

Package ‘diceplot’

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Title High Dimensional Categorical Data Visualization

Description Easy visualization for datasets with more than two categorical variables and additional continuous variables. 'diceplot' is particularly useful for exploring complex categorical data in the context of pathway analysis across multiple conditions. For a detailed documentation please visit <<https://dice-and-domino-plot.readthedocs.io/en/latest/>>.

Version 0.2.0

URL <https://dice-and-domino-plot.readthedocs.io/en/latest/>,
<https://github.com/maflot/Diceplot>

BugReports <https://github.com/maflot/Diceplot/issues>

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calculate_dot_size	<i>Calculate Dynamic Dot Size</i>
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Description

Calculates the dot size based on the number of variables.

Usage

```
calculate_dot_size(num_vars, max_size, min_size)
```

Arguments

num_vars	Number of variables.
max_size	Maximal dot size for the plot to scale the dot sizes.
min_size	Minimal dot size for the plot to scale the dot sizes.

Value

A numeric value representing the dot size.

create_custom_legends	<i>Create Custom Legends</i>
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Description

Creates custom legend plots for cat_c and group.

Usage

```
create_custom_legends(  
  data,  
  cat_c,  
  group,  
  cat_c_colors,  
  group_colors,  
  var_positions,  
  num_vars,  
  dot_size  
)
```

Arguments

<code>data</code>	The original data frame.
<code>cat_c</code>	The name of the <code>cat_c</code> variable.
<code>group</code>	The name of the group variable.
<code>cat_c_colors</code>	A named vector of colors for <code>cat_c</code> .
<code>group_colors</code>	A named vector of colors for the group variable.
<code>var_positions</code>	Data frame with variable positions.
<code>num_vars</code>	Number of variables in <code>cat_c</code> .
<code>dot_size</code>	The size of the dots used in the plot.

Value

A combined ggplot object of the custom legends.

`create_var_positions` *Create Variable Positions*

Description

Generates a data frame containing variable names from `cat_c_colors` and corresponding x and y offsets based on the number of variables.

Usage

```
create_var_positions(cat_c_colors, num_vars)
```

Arguments

<code>cat_c_colors</code>	A named vector of colors for variables in category C. The names correspond to variable names.
<code>num_vars</code>	The number of variables. Supported values are "3", "4", "5", or "6".

Value

A data frame with columns:

var Factor of variable names from `cat_c_colors`.

x_offset Numeric x-axis offset for plotting.

y_offset Numeric y-axis offset for plotting.

Examples

```
library(dplyr)
cat_c_colors <- c("Var1" = "red", "Var2" = "blue", "Var3" = "green")
create_var_positions(cat_c_colors, 3)
```

dice_facet_plot

Domino Plot Visualization with Categorical Colors

Description

This function generates a plot to visualize categorical data in a domino plot format. The size of the dots is fixed, and the plot can be saved to an output file if specified. This version supports categorical colors and allows setting colors for left and right rectangle plots.

Usage

```
dice_facet_plot(  
  data,  
  gene_list,  
  x = "gene",  
  y = "Celltype",  
  contrast = "Contrast",  
  var_id = "var",  
  spacing_factor = 3,  
  categorical_colors = NULL,  
  color_scale_name = "Category",  
  left_rect_color = "lightblue",  
  right_rect_color = "lightpink",  
  rect_alpha = 0.5,  
  axis_text_size = 8,  
  x_axis_text_size = NULL,  
  y_axis_text_size = NULL,  
  legend_text_size = 8,  
  cluster_method = "complete",  
  cluster_y_axis = TRUE,  
  cluster_var_id = TRUE,  
  base_width = 5,  
  base_height = 4,  
  show_legend = TRUE,  
  legend_width = 0.25,  
  legend_height = 0.5,  
  custom_legend = TRUE,  
  aspect_ratio = NULL,  
  switch_axis = FALSE,  
  reverse_y_ordering = FALSE,  
  show_var_positions = FALSE,  
  output_file = NULL,  
  feature_col = NULL,  
  celltype_col = NULL,  
  contrast_col = NULL  
)
```

Arguments

<code>data</code>	A data frame containing the categorical data.
<code>gene_list</code>	A character vector of gene names to include in the plot.
<code>x</code>	A string representing the column name in data for the feature variable (e.g., genes). Default is "gene".
<code>y</code>	A string representing the column name in data for the cell type variable. Default is "Celltype".
<code>contrast</code>	A string representing the column name in data for the contrast variable. Default is "Contrast".
<code>var_id</code>	A string representing the column name in data for the variable identifier. Default is "var".
<code>spacing_factor</code>	A numeric value indicating the spacing between gene pairs. Default is 3.
<code>categorical_colors</code>	A named vector of colors to use for categorical values in the data. Default is NULL.
<code>color_scale_name</code>	A string specifying the name of the color scale in the legend. Default is "Category".
<code>left_rect_color</code>	A string specifying the color for the left rectangles. Default is "lightblue".
<code>right_rect_color</code>	A string specifying the color for the right rectangles. Default is "lightpink".
<code>rect_alpha</code>	A numeric value between 0 and 1 indicating the transparency of the rectangles. Default is 0.5.
<code>axis_text_size</code>	A numeric value specifying the size of the axis text. Default is 8.
<code>x_axis_text_size</code>	A numeric value specifying the size of the x-axis text. If NULL, uses <code>axis_text_size</code> . Default is NULL.
<code>y_axis_text_size</code>	A numeric value specifying the size of the y-axis text. If NULL, uses <code>axis_text_size</code> . Default is NULL.
<code>legend_text_size</code>	A numeric value specifying the size of the legend text. Default is 8.
<code>cluster_method</code>	The clustering method to use. Default is "complete".
<code>cluster_y_axis</code>	A logical value indicating whether to cluster the y-axis (cell types). Default is TRUE.
<code>cluster_var_id</code>	A logical value indicating whether to cluster the <code>var_id</code> . Default is TRUE.
<code>base_width</code>	A numeric value specifying the base width for saving the plot. Default is 5.
<code>base_height</code>	A numeric value specifying the base height for saving the plot. Default is 4.
<code>show_legend</code>	A logical value indicating whether to show the legend. Default is TRUE.
<code>legend_width</code>	A numeric value specifying the relative width of the legend. Default is 0.25.
<code>legend_height</code>	A numeric value specifying the relative height of the legend. Default is 0.5.
<code>custom_legend</code>	A logical value indicating whether to use a custom legend. Default is TRUE.

aspect_ratio	A numeric value specifying the aspect ratio of the plot. If NULL, it's calculated automatically. Default is NULL.
switch_axis	A logical value indicating whether to switch the x and y axes. Default is FALSE.
reverse_y_ordering	A logical value indicating whether to reverse the y-axis ordering after clustering. Default is FALSE.
show_var_positions	A logical value indicating whether to show the intermediate variable positions plot. Default is FALSE. When output_file is specified with a PDF extension, both plots will be saved to a multi-page PDF if this is TRUE. A warning will be shown if show_var_positions is TRUE but the output file is not a PDF.
output_file	An optional string specifying the path to save the plot. If NULL, the plot is not saved. Default is NULL.
feature_col	Deprecated. Use x instead.
celltype_col	Deprecated. Use y instead.
contrast_col	Deprecated. Use contrast instead.

Value

A list containing the domino plot and optionally the variable positions plot.

dice_plot	<i>Dice Plot Visualization</i>
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Description

This function generates a custom plot based on three categorical variables and a group variable. It adapts to the number of unique categories in z and allows customization of various plot aesthetics.

Usage

```
dice_plot(
  data,
  x = NULL,
  y = NULL,
  z = NULL,
  group = NULL,
  group_alpha = 0.5,
  title = NULL,
  z_colors = NULL,
  group_colors = NULL,
  custom_theme = theme_minimal(),
  max_dot_size = 5,
  min_dot_size = 2,
  legend_width = 0.25,
```

```

    legend_height = 0.5,
    base_width_per_x = 0.5,
    base_height_per_y = 0.3,
    reverse_ordering = FALSE,
    cluster_by_row = TRUE,
    cluster_by_column = TRUE,
    show_legend = TRUE,
    cat_a = NULL,
    cat_b = NULL,
    cat_c = NULL,
    cat_c_colors = NULL,
    cat_b_order = NULL,
    base_width_per_cat_a = NULL,
    base_height_per_cat_b = NULL
  )

```

Arguments

<code>data</code>	A data frame containing the categorical and group variables for plotting.
<code>x</code>	A string representing the column name in <code>data</code> for the first categorical variable.
<code>y</code>	A string representing the column name in <code>data</code> for the second categorical variable.
<code>z</code>	A string representing the column name in <code>data</code> for the third categorical variable.
<code>group</code>	A string representing the column name in <code>data</code> for the grouping variable.
<code>group_alpha</code>	A numeric value for the transparency level of the group rectangles. Default is 0.5.
<code>title</code>	An optional string for the plot title. Defaults to NULL.
<code>z_colors</code>	A named vector of colors for <code>z</code> categories or a string to chose a colorbrewer palette. Defaults to NULL using the first suitable colorbrewer palette to use.
<code>group_colors</code>	A named vector of colors for the group variable or a string to chose a colorbrewer palette. Defaults to NULL using the first suitable colorbrewer palette to use.
<code>custom_theme</code>	A ggplot2 theme for customizing the plot's appearance. Defaults to <code>theme_minimal()</code> .
<code>max_dot_size</code>	Maximal dot size for the plot to scale the dot sizes.
<code>min_dot_size</code>	Minimal dot size for the plot to scale the dot sizes.
<code>legend_width</code>	Relative width of your legend. Default is 0.25.
<code>legend_height</code>	Relative width of your legend. Default is 0.5.
<code>base_width_per_x</code>	Used for dynamically scaling the width. Default is 0.5.
<code>base_height_per_y</code>	Used for dynamically scaling the height. Default is 0.3.
<code>reverse_ordering</code>	Should the cluster ordering be reversed?. Default is FALSE.
<code>cluster_by_row</code>	Cluster rows, defaults to TRUE

cluster_by_column	Cluster columns, defaults to TRUE
show_legend	Do you want to show the legend? Default is TRUE
cat_a	Deprecated. Use x instead.
cat_b	Deprecated. Use y instead.
cat_c	Deprecated. Use z instead.
cat_c_colors	Deprecated. Use z_colors instead.
cat_b_order	Deprecated. Use cluster_by_row instead. Will be removed in a future version.
base_width_per_cat_a	Deprecated. Use base_width_per_x instead.
base_height_per_cat_b	Deprecated. Use base_height_per_y instead.

Value

A ggplot object representing the dice plot.

domino_plot	<i>Domino Plot Visualization</i>
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Description

This function generates a plot to visualize gene expression levels for a given list of genes. The size of the dots can be customized, and the plot can be saved to an output file if specified.

Usage

```
domino_plot(
  data,
  gene_list,
  x = "gene",
  y = "Celltype",
  contrast = "Contrast",
  var_id = "var",
  log_fc = "avg_log2FC",
  p_val = "p_val_adj",
  min_dot_size = 1,
  max_dot_size = 5,
  spacing_factor = 3,
  logfc_colors = c(low = "blue", mid = "white", high = "red"),
  color_scale_name = "Log2 Fold Change",
  size_scale_name = "-log10(adj. p-value)",
  p_label_formatter = function(lp) sprintf("%.2g", 10^-lp),
  axis_text_size = 8,
  x_axis_text_size = NULL,
```

```

y_axis_text_size = NULL,
legend_text_size = 8,
cluster_method = "complete",
cluster_y_axis = TRUE,
cluster_var_id = TRUE,
base_width = 5,
base_height = 4,
show_legend = TRUE,
legend_width = 0.25,
legend_height = 0.5,
custom_legend = TRUE,
logfc_limits = NULL,
aspect_ratio = NULL,
switch_axis = FALSE,
reverse_y_ordering = FALSE,
show_var_positions = FALSE,
output_file = NULL,
feature_col = NULL,
celltype_col = NULL,
contrast_col = NULL,
logfc_col = NULL,
pval_col = NULL
)

```

Arguments

<code>data</code>	A data frame containing gene expression data.
<code>gene_list</code>	A character vector of gene names to include in the plot.
<code>x</code>	A string representing the column name in data for the feature variable (e.g., genes). Default is "gene".
<code>y</code>	A string representing the column name in data for the cell type variable. Default is "Celltype".
<code>contrast</code>	A string representing the column name in data for the contrast variable. Default is "Contrast".
<code>var_id</code>	A string representing the column name in data for the variable identifier. Default is "var".
<code>log_fc</code>	A string representing the column name in data for the log fold change values. Default is "avg_log2FC".
<code>p_val</code>	A string representing the column name in data for the adjusted p-values. Default is "p_val_adj".
<code>min_dot_size</code>	A numeric value indicating the minimum dot size in the plot. Default is 1.
<code>max_dot_size</code>	A numeric value indicating the maximum dot size in the plot. Default is 5.
<code>spacing_factor</code>	A numeric value indicating the spacing between gene pairs. Default is 3.
<code>logfc_colors</code>	A named vector specifying the colors for the low, mid, and high values in the color scale. Default is <code>c(low = "blue", mid = "white", high = "red")</code> .

color_scale_name	A string specifying the name of the color scale in the legend. Default is "Log2 Fold Change".
size_scale_name	A string specifying the name of the size scale in the legend. Default is "-log10(adj. p-value)".
p_label_formatter	A function used to format the size legend labels (typically for p-values). Default is <code>function(lp) sprintf("%.2g", 10^-lp)</code> .
axis_text_size	A numeric value specifying the size of the axis text. Default is 8.
x_axis_text_size	A numeric value specifying the size of the x-axis text. If NULL, uses <code>axis_text_size</code> . Default is NULL.
y_axis_text_size	A numeric value specifying the size of the y-axis text. If NULL, uses <code>axis_text_size</code> . Default is NULL.
legend_text_size	A numeric value specifying the size of the legend text. Default is 8.
cluster_method	The clustering method to use. Default is "complete".
cluster_y_axis	A logical value indicating whether to cluster the y-axis (cell types). Default is TRUE.
cluster_var_id	A logical value indicating whether to cluster the <code>var_id</code> . Default is TRUE.
base_width	A numeric value specifying the base width for saving the plot. Default is 5.
base_height	A numeric value specifying the base height for saving the plot. Default is 4.
show_legend	A logical value indicating whether to show the legend. Default is TRUE.
legend_width	A numeric value specifying the relative width of the legend. Default is 0.25.
legend_height	A numeric value specifying the relative height of the legend. Default is 0.5.
custom_legend	A logical value indicating whether to use a custom legend. Default is TRUE.
logfc_limits	A numeric vector of length 2 specifying the limits for the log fold change color scale. If NULL (default), no limits are applied.
aspect_ratio	A numeric value specifying the aspect ratio of the plot. If NULL, it's calculated automatically. Default is NULL.
switch_axis	A logical value indicating whether to switch the x and y axes. Default is FALSE.
reverse_y_ordering	A logical value indicating whether to reverse the y-axis ordering after clustering. Default is FALSE.
show_var_positions	A logical value indicating whether to show the intermediate variable positions plot. Default is FALSE. When <code>output_file</code> is specified with a PDF extension, both plots will be saved to a multi-page PDF if this is TRUE. A warning will be shown if <code>show_var_positions</code> is TRUE but the output file is not a PDF.
output_file	An optional string specifying the path to save the plot. If NULL, the plot is not saved. Default is NULL.

feature_col	Deprecated. Use x instead.
celltype_col	Deprecated. Use y instead.
contrast_col	Deprecated. Use contrast instead.
logfc_col	Deprecated. Use log_fc instead.
pval_col	Deprecated. Use p_val instead.

Value

A list containing the domino plot and optionally the variable positions plot.

geom_dice_sf	<i>Plot Dice Representations on sf Objects</i>
--------------	--

Description

Creates a ggplot2 layer that places dice representations on spatial features in an sf object. The dice values are determined by a column in the sf object.

Creates a ggplot2 layer that places dice representations on spatial features in an sf object. The dice values are determined by a column in the sf object.

Usage

```
geom_dice_sf(
  sf_data,
  dice_value_col = "dice",
  face_color = NULL,
  dice_color = "white",
  dice_size = 3,
  dot_size = NULL,
  rectangle_padding = 0.05,
  ...
)
```

```
geom_dice_sf(
  sf_data,
  dice_value_col = "dice",
  face_color = NULL,
  dice_color = "white",
  dice_size = 3,
  dot_size = NULL,
  rectangle_padding = 0.05,
  ...
)
```

Arguments

<code>sf_data</code>	An sf object containing the spatial features.
<code>dice_value_col</code>	Character. Name of the column in <code>sf_data</code> containing dice values (1-6). Default is "dice".
<code>face_color</code>	Character vector. Column names in <code>sf_data</code> containing color information for each dice dot. If NULL (default), all dots are black.
<code>dice_color</code>	Character. Background color of the dice. Default is "white".
<code>dice_size</code>	Numeric. Size of the dice. Default is 3.
<code>dot_size</code>	Numeric. Size of the dots on the dice. If NULL (default), it's calculated as 20% of <code>dice_size</code> .
<code>rectangle_padding</code>	Numeric. Padding of the rectangle around the dots, as a proportion of <code>dice_size</code> . Default is 0.05.
<code>...</code>	Additional arguments passed to <code>geom_point</code> for the dots.

Value

A list of ggplot2 layers (rectangle layer and dots layer).

A list of ggplot2 layers (rectangle layer and dots layer).

Examples

```
## Not run:
library(ggplot2)
library(sf)

# Create sample sf data with dice values
nc <- st_read(system.file("shape/nc.shp", package = "sf"))
nc$dice <- sample(1:6, nrow(nc), replace = TRUE)

# Basic plot with dice
ggplot(nc) +
  geom_sf() +
  geom_dice_sf(sf_data = nc)

# Customized dice
ggplot(nc) +
  geom_sf() +
  geom_dice_sf(sf_data = nc, dice_color = "lightblue", dice_size = 5)

## End(Not run)

## Not run:
library(ggplot2)
library(sf)

# Create sample sf data with dice values
nc <- st_read(system.file("shape/nc.shp", package = "sf"))
```

```

nc$dice <- sample(1:6, nrow(nc), replace = TRUE)

# Basic plot with dice
ggplot(nc) +
  geom_sf() +
  geom_dice_sf(sf_data = nc)

# Customized dice
ggplot(nc) +
  geom_sf() +
  geom_dice_sf(sf_data = nc, dice_color = "lightblue", dice_size = 5)

## End(Not run)

```

order_cat_b	<i>Order Category B</i>
-------------	-------------------------

Description

Determines the ordering of category B based on the counts within each group, ordered by group and count.

Usage

```
order_cat_b(data, group, cat_b, group_colors, reverse_order = FALSE)
```

Arguments

data	A data frame containing the variables.
group	The name of the column representing the grouping variable.
cat_b	The name of the column representing category B.
group_colors	A named vector of colors for each group. The names correspond to group names.
reverse_order	Reverse the ordering? Default is FALSE.

Value

A vector of category B labels ordered according to group and count.

Examples

```

library(dplyr)
data <- data.frame(
  group = rep(c("G1", "G2"), each = 5),
  cat_b = sample(LETTERS[1:3], 10, replace = TRUE)
)
group_colors <- c("G1" = "red", "G2" = "blue")
order_cat_b(data, "group", "cat_b", group_colors)

```

perform_clustering	<i>Perform Hierarchical Clustering on Category A</i>
--------------------	--

Description

Performs hierarchical clustering on category A based on the binary presence of combinations of categories B and C.

Usage

```
perform_clustering(data, cat_a, cat_b, cat_c)
```

Arguments

data	A data frame containing the variables.
cat_a	The name of the column representing category A.
cat_b	The name of the column representing category B.
cat_c	The name of the column representing category C.

Value

A vector of category A labels ordered according to the hierarchical clustering.

Examples

```
library(dplyr)
library(tidyr)
library(tibble)
data <- data.frame(
  cat_a = rep(letters[1:5], each = 4),
  cat_b = rep(LETTERS[1:2], times = 10),
  cat_c = sample(c("Var1", "Var2", "Var3"), 20, replace = TRUE)
)
perform_clustering(data, "cat_a", "cat_b", "cat_c")
```

prepare_box_data	<i>Prepare Box Data</i>
------------------	-------------------------

Description

Prepares data for plotting boxes by calculating box boundaries based on category positions.

Usage

```
prepare_box_data(data, cat_a, cat_b, group, cat_a_order, cat_b_order)
```

Arguments

data	A data frame containing the variables.
cat_a	The name of the column representing category A.
cat_b	The name of the column representing category B.
group	The name of the column representing the grouping variable.
cat_a_order	A vector specifying the order of category A.
cat_b_order	A vector specifying the order of category B.

Value

A data frame with box boundaries for plotting.

Examples

```
library(dplyr)
data <- data.frame(
  cat_a = rep(letters[1:3], each = 2),
  cat_b = rep(LETTERS[1:2], times = 3),
  group = rep(c("G1", "G2"), times = 3)
)
cat_a_order <- c("a", "b", "c")
cat_b_order <- c("A", "B")
prepare_box_data(data, "cat_a", "cat_b", "group", cat_a_order, cat_b_order)
```

prepare_plot_data	<i>Prepare Plot Data</i>
-------------------	--------------------------

Description

Prepares data for plotting by calculating positions based on provided variable positions and orders.

Usage

```
prepare_plot_data(
  data,
  cat_a,
  cat_b,
  cat_c,
  group,
  var_positions,
  cat_a_order,
  cat_b_order
)
```

Arguments

<code>data</code>	A data frame containing the variables.
<code>cat_a</code>	The name of the column representing category A.
<code>cat_b</code>	The name of the column representing category B.
<code>cat_c</code>	The name of the column representing category C.
<code>group</code>	The name of the column representing the grouping variable.
<code>var_positions</code>	A data frame with variable positions, typically output from <code>create_var_positions</code> .
<code>cat_a_order</code>	A vector specifying the order of category A.
<code>cat_b_order</code>	A vector specifying the order of category B.

Value

A data frame ready for plotting with added `x_pos` and `y_pos` columns.

Examples

```
library(dplyr)
data <- data.frame(
  cat_a = rep(letters[1:3], each = 4),
  cat_b = rep(LETTERS[1:2], times = 6),
  cat_c = rep(c("Var1", "Var2"), times = 6),
  group = rep(c("G1", "G2"), times = 6)
)
var_positions <- data.frame(
  var = c("Var1", "Var2"),
  x_offset = c(0.1, -0.1),
  y_offset = c(0.1, -0.1)
)
cat_a_order <- c("a", "b", "c")
cat_b_order <- c("A", "B")
prepare_plot_data(data, "cat_a", "cat_b", "cat_c", "group", var_positions, cat_a_order, cat_b_order)
```

```
prepare_simple_box_data
```

Prepare Simple Box Data (no grouping)

Description

Prepares data for plotting boxes without grouping by calculating box boundaries based on category positions.

Usage

```
prepare_simple_box_data(data, cat_a, cat_b, cat_a_order, cat_b_order)
```

Arguments

<code>data</code>	A data frame containing the variables.
<code>cat_a</code>	The name of the column representing category A.
<code>cat_b</code>	The name of the column representing category B.
<code>cat_a_order</code>	A vector specifying the order of category A.
<code>cat_b_order</code>	A vector specifying the order of category B.

Value

A data frame with box boundaries for plotting.

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