans: Default font family.

`axis.text.x.angle` **numeric** | Degree to rotate the X labels. One of: 0, 45, 90.

min.cutoff, max.cutoff **numeric** | Set the min/max ends of the color scale. Any cell/group with a value lower than min.cutoff will turn into min.cutoff and any cell with a value higher than max.cutoff will turn into max.cutoff. In FeaturePlots, provide as many values as features. Use NAs to skip a feature.

na.value **character** | Color value for NA.

grid.color **character** | Color of the grid in the plot. In heatmaps, color of the border of the cells.

border.color **character** | Color for the border of the heatmap body.

plot.title.face, plot.subtitle.face, plot.caption.face, axis.title.face, axis.text.face, legend.title **character** | Controls the style of the font for the corresponding theme element. One of:

- plain: For normal text.
- italic: For text in italic.
- bold: For text in bold.
- bold.italic: For text both in italic and bold.

Value

A heatmap composed of 3 main panels: $-\log_{10}(\text{adjusted } p\text{-value})$, $\log_2(\text{FC})$ and mean expression by cluster.

Examples

```
# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_GroupwiseDEPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your Seurat object.
  sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))

  # Compute DE genes and transform to a tibble.
  de_genes <- readRDS(system.file("extdata/de_genes_example.rds", package = "SCpubr"))

  # Default output.
  p <- SCpubr::do_GroupwiseDEPlot(sample = sample,
                                  de_genes = de_genes)

  p
} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies`.")
}
```

do_NebulosaPlot *Wrapper for Nebulosa::plot_density in Seurat.*

Description

Wrapper for Nebulosa::plot_density in Seurat.

Usage

```
do_NebulosaPlot(  
  sample,  
  features,  
  slot = NULL,  
  dims = c(1, 2),  
  pt.size = 1,  
  reduction = NULL,  
  combine = TRUE,  
  method = c("ks", "wkde"),  
  joint = FALSE,  
  return_only_joint = FALSE,  
  plot.title = NULL,  
  plot.subtitle = NULL,  
  plot.caption = NULL,  
  legend.type = "colorbar",  
  legend.framewidth = 0.5,  
  legend.tickwidth = 0.5,  
  legend.length = 20,  
  legend.width = 1,  
  legend.framecolor = "grey50",  
  legend.tickcolor = "white",  
  font.size = 14,  
  font.type = "sans",  
  legend.position = "bottom",  
  plot_cell_borders = TRUE,  
  border.size = 2,  
  border.color = "black",  
  viridis.palette = "G",  
  viridis.direction = 1,  
  verbose = TRUE,  
  na.value = "grey75",  
  plot.axes = FALSE,  
  number.breaks = 5,  
  use_viridis = FALSE,  
  sequential.palette = "YlGnBu",  
  sequential.direction = 1,  
  plot.title.face = "bold",  
  plot.subtitle.face = "plain",
```

```

    plot.caption.face = "italic",
    axis.title.face = "bold",
    axis.text.face = "plain",
    legend.title.face = "bold",
    legend.text.face = "plain"
  )

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
features	character Features to represent.
slot	character Data slot to use. Only one of: counts, data, scale.data. Defaults to "data".
dims	numeric Vector of 2 numerics indicating the dimensions to plot out of the selected reduction. Defaults to c(1, 2) if not specified.
pt.size	numeric Size of the dots.
reduction	character Reduction to use. Can be the canonical ones such as "umap", "pca", or any custom ones, such as "diffusion". If you are unsure about which reductions you have, use <code>Seurat::Reductions(sample)</code> . Defaults to "umap" if present or to the last computed reduction if the argument is not provided.
combine	logical Whether to create a single plot out of multiple features.
method	Kernel density estimation method: <ul style="list-style-type: none"> • ks: Computes density using the kde function from the ks package. • wkde: Computes density using a modified version of the kde2d function from the MASS package to allow weights. Bandwidth selection from the ks package is used instead.
joint	logical Whether to plot different features as joint density.
return_only_joint	logical Whether to only return the joint density panel.
plot.title, plot.subtitle, plot.caption	character Title, subtitle or caption to use in the plot.
legend.type	character Type of legend to display. One of: <ul style="list-style-type: none"> • normal: Default legend displayed by ggplot2. • colorbar: Redefined colorbar legend, using guide_colorbar.
legend.framewidth, legend.tickwidth	numeric Width of the lines of the box in the legend.
legend.length, legend.width	numeric Length and width of the legend. Will adjust automatically depending on legend side.
legend.framecolor	character Color of the lines of the box in the legend.
legend.tickcolor	character Color of the ticks of the box in the legend.

font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
legend.position	character Position of the legend in the plot. One of: <ul style="list-style-type: none"> • top: Top of the figure. • bottom: Bottom of the figure. • left: Left of the figure. • right: Right of the figure. • none: No legend is displayed.
plot.cell.borders	logical Whether to plot border around cells.
border.size	numeric Width of the border of the cells.
border.color	character Color for the border of the heatmap body.
viridis.palette	character A capital letter from A to H or the scale name as in scale_fill_viridis .
viridis.direction	numeric Either 1 or -1. Controls how the gradient of viridis scale is formed.
verbose	logical Whether to show extra comments, warnings, etc.
na.value	character Color value for NA.
plot.axes	logical Whether to plot axes or not.
number.breaks	numeric Controls the number of breaks in continuous color scales of ggplot2-based plots.
use_viridis	logical Whether to use viridis color scales.
sequential.palette	character Type of sequential color palette to use. Out of the sequential palettes defined in brewer.pal .
sequential.direction	numeric Direction of the sequential color scale. Either 1 or -1.
plot.title.face, plot.subtitle.face, plot.caption.face, axis.title.face, axis.text.face, legend.title	character Controls the style of the font for the corresponding theme element. One of: <ul style="list-style-type: none"> • plain: For normal text. • italic: For text in italic. • bold: For text in bold. • bold.italic: For text both in italic and bold.

Value

A ggplot2 object containing a Nebulosa plot.

Examples

```

# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_NebulosaPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your Seurat object.
  sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))

  # Basic Nebulosa plot.
  p <- SCpubr::do_NebulosaPlot(sample = sample,
                               features = "EPC1")

  # Compute joint density.
  p <- SCpubr::do_NebulosaPlot(sample = sample,
                               features = c("EPC1", "TOX2"),
                               joint = TRUE)

} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`.")
}

```

do_PathwayActivityPlot

Plot Pathway Activities from decoupleR using Progeny prior knowledge.

Description

Plot Pathway Activities from decoupleR using Progeny prior knowledge.

Usage

```

do_PathwayActivityPlot(
  sample,
  activities,
  group.by = NULL,
  split.by = NULL,
  slot = "scale.data",
  statistic = "norm_wmean",
  pt.size = 1,
  border.size = 2,
  na.value = "grey75",
  legend.position = "bottom",

```

```

legend.width = 1,
legend.length = 20,
legend.framewidth = 0.5,
legend.tickwidth = 0.5,
legend.framecolor = "grey50",
legend.tickcolor = "white",
legend.type = "colorbar",
font.size = 14,
font.type = "sans",
axis.text.x.angle = 45,
enforce_symmetry = TRUE,
min.cutoff = NA,
max.cutoff = NA,
number.breaks = 5,
diverging.palette = "RdBu",
diverging.direction = -1,
use_viridis = FALSE,
viridis.palette = "G",
viridis.direction = -1,
sequential.palette = "YlGnBu",
sequential.direction = 1,
flip = FALSE,
return_object = FALSE,
grid.color = "white",
border.color = "black",
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
activities	tibble Result of running decoupleR method with progeny regulon prior knowledge.
group.by	character Metadata variable to group the output by. Has to be a character of factor column.
split.by	character Secondary metadata variable to further group (split) the output by. Has to be a character of factor column.
slot	character Data slot to use. Only one of: counts, data, scale.data. Defaults to "data".
statistic	character DecoupleR statistic to use. One of: <ul style="list-style-type: none"> wmean: For weighted mean.

	<ul style="list-style-type: none"> • norm_wmean: For normalized weighted mean. • corr_wmean: For corrected weighted mean.
pt.size	numeric Size of the dots.
border.size	numeric Width of the border of the cells.
na.value	character Color value for NA.
legend.position	<p>character Position of the legend in the plot. One of:</p> <ul style="list-style-type: none"> • top: Top of the figure. • bottom: Bottom of the figure. • left: Left of the figure. • right: Right of the figure. • none: No legend is displayed.
legend.length, legend.width	<p>numeric Length and width of the legend. Will adjust automatically depending on legend side.</p>
legend.framewidth, legend.tickwidth	<p>numeric Width of the lines of the box in the legend.</p>
legend.framecolor	<p>character Color of the lines of the box in the legend.</p>
legend.tickcolor	<p>character Color of the ticks of the box in the legend.</p>
legend.type	<p>character Type of legend to display. One of:</p> <ul style="list-style-type: none"> • normal: Default legend displayed by ggplot2. • colorbar: Redefined colorbar legend, using <code>guide_colorbar</code>.
font.size	<p>numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.</p>
font.type	<p>character Base font family for the plot. One of:</p> <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
axis.text.x.angle	<p>numeric Degree to rotate the X labels. One of: 0, 45, 90.</p>
enforce_symmetry	<p>logical Return a symmetrical plot axes-wise or continuous color scale-wise, when applicable.</p>
min.cutoff, max.cutoff	<p>numeric Set the min/max ends of the color scale. Any cell/group with a value lower than min.cutoff will turn into min.cutoff and any cell with a value higher than max.cutoff will turn into max.cutoff. In FeaturePlots, provide as many values as features. Use NAs to skip a feature.</p>
number.breaks	<p>numeric Controls the number of breaks in continuous color scales of ggplot2-based plots.</p>

`diverging.palette` **character** | Type of symmetrical color palette to use. Out of the diverging palettes defined in `brewer.pal`.

`diverging.direction` **numeric** | Either 1 or -1. Direction of the diverging palette. This basically flips the two ends.

`use_viridis` **logical** | Whether to use viridis color scales.

`viridis.palette` **character** | A capital letter from A to H or the scale name as in `scale_fill_viridis`.

`viridis.direction` **numeric** | Either 1 or -1. Controls how the gradient of viridis scale is formed.

`sequential.palette` **character** | Type of sequential color palette to use. Out of the sequential palettes defined in `brewer.pal`.

`sequential.direction` **numeric** | Direction of the sequential color scale. Either 1 or -1.

`flip` **logical** | Whether to invert the axis of the displayed plot.

`return_object` **logical** | Returns the Seurat object with the modifications performed in the function. Normally, this contains a new assay with the data that can then be used for any other visualization desired.

`grid.color` **character** | Color of the grid in the plot. In heatmaps, color of the border of the cells.

`border.color` **character** | Color for the border of the heatmap body.

`plot.title.face`, `plot.subtitle.face`, `plot.caption.face`, `axis.title.face`, `axis.text.face`, `legend.title` **character** | Controls the style of the font for the corresponding theme element. One of:

- `plain`: For normal text.
- `italic`: For text in italic.
- `bold`: For text in bold.
- `bold.italic`: For text both in italic and bold.

Value

A `ggplot2` object.

Examples

```
# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_PathwayActivityPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your Seurat object.
  sample <- readRDS(system.file("extdata/seurat_dataset_example.rds",
```



```

        package = "SCpubr"))

# Define your activities object.
progeny_activities <- readRDS(system.file("extdata/progeny_activities_example.rds",
                                         package = "SCpubr"))

# General heatmap.
out <- SCpubr::do_PathwayActivityPlot(sample = sample,
                                     activities = progeny_activities)

p <- out$heatmaps$average_scores
p

} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`.")
}

```

do_RidgePlot

Create ridge plots.

Description

This function computes ridge plots based on the **ggridges** package.

Usage

```

do_RidgePlot(
  sample,
  feature,
  group.by = NULL,
  split.by = NULL,
  assay = "SCT",
  slot = "data",
  continuous_scale = FALSE,
  legend.title = NULL,
  legend.ncol = NULL,
  legend.nrow = NULL,
  legend.byrow = FALSE,
  legend.position = NULL,
  legend.width = 1,
  legend.length = 20,
  legend.framewidth = 0.5,
  legend.tickwidth = 0.5,
  legend.framecolor = "grey50",
  legend.tickcolor = "white",
  legend.type = "colorbar",
  colors.use = NULL,

```

```

font.size = 14,
font.type = "sans",
axis.text.x.angle = 45,
plot.title = NULL,
plot.subtitle = NULL,
plot.caption = NULL,
xlab = NULL,
ylab = NULL,
compute_quantiles = FALSE,
compute_custom_quantiles = FALSE,
quantiles = c(0.25, 0.5, 0.75),
compute_distribution_tails = FALSE,
prob_tails = 0.025,
color_by_probabilities = FALSE,
use_viridis = TRUE,
viridis.palette = "G",
viridis.direction = 1,
sequential.palette = "YlGnBu",
sequential.direction = 1,
plot.grid = TRUE,
grid.color = "grey75",
grid.type = "dashed",
flip = FALSE,
number.breaks = 5,
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
feature	character Feature to represent.
group.by	character Metadata variable to group the output by. Has to be a character of factor column.
split.by	character Secondary metadata variable to further group (split) the output by. Has to be a character of factor column.
assay	character Assay to use. Defaults to the current assay.
slot	character Data slot to use. Only one of: counts, data, scale.data. Defaults to "data".
continuous_scale	logical Whether to color the ridges depending on a categorical or continuous scale.

legend.title	character	Title for the legend.
legend.ncol	numeric	Number of columns in the legend.
legend.nrow	numeric	Number of rows in the legend.
legend.byrow	logical	Whether the legend is filled by row or not.
legend.position	character	Position of the legend in the plot. One of: <ul style="list-style-type: none"> • top: Top of the figure. • bottom: Bottom of the figure. • left: Left of the figure. • right: Right of the figure. • none: No legend is displayed.
legend.length, legend.width	numeric	Length and width of the legend. Will adjust automatically depending on legend side.
legend.framewidth, legend.tickwidth	numeric	Width of the lines of the box in the legend.
legend.framecolor	character	Color of the lines of the box in the legend.
legend.tickcolor	character	Color of the ticks of the box in the legend.
legend.type	character	Type of legend to display. One of: <ul style="list-style-type: none"> • normal: Default legend displayed by ggplot2. • colorbar: Redefined colorbar legend, using guide_colorbar.
colors.use	character	Named vector of colors to use. Has to match the unique values of group.by or color.by (if used) when scale_type is set to categorical.
font.size	numeric	Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character	Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
axis.text.x.angle	numeric	Degree to rotate the X labels. One of: 0, 45, 90.
plot.title, plot.subtitle, plot.caption	character	Title, subtitle or caption to use in the plot.
xlab, ylab	character	Titles for the X and Y axis.
compute_quantiles	logical	Whether to compute quantiles of the distribution and color the ridge plots by them.
compute_custom_quantiles	logical	Whether to compute custom quantiles.
quantiles	numeric	Numeric vector of quantiles.

<code>compute_distribution_tails</code>	logical Whether to compute distribution tails and color them.
<code>prob_tails</code>	numeric The accumulated probability that the tails should contain.
<code>color_by_probabilities</code>	logical Whether to color the ridges depending on the probability.
<code>use_viridis</code>	logical Whether to use viridis color scales.
<code>viridis.palette</code>	character A capital letter from A to H or the scale name as in <code>scale_fill_viridis</code> .
<code>viridis.direction</code>	numeric Either 1 or -1. Controls how the gradient of viridis scale is formed.
<code>sequential.palette</code>	character Type of sequential color palette to use. Out of the sequential palettes defined in <code>brewer.pal</code> .
<code>sequential.direction</code>	numeric Direction of the sequential color scale. Either 1 or -1.
<code>plot.grid</code>	logical Whether to plot grid lines.
<code>grid.color</code>	character Color of the grid in the plot. In heatmaps, color of the border of the cells.
<code>grid.type</code>	character One of the possible linetype options: <ul style="list-style-type: none"> • blank. • solid. • dashed. • dotted. • dotdash. • longdash. • twodash.
<code>flip</code>	logical Whether to invert the axis of the displayed plot.
<code>number.breaks</code>	numeric Controls the number of breaks in continuous color scales of <code>ggplot2</code> -based plots.
<code>plot.title.face</code> , <code>plot.subtitle.face</code> , <code>plot.caption.face</code> , <code>axis.title.face</code> , <code>axis.text.face</code> , <code>legend.title</code>	character Controls the style of the font for the corresponding theme element. One of: <ul style="list-style-type: none"> • plain: For normal text. • italic: For text in italic. • bold: For text in bold. • bold.italic: For text both in italic and bold.

Value

A `ggplot2` object.

Examples

```

# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_RidgePlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your Seurat object.
sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))

  # Compute the most basic ridge plot.
p <- SCpubr::do_RidgePlot(sample = sample,
                          feature = "nFeature_RNA")

p

  # Use continuous color scale.
p <- SCpubr::do_RidgePlot(sample = sample,
                          feature = "nFeature_RNA",
                          continuous_scale = TRUE,
                          viridis.direction = 1)

p

  # Draw quantiles of the distribution.
p <- SCpubr::do_RidgePlot(sample = sample,
                          feature = "nFeature_RNA",
                          continuous_scale = TRUE,
                          compute_quantiles = TRUE,
                          compute_custom_quantiles = TRUE)

p

  # Draw probability tails.
p <- SCpubr::do_RidgePlot(sample = sample,
                          feature = "nFeature_RNA",
                          continuous_scale = TRUE,
                          compute_quantiles = TRUE,
                          compute_distribution_tails = TRUE)

p

  # Draw probability tails.
p <- SCpubr::do_RidgePlot(sample = sample,
                          feature = "nFeature_RNA",
                          continuous_scale = TRUE,
                          compute_quantiles = TRUE,
                          color_by_probabilities = TRUE)

p
} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`.")
}

```

do_TermEnrichmentPlot *Display the enriched terms for a given list of genes.*

Description

Display the enriched terms for a given list of genes.

Usage

```
do_TermEnrichmentPlot(
  enriched_terms,
  nchar_wrap = 20,
  nterms = 10,
  font.size = 14,
  font.type = "sans",
  plot.title = NULL,
  plot.subtitle = NULL,
  plot.caption = NULL,
  legend.position = "bottom",
  legend.type = "colorbar",
  colors.use = NULL,
  text_labels_size = 4,
  legend.length = 30,
  legend.width = 1,
  legend.framewidth = 0.5,
  legend.tickwidth = 0.5,
  legend.framecolor = "grey50",
  legend.tickcolor = "white",
  plot.title.face = "bold",
  plot.subtitle.face = "plain",
  plot.caption.face = "italic",
  axis.title.face = "bold",
  axis.text.face = "plain",
  legend.title.face = "bold",
  legend.text.face = "plain"
)
```

Arguments

- enriched_terms **list** | List containing the output(s) of running Enrichr.
- nchar_wrap **numeric** | Number of characters to use as a limit to wrap the term names. The higher this value, the longer the lines would be for each term in the plots. Defaults to 60.
- nterms **numeric** | Number of terms to report for each database. Terms are arranged by adjusted p-value and selected from lowest to highest. Defaults to 5.
- Enrichr.

	<ul style="list-style-type: none"> • FlyEnrichr. • WormEnrichr. • YeastEnrichr. • FishEnrichr.
font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
plot.title, plot.subtitle, plot.caption	character Title, subtitle or caption to use in the plot.
legend.position	character Position of the legend in the plot. One of: <ul style="list-style-type: none"> • top: Top of the figure. • bottom: Bottom of the figure. • left: Left of the figure. • right: Right of the figure. • none: No legend is displayed.
legend.type	character Type of legend to display. One of: <ul style="list-style-type: none"> • normal: Default legend displayed by ggplot2. • colorbar: Redefined colorbar legend, using guide_colorbar.
colors.use	character Character vector of 2 colors (low and high ends of the color scale) to generate the gradient.
text_labels_size	numeric Controls how big or small labels are in the plot.
legend.length, legend.width	numeric Length and width of the legend. Will adjust automatically depending on legend side.
legend.framewidth, legend.tickwidth	numeric Width of the lines of the box in the legend.
legend.framecolor	character Color of the lines of the box in the legend.
legend.tickcolor	character Color of the ticks of the box in the legend.
plot.title.face, plot.subtitle.face, plot.caption.face, axis.title.face, axis.text.face, legend.title	character Controls the style of the font for the corresponding theme element. One of: <ul style="list-style-type: none"> • plain: For normal text. • italic: For text in italic. • bold: For text in bold. • bold.italic: For text both in italic and bold.

Value

A ggplot2 object with enriched terms.

Examples

```
# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_TermEnrichmentPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your enriched terms.
  enriched_terms <- readRDS(system.file("extdata/enriched_terms_example.rds", package = "SCpubr"))
  enriched_terms$GO_Cellular_Component_2021 <- NULL
  enriched_terms$Azimuth_Cell_Types_2021 <- NULL

  # Default plot.
  p <- SCpubr::do_TermEnrichmentPlot(enriched_terms = enriched_terms)
  p
} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`.")
}
```

do_TFActivityPlot

Plot TF Activities from decoupleR using Dorothea prior knowledge.

Description

Plot TF Activities from decoupleR using Dorothea prior knowledge.

Usage

```
do_TFActivityPlot(
  sample,
  activities,
  n_tfs = 25,
  slot = "scale.data",
  statistic = "norm_wmean",
  tfs.use = NULL,
  group.by = NULL,
  split.by = NULL,
  na.value = "grey75",
  legend.position = "bottom",
  legend.width = 1,
  legend.length = 20,
```



```

legend.framewidth = 0.5,
legend.tickwidth = 0.5,
legend.framecolor = "grey50",
legend.tickcolor = "white",
legend.type = "colorbar",
font.size = 14,
font.type = "sans",
axis.text.x.angle = 45,
enforce_symmetry = TRUE,
diverging.palette = "RdBu",
diverging.direction = -1,
use_viridis = FALSE,
viridis.palette = "G",
viridis.direction = -1,
sequential.palette = "YlGnBu",
sequential.direction = 1,
min.cutoff = NA,
max.cutoff = NA,
number.breaks = 5,
flip = FALSE,
return_object = FALSE,
grid.color = "white",
border.color = "black",
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
activities	tibble Result of running decoupleR method with dorothea regulon prior knowledge.
n_tfs	numeric Number of top regulons to consider for downstream analysis.
slot	character Data slot to use. Only one of: counts, data, scale.data. Defaults to "data".
statistic	character DecoupleR statistic to use. One of: <ul style="list-style-type: none"> wmean: For weighted mean. norm_wmean: For normalized weighted mean. corr_wmean: For corrected weighted mean.
tfs.use	character Restrict the analysis to given regulons.
group.by	character Metadata variable to group the output by. Has to be a character of factor column.

split.by	character Secondary metadata variable to further group (split) the output by. Has to be a character of factor column.
na.value	character Color value for NA.
legend.position	character Position of the legend in the plot. One of: <ul style="list-style-type: none"> • top: Top of the figure. • bottom: Bottom of the figure. • left: Left of the figure. • right: Right of the figure. • none: No legend is displayed.
legend.length, legend.width	numeric Length and width of the legend. Will adjust automatically depending on legend side.
legend.framewidth, legend.tickwidth	numeric Width of the lines of the box in the legend.
legend.framecolor	character Color of the lines of the box in the legend.
legend.tickcolor	character Color of the ticks of the box in the legend.
legend.type	character Type of legend to display. One of: <ul style="list-style-type: none"> • normal: Default legend displayed by ggplot2. • colorbar: Redefined colorbar legend, using guide_colorbar.
font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
axis.text.x.angle	numeric Degree to rotate the X labels. One of: 0, 45, 90.
enforce_symmetry	logical Whether the geyser and feature plot has a symmetrical color scale.
diverging.palette	character Type of symmetrical color palette to use. Out of the diverging palettes defined in brewer.pal .
diverging.direction	numeric Either 1 or -1. Direction of the diverging palette. This basically flips the two ends.
use_viridis	logical Whether to use viridis color scales.
viridis.palette	character A capital letter from A to H or the scale name as in scale_fill_viridis .
viridis.direction	numeric Either 1 or -1. Controls how the gradient of viridis scale is formed.


```

# General heatmap.
out <- SCpubr::do_TFActivityPlot(sample = sample,
                                activities = dorothea_activities)
p <- out$heatmaps$saverage_scores
p

} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`.")
}

```

do_ViolinPlot

Wrapper for [VlnPlot](#).

Description

Wrapper for [VlnPlot](#).

Usage

```

do_ViolinPlot(
  sample,
  features,
  assay = NULL,
  slot = NULL,
  group.by = NULL,
  split.by = NULL,
  colors.use = NULL,
  pt.size = 0,
  line_width = 0.5,
  y_cut = rep(NA, length(features)),
  plot_boxplot = TRUE,
  boxplot_width = 0.2,
  legend.position = "none",
  plot.title = NULL,
  plot.subtitle = NULL,
  plot.caption = NULL,
  xlab = rep(NA, length(features)),
  ylab = rep(NA, length(features)),
  font.size = 14,
  font.type = "sans",
  axis.text.x.angle = 45,
  plot.grid = TRUE,
  grid.color = "grey75",
  grid.type = "dashed",
  flip = FALSE,

```

```

ncol = NULL,
share.y.lims = FALSE,
legend.title = NULL,
legend.ncol = NULL,
legend.nrow = NULL,
legend.byrow = FALSE,
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
features	character Features to represent.
assay	character Assay to use. Defaults to the current assay.
slot	character Data slot to use. Only one of: counts, data, scale.data. Defaults to "data".
group.by	character Metadata variable to group the output by. Has to be a character of factor column.
split.by	character Secondary metadata variable to further group (split) the output by. Has to be a character of factor column.
colors.use	named_vector Named vector of valid color representations (either name of HEX codes) with as many named colors as unique values of group.by. If group.by is not provided, defaults to the unique values of Idents . If not provided, a color scale will be set by default.
pt.size	numeric Size of points in the Violin plot.
line_width	numeric Width of the lines drawn in the plot. Defaults to 1.
y_cut	numeric Vector with the values in which the Violins should be cut. Only works for one feature.
plot_boxplot	logical Whether to plot a Box plot inside the violin or not.
boxplot_width	numeric Width of the boxplots. Defaults to 0.2.
legend.position	character Position of the legend in the plot. One of: <ul style="list-style-type: none"> • top: Top of the figure. • bottom: Bottom of the figure. • left: Left of the figure. • right: Right of the figure. • none: No legend is displayed.

plot.title, plot.subtitle, plot.caption	character Title, subtitle or caption to use in the plot.
xlab, ylab	character Titles for the X and Y axis.
font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
axis.text.x.angle	numeric Degree to rotate the X labels. One of: 0, 45, 90.
plot.grid	logical Whether to plot grid lines.
grid.color	character Color of the grid in the plot. In heatmaps, color of the border of the cells.
grid.type	character One of the possible linetype options: <ul style="list-style-type: none"> • blank. • solid. • dashed. • dotted. • dotdash. • longdash. • twodash.
flip	logical Whether to invert the axis of the displayed plot.
ncol	numeric Number of columns used in the arrangement of the output plot using "split.by" parameter.
share.y.lims	logical When querying multiple features, force the Y axis of all of them to be on the same range of values (this being the max and min of all features combined).
legend.title	character Title for the legend.
legend.ncol	numeric Number of columns in the legend.
legend.nrow	numeric Number of rows in the legend.
legend.byrow	logical Whether the legend is filled by row or not.
plot.title.face, plot.subtitle.face, plot.caption.face, axis.title.face, axis.text.face, legend.title	character Controls the style of the font for the corresponding theme element. One of: <ul style="list-style-type: none"> • plain: For normal text. • italic: For text in italic. • bold: For text in bold. • bold.italic: For text both in italic and bold.

Value

A ggplot2 object containing a Violin Plot.

Examples

```

# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_ViolinPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your Seurat object.
  sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))

  # Basic violin plot.
  p <- SCpubr::do_ViolinPlot(sample = sample,
                             feature = "nCount_RNA")

  p

  # Remove the box plots.
  p <- SCpubr::do_ViolinPlot(sample = sample,
                             feature = "nCount_RNA",
                             plot_boxplot = FALSE)

  p

} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies()`.")
}

```

do_VolcanoPlot

Compute a Volcano plot out of DE genes.

Description

Compute a Volcano plot out of DE genes.

Usage

```

do_VolcanoPlot(
  sample,
  de_genes,
  pval_cutoff = 0.05,
  FC_cutoff = 2,
  pt.size = 2,
  border.size = 1.5,
  border.color = "black",
  font.size = 14,
  font.type = "sans",
  plot.title = NULL,
  plot.subtitle = NULL,

```

```

plot.caption = NULL,
plot_lines = TRUE,
line_color = "grey75",
line_size = 0.5,
add_gene_tags = TRUE,
order_tags_by = "both",
n_genes = 5,
use_labels = FALSE,
colors.use = "steelblue",
plot.title.face = "bold",
plot.subtitle.face = "plain",
plot.caption.face = "italic",
axis.title.face = "bold",
axis.text.face = "plain",
legend.title.face = "bold",
legend.text.face = "plain"
)

```

Arguments

sample	Seurat A Seurat object, generated by CreateSeuratObject .
de_genes	tibble Output of <code>Seurat::FindMarkers()</code> .
pval_cutoff	numeric Cutoff for the p-value.
FC_cutoff	numeric Cutoff for the avg_log2FC.
pt.size	numeric Size of the dots.
border.size	numeric Width of the border of the cells.
border.color	character Color for the border of the heatmap body.
font.size	numeric Overall font size of the plot. All plot elements will have a size relationship with this font size.
font.type	character Base font family for the plot. One of: <ul style="list-style-type: none"> • mono: Mono spaced font. • serif: Serif font family. • sans: Default font family.
plot.title, plot.subtitle, plot.caption	character Title, subtitle or caption to use in the plot.
plot_lines	logical Whether to plot the division lines.
line_color	character Color for the lines.
line_size	numeric Size of the lines in the plot.
add_gene_tags	logical Whether to plot the top genes.
order_tags_by	character Either "both", "pvalue" or "logfc".
n_genes	numeric Number of top genes in each side to plot.
use_labels	logical Whether to use labels instead of text for the tags.
colors.use	character Color to generate a tetradic color scale with.

plot.title.face, plot.subtitle.face, plot.caption.face, axis.title.face, axis.text.face, legend.title, **character** | Controls the style of the font for the corresponding theme element.

One of:

- plain: For normal text.
- italic: For text in italic.
- bold: For text in bold.
- bold.italic: For text both in italic and bold.

Value

A volcano plot as a ggplot2 object.

Examples

```
# Check Suggests.
value <- SCpubr:::check_suggests(function_name = "do_VolcanoPlot", passive = TRUE)

if (isTRUE(value)){
  # Consult the full documentation in https://enblacar.github.io/SCpubr-book/

  # Define your Seurat object.
  sample <- readRDS(system.file("extdata/seurat_dataset_example.rds", package = "SCpubr"))

  # Retrieve DE genes.
  de_genes <- readRDS(system.file("extdata/de_genes_example.rds", package = "SCpubr"))

  # Generate a volcano plot.
  p <- SCpubr::do_VolcanoPlot(sample = sample,
                              de_genes = de_genes)

  p

} else if (base::isFALSE(value)){
  message("This function can not be used without its suggested packages.")
  message("Check out which ones are needed using `SCpubr::state_dependencies`.`")
}
```

human_chr_locations *Chromosome arm locations for human genome GRCh38.*

Description

A tibble containing the chromosome, arm and start and end coordinates.

Usage

```
data(human_chr_locations)
```

Format

A tibble with 48 rows and 4 columns:

chr Chromosome.

arm Chromosome arm.

start Start coordinates.

end End coordinates.

package_report

Generate a status report of SCpubr and its dependencies.

Description

This function generates a summary report of the installation status of SCpubr, which packages are still missing and which functions can or can not currently be used.

Usage

```
package_report(startup = FALSE, extended = FALSE)
```

Arguments

startup [logical](#) | Whether the message should be displayed at startup, therefore, also containing welcoming messages and tips. If FALSE, only the report itself will be printed.

extended [logical](#) | Whether the message should also include installed packages, current and available version, and which SCpubr functions can be used with the currently installed packages.

Value

None

Examples

```
# Print a package report.  
SCpubr::package_report(startup = FALSE, extended = FALSE)
```

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