

Package ‘plotthis’

April 7, 2025

Title High-Level Plotting Built Upon 'ggplot2' and Other Plotting Packages

Version 0.6.1

Description Provides high-level API and a wide range of options to create stunning, publication-quality plots effortlessly.

It is built upon 'ggplot2' and other plotting packages, and is designed to be easy to use and to work seamlessly with 'ggplot2' objects.

It is particularly useful for creating complex plots with multiple layers, facets, and annotations. It also provides a set of functions to create plots for specific types of data, such as Venn diagrams, alluvial diagrams, and phylogenetic trees.

The package is designed to be flexible and customizable, and to work well with the 'ggplot2' ecosystem.

The API can be found at <https://pwwang.github.io/plotthis/reference/index.html>.

License GPL (>= 3)

Encoding UTF-8

URL <https://github.com/pwwang/plotthis>

<https://pwwang.github.io/plotthis/>

BugReports <https://github.com/pwwang/plotthis/issues>

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AreaPlot	<i>Area plot</i>
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Description

A plot showing how one or more groups' numeric values change over the progression of a another variable

Usage

```
AreaPlot(  
  data,  
  x,  
  y = NULL,  
  x_sep = "_",  
  split_by = NULL,  
  split_by_sep = "_",  
  group_by = NULL,  
  group_by_sep = "_",  
  group_name = NULL,  
  scale_y = FALSE,  
  theme = "theme_this",  
  theme_args = list(),  
  palette = "Paired",  
  palcolor = NULL,  
  alpha = 1,  
  facet_by = NULL,  
  facet_scales = "fixed",  
  facet_ncol = NULL,  
  facet_nrow = NULL,  
  facet_byrow = TRUE,  
  x_text_angle = 0,  
  aspect.ratio = 1,  
  legend.position = waiver(),  
  legend.direction = "vertical",  
  title = NULL,  
  subtitle = NULL,  
  xlab = NULL,  
  ylab = NULL,  
  keep_empty = FALSE,  
  seed = 8525,  
  combine = TRUE,  
  nrow = NULL,  
  ncol = NULL,  
  byrow = TRUE,  
  axes = NULL,
```

```

    axis_titles = axes,
    guides = NULL,
    design = NULL,
    ...
)

```

Arguments

<code>data</code>	A data frame.
<code>x</code>	A character string specifying the column name of the data frame to plot for the x-axis.
<code>y</code>	A character string specifying the column name of the data frame to plot for the y-axis.
<code>x_sep</code>	A character string to concatenate the columns in <code>x</code> , if multiple columns are provided.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>group_by</code>	Columns to group the data for plotting For those plotting functions that do not support multiple groups, They will be concatenated into one column, using <code>group_by_sep</code> as the separator
<code>group_by_sep</code>	The separator for multiple <code>group_by</code> columns. See <code>group_by</code>
<code>group_name</code>	A character string to name the legend of fill.
<code>scale_y</code>	A logical value to scale the y-axis by the total number in each x-axis group.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be <code>NULL</code> for those values).
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is <code>TRUE</code> .

<code>x_text_angle</code>	A numeric value specifying the angle of the x-axis text.
<code>aspect_ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend_position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend_direction</code>	A character string specifying the direction of the legend.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>keep_empty</code>	A logical value indicating whether to keep empty groups. If <code>FALSE</code> , empty groups will be removed.
<code>seed</code>	The random seed to use. Default is 8525.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is <code>FALSE</code> . Default is <code>TRUE</code> .
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none">• 'keep' will retain all axes in individual plots.• 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout.• 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none">• 'keep' will retain all axis titles in individual plots.• 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction.• 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none">• 'collect' will collect guides below to the given nesting level, removing duplicates.• 'keep' will stop collection at this level and let guides be placed alongside their plot.• 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.

design	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
...	Additional arguments.

Value

A `ggplot` object or `wrap_plots` object or a list of `ggplot` objects

Examples

```
data <- data.frame(
  x = rep(c("A", "B", "C", "D"), 2),
  y = c(1, 3, 6, 4, 2, 5, 7, 8),
  group = rep(c("F1", "F2"), each = 4),
  split = rep(c("X", "Y"), 4)
)
AreaPlot(data, x = "x", y = "y", group_by = "group")
AreaPlot(data, x = "x", y = "y", group_by = "group",
  scale_y = TRUE)
AreaPlot(data, x = "x", y = "y", split_by = "group")
AreaPlot(data, x = "x", y = "y", split_by = "group", palette = c(F1 = "Blues", F2 = "Reds"))
AreaPlot(data, x = "x", y = "y", group_by = "group", split_by = "split",
  legend.direction = c(X = "horizontal", Y = "vertical"),
  legend.position = c(X = "top", Y = "right"))
```

BarPlot

Bar Plot

Description

- `BarPlot` is used to create a bar plot.
- `SplitBarPlot` (a.k.a `WaterfallPlot`) is used to create a bar plot with splitting the bars on the two sides.

Usage

```
BarPlot(
  data,
  x,
  x_sep = "_",
  y = NULL,
  flip = FALSE,
  fill_by_x_if_no_group = TRUE,
  line_name = NULL,
  label_nudge = 0,
  label = NULL,
```

```
label_fg = "black",
label_size = 4,
label_bg = "white",
label_bg_r = 0.1,
group_by = NULL,
group_by_sep = "_",
group_name = NULL,
split_by = NULL,
split_by_sep = "_",
facet_by = NULL,
facet_scales = "fixed",
facet_ncol = NULL,
facet_nrow = NULL,
facet_byrow = TRUE,
facet_args = list(),
add_bg = FALSE,
bg_palette = "stripe",
bg_palcolor = NULL,
bg_alpha = 0.2,
add_line = NULL,
line_color = "red2",
line_width = 0.6,
line_type = 2,
add_trend = FALSE,
trend_color = "black",
trend_linewidth = 1,
trend_ptsize = 2,
theme = "theme_this",
theme_args = list(),
palette = "Paired",
palcolor = NULL,
alpha = 1,
x_text_angle = 0,
aspect.ratio = 1,
y_min = NULL,
y_max = NULL,
position = "auto",
position_dodge_preserve = "total",
legend.position = "right",
legend.direction = "vertical",
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
keep_empty = FALSE,
expand = waiver(),
width = waiver(),
combine = TRUE,
```

```

nrow = NULL,
ncol = NULL,
byrow = TRUE,
seed = 8525,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

SplitBarPlot(
  data,
  x,
  y,
  y_sep = "_",
  flip = FALSE,
  split_by = NULL,
  split_by_sep = "_",
  alpha_by = NULL,
  alpha_reverse = FALSE,
  alpha_name = NULL,
  order_y = list(`+` = c("x_desc", "alpha_desc"), `-` = c("x_desc", "alpha_asc")),
  bar_height = 0.9,
  lineheight = 0.5,
  max_charwidth = 80,
  fill_by = NULL,
  fill_by_sep = "_",
  fill_name = NULL,
  direction_pos_name = "positive",
  direction_neg_name = "negative",
  theme = "theme_this",
  theme_args = list(),
  palette = "Spectral",
  palcolor = NULL,
  facet_by = NULL,
  facet_scales = "free_y",
  facet_nrow = NULL,
  facet_ncol = NULL,
  facet_byrow = TRUE,
  aspect.ratio = 1,
  x_min = NULL,
  x_max = NULL,
  legend.position = "right",
  legend.direction = "vertical",
  title = NULL,
  subtitle = NULL,
  xlab = NULL,

```



```
  ylab = NULL,
  keep_empty = FALSE,
  combine = TRUE,
  nrow = NULL,
  ncol = NULL,
  byrow = TRUE,
  seed = 8525,
  axes = NULL,
  axis_titles = axes,
  guides = NULL,
  design = NULL,
  ...
)

WaterfallPlot(
  data,
  x,
  y,
  y_sep = "_",
  flip = FALSE,
  split_by = NULL,
  split_by_sep = "_",
  alpha_by = NULL,
  alpha_reverse = FALSE,
  alpha_name = NULL,
  order_y = list(`+` = c("x_desc", "alpha_desc"), `^-` = c("x_desc", "alpha_asc")),
  bar_height = 0.9,
  lineheight = 0.5,
  max_charwidth = 80,
  fill_by = NULL,
  fill_by_sep = "_",
  fill_name = NULL,
  direction_pos_name = "positive",
  direction_neg_name = "negative",
  theme = "theme_this",
  theme_args = list(),
  palette = "Spectral",
  palcolor = NULL,
  facet_by = NULL,
  facet_scales = "free_y",
  facet_nrow = NULL,
  facet_ncol = NULL,
  facet_byrow = TRUE,
  aspect.ratio = 1,
  x_min = NULL,
  x_max = NULL,
  legend.position = "right",
  legend.direction = "vertical",
```

```

    title = NULL,
    subtitle = NULL,
    xlab = NULL,
    ylab = NULL,
    keep_empty = FALSE,
    combine = TRUE,
    nrow = NULL,
    ncol = NULL,
    byrow = TRUE,
    seed = 8525,
    axes = NULL,
    axis_titles = axes,
    guides = NULL,
    design = NULL,
    ...
)

```

Arguments

<code>data</code>	A data frame.
<code>x</code>	A character string specifying the column name of the data frame to plot for the x-axis.
<code>x_sep</code>	A character string to concatenate the columns in <code>x</code> , if multiple columns are provided.
<code>y</code>	A character string specifying the column name of the data frame to plot for the y-axis.
<code>flip</code>	A logical value indicating whether to flip the x and y axes.
<code>fill_by_x_if_no_group</code>	A logical value indicating whether to fill the bars by the x-axis values if there is no <code>group_by</code> .
<code>line_name</code>	A character string indicating the name of the line.
<code>label_nudge</code>	A numeric value to nudge the labels (the distance between the label and the top of the bar).
<code>label</code>	A column name for the values to be displayed on the top of the bars. If <code>TRUE</code> , the y values will be displayed.
<code>label_fg</code>	A character string indicating the color of the label.
<code>label_size</code>	A numeric value indicating the size of the label.
<code>label_bg</code>	A character string indicating the background color of the label.
<code>label_bg_r</code>	A numeric value indicating the radius of the background.
<code>group_by</code>	Columns to group the data for plotting For those plotting functions that do not support multiple groups, They will be concatenated into one column, using <code>group_by_sep</code> as the separator
<code>group_by_sep</code>	The separator for multiple <code>group_by</code> columns. See <code>group_by</code>
<code>group_name</code>	A character string to specify the name of the <code>group_by</code> in the legend.

<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is TRUE.
<code>facet_args</code>	A list of arguments to pass to <code>ggplot2::facet_grid</code> or <code>ggplot2::facet_wrap</code> .
<code>add_bg</code>	A logical value indicating whether to add a background to the plot.
<code>bg_palette</code>	A character string indicating the palette to use for the background.
<code>bg_palcolor</code>	A character string indicating the color to use for the background.
<code>bg_alpha</code>	A numeric value indicating the alpha of the background.
<code>add_line</code>	A numeric value indicating the y value to add a horizontal line.
<code>line_color</code>	A character string indicating the color of the line.
<code>line_width</code>	A numeric value indicating the size of the line.
<code>line_type</code>	A numeric value indicating the type of the line.
<code>add_trend</code>	A logical value to add trend line to the plot.
<code>trend_color</code>	A character string to specify the color of the trend line.
<code>trend_linewidth</code>	A numeric value to specify the width of the trend line.
<code>trend_ptsize</code>	A numeric value to specify the size of the trend line points.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be NULL for those values).
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>x_text_angle</code>	A numeric value specifying the angle of the x-axis text.
<code>aspect.ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>y_min</code>	A numeric value to specify the minimum value of the y axis.
<code>y_max</code>	A numeric value to specify the maximum value of the y axis.

position	A character string indicating the position of the bars. If "auto", the position will be "stack" if group_by has more than 5 levels, otherwise "dodge". "fill" is also a valid option. Only works when group_by is not NULL.
position_dodge_preserve	Should dodging preserve the "total" width of all elements at a position, or the width of a "single" element?
legend.position	A character string specifying the position of the legend. if waiver(), for single groups, the legend will be "none", otherwise "right".
legend.direction	A character string specifying the direction of the legend.
title	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when split_by is used and the title needs to be dynamic.
subtitle	A character string specifying the subtitle of the plot.
xlab	A character string specifying the x-axis label.
ylab	A character string specifying the y-axis label.
keep_empty	A logical value indicating whether to keep empty groups. If FALSE, empty groups will be removed.
expand	The values to expand the x and y axes. It is like CSS padding. When a single value is provided, it is used for both axes on both sides. When two values are provided, the first value is used for the top/bottom side and the second value is used for the left/right side. When three values are provided, the first value is used for the top side, the second value is used for the left/right side, and the third value is used for the bottom side. When four values are provided, the values are used for the top, right, bottom, and left sides, respectively. You can also use a named vector to specify the values for each side. When the axis is discrete, the values will be applied as 'add' to the 'expansion' function. When the axis is continuous, the values will be applied as 'mult' to the 'expansion' function. See also https://ggplot2.tidyverse.org/reference/expansion.html
width	A numeric value specifying the width of the bars.
combine	Whether to combine the plots into one when facet is FALSE. Default is TRUE.
nrow	A numeric value specifying the number of rows in the facet.
ncol	A numeric value specifying the number of columns in the facet.
byrow	A logical value indicating whether to fill the plots by row.
seed	The random seed to use. Default is 8525.
axes	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when split_by is used and combine is TRUE. Options are: <ul style="list-style-type: none"> 'keep' will retain all axes in individual plots. 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.

axis_titles	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
guides	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
design	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
...	Additional arguments.
y_sep	A character string to concatenate the x columns if there are multiple.
alpha_by	A character string indicating the column name to use for the transparency of the bars.
alpha_reverse	A logical value indicating whether to reverse the transparency.
alpha_name	A character string indicating the legend name of the transparency.
order_y	A list of character strings indicating the order of the y axis. The keys are "+", "-", or "". <i>However, "+/-" should not be mixed with ""</i> . The values are "x_asc", "x_desc", "alpha_asc", or "alpha_desc", indicating how to order the y axis. The default is <code>list("+ = c("x_desc", "alpha_desc"), "-" = c("x_desc", "alpha_asc"))</code> , meaning the positive values are ordered by the x-axis values in descending order and the alpha values in descending order, and the negative values are ordered by the x-axis values in descending order and the alpha values in ascending order. The "*" key is used to order the y axis without considering the direction.
bar_height	A numeric value indicating the height of the bars.
lineheight	A numeric value indicating the height of the text.
max_charwidth	A numeric value indicating the maximum width of the text.
fill_by	A character string indicating the column name to use for the fill of the bars.
fill_by_sep	A character string to concatenate the fill columns if there are multiple.
fill_name	A character string indicating the legend name of the fill.
direction_pos_name	A character string indicating the name of the positive direction.

direction_neg_name A character string indicating the name of the negative direction.

x_min A numeric value indicating the minimum value of the x axis.

x_max A numeric value indicating the maximum value of the x axis.

Value

A ggplot object or wrap_plots object or a list of ggplot objects

Examples

```
data <- data.frame(
  x = c("A", "B", "C", "D", "E", "F", "G", "H"),
  y = c(10, 8, 16, 4, 6, 12, 14, 2),
  group = c("G1", "G1", "G2", "G2", "G3", "G3", "G4", "G4"),
  facet = c("F1", "F2", "F3", "F4", "F1", "F2", "F3", "F4")
)

BarPlot(data, x = "x", y = "y")
BarPlot(data, x = "x", y = "y", fill_by_x_if_no_group = FALSE)
BarPlot(data, x = "x", y = "y", label = TRUE)
BarPlot(data, x = "x", y = "y", label = "facet", label_nudge = 1)
BarPlot(data, x = "group", y = "y", group_by = "x")
BarPlot(data,
  x = "group", y = "y", group_by = "x",
  position = "dodge", add_bg = TRUE
)
BarPlot(data,
  x = "x", y = "y", split_by = "group",
  facet_by = "facet", position = "dodge", facet_ncol = 1
)
BarPlot(data,
  x = "x", y = "y", split_by = "group", facet_by = "facet",
  position = "dodge", facet_ncol = 1, guides = 'collect'
)
BarPlot(data,
  x = "x", y = "y", split_by = "group",
  palette = list(G1 = "Reds", G2 = "Blues", G3 = "Greens", G4 = "Purp"),
  facet_by = "facet", position = "dodge", facet_ncol = 1
)
BarPlot(data,
  x = "group", y = "y", group_by = "x",
  position = "dodge", add_bg = TRUE, bg_palette = "Spectral"
)
# use the count
BarPlot(data, x = "group", ylab = "count")
# flip the plot
BarPlot(data, x = "group", flip = TRUE, ylab = "count")

data <- data.frame(
  word = c("apple", "banana", "cherry", "date", "elderberry",
    "It is a very long term with a lot of words"),
```

```

count = c(-10, 20, -30, 40, 50, 34),
score = c(1, 2, 3, 4, 5, 3.2),
group = c("A", "A", "B", "B", "C", "C")
)
SplitBarPlot(data, x = "count", y = "word", alpha_by = "score")
SplitBarPlot(data, x = "count", y = "word", alpha_by = "score",
             max_charwidth = 30, lineheight = 1.1)
SplitBarPlot(data, x = "count", y = "word", fill_by = "group")
SplitBarPlot(data, x = "count", y = "word", facet_by = "group",
             fill_name = "Direction")
SplitBarPlot(data, x = "count", y = "word", alpha_by = "score", split_by="group",
             palette = c(A = "Reds", B = "Blues", C = "Greens"))

```

BoxPlot

Box / Violin Plot

Description

Box plot or violin plot with optional jitter points, trend line, statistical test, background, line, and highlight.

Usage

```

BoxPlot(
  data,
  x,
  x_sep = "_",
  y = NULL,
  in_form = c("long", "wide"),
  split_by = NULL,
  split_by_sep = "_",
  sort_x = c("none", "mean_asc", "mean_desc", "mean", "median_asc", "median_desc",
            "median"),
  flip = FALSE,
  keep_empty = FALSE,
  group_by = NULL,
  group_by_sep = "_",
  group_name = NULL,
  x_text_angle = ifelse(isTRUE(flip) && isTRUE(stack), 90, 45),
  fill_mode = ifelse(!is.null(group_by), "dodge", "x"),
  fill_reverse = FALSE,
  theme = "theme_this",
  theme_args = list(),
  palette = "Paired",
  palcolor = NULL,
  alpha = 1,
  aspect.ratio = NULL,
  legend.position = "right",

```

```
legend.direction = "vertical",
add_point = FALSE,
pt_color = "grey30",
pt_size = NULL,
pt_alpha = 1,
jitter_width = 0.5,
jitter_height = 0.1,
stack = FALSE,
y_max = NULL,
y_min = NULL,
add_trend = FALSE,
trend_color = NULL,
trend_linewidth = 1,
trend_ptsize = 2,
add_stat = NULL,
stat_name = NULL,
stat_color = "black",
stat_size = 1,
stat_stroke = 1,
stat_shape = 25,
add_bg = FALSE,
bg_palette = "stripe",
bg_palcolor = NULL,
bg_alpha = 0.2,
add_line = NULL,
line_color = "red2",
line_width = 0.6,
line_type = 2,
highlight = NULL,
highlight_color = "red2",
highlight_size = 1,
highlight_alpha = 1,
comparisons = NULL,
ref_group = NULL,
pairwise_method = "wilcox.test",
multiplegroup_comparisons = FALSE,
multiple_method = "kruskal.test",
sig_label = c("p.signif", "p.format"),
sig_labelsize = 3.5,
facet_by = NULL,
facet_scales = "fixed",
facet_ncol = NULL,
facet_nrow = NULL,
facet_byrow = TRUE,
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
```



```
seed = 8525,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
...
)

ViolinPlot(
  data,
  x,
  x_sep = "_",
  y = NULL,
  in_form = c("long", "wide"),
  split_by = NULL,
  split_by_sep = "_",
  sort_x = c("none", "mean_asc", "mean_desc", "mean", "median_asc", "median_desc",
    "median"),
  flip = FALSE,
  keep_empty = FALSE,
  group_by = NULL,
  group_by_sep = "_",
  group_name = NULL,
  x_text_angle = ifelse(isTRUE(flip) && isTRUE(stack), 90, 45),
  fill_mode = ifelse(!is.null(group_by), "dodge", "x"),
  fill_reverse = FALSE,
  theme = "theme_this",
  theme_args = list(),
  palette = "Paired",
  palcolor = NULL,
  alpha = 1,
  aspect.ratio = NULL,
  legend.position = "right",
  legend.direction = "vertical",
  add_point = FALSE,
  pt_color = "grey30",
  pt_size = NULL,
  pt_alpha = 1,
  jitter_width = 0.5,
  jitter_height = 0.1,
  stack = FALSE,
  y_max = NULL,
  y_min = NULL,
  add_box = FALSE,
  box_color = "black",
```

```
box_width = 0.1,
box_ptsize = 2.5,
add_trend = FALSE,
trend_color = NULL,
trend_linewidth = 1,
trend_ptsize = 2,
add_stat = NULL,
stat_name = NULL,
stat_color = "black",
stat_size = 1,
stat_stroke = 1,
stat_shape = 25,
add_bg = FALSE,
bg_palette = "stripe",
bg_palcolor = NULL,
bg_alpha = 0.2,
add_line = NULL,
line_color = "red2",
line_width = 0.6,
line_type = 2,
highlight = NULL,
highlight_color = "red2",
highlight_size = 1,
highlight_alpha = 1,
comparisons = NULL,
ref_group = NULL,
pairwise_method = "wilcox.test",
multiplegroup_comparisons = FALSE,
multiple_method = "kruskal.test",
sig_label = c("p.signif", "p.format"),
sig_labelsize = 3.5,
facet_by = NULL,
facet_scales = "fixed",
facet_ncol = NULL,
facet_nrow = NULL,
facet_byrow = TRUE,
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
seed = 8525,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
```

```
    ...
  )
```

Arguments

<code>data</code>	A data frame.
<code>x</code>	A character string specifying the column name of the data frame to plot for the x-axis.
<code>x_sep</code>	A character string to concatenate the columns in <code>x</code> , if multiple columns are provided. When <code>in_form</code> is "wide", <code>x</code> columns will not be concatenated.
<code>y</code>	A character string specifying the column name of the data frame to plot for the y-axis.
<code>in_form</code>	A character string to specify the input data type. Either "long" or "wide".
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>sort_x</code>	A character string to specify the sorting of x-axis. Either "none", "mean_asc", "mean_desc", "mean", "median_asc", "median_desc", "median".
<code>flip</code>	A logical value to flip the plot.
<code>keep_empty</code>	A logical value indicating whether to keep empty groups. If FALSE, empty groups will be removed.
<code>group_by</code>	Columns to group the data for plotting For those plotting functions that do not support multiple groups, They will be concatenated into one column, using <code>group_by_sep</code> as the separator
<code>group_by_sep</code>	The separator for multiple <code>group_by</code> columns. See <code>group_by</code>
<code>group_name</code>	A character string to name the legend of dodge.
<code>x_text_angle</code>	A numeric value specifying the angle of the x-axis text.
<code>fill_mode</code>	A character string to specify the fill mode. Either "dodge", "x", "mean", "median".
<code>fill_reverse</code>	A logical value to reverse the fill colors for gradient fill (mean/median).
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be NULL for those values).
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>aspect.ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".

<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>add_point</code>	A logical value to add (jitter) points to the plot.
<code>pt_color</code>	A character string to specify the color of the points.
<code>pt_size</code>	A numeric value to specify the size of the points.
<code>pt_alpha</code>	A numeric value to specify the transparency of the points.
<code>jitter_width</code>	A numeric value to specify the width of the jitter.
<code>jitter_height</code>	A numeric value to specify the height of the jitter.
<code>stack</code>	A logical value whether to stack the faceted plot by 'facet_by'.
<code>y_max</code>	A numeric value or a character string to specify the maximum value of the y-axis.
<code>y_min</code>	A numeric value or a character string to specify the minimum value of the y-axis.
<code>add_trend</code>	A logical value to add trend line to the plot.
<code>trend_color</code>	A character string to specify the color of the trend line.
<code>trend_linewidth</code>	A numeric value to specify the width of the trend line.
<code>trend_ptsize</code>	A numeric value to specify the size of the trend line points.
<code>add_stat</code>	A character string to add statistical test to the plot.
<code>stat_name</code>	A character string to specify the name of the stat legend.
<code>stat_color</code>	A character string to specify the color of the statistical test.
<code>stat_size</code>	A numeric value to specify the size of the statistical test.
<code>stat_stroke</code>	A numeric value to specify the stroke of the statistical test.
<code>stat_shape</code>	A numeric value to specify the shape of the statistical test.
<code>add_bg</code>	A logical value to add background to the plot.
<code>bg_palette</code>	A character string to specify the palette of the background.
<code>bg_palcolor</code>	A character vector to specify the colors of the background.
<code>bg_alpha</code>	A numeric value to specify the transparency of the background.
<code>add_line</code>	A character string to add a line to the plot.
<code>line_color</code>	A character string to specify the color of the line.
<code>line_width</code>	A numeric value to specify the size of the line.
<code>line_type</code>	A numeric value to specify the type of the line.
<code>highlight</code>	A vector of character strings to highlight the points. It should be a subset of the row names of the data. If TRUE, it will highlight all points.
<code>highlight_color</code>	A character string to specify the color of the highlighted points.
<code>highlight_size</code>	A numeric value to specify the size of the highlighted points.
<code>highlight_alpha</code>	A numeric value to specify the transparency of the highlighted points.
<code>comparisons</code>	A logical value or a list of vectors to perform pairwise comparisons. If TRUE, it will perform pairwise comparisons for all pairs.

<code>ref_group</code>	A character string to specify the reference group for comparisons.
<code>pairwise_method</code>	A character string to specify the pairwise comparison method.
<code>multiplegroup_comparisons</code>	A logical value to perform multiple group comparisons.
<code>multiple_method</code>	A character string to specify the multiple group comparison method.
<code>sig_label</code>	A character string to specify the label of the significance test.
<code>sig_labelsize</code>	A numeric value to specify the size of the significance test label.
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is TRUE.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>seed</code>	The random seed to use. Default is 8525.
<code>combine</code>	Whether to combine the plots into one when facet is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction.

	<ul style="list-style-type: none"> • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
guides	<p>A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code>. Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are:</p> <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
...	Additional arguments.
add_box	A logical value to add box plot to the plot.
box_color	A character string to specify the color of the box plot.
box_width	A numeric value to specify the width of the box plot.
box_ptsize	A numeric value to specify the size of the box plot points in the middle.

Value

The Box / Violin plot(s). When `split_by` is not provided, it returns a ggplot object. When `split_by` is provided, it returns a object of plots wrapped by `patchwork::wrap_plots` if `combine = TRUE`; otherwise, it returns a list of ggplot objects.

Examples

```
set.seed(8525)
data <- data.frame(
  x = rep(LETTERS[1:8], 40),
  y = rnorm(320),
  group1 = sample(c("g1", "g2"), 320, replace = TRUE),
  group2 = sample(c("h1", "h2", "h3", "h4"), 320, replace = TRUE)
)

BoxPlot(data, x = "x", y = "y")
BoxPlot(data,
  x = "x", y = "y",
  stack = TRUE, flip = TRUE, facet_by = "group1",
  add_bg = TRUE, bg_palette = "Paired"
)
BoxPlot(data,
  x = "x", y = "y",
  stack = TRUE, flip = TRUE, split_by = "group1",
  add_bg = TRUE, bg_palette = "Paired",
  palcolor = list(g1 = c("red", "blue"), g2 = c("blue", "red"))
)

# wide form data
data_wide <- data.frame(
  A = rnorm(100),
  B = rnorm(100),
```

```

    C = rnorm(100)
  )
  BoxPlot(data_wide, x = c("A", "B", "C"), in_form = "wide")

  ViolinPlot(data, x = "x", y = "y")
  ViolinPlot(data, x = "x", y = "y", add_box = TRUE)
  ViolinPlot(data, x = "x", y = "y", add_point = TRUE)
  ViolinPlot(data, x = "x", y = "y", add_trend = TRUE)
  ViolinPlot(data, x = "x", y = "y", add_stat = mean)
  ViolinPlot(data, x = "x", y = "y", add_bg = TRUE)
  ViolinPlot(data, x = "x", y = "y", add_line = 0)
  ViolinPlot(data, x = "x", y = "y", group_by = "group1")
  ViolinPlot(data,
    x = "x", y = "y", group_by = "group1",
    facet_by = "group2", add_box = TRUE
  )
  ViolinPlot(data, x = "x", y = "y", add_point = TRUE, highlight = 'group1 == "g1"',
    alpha = 0.8, highlight_size = 1.5, pt_size = 1, add_box = TRUE)
  ViolinPlot(data,
    x = "x", y = "y", group_by = "group1",
    comparisons = TRUE
  )
  ViolinPlot(data,
    x = "x", y = "y", sig_label = "p.format",
    facet_by = "group2", comparisons = list(c("A", "B"))
  )
  ViolinPlot(data,
    x = "x", y = "y", fill_mode = "mean",
    facet_by = "group2", palette = "Blues"
  )
  ViolinPlot(data,
    x = "x", y = "y", fill_mode = "mean",
    split_by = "group1", palette = c(g1 = "Blues", g2 = "Reds")
  )
  ViolinPlot(data,
    x = "x", y = "y", stack = TRUE,
    facet_by = "group2", add_box = TRUE, add_bg = TRUE,
    bg_palette = "Paired"
  )
)

```

ChordPlot

Chord / Circos plot

Description

ChordPlot is used to create a chord plot to visualize the relationships between two categorical variables. CircosPlot is an alias of ChordPlot.

Usage

```
ChordPlot(  
  data,  
  y = NULL,  
  from = NULL,  
  from_sep = "_",  
  to = NULL,  
  to_sep = "_",  
  split_by = NULL,  
  split_by_sep = "_",  
  flip = FALSE,  
  links_color = c("from", "to"),  
  theme = "theme_this",  
  theme_args = list(),  
  palette = "Paired",  
  palcolor = NULL,  
  alpha = 0.5,  
  labels_rot = FALSE,  
  title = NULL,  
  subtitle = NULL,  
  seed = 8525,  
  combine = TRUE,  
  nrow = NULL,  
  ncol = NULL,  
  byrow = TRUE,  
  axes = NULL,  
  axis_titles = axes,  
  guides = NULL,  
  design = NULL,  
  ...  
)
```

```
CircosPlot(  
  data,  
  y = NULL,  
  from = NULL,  
  from_sep = "_",  
  to = NULL,  
  to_sep = "_",  
  split_by = NULL,  
  split_by_sep = "_",  
  flip = FALSE,  
  links_color = c("from", "to"),  
  theme = "theme_this",  
  theme_args = list(),  
  palette = "Paired",  
  palcolor = NULL,  
  alpha = 0.5,
```



```

    labels_rot = FALSE,
    title = NULL,
    subtitle = NULL,
    seed = 8525,
    combine = TRUE,
    nrow = NULL,
    ncol = NULL,
    byrow = TRUE,
    axes = NULL,
    axis_titles = axes,
    guides = NULL,
    design = NULL,
    ...
)

```

Arguments

<code>data</code>	A data frame.
<code>y</code>	A character string specifying the column name of the data frame to plot for the y-axis.
<code>from</code>	A character string of the column name to plot for the source. A character/factor column is expected.
<code>from_sep</code>	A character string to concatenate the columns in <code>from</code> , if multiple columns are provided.
<code>to</code>	A character string of the column name to plot for the target. A character/factor column is expected.
<code>to_sep</code>	A character string to concatenate the columns in <code>to</code> , if multiple columns are provided.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>flip</code>	A logical value to flip the source and target.
<code>links_color</code>	A character string to specify the color of the links. Either "from" or "to".
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be <code>NULL</code> for those values).
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>labels_rot</code>	A logical value to rotate the labels by 90 degrees.

<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>seed</code>	The random seed to use. Default is 8525.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is <code>FALSE</code> . Default is <code>TRUE</code> .
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
<code>...</code>	Additional arguments.

Value

A combined plot or a list of plots

Examples

```

set.seed(8525)
data <- data.frame(
  nodes1 = sample(c("Source1", "Source2", "Source3"), 10, replace = TRUE),
  nodes2 = sample(letters[1:3], 10, replace = TRUE),
  y = sample(1:5, 10, replace = TRUE)
)

ChordPlot(data, from = "nodes1", to = "nodes2")
ChordPlot(data, from = "nodes1", to = "nodes2",
  links_color = "to", labels_rot = TRUE)
ChordPlot(data, from = "nodes1", to = "nodes2", y = "y")
ChordPlot(data, from = "nodes1", to = "nodes2", split_by = "y")
ChordPlot(data, from = "nodes1", to = "nodes2", split_by = "y",
  palette = c("1" = "Reds", "2" = "Blues", "3" = "Greens", "4" = "Purp"))
ChordPlot(data, from = "nodes1", to = "nodes2", flip = TRUE)

```

ClustreePlot

Clustree Plot

Description

A plot visualizing Clusterings at Different Resolutions

Usage

```

ClustreePlot(
  data,
  prefix,
  flip = FALSE,
  split_by = NULL,
  split_by_sep = "_",
  palette = "Paired",
  palcolor = NULL,
  edge_palette = "Spectral",
  edge_palcolor = NULL,
  aspect.ratio = 1,
  legend.position = "right",
  legend.direction = "vertical",
  title = NULL,
  subtitle = NULL,
  xlab = NULL,
  ylab = NULL,
  expand = c(0.1, 0.1),
  theme = "theme_this",
  theme_args = list(),
  combine = TRUE,

```

```

nrow = NULL,
ncol = NULL,
byrow = TRUE,
seed = 8525,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

<code>data</code>	A data frame.
<code>prefix</code>	A character string of the prefix of the columns to plot. The columns with the prefix will be used to plot the tree.
<code>flip</code>	A logical value to flip the tree.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be <code>NULL</code> for those values).
<code>edge_palette</code>	A character string of the palette name to color the edges.
<code>edge_palcolor</code>	A character vector of colors to color the edges.
<code>aspect.ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>expand</code>	The values to expand the x and y axes. It is like CSS padding. When a single value is provided, it is used for both axes on both sides. When two values are provided, the first value is used for the top/bottom side and the second value is used for the left/right side. When three values are provided, the first value is used for the top side, the second value is used for the left/right side, and the third

value is used for the bottom side. When four values are provided, the values are used for the top, right, bottom, and left sides, respectively. You can also use a named vector to specify the values for each side. When the axis is discrete, the values will be applied as 'add' to the 'expansion' function. When the axis is continuous, the values will be applied as 'mult' to the 'expansion' function. See also <https://ggplot2.tidyverse.org/reference/expansion.html>

theme	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
theme_args	A list of arguments to pass to the theme function.
combine	Whether to combine the plots into one when facet is FALSE. Default is TRUE.
nrow	A numeric value specifying the number of rows in the facet.
ncol	A numeric value specifying the number of columns in the facet.
byrow	A logical value indicating whether to fill the plots by row.
seed	The random seed to use. Default is 8525.
axes	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
axis_titles	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
guides	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
design	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
...	Additional arguments.

Value

A ggplot object or wrap_plots object or a list of ggplot objects

Examples

```
set.seed(8525)
N = 100
data <- data.frame(
  p.0.4 = sample(LETTERS[1:5], N, replace = TRUE),
  p.0.5 = sample(LETTERS[1:6], N, replace = TRUE),
  p.0.6 = sample(LETTERS[1:7], N, replace = TRUE),
  p.0.7 = sample(LETTERS[1:8], N, replace = TRUE),
  p.0.8 = sample(LETTERS[1:9], N, replace = TRUE),
  p.0.9 = sample(LETTERS[1:10], N, replace = TRUE),
  p.1 = sample(LETTERS[1:30], N, replace = TRUE),
  split = sample(1:2, N, replace = TRUE)
)

ClustreePlot(data, prefix = "p")
ClustreePlot(data, prefix = "p", flip = TRUE)
ClustreePlot(data, prefix = "p", split_by = "split")
ClustreePlot(data, prefix = "p", split_by = "split",
  palette = c("1" = "Set1", "2" = "Paired"))
```

CorPairsPlot

CorPairsPlot

Description

Generate a grid of scatter correlation plots for all pairs of variables.

Usage

```
CorPairsPlot(
  data,
  columns = NULL,
  group_by = NULL,
  group_by_sep = "_",
  group_name = NULL,
  split_by = NULL,
  split_by_sep = "_",
  diag_type = NULL,
  diag_args = list(),
  layout = c(".\\", "\\.", "/.", "./" ),
  cor_method = c("pearson", "spearman", "kendall"),
  cor_palette = "RdBu",
  cor_palcolor = NULL,
  cor_size = 3,
```

```

cor_format = "corr: {round(corr, 2)}",
cor_fg = "black",
cor_bg = "white",
cor_bg_r = 0.1,
theme = "theme_this",
theme_args = list(),
palette = ifelse(is.null(group_by), "Spectral", "Paired"),
palcolor = NULL,
title = NULL,
subtitle = NULL,
facet_by = NULL,
legend.position = "right",
legend.direction = "vertical",
seed = 8525,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

data	A data frame.
columns	The column names of the data to be plotted. If NULL, all columns, except group_by, will be used.
group_by	Columns to group the data for plotting For those plotting functions that do not support multiple groups, They will be concatenated into one column, using group_by_sep as the separator
group_by_sep	The separator for multiple group_by columns. See group_by
group_name	The name of the group in the legend.
split_by	The column(s) to split data by and plot separately.
split_by_sep	The separator for multiple split_by columns. See split_by
diag_type	The type of the diagonal plots. Available types: "density", "violin", "histogram", "box", "none".
diag_args	A list of additional arguments to be passed to the diagonal plots.
layout	The layout of the plots. Available layouts: ".\", "\.", "/.", "/.". <ul style="list-style-type: none"> • '\ or '/' means the diagonal plots are on the top-left to bottom-right diagonal. • './ means where the scatter plots are.

<code>cor_method</code>	The method to calculate the correlation. Available methods: "pearson", "spearman", "kendall". The correlation will be shown in the other triangle of the scatter plots.
<code>cor_palette</code>	The color palette for the correlation tile plots.
<code>cor_palcolor</code>	Custom colors used to create a color palette for the correlation tile plots.
<code>cor_size</code>	The size of the correlation text.
<code>cor_format</code>	The format of the correlation text. Default is "corr: %.2f". It will be formatted using <code>sprintf(cor_format, corr)</code> .
<code>cor_fg</code>	The color of the correlation text.
<code>cor_bg</code>	The background color of the correlation text.
<code>cor_bg_r</code>	The radius of the background of the correlation text.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be NULL for those values).
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>seed</code>	The random seed to use. Default is 8525.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout.

	<ul style="list-style-type: none"> • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
axis_titles	<p>A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code>. Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are:</p> <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
guides	<p>A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code>. Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are:</p> <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
design	<p>Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code>. Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code>, <code>ncol</code>, and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.</p>
...	Additional arguments.

Value

A `patch_work::wrap_plots` object or a list of them if `combine` is FALSE.

Examples

```
set.seed(8525)
data <- data.frame(x = rnorm(100))
data$y <- rnorm(100, 10, sd = 0.5)
data$z <- -data$x + data$y + rnorm(100, 20, 1)
data$g <- sample(1:4, 100, replace = TRUE)

CorPairsPlot(data, diag_type = "histogram", diag_args = list(bins = 30, palette = "Paired"),
  layout = "/.")

CorPairsPlot(data, group_by = "g", diag_type = "none", layout = "/.",
  theme_args = list(axis.title = element_textbox(
    color = "black", box.color = "grey20", size = 16, halign = 0.5, fill = "grey90",
    linetype = 1, width = grid::unit(1, "npc"), padding = ggplot2::margin(5, 5, 5, 5))))

CorPairsPlot(data, group_by = "g", diag_type = "violin", layout = "\\.",
  cor_format = "{x}\\n{y}\\ncorr: {round(corr, 2)}")

CorPairsPlot(data, split_by = "g", diag_type = "none", layout = ".\\.",
  legend.position = "bottom", legend.direction = "horizontal", group_name = "group")
```

```
CorPairsPlot(data, split_by = "g",
             palcolor = list("1" = "red", "2" = "blue", "3" = "green", "4" = "yellow"))
```

CorPlot

CorPlot

Description

Generate scatter correlation plot for two variables.

Usage

```
CorPlot(
  data,
  x,
  y,
  group_by = NULL,
  group_by_sep = "_",
  group_name = NULL,
  split_by = NULL,
  split_by_sep = "_",
  pt_size = 2,
  pt_shape = 16,
  raster = FALSE,
  alpha = 1,
  raster_dpi = c(512, 512),
  highlight = NULL,
  highlight_color = "black",
  highlight_size = 1,
  highlight_alpha = 1,
  highlight_stroke = 0.8,
  anno_items = c("eq", "r2", "p"),
  anno_size = 3,
  anno_fg = "black",
  anno_bg = "white",
  anno_bg_r = 0.1,
  anno_position = c("topleft", "topright", "bottomleft", "bottomright", "tl", "tr", "bl",
                    "br"),
  add_smooth = TRUE,
  smooth_color = "red2",
  smooth_width = 1.5,
  smooth_se = FALSE,
  theme = "theme_this",
  theme_args = list(),
  palette = ifelse(is.null(group_by), "Spectral", "Paired"),
```

```

    palcolor = NULL,
    title = NULL,
    subtitle = NULL,
    xlab = NULL,
    ylab = NULL,
    facet_by = NULL,
    facet_scales = "fixed",
    facet_ncol = NULL,
    facet_nrow = NULL,
    facet_byrow = TRUE,
    aspect.ratio = 1,
    legend.position = waiver(),
    legend.direction = "vertical",
    seed = 8525,
    combine = TRUE,
    nrow = NULL,
    ncol = NULL,
    byrow = TRUE,
    axes = NULL,
    axis_titles = axes,
    guides = NULL,
    design = NULL,
    ...
)

```

Arguments

<code>data</code>	A data frame.
<code>x</code>	A character string specifying the column name of the data frame to plot for the x-axis.
<code>y</code>	A character string specifying the column name of the data frame to plot for the y-axis.
<code>group_by</code>	Columns to group the data for plotting For those plotting functions that do not support multiple groups, They will be concatenated into one column, using <code>group_by_sep</code> as the separator
<code>group_by_sep</code>	The separator for multiple <code>group_by</code> columns. See <code>group_by</code>
<code>group_name</code>	The name of the group in the legend.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>pt_size</code>	The size of the points.
<code>pt_shape</code>	The shape of the points.
<code>raster</code>	Whether to use raster graphics for plotting.
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>raster_dpi</code>	The DPI of the raster graphics.

<code>highlight</code>	The items to be highlighted. Could be either a vector of rownames if data has rownames, or a vector of indices, or An expression that can be evaluated by <code>dplyr::filter</code> to get the highlighted items.
<code>highlight_color</code>	The color of the highlighted points.
<code>highlight_size</code>	The size of the highlighted points.
<code>highlight_alpha</code>	The alpha of the highlighted points.
<code>highlight_stroke</code>	The stroke of the highlighted points.
<code>anno_items</code>	The items to be annotated on the plot. Available items: "eq", "r2", "p", "spearman", "pearson", "kendall", "n".
<code>anno_size</code>	The size of the annotation text.
<code>anno_fg</code>	The color of the annotation text.
<code>anno_bg</code>	The background color of the annotation text.
<code>anno_bg_r</code>	The radius of the background of the annotation text.
<code>anno_position</code>	The position of the annotation text. Available positions: "topleft", "topright", "bottomleft", "bottomright". Shortcuts: "tl", "tr", "bl", "br".
<code>add_smooth</code>	Whether to add a linear regression line.
<code>smooth_color</code>	The color of the regression line.
<code>smooth_width</code>	The width of the regression line.
<code>smooth_se</code>	Whether to add the standard error band to the regression line.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be NULL for those values).
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>

<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is <code>TRUE</code> .
<code>aspect.ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. If <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>seed</code>	The random seed to use. Default is 8525.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is <code>FALSE</code> . Default is <code>TRUE</code> .
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none">• 'keep' will retain all axes in individual plots.• 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout.• 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none">• 'keep' will retain all axis titles in individual plots.• 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction.• 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none">• 'collect' will collect guides below to the given nesting level, removing duplicates.• 'keep' will stop collection at this level and let guides be placed alongside their plot.• 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
<code>...</code>	Additional arguments.

Value

A ggplot object or a list of ggplot objects if combine is FALSE.

Examples

```
data(iris)
CorPlot(iris, "Sepal.Length", "Sepal.Width", group_by = "Species")
CorPlot(iris, "Sepal.Length", "Sepal.Width", group_by = "Species",
  highlight = 'Species == "setosa"', highlight_stroke = 1.5,
  anno_items = c("eq", "pearson"), anno_position = "bottomright")
CorPlot(iris, "Sepal.Length", "Sepal.Width", facet_by = "Species", facet_scales = "free")
CorPlot(iris, "Sepal.Length", "Sepal.Width", split_by = "Species",
  palette = c(setosa = "Set1", versicolor = "Dark2", virginica = "Paired"))
```

 DensityPlot

Density Plot / Histogram

Description

Density plot and histogram to illustrate the distribution of the data.

Usage

```
DensityPlot(
  data,
  x,
  group_by = NULL,
  group_by_sep = "_",
  group_name = NULL,
  xtrans = "identity",
  ytrans = "identity",
  split_by = NULL,
  split_by_sep = "_",
  flip = FALSE,
  position = "identity",
  palette = "Paired",
  palcolor = NULL,
  alpha = 0.5,
  theme = "theme_this",
  theme_args = list(),
  addBars = FALSE,
  bar_height = 0.025,
  bar_alpha = 1,
  bar_width = 0.1,
  title = NULL,
  subtitle = NULL,
  xlab = NULL,
```

```
ylab = NULL,  
expand = c(bottom = 0, left = 0, right = 0),  
facet_by = NULL,  
facet_scales = "free_y",  
facet_ncol = NULL,  
facet_nrow = NULL,  
facet_byrow = TRUE,  
legend.position = ifelse(is.null(group_by), "none", "right"),  
legend.direction = "vertical",  
seed = 8525,  
combine = TRUE,  
nrow = NULL,  
ncol = NULL,  
byrow = TRUE,  
axes = NULL,  
axis_titles = axes,  
guides = NULL,  
design = NULL,  
...  
)
```

```
Histogram(  
  data,  
  x,  
  group_by = NULL,  
  group_by_sep = "_",  
  group_name = NULL,  
  xtrans = "identity",  
  ytrans = "identity",  
  split_by = NULL,  
  split_by_sep = "_",  
  flip = FALSE,  
  bins = NULL,  
  binwidth = NULL,  
  trend_skip_zero = FALSE,  
  addBars = FALSE,  
  bar_height = 0.025,  
  bar_alpha = 1,  
  bar_width = 0.1,  
  position = "identity",  
  use_trend = FALSE,  
  add_trend = FALSE,  
  trend_alpha = 1,  
  trend_linewidth = 0.8,  
  trend_pt_size = 1.5,  
  palette = "Paired",  
  palcolor = NULL,  
  alpha = 0.5,
```

```

theme = "theme_this",
theme_args = list(),
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
expand = c(bottom = 0, left = 0, right = 0),
facet_by = NULL,
facet_scales = "free_y",
facet_ncol = NULL,
facet_nrow = NULL,
facet_byrow = TRUE,
legend.position = ifelse(is.null(group_by), "none", "right"),
legend.direction = "vertical",
seed = 8525,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

<code>data</code>	A data frame.
<code>x</code>	A character string specifying the column name of the data frame to plot for the x-axis.
<code>group_by</code>	Columns to group the data for plotting For those plotting functions that do not support multiple groups, They will be concatenated into one column, using <code>group_by_sep</code> as the separator
<code>group_by_sep</code>	The separator for multiple <code>group_by</code> columns. See <code>group_by</code>
<code>group_name</code>	A character string to name the legend of <code>group_by</code>
<code>xtrans</code>	A character string specifying the transformation of the x-axis. Default is "identity". Other options see transform of scale_x_continuous .
<code>ytrans</code>	A character string specifying the transformation of the y-axis. Default is "identity". Other options see transform of scale_y_continuous .
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>flip</code>	A logical value. If TRUE, the plot will be flipped.
<code>position</code>	How should we position the values in each bin? Default is "identity". Unlike the default position = "stack" in <code>ggplot2::geom_histogram</code> or <code>ggplot2::geom_density</code> , the default position is "identity" to show the actual count or density for each group.

palette	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
palcolor	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (palcolor will be NULL for those values).
alpha	A numeric value specifying the transparency of the plot.
theme	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
theme_args	A list of arguments to pass to the theme function.
add_bars	A logical value. If TRUE, add lines to the plot to show the data distribution on the bottom.
bar_height	A numeric value specifying the height of the bars. The actual height will be calculated based on the maximum density or count.
bar_alpha	A numeric value specifying the alpha of the bars.
bar_width	A numeric value specifying the width of the bars.
title	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
subtitle	A character string specifying the subtitle of the plot.
xlab	A character string specifying the x-axis label.
ylab	A character string specifying the y-axis label.
expand	The values to expand the x and y axes. It is like CSS padding. When a single value is provided, it is used for both axes on both sides. When two values are provided, the first value is used for the top/bottom side and the second value is used for the left/right side. When three values are provided, the first value is used for the top side, the second value is used for the left/right side, and the third value is used for the bottom side. When four values are provided, the values are used for the top, right, bottom, and left sides, respectively. You can also use a named vector to specify the values for each side. When the axis is discrete, the values will be applied as 'add' to the 'expansion' function. When the axis is continuous, the values will be applied as 'mult' to the 'expansion' function. See also https://ggplot2.tidyverse.org/reference/expansion.html
facet_by	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
facet_scales	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
facet_ncol	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
facet_nrow	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
facet_byrow	A logical value indicating whether to fill the plots by row. Default is TRUE.

<code>legend.position</code>	A character string specifying the position of the legend. If <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>seed</code>	The random seed to use. Default is 8525.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
<code>...</code>	Additional arguments.
<code>bins</code>	A numeric value specifying the number of bins for the histogram.
<code>binwidth</code>	A numeric value specifying the width of the bins for the histogram.
<code>trend_skip_zero</code>	A logical value. If TRUE, skip the zero count when drawing the trend line.
<code>use_trend</code>	A logical value. If TRUE, use trend line instead of histogram.

<code>add_trend</code>	A logical value. If TRUE, add trend line to the histogram.
<code>trend_alpha</code>	A numeric value specifying the alpha of the trend line and points
<code>trend_linewidth</code>	A numeric value specifying the width of the trend line
<code>trend_pt_size</code>	A numeric value specifying the size of the trend points

Value

A ggplot object or wrap_plots object or a list of ggplot objects

Examples

```
set.seed(8525)
data <- data.frame(
  x = c(rnorm(500, -1), rnorm(500, 1)),
  group = rep(c("A", "B"), each = 500),
  facet = sample(c("F1", "F2"), 1000, replace = TRUE)
)

DensityPlot(data, x = "x")
DensityPlot(data, x = "x", group_by = "group", facet_by = "facet")
DensityPlot(data, x = "x", split_by = "facet", add_bars = TRUE)
DensityPlot(data, x = "x", split_by = "facet", add_bars = TRUE,
  palette = c(F1 = "Set1", F2 = "Set2"))
set.seed(8525)
data <- data.frame(
  x = sample(setdiff(1:100, c(30:36, 50:55, 70:77)), 1000, replace = TRUE),
  group = factor(rep(c("A", "B"), each = 500), levels = c("A", "B")),
  facet = sample(c("F1", "F2"), 1000, replace = TRUE)
)

Histogram(data, x = "x")
Histogram(data, x = "x", group_by = "group")
Histogram(data, x = "x", split_by = "facet", add_bars = TRUE)
Histogram(data, x = "x", group_by = "group", add_trend = TRUE)
Histogram(data, x = "x", group_by = "group", add_trend = TRUE, trend_skip_zero = TRUE)
Histogram(data, x = "x", group_by = "group", split_by = "facet",
  use_trend = TRUE, trend_pt_size = 3)
Histogram(data, x = "x", group_by = "group", split_by = "facet",
  palette = c(F1 = "Paired", F2 = "Spectral"))
```

Description

Visualizing the dimension reduction data. FeatureDimPlot is used to plot the feature numeric values on the dimension reduction plot.

Usage

```
DimPlot(  
  data,  
  dims = 1:2,  
  group_by,  
  group_by_sep = "_",  
  split_by = NULL,  
  split_by_sep = "_",  
  pt_size = NULL,  
  pt_alpha = 1,  
  bg_color = "grey80",  
  label_insitu = FALSE,  
  show_stat = !identical(theme, "theme_blank"),  
  label = FALSE,  
  label_size = 4,  
  label_fg = "white",  
  label_bg = "black",  
  label_bg_r = 0.1,  
  label_repel = FALSE,  
  label_repulsion = 20,  
  label_pt_size = 1,  
  label_pt_color = "black",  
  label_segment_color = "black",  
  highlight = NULL,  
  highlight_alpha = 1,  
  highlight_size = 1,  
  highlight_color = "black",  
  highlight_stroke = 0.8,  
  add_mark = FALSE,  
  mark_type = c("hull", "ellipse", "rect", "circle"),  
  mark_expand = unit(3, "mm"),  
  mark_alpha = 0.1,  
  mark_linetype = 1,  
  stat_by = NULL,  
  stat_plot_type = c("pie", "ring", "bar", "line"),  
  stat_plot_size = 0.1,  
  stat_args = list(palette = "Set1"),  
  graph = NULL,  
  edge_size = c(0.05, 0.5),  
  edge_alpha = 0.1,  
  edge_color = "grey40",  
  add_density = FALSE,  
  density_color = "grey80",  
  density_filled = FALSE,  
  density_filled_palette = "Greys",  
  density_filled_palcolor = NULL,  
  lineages = NULL,  
  lineages_trim = c(0.01, 0.99),
```

```
  lineages_span = 0.75,
  lineages_palette = "Dark2",
  lineages_palcolor = NULL,
  lineages_arrow = arrow(length = unit(0.1, "inches")),
  lineages_linewidth = 1,
  lineages_line_bg = "white",
  lineages_line_bg_stroke = 0.5,
  lineages_whiskers = FALSE,
  lineages_whiskers_linewidth = 0.5,
  lineages_whiskers_alpha = 0.5,
  facet_by = NULL,
  facet_scales = "fixed",
  facet_nrow = NULL,
  facet_ncol = NULL,
  facet_byrow = TRUE,
  title = NULL,
  subtitle = NULL,
  xlab = NULL,
  ylab = NULL,
  theme = "theme_this",
  theme_args = list(),
  aspect.ratio = 1,
  legend.position = "right",
  legend.direction = "vertical",
  raster = NULL,
  raster_dpi = c(512, 512),
  hex = FALSE,
  hex_linewidth = 0.5,
  hex_count = TRUE,
  hex_bins = 50,
  hex_binwidth = NULL,
  palette = "Paired",
  palcolor = NULL,
  seed = 8525,
  combine = TRUE,
  nrow = NULL,
  ncol = NULL,
  byrow = TRUE,
  axes = NULL,
  axis_titles = axes,
  guides = NULL,
  design = NULL,
  ...
)

FeatureDimPlot(
  data,
  dims = 1:2,
```

```
features,
split_by = NULL,
split_by_sep = "_",
lower_quantile = 0,
upper_quantile = 0.99,
lower_cutoff = NULL,
upper_cutoff = NULL,
pt_size = NULL,
pt_alpha = 1,
bg_color = "grey80",
bg_cutoff = NULL,
label_insitu = FALSE,
show_stat = !identical(theme, "theme_blank"),
color_name = "",
label = FALSE,
label_size = 4,
label_fg = "white",
label_bg = "black",
label_bg_r = 0.1,
label_repel = FALSE,
label_repulsion = 20,
label_pt_size = 1,
label_pt_color = "black",
label_segment_color = "black",
highlight = NULL,
highlight_alpha = 1,
highlight_size = 1,
highlight_color = "black",
highlight_stroke = 0.8,
add_mark = FALSE,
mark_type = c("hull", "ellipse", "rect", "circle"),
mark_expand = unit(3, "mm"),
mark_alpha = 0.1,
mark_linetype = 1,
stat_by = NULL,
stat_plot_type = c("pie", "ring", "bar", "line"),
stat_plot_size = 0.1,
stat_args = list(palette = "Set1"),
graph = NULL,
edge_size = c(0.05, 0.5),
edge_alpha = 0.1,
edge_color = "grey40",
add_density = FALSE,
density_color = "grey80",
density_filled = FALSE,
density_filled_palette = "Greys",
density_filled_palcolor = NULL,
lineages = NULL,
```

```
lineages_trim = c(0.01, 0.99),
lineages_span = 0.75,
lineages_palette = "Dark2",
lineages_palcolor = NULL,
lineages_arrow = arrow(length = unit(0.1, "inches")),
lineages_linewidth = 1,
lineages_line_bg = "white",
lineages_line_bg_stroke = 0.5,
lineages_whiskers = FALSE,
lineages_whiskers_linewidth = 0.5,
lineages_whiskers_alpha = 0.5,
facet_by = NULL,
facet_scales = "fixed",
facet_nrow = NULL,
facet_ncol = NULL,
facet_byrow = TRUE,
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
theme = "theme_this",
theme_args = list(),
aspect.ratio = 1,
legend.position = "right",
legend.direction = "vertical",
raster = NULL,
raster_dpi = c(512, 512),
hex = FALSE,
hex_linewidth = 0.5,
hex_count = FALSE,
hex_bins = 50,
hex_binwidth = NULL,
palette = "Spectral",
palcolor = NULL,
seed = 8525,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)
```

Arguments

data A data frame.

<code>dims</code>	A character vector of the column names to plot on the x and y axes or a numeric vector of the column indices.
<code>group_by</code>	Columns to group the data for plotting For those plotting functions that do not support multiple groups, They will be concatenated into one column, using <code>group_by_sep</code> as the separator
<code>group_by_sep</code>	The separator for multiple <code>group_by</code> columns. See <code>group_by</code>
<code>split_by</code>	A character vector of column names to split the data and plot separately If TRUE, we will split the data by the features. Each feature will be plotted separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>pt_size</code>	A numeric value of the point size. If NULL, the point size will be calculated based on the number of data points.
<code>pt_alpha</code>	A numeric value of the point transparency. Default is 1.
<code>bg_color</code>	A character string of the background or NA points. Default is "grey80".
<code>label_insitu</code>	Whether to place the raw labels (group names) in the center of the points with the corresponding group. Default is FALSE, which using numbers instead of raw labels.
<code>show_stat</code>	Whether to show the number of points in the subtitle. Default is TRUE.
<code>label</code>	Whether to show the labels of groups. Default is FALSE.
<code>label_size</code>	A numeric value of the label size. Default is 4.
<code>label_fg</code>	A character string of the label foreground color. Default is "white".
<code>label_bg</code>	A character string of the label background color. Default is "black".
<code>label_bg_r</code>	A numeric value of the background ratio of the labels. Default is 0.1.
<code>label_repel</code>	Whether to repel the labels. Default is FALSE.
<code>label_repulsion</code>	A numeric value of the label repulsion. Default is 20.
<code>label_pt_size</code>	A numeric value of the label point size. Default is 1.
<code>label_pt_color</code>	A character string of the label point color. Default is "black".
<code>label_segment_color</code>	A character string of the label segment color. Default is "black".
<code>highlight</code>	A character vector of the row names to highlight. Default is NULL.
<code>highlight_alpha</code>	A numeric value of the highlight transparency. Default is 1.
<code>highlight_size</code>	A numeric value of the highlight size. Default is 1.
<code>highlight_color</code>	A character string of the highlight color. Default is "black".
<code>highlight_stroke</code>	A numeric value of the highlight stroke. Default is 0.5.
<code>add_mark</code>	Whether to add mark to the plot. Default is FALSE.
<code>mark_type</code>	A character string of the mark type. Default is "hull".
<code>mark_expand</code>	A unit value of the mark expand. Default is 3mm.

mark_alpha	A numeric value of the mark transparency. Default is 0.1.
mark_linetype	A numeric value of the mark line type. Default is 1.
stat_by	A character string of the column name to calculate the statistics. Default is NULL.
stat_plot_type	A character string of the statistic plot type. Default is "pie".
stat_plot_size	A numeric value of the statistic plot size. Default is 0.1.
stat_args	A list of additional arguments to the statistic plot. Default is list(palette = "Set1").
graph	A character string of column names or the indexes in the data for the graph data. Default is NULL. If "@graph" is provided, the graph data will be extracted from the data attribute 'graph'.
edge_size	A numeric vector of the edge size range. Default is c(0.05, 0.5).
edge_alpha	A numeric value of the edge transparency. Default is 0.1.
edge_color	A character string of the edge color. Default is "grey40".
add_density	Whether to add density plot. Default is FALSE.
density_color	A character string of the density color. Default is "grey80".
density_filled	Whether to fill the density plot. Default is FALSE.
density_filled_palette	A character string of the filled density palette. Default is "Greys".
density_filled_palcolor	A character vector of the filled density palette colors. Default is NULL.
lineages	A character vector of the column names for lineages. Default is NULL.
lineages_trim	A numeric vector of the trim range for lineages. Default is c(0.01, 0.99).
lineages_span	A numeric value of the lineages span. Default is 0.75.
lineages_palette	A character string of the lineages palette. Default is "Dark2".
lineages_palcolor	A character vector of the lineages palette colors. Default is NULL.
lineages_arrow	An arrow object for the lineages. Default is arrow(length = unit(0.1, "inches")).
lineages_linewidth	A numeric value of the lineages line width. Default is 1.
lineages_line_bg	A character string of the lineages line background color. Default is "white".
lineages_line_bg_stroke	A numeric value of the lineages line background stroke. Default is 0.5.
lineages_whiskers	Whether to add whiskers to the lineages. Default is FALSE.
lineages_whiskers_linewidth	A numeric value of the lineages whiskers line width. Default is 0.5.
lineages_whiskers_alpha	A numeric value of the lineages whiskers transparency. Default is 0.5.

<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is TRUE.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>aspect.ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>raster</code>	Whether to raster the plot. Default is NULL.
<code>raster_dpi</code>	A numeric vector of the raster dpi. Default is <code>c(512, 512)</code> .
<code>hex</code>	Whether to use hex plot. Default is FALSE.
<code>hex_linewidth</code>	A numeric value of the hex line width. Default is 0.5.
<code>hex_count</code>	Whether to count the hex.
<code>hex_bins</code>	A numeric value of the hex bins. Default is 50.
<code>hex_binwidth</code>	A numeric value of the hex bin width. Default is NULL.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be NULL for those values).
<code>seed</code>	The random seed to use. Default is 8525.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.

<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
<code>...</code>	Additional arguments.
<code>features</code>	A character vector of the column names to plot as features.
<code>lower_quantile</code> , <code>upper_quantile</code> , <code>lower_cutoff</code> , <code>upper_cutoff</code>	Vector of minimum and maximum cutoff values or quantile values for each feature.
<code>bg_cutoff</code>	A numeric value to be used a cutoff to set the feature values to NA. Default is <code>NULL</code> .
<code>color_name</code>	A character string of the color legend name. Default is <code>""</code> .

Value

A `ggplot` object or `wrap_plots` object or a list of `ggplot` objects

A `ggplot` object or `wrap_plots` object or a list of `ggplot` objects

Examples

```

# generate a PCA dimension data for DimPlot
set.seed(8525)
df <- matrix(c(rnorm(333), rnorm(334, 0.2), rnorm(333, .4)), ncol = 10)
# run PCA
pca <- prcomp(df)
# get coordinates
data <- pca$x[, 1:2]
# kmeans clustering
km <- kmeans(data, 3)
data <- as.data.frame(data)
data$cluster <- factor(paste0("C", km$cluster))
data$group <- sample(c("A", "B"), nrow(data), replace = TRUE)

graph <- rnorm(nrow(data) * nrow(data))
graph[sample(1:(nrow(data) * nrow(data)), 5000)] <- NA
graph <- matrix(graph, nrow = nrow(data))
rownames(graph) <- colnames(graph) <- rownames(data)

attr(data, "graph") <- graph

data$L1 <- rnorm(nrow(data), 0, 0.1)
data$L2 <- rnorm(nrow(data), 1, 0.2)
data$L3 <- rnorm(nrow(data), 2, 0.3)

DimPlot(data, group_by = "cluster")
DimPlot(data, group_by = "cluster", theme = "theme_blank")
DimPlot(data, group_by = "cluster", theme = ggplot2::theme_classic,
        theme_args = list(base_size = 16), palette = "seurat")
DimPlot(data, group_by = "cluster", raster = TRUE, raster_dpi = 30)
DimPlot(data, group_by = "cluster", highlight = 1:20,
        highlight_color = "red2", highlight_stroke = 0.8)
DimPlot(data, group_by = "cluster", highlight = TRUE, facet_by = "group",
        theme = "theme_blank")
DimPlot(data, group_by = "cluster", label = TRUE)
DimPlot(data, group_by = "cluster", label = TRUE, label_fg = "red",
        label_bg = "yellow", label_size = 5)
DimPlot(data, group_by = "cluster", label = TRUE, label_insitu = TRUE)
DimPlot(data, group_by = "cluster", add_mark = TRUE)
DimPlot(data, group_by = "cluster", add_mark = TRUE, mark_linetype = 2)
DimPlot(data, group_by = "cluster", add_mark = TRUE, mark_type = "ellipse")
DimPlot(data, group_by = "cluster", add_density = TRUE)
DimPlot(data, group_by = "cluster", add_density = TRUE, density_filled = TRUE)
DimPlot(data, group_by = "cluster", add_density = TRUE, density_filled = TRUE,
        density_filled_palette = "Blues", highlight = TRUE)
DimPlot(data, group_by = "cluster", stat_by = "group")
DimPlot(data, group_by = "cluster", stat_by = "group", stat_plot_type = "bar")
DimPlot(data, group_by = "cluster", hex = TRUE)
DimPlot(data, group_by = "cluster", hex = TRUE, hex_bins = 20)
DimPlot(data, group_by = "cluster", hex = TRUE, hex_count = FALSE)
DimPlot(data, group_by = "cluster", graph = "@graph", edge_color = "grey80")
DimPlot(data, group_by = "cluster", lineages = c("L1", "L2", "L3"))

```

```

DimPlot(data, group_by = "cluster", lineages = c("L1", "L2", "L3"),
        lineages_whiskers = TRUE)
DimPlot(data, group_by = "cluster", lineages = c("L1", "L2", "L3"),
        lineages_span = 1)
DimPlot(data, group_by = "cluster", split_by = "cluster",
        palcolor = list(C1 = "red", C2 = "blue", C3 = "green"))

# Feature Dim Plot
FeatureDimPlot(data, features = "L1", pt_size = 2)
FeatureDimPlot(data, features = "L1", pt_size = 2, bg_cutoff = -Inf)
FeatureDimPlot(data, features = "L1", raster = TRUE, raster_dpi = 30)
FeatureDimPlot(data, features = c("L1", "L2"), pt_size = 2)
FeatureDimPlot(data, features = c("L1"), pt_size = 2, facet_by = "group")
# Can't facet multiple features
FeatureDimPlot(data, features = c("L1", "L2", "L3"), pt_size = 2)
# We can use split_by
FeatureDimPlot(data, features = c("L1", "L2", "L3"), split_by = "group", nrow = 2)
FeatureDimPlot(data, features = c("L1", "L2", "L3"), highlight = TRUE)
FeatureDimPlot(data, features = c("L1", "L2", "L3"), hex = TRUE, hex_bins = 15)
FeatureDimPlot(data, features = c("L1", "L2", "L3"), hex = TRUE, hex_bins = 15,
        split_by = "cluster", palette = list(C1 = "Reds", C2 = "Blues", C3 = "Greens"))

```

DotPlot

Dot Plot / Scatter Plot / Lollipop Plot

Description

For DotPlot, X-axis and Y-axis could be either numeric or factor/character. When x-axis and y-axis are both numeric, the plot works as a scatter plot. LollipopPlot is an alias of DotPlot when `lollipop = TRUE`.

Usage

```

DotPlot(
  data,
  x,
  y,
  x_sep = "_",
  y_sep = "_",
  flip = FALSE,
  split_by = NULL,
  split_by_sep = "_",
  size_name = NULL,
  fill_name = NULL,
  fill_cutoff_name = NULL,
  add_bg = FALSE,
  bg_palette = "stripe",

```

```
bg_palcolor = NULL,  
bg_alpha = 0.2,  
bg_direction = c("vertical", "horizontal", "v", "h"),  
size_by = NULL,  
fill_by = NULL,  
fill_cutoff = NULL,  
fill_reverse = FALSE,  
theme = "theme_this",  
theme_args = list(),  
palette = "Spectral",  
palcolor = NULL,  
alpha = 1,  
facet_by = NULL,  
facet_scales = "fixed",  
facet_ncol = NULL,  
facet_nrow = NULL,  
facet_byrow = TRUE,  
x_text_angle = 0,  
seed = 8525,  
aspect.ratio = 1,  
legend.position = "right",  
legend.direction = "vertical",  
title = NULL,  
subtitle = NULL,  
xlab = NULL,  
ylab = NULL,  
keep_empty = FALSE,  
combine = TRUE,  
nrow = NULL,  
ncol = NULL,  
byrow = TRUE,  
axes = NULL,  
axis_titles = axes,  
guides = NULL,  
design = NULL,  
...  
)  
  
LollipopPlot(  
  data,  
  x,  
  y,  
  y_sep = NULL,  
  flip = FALSE,  
  split_by = NULL,  
  split_by_sep = "_",  
  size_name = NULL,  
  fill_name = NULL,
```

```

fill_cutoff_name = NULL,
size_by = NULL,
fill_by = NULL,
fill_cutoff = NULL,
fill_reverse = FALSE,
theme = "theme_this",
theme_args = list(),
palette = "Spectral",
palcolor = NULL,
alpha = 1,
facet_by = NULL,
facet_scales = "fixed",
facet_ncol = NULL,
facet_nrow = NULL,
facet_byrow = TRUE,
x_text_angle = 0,
seed = 8525,
aspect.ratio = 1,
legend.position = "right",
legend.direction = "vertical",
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
keep_empty = FALSE,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

<code>data</code>	A data frame.
<code>x</code>	A character vector specifying the column to use for the x-axis. A numeric column is expected.
<code>y</code>	A character vector specifying the column to use for the y-axis. A factor/character column is expected.
<code>x_sep</code>	A character vector to concatenate multiple columns in x. Default is "_".
<code>y_sep</code>	A character vector to concatenate multiple columns in y. Default is "_".
<code>flip</code>	A logical value indicating whether to flip the x and y axes. Default is FALSE.
<code>split_by</code>	The column(s) to split data by and plot separately.

<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>size_name</code>	A character vector specifying the name for the size legend.
<code>fill_name</code>	A character vector specifying the name for the fill legend.
<code>fill_cutoff_name</code>	A character vector specifying the name for the fill cutoff legend.
<code>add_bg</code>	A logical value indicating whether to add a background color to the plot. Default is FALSE.
<code>bg_palette</code>	A character vector specifying the palette for the background color. Default is "stripe".
<code>bg_palcolor</code>	A character vector specifying the color for the background color.
<code>bg_alpha</code>	A numeric value specifying the alpha for the background color. Default is 0.2.
<code>bg_direction</code>	A character vector specifying the direction for the background color. Default is "vertical". Other options are "horizontal". "h" and "v" are also accepted.
<code>size_by</code>	Which column to use as the size of the dots. It must be a numeric column. If not provided, the size will be the count of the instances for each 'y' in 'x'. For 'ScatterPlot', it can be a single numeric value to specify the size of the dots.
<code>fill_by</code>	Which column to use as the fill the dots. It must be a numeric column. If not provided, all dots will be filled with the same color at the middle of the palette.
<code>fill_cutoff</code>	A numeric value specifying the cutoff for the fill column.
<code>fill_reverse</code>	A logical value indicating whether to reverse the fill direction. Default is FALSE. By default, the fill direction is "up". If TRUE, the fill direction is "down". When the direction is "up", the values less than the cutoff will be filled with grey. When the direction is "down", the values greater than the cutoff will be filled with grey.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be NULL for those values).
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.

facet_byrow	A logical value indicating whether to fill the plots by row. Default is TRUE.
x_text_angle	A numeric value specifying the angle of the x-axis text.
seed	The random seed to use. Default is 8525.
aspect_ratio	A numeric value specifying the aspect ratio of the plot.
legend_position	A character string specifying the position of the legend. If <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
legend_direction	A character string specifying the direction of the legend.
title	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
subtitle	A character string specifying the subtitle of the plot.
xlab	A character string specifying the x-axis label.
ylab	A character string specifying the y-axis label.
keep_empty	A logical value indicating whether to keep empty groups. If FALSE, empty groups will be removed.
combine	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
nrow	A numeric value specifying the number of rows in the facet.
ncol	A numeric value specifying the number of columns in the facet.
byrow	A logical value indicating whether to fill the plots by row.
axes	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none">• 'keep' will retain all axes in individual plots.• 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout.• 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
axis_titles	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none">• 'keep' will retain all axis titles in individual plots.• 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction.• 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
guides	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none">• 'collect' will collect guides below to the given nesting level, removing duplicates.• 'keep' will stop collection at this level and let guides be placed alongside their plot.

- 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
- design Specification of the location of areas in the layout, passed to `patchwork::wrap_plots()`. Only relevant when `split_by` is used and `combine` is TRUE. When specified, `nrow`, `ncol`, and `byrow` are ignored. See `patchwork::wrap_plots()` for more details.
- ... Additional arguments.

Value

A ggplot object or `wrap_plots` object or a list of ggplot objects

A ggplot object or `wrap_plots` object or a list of ggplot objects

Examples

```
mtcars <- datasets::mtcars
mtcars$carb <- factor(mtcars$carb)
mtcars$gear <- factor(mtcars$gear)
DotPlot(mtcars, x = "carb", y = "gear", size_by = "wt",
        fill_by = "mpg", fill_cutoff = 18)
DotPlot(mtcars, x = "carb", y = "gear", size_by = "wt",
        fill_by = "mpg", fill_cutoff = 18, add_bg = TRUE)
DotPlot(mtcars, x = "carb", y = "gear", size_by = "wt",
        fill_by = "mpg", fill_cutoff = 18, add_bg = TRUE,
        bg_direction = "h")
DotPlot(mtcars, x = "carb", y = "gear", size_by = "wt",
        fill_by = "mpg", fill_cutoff = 18, facet_by = "cyl")
DotPlot(mtcars, x = "carb", y = "gear", size_by = "wt",
        fill_by = "mpg", fill_cutoff = 18, facet_by = "cyl",
        facet_scales = "free_x")
DotPlot(mtcars, x = "carb", y = "gear", size_by = "wt",
        fill_by = "mpg", fill_cutoff = 18, split_by = "cyl")
DotPlot(mtcars, x = "carb", y = "gear", size_by = "wt",
        fill_by = "mpg", fill_cutoff = 18, split_by = "cyl",
        palette = list("4" = "Set1", "6" = "Paired", "8" = "Reds"))
# works as a scatter plot
DotPlot(mtcars, x = "qsec", y = "drat", size_by = "wt",
        fill_by = "mpg", fill_cutoff = 18, fill_cutoff_name = "Small mpgs")
LollipopPlot(mtcars, x = "qsec", y = "drat", size_by = "wt",
            fill_by = "mpg")
LollipopPlot(mtcars, x = "qsec", y = "drat", size_by = "wt",
            fill_by = "mpg", fill_cutoff = 18, facet_by = "cyl",
            facet_scales = "free_y")
LollipopPlot(mtcars, x = "qsec", y = "drat", size_by = "wt",
            split_by = "vs", palette = list("0" = "Reds", "1" = "Blues"))
```

element_textbox	<i>Theme element that add a box to the text</i>
-----------------	---

Description

Code grabbed from the ggtext package. See the original code at: <https://github.com/wilkelab/ggtext>
This is used to create a text box around the text, primarily to be used in CorPairsPlot.

Usage

```
element_textbox(  
  family = NULL,  
  face = NULL,  
  size = NULL,  
  colour = NULL,  
  fill = NULL,  
  box.colour = NULL,  
  linetype = NULL,  
  linewidth = NULL,  
  hjust = NULL,  
  vjust = NULL,  
  halign = NULL,  
  valign = NULL,  
  lineheight = NULL,  
  margin = NULL,  
  padding = NULL,  
  width = NULL,  
  height = NULL,  
  minwidth = NULL,  
  maxwidth = NULL,  
  minheight = NULL,  
  maxheight = NULL,  
  r = NULL,  
  orientation = NULL,  
  color = NULL,  
  box.color = NULL,  
  debug = FALSE,  
  inherit.blank = FALSE  
)  
  
## S3 method for class 'element_textbox'  
element_grob(  
  element,  
  label = "",  
  x = NULL,  
  y = NULL,  
  family = NULL,
```

```

    face = NULL,
    colour = NULL,
    size = NULL,
    hjust = NULL,
    vjust = NULL,
    lineheight = NULL,
    margin = NULL,
    ...
  )

```

Arguments

family	Font family
face	Font face
size	Font size (in pt)
colour, color	Text color
fill	Fill color of the enclosing box
box.colour, box.color	Line color of the enclosing box (if different from the text color)
linetype	Line type of the enclosing box (like lty in base R)
linewidth	Line width of the enclosing box (measured in mm, just like size in <code>ggplot2::element_line()</code>).
hjust	Horizontal justification
vjust	Vertical justification
halign	Horizontal justification
valign	Vertical justification
lineheight	Line height, in multiples of the font size
padding, margin	Padding and margins around the text box. See <code>gridtext::textbox_grob()</code> for details.
width, height	Unit objects specifying the width and height of the textbox, as in <code>gridtext::textbox_grob()</code> .
minwidth, minheight, maxwidth, maxheight	Min and max values for width and height. Set to NULL to impose neither a minimum nor a maximum.
r	Unit value specifying the corner radius of the box
orientation	Orientation of the text box. See <code>gridtext::textbox_grob()</code> for details.
debug	Not implemented.
inherit.blank	See <code>ggplot2::margin()</code> for details.
element	A theme element created by <code>element_textbox()</code> .
label	Text to display in the textbox.
x, y	Position of the textbox.
...	Other arguments passed to <code>gridtext::textbox_grob()</code> .

Value

A ggplot2 theme element that can be used inside a `ggplot2::theme()` call.

enrich_example *A example of clusterProfiler enrichment result*

Description

A example of clusterProfiler enrichment result

Examples

```
## Not run:
if (interactive()) {
  data(geneList, package="DOSE")
  de <- names(geneList)[abs(geneList) > 1.5]
  enrich_example <- clusterProfiler::enrichPathway(gene=de, pvalueCutoff = 0.05, readable=TRUE)
  enrich_example <- as.data.frame(enrich_example)
}

## End(Not run)
```

enrich_multidb_example *A example of clusterProfiler enrichment result with multiple databases*

Description

A example of clusterProfiler enrichment result with multiple databases

Examples

```
## Not run:
if (interactive()) {
  data(enrich_example, package="plotthis")
  enrich_example$Database <- "DB1"
  enrich_example2 <- enrich_example
  enrich_example2$Database <- "DB2"
  enrich_example2$ID <- paste0(enrich_example2$ID, "_DB2")
  enrich_example2$Description <- paste0(enrich_example2$Description, " (DB2)")
  enrich_multidb_example <- rbind(enrich_example, enrich_example2)
}

## End(Not run)
```

gsea_example

A example of GSEA result from fgsea package

Description

A example of GSEA result from fgsea package

Examples

```
## Not run:
if (interactive()) {
  set.seed(1234)
  data(geneList, package="DOSE")
  gsea_example <- DOSE::gseD0(geneList)
  gene_ranks <- gsea_example@geneList
  gene_sets <- gsea_example@geneSets
  gsea_example_pos <- gsea_example[gsea_example$p.adjust < 0.05 & gsea_example$NES > 0, ]
  gsea_example_neg <- gsea_example[gsea_example$p.adjust < 0.05 & gsea_example$NES < 0, ]
  gsea_example <- rbind(
    gsea_example_pos[sample(1:nrow(gsea_example_pos), 5), ],
    gsea_example_neg[sample(1:nrow(gsea_example_neg), 5), ]
  )

  attr(gsea_example, "gene_ranks") <- gene_ranks
  attr(gsea_example, "gene_sets") <- gene_sets[gsea_example$ID]
}

## End(Not run)
```

Heatmap

Heatmap

Description

Heatmap is a popular way to visualize data in matrix format. It is widely used in biology to visualize gene expression data in microarray and RNA-seq data. The heatmap is a matrix where rows represent the samples and columns represent the features. The color of each cell represents the value of the feature in the sample. The color can be continuous or discrete. The heatmap can be split by the columns or rows to show the subgroups in the data. The heatmap can also be annotated by the columns or rows to show the additional information of the samples or features.

Usage

```
Heatmap(
  data,
  rows,
  columns_by,
```

```
rows_name = "rows",
columns_name = "columns",
split_by = NULL,
split_by_sep = "_",
split_rows_data = FALSE,
name = "value",
border = TRUE,
rows_palette = "Paired",
rows_palcolor = NULL,
title = NULL,
pie_group_by = NULL,
pie_group_by_sep = "_",
pie_palette = "Spectral",
pie_palcolor = NULL,
pie_size = NULL,
pie_name = NULL,
pie_size_name = "size",
pie_values = "count",
legend_items = NULL,
legend_discrete = FALSE,
lower_quantile = 0,
upper_quantile = 0.99,
lower_cutoff = NULL,
upper_cutoff = NULL,
columns_by_sep = "_",
columns_split_by = NULL,
columns_split_name = NULL,
columns_palette = "Paired",
columns_palcolor = NULL,
columns_split_by_sep = "_",
columns_split_palette = "simspec",
columns_split_palcolor = NULL,
rows_data = NULL,
rows_split_by = NULL,
rows_split_by_sep = "_",
rows_split_palette = "simspec",
rows_split_palcolor = NULL,
column_name_annotation = TRUE,
column_name_legend = isFALSE(show_column_names) && !identical(legend.position, "none"),
row_name_annotation = TRUE,
row_name_legend = isFALSE(show_row_names) && !identical(legend.position, "none"),
cluster_columns = TRUE,
cluster_rows = TRUE,
show_row_names = !row_name_annotation,
show_column_names = !column_name_annotation,
column_title = character(0),
row_title = character(0),
na_col = "grey85",
```

```
row_names_side = "right",
column_names_side = "bottom",
bars_sample = 100,
flip = FALSE,
label_size = 10,
label_cutoff = NULL,
label_accuracy = 0.01,
layer_fun_callback = NULL,
cell_type = c("tile", "bars", "label", "dot", "violin", "boxplot", "pie"),
cell_agg = mean,
add_bg = FALSE,
bg_alpha = 0.5,
violin_fill = NULL,
boxplot_fill = NULL,
dot_size = 8,
dot_size_name = "size",
column_annotation = NULL,
column_annotation_side = "top",
column_annotation_palette = "Paired",
column_annotation_palcolor = NULL,
column_annotation_type = "auto",
column_annotation_params = list(),
column_annotation_agg = NULL,
row_annotation = NULL,
row_annotation_side = "left",
row_annotation_palette = "Paired",
row_annotation_palcolor = NULL,
row_annotation_type = "auto",
row_annotation_params = list(),
row_annotation_agg = NULL,
add_reticle = FALSE,
reticle_color = "grey",
palette = "RdBu",
palcolor = NULL,
alpha = 1,
legend.position = "right",
legend.direction = "vertical",
seed = 8525,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)
```


Arguments

<code>data</code>	A data frame used to create the heatmap. The data should be in a long form where each row represents a instance in the heatmap. The rows should be multiple columns if you want to plot as rows, which you can refer as "features".
<code>rows</code>	A character string/vector of the column name(s) to plot for the rows Multiple columns in the data frame can be used as the rows.
<code>columns_by</code>	A character string of the column name to plot for the columns A character/factor column is expected. Multiple columns are also supported. If so, NAs can be used to exclude rows in that group. If there is a single value in each group (other than NA), the group name, rather than the value, will be shown in the column group annotation.
<code>rows_name</code>	A character string specifying the name of rows, which will be shown in the row group annotation and the legend of it.
<code>columns_name</code>	A character string specifying the name of columns, which will be shown in the column group annotation and the legend of it. Only used when <code>columns_by</code> has multiple columns.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>split_rows_data</code>	A logical value indicating whether to split the rows data as well using <code>'split_by'</code> and <code>'split_by_sep'</code> .
<code>name</code>	A character string specifying the name of the main legend of the heatmap
<code>border</code>	A logical value indicating whether to draw the border of the heatmap. If TRUE, the borders of the slices will be also drawn.
<code>rows_palette</code>	A character string specifying the palette of the row group annotation. The default is "Paired".
<code>rows_palcolor</code>	A character vector of colors to override the palette of the row group annotation.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>pie_group_by</code>	A character string of the column name to group the data for the pie chart.
<code>pie_group_by_sep</code>	A character string to concatenate the columns in <code>pie_group_by</code> if there are multiple columns.
<code>pie_palette</code>	A character string specifying the palette of the pie chart.
<code>pie_palcolor</code>	A character vector of colors to override the palette of the pie chart.
<code>pie_size</code>	A numeric value or a function specifying the size of the pie chart. If it is a function, the function should take count as the argument and return the size.
<code>pie_name</code>	A character string specifying the name of the legend for the pie chart.
<code>pie_size_name</code>	A character string specifying the name of the legend for the pie size.
<code>pie_values</code>	How to calculate the values for the pie chart. Default is "count". Other options are "value" and a function.

- "count": Count the number of instances in `pie_group_by`.
 - "value": Use the values in the columns specified by rows as the values. If there are multiple values for a single group in `pie_group_by`, a function should be provided to aggregate the values. If not, the sum of the values will be used and a warning will be shown.
 - A function: The function should take a vector of values as the argument and return a single value, for each group in `pie_group_by`.
- `legend_items` A numeric vector with names to specify the items in the main legend. The names will be working as the labels of the legend items.
- `legend_discrete` A logical value indicating whether the main legend is discrete.
- `lower_quantile, upper_quantile, lower_cutoff, upper_cutoff` Vector of minimum and maximum cutoff values or quantile values for each feature. It's applied to aggregated values when aggregated values are used (e.g. `plot_type` tile, label, etc). It's applied to raw values when raw values are used (e.g. `plot_type` bars, etc).
- `columns_by_sep` A character string to concatenate the columns in `columns_by` if there are multiple columns.
- `columns_split_by` A character string of the column name to split the heatmap columns into slices. A character/factor column or multiple columns are expected.
- `columns_split_name` A character string specifying the name of the column split annotation.
- `columns_palette` A character string specifying the palette of the column group annotation. The default is "Paired".
- `columns_palcolor` A character vector of colors to override the palette of the column group annotation.
- `columns_split_by_sep` A character string to concatenate the columns in `columns_split_by` if there are multiple columns.
- `columns_split_palette` A character string specifying the palette of the column split annotation. The default is "simspec".
- `columns_split_palcolor` A character vector of colors to override the palette of the column split annotation.
- `rows_data` A character string of the column name to use as the data for the row group annotation. If it starts with "@", it will be treated as an attribute of the data.
- `rows_split_by` A character string of the column name to split the heatmap rows into slices. A character/factor column or multiple columns are expected.
- `rows_split_by_sep` A character string to concatenate the columns in `rows_split_by` if there are multiple columns.

<code>rows_split_palette</code>	A character string specifying the palette of the row split annotation. The default is "simspec".
<code>rows_split_palcolor</code>	A character vector of colors to override the palette of the row split annotation.
<code>column_name_annotation</code>	A logical value indicating whether to add the column annotation for the column names. which is a simple annotation indicating the column names.
<code>column_name_legend</code>	A logical value indicating whether to show the legend of the column name annotation.
<code>row_name_annotation</code>	A logical value indicating whether to add the row annotation for the row names. which is a simple annotation indicating the row names.
<code>row_name_legend</code>	A logical value indicating whether to show the legend of the row name annotation.
<code>cluster_columns</code>	A logical value indicating whether to cluster the columns. If TRUE and <code>columns_split_by</code> is provided, the clustering will only be applied to the columns within the same split.
<code>cluster_rows</code>	A logical value indicating whether to cluster the rows. If TRUE and <code>rows_split_by</code> is provided, the clustering will only be applied to the rows within the same split.
<code>show_row_names</code>	A logical value indicating whether to show the row names. If TRUE, the legend of the row group annotation will be hidden.
<code>show_column_names</code>	A logical value indicating whether to show the column names. If TRUE, the legend of the column group annotation will be hidden.
<code>column_title</code>	A character string/vector of the column name(s) to use as the title of the column group annotation.
<code>row_title</code>	A character string/vector of the column name(s) to use as the title of the row group annotation.
<code>na_col</code>	A character string specifying the color for missing values. The default is "grey85".
<code>row_names_side</code>	A character string specifying the side of the row names. The default is "right".
<code>column_names_side</code>	A character string specifying the side of the column names. The default is "bottom".
<code>bars_sample</code>	An integer specifying the number of samples to draw the bars.
<code>flip</code>	A logical value indicating whether to flip the heatmap.
<code>label_size</code>	A numeric value specifying the size of the labels when <code>cell_type = "label"</code> .
<code>label_cutoff</code>	A numeric value specifying the cutoff to show the labels when <code>cell_type = "label"</code> .
<code>label_accuracy</code>	A numeric value specifying the accuracy of the labels when <code>cell_type = "label"</code> .

<code>layer_fun_callback</code>	A function to add additional layers to the heatmap. The function should have the following arguments: <code>j</code> , <code>i</code> , <code>x</code> , <code>y</code> , <code>w</code> , <code>h</code> , <code>fill</code> , <code>sr</code> and <code>sc</code> . Please also refer to the <code>layer_fun</code> argument in <code>ComplexHeatmap::Heatmap</code> .
<code>cell_type</code>	A character string specifying the type of the heatmap cells. The default is <code>values</code> . Other options are <code>"bars"</code> , <code>"label"</code> , <code>"dot"</code> , <code>"violin"</code> , <code>"boxplot"</code> . Note that for pie chart, the values under columns specified by rows will not be used directly. Instead, the values will just be counted in different <code>pie_group_by</code> groups. <code>NA</code> values will not be counted.
<code>cell_agg</code>	A function to aggregate the values in the cell, for the cell type <code>"tile"</code> and <code>"label"</code> . The default is <code>mean</code> .
<code>add_bg</code>	A logical value indicating whether to add a background to the heatmap. Does not work with <code>cell_type = "bars"</code> or <code>cell_type = "tile"</code> .
<code>bg_alpha</code>	A numeric value between 0 and 1 specifying the transparency of the background.
<code>violin_fill</code>	A character vector of colors to override the fill color of the violin plot. If <code>NULL</code> , the fill color will be the same as the annotation.
<code>boxplot_fill</code>	A character vector of colors to override the fill color of the boxplot. If <code>NULL</code> , the fill color will be the same as the annotation.
<code>dot_size</code>	A numeric value specifying the size of the dot or a function to calculate the size from the values in the cell.
<code>dot_size_name</code>	A character string specifying the name of the legend for the dot size.
<code>column_annotation</code>	A character string/vector of the column name(s) to use as the column annotation. Or a list with the keys as the names of the annotation and the values as the column names.
<code>column_annotation_side</code>	A character string specifying the side of the column annotation. Could be a list with the keys as the names of the annotation and the values as the sides.
<code>column_annotation_palette</code>	A character string specifying the palette of the column annotation. The default is <code>"Paired"</code> . Could be a list with the keys as the names of the annotation and the values as the palettes.
<code>column_annotation_palcolor</code>	A character vector of colors to override the palette of the column annotation. Could be a list with the keys as the names of the annotation and the values as the palcolors.
<code>column_annotation_type</code>	A character string specifying the type of the column annotation. The default is <code>"auto"</code> . Other options are <code>"simple"</code> , <code>"pie"</code> , <code>"ring"</code> , <code>"bar"</code> , <code>"violin"</code> , <code>"boxplot"</code> , <code>"density"</code> . Could be a list with the keys as the names of the annotation and the values as the types. If the type is <code>"auto"</code> , the type will be determined by the type and number of the column data.
<code>column_annotation_params</code>	A list of parameters passed to the annotation function. Could be a list with the keys as the names of the annotation and the values as the parameters.

<code>column_annotation_agg</code>	A function to aggregate the values in the column annotation.
<code>row_annotation</code>	A character string/vector of the column name(s) to use as the row annotation. Or a list with the keys as the names of the annotation and the values as the column names.
<code>row_annotation_side</code>	A character string specifying the side of the row annotation. Could be a list with the keys as the names of the annotation and the values as the sides.
<code>row_annotation_palette</code>	A character string specifying the palette of the row annotation. The default is "Paired". Could be a list with the keys as the names of the annotation and the values as the palettes.
<code>row_annotation_palcolor</code>	A character vector of colors to override the palette of the row annotation. Could be a list with the keys as the names of the annotation and the values as the palcolors.
<code>row_annotation_type</code>	A character string specifying the type of the row annotation. The default is "auto". Other options are "simple", "pie", "ring", "bar", "violin", "boxplot", "density". Could be a list with the keys as the names of the annotation and the values as the types. If the type is "auto", the type will be determined by the type and number of the row data.
<code>row_annotation_params</code>	A list of parameters passed to the annotation function. Could be a list with the keys as the names of the annotation and the values as the parameters.
<code>row_annotation_agg</code>	A function to aggregate the values in the row annotation.
<code>add_reticle</code>	A logical value indicating whether to add a reticle to the heatmap.
<code>reticle_color</code>	A character string specifying the color of the reticle.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (palcolor will be NULL for those values).
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>seed</code>	The random seed to use. Default is 8525.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.

<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
<code>...</code>	Additional arguments.

Value

The heatmap(s). When `split_by` is not provided, the function returns a single heatmap (`ComplexHeatmap::Heatmap`-class object). When `split_by` is provided, the function returns a combined plot of multiple heatmaps wrapped by `patchwork::wrap_plots` if `combine = TRUE`, otherwise, it returns a list of heatmaps.

See Also

[anno_simple](#), [anno_points](#), [anno_lines](#), [anno_pie](#), [anno_violin](#), [anno_boxplot](#), [anno_density](#)

Examples

```
set.seed(8525)
data <- data.frame(
  F1 = rnorm(100, 0.1),
```

```

F2 = rnorm(100, 0.2),
F3 = rnorm(100),
F4 = rnorm(100, 0.3),
F5 = rnorm(100, -0.1),
F6 = rnorm(100, -0.2),
c = sample(letters[1:8], 100, replace = TRUE),
s = sample(LETTERS[1:2], 100, replace = TRUE),
p = sample(c("X", "Y", "Z"), 100, replace = TRUE),
a = sample(1:5, 100, replace = TRUE),
p1 = c(sample(c(1, NA), 100, replace = TRUE)),
p2 = c(sample(c(1, NA), 100, replace = TRUE)),
p3 = c(sample(c(1, NA), 100, replace = TRUE))
)
rows <- c("F1", "F2", "F3", "F4", "F5", "F6")
rows_data <- data.frame(
  rows = rep(c("F1", "F2", "F3", "F4", "F5", "F6"), each = 10),
  rows1 = rep(c("F1", "F2", "F3", "F4", "F5", "F6"), each = 10),
  rs = rep(letters[1:2], each = 30),
  rp = sample(c("X", "Y", "Z"), 60, replace = TRUE),
  rv = rnorm(60, 0.5)
)

if (requireNamespace("cluster", quietly = TRUE)) {
  Heatmap(data, rows = rows, columns_by = "c")
}
if (requireNamespace("cluster", quietly = TRUE)) {
  Heatmap(data, rows = list(RG1 = c("F1", "F2", "F3"), RG2 = c("F4", "F5", "F6")),
    columns_by = "c")
}
if (requireNamespace("cluster", quietly = TRUE)) {
  # Multiple columns_by, each as a split
  Heatmap(data, rows = rows, columns_by = c("c", "s"), columns_by_sep = "/" )
}
if (requireNamespace("cluster", quietly = TRUE)) {
  Heatmap(data, rows = rows, columns_by = c("p1", "p2", "p3"))
}
if (requireNamespace("cluster", quietly = TRUE)) {
  Heatmap(data, rows = rows, columns_by = "c", split_by = "s",
    upper_cutoff = 2, lower_cutoff = -2, legend.position = c("none", "right"),
    design = "AAAAAA#BBBBBBB")
}
if (requireNamespace("cluster", quietly = TRUE)) {
  Heatmap(data, rows = rows, columns_by = "c", columns_split_by = "s")
}
if (requireNamespace("cluster", quietly = TRUE)) {
  Heatmap(data, rows = rows, columns_by = "c", columns_split_by = "s",
    rows_data = rows_data, rows_split_by = "rs")
}
if (requireNamespace("cluster", quietly = TRUE)) {
  Heatmap(data, rows = rows, columns_by = "c", columns_split_by = "s",
    rows_data = rows_data, rows_split_by = "rs", flip = TRUE)
}
if (requireNamespace("cluster", quietly = TRUE)) {

```

```

Heatmap(data, rows = rows, columns_by = "c", cell_type = "bars")
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, rows = rows, columns_by = "c", cell_type = "bars",
        bars_sample = 3)
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, rows = rows, columns_by = "c", cell_type = "label")
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, rows = rows, columns_by = "c", cell_type = "label",
        label_cutoff = 0)
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, rows = rows, columns_by = "c", cell_type = "dot")
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, rows = rows, columns_by = "c", cell_type = "dot",
        dot_size = mean)
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, rows = rows, columns_by = "c", cell_type = "dot",
        dot_size = mean, row_name_annotation = FALSE, column_name_annotation = FALSE,
        row_names_side = "left", cluster_rows = FALSE, cluster_columns = FALSE)
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, rows = rows, columns_by = "c", cell_type = "dot",
        dot_size = mean, add_bg = TRUE)
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, rows = rows, columns_by = "c", cell_type = "dot",
        dot_size = mean, add_reticle = TRUE)
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, cluster_rows = FALSE, cluster_columns = FALSE, columns_by = "p",
        rows = c("p1", "p2", "p3"), name = "Category", pie_group_by = "c",
        cell_type = "pie")
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, cluster_rows = FALSE, cluster_columns = FALSE, columns_by = "p",
        rows = c("p1", "p2", "p3"), name = "Category", pie_group_by = "c",
        cell_type = "pie", pie_size = sqrt, add_bg = TRUE)
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, rows = rows, columns_by = "c", cell_type = "violin")
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, rows = rows, columns_by = "c", cell_type = "boxplot")
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, rows = rows, columns_by = "c", rows_data = rows_data,
        column_annotation = list(p1 = "p", p2 = "p", F1 = "F1"),
        column_annotation_type = list(p1 = "ring", p2 = "bar", F1 = "violin"),

```



```

column_annotation_params = list(
  p1 = list(height = grid::unit(10, "mm"), show_legend = FALSE),
  F1 = list(height = grid::unit(18, "mm"))),
rows_split_by = "rs",
row_annotation = c("rp", "rv", "rows1"),
row_annotation_side = "right",
row_annotation_type = list(rp = "pie", rv = "density", rows1 = "simple"),
row_annotation_params = list(rp = list(width = grid::unit(12, "mm"))),
show_row_names = TRUE, show_column_names = TRUE)
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, rows = rows, columns_by = "c", rows_data = rows_data,
  column_annotation = list(p1 = "p", p2 = "p", F1 = "F1"),
  column_annotation_type = list(p1 = "ring", p2 = "bar", F1 = "violin"),
  column_annotation_params = list(
    p1 = list(height = grid::unit(10, "mm"), show_legend = FALSE),
    F1 = list(height = grid::unit(18, "mm"))),
  rows_split_by = "rs",
  row_annotation = c("rp", "rv", "rows1"),
  row_annotation_side = "right",
  row_annotation_type = list(rp = "pie", rv = "density", rows1 = "simple"),
  row_annotation_params = list(rp = list(width = grid::unit(12, "mm"))),
  show_row_names = TRUE, show_column_names = TRUE, flip = TRUE)
}
if (requireNamespace("cluster", quietly = TRUE)) {
Heatmap(data, rows = rows, columns_by = "c", split_by = "p",
  palette = list(X = "Reds", Y = "Blues", Z = "Purp"))
}
}

```

LinePlot

Line Plot

Description

Visualizing the change of a numeric value over the progression of a categorical variable.

Usage

```

LinePlot(
  data,
  x,
  y = NULL,
  group_by = NULL,
  group_by_sep = "_",
  split_by = NULL,
  split_by_sep = "_",
  fill_point_by_x_if_no_group = TRUE,
  color_line_by_x_if_no_group = TRUE,

```

```
add_bg = FALSE,
bg_palette = "stripe",
bg_palcolor = NULL,
bg_alpha = 0.2,
add_errorbars = FALSE,
errorbar_width = 0.1,
errorbar_alpha = 1,
errorbar_color = "grey30",
errorbar_linewidth = 0.75,
errorbar_min = NULL,
errorbar_max = NULL,
errorbar_sd = NULL,
highlight = NULL,
highlight_size = pt_size - 0.75,
highlight_color = "red2",
highlight_alpha = 0.8,
pt_alpha = 1,
pt_size = 5,
line_type = "solid",
line_width = 1,
line_alpha = 0.8,
theme = "theme_this",
theme_args = list(),
palette = "Paired",
palcolor = NULL,
x_text_angle = 0,
aspect.ratio = 1,
legend.position = "right",
legend.direction = "vertical",
facet_by = NULL,
facet_scales = "fixed",
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
facet_nrow = NULL,
facet_ncol = NULL,
facet_byrow = TRUE,
facet_args = list(),
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
keep_empty = FALSE,
seed = 8525,
axes = NULL,
axis_titles = axes,
guides = NULL,
```

```

    design = NULL,
    ...
)

```

Arguments

<code>data</code>	A data frame.
<code>x</code>	A character string specifying the column name of the data frame to plot for the x-axis.
<code>y</code>	A character string specifying the column name of the data frame to plot for the y-axis.
<code>group_by</code>	Columns to group the data for plotting For those plotting functions that do not support multiple groups, They will be concatenated into one column, using <code>group_by_sep</code> as the separator
<code>group_by_sep</code>	A character string specifying the separator to use when concatenating multiple columns.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>fill_point_by_x_if_no_group</code>	A logical value indicating whether to color the points by the x-axis values when there is no <code>group_by</code> column.
<code>color_line_by_x_if_no_group</code>	A logical value indicating whether to color the lines by the x-axis values
<code>add_bg</code>	A logical value indicating whether to add a background to the plot.
<code>bg_palette</code>	The palette to use for the background.
<code>bg_palcolor</code>	The color to use for the background.
<code>bg_alpha</code>	The alpha value of the background.
<code>add_errorbars</code>	A logical value indicating whether to add error bars to the plot.
<code>errorbar_width</code>	The width of the error bars.
<code>errorbar_alpha</code>	The alpha value of the error bars.
<code>errorbar_color</code>	The color to use for the error bars. If "line", the error bars will be colored the same as the lines.
<code>errorbar_linewidth</code>	The line width of the error bars.
<code>errorbar_min</code>	The column in the data frame containing the lower bound of the error bars.
<code>errorbar_max</code>	The column in the data frame containing the upper bound of the error bars.
<code>errorbar_sd</code>	The column in the data frame containing the standard deviation of the error bars. If <code>errorbar_min</code> and <code>errorbar_max</code> are not provided, this column will be used to calculate the error bars. $errorbar_min = y - errorbar_sd$, $errorbar_max = y + errorbar_sd$. If <code>errorbar_min</code> and <code>errorbar_max</code> are provided, this column will be ignored.
<code>highlight</code>	A vector of indexes or rownames to select the points to highlight. It could also be an expression (in string) to filter the data.

<code>highlight_size</code>	The size of the highlighted points.
<code>highlight_color</code>	A character vector specifying the color of the highlighted points. Default is "red".
<code>highlight_alpha</code>	A numeric value specifying the transparency of the highlighted points. Default is 1.
<code>pt_alpha</code>	The alpha value of the points.
<code>pt_size</code>	The size of the points.
<code>line_type</code>	The type of line to draw.
<code>line_width</code>	The width of the line.
<code>line_alpha</code>	The alpha value of the line.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be NULL for those values).
<code>x_text_angle</code>	A numeric value specifying the angle of the x-axis text.
<code>aspect.ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
<code>combine</code>	Whether to combine the plots into one when facet is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is TRUE.

facet_args	A list of arguments to pass to <code>ggplot2::facet_wrap()</code> or <code>ggplot2::facet_grid()</code> . when there is no <code>group_by</code> column.
title	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
subtitle	A character string specifying the subtitle of the plot.
xlab	A character string specifying the x-axis label.
ylab	A character string specifying the y-axis label.
keep_empty	A logical value indicating whether to keep empty groups. If FALSE, empty groups will be removed.
seed	The random seed to use. Default is 8525.
axes	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
axis_titles	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
guides	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
design	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
...	Additional arguments.

Value

A ggplot object or `wrap_plots` object or a list of ggplot objects

Examples

```

data <- data.frame(
  x = factor(c("A", "B", "C", "D", "A", "B", "C", "D"), levels = LETTERS[1:6]),
  y = c(10, 8, 16, 4, 6, 12, 14, 2),
  group = c("G1", "G1", "G1", "G1", "G2", "G2", "G2", "G2"),
  facet = c("F1", "F1", "F2", "F2", "F3", "F3", "F4", "F4")
)

LinePlot(data, x = "x", y = "y")
LinePlot(data, x = "x", y = "y", highlight = "group == 'G1'",
  fill_point_by_x_if_no_group = FALSE, color_line_by_x_if_no_group = FALSE)
LinePlot(data, x = "x", y = "y", group_by = "group")
LinePlot(data, x = "x", y = "y", group_by = "group", add_bg = TRUE,
  highlight = "y > 10")
LinePlot(data, x = "x", y = "y", group_by = "group", facet_by = "facet")
LinePlot(data, x = "x", y = "y", group_by = "group", split_by = "facet")
LinePlot(data, x = "x", y = "y", split_by = "group",
  palcolor = list(G1 = c("red", "blue"), G2 = c("green", "black")))

```

ManhattanPlot

ManhattanPlot

Description

This function is borrowed from `ggmanh:manhattan_plot()` with following customizations:

Usage

```

ManhattanPlot(
  data,
  chr_by,
  pos_by,
  pval_by,
  split_by = NULL,
  split_by_sep = "_",
  label_by = NULL,
  chromosomes = NULL,
  pt_size = 0.75,
  pt_color = NULL,
  pt_alpha = alpha,
  pt_shape = 19,
  label_size = 3,
  label_fg = NULL,
  highlight = NULL,
  highlight_color = NULL,
  highlight_size = 1.5,
  highlight_alpha = 1,
  highlight_shape = 19,

```

```

preserve_position = TRUE,
chr_gap_scaling = 1,
pval_transform = "-log10",
signif = c(5e-08, 1e-05),
signif_color = NULL,
signif_rel_pos = 0.2,
signif_label = TRUE,
signif_label_size = 3.5,
signif_label_pos = c("left", "right"),
thin = NULL,
thin_n = 1000,
thin_bins = 200,
rescale = TRUE,
rescale_ratio_threshold = 5,
palette = "Dark2",
palcolor = NULL,
palreverse = FALSE,
alpha = 1,
theme = "theme_this",
theme_args = list(),
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = expression("-" * log[10](p)),
seed = 8525,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
facet_by = NULL,
design = NULL,
...
)

```

Arguments

<code>data</code>	A data frame.
<code>chr_by</code>	Column name for chromosome (default: "chr").
<code>pos_by</code>	Column name for position (default: "pos").
<code>pval_by</code>	Column name for p-value (default: "pval").
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>label_by</code>	Column name for the variants to be labeled (default: NULL). Only the variants with values in this column will be labeled.

chromosomes	A vector of chromosomes to be plotted (default: NULL). If NULL, all chromosomes will be plotted. It is more of a combination of the chromosome and chr.order arguments of <code>ggmanh::manhattan_plot()</code> . We can use it to select chromosomes to be plotted or to set the order of the chromosomes.
pt_size	A numeric value to specify the size of the points in the plot.
pt_color	A character string to specify the color of the points in the plot. By default, the color of the points will be controlled by <code>palette</code> or <code>palcolor</code> arguments. This is useful to color the background points when <code>highlight</code> and <code>highlight_color</code> are specified.
pt_alpha	A numeric value to specify the transparency of the points in the plot.
pt_shape	A numeric value to specify the shape of the points in the plot.
label_size	A numeric value to specify the size of the labels in the plot.
label_fg	A character string to specify the color of the labels in the plot. If NULL, the color of the labels will be the same as the points.
highlight	Either a vector of indices or a character of expression to select the variants to be highlighted (default: NULL). If NULL, no variants will be highlighted.
highlight_color	A character string to specify the color of the highlighted points.
highlight_size	A numeric value to specify the size of the highlighted points.
highlight_alpha	A numeric value to specify the transparency of the highlighted points.
highlight_shape	A numeric value to specify the shape of the highlighted points.
preserve_position	If TRUE, the width of each chromosome reflect the number of variants and the position of each variant is correctly scaled? If FALSE, the width of each chromosome is equal and the variants are equally spaced.
chr_gap_scaling	A numeric value to specify the scaling of the gap between chromosomes. It is used to adjust the gap between chromosomes in the plot.
pval_transform	A function to transform the p-values (default: <code>-log10</code>). If it is a character, it will be evaluated as a function.
signif	A vector of significance thresholds (default: <code>c(5e-08, 1e-05)</code>).
signif_color	A character vector of equal length as <code>signif</code> . It contains colors for the lines drawn at <code>signif</code> . If NULL, the smallest value is colored black while others are grey.
signif_rel_pos	A numeric between 0.1 and 0.9. If the plot is rescaled,
signif_label	A logical value indicating whether to label the significance thresholds (default: TRUE).
signif_label_size	A numeric value to specify the size of the significance labels.
signif_label_pos	A character string specifying the position of the significance labels. where should the significance threshold be positioned? It can be either "left" or "right" (default: "left").

<code>thin</code>	A logical value indicating whether to thin the data (default: <code>NULL</code>). Defaults to <code>TRUE</code> when <code>chromosomes</code> is specified and the length of it is less than the number of chromosomes in the data. Defaults to <code>FALSE</code> otherwise.
<code>thin_n</code>	Number of max points per horizontal partitions of the plot. Defaults to 1000.
<code>thin_bins</code>	Number of bins to partition the data. Defaults to 200.
<code>rescale</code>	A logical value indicating whether to rescale the plot (default: <code>TRUE</code>).
<code>rescale_ratio_threshold</code>	A numeric value to specify the ratio threshold for rescaling.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be <code>NULL</code> for those values).
<code>palreverse</code>	A logical value indicating whether to reverse the palette for chromosomes (default: <code>FALSE</code>).
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>seed</code>	The random seed to use. Default is 8525.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is <code>FALSE</code> . Default is <code>TRUE</code> .
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots.

	<ul style="list-style-type: none"> • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
guides	<p>A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code>. Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are:</p> <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
facet_by	<p>A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code></p>
design	<p>Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code>. Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code>, <code>ncol</code>, and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.</p>
...	<p>Additional arguments.</p>

Details

- The dots in argument names are replaced with underscores wherever possible.
- `chr.colname`, `pos.colname`, `pval.colname` and `label.colname` are replaced with `chr_by`, `pos_by`, `pval_by` and `label_by` respectively.
- The chromosome and `chr.order` arguments are merged into a single argument `chromosomes`.
- The `highlight.colname` argument is replaced with `highlight`, which can be a vector of indices or a character of expression to select the variants to be highlighted, instead of a column name.
- `point.size` is replaced with `pt_size`
- When `highlight` is specified, the colors of the points will be controlled by `pt_color` and `highlight_color` arguments.
- The labels get more controlled by `label_*` arguments.
- The highlighted points get more controlled by `highlight_*` arguments.
- The `pval_log_transform` argument is replaced with `pval_transform`, which allows to specify a function to transform the p-values.

Value

A ggplot object or `wrap_plots` object or a list of ggplot objects. If no `split_by` is provided, a single plot (ggplot object) will be returned. If 'combine' is TRUE, a `wrap_plots` object will be returned. If 'combine' is FALSE, a list of ggplot objects will be returned.

Examples

```

set.seed(1000)

nsim <- 50000

simdata <- data.frame(
  "chromosome" = sample(c(1:22,"X"), size = nsim, replace = TRUE),
  "position" = sample(1:100000000, size = nsim),
  "P.value" = rbeta(nsim, shape1 = 5, shape2 = 1)^7,
  "cohort" = sample(c("A", "B"), size = nsim, replace = TRUE)
)
simdata$chromosome <- factor(simdata$chromosome, c(1:22, "X"))
options(repr.plot.width=10, repr.plot.height=5)

if (requireNamespace("ggmanh", quietly = TRUE)) {
  ManhattanPlot(
    simdata, pval_by = "P.value", chr_by = "chromosome", pos_by = "position",
    title = "Simulated P.Values", ylab = "P")
}

if (requireNamespace("ggmanh", quietly = TRUE)) {
  # split_by
  ManhattanPlot(
    simdata, pval_by = "P.value", chr_by = "chromosome", pos_by = "position",
    title = "Simulated P.Values", ylab = "P", split_by = "cohort", ncol = 1)
}

if (requireNamespace("ggmanh", quietly = TRUE)) {
  # Customized p-value transformation and significance threshold line colors
  ManhattanPlot(
    simdata, pval_by = "P.value", chr_by = "chromosome", pos_by = "position",
    title = "Simulated -Log2 P.Values", ylab = "-log2(P)", pval_transform = "-log2",
    signif_color = c("red", "blue"))
}

if (requireNamespace("ggmanh", quietly = TRUE)) {
  # Use a different palette and don't show significance threshold labels
  ManhattanPlot(
    simdata, pval_by = "P.value", chr_by = "chromosome", pos_by = "position",
    palette = "Set1", signif_label = FALSE)
}

if (requireNamespace("ggmanh", quietly = TRUE)) {
  # Reverse the palette and show significance threshold labels on the right
  ManhattanPlot(
    simdata, pval_by = "P.value", chr_by = "chromosome", pos_by = "position",
    palette = "Set1", palreverse = TRUE, signif_label_pos = "right")
}

if (requireNamespace("ggmanh", quietly = TRUE)) {
  # Use chromosomes to show a single selected chromosome
  ManhattanPlot(

```

```

simdata, pval_by = "P.value", chr_by = "chromosome", pos_by = "position",
title = "Simulated P.Values", chromosomes = 5)
}

if (requireNamespace("ggmanh", quietly = TRUE)) {
# Subset and reorder chromosomes
ManhattanPlot(
  simdata, pval_by = "P.value", chr_by = "chromosome", pos_by = "position",
  title = "Simulated P.Values", chromosomes = c(20, 4, 6))
}

tmpdata <- data.frame(
  "chromosome" = c(rep(5, 10), rep(21, 5)),
  "position" = c(sample(250000:250100, 10, replace = FALSE),
  sample(590000:600000, 5, replace = FALSE)),
  "P.value" = c(10^-(rnorm(10, 100, 3)), 10^-rnorm(5, 9, 1)),
  "cohort" = c(rep("A", 10), rep("B", 5))
)

simdata <- rbind(simdata, tmpdata)
simdata$chromosome <- factor(simdata$chromosome, c(1:22, "X"))

if (requireNamespace("ggmanh", quietly = TRUE)) {
# Don't rescale the plot (y-axis)
ManhattanPlot(
  simdata, pval_by = "P.value", chr_by = "chromosome", pos_by = "position",
  title = "Simulated P.Values - Significant", rescale = FALSE)
}

if (requireNamespace("ggmanh", quietly = TRUE)) {
# Rescale the plot (y-axis) and put the breaking point in the middle of the y-axis
ManhattanPlot(
  simdata, pval_by = "P.value", chr_by = "chromosome", pos_by = "position",
  title = "Simulated P.Values - Significant", rescale = TRUE, signif_rel_pos = 0.5)
}

sig <- simdata$P.value < 5e-07

simdata$label <- ""
simdata$label[sig] <- sprintf("Label: %i", 1:sum(sig))
simdata$label2 <- ""
i <- (simdata$chromosome == 5) & (simdata$P.value < 5e-8)
simdata$label2[i] <- paste("Chromosome 5 label", 1:sum(i))

if (requireNamespace("ggmanh", quietly = TRUE)) {
# Label the points with labels
ManhattanPlot(simdata, label_by = "label", pval_by = "P.value", chr_by = "chromosome",
  pos_by = "position", title = "Simulated P.Values with labels", label_size = 4)
}

if (requireNamespace("ggmanh", quietly = TRUE)) {
# Label the points with labels and use a different color for the labels
ManhattanPlot(simdata, label_by = "label2", pval_by = "P.value", chr_by = "chromosome",

```

```

    pos_by = "position", title = "Simulated P.Values with labels",
    label_size = 3, label_fg = "black")
}

simdata$color <- "Not Significant"
simdata$color[simdata$P.value <= 5e-8] <- "Significant"

if (requireNamespace("ggmanh", quietly = TRUE)) {
# Highlight points with shapes
ManhattanPlot(simdata, title = "Highlight Points with shapes",
  pval_by = "P.value", chr_by = "chromosome", pos_by = "position",
  highlight = "color == 'Significant'", highlight_color = NULL, highlight_shape = 6,
  highlight_size = 5, pt_alpha = 0.2, pt_size = 1)
}

if (requireNamespace("ggmanh", quietly = TRUE)) {
# Highlight points with colors
ManhattanPlot(simdata, title = "Highlight Points",
  pval_by = "P.value", chr_by = "chromosome", pos_by = "position",
  highlight = "color == 'Significant'", highlight_color = "black",
  pt_color = "lightblue", pt_alpha = 0.2, pt_size = 0.1)
}

```

Network

Network

Description

Plot a network graph

Usage

```

Network(
  links,
  nodes = NULL,
  split_by = NULL,
  split_by_sep = "_",
  split_nodes = FALSE,
  from = NULL,
  from_sep = "_",
  to = NULL,
  to_sep = "_",
  node_by = NULL,
  node_by_sep = "_",
  link_weight_by = 2,
  link_weight_name = NULL,
  link_type_by = "solid",
  link_type_name = NULL,

```

```
node_size_by = 15,
node_size_name = NULL,
node_color_by = "black",
node_color_name = NULL,
node_shape_by = 21,
node_shape_name = NULL,
node_fill_by = "grey20",
node_fill_name = NULL,
link_alpha = 1,
node_alpha = 0.95,
node_stroke = 1.5,
cluster_scale = c("fill", "color", "shape"),
node_size_range = c(5, 20),
link_weight_range = c(0.5, 5),
link_arrow_offset = 20,
link_curvature = 0,
link_color_by = "from",
link_color_name = NULL,
palette = "Paired",
palcolor = NULL,
link_palette = ifelse(link_color_by %in% c("from", "to"), palette, "Set1"),
link_palcolor = if (link_color_by %in% c("from", "to")) palcolor else NULL,
directed = TRUE,
layout = "circle",
cluster = "none",
add_mark = FALSE,
mark_expand = ggplot2::unit(10, "mm"),
mark_type = c("hull", "ellipse", "rect", "circle"),
mark_alpha = 0.1,
mark_linetype = 1,
add_label = TRUE,
label_size = 3,
label_fg = "white",
label_bg = "black",
label_bg_r = 0.1,
arrow = ggplot2::arrow(type = "closed", length = ggplot2::unit(0.1, "inches")),
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
aspect.ratio = 1,
theme = "theme_this",
theme_args = list(),
legend.position = "right",
legend.direction = "vertical",
seed = 8525,
combine = TRUE,
nrow = NULL,
```

```

    ncol = NULL,
    byrow = TRUE,
    axes = NULL,
    axis_titles = axes,
    guides = NULL,
    design = NULL,
    ...
)

```

Arguments

links	A data frame containing the links between nodes.
nodes	A data frame containing the nodes. This is optional. The names of the nodes are extracted from the links data frame. If "@nodes" is provided, the nodes data frame will be extracted from the attribute nodes of the links data frame.
split_by	The column(s) to split data by and plot separately.
split_by_sep	The separator for multiple split_by columns. See split_by
split_nodes	A logical value specifying whether to split the nodes data. If TRUE, the nodes data will also be split by the split_by column.
from	A character string specifying the column name of the links data frame for the source nodes. Default is the first column of the links data frame.
from_sep	A character string to concatenate the columns in from, if multiple columns are provided.
to	A character string specifying the column name of the links data frame for the target nodes. Default is the second column of the links data frame.
to_sep	A character string to concatenate the columns in to, if multiple columns are provided.
node_by	A character string specifying the column name of the nodes data frame for the node names. Default is the first column of the nodes data frame.
node_by_sep	A character string to concatenate the columns in node_by, if multiple columns are provided.
link_weight_by	A numeric value or a character string specifying the column name of the links data frame for the link weight. If a numeric value is provided, all links will have the same weight. This determines the width of the links.
link_weight_name	A character string specifying the name of the link weight in the legend.
link_type_by	A character string specifying the type of the links. This can be "solid", "dashed", "dotted", or a column name from the links data frame. It has higher priority when it is a column name.
link_type_name	A character string specifying the name of the link type in the legend.
node_size_by	A numeric value or a character string specifying the column name of the nodes data frame for the node size. If a numeric value is provided, all nodes will have the same size.
node_size_name	A character string specifying the name of the node size in the legend.

<code>node_color_by</code>	A character string specifying the color of the nodes. This can be a color name, a hex code, or a column name from the nodes data frame. It has higher priority when it is a column name.
<code>node_color_name</code>	A character string specifying the name of the node color in the legend.
<code>node_shape_by</code>	A numeric value or a character string specifying the column name of the nodes data frame for the node shape. If a numeric value is provided, all nodes will have the same shape.
<code>node_shape_name</code>	A character string specifying the name of the node shape in the legend.
<code>node_fill_by</code>	A character string specifying the fill color of the nodes. This can be a color name, a hex code, or a column name from the nodes data frame. It has higher priority when it is a column name.
<code>node_fill_name</code>	A character string specifying the name of the node fill in the legend.
<code>link_alpha</code>	A numeric value specifying the transparency of the links.
<code>node_alpha</code>	A numeric value specifying the transparency of the nodes. It only works when the nodes are filled.
<code>node_stroke</code>	A numeric value specifying the stroke of the nodes.
<code>cluster_scale</code>	A character string specifying how to scale the clusters. It can be "fill", "color", or "shape".
<code>node_size_range</code>	A numeric vector specifying the range of the node size.
<code>link_weight_range</code>	A numeric vector specifying the range of the link weight.
<code>link_arrow_offset</code>	A numeric value specifying the offset of the link arrows. So that they won't overlap with the nodes.
<code>link_curvature</code>	A numeric value specifying the curvature of the links.
<code>link_color_by</code>	A character string specifying the colors of the link. It can be: <ul style="list-style-type: none"> • "from" means the color of the link is determined by the source node. • "to" means the color of the link is determined by the target node. • Otherwise, the color of the link is determined by the column name from the links data frame.
<code>link_color_name</code>	A character string specifying the name of the link color in the legend. Only used when <code>link_color_by</code> is a column name.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (palcolor will be NULL for those values).
<code>link_palette</code>	A character string specifying the palette of the links. When <code>link_color_by</code> is "from" or "to", the palette of the links defaults to the palette of the nodes.

<code>link_palcolor</code>	A character vector specifying the colors of the link palette. When <code>link_color_by</code> is "from" or "to", the colors of the link palette defaults to the colors of the node palette.
<code>directed</code>	A logical value specifying whether the graph is directed.
<code>layout</code>	A character string specifying the layout of the graph. It can be "circle", "tree", "grid", or a layout function from <code>igraph</code> .
<code>cluster</code>	A character string specifying the clustering method. It can be "none", "fast_greedy", "walktrap", "edge_betweenness", "infomap", or a clustering function from <code>igraph</code> .
<code>add_mark</code>	A logical value specifying whether to add mark for the clusters to the plot.
<code>mark_expand</code>	A unit value specifying the expansion of the mark.
<code>mark_type</code>	A character string specifying the type of the mark. It can be "hull", "ellipse", "rect", "circle", or a mark function from <code>ggforce</code> .
<code>mark_alpha</code>	A numeric value specifying the transparency of the mark.
<code>mark_linetype</code>	A numeric value specifying the line type of the mark.
<code>add_label</code>	A logical value specifying whether to add label to the nodes to the plot.
<code>label_size</code>	A numeric value specifying the size of the label.
<code>label_fg</code>	A character string specifying the foreground color of the label.
<code>label_bg</code>	A character string specifying the background color of the label.
<code>label_bg_r</code>	A numeric value specifying the background ratio of the label.
<code>arrow</code>	An arrow object for the links.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>aspect.ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>seed</code>	The random seed to use. Default is 8525.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.

<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
<code>...</code>	Additional arguments.

Value

A ggplot object or `wrap_plots` object or a list of ggplot objects

Examples

```
actors <- data.frame(
  name = c("Alice", "Bob", "Cecil", "David", "Esmeralda"),
  age = c(48, 33, 45, 34, 21),
  shape = c(21, 22, 21, 22, 23),
  gender = c("F", "M", "F", "M", "F")
)
relations <- data.frame(
  from = c("Bob", "Cecil", "Cecil", "David", "David", "Esmeralda", "Bob", "Alice",
    "Cecil", "David"),
  to = c("Alice", "Bob", "Alice", "Alice", "Bob", "Alice", "Bob", "Alice", "Cecil",
    "David"),
  friendship = c(4, 5, 5, 2, 1, 1, 2, 1, 3, 4),
  type = c(1, 1, 1, 1, 1, 2, 2, 2, 2, 2)
```

```

)
Network(relations, actors)
Network(relations, actors, theme = "theme_blank", theme_args = list(add_coord = FALSE))
Network(relations, actors, link_weight_by = "friendship", node_size_by = "age",
  link_weight_name = "FRIENDSHIP", node_fill_by = "gender", link_color_by = "to",
  link_type_by = "type", node_color_by = "black", layout = "circle", link_curvature = 0.2)
Network(relations, actors, layout = "tree", directed = FALSE, cluster = "fast_greedy",
  add_mark = TRUE)
Network(relations, actors, split_by = "type")

```

palette_list

A list of palettes for use in data visualization

Description

A list of palettes for use in data visualization

Examples

```

## Not run:
if (interactive()) {
  library(stringr)
  library(RColorBrewer)
  library(Redmonder)
  library(rcartocolor)
  library(nord)
  library(viridis)
  library(pals)
  library(dichromat)
  library(jcolors)
  library(scales)
  sypals <- utils::getFromNamespace("sypals", "pals")
  brewer.pal.info <- RColorBrewer::brewer.pal.info
  ggsci_db <- utils::getFromNamespace("ggsci_db", "ggsci")
  redmonder.pal.info <- Redmonder::redmonder.pal.info
  metacartocolors <- rcartocolor::metacartocolors
  rownames(metacartocolors) <- metacartocolors$Name
  nord_palettes <- nord::nord_palettes
  viridis_names <- c("magma", "inferno", "plasma", "viridis", "cividis", "rocket",
    "mako", "turbo")
  viridis_palettes <- lapply(setNames(viridis_names, viridis_names),
    function(x) viridis::viridis(100, option = x))
  ocean_names <- names(sypals)[grep("ocean", names(sypals))]
  ocean_palettes <- sypals[ocean_names]
  dichromat_palettes <- dichromat::color schemes
  jcolors_names <- paste0("jcolors-", c("default", "pal2", "pal3", "pal4", "pal5",
    "pal6", "pal7", "pal8", "pal9", "pal10", "pal11", "pal12", "rainbow"))
  custom_names <- c("jet", "simspec", "GdRd")
  custom_palettes <- list(

```

```

oompaBase::jetColors(N = 100),
c("#c22b86", "#f769a1", "#fcc5c1", "#253777", "#1d92c0", "#9ec9e1", "#015b33",
  "#42aa5e", "#d9f0a2", "#E66F00", "#f18c28", "#FFBB61"),
c("gold", "red3")
)
names(custom_palettes) <- custom_names
seurat_discrete_palettes <- list(
  alphabet = c(
    "#F0A0FF", "#0075DC", "#993F00", "#4C005C", "#191919", "#005C31",
    "#2BCE48", "#FFCC99", "#808080", "#94FFB5", "#8F7C00", "#9DCC00",
    "#C20088", "#003380", "#FFA405", "#FFA8BB", "#426600", "#FF0010",
    "#5EF1F2", "#00998F", "#E0FF66", "#740AFF", "#990000", "#FFFF80",
    "#FFE100", "#FF5005"
  ),
  alphabet2 = c(
    "#AA0DFE", "#3283FE", "#85660D", "#782AB6", "#565656", "#1C8356",
    "#16FF32", "#F7E1A0", "#E2E2E2", "#1CBE4F", "#C4451C", "#DEA0FD",
    "#FE00FA", "#325A9B", "#FEAF16", "#F8A19F", "#90AD1C", "#F6222E",
    "#1CFFCE", "#2ED9FF", "#B10DA1", "#C075A6", "#FC1CBF", "#B00068",
    "#FBE426", "#FA0087"
  ),
  glasbey = c(
    "#0000FF", "#FF0000", "#00FF00", "#000033", "#FF00B6", "#005300",
    "#FFD300", "#009FFF", "#9A4D42", "#00FFBE", "#783FC1", "#1F9698",
    "#FFACFD", "#B1CC71", "#F1085C", "#FE8F42", "#DD00FF", "#201A01",
    "#720055", "#766C95", "#02AD24", "#C8FF00", "#886C00", "#FFB79F",
    "#858567", "#A10300", "#14F9FF", "#00479E", "#DC5E93", "#93D4FF",
    "#004CFF", "#F2F318"
  ),
  polychrome = c(
    "#5A5156", "#E4E1E3", "#F6222E", "#FE00FA", "#16FF32", "#3283FE",
    "#FEAF16", "#B00068", "#1CFFCE", "#90AD1C", "#2ED9FF", "#DEA0FD",
    "#AA0DFE", "#F8A19F", "#325A9B", "#C4451C", "#1C8356", "#85660D",
    "#B10DA1", "#FBE426", "#1CBE4F", "#FA0087", "#FC1CBF", "#F7E1A0",
    "#C075A6", "#782AB6", "#AAF400", "#BDCDFE", "#822E1C", "#B5E5B5",
    "#7ED7D1", "#1C7F93", "#D85FF7", "#683B79", "#66B0FF", "#3B00FB"
  ),
  stepped = c(
    "#990F26", "#B33E52", "#CC7A88", "#E6B8BF", "#99600F", "#B3823E",
    "#CCAA7A", "#E6D2B8", "#54990F", "#78B33E", "#A3CC7A", "#CFE6B8",
    "#0F8299", "#3E9FB3", "#7ABECC", "#B8DEE6", "#3D0F99", "#653EB3",
    "#967ACC", "#C7B8E6", "#333333", "#666666", "#999999", "#CCCCCC"
  ),
  parade = c(
    '#ff6969', '#9b37ff', '#cd3737', '#69cdf', '#ffff69', '#69cdcd',
    '#9b379b', '#3737cd', '#ffff9b', '#cdf69', '#ff9b37', '#37ffff',
    '#9b69ff', '#37cd69', '#ff3769', '#ff3737', '#37ff9b', '#cdcd37',
    '#3769cd', '#37cdf', '#9b3737', '#ff699b', '#9b9bff', '#cd9b37',
    '#69ff37', '#cd3769', '#cd69cd', '#cd6937', '#3737ff', '#cdcd69',
    '#ff9b69', '#cd37cd', '#9bff37', '#cd379b', '#cd6969', '#69ff9b',
    '#ff379b', '#9bff9b', '#6937ff', '#69cd37', '#cdf69', '#9bff69',
    '#9b37cd', '#ff37ff', '#ff37cd', '#ffff37', '#37cd9b', '#379bff',
    '#ffcd37', '#379b37', '#ff9bff', '#379b9b', '#69ffcd', '#379bcd',

```

```

      '#ff69ff', '#ff9b9b', '#37ff69', '#ff6937', '#6969ff', '#699bff',
      '#ffcd69', '#69ffff', '#37ff37', '#6937cd', '#37cd37', '#3769ff',
      '#cd69ff', '#6969cd', '#9bcd37', '#69ff69', '#37cdcd', '#cd37ff',
      '#37379b', '#37ffcd', '#69cd69'
    )
  )
  seurat_continuous_palettes <- list(
    seurat.16 = hue_pal()(16),
    seurat.32 = hue_pal()(32),
    seurat.64 = hue_pal()(64)
  )

  palette_list <- list()
  all_colors <- c(
    rownames(brewer.pal.info), names(ggsci_db), rownames(redmonder.pal.info),
    rownames(metacartocolors), names(nord_palettes), names(viridis_palettes),
    ocean_names, names(dichromat_palettes), jcolors_names, names(seurat_palettes),
    names(seurat_continuous_palettes), custom_names
  )
  for (pal in all_colors) {
    if (!pal %in% all_colors) {
      stop(paste0("Invalid pal Must be one of ", paste0(all_colors, collapse = ",")))
    }
    if (pal %in% rownames(brewer.pal.info)) {
      pal_n <- brewer.pal.info[pal, "maxcolors"]
      pal_category <- brewer.pal.info[pal, "category"]
      if (pal_category == "div") {
        palcolor <- rev(brewer.pal(name = pal, n = pal_n))
      } else {
        if (pal == "Paired") {
          palcolor <- brewer.pal(12, "Paired")[c(1:4, 7, 8, 5, 6, 9, 10, 11, 12)]
        } else {
          palcolor <- brewer.pal(name = pal, n = pal_n)
        }
      }
    }
    if (pal_category == "qual") {
      attr(palcolor, "type") <- "discrete"
    } else {
      attr(palcolor, "type") <- "continuous"
    }
  }
  } else if (pal %in% names(ggsci_db)) {
    if (pal %in% c("d3", "uchicago", "material")) {
      for (subpal in names(ggsci_db[[pal]])) {
        palcolor <- ggsci_db[[pal]][[subpal]]
        if (pal == "material") {
          attr(palcolor, "type") <- "continuous"
        } else {
          attr(palcolor, "type") <- "discrete"
        }
      }
      palette_list[[paste0(pal, "-", subpal)]] <- palcolor
    }
    next
  } else {

```

```

    palcolor <- ggsci_db[[pal]][[1]]
    if (pal == "gsea") {
      attr(palcolor, "type") <- "continuous"
    } else {
      attr(palcolor, "type") <- "discrete"
    }
  }
} else if (pal %in% rownames(redmonder.pal.info)) {
  pal_n <- redmonder.pal.info[pal, "maxcolors"]
  pal_category <- redmonder.pal.info[pal, "category"]
  if (pal_category == "div") {
    palcolor <- rev(redmonder.pal(name = pal, n = pal_n))
  } else {
    palcolor <- redmonder.pal(name = pal, n = pal_n)
  }
  if (pal_category == "qual") {
    attr(palcolor, "type") <- "discrete"
  } else {
    attr(palcolor, "type") <- "continuous"
  }
} else if (pal %in% rownames(metacartocolors)) {
  pal_n <- metacartocolors[pal, "Max_n"]
  palcolor <- carto_pal(name = pal, n = pal_n)
  if (pal_category == "qualitative") {
    attr(palcolor, "type") <- "discrete"
  } else {
    attr(palcolor, "type") <- "continuous"
  }
} else if (pal %in% names(nord_palettes)) {
  palcolor <- nord_palettes[[pal]]
  attr(palcolor, "type") <- "discrete"
} else if (pal %in% names(viridis_palettes)) {
  palcolor <- viridis_palettes[[pal]]
  attr(palcolor, "type") <- "continuous"
} else if (pal %in% names(ocean_palettes)) {
  palcolor <- ocean_palettes[[pal]]
  attr(palcolor, "type") <- "continuous"
} else if (pal %in% names(dichromat_palettes)) {
  palcolor <- dichromat_palettes[[pal]]
  if (pal %in% c("Categorical.12", "SteppedSequential.5")) {
    attr(palcolor, "type") <- "discrete"
  } else {
    attr(palcolor, "type") <- "continuous"
  }
} else if (pal %in% jcolors_names) {
  palcolor <- jcolors(palette = gsub("jcolors-", "", pal))
  if (pal %in% paste0("jcolors-", c("pal10", "pal11", "pal12", "rainbow"))) {
    attr(palcolor, "type") <- "continuous"
  } else {
    attr(palcolor, "type") <- "discrete"
  }
} else if (pal %in% custom_names) {
  palcolor <- custom_palettes[[pal]]

```

```

    if (pal %in% c("jet")) {
      attr(palcolor, "type") <- "continuous"
    } else {
      attr(palcolor, "type") <- "discrete"
    }
  } else if (pal %in% names(seurat_discrete_palettes)) {
    palcolor <- seurat_discrete_palettes[[pal]]
    attr(palcolor, "type") <- "discrete"
  } else if (pal %in% names(seurat_continuous_palettes)) {
    palcolor <- seurat_continuous_palettes[[pal]]
    attr(palcolor, "type") <- "continuous"
  }
  palette_list[[pal]] <- palcolor
}
}

## End(Not run)

```

palette_this

Color palettes collected in plotthis.

Description

Color palettes collected in plotthis.

Usage

```

palette_this(
  x,
  n = 100,
  palette = "Paired",
  palcolor = NULL,
  type = "auto",
  keep_names = TRUE,
  alpha = 1,
  matched = FALSE,
  reverse = FALSE,
  NA_keep = FALSE,
  NA_color = "grey80",
  transparent = TRUE
)

```

Arguments

x	A vector of character/factor or numeric values. If missing, numeric values 1:n will be used as x.
n	The number of colors to return for numeric values.
palette	Palette name. All available palette names can be queried with show_palettes().

palcolor	Custom colors used to create a color palette.
type	Type of x. Can be one of "auto", "discrete" or "continuous". The default is "auto", which automatically detects if x is a numeric value.
keep_names	Whether to keep the names of the color vector.
alpha	The alpha value of the colors. Default is 1.
matched	If TRUE, will return a color vector of the same length as x.
reverse	Whether to invert the colors.
NA_keep	Whether to keep the color assignment to NA in x.
NA_color	Color assigned to NA if NA_keep is TRUE.
transparent	Whether to make the colors transparent when alpha < 1. When TRUE, <code>ggplot2::alpha()</code> is used to make the colors transparent. Otherwise, <code>adjcolors</code> is used to adjust the colors based on the alpha. The color will be not be actually transparent. For example, <code>ggplot2::alpha("red", 0.5) == "#FF000080"</code> ; while <code>adjcolors("red", 0.5) == "#FF8080"</code> .

Value

A vector of colors.

PieChart

Pie Chart

Description

Pie chart to illustrate numerical proportion of each group.

Usage

```
PieChart(
  data,
  x,
  y = NULL,
  label = y,
  split_by = NULL,
  split_by_sep = "_",
  clockwise = TRUE,
  facet_by = NULL,
  facet_scales = "free_y",
  facet_ncol = NULL,
  facet_nrow = NULL,
  facet_byrow = TRUE,
  theme = "theme_this",
  theme_args = list(),
  palette = "Paired",
  palcolor = NULL,
```



```

alpha = 1,
aspect.ratio = 1,
legend.position = "right",
legend.direction = "vertical",
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
keep_empty = FALSE,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
seed = 8525,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

<code>data</code>	A data frame.
<code>x</code>	A character string specifying the column name of the data frame to plot for the x-axis.
<code>y</code>	A character string of the column name to plot on the y-axis. A numeric column is expected. If <code>NULL</code> , the count of each x column will be used.
<code>label</code>	Which column to use as the label. <code>NULL</code> means no label. Default is the same as <code>y</code> . If <code>y</code> is <code>NULL</code> , you should use <code>".y"</code> to specify the count as the label.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>clockwise</code>	A logical value to draw the pie chart clockwise or not.
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is <code>TRUE</code> .
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is <code>"theme_this"</code> .

<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (palcolor will be NULL for those values).
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>aspect.ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>keep_empty</code>	A logical value indicating whether to keep empty groups. If FALSE, empty groups will be removed.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>seed</code>	The random seed to use. Default is 8525.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.

guides	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
design	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
...	Additional arguments.

Value

A ggplot object or `wrap_plots` object or a list of ggplot objects

Examples

```
data <- data.frame(
  x = c("A", "B", "C", "D", "E", "F", "G", "H"),
  y = c(10, 8, 16, 4, 6, 12, 14, 2),
  group = c("G1", "G1", "G2", "G2", "G3", "G3", "G4", "G4"),
  facet = c("F1", "F2", "F3", "F4", "F1", "F2", "F3", "F4")
)

PieChart(data, x = "x", y = "y")
PieChart(data, x = "x", y = "y", clockwise = FALSE)
PieChart(data, x = "x", y = "y", label = "group")
PieChart(data, x = "x", y = "y", facet_by = "facet")
PieChart(data, x = "x", y = "y", split_by = "group")
PieChart(data, x = "x", y = "y", split_by = "group",
  palette = list(G1 = "Reds", G2 = "Blues", G3 = "Greens", G4 = "Purp"))

# y from count
PieChart(data, x = "group")
# add label
PieChart(data, x = "group", label = ".y")
```

PrepareEnrichResult *Enrichment Map/Network*

Description

`PrepareEnrichResult` is a function to process the enrichment results from `Enrichr`. `EnrichMap` is a function to plot the enrichment map. `EnrichNetwork` is a function to plot the enrichment network.

Usage

```
PrepareEnrichResult(data, n_input = NULL)
```

```
EnrichMap(  
  data,  
  split_by = NULL,  
  split_by_sep = "_",  
  top_term = 10,  
  metric = "p.adjust",  
  layout = "fr",  
  minchar = 2,  
  cluster = "fast_greedy",  
  show_keyword = FALSE,  
  nlabel = 4,  
  character_width = 50,  
  mark = "ellipse",  
  label = c("term", "feature"),  
  labelsize = 5,  
  expand = c(0.4, 0.4),  
  theme = "theme_this",  
  theme_args = list(),  
  palette = "Paired",  
  palcolor = NULL,  
  alpha = 1,  
  aspect.ratio = 1,  
  legend.position = "right",  
  legend.direction = "vertical",  
  title = NULL,  
  subtitle = NULL,  
  xlab = NULL,  
  ylab = NULL,  
  seed = 8525,  
  combine = TRUE,  
  nrow = NULL,  
  ncol = NULL,  
  byrow = TRUE,  
  axes = NULL,  
  axis_titles = axes,  
  guides = NULL,  
  design = NULL,  
  ...  
)
```

```
EnrichNetwork(  
  data,  
  split_by = NULL,  
  split_by_sep = "_",  
  top_term = 10,
```

```
metric = "p.adjust",
character_width = 50,
layout = "fr",
layoutadjust = TRUE,
adjscale = 60,
adjiter = 100,
blendmode = "blend",
labelsize = 5,
theme = "theme_this",
theme_args = list(),
palette = "Paired",
palcolor = NULL,
alpha = 1,
aspect.ratio = 1,
legend.position = "right",
legend.direction = "vertical",
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
seed = 8525,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)
```

Arguments

data A data frame containing the data to be plotted. It should be in the format of clusterProfiler enrichment result, which includes the columns: ID, Description, GeneRatio, BgRatio, pvalue, p.adjust, qvalue, geneID and Count.

- The ID, qvalue and Count columns are optional.
- The Description is the description of the term.
- The GeneRatio is the number of genes in the term divided by the total number of genes in the input list.
- The BgRatio is the number of genes in the term divided by the total number of genes in the background list (all terms).
- The Count column, if given, should be the same as the first number in GeneRatio.

If you have enrichment results from multiple databases, you can combine them into one data frame and add a column (e.g. Database) to indicate the database.

You can plot them in a single plot using the `split_by` argument (e.g. `split_by = "Database"`).

<code>n_input</code>	An integer specifying the number of input genes. Enrichr result doesn't ship with the number of input genes. You can either provide the number directly or we will infer it. See details.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>top_term</code>	An integer specifying the number of top terms to show.
<code>metric</code>	A character string specifying the metric to use for the size of the nodes. It is also used to order the terms when selected the top terms. Either "pvalue" or "p.adjust". The default is "p.adjust".
<code>layout</code>	A character string specifying the layout of the graph. Either "circle", "tree", "grid" or other layout functions in <code>igraph</code> .
<code>minchar</code>	An integer specifying the minimum number of characters to show in the keyword.
<code>cluster</code>	A character string specifying the clustering method. Either "fast_greedy", "walktrap", "edge_betweenness", "infomap" or other clustering functions in <code>igraph</code> .
<code>show_keyword</code>	A logical value specifying whether to show the keyword instead of Description/Term in the plot.
<code>nlabel</code>	An integer specifying the number of labels to show in each cluster.
<code>character_width</code>	The width of the characters used to wrap the keyword.
<code>mark</code>	A character string specifying the mark to use for the nodes. Either "ellipse", "rect", "circle", "text" or other mark functions in <code>ggforce</code> .
<code>label</code>	A character string specifying the label to show in the legend. Either "term" or "feature". The default is "term".
<code>labelsize</code>	A numeric value specifying the size of the label.
<code>expand</code>	The values to expand the x and y axes. It is like CSS padding. When a single value is provided, it is used for both axes on both sides. When two values are provided, the first value is used for the top/bottom side and the second value is used for the left/right side. When three values are provided, the first value is used for the top side, the second value is used for the left/right side, and the third value is used for the bottom side. When four values are provided, the values are used for the top, right, bottom, and left sides, respectively. You can also use a named vector to specify the values for each side. When the axis is discrete, the values will be applied as 'add' to the 'expansion' function. When the axis is continuous, the values will be applied as 'mult' to the 'expansion' function. See also https://ggplot2.tidyverse.org/reference/expansion.html
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.

palcolor	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (palcolor will be NULL for those values).
alpha	A numeric value specifying the transparency of the plot.
aspect.ratio	A numeric value specifying the aspect ratio of the plot.
legend.position	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
legend.direction	A character string specifying the direction of the legend.
title	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
subtitle	A character string specifying the subtitle of the plot.
xlab	A character string specifying the x-axis label.
ylab	A character string specifying the y-axis label.
seed	The random seed to use. Default is 8525.
combine	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
nrow	A numeric value specifying the number of rows in the facet.
ncol	A numeric value specifying the number of columns in the facet.
byrow	A logical value indicating whether to fill the plots by row.
axes	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none">• 'keep' will retain all axes in individual plots.• 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout.• 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
axis_titles	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none">• 'keep' will retain all axis titles in individual plots.• 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction.• 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
guides	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none">• 'collect' will collect guides below to the given nesting level, removing duplicates.• 'keep' will stop collection at this level and let guides be placed alongside their plot.

- 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.

design	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
...	Additional arguments.
layoutadjust	A logical value specifying whether to adjust the layout of the network.
adjscale	A numeric value specifying the scale of the adjustment.
adjiter	A numeric value specifying the number of iterations for the adjustment.
blendmode	A character string specifying the blend mode of the colors. Either "blend", "average", "multiply" and "screen".

Details

In order to use the `EnrichMap` and `EnrichNetwork` functions and other visualization functions in `plotthis`, the enrichment results from `Enrichr` need to be processed by the `PrepareEnrichrResult` function. The following columns are renamed:

- Term -> Description
- Genes -> geneID (separated replaced by /)
- P.value -> pvalue
- Adjusted.P.value -> p.adjust Additionally, `GeneRatio` and `BgRatio` columns are inferred. From [enrichr's documentation](#), the `oddsRatio` is defined as: $oddsRatio = (A * (D - B - C + A) / \max((B - A) * (C - A), 1))$ where A is the overlapping genes; B is the total genes in the gene set; C (`n_input`) is the genes in input list; D is the total genes in the background. D is not provided by `Enrichr`. To infer it, $D = oddsRatio * \max((B - A) * (C - A), 1) / A + B + C - A$.
- `Overlap` = A / B (from `Enrichr`)
- `GeneRatio` = A / C (from `ClusterProfiler`)
- `BgRatio` = B / D (from `ClusterProfiler`) `C` (`n_input`), if not provided, will be inferred when D for all terms are equal. When starting inference, the minimum value to try will be unique genes in `data$Genes/data$geneID`.

Value

A data frame that can be used in `EnrichMap`.

A `ggplot` object or `wrap_plots` object or a list of `ggplot` objects

Examples

```
data(enrich_example)
EnrichMap(enrich_example)
EnrichMap(enrich_example, label = "feature")
EnrichMap(enrich_example, show_keyword = TRUE, label = "term")
EnrichMap(enrich_example, show_keyword = TRUE, label = "feature")
```



```
data(enrich_multidb_example)
EnrichMap(enrich_multidb_example, split_by = "Database")
EnrichMap(enrich_multidb_example, split_by = "Database",
          palette = list(DB1 = "Paired", DB2 = "Set1"))
EnrichNetwork(enrich_example, top_term = 5)
```

PrepareFGSEAResult *GSEA plots*

Description

- GSEASummaryPlot is used to plot a summary of the results of a GSEA analysis.
- GSEAPlot is used to plot the results of a GSEA analysis.
- PrepareFGSEA is used to prepare the result of GSEA from the fgsea package for plotting.

Usage

```
PrepareFGSEAResult(data, gene_ranks, gene_sets)
```

```
GSEASummaryPlot(
  data,
  gene_ranks = "@gene_ranks",
  gene_sets = "@gene_sets",
  top_term = 10,
  metric = "p.adjust",
  cutoff = 0.05,
  character_width = 50,
  line_plot_size = 0.25,
  metric_name = paste0("-log10(", metric, ")"),
  nonsig_name = "Non-significant",
  linewidth = 0.2,
  line_by = c("prerank", "running_score"),
  title = NULL,
  subtitle = NULL,
  xlab = NULL,
  ylab = NULL,
  alpha = 0.6,
  aspect.ratio = 1,
  legend.position = "right",
  legend.direction = "vertical",
  theme = "theme_this",
  theme_args = list(),
  palette = "Spectral",
  palcolor = NULL,
  seed = 8525,
  ...
)
```

```

GSEAPlot(
  data,
  gene_ranks = "@gene_ranks",
  gene_sets = "@gene_sets",
  sample_coregenes = FALSE,
  line_width = 1.5,
  line_alpha = 1,
  line_color = "#6BB82D",
  n_coregenes = 10,
  genes_label = NULL,
  label_fg = "black",
  label_bg = "white",
  label_bg_r = 0.1,
  label_size = 4,
  title = NULL,
  subtitle = NULL,
  xlab = NULL,
  ylab = NULL,
  combine = TRUE,
  nrow = NULL,
  ncol = NULL,
  byrow = TRUE,
  seed = 8525,
  axes = NULL,
  axis_titles = axes,
  guides = NULL,
  design = NULL,
  ...
)

```

Arguments

<code>data</code>	A data frame of GSEA results For example, from <code>DOSE::gseDO()</code> . Required columns are ID, Description, NES, <code>p.adjust</code> , <code>pvalue</code> . The ID column is used to match the gene sets.
<code>gene_ranks</code>	A numeric vector of gene ranks with genes as names The gene ranks are used to plot the gene sets. If <code>gene_ranks</code> is a character vector starting with @, the gene ranks will be taken from the attribute of <code>data</code> .
<code>gene_sets</code>	A list of gene sets, typically from a record of a GMT file The names of the list should match the ID column of <code>data</code> . If <code>gene_sets</code> is a character vector starting with @, the gene sets will be taken from the attribute of <code>data</code> . The GSEA plots will be plotted for each gene set. So, the number of plots will be the number of gene sets. If you only want to plot a subset of gene sets, you can subset the <code>gene_sets</code> before passing it to this function.
<code>top_term</code>	An integer to select the top terms
<code>metric</code>	The metric to use for the significance of the terms

cutoff	The cutoff for the significance of the terms. The terms will not be filtered with this cutoff; they are only filtered by the top_term ranked by the metric. The cutoff here is used to show the significance of the terms on the plot. For the terms that are not significant, the color will be grey.
character_width	The width of the characters in the y-axis
line_plot_size	The size of the line plots
metric_name	The name of the metric to show in the color bar
nonsig_name	The name of the legend for the nonsignificant terms
linewidth	The width of the lines in the line plots
line_by	The method to calculate the line plots. <ul style="list-style-type: none"> • prerank: Use the gene ranks as heights to plot the line plots. • running_score: Use the running score to plot the line plots.
title	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when split_by is used and the title needs to be dynamic.
subtitle	A character string specifying the subtitle of the plot.
xlab	A character string specifying the x-axis label.
ylab	A character string specifying the y-axis label.
alpha	A numeric value specifying the transparency of the plot.
aspect.ratio	A numeric value specifying the aspect ratio of the plot.
legend.position	A character string specifying the position of the legend. if waiver(), for single groups, the legend will be "none", otherwise "right".
legend.direction	A character string specifying the direction of the legend.
theme	A character string or a theme class (i.e. ggplot2::theme_classic) specifying the theme to use. Default is "theme_this".
theme.args	A list of arguments to pass to the theme function.
palette	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different split_by values.
palcolor	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different split_by values. If some values are missing, the values from the palette will be used (palcolor will be NULL for those values).
seed	The random seed to use. Default is 8525.
...	Additional arguments.
sample_coregenes	A logical value to sample the core genes from the core_enrichment; if FALSE, the first n_coregenes will be used
line_width	The width of the line in the running score plot

<code>line_alpha</code>	The alpha of the line in the running score plot
<code>line_color</code>	The color of the line in the running score plot
<code>n_coregenes</code>	The number of core genes to label
<code>genes_label</code>	The genes to label. If set, <code>n_coregenes</code> will be ignored
<code>label_fg</code>	The color of the label text
<code>label_bg</code>	The background color of the label
<code>label_bg_r</code>	The radius of the background color of the label
<code>label_size</code>	The size of the label text
<code>combine</code>	Whether to combine the plots into one when facet is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.

Value

A data frame with the desired columns for plotting and the gene ranks and gene sets as attributes

Examples

```
data(gsea_example)
GSEASummaryPlot(gsea_example)
GSEASummaryPlot(gsea_example, line_by = "running_score")
GSEASummaryPlot(gsea_example, cutoff = 0.01)

GSEAPlot(gsea_example, gene_sets = attr(gsea_example, "gene_sets")[1])
GSEAPlot(gsea_example, gene_sets = attr(gsea_example, "gene_sets")[1:4])
```

PrepareUpsetData	<i>Upset Plot</i>
------------------	-------------------

Description

PrepareUpsetData is used to process the input data for Upset plot. UpsetPlot is used to plot the processed data.

Usage

```
PrepareUpsetData(
  data,
  in_form = NULL,
  group_by = NULL,
  group_by_sep = "_",
  id_by = NULL,
  specific = TRUE
)

UpsetPlot(
  data,
  in_form = NULL,
  split_by = NULL,
  split_by_sep = "_",
  group_by = NULL,
  group_by_sep = "_",
  id_by = NULL,
  label = TRUE,
  label_fg = "black",
  label_size = NULL,
  label_bg = "white",
  label_bg_r = 0.1,
  palette = "material-indigo",
  palcolor = NULL,
  alpha = 1,
  specific = TRUE,
```

```

theme = "theme_this",
theme_args = list(),
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
aspect.ratio = 0.6,
legend.position = "right",
legend.direction = "vertical",
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
seed = 8525,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

data A data frame or a list or an UpsetPlotData object.

in_form A character string indicating the datatype of the input data. Possible values are "long", "wide", "list", "upset" or NULL. "long" indicates the data is in long format. "wide" indicates the data is in wide format. "list" indicates the data is a list. "upset" indicates the data is a UpsetPlotData object. NULL indicates the function will detect the datatype of the input data.

A long format data would look like:

```

group_by id_by
A      a1
A      a2
B      a1
B      a3
...

```

A wide format data would look like:

```

A      B
TRUE TRUE
TRUE FALSE
FALSE TRUE
...

```

A list format data would look like:

```
list(A = c("a1", "a2"), B = c("a1", "a3"))
```

An UpsetPlotData object is generated by PrepareUpsetData() would look like:

	<pre> group_by ----- list("A") # a2 list("B") # a3 list(c("A", "B")) # a1 ... </pre>
group_by	A character string specifying the column name of the data frame to group the data.
group_by_sep	A character string to concatenate the columns in group_by, if multiple columns are provided and the in_form is "long".
id_by	A character string specifying the column name of the data frame to identify the instances. Required when group_by is a single column and data is a data frame.
specific	A logical value to show the specific intersections only. ggVennDiagram, by default, only return the specific subsets of a region. However, sometimes, we want to show all the overlapping items for two or more sets. See https://github.com/gaospecial/ggVennDiagram/issues/64 for more details.
split_by	The column(s) to split data by and plot separately.
split_by_sep	The separator for multiple split_by columns. See split_by
label	A logical value to show the labels on the bars.
label_fg	A character string specifying the color of the label text.
label_size	A numeric value specifying the size of the label text.
label_bg	A character string specifying the background color of the label.
label_bg_r	A numeric value specifying the radius of the background of the label.
palette	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different split_by values.
palcolor	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different split_by values. If some values are missing, the values from the palette will be used (palcolor will be NULL for those values).
alpha	A numeric value specifying the transparency of the plot.
theme	A character string or a theme class (i.e. ggplot2::theme_classic) specifying the theme to use. Default is "theme_this".
theme_args	A list of arguments to pass to the theme function.
title	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when split_by is used and the title needs to be dynamic.
subtitle	A character string specifying the subtitle of the plot.
xlab	A character string specifying the x-axis label.
ylab	A character string specifying the y-axis label.
aspect.ratio	A numeric value specifying the aspect ratio of the plot.
legend.position	A character string specifying the position of the legend. if waiver(), for single groups, the legend will be "none", otherwise "right".

<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is <code>FALSE</code> . Default is <code>TRUE</code> .
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>seed</code>	The random seed to use. Default is 8525.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
<code>...</code>	Additional arguments.

Value

A `UpsetPlotData` object

A `ggplot` object or `wrap_plots` object or a list of `ggplot` objects

Examples

```
data <- list(
  A = 1:5,
  B = 2:6,
  C = 3:7,
  D = 4:8
)
UpsetPlot(data)
UpsetPlot(data, label = FALSE)
UpsetPlot(data, palette = "Reds", specific = FALSE)
```

PrepareVennData

VennDiagram

Description

PrepareVennData is helper function to process the input data for Venn diagram.

Usage

```
PrepareVennData(
  data,
  in_form = NULL,
  group_by = NULL,
  group_by_sep = "_",
  id_by = NULL
)

VennDiagram(
  data,
  in_form = NULL,
  split_by = NULL,
  split_by_sep = "_",
  group_by = NULL,
  group_by_sep = "_",
  id_by = NULL,
  label = "count",
  label_fg = "black",
  label_size = NULL,
  label_bg = "white",
  label_bg_r = 0.1,
  fill_mode = "count",
  fill_name = NULL,
  palette = ifelse(fill_mode == "set", "Paired", "Spectral"),
  palcolor = NULL,
  alpha = 1,
  theme = "theme_this",
```

```

theme_args = list(),
title = NULL,
subtitle = NULL,
legend.position = "right",
legend.direction = "vertical",
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
seed = 8525,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

- | | |
|--------------|--|
| data | A data frame or a list or a VennPlotData object. |
| in_form | <p>A character string indicating the datatype of the input data. Possible values are "long", "wide", "list", "venn" or NULL. "long" indicates the data is in long format. "wide" indicates the data is in wide format. "list" indicates the data is a list. "venn" indicates the data is a VennPlotData object. NULL indicates the function will detect the datatype of the input data.</p> <p>A long format data would look like:</p> <pre> group_by id_by A a1 A a2 B a1 B a3 ... </pre> <p>A wide format data would look like:</p> <pre> A B TRUE TRUE TRUE FALSE FALSE TRUE ... </pre> <p>A list format data would look like:</p> <pre> list(A = c("a1", "a2"), B = c("a1", "a3")) </pre> |
| group_by | A character string specifying the column name of the data frame to group the data. |
| group_by_sep | A character string to concatenate the columns in group_by, if multiple columns are provided and the in_form is "long". |

<code>id_by</code>	A character string specifying the column name of the data frame to identify the instances. Required when <code>group_by</code> is a single column and data is a data frame.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>label</code>	A character string specifying the label to show on the Venn diagram. Possible values are "count", "percent", "both", "none" and a function. "count" indicates the count of the intersection. "percent" indicates the percentage of the intersection. "both" indicates both the count and the percentage of the intersection. "none" indicates no label. If it is a function, it takes a data frame as input and returns a character vector as label. The data frame has columns "id", "X", "Y", "name", "item" and "count".
<code>label_fg</code>	A character string specifying the color of the label text.
<code>label_size</code>	A numeric value specifying the size of the label text.
<code>label_bg</code>	A character string specifying the background color of the label.
<code>label_bg_r</code>	A numeric value specifying the radius of the background of the label.
<code>fill_mode</code>	A character string specifying the fill mode of the Venn diagram. Possible values are "count", "set", "count_rev". "count" indicates the fill color is based on the count of the intersection. "set" indicates the fill color is based on the set of the intersection. "count_rev" indicates the fill color is based on the count of the intersection in reverse order. The palette will be continuous for "count" and "count_rev". The palette will be discrete for "set".
<code>fill_name</code>	A character string to name the legend of colorbar.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (palcolor will be NULL for those values).
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. If <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.

<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>seed</code>	The random seed to use. Default is 8525.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
<code>...</code>	Additional arguments.

Value

A `VennPlotData` object

A combined `ggplot` object or `wrap_plots` object or a list of `ggplot` objects

Examples

```
set.seed(8525)
data = list(
  A = sort(sample(letters, 8)),
  B = sort(sample(letters, 8)),
  C = sort(sample(letters, 8)),
  D = sort(sample(letters, 8))
)
```

```
VennDiagram(data)
VennDiagram(data, fill_mode = "set")
VennDiagram(data, label = "both")
# label with a function
VennDiagram(data, label = function(df) df$name)
VennDiagram(data, palette = "material-indigo", alpha = 0.6)
```

QQPlot

QQ plot

Description

QQ plot is a graphical tool to compare two distributions by plotting their quantiles against each other.

Usage

```
QQPlot(
  data,
  val,
  val_trans = NULL,
  type = c("qq", "pp"),
  split_by = NULL,
  split_by_sep = "_",
  band = NULL,
  line = list(),
  point = list(),
  fill_name = "Bands",
  band_alpha = 0.5,
  theme = "theme_this",
  theme_args = list(),
  palette = "Spectral",
  palcolor = NULL,
  facet_by = NULL,
  facet_scales = "fixed",
  facet_ncol = NULL,
  facet_nrow = NULL,
  facet_byrow = TRUE,
  aspect.ratio = 1,
  legend.position = waiver(),
  legend.direction = "vertical",
  title = NULL,
  subtitle = NULL,
  xlim = NULL,
  ylim = NULL,
  xlab = ifelse(type == "qq", "Theoretical Quantiles", "Probability Points"),
```

```

ylab = ifelse(type == "qq", "Sample Quantiles", "Cumulative Probability"),
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
seed = 8525,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

<code>data</code>	A data frame.
<code>val</code>	A character string of the column name for the values to plot. A numeric column is expected.
<code>val_trans</code>	A function to transform the values before plotting. Default is <code>NULL</code> , which means no transformation.
<code>type</code>	A character string to specify the type of plot. Default is "qq", which means QQ plot. Other options are "pp", which means PP plot.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>band</code>	A list of arguments to pass to <code>qqplotr::stat_qq_band()</code> or <code>qqplotr::stat_pp_band()</code> , depending on the value of <code>type</code> . Default is <code>NULL</code> , which means no band. If an empty list or <code>TRUE</code> is provided, the default arguments will be used. Multiple bands can be added by providing a list of lists.
<code>line</code>	A list of arguments to pass to <code>qqplotr::stat_qq_line()</code> or <code>qqplotr::stat_pp_line()</code> , depending on the value of <code>type</code> . Default is <code>list()</code> , which means to add a line with default arguments. If <code>NULL</code> is provided, no line will be added.
<code>point</code>	A list of arguments to pass to <code>qqplotr::stat_qq_point()</code> or <code>qqplotr::stat_pp_point()</code> , depending on the value of <code>type</code> . Default is <code>list()</code> , which means to add points with default arguments. If <code>NULL</code> is provided, no points will be added (not recommended).
<code>fill_name</code>	A character string to name the legend of fill. Default is "Band Type".
<code>band_alpha</code>	A numeric value to set the alpha of all bands. Default is 0.5. It is a shortcut for setting alpha of all bands. You can override it by setting <code>alpha</code> in <code>band</code> argument. For example, <code>band = list(list(alpha = 0.3), list(alpha = 0.7))</code> .
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.

<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be <code>NULL</code> for those values).
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is <code>TRUE</code> .
<code>aspect.ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlim</code>	A numeric vector of length 2 to set the x-axis limits.
<code>ylim</code>	A numeric vector of length 2 to set the y-axis limits.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is <code>FALSE</code> . Default is <code>TRUE</code> .
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>seed</code>	The random seed to use. Default is 8525.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are:

	<ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
guides	<p>A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code>. Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are:</p> <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
design	<p>Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code>. Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code>, <code>ncol</code>, and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.</p>
...	Additional arguments.

Value

A ggplot object or `wrap_plots` object or a list of ggplot objects

Examples

```
set.seed(8525)
data <- data.frame(norm = rnorm(100))

QQPlot(data, val = "norm", band = TRUE)
QQPlot(data, val = "norm", band = list(
  list(bandType = "ks", mapping = ggplot2::aes(fill = "KS"), alpha = 0.3),
  list(bandType = "ts", mapping = ggplot2::aes(fill = "TS")),
  list(bandType = "pointwise", mapping = ggplot2::aes(fill = "Normal")),
  list(bandType = "boot", mapping = ggplot2::aes(fill = "Bootstrap"))
), band_alpha = 0.6)

data(airquality, package = "datasets")
di <- "exp" # exponential distribution
dp <- list(rate = 2) # exponential rate parameter
QQPlot(airquality, val = "Ozone",
  band = list(distribution = di, dparams = dp),
  line = list(distribution = di, dparams = dp),
  point = list(distribution = di, dparams = dp)
)

de <- TRUE # enabling the detrend option
QQPlot(airquality, val = "Ozone",
  band = list(distribution = di, dparams = dp, detrend = de),
  line = list(distribution = di, dparams = dp, detrend = de),
```



```

    point = list(distribution = di, dparams = dp, detrend = de)
  )

  QQPlot(data, val = "norm", type = "pp", band = TRUE)

  dp <- list(mean = 2, sd = 2) # shifted and rescaled Normal parameters
  QQPlot(data, val = "norm", type = "pp",
    band = list(dparams = dp),
    point = list(dparams = dp))

  QQPlot(data, val = "norm", type = "pp", band = TRUE,
    line = list(ab = c(.2, .5)))

  di <- "exp"
  dp <- list(rate = .022) # value is based on some empirical tests
  de <- TRUE
  QQPlot(airquality, val = "Ozone", type = "pp",
    band = list(distribution = di, detrend = de, dparams = dp),
    line = list(detrend = de),
    point = list(distribution = di, detrend = de, dparams = dp),
    ylim = c(-.5, .5)
  )

```

RadarPlot

Radar plot / Spider plot

Description

Create a radar plot or spider plot for a series of data. Radar plot uses circles as the plot grid and Spider plot uses polygons.

Usage

```

RadarPlot(
  data,
  x,
  x_sep = "_",
  group_by = NULL,
  group_by_sep = "_",
  y = NULL,
  group_name = NULL,
  scale_y = c("group", "global", "x", "none"),
  y_min = 0,
  y_max = NULL,
  y_nbreaks = 4,
  fill = TRUE,
  linewidth = 1,
  pt_size = 4,
  max_charwidth = 16,

```

```
split_by = NULL,
split_by_sep = "_",
theme = "theme_this",
theme_args = list(),
palette = "Paired",
palcolor = NULL,
facet_by = NULL,
facet_scales = "fixed",
facet_ncol = NULL,
facet_nrow = NULL,
facet_byrow = TRUE,
alpha = 0.2,
aspect.ratio = 1,
legend.position = waiver(),
legend.direction = "vertical",
title = NULL,
subtitle = NULL,
seed = 8525,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

SpiderPlot(
  data,
  x,
  x_sep = "_",
  group_by = NULL,
  group_by_sep = "_",
  y = NULL,
  group_name = NULL,
  scale_y = c("group", "global", "x", "none"),
  y_min = 0,
  y_max = NULL,
  y_nbreaks = 4,
  fill = TRUE,
  linewidth = 1,
  pt_size = 4,
  max_charwidth = 16,
  split_by = NULL,
  split_by_sep = "_",
  theme = "theme_this",
```

```

theme_args = list(),
palette = "Paired",
palcolor = NULL,
facet_by = NULL,
facet_scales = "fixed",
facet_ncol = NULL,
facet_nrow = NULL,
facet_byrow = TRUE,
alpha = 0.2,
aspect.ratio = 1,
legend.position = waiver(),
legend.direction = "vertical",
title = NULL,
subtitle = NULL,
seed = 8525,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

<code>data</code>	A data frame.
<code>x</code>	A character string specifying the column name of the data frame to plot for the x-axis.
<code>x_sep</code>	A character string to concatenate the columns in <code>x</code> , if multiple columns are provided.
<code>group_by</code>	Columns to group the data for plotting For those plotting functions that do not support multiple groups, They will be concatenated into one column, using <code>group_by_sep</code> as the separator
<code>group_by_sep</code>	The separator for multiple <code>group_by</code> columns. See <code>group_by</code>
<code>y</code>	A character string specifying the column name of the data frame to plot for the y-axis.
<code>group_name</code>	A character string to name the legend of group.
<code>scale_y</code>	How should the y-axis be scaled? Default is "group". Other options are "global", "x" and "none". <ul style="list-style-type: none"> • If "group", the y-axis will be scaled to the fraction within each group. • If "global", the y-axis will be scaled to the fraction of the total. • If "x", the y-axis will be scaled to the fraction of the total within each x-axis group.

	<ul style="list-style-type: none"> • If "none", the y-axis will be scaled to the count of each x-axis group.
y_min	A numeric value to set the minimum value of the y-axis.
y_max	A numeric value to set the maximum value of the y-axis.
y_nbreaks	A numeric value to set the number of breaks in the y-axis.
fill	A logical value to fill the polygons with colors.
linewidth	A numeric value to set the width of the lines.
pt_size	A numeric value to set the size of the points.
max_charwidth	A numeric value to set the maximum character width for the x labels.
split_by	The column(s) to split data by and plot separately.
split_by_sep	The separator for multiple split_by columns. See split_by
theme	A character string or a theme class (i.e. ggplot2::theme_classic) specifying the theme to use. Default is "theme_this".
theme_args	A list of arguments to pass to the theme function.
palette	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different split_by values.
palcolor	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different split_by values. If some values are missing, the values from the palette will be used (palcolor will be NULL for those values).
facet_by	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by split_by and generate multiple plots and combine them into one using patchwork::wrap_plots
facet_scales	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See ggplot2::facet_wrap
facet_ncol	A numeric value specifying the number of columns in the facet. When facet_by is a single column and facet_wrap is used.
facet_nrow	A numeric value specifying the number of rows in the facet. When facet_by is a single column and facet_wrap is used.
facet_byrow	A logical value indicating whether to fill the plots by row. Default is TRUE.
alpha	A numeric value specifying the transparency of the plot.
aspect_ratio	A numeric value specifying the aspect ratio of the plot.
legend.position	A character string specifying the position of the legend. if waiver(), for single groups, the legend will be "none", otherwise "right".
legend.direction	A character string specifying the direction of the legend.
title	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when split_by is used and the title needs to be dynamic.
subtitle	A character string specifying the subtitle of the plot.
seed	The random seed to use. Default is 8525.

combine	Whether to combine the plots into one when facet is FALSE. Default is TRUE.
nrow	A numeric value specifying the number of rows in the facet.
ncol	A numeric value specifying the number of columns in the facet.
byrow	A logical value indicating whether to fill the plots by row.
axes	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
axis_titles	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
guides	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
design	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
...	Additional arguments.

Value

A ggplot object or `wrap_plots` object or a list of ggplot objects

Examples

```
# use the count
data <- data.frame(
  x = c(rep("A", 2), rep("B", 3), rep("C", 3), rep("D", 4), rep("E", 5)),
  group = sample(paste0("G", 1:4), 17, replace = TRUE)
)
RadarPlot(data, x = "x")
RadarPlot(data, x = "x", scale_y = "none")
```

```

RadarPlot(data, x = "x", group_by = "group")
SpiderPlot(data, x = "x")
SpiderPlot(data, x = "x", group_by = "group")

# use the y value
data <- data.frame(
  x = rep(LETTERS[1:5], 2),
  y = c(1, 3, 6, 4, 2, 5, 7, 8, 9, 10),
  group = rep(c("G1", "G2"), each = 5)
)
RadarPlot(data, x = "x", y = "y", scale_y = "none", group_by = "group")
RadarPlot(data, x = "x", y = "y", facet_by = "group")
RadarPlot(data, x = "x", y = "y", split_by = "group")
RadarPlot(data, x = "x", y = "y", split_by = "group",
           palette = c(G1 = "Set1", G2 = "Paired"))

```

RarefactionPlot

RarefactionPlot

Description

This function generates a rarefaction plot for a given dataset.

Usage

```

RarefactionPlot(
  data,
  type = 1,
  se = NULL,
  group_by = "group",
  group_by_sep = "_",
  group_name = NULL,
  split_by = NULL,
  split_by_sep = "_",
  theme = "theme_this",
  theme_args = list(),
  palette = "Spectral",
  palcolor = NULL,
  alpha = 0.2,
  pt_size = 3,
  line_width = 1,
  facet_by = NULL,
  facet_scales = "fixed",
  facet_ncol = NULL,
  facet_nrow = NULL,
  facet_byrow = TRUE,
  aspect.ratio = 1,
  legend.position = "right",

```

```

    legend.direction = "vertical",
    title = NULL,
    subtitle = NULL,
    xlab = NULL,
    ylab = NULL,
    seed = 8525,
    combine = TRUE,
    nrow = NULL,
    ncol = NULL,
    byrow = TRUE,
    axes = NULL,
    axis_titles = axes,
    guides = NULL,
    design = NULL,
    ...
  )

```

Arguments

<code>data</code>	A data frame.
<code>type</code>	three types of plots: sample-size-based rarefaction/extrapolation curve (<code>type = 1</code>); sample completeness curve (<code>type = 2</code>); coverage-based rarefaction/extrapolation curve (<code>type = 3</code>).
<code>se</code>	a logical variable to display confidence interval around the estimated sampling curve. Default to <code>NULL</code> which means <code>TRUE</code> if the data has the lower and upper bounds.
<code>group_by</code>	Columns to group the data for plotting For those plotting functions that do not support multiple groups, They will be concatenated into one column, using <code>group_by_sep</code> as the separator
<code>group_by_sep</code>	A character string indicating how to separate the <code>group_by</code> column if both " <code>q</code> " and " <code>group</code> " are used. for ' <code>group_by</code> '. Default to " <code>_</code> ".
<code>group_name</code>	A character string indicating the name of the group, showing as the legend title.
<code>split_by</code>	A character string indicating how to split the data and plots Possible values are " <code>q</code> " and " <code>group</code> "
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is " <code>theme_this</code> ".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be <code>NULL</code> for those values).
<code>alpha</code>	A numeric value specifying the transparency of the plot.

<code>pt_size</code>	A numeric value specifying the size of the points.
<code>line_width</code>	A numeric value specifying the width of the lines.
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is TRUE.
<code>aspect_ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>seed</code>	The random seed to use. Default is 8525.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction.

	<ul style="list-style-type: none"> • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
guides	<p>A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code>. Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are:</p> <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
design	<p>Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code>. Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code>, <code>ncol</code>, and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.</p>
...	Additional arguments.

Value

A ggplot object or wrap_plots object or a list of ggplot objects

Examples

```
set.seed(8525)
spider <- list(
  Girdled = c(46, 22, 17, 15, 15, 9, 8, 6, 6, 4, rep(2, 4), rep(1, 12)),
  Logged = c(88, 22, 16, 15, 13, 10, 8, 8, 7, 7, 7, 5, 4, 4, 4, 3, 3, 3, 3,
    2, 2, 2, 2, rep(1, 14))
)

RarefactionPlot(spider)
RarefactionPlot(spider, q = c(0, 1, 2), facet_by = "q")
RarefactionPlot(spider, q = c(0, 1, 2), split_by = "q")
RarefactionPlot(spider, q = c(0, 1, 2), split_by = "q",
  palette = c("0" = "Paired", "1" = "Set1", "2" = "Dark2"))
RarefactionPlot(spider, q = c(0, 1, 2), group_by = "q",
  facet_by = "group", palette = "Set1", type = 3)
```

RidgePlot

Ridge Plot

Description

Ridge plot to illustrate the distribution of the data in different groups.

Usage

```
RidgePlot(  
  data,  
  x = NULL,  
  in_form = c("long", "wide"),  
  split_by = NULL,  
  split_by_sep = "_",  
  group_by = NULL,  
  group_by_sep = "_",  
  group_name = NULL,  
  scale = NULL,  
  flip = FALSE,  
  alpha = 1,  
  theme = "theme_this",  
  theme_args = list(),  
  palette = "Paired",  
  palcolor = NULL,  
  title = NULL,  
  subtitle = NULL,  
  xlab = NULL,  
  ylab = NULL,  
  x_text_angle = 90,  
  keep_empty = FALSE,  
  reverse = FALSE,  
  facet_by = NULL,  
  facet_scales = "fixed",  
  facet_ncol = NULL,  
  facet_nrow = NULL,  
  facet_byrow = TRUE,  
  aspect.ratio = 1,  
  legend.position = "none",  
  legend.direction = "vertical",  
  combine = TRUE,  
  nrow = NULL,  
  ncol = NULL,  
  byrow = TRUE,  
  seed = 8525,  
  axes = NULL,  
  axis_titles = axes,  
  guides = NULL,  
  design = NULL,  
  ...  
)
```

Arguments

<code>data</code>	A data frame.
<code>x</code>	A character string specifying the column name of the data frame to plot for the

	x-axis.
<code>in_form</code>	A character string specifying the form of the data. Default is "long".
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>group_by</code>	Columns to group the data for plotting For those plotting functions that do not support multiple groups, They will be concatenated into one column, using <code>group_by_sep</code> as the separator
<code>group_by_sep</code>	The separator for multiple <code>group_by</code> columns. See <code>group_by</code>
<code>group_name</code>	A character string to name the legend of 'group_by', if 'legend.position' is not "none".
<code>scale</code>	A numeric value to scale the ridges. See also geom_density_ridges .
<code>flip</code>	A logical value. If TRUE, the plot will be flipped.
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be NULL for those values).
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>x_text_angle</code>	A numeric value specifying the angle of the x-axis text.
<code>keep_empty</code>	A logical value indicating whether to keep empty groups. If FALSE, empty groups will be removed.
<code>reverse</code>	A logical value. If TRUE, reverse the order of the groups on the y-axis.
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.

<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is TRUE.
<code>aspect_ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend_position</code>	A character string specifying the position of the legend. If <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend_direction</code>	A character string specifying the direction of the legend.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>seed</code>	The random seed to use. Default is 8525.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
<code>...</code>	Additional arguments.

Value

A ggplot object or `wrap_plots` object or a list of ggplot objects. If no `split_by` is provided, a single plot (ggplot object) will be returned. If 'combine' is TRUE, a `wrap_plots` object will be returned. If 'combine' is FALSE, a list of ggplot objects will be returned.

Examples

```

set.seed(8525)
data <- data.frame(
  x = c(rnorm(250, -1), rnorm(250, 1)),
  group = rep(LETTERS[1:5], each = 100)
)
RidgePlot(data, x = "x", group_by = "group")
RidgePlot(data, x = "x", group_by = "group", reverse = TRUE)

# wide form
data_wide <- data.frame(
  A = rnorm(100),
  B = rnorm(100),
  C = rnorm(100),
  D = rnorm(100),
  E = rnorm(100),
  group = sample(letters[1:4], 100, replace = TRUE)
)
RidgePlot(data_wide, group_by = LETTERS[1:5], in_form = "wide")
RidgePlot(data_wide, group_by = LETTERS[1:5], in_form = "wide", facet_by = "group")
RidgePlot(data_wide, group_by = LETTERS[1:5], in_form = "wide", split_by = "group",
  palette = list(a = "Reds", b = "Blues", c = "Greens", d = "Purples"))

```

RingPlot

Ring Plot

Description

A ring plot is like pie chart but with multiple rings.

Usage

```

RingPlot(
  data,
  x = NULL,
  y = NULL,
  group_by = NULL,
  group_by_sep = "_",
  group_name = NULL,
  label = NULL,
  split_by = NULL,
  split_by_sep = "_",
  facet_by = NULL,
  facet_scales = "free_y",
  facet_ncol = NULL,
  facet_nrow = NULL,
  facet_byrow = TRUE,
  theme = "theme_this",

```

```

theme_args = list(),
palette = "Paired",
palcolor = NULL,
alpha = 1,
aspect.ratio = 1,
legend.position = "right",
legend.direction = "vertical",
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
keep_empty = FALSE,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
seed = 8525,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

<code>data</code>	A data frame.
<code>x</code>	A character vector specifying the column as the rings of the plot.
<code>y</code>	A character vector specifying the column as the y axis of the plot. Default is NULL, meaning the y axis is the count of the data.
<code>group_by</code>	A character vector specifying the column as the <code>group_by</code> of the plot. How the ring is divided.
<code>group_by_sep</code>	A character string to concatenate the columns in <code>group_by</code> , if multiple columns are provided.
<code>group_name</code>	A character string to specify the name of the <code>group_by</code> in the legend.
<code>label</code>	A logical value indicating whether to show the labels on the rings. The labels should be the values of <code>group_by</code> . Default is NULL, meaning no labels for one ring and showing the labels for multiple rings.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>

<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is TRUE.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be NULL for those values).
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>aspect.ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. If <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>keep_empty</code>	A logical value indicating whether to keep empty groups. If FALSE, empty groups will be removed.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>seed</code>	The random seed to use. Default is 8525.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none">• 'keep' will retain all axes in individual plots.• 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout.• 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.

<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
<code>...</code>	Additional arguments.

Value

A ggplot object or `wrap_plots` object or a list of ggplot objects

See Also

[PieChart](#)

Examples

```
RingPlot(datasets::iris, group_by = "Species")

data <- data.frame(
  x = c("A", "B", "C", "A", "B", "C"),
  y = c(1, 2, 3, 4, 5, 6),
  group = c("a", "a", "a", "b", "b", "b")
)
RingPlot(data, x = "x", y = "y", group_by = "group")
RingPlot(datasets::mtcars, x = "cyl", group_by = "carb", facet_by = "vs")
RingPlot(datasets::mtcars, x = "cyl", group_by = "carb", split_by = "vs",
  palette = c("0" = "Set1", "1" = "Paired"))
```

`ROCCurve`*ROC curve*

Description

A wrapped function around `plotROC` package to create ROC curves.

Usage

```
ROCCurve(  
  data,  
  truth_by,  
  score_by,  
  pos_label = NULL,  
  split_by = NULL,  
  split_by_sep = "_",  
  group_by = NULL,  
  group_by_sep = "_",  
  group_name = NULL,  
  x_axis_reverse = FALSE,  
  percent = FALSE,  
  ci = NULL,  
  n_cuts = 0,  
  cutoffs_at = NULL,  
  cutoffs_labels = NULL,  
  cutoffs_accuracy = 0.01,  
  cutoffs_pt_size = 5,  
  cutoffs_pt_shape = 4,  
  cutoffs_pt_stroke = 1,  
  cutoffs_labal_fg = "black",  
  cutoffs_label_size = 4,  
  cutoffs_label_bg = "white",  
  cutoffs_label_bg_r = 0.1,  
  show_auc = c("auto", "none", "legend", "plot"),  
  auc_accuracy = 0.01,  
  auc_size = 4,  
  theme = "theme_this",  
  theme_args = list(),  
  palette = "Spectral",  
  palcolor = NULL,  
  alpha = 1,  
  facet_by = NULL,  
  facet_scales = "fixed",  
  facet_ncol = NULL,  
  facet_nrow = NULL,  
  facet_byrow = TRUE,  
  aspect.ratio = 1,
```

```

legend.position = waiver(),
legend.direction = "vertical",
title = NULL,
subtitle = NULL,
xlab = ifelse(x_axis_reverse, "Specificity", "1 - Specificity"),
ylab = "Sensitivity",
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
seed = 8525,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

<code>data</code>	A data frame.
<code>truth_by</code>	A character string of the column name that contains the true class labels. (a.k.a. the binary outcome, 1/0 or TRUE/FALSE.)
<code>score_by</code>	character strings of the column names that contains the predicted scores. When multiple columns are provided, the ROC curve is plotted for each column.
<code>pos_label</code>	A character string of the positive class label. When NULL, the labels will be handled by the <code>plotROC</code> package.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>group_by</code>	Columns to group the data for plotting For those plotting functions that do not support multiple groups, They will be concatenated into one column, using <code>group_by_sep</code> as the separator
<code>group_by_sep</code>	The separator for multiple <code>group_by</code> columns. See <code>group_by</code>
<code>group_name</code>	A character string to name the legend of the ROC curve groups.
<code>x_axis_reverse</code>	A logical to reverse the x-axis, that is from 1 to 0.
<code>percent</code>	A logical to display the x and y axis as percentages.
<code>ci</code>	A list of arguments to pass to <code>plotROC::geom_rocci()</code> to add confidence intervals. When NULL, no confidence intervals are added.
<code>n_cuts</code>	An integer to specify the number of cutpoints on the ROC curve. It will be the quantiles of the predicted scores.
<code>cutoffs_at</code>	Vector of user supplied cutoffs to plot as points. If non-NULL, it will override the values of <code>n_cuts</code> and plot the observed cutoffs closest to the user-supplied ones. Both <code>cutoffs_at</code> and <code>cutoffs.labels</code> will be passed to <code>plotROC::geom_roc()</code> . Other than numeric values, the following special values are allowed. These values are the methods of <code>OptimalCutpoints::optimal.cutpoints()</code> , they are literally:

- "CB" (cost-benefit method);
- "MCT" (minimizes Misclassification Cost Term);
- "MinValueSp" (a minimum value set for Specificity);
- "MinValueSe" (a minimum value set for Sensitivity);
- "ValueSe" (a value set for Sensitivity);
- "MinValueSpSe" (a minimum value set for Specificity and Sensitivity);
- "MaxSp" (maximizes Specificity);
- "MaxSe" (maximizes Sensitivity);
- "MaxSpSe" (maximizes Sensitivity and Specificity simultaneously);
- "MaxProdSpSe" (maximizes the product of Sensitivity and Specificity or Accuracy Area);
- "ROC01" (minimizes distance between ROC plot and point (0,1));
- "SpEqualSe" (Sensitivity = Specificity);
- "Youden" (Youden Index);
- "MaxEfficiency" (maximizes Efficiency or Accuracy, similar to minimize Error Rate);
- "Minimax" (minimizes the most frequent error);
- "MaxDOR" (maximizes Diagnostic Odds Ratio);
- "MaxKappa" (maximizes Kappa Index);
- "MinValueNPV" (a minimum value set for Negative Predictive Value);
- "MinValuePPV" (a minimum value set for Positive Predictive Value);
- "ValueNPV" (a value set for Negative Predictive Value);
- "ValuePPV" (a value set for Positive Predictive Value);
- "MinValueNPVPPV" (a minimum value set for Predictive Values);
- "PROC01" (minimizes distance between PROC plot and point (0,1));
- "NPVEqualPPV" (Negative Predictive Value = Positive Predictive Value);
- "MaxNPVPPV" (maximizes Positive Predictive Value and Negative Predictive Value simultaneously);
- "MaxSumNPVPPV" (maximizes the sum of the Predictive Values);
- "MaxProdNPVPPV" (maximizes the product of Predictive Values);
- "ValueDLR.Negative" (a value set for Negative Diagnostic Likelihood Ratio);
- "ValueDLR.Positive" (a value set for Positive Diagnostic Likelihood Ratio);
- "MinPvalue" (minimizes p-value associated with the statistical Chi-squared test which measures the association between the marker and the binary result obtained on using the cutpoint);
- "ObservedPrev" (The closest value to observed prevalence);
- "MeanPrev" (The closest value to the mean of the diagnostic test values);
- "PrevalenceMatching" (The value for which predicted prevalence is practically equal to observed prevalence).

`cutoffs_labels` vector of user-supplied labels for the cutoffs. Must be a character vector of the same length as `cutoffs_at`.

`cutoffs_accuracy`

A numeric to specify the accuracy of the cutoff values to show.

<code>cutoffs_pt_size</code>	A numeric to specify the size of the cutoff points.
<code>cutoffs_pt_shape</code>	A numeric to specify the shape of the cutoff points.
<code>cutoffs_pt_stroke</code>	A numeric to specify the stroke of the cutoff points.
<code>cutoffs_labal_fg</code>	A character string to specify the color of the cutoff labels.
<code>cutoffs_label_size</code>	A numeric to specify the size of the cutoff labels.
<code>cutoffs_label_bg</code>	A character string to specify the background color of the cutoff labels.
<code>cutoffs_label_bg_r</code>	A numeric to specify the radius of the background of the cutoff labels.
<code>show_auc</code>	A character string to specify the position of the AUC values. <ul style="list-style-type: none"> • "auto" (default): Automatically determine the position based on the plot. When there is a single group or 'facet_by' is provided, the AUC is placed on the plot. Otherwise, the AUC is placed in the legend. • "none": Do not display the AUC values. • "legend": Display the AUC values in the legend. • "plot": Display the AUC values on the plot (left/right bottom corner).
<code>auc_accuracy</code>	A numeric to specify the accuracy of the AUC values.
<code>auc_size</code>	A numeric to specify the size of the AUC values when they are displayed on the plot.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be NULL for those values).
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.

<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is TRUE.
<code>aspect.ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>seed</code>	The random seed to use. Default is 8525.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
<code>...</code>	Additional arguments.

Value

A `patch_work::wrap_plots` object or a list of them if `combine` is `FALSE`. You can retrieve the AUC values using `attr(p, "auc")` if `combine` is `TRUE`. If `combine` is `FALSE`, The AUC value of each plot can be retrieved using `attr(p[[i]], "auc")`.

Examples

```
set.seed(8525)

D.ex <- rbinom(200, size = 1, prob = .5)
M1 <- rnorm(200, mean = D.ex, sd = .65)
M2 <- rnorm(200, mean = D.ex, sd = 1.5)
gender <- c("Male", "Female")[rbinom(200, 1, .49) + 1]

data <- data.frame(D = D.ex, D.str = c("Healthy", "Ill")[D.ex + 1],
  gender = gender, M1 = M1, M2 = M2)

ROCCurve(data, truth_by = "D", score_by = "M1")
# will warn about the positive label
ROCCurve(data, truth_by = "D.str", score_by = "M1")
ROCCurve(data, truth_by = "D", score_by = "M1", increasing = FALSE)
# Multiple ROC curves
ROCCurve(data, truth_by = "D", score_by = c("M1", "M2"), group_name = "Method")
ROCCurve(data, truth_by = "D", score_by = "M1", group_by = "gender", show_auc = "plot")
# Reverse the x-axis and display the axes as percentages
ROCCurve(data, truth_by = "D", score_by = "M1", x_axis_reverse = TRUE, percent = TRUE)
# Pass additional arguments to geom_roc and make the curve black
ROCCurve(data, truth_by = "D", score_by = "M1", n_cuts = 10, palcolor = "black")
# Add confidence intervals
ROCCurve(data, truth_by = "D", score_by = "M1", ci = list(sig.level = .01))
# Facet by a column
ROCCurve(data, truth_by = "D", score_by = "M1", facet_by = "gender")
# Show cutoffs
ROCCurve(data, truth_by = "D", score_by = "M1", cutoffs_at = c(0, "ROC01", "SpEqualSe"))
# Split by a column
p <- ROCCurve(data, truth_by = "D", score_by = "M1", split_by = "gender")
p
# Retrieve the AUC values
attr(p, "auc")
```

SankeyPlot

Sankey / Alluvial Plot

Description

A plot visualizing flow/movement/change from one state to another or one time to another. `AlluvialPlot` is an alias of `SankeyPlot`.

Usage

```
SankeyPlot(  
  data,  
  in_form = c("auto", "long", "lodes", "wide", "alluvia", "counts"),  
  x,  
  x_sep = "_",  
  y = NULL,  
  stratum = NULL,  
  stratum_sep = "_",  
  alluvium = NULL,  
  alluvium_sep = "_",  
  split_by = NULL,  
  split_by_sep = "_",  
  keep_empty = TRUE,  
  flow = FALSE,  
  expand = c(0, 0, 0, 0),  
  nodes_legend = c("auto", "separate", "merge", "none"),  
  nodes_color = "grey30",  
  links_fill_by = NULL,  
  links_fill_by_sep = "_",  
  links_name = NULL,  
  links_color = "gray80",  
  nodes_palette = "Paired",  
  nodes_palcolor = NULL,  
  nodes_alpha = 1,  
  nodes_label = FALSE,  
  nodes_label_miny = 0,  
  nodes_width = 0.25,  
  links_palette = "Paired",  
  links_palcolor = NULL,  
  links_alpha = 0.6,  
  legend.box = "vertical",  
  x_text_angle = 0,  
  aspect.ratio = 1,  
  legend.position = "right",  
  legend.direction = "vertical",  
  flip = FALSE,  
  theme = "theme_this",  
  theme_args = list(),  
  title = NULL,  
  subtitle = NULL,  
  xlab = NULL,  
  ylab = NULL,  
  facet_by = NULL,  
  facet_scales = "fixed",  
  facet_ncol = NULL,  
  facet_nrow = NULL,  
  facet_byrow = TRUE,
```

```
seed = 8525,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

AlluvialPlot(
  data,
  in_form = c("auto", "long", "lodes", "wide", "alluvia", "counts"),
  x,
  x_sep = "_",
  y = NULL,
  stratum = NULL,
  stratum_sep = "_",
  alluvium = NULL,
  alluvium_sep = "_",
  split_by = NULL,
  split_by_sep = "_",
  keep_empty = TRUE,
  flow = FALSE,
  expand = c(0, 0, 0, 0),
  nodes_legend = c("auto", "separate", "merge", "none"),
  nodes_color = "grey30",
  links_fill_by = NULL,
  links_fill_by_sep = "_",
  links_name = NULL,
  links_color = "gray80",
  nodes_palette = "Paired",
  nodes_palcolor = NULL,
  nodes_alpha = 1,
  nodes_label = FALSE,
  nodes_label_miny = 0,
  nodes_width = 0.25,
  links_palette = "Paired",
  links_palcolor = NULL,
  links_alpha = 0.6,
  legend.box = "vertical",
  x_text_angle = 0,
  aspect.ratio = 1,
  legend.position = "right",
  legend.direction = "vertical",
  flip = FALSE,
```



```

theme = "theme_this",
theme_args = list(),
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
facet_by = NULL,
facet_scales = "fixed",
facet_ncol = NULL,
facet_nrow = NULL,
facet_byrow = TRUE,
seed = 8525,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

data	<p>A data frame in following possible formats:</p> <ul style="list-style-type: none"> • "long" or "lodes": A long format with columns for x, stratum, alluvium, and y. x (required, single columns or concatenated by x_sep) is the column name to plot on the x-axis, stratum (defaults to links_fill_by) is the column name to group the nodes for each x, alluvium (required) is the column name to define the links, and y is the frequency of each x, stratum, and alluvium. • "wide" or "alluvia": A wide format with columns for x. x (required, multiple columns, x_sep won't be used) are the columns to plot on the x-axis, stratum and alluvium will be ignored. See ggalluvial::to_lodes_form for more details. • "counts": A format with counts being provides under each x. x (required, multiple columns, x_sep won't be used) are the columns to plot on the x-axis. When the first element of x is ".", values of links_fill_by (required) will be added to the plot as the first column of nodes. It is useful to show how the links are flowed from the source to the targets. • "auto" (default): Automatically determine the format based on the columns provided. When the length of x is greater than 1 and all x columns are numeric, "counts" format will be used. When the length of x is greater than 1 and ggalluvial::is_alluvia_form returns TRUE, "alluvia" format will be used. Otherwise, "lodes" format will be tried.
in_form	<p>A character string to specify the format of the data. Possible values are "auto", "long", "lodes", "wide", "alluvia", and "counts".</p>

x	A character string specifying the column name of the data frame to plot for the x-axis.
x_sep	A character string to concatenate the columns in x, if multiple columns are provided.
y	A character string specifying the column name of the data frame to plot for the y-axis.
stratum	A character string of the column name to group the nodes for each x. See data for more details.
stratum_sep	A character string to concatenate the columns in stratum, if multiple columns are provided.
alluvium	A character string of the column name to define the links. See data for more details.
alluvium_sep	A character string to concatenate the columns in alluvium, if multiple columns are provided.
split_by	The column(s) to split data by and plot separately.
split_by_sep	The separator for multiple split_by columns. See split_by
keep_empty	A logical value indicating whether to keep empty groups. If FALSE, empty groups will be removed.
flow	A logical value to use <code>ggalluvial::geom_flow</code> instead of <code>ggalluvial::geom_alluvium</code> .
expand	The values to expand the x and y axes. It is like CSS padding. When a single value is provided, it is used for both axes on both sides. When two values are provided, the first value is used for the top/bottom side and the second value is used for the left/right side. When three values are provided, the first value is used for the top side, the second value is used for the left/right side, and the third value is used for the bottom side. When four values are provided, the values are used for the top, right, bottom, and left sides, respectively. You can also use a named vector to specify the values for each side. When the axis is discrete, the values will be applied as 'add' to the 'expansion' function. When the axis is continuous, the values will be applied as 'mult' to the 'expansion' function. See also https://ggplot2.tidyverse.org/reference/expansion.html
nodes_legend	Controls how the legend of nodes will be shown. Possible values are: <ul style="list-style-type: none"> "merge": Merge the legends of nodes. That is only one legend will be shown for all nodes. "separate": Show the legends of nodes separately. That is, nodes on each x will have their own legend. "none": Do not show the legend of nodes. "auto": Automatically determine how to show the legend. When nodes_label is TRUE, "none" will apply. When nodes_label is FALSE, and if stratum is the same as links_fill_by, "none" will apply. If there is any overlapping values between the nodes on different x, "merge" will apply. Otherwise, "separate" will apply.
nodes_color	A character string to color the nodes. Use a special value ".fill" to use the same color as the fill.
links_fill_by	A character string of the column name to fill the links.

<code>links_fill_by_sep</code>	A character string to concatenate the columns in <code>links_fill_by</code> , if multiple columns are provided.
<code>links_name</code>	A character string to name the legend of links.
<code>links_color</code>	A character string to color the borders of links. Use a special value <code>".fill"</code> to use the same color as the fill.
<code>nodes_palette</code>	A character string to specify the palette of nodes fill.
<code>nodes_palcolor</code>	A character vector to specify the colors of nodes fill.
<code>nodes_alpha</code>	A numeric value to specify the transparency of nodes fill.
<code>nodes_label</code>	A logical value to show the labels on the nodes.
<code>nodes_label_min</code>	A numeric value to specify the minimum y (frequency) to show the labels.
<code>nodes_width</code>	A numeric value to specify the width of nodes.
<code>links_palette</code>	A character string to specify the palette of links fill.
<code>links_palcolor</code>	A character vector to specify the colors of links fill.
<code>links_alpha</code>	A numeric value to specify the transparency of links fill.
<code>legend.box</code>	A character string to specify the box of the legend, either <code>"vertical"</code> or <code>"horizontal"</code> .
<code>x_text_angle</code>	A numeric value specifying the angle of the x-axis text.
<code>aspect.ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be <code>"none"</code> , otherwise <code>"right"</code> .
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>flip</code>	A logical value to flip the plot.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is <code>"theme_this"</code> .
<code>theme.args</code>	A list of arguments to pass to the theme function.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is <code>"fixed"</code> Other options are <code>"free"</code> , <code>"free_x"</code> , <code>"free_y"</code> . See <code>ggplot2::facet_wrap</code>

facet_ncol	A numeric value specifying the number of columns in the facet. When facet_by is a single column and facet_wrap is used.
facet_nrow	A numeric value specifying the number of rows in the facet. When facet_by is a single column and facet_wrap is used.
facet_byrow	A logical value indicating whether to fill the plots by row. Default is TRUE.
seed	The random seed to use. Default is 8525.
combine	Whether to combine the plots into one when facet is FALSE. Default is TRUE.
nrow	A numeric value specifying the number of rows in the facet.
ncol	A numeric value specifying the number of columns in the facet.
byrow	A logical value indicating whether to fill the plots by row.
axes	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
axis_titles	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
guides	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
design	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
...	Additional arguments.

Value

A ggplot object or wrap_plots object or a list of ggplot objects

Examples

```

# Reproduce the examples in ggalluvial
set.seed(8525)

data(UCBAdmissions, package = "datasets")
UCBAdmissions <- as.data.frame(UCBAdmissions)
SankeyPlot(as.data.frame(UCBAdmissions), x = c("Gender", "Dept"),
  y = "Freq", nodes_width = 1/12, links_fill_by = "Admit", nodes_label = TRUE,
  nodes_palette = "simspec", links_palette = "Set1", links_alpha = 0.5,
  nodes_palcolor = "black", links_color = "transparent")

data(HairEyeColor, package = "datasets")
SankeyPlot(as.data.frame(HairEyeColor), x = c("Hair", "Eye", "Sex"),
  y = "Freq", links_fill_by = "Eye", nodes_width = 1/8, nodes_alpha = 0.4,
  flip = TRUE, reverse = FALSE, knot.pos = 0, links_color = "transparent",
  ylab = "Freq", links_alpha = 0.5, links_name = "Eye (links)", links_palcolor = c(
    Brown = "#70493D", Hazel = "#E2AC76", Green = "#3F752B", Blue = "#81B0E4"))

data(Refugees, package = "alluvial")
country_regions <- c(
  Afghanistan = "Middle East",
  Burundi = "Central Africa",
  `Congo DRC` = "Central Africa",
  Iraq = "Middle East",
  Myanmar = "Southeast Asia",
  Palestine = "Middle East",
  Somalia = "Horn of Africa",
  Sudan = "Central Africa",
  Syria = "Middle East",
  Vietnam = "Southeast Asia"
)
Refugees$region <- country_regions[Refugees$country]
SankeyPlot(Refugees, x = "year", y = "refugees", alluvium = "country",
  links_fill_by = "country", links_color = ".fill", links_alpha = 0.75,
  links_palette = "Set3", facet_by = "region", x_text_angle = -45, nodes_legend = "none",
  theme_args = list(strip.background = ggplot2::element_rect(fill="grey80")),
  decreasing = FALSE, nodes_width = 0, nodes_color = "transparent", ylab = "refugees",
  title = "Refugee volume by country and region of origin")

data(majors, package = "ggalluvial")
majors$curriculum <- as.factor(majors$curriculum)
SankeyPlot(majors, x = "semester", stratum = "curriculum", alluvium = "student",
  links_fill_by = "curriculum", flow = TRUE, stat = "alluvium", nodes_palette = "Set2",
  links_palette = "Set2")

data(vaccinations, package = "ggalluvial")
vaccinations <- transform(vaccinations,
  response = factor(response, rev(levels(response))))
SankeyPlot(vaccinations, x = "survey", stratum = "response", alluvium = "subject",
  y = "freq", links_fill_by = "response", nodes_label = TRUE, nodes_alpha = 0.5,
  nodes_palette = "seurat", links_palette = "seurat", links_alpha = 0.5,
  legend.position = "none", flow = TRUE, expand = c(0, 0, 0, .15), stat = "alluvium",

```

```

    title = "vaccination survey responses at three points in time")

data(Titanic, package = "datasets")
SankeyPlot(as.data.frame(Titanic), x = c("Class", "Sex"), y = "Freq",
  links_fill_by = "Survived", flow = TRUE, facet_by = "Age", facet_scales = "free_y",
  nodes_label = TRUE, expand = c(0.05, 0), xlab = "", links_palette = "Set1",
  nodes_palcolor = "white", nodes_label_min = 10)

# Simulated examples
df <- data.frame(
  Clone = paste0("clone", 1:10),
  Timepoint1 = sample(c(rep(0, 30), 1:100), 10),
  Timepoint2 = sample(c(rep(0, 30), 1:100), 10)
)
SankeyPlot(df, x = c("Timepoint1", "Timepoint2"), alluvium = "Clone",
  links_color = ".fill")

df <- data.frame(
  Clone = rep(paste0("clone", 1:6), each = 2),
  Timepoint1 = sample(c(rep(0, 30), 1:100), 6),
  Timepoint2 = sample(c(rep(0, 30), 1:100), 6),
  Group = rep(c("A", "B"), 6)
)
SankeyPlot(df, x = c(".", "Timepoint1", "Timepoint2"),
  stratum = "Group", links_fill_by = "Clone", links_color = ".fill")

```

ScatterPlot

Scatter Plot

Description

Scatter Plot

Usage

```

ScatterPlot(
  data,
  x,
  y,
  size_by = 2,
  size_name = NULL,
  color_by = NULL,
  color_name = NULL,
  color_reverse = FALSE,
  split_by = NULL,
  split_by_sep = "_",
  shape = 21,
  alpha = ifelse(shape %in% 21:25, 0.65, 1),

```

```

border_color = "black",
highlight = NULL,
highlight_shape = 16,
highlight_size = 3,
highlight_color = "red",
highlight_alpha = 1,
theme = "theme_this",
theme_args = list(),
palette = ifelse(!is.null(color_by) && !is.numeric(data[[color_by]]), "Paired",
  "Spectral"),
palcolor = NULL,
facet_by = NULL,
facet_scales = "fixed",
facet_ncol = NULL,
facet_nrow = NULL,
facet_byrow = TRUE,
aspect.ratio = 1,
legend.position = "right",
legend.direction = "vertical",
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
seed = 8525,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

<code>data</code>	A data frame.
<code>x</code>	A character string specifying the column name of the data frame to plot for the x-axis.
<code>y</code>	A character string specifying the column name of the data frame to plot for the y-axis.
<code>size_by</code>	Which column to use as the size of the dots. It must be a numeric column. Or it can be a numeric value to specify the size of the dots.
<code>size_name</code>	A character vector specifying the name for the size legend.
<code>color_by</code>	Which column to use as the color of the dots. It could be a numeric column or a factor/character column. For shapes 21-25, the color is applied to the fill color.

<code>color_name</code>	A character vector specifying the name for the color legend.
<code>color_reverse</code>	A logical value indicating whether to reverse the color direction. Default is FALSE.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>shape</code>	A numeric value specifying the shape of the points. Default is 21.
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>border_color</code>	A character vector specifying the color for the border of the points. Or TRUE to use the fill color as the border color.
<code>highlight</code>	A vector of indexes or rownames to select the points to highlight. It could also be an expression (in string) to filter the data.
<code>highlight_shape</code>	A numeric value specifying the shape of the highlighted points. Default is 16.
<code>highlight_size</code>	A numeric value specifying the size of the highlighted points. Default is 3.
<code>highlight_color</code>	A character vector specifying the color of the highlighted points. Default is "red".
<code>highlight_alpha</code>	A numeric value specifying the transparency of the highlighted points. Default is 1.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be NULL for those values).
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is TRUE.
<code>aspect_ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".

<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is <code>FALSE</code> . Default is <code>TRUE</code> .
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>seed</code>	The random seed to use. Default is 8525.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
<code>...</code>	Additional arguments.

Value

A ggplot object or `wrap_plots` object or a list of ggplot objects

Examples

```

set.seed(8525)

data <- data.frame(
  x = rnorm(20),
  y = rnorm(20),
  w = abs(rnorm(20)),
  t = sample(c("A", "B"), 20, replace = TRUE)
)
ScatterPlot(data, x = "x", y = "y")

# highlight points
ScatterPlot(data, x = "x", y = "y", highlight = 'x > 0')

# size_by is a numeric column
ScatterPlot(data, x = "x", y = "y", size_by = "w")

# color_by is a numeric column
ScatterPlot(data, x = "x", y = "y", color_by = "w")

# color_by is a factor/character column and set a border_color
ScatterPlot(data, x = "x", y = "y", size_by = "w", color_by = "t",
  border_color = "red")

# Same border_color as the fill color
ScatterPlot(data, x = "x", y = "y", size_by = "w", color_by = "t",
  border_color = TRUE)

# Shape doesn't have fill color
ScatterPlot(data, x = "x", y = "y", size_by = "w", color_by = "t",
  shape = 1, palette = "Set1")

# Change color per plot
ScatterPlot(data, x = "x", y = "y", split_by = "t",
  palcolor = list(A = "blue", B = "red"))

```

show_palettes

Show the color palettes

Description

This function displays color palettes using ggplot2.

Usage

```

show_palettes(
  palettes = NULL,
  type = c("discrete", "continuous"),
  index = NULL,

```

```

    palette_names = NULL,
    return_names = TRUE,
    return_palettes = FALSE
  )

```

Arguments

palettes	A list of color palettes. If NULL, uses default palettes.
type	A character vector specifying the type of palettes to include. Default is "discrete".
index	A numeric vector specifying the indices of the palettes to include. Default is NULL.
palette_names	A character vector specifying the names of the SCP palettes to include. Default is NULL.
return_names	A logical value indicating whether to return the names of the selected palettes. Default is TRUE.
return_palettes	A logical value indicating whether to return the colors of selected palettes. Default is FALSE.

Value

A list of palette names or a list of palettes.

See Also

[palette_list](#)

[All available palettes](#)

Examples

```

show_palettes(palettes = list(c("red", "blue", "green"), c("yellow", "purple", "orange")))
all_palettes <- show_palettes(return_palettes = TRUE)
names(all_palettes)
all_palettes[["simspec"]]
show_palettes(index = 1:10)
show_palettes(type = "discrete", index = 1:10)
show_palettes(type = "continuous", index = 1:10)
show_palettes(
  palette_names = c("Paired", "nejm", "simspec", "Spectral", "jet"),
  return_palettes = TRUE
)

```

`theme_blank`*Blank theme*

Description

This function creates a theme with all elements blank except for axis lines and labels. It can optionally add coordinate axes in the plot.

Usage

```
theme_blank(  
  add_coord = TRUE,  
  xlen_npc = 0.15,  
  ylen_npc = 0.15,  
  xlab = "",  
  ylab = "",  
  lab_size = 12,  
  ...  
)
```

Arguments

<code>add_coord</code>	Whether to add coordinate arrows. Default is TRUE.
<code>xlen_npc</code>	The length of the x-axis arrow in "npc".
<code>ylen_npc</code>	The length of the y-axis arrow in "npc".
<code>xlab</code>	x-axis label.
<code>ylab</code>	y-axis label.
<code>lab_size</code>	Label size.
<code>...</code>	Arguments passed to the theme .

Value

A ggplot2 theme.

Examples

```
library(ggplot2)  
p <- ggplot(mtcars, aes(x = wt, y = mpg, colour = factor(cyl))) +  
  geom_point()  
p + theme_blank()  
p + theme_blank(xlab = "x-axis", ylab = "y-axis", lab_size = 16)
```

theme_this	<i>A ggplot2 theme and palettes for plotthis Borrowed from the theme_this function in the SCP pipeline</i>
------------	--

Description

A ggplot2 theme and palettes for plotthis Borrowed from the theme_this function in the SCP pipeline

Usage

```
theme_this(aspect.ratio = NULL, base_size = 12, font_family = NULL, ...)
```

Arguments

aspect.ratio	The aspect ratio of the plot
base_size	The base size of the text
font_family	The font family of the text
...	Other arguments for theme()

Value

A ggplot2 theme

See Also

<https://github.com/zhanghao-njmu/SCP>

TrendPlot	<i>Trend plot</i>
-----------	-------------------

Description

A trend plot is like an area plot but with gaps between the bars.

Usage

```
TrendPlot(  
  data,  
  x,  
  y = NULL,  
  x_sep = "_",  
  split_by = NULL,  
  split_by_sep = "_",  
  group_by = NULL,
```

```

group_by_sep = "_",
group_name = NULL,
scale_y = FALSE,
theme = "theme_this",
theme_args = list(),
palette = "Paired",
palcolor = NULL,
alpha = 1,
facet_by = NULL,
facet_scales = "fixed",
facet_ncol = NULL,
facet_nrow = NULL,
facet_byrow = TRUE,
x_text_angle = 0,
aspect.ratio = 1,
legend.position = waiver(),
legend.direction = "vertical",
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
seed = 8525,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

<code>data</code>	A data frame.
<code>x</code>	A character string specifying the column name of the data frame to plot for the x-axis.
<code>y</code>	A character string specifying the column name of the data frame to plot for the y-axis.
<code>x_sep</code>	A character string to concatenate the columns in <code>x</code> , if multiple columns are provided.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>group_by</code>	Columns to group the data for plotting For those plotting functions that do not support multiple groups, They will be concatenated into one column, using <code>group_by_sep</code> as the separator

<code>group_by_sep</code>	The separator for multiple <code>group_by</code> columns. See <code>group_by</code>
<code>group_name</code>	A character string to name the legend of fill.
<code>scale_y</code>	A logical value to scale the y-axis by the total number in each x-axis group.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be NULL for those values).
<code>alpha</code>	A numeric value specifying the transparency of the plot.
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is TRUE.
<code>x_text_angle</code>	A numeric value specifying the angle of the x-axis text.
<code>aspect.ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>xlab</code>	A character string specifying the x-axis label.
<code>ylab</code>	A character string specifying the y-axis label.
<code>seed</code>	The random seed to use. Default is 8525.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.

<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . Options are: <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is <code>TRUE</code> . When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
<code>...</code>	Additional arguments.

Value

A ggplot object or `wrap_plots` object or a list of ggplot objects

See Also

[AreaPlot](#)

Examples

```
data <- data.frame(
  x = rep(c("A", "B", "C", "D"), 2),
  y = c(1, 3, 6, 4, 2, 5, 7, 8),
  group = rep(c("F1", "F2"), each = 4)
)
TrendPlot(data, x = "x", y = "y", group_by = "group")
TrendPlot(data, x = "x", y = "y", group_by = "group",
  scale_y = TRUE)
TrendPlot(data, x = "x", y = "y", split_by = "group")
```



```
TrendPlot(data, x = "x", y = "y", split_by = "group",  
          palette = c(F1 = "Set1", F2 = "Paired"))
```

VolcanoPlot

Volcano plot

Description

A volcano plot is a type of scatter plot that shows statistical significance (usually on the y-axis) versus magnitude of change (usually on the x-axis).

Usage

```
VolcanoPlot(  
  data,  
  x,  
  y,  
  ytrans = function(n) -log10(n),  
  color_by = NULL,  
  color_name = NULL,  
  xlim = NULL,  
  flip_negatives = FALSE,  
  x_cutoff = NULL,  
  y_cutoff = 0.05,  
  split_by = NULL,  
  split_by_sep = "_",  
  x_cutoff_name = NULL,  
  y_cutoff_name = NULL,  
  x_cutoff_color = "red2",  
  y_cutoff_color = "blue2",  
  x_cutoff_linetype = "dashed",  
  y_cutoff_linetype = "dashed",  
  x_cutoff_linewidth = 0.5,  
  y_cutoff_linewidth = 0.5,  
  pt_size = 2,  
  pt_alpha = 0.5,  
  nlabel = 5,  
  labels = NULL,  
  label_size = 3,  
  label_fg = "black",  
  label_bg = "white",  
  label_bg_r = 0.1,  
  highlight = NULL,  
  highlight_color = "red",  
  highlight_size = 2,  
  highlight_alpha = 1,  
  highlight_stroke = 0.5,
```

```

trim = c(0, 1),
facet_by = NULL,
facet_scales = "fixed",
facet_ncol = NULL,
facet_nrow = NULL,
facet_byrow = TRUE,
theme = "theme_this",
theme_args = list(),
palette = "Spectral",
palcolor = NULL,
title = NULL,
subtitle = NULL,
xlab = NULL,
ylab = NULL,
aspect.ratio = 1,
legend.position = "right",
legend.direction = "vertical",
seed = 8525,
combine = TRUE,
nrow = NULL,
ncol = NULL,
byrow = TRUE,
axes = NULL,
axis_titles = axes,
guides = NULL,
design = NULL,
...
)

```

Arguments

<code>data</code>	A data frame.
<code>x</code>	A character string specifying the column name of the data frame to plot for the x-axis.
<code>y</code>	A character string specifying the column name of the data frame to plot for the y-axis.
<code>ytrans</code>	A function to transform the y-axis values.
<code>color_by</code>	A character vector of column names to color the points by. If NULL, the points will be filled by the x and y cutoff value.
<code>color_name</code>	A character string to name the legend of color.
<code>xlim</code>	A numeric vector of length 2 to set the x-axis limits.
<code>flip_negatives</code>	A logical value to flip the y-axis for negative x values.
<code>x_cutoff</code>	A numeric value to set the x-axis cutoff. Both negative and positive of this value will be used.
<code>y_cutoff</code>	A numeric value to set the y-axis cutoff. Note that the y-axis cutoff will be transformed by <code>ytrans</code> . So you should provide the original value.

<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>x_cutoff_name</code>	A character string to name the x-axis cutoff. If "none", the legend for the x-axis cutoff will not be shown.
<code>y_cutoff_name</code>	A character string to name the y-axis cutoff. If "none", the legend for the y-axis cutoff will not be shown.
<code>x_cutoff_color</code>	A character string to color the x-axis cutoff line.
<code>y_cutoff_color</code>	A character string to color the y-axis cutoff line.
<code>x_cutoff_linetype</code>	A character string to set the x-axis cutoff line type.
<code>y_cutoff_linetype</code>	A character string to set the y-axis cutoff line type.
<code>x_cutoff_linewidth</code>	A numeric value to set the x-axis cutoff line size.
<code>y_cutoff_linewidth</code>	A numeric value to set the y-axis cutoff line size.
<code>pt_size</code>	A numeric value to set the point size.
<code>pt_alpha</code>	A numeric value to set the point transparency.
<code>nlabel</code>	A numeric value to set the number of labels to show. The points will be ordered by the distance to the origin. Top <code>nlabel</code> points will be labeled.
<code>labels</code>	A character vector of row names or indexes to label the points.
<code>label_size</code>	A numeric value to set the label size.
<code>label_fg</code>	A character string to set the label color.
<code>label_bg</code>	A character string to set the label background color.
<code>label_bg_r</code>	A numeric value specifying the radius of the background of the label.
<code>highlight</code>	A character vector of row names or indexes to highlight the points.
<code>highlight_color</code>	A character string to set the highlight color.
<code>highlight_size</code>	A numeric value to set the highlight size.
<code>highlight_alpha</code>	A numeric value to set the highlight transparency.
<code>highlight_stroke</code>	A numeric value to set the highlight stroke size.
<code>trim</code>	A numeric vector of length 2 to trim the x-axis values. The values must be in the range from 0 to 1, which works as quantile to trim the x-axis values. For example, <code>c(0.01, 0.99)</code> will trim the 1% and 99% quantile of the x-axis values. If the values are less than 1% or greater than 99% quantile, the values will be set to the 1% or 99% quantile.
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>

facet_scales	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
facet_ncol	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
facet_nrow	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
facet_byrow	A logical value indicating whether to fill the plots by row. Default is TRUE.
theme	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
theme_args	A list of arguments to pass to the theme function.
palette	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
palcolor	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be NULL for those values).
title	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
subtitle	A character string specifying the subtitle of the plot.
xlab	A character string specifying the x-axis label.
ylab	A character string specifying the y-axis label.
aspect.ratio	A numeric value specifying the aspect ratio of the plot.
legend.position	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
legend.direction	A character string specifying the direction of the legend.
seed	The random seed to use. Default is 8525.
combine	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
nrow	A numeric value specifying the number of rows in the facet.
ncol	A numeric value specifying the number of columns in the facet.
byrow	A logical value indicating whether to fill the plots by row.
axes	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none"> • 'keep' will retain all axes in individual plots. • 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout. • 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
axis_titles	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are:

	<ul style="list-style-type: none"> • 'keep' will retain all axis titles in individual plots. • 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction. • 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
guides	<p>A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code>. Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are:</p> <ul style="list-style-type: none"> • 'collect' will collect guides below to the given nesting level, removing duplicates. • 'keep' will stop collection at this level and let guides be placed alongside their plot. • 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
design	<p>Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code>. Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code>, <code>ncol</code>, and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.</p>
...	Additional arguments.

Value

A list of ggplot objects or a `wrap_plots` object

Examples

```
set.seed(8525)
# Obtained by Seurat::FindMarkers for the first cluster of pbmc_small
data <- data.frame(
  avg_log2FC = c(
    -3.69, -4.10, -2.68, -3.51, -3.09, -2.52, -3.53, -3.35, -2.82, -2.71, -3.16, -2.24,
    -5.62, -3.10, -3.42, -2.72, -3.23, -3.25, -4.68, 3.67, -2.66, 4.79, -2.99, 10.14,
    -1.78, -2.67, -2.26, -2.59, -3.39, 5.36, 4.56, 4.62, -2.94, -9.47, -9.12, -1.63,
    -2.77, 3.31, -1.53, -3.89, -4.21, 4.72, -2.98, -2.29, -1.41, -9.48, -4.30, 3.01,
    -1.19, -4.83, -1.35, -1.68, -1.63, -2.70, 3.86, 3.81, 7.23, -1.45, -0.92, -2.45,
    3.91, -4.45, -9.33, 3.56, 2.27, -1.60, -1.15, 11.40, -9.77, -8.32, 2.61, -1.25,
    -1.72, 10.61, 11.34, 10.02, 2.78, -3.48, -1.98, 5.86, 5.57, 4.57, 9.75, 9.97,
    10.90, 9.19, 2.93, 5.10, -1.52, -3.93, -1.95, -2.46, -0.64, 4.60, -1.82, -0.80,
    9.34, 7.51, 6.45, 5.23, 4.41, 3.60, -1.94, -1.15),
  p_val_adj = c(
    3.82e-09, 1.52e-07, 1.79e-07, 4.68e-07, 4.83e-07, 6.26e-07, 2.61e-06, 1.33e-05,
    1.79e-05, 3.71e-05, 5.21e-05, 5.36e-05, 5.83e-05, 6.66e-05, 8.22e-05, 2.89e-04,
    3.00e-04, 4.94e-04, 7.62e-04, 8.93e-04, 9.55e-04, 9.61e-04, 1.12e-03, 1.47e-03,
    1.66e-03, 1.95e-03, 2.06e-03, 3.01e-03, 3.26e-03, 4.35e-03, 4.85e-03, 5.12e-03,
    5.40e-03, 7.18e-03, 7.18e-03, 1.04e-02, 1.24e-02, 1.90e-02, 1.94e-02, 1.97e-02,
    2.09e-02, 2.13e-02, 2.25e-02, 2.61e-02, 3.18e-02, 3.27e-02, 3.69e-02, 3.80e-02,
    4.95e-02, 5.73e-02, 5.77e-02, 6.10e-02, 6.22e-02, 6.31e-02, 6.72e-02, 9.23e-02,
    9.85e-02, 1.06e-01, 1.07e-01, 1.11e-01, 1.31e-01, 1.38e-01, 1.40e-01, 1.43e-01,
    2.00e-01, 2.39e-01, 2.49e-01, 2.57e-01, 2.86e-01, 2.86e-01, 2.98e-01, 3.32e-01,
    4.15e-01, 4.91e-01, 4.91e-01, 4.91e-01, 5.97e-01, 7.11e-01, 7.59e-01, 8.38e-01,
```

```

9.20e-01, 9.20e-01, 9.29e-01, 9.29e-01, 9.29e-01, 9.29e-01, 9.34e-01, 9.68e-01,
1.00e+00, 1.00e+00, 1.00e+00, 1.00e+00, 1.00e+00, 1.00e+00, 1.00e+00, 1.00e+00,
1.00e+00, 1.00e+00, 1.00e+00, 1.00e+00, 1.00e+00, 1.00e+00, 1.00e+00, 1.00e+00),
gene = c(
  "HLA-DPB1", "LYZ", "HLA-DRA", "TYMP", "HLA-DPA1", "HLA-DRB1", "CST3", "HLA-DQB1",
  "HLA-DRB5", "LST1", "HLA-DQA1", "AIF1", "S100A8", "IFITM3", "HLA-DMB", "FCGRT",
  "SERPINA1", "IFI30", "S100A9", "CCL5", "GRN", "LCK", "HLA-DMA", "MS4A6A", "CTSS",
  "CFP", "FCN1", "BID", "CFD", "CD3D", "CD7", "CD3E", "LGALS2", "CD14", "SMCO4",
  "LINC00936", "HCK", "CTSW", "LGALS1", "HLA-DQA2", "LRRC25", "GZMM", "RNF130",
  "LGALS3", "S100A11", "C5AR1", "IL1B", "GZMA", "FCER1G", "MPEG1", "TYROBP", "TSPO",
  "GSTP1", "CTSB", "IL32", "CD247", "GNLY", "COTL1", "NFKBIA", "NUP214", "LAMP1",
  "FPR1", "CLEC10A", "CST7", "PRF1", "BLVRA", "PSAP", "GZMH", "EAF2", "ASGR1",
  "RARRES3", "SAT1", "LY86", "GP9", "TUBB1", "NGFRAP1", "XBP1", "SC02", "RGS2", "GZMB",
  "HIST1H2AC", "KLRD1", "PGRMC1", "AKR1C3", "PTGDR", "IL2RB", "GYPC", "CCL4", "CD68",
  "FCER1A", "CD79B", "MS4A7", "CARD16", "ACAP1", "CD79A", "ANXA2", "TMEM40", "PF4",
  "GNG11", "CLU", "CD9", "FGFBP2", "TNFRSF1B", "IFI6"),
pct_diff = c(
  -0.752, -0.457, -0.460, -0.671, -0.626, -0.701, -0.502, -0.619, -0.623, -0.598,
  -0.566, -0.626, -0.543, -0.566, -0.541, -0.542, -0.515, -0.489, -0.444, 0.428,
  -0.517, 0.461, -0.491, -0.410, -0.480, -0.491, -0.521, -0.491, -0.438, 0.411,
  0.411, 0.409, -0.438, -0.359, -0.359, -0.440, -0.386, 0.385, -0.332, -0.361, -0.361,
  0.364, -0.387, -0.415, -0.454, -0.308, -0.335, 0.364, -0.454, -0.309, -0.379, -0.427,
  -0.377, -0.389, 0.335, 0.315, 0.313, -0.284, -0.502, -0.309, 0.313, -0.284, -0.256,
  0.309, 0.313, -0.364, -0.406, 0.244, -0.231, -0.231, 0.281, -0.311, -0.312, 0.220,
  0.220, 0.220, 0.261, -0.232, -0.367, 0.240, 0.218, 0.218, 0.195, 0.195, 0.195, 0.195,
  0.262, 0.218, -0.288, -0.207, -0.290, -0.233, -0.367, 0.217, -0.233, -0.403, 0.171,
  0.194, 0.194, 0.194, 0.194, 0.213, -0.235, -0.292),
group = sample(LETTERS[1:2], 104, replace = TRUE)
)
rownames(data) <- data$gene

VolcanoPlot(data, x = "avg_log2FC", y = "p_val_adj", color_by = "pct_diff",
  y_cutoff_name = "-log10(0.05)")
VolcanoPlot(data, x = "avg_log2FC", y = "p_val_adj", y_cutoff_name = "none",
  flip_negatives = TRUE)
VolcanoPlot(data, x = "avg_log2FC", y = "p_val_adj", y_cutoff_name = "none",
  flip_negatives = TRUE, facet_by = "group")
VolcanoPlot(data, x = "avg_log2FC", y = "p_val_adj", y_cutoff_name = "none",
  flip_negatives = TRUE, split_by = "group")
VolcanoPlot(data, x = "avg_log2FC", y = "p_val_adj", y_cutoff_name = "none",
  highlight = c("ANXA2", "TMEM40", "PF4", "GNG11", "CLU", "CD9", "FGFBP2",
  "TNFRSF1B", "IFI6"))
VolcanoPlot(data, x = "avg_log2FC", y = "p_val_adj", color_by = "pct_diff",
  y_cutoff_name = "-log10(0.05)", split_by = "group",
  palette = c(A = "Set1", B = "Dark2"))

```

Description

Word cloud plot to illustrate the count/frequency of words.

Usage

```
WordCloudPlot(  
  data,  
  word_by = NULL,  
  sentence_by = NULL,  
  count_by = NULL,  
  score_by = NULL,  
  count_name = NULL,  
  score_name = NULL,  
  split_by = NULL,  
  split_by_sep = "_",  
  words_excluded = plotthis::words_excluded,  
  score_agg = mean,  
  minchar = 2,  
  word_size = c(2, 8),  
  top_words = 100,  
  facet_by = NULL,  
  facet_scales = "fixed",  
  facet_ncol = NULL,  
  facet_nrow = NULL,  
  facet_byrow = TRUE,  
  theme = "theme_this",  
  theme_args = list(),  
  palette = "Spectral",  
  palcolor = NULL,  
  alpha = 1,  
  palreverse = FALSE,  
  aspect.ratio = 1,  
  legend.position = "right",  
  legend.direction = "vertical",  
  title = NULL,  
  subtitle = NULL,  
  seed = 8525,  
  combine = TRUE,  
  nrow = NULL,  
  ncol = NULL,  
  byrow = TRUE,  
  axes = NULL,  
  axis_titles = axes,  
  guides = NULL,  
  design = NULL,  
  ...  
)
```

Arguments

<code>data</code>	A data frame.
<code>word_by</code>	A character string of the column name to use as the word. A character column is expected.
<code>sentence_by</code>	A character string of the column name to split the sentence. A character column is expected. Either <code>word_by</code> or <code>sentence_by</code> should be specified.
<code>count_by</code>	A character string of the column name for the count of the word/sentence. A numeric column is expected. If NULL, the count of the word/sentence will be used.
<code>score_by</code>	A character string of the column name for the score of the word/sentence. A numeric column is expected, used for the color of the word cloud. If NULL, the score will be set to 1.
<code>count_name</code>	A character string to name the legend of count.
<code>score_name</code>	A character string to name the legend of score.
<code>split_by</code>	The column(s) to split data by and plot separately.
<code>split_by_sep</code>	The separator for multiple <code>split_by</code> columns. See <code>split_by</code>
<code>words_excluded</code>	A character vector of words to exclude from the word cloud.
<code>score_agg</code>	A function to aggregate the scores. Default is mean.
<code>minchar</code>	A numeric value specifying the minimum number of characters for the word.
<code>word_size</code>	A numeric vector specifying the range of the word size.
<code>top_words</code>	A numeric value specifying the number of top words to show.
<code>facet_by</code>	A character string specifying the column name of the data frame to facet the plot. Otherwise, the data will be split by <code>split_by</code> and generate multiple plots and combine them into one using <code>patchwork::wrap_plots</code>
<code>facet_scales</code>	Whether to scale the axes of facets. Default is "fixed" Other options are "free", "free_x", "free_y". See <code>ggplot2::facet_wrap</code>
<code>facet_ncol</code>	A numeric value specifying the number of columns in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_nrow</code>	A numeric value specifying the number of rows in the facet. When <code>facet_by</code> is a single column and <code>facet_wrap</code> is used.
<code>facet_byrow</code>	A logical value indicating whether to fill the plots by row. Default is TRUE.
<code>theme</code>	A character string or a theme class (i.e. <code>ggplot2::theme_classic</code>) specifying the theme to use. Default is "theme_this".
<code>theme_args</code>	A list of arguments to pass to the theme function.
<code>palette</code>	A character string specifying the palette to use. A named list or vector can be used to specify the palettes for different <code>split_by</code> values.
<code>palcolor</code>	A character string specifying the color to use in the palette. A named list can be used to specify the colors for different <code>split_by</code> values. If some values are missing, the values from the palette will be used (<code>palcolor</code> will be NULL for those values).
<code>alpha</code>	A numeric value specifying the transparency of the plot.

<code>palreverse</code>	A logical value to reverse the palette colors.
<code>aspect.ratio</code>	A numeric value specifying the aspect ratio of the plot.
<code>legend.position</code>	A character string specifying the position of the legend. if <code>waiver()</code> , for single groups, the legend will be "none", otherwise "right".
<code>legend.direction</code>	A character string specifying the direction of the legend.
<code>title</code>	A character string specifying the title of the plot. A function can be used to generate the title based on the default title. This is useful when <code>split_by</code> is used and the title needs to be dynamic.
<code>subtitle</code>	A character string specifying the subtitle of the plot.
<code>seed</code>	The random seed to use. Default is 8525.
<code>combine</code>	Whether to combine the plots into one when <code>facet</code> is FALSE. Default is TRUE.
<code>nrow</code>	A numeric value specifying the number of rows in the facet.
<code>ncol</code>	A numeric value specifying the number of columns in the facet.
<code>byrow</code>	A logical value indicating whether to fill the plots by row.
<code>axes</code>	A string specifying how axes should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none">• 'keep' will retain all axes in individual plots.• 'collect' will remove duplicated axes when placed in the same run of rows or columns of the layout.• 'collect_x' and 'collect_y' will remove duplicated x-axes in the columns or duplicated y-axes in the rows respectively.
<code>axis_titles</code>	A string specifying how axis titles should be treated. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none">• 'keep' will retain all axis titles in individual plots.• 'collect' will remove duplicated titles in one direction and merge titles in the opposite direction.• 'collect_x' and 'collect_y' control this for x-axis titles and y-axis titles respectively.
<code>guides</code>	A string specifying how guides should be treated in the layout. Passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. Options are: <ul style="list-style-type: none">• 'collect' will collect guides below to the given nesting level, removing duplicates.• 'keep' will stop collection at this level and let guides be placed alongside their plot.• 'auto' will allow guides to be collected if a upper level tries, but place them alongside the plot if not.
<code>design</code>	Specification of the location of areas in the layout, passed to <code>patchwork::wrap_plots()</code> . Only relevant when <code>split_by</code> is used and <code>combine</code> is TRUE. When specified, <code>nrow</code> , <code>ncol</code> , and <code>byrow</code> are ignored. See <code>patchwork::wrap_plots()</code> for more details.
<code>...</code>	Additional arguments.

Value

A ggplot object or wrap_plots object or a list of ggplot objects

Examples

```
data <- data.frame(  
  word = c("apple", "banana", "cherry", "date", "elderberry"),  
  count = c(10, 20, 30, 40, 50),  
  score = c(1, 2, 3, 4, 5)  
)  
WordCloudPlot(data, word_by = "word", count_by = "count", score_by = "score")
```

words_excluded

Excluded words in keyword enrichment analysis and extraction

Description

The variable "words_excluded" represents the words that are excluded during keyword enrichment analysis or keyword extraction process. These mainly include words that are excessively redundant or of little value.

Examples

```
## Not run:  
if (interactive()) {  
  words_excluded <- c(  
    "the", "is", "and", "or", "a", "in", "on", "under", "between", "of", "through",  
    "via", "along", "that", "for", "with", "within", "without", "cell", "cellular",  
    "dna", "rna", "protein", "peptide", "amino", "acid", "development", "involved",  
    "organization", "system", "regulation", "regulated", "positive", "negative",  
    "response", "process", "processing", "small", "large", "change", "disease"  
  )  
}  
  
## End(Not run)
```

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