Package ‘ggpubr’

November 16, 2022

Type Package
Title 'ggplot2' Based Publication Ready Plots
Version 0.5.0
Date 2022-11-14
Description The 'ggplot2' package is excellent and flexible for elegant data visualization in R. However the default generated plots requires some formatting before we can send them for publication. Furthermore, to customize a 'ggplot', the syntax is opaque and this raises the level of difficulty for researchers with no advanced R programming skills. 'ggpubr' provides some easy-to-use functions for creating and customizing 'ggplot2'- based publication ready plots.
License GPL-2
LazyData TRUE
Encoding UTF-8
Depends R (>= 3.1.0), ggplot2 (>= 3.4.0)
Imports ggrepel, grid, ggsci, stats, utils, tidyr, purrr, dplyr (>= 0.7.1), cowplot, ggsignif, scales, gridExtra, glue, polynom, rlang (>= 0.4.6), rstatix (>= 0.7.1), tibble, magrittr
Suggests grDevices, knitr, RColorBrewer, gtable, testthat
URL https://rpkgs.datanovia.com/ggpubr/
BugReports https://github.com/kassambara/ggpubr/issues
RoxygenNote 7.1.0
Collate 'utilities_color.R' 'utilities_base.R' 'desc_statby.R'
'as_npc.R' 'axis_scale.R' 'background_image.R' 'bgcolor.R'
'border.R' 'compare_means.R' 'create_aes.R' 'diff_expr.R'
'facet.R' 'font.R' 'gene_citation.R' 'geom_bracket.R'
'geom_exec.R' 'utils-aes.R' 'utils_stat_test_label.R'
'geom_pwc.R' 'get_breaks.R' 'get_coord.R' 'get_legend.R'
'get_palette.R' 'gga.R' 'ggarrange.R' 'ggbarplot.R'
'ggcheck.R' 'ggcircleplot.R' 'ggdensity.R' 'ggepie.R'
'ggdonutchart.R' 'stat_conf_ellipse.R' 'stat_chull.R
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**NeedsCompilation**: no

**Author**: Alboukadel Kassambara [aut, cre]

**Maintainer**: Alboukadel Kassambara <alboukadel.kassambara@gmail.com>

**Repository**: CRAN

**Date/Publication**: 2022-11-16 12:10:54 UTC
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Description

add summary statistics onto a ggplot.

Usage

```r
add_summary(
  p,
  fun = "mean_se",
  error.plot = "pointrange",
  color = "black",
  fill = "white",
  group = 1,
  width = NULL,
  shape = 19,
  size = 1,
  linetype = 1,
  show.legend = NA,
  ci = 0.95,
  data = NULL,
  position = position_dodge(0.8)
)
```

```r
mean_se_(x, error.limit = "both")
mean_sd(x, error.limit = "both")
mean_ci(x, ci = 0.95, error.limit = "both")
mean_range(x, error.limit = "both")
median_iqr(x, error.limit = "both")
median_hilow_(x, ci = 0.95, error.limit = "both")
```
add_summary

median_q1q3(x, error.limit = "both")

median_mad(x, error.limit = "both")

median_range(x, error.limit = "both")

Arguments

p             a ggplot on which you want to add summary statistics.
fun           a function that is given the complete data and should return a data frame with variables ymin, y, and ymax. Allowed values are one of: "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", "median", "median_iqr", "median_hilow", "median_q1q3", "median_mad", "median_range".
error.plot    plot type used to visualize error. Allowed values are one of c("pointrange", "linerange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linerange", "lower_linerange"). Default value is "pointrange".
color         point or outline color.
fill           fill color. Used only when error.plot = "crossbar".
group         grouping variable. Allowed values are 1 (for one group) or a character vector specifying the name of the grouping variable. Used only for adding statistical summary per group.
width         numeric value between 0 and 1 specifying bar or box width. Example width = 0.8. Used only when error.plot is one of c("crossbar", "errorbar").
shape         point shape. Allowed values can be displayed using the function show_point_shapes().
size          numeric value in [0-1] specifying point and line size.
linetype      line type.
show.legend   logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
ci            the percent range of the confidence interval (default is 0.95).
data          a data.frame to be displayed. If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot.
position      position adjustment, either as a string, or the result of a call to a position adjustment function. Used to adjust position for multiple groups.
x             a numeric vector.
error.limit   allowed values are one of ("both", "lower", "upper", "none") specifying whether to plot the lower and/or the upper limits of error interval.

Functions

- add_summary: add summary statistics onto a ggplot.
- mean_se_: returns the mean and the error limits defined by the standard error. We used the name mean_se_() to avoid masking mean_se().
• **mean_sd**: returns the mean and the error limits defined by the standard deviation.
• **mean_ci**: returns the mean and the error limits defined by the confidence interval.
• **mean_range**: returns the mean and the error limits defined by the range = max - min.
• **median_iqr**: returns the median and the error limits defined by the interquartile range.
• **median_hilow_**: computes the sample median and a selected pair of outer quantiles having equal tail areas. This function is a reformatted version of Hmisc::smedian.hilow(). The confidence limits are computed as follow: lower.limits = (1-ci)/2 percentiles; upper.limits = (1+ci)/2 percentiles. By default (ci = 0.95), the 2.5th and the 97.5th percentiles are used as the lower and the upper confidence limits, respectively. If you want to use the 25th and the 75th percentiles as the confidence limits, then specify ci = 0.5 or use the function median_q1q3().
• **median_q1q3**: computes the sample median and the 25th and 75th percentiles. Wrapper around the function median_hilow() using ci = 0.5.
• **median_mad**: returns the median and the error limits defined by the median absolute deviation.
• **median_range**: returns the median and the error limits defined by the range = max - min.

**Examples**

```r
# Basic violin plot
p <- ggviolin(ToothGrowth, x = "dose", y = "len", add = "none")
p

# Add mean_sd
add_summary(p, "mean_sd")
```

### annotate_figure

**Annotate Arranged Figure**

**Description**

Annotate figures including: i) ggplots, ii) arranged ggplots from ggarrange(), grid.arrange() and plot_grid().

**Usage**

```r
annotate_figure(
p,
  top = NULL,
  bottom = NULL,
  left = NULL,
  right = NULL,
  fig.lab = NULL,
  fig.lab.pos = c("top.left", "top", "top.right", "bottom.left", "bottom",
```
annotate_figure

    "bottom.right"),
    fig.lab.size,
    fig.lab.face
}

Arguments

  p  (arranged) ggplots.
  top, bottom, left, right
    optional string, or grob.
  fig.lab  figure label (e.g.: "Figure 1").
  fig.lab.pos  position of the figure label, can be one of "top.left", "top", "top.right", "bottom.left", "bottom", "bottom.right". Default is "top.left".
  fig.lab.size  optional size of the figure label.
  fig.lab.face  optional font face of the figure label. Allowed values include: "plain", "bold", "italic", "bold.italic".

Author(s)

Alboukadel Kassambara <alboukadel.kassambara@gmail.com>

See Also

  ggarrange()

Examples

data("ToothGrowth")
df <- ToothGrowth
df$dose <- as.factor(df$dose)

# Create some plots
# ::::::::::::::::::::::::::::::::::::::::::::::::::
# Box plot
bxp <- ggboxplot(df, x = "dose", y = "len",
                 color = "dose", palette = "jco")
# Dot plot
dp <- ggdotplot(df, x = "dose", y = "len",
                color = "dose", palette = "jco")
# Density plot
dens <- ggdensity(df, x = "len", fill = "dose", palette = "jco")

# Arrange and annotate
# ::::::::::::::::::::::::::::::::::::::::::::::::::
figure <- ggarrange(bxp, dp, dens, ncol = 2, nrow = 2)
annotate_figure(figure,
    top = text_grob("Visualizing Tooth Growth", color = "red", face = "bold", size = 14),
    bottom = text_grob("Data source: \nToothGrowth data set", color = "blue",
                      hjust = 1, x = 1, face = "italic", size = 10),
    left = text_grob("Figure arranged using ggpubr", color = "green", rot = 90),
    ... )
as_ggplot  Storing grid.arrange() arrangeGrob() and plots

Description

Transform the output of arrangeGrob() and grid.arrange() to a an object of class ggplot.

Usage

as_ggplot(x)

Arguments

x  an object of class gtable or grob as returned by the functions arrangeGrob() and grid.arrange().

Value

an object of class ggplot.

Examples

# Create some plots
bxp <- ggboxplot(iris, x = "Species", y = "Sepal.Length")
vp <- ggviolin(iris, x = "Species", y = "Sepal.Length",
               add = "mean_sd")

# Arrange the plots in one page
# Returns a gtable (grob) object
library(gridExtra)
gt <- arrangeGrob(bxp, vp, ncol = 2)

# Transform to a ggplot and print
as_ggplot(gt)
as_npc  

Convert Character Coordinates into Normalized Parent Coordinates (NPC)

Description

Convert character coordinates to npc units and shift positions to avoid overlaps when grouping is active. If numeric validate npc values.

Usage

```r
as_npc(
  value,
  group = 1L,
  step = 0.1,
  margin.npc = 0.05,
  axis = c("xy", "x", "y")
)
```

```r
as_npcx(value, group = 1L, step = 0.1, margin.npc = 0.05)
```

```r
as_npcy(value, group = 1L, step = 0.1, margin.npc = 0.05)
```

Arguments

- `value` numeric (in [0-1]) or character vector of coordinates. If character, should be one of c("right", "left", "bottom", "top", "center", "centre", "middle").
- `group` integer ggplot’s group id. Used to shift coordinates to avoid overlaps.
- `step` numeric value in [0-1]. The step size for shifting coordinates in npc units. Considered as horizontal step for x-axis and vertical step for y-axis. For y-axis, the step value can be negative to reverse the order of groups.
- `margin.npc` numeric [0-1] The margin added towards the nearest plotting area edge when converting character coordinates into npc.
- `axis` the concerned axis. Should be one of c("xy", "x", "y").

Details

the `as_npc()` function is an adaptation from `ggpmisc::compute_npc()`.

Value

A numeric vector with values in the range [0-1] representing npc coordinates.
Functions

• **as_npc**: converts x or y coordinate values into npc. Input values should be numeric or one of the following values `c( 'right', 'left', 'bottom', 'top', 'center', 'centre', 'middle')`.

• **as_npcx**: converts x coordinate values into npc. Input values should be numeric or one of the following values `c( 'right', 'left', 'center', 'centre', 'middle')`. Wrapper around `as_npc(axis = "x")`.

• **as_npcy**: converts y coordinate values into npc. Input values should be numeric or one of the following values `c( 'bottom', 'top', 'center', 'centre', 'middle')`. Wrapper around `as_npc(axis = "y")`.

See Also

`npc_to_data_coord`, `get_coord`.

Examples

```r
as_npc(c("left", "right"))
as_npc(c("top", "right"))
```

### Description

Change axis scale.

• **xscale**: change x axis scale.

• **yscale**: change y axis scale.

#### Usage

```r
xscale(.scale, .format = FALSE)
yscale(.scale, .format = FALSE)
```

#### Arguments

- **.scale**: axis scale. Allowed values are one of `c("none", "log2", "log10", "sqrt", "percent", "dollar", "scientific")`; e.g.: `.scale = "log2"`.

- **.format**: logical value. If TRUE, axis tick mark labels will be formatted when `.scale = "log2"` or "log10".
Examples

# Basic scatter plots
data(cars)
p <- ggscatter(cars, x = "speed", y = "dist")
p
# Set log scale
p + yscale("log2", .format = TRUE)

Description

Add background image to ggplot2.

Usage

background_image(raster.img)

Arguments

raster.img  raster object to display, as returned by the function readPNG() [in png package] and readJPEG() [in jpeg package].

Author(s)

Alboukadel Kassambara <alboukadel.kassambara@gmail.com>

Examples

## Not run:
install.packages("png")

# Import the image
ing.file <- system.file(file.path("images", "background-image.png"),
                          package = "ggpubr")
ing <- png::readPNG(img.file)

# Plot with background image
ggplot(iris, aes(Species, Sepal.Length))+
background_image(img)+
geom_boxplot(aes(fill = Species), color = "white")+
fill_palette("jco")

## End(Not run)
bgcolor

Change ggplot Panel Background Color

Description

Change ggplot panel background color.

Usage

bgcolor(color)

Arguments

color background color.

See Also

border().

Examples

# Load data
data("ToothGrowth")
df <- ToothGrowth

# Basic plot
p <- ggboxplot(df, x = "dose", y = "len")

# Change panel background color
p +
   bgcolor("#BFD5E3")+
   border("#BFD5E3")

border

Set ggplot Panel Border Line

Description

Change or set ggplot panel border.

Usage

border(color = "black", size = 0.8, linetype = NULL)
Arguments

- **color**: border line color.
- **size**: numeric value specifying border line size.
- **linetype**: line type. An integer (0:8), a name (blank, solid, dashed, dotted, dotdash, long-dash, twodash). See `show_line_types`.

Examples

```r
# Load data
data("ToothGrowth")
df <- ToothGrowth

# Basic plot
p <- ggboxplot(df, x = "dose", y = "len")
p

# Add border
p + border()
```

```
c assemble means  Comparison of Means

Description

Performs one or multiple mean comparisons.

Usage

```r
compare_means(
  formula,
  data,
  method = "wilcoxon.test",
  paired = FALSE,
  group.by = NULL,
  ref.group = NULL,
  symnum.args = list(),
  p.adjust.method = "holm",
  ...
)
```

Arguments

- **formula**: a formula of the form `x ~ group` where `x` is a numeric variable giving the data values and `group` is a factor with one or multiple levels giving the corresponding groups. For example, `formula = TP53 ~ cancer_group`.

  It's also possible to perform the test for multiple response variables at the same time. For example, `formula = c(TP53, PTEN) ~ cancer_group`. 
compare_means

data a data.frame containing the variables in the formula.

method the type of test. Default is wilcox.test. Allowed values include:

- t.test (parametric) and wilcox.test (non-parametric). Perform comparison between two groups of samples. If the grouping variable contains more than two levels, then a pairwise comparison is performed.
- anova (parametric) and kruskal.test (non-parametric). Perform one-way ANOVA test comparing multiple groups.

paired a logical indicating whether you want a paired test. Used only in t.test and in wilcox.test.

group.by a character vector containing the name of grouping variables.

ref.group a character string specifying the reference group. If specified, for a given grouping variable, each of the group levels will be compared to the reference group (i.e. control group).

ref.group can be also ".all.". In this case, each of the grouping variable levels is compared to all (i.e. basemean).

symnum.args a list of arguments to pass to the function symnum for symbolic number coding of p-values. For example, symnum.args <- list(cutpoints = c(0, 0.0001, 0.001, 0.01, 0.05, Inf), symbols = c("****", "***", "+", "ns").

In other words, we use the following convention for symbols indicating statistical significance:

- ns: p > 0.05
- *: p <= 0.05
- **: p <= 0.01
- ***: p <= 0.001
- ****: p <= 0.0001

p.adjust.method method for adjusting p values (see p.adjust). Has impact only in a situation, where multiple pairwise tests are performed; or when there are multiple grouping variables. Allowed values include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". If you don’t want to adjust the p value (not recommended), use p.adjust.method = "none".

Note that, when the formula contains multiple variables, the p-value adjustment is done independently for each variable.

Value

return a data frame with the following columns:

- .y.: the y variable used in the test.
- group1,group2: the compared groups in the pairwise tests. Available only when method = "t.test" or method = "wilcox.test".
- p: the p-value.
- p.adj: the adjusted p-value. Default for p.adjust.method = "holm".
• \texttt{p.format}: the formatted p-value.
• \texttt{p.signif}: the significance level.
• \texttt{method}: the statistical test used to compare groups.

Examples

# Load data
#:::::::::::::::::::::::::::::::::::::::
data("ToothGrowth")
df <- ToothGrowth

# One-sample test
#:::::::::::::::::::::::::::::::::::::::::
compare_means(len ~ 1, df, mu = 0)

# Two-samples unpaired test
#:::::::::::::::::::::::::::::::::::::::::
compare_means(len ~ supp, df)

# Two-samples paired test
#:::::::::::::::::::::::::::::::::::::::::
compare_means(len ~ supp, df, paired = TRUE)

# Compare supp levels after grouping the data by "dose"
#:::::::::::::::::::::::::::::::::::::::::
compare_means(len ~ supp, df, group.by = "dose")

# pairwise comparisons
#:::::::::::::::::::::::::::::::::::::::::
# As dose contains more than two levels =>
# pairwise test is automatically performed.
compare_means(len ~ dose, df)

# Comparison against reference group
#:::::::::::::::::::::::::::::::::::::::::
compare_means(len ~ dose, df, ref.group = "0.5")

# Comparison against all
#:::::::::::::::::::::::::::::::::::::::::
compare_means(len ~ dose, df, ref.group = ".all.")

# Anova and kruskal.test
#:::::::::::::::::::::::::::::::::::::::::
compare_means(len ~ dose, df, method = "anova")
compare_means(len ~ dose, df, method = "kruskal.test")

---
create_aes | Create Aes Mapping from a List
---
Description
Create aes mapping to make programming easy with ggplot2.

Usage
create_aes(.list, parse = TRUE)

Arguments

.list a list of aesthetic arguments; for example .list = list(x = "dose", y = "len", color = "dose").
parse logical. If TRUE, parse the input as an expression.

Examples

# Simple aes creation
create_aes(list(x = "Sepal.Length", y = "Petal.Length" ))

# Parse an expression
x <- "log2(Sepal.Length)"
y <- "log2(Petal.Length)"
create_aes(list(x = x, y = y ), parse = TRUE)

# Create a ggplot
mapping <- create_aes(list(x = x, y = y ), parse = TRUE)
ggplot(iris, mapping) + geom_point()

desc_statby

Descriptive statistics by groups

Description
Computes descriptive statistics by groups for a measure variable.

Usage
desc_statby(data, measure.var, grps, ci = 0.95)

Arguments

data a data frame.
measure.var the name of a column containing the variable to be summarized.
grps a character vector containing grouping variables; e.g.: grps = c("grp1", "grp2")
ci the percent range of the confidence interval (default is 0.95).
Value

A data frame containing descriptive statistics, such as:

- **length**: the number of elements in each group
- **min**: minimum
- **max**: maximum
- **median**: median
- **mean**: mean
- **iqr**: interquartile range
- **mad**: median absolute deviation (see ?MAD)
- **sd**: standard deviation of the mean
- **se**: standard error of the mean
- **ci**: confidence interval of the mean
- **range**: the range = max - min
- **cv**: coefficient of variation, sd/mean
- **var**: variance, sd^2

Examples

```r
# Load data
data("ToothGrowth")

# Descriptive statistics
res <- desc_statby(ToothGrowth, measure.var = "len",
                   grps = c("dose", " supp"))
head(res[, 1:10])
```

---

**diff_express**  
* Differential gene expression analysis results

**Description**

Differential gene expression analysis results obtained from comparing the RNAseq data of two different cell populations using DESeq2

**Usage**

```r
data("diff_express")
```
### Format

A data frame with 36028 rows and 5 columns.

- **name** gene names
- **baseMean** mean expression signal across all samples
- **log2FoldChange** log2 fold change
- **padj** Adjusted p-value
- **detection_call** a numeric vector specifying whether the genes is expressed (value = 1) or not (value = 0).

### Examples

```r
data(diff_express)

# Default plot
ggmaplot(diff_express, main = expression("Group 1" %->% "Group 2"),
         fdr = 0.05, fc = 2, size = 0.4,
         palette = c("#B31B21", "#1465AC", "darkgray"),
         genenames = as.vector(diff_express$name),
         legend = "top", top = 20,
         font.label = c("bold", 11),
         font.legend = "bold",
         font.main = "bold",
         ggtheme = ggplot2::theme_minimal())

# Add rectangle around labels
ggmaplot(diff_express, main = expression("Group 1" %->% "Group 2"),
         fdr = 0.05, fc = 2, size = 0.4,
         palette = c("#B31B21", "#1465AC", "darkgray"),
         genenames = as.vector(diff_express$name),
         legend = "top", top = 20,
         font.label = c("bold", 11), label.rectangle = TRUE,
         font.legend = "bold",
         font.main = "bold",
         ggtheme = ggplot2::theme_minimal())
```

---

**facet**

*Facet a ggplot into Multiple Panels*

---

**Description**

Create multi-panel plots of a data set grouped by one or two grouping variables. Wrapper around `facet_wrap`
facet

Usage

```r
facet(
  p,
  facet.by,
  nrow = NULL,
  ncol = NULL,
  scales = "fixed",
  short.panel.labs = TRUE,
  labeller = "label_value",
  panel.labs = NULL,
  panel.labs.background = list(color = NULL, fill = NULL),
  panel.labs.font = list(face = NULL, color = NULL, size = NULL, angle = NULL),
  panel.labs.font.x = panel.labs.font,
  panel.labs.font.y = panel.labs.font,
  strip.position = "top",
  ...
)
```

Arguments

- **p**: a `ggplot`
- **facet.by**: character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
- **nrow, ncol**: Number of rows and columns in the panel. Used only when the data is faceted by one grouping variable.
- **scales**: should axis scales of panels be fixed ("fixed", the default), free ("free"), or free in one dimension ("free_x", "free_y").
- **short.panel.labs**: logical value. Default is TRUE. If TRUE, create short labels for panels by omitting variable names; in other words panels will be labelled only by variable grouping levels.
- **labeller**: Character vector. An alternative to the argument `short.panel.labs`. Possible values are one of "label_both" (panel labelled by both grouping variable names and levels) and "label_value" (panel labelled with only grouping levels).
- **panel.labs**: a list of one or two character vectors to modify facet panel labels. For example, `panel.labs = list(sex = c("Male", "Female"))` specifies the labels for the "sex" variable. For two grouping variables, you can use for example `panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))`.
- **panel.labs.background**: a list to customize the background of panel labels. Should contain the combination of the following elements:
  - `color`, `linetype`, `size`: background line color, type and size
  - `fill`: background fill color.

For example, `panel.labs.background = list(color = "blue", fill = "pink", linetype = "dashed", size = 0.5)`. 
font

panel.labs.font
a list of aesthetics indicating the size (e.g.: 14), the face/style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") and the orientation angle (e.g.: 45) of panel labels.

panel.labs.font.x, panel.labs.font.y
same as panel.labs.font but for only x and y direction, respectively.

strip.position (used only in facet_wrap()). By default, the labels are displayed on the top of the plot. Using strip.position it is possible to place the labels on either of the four sides by setting strip.position = c("top", "bottom", "left", "right")

Examples

```r
p <- ggboxplot(ToothGrowth, x = "dose", y = "len",
               color = "supp")
print(p)

facet(p, facet.by = "supp")

# Customize
facet(p + theme_bw(), facet.by = "supp",
      short.panel.labs = FALSE,  # Allow long labels in panels
      panel.labs.background = list(fill = "steelblue", color = "steelblue")
)
```

Arguments

object character string specifying the plot components. Allowed values include:
- "title" for the main title
- "subtitle" for the plot subtitle
- "caption" for the plot caption
- "legend.title" for the legend title
- "legend.text" for the legend text
- "x", "xlab", or "x.title" for x axis label

Description

Change the appearance of the main title, subtitle, caption, axis labels and text, as well as the legend title and texts. Wrapper around element_text().

Usage

```r
font(object, size = NULL, color = NULL, face = NULL, family = NULL, ...)
```

Examples

```r
p <- ggboxplot(ToothGrowth, x = "dose", y = "len",
               color = "supp")
print(p)

facet(p, facet.by = "supp")

# Customize
facet(p + theme_bw(), facet.by = "supp",
      short.panel.labs = FALSE,  # Allow long labels in panels
      panel.labs.background = list(fill = "steelblue", color = "steelblue")
)
```
• "y", "ylab", or "y.title" for y axis label
• "xy", "xylab", "xy.title" or "axis.title" for both x and y axis labels
• "x.text" for x axis texts (x axis tick labels)
• "y.text" for y axis texts (y axis tick labels)
• "xy.text" or "axis.text" for both x and y axis texts

size numeric value specifying the font size, (e.g.: size = 12).
color character string specifying the font color, (e.g.: color = "red").
face the font face or style. Allowed values include one of "plain", "bold", "italic", "bold.italic", (e.g.: face = "bold.italic").
family the font family.

Examples

# Load data
data("ToothGrowth")

# Basic plot
p <- ggboxplot(ToothGrowth, x = "dose", y = "len", color = "dose",
title = "Box Plot created with ggpubr",
subtitle = "Length by dose",
caption = "Source: ggpubr",
xlab = "Dose (mg)", ylab = "Teeth length")
p

# Change the appearance of titles and labels
p +
  font("title", size = 14, color = "red", face = "bold.italic")+
  font("subtitle", size = 10, color = "orange")+
  font("caption", size = 10, color = "orange")+
  font("xlab", size = 12, color = "blue")+
  font("ylab", size = 12, color = "#993333")+
  font("xy.text", size = 12, color = "gray", face = "bold")

# Change the appearance of legend title and texts
p +
  font("legend.title", color = "blue", face = "bold")+
  font("legend.text", color = "red")

---

gene_citation Gene Citation Index

Description

Contains the mean citation index of 66 genes obtained by assessing PubMed abstracts and annotations using two key words i) Gene name + b cell differentiation and ii) Gene name + plasma cell differentiation.
Usage

```r
data("gene_citation")
```

Format

A data frame with 66 rows and 2 columns.

- `gene`  gene names
- `citation_index`  mean citation index

Examples

```r
data(gene_citation)
# Some key genes of interest to be highlighted
# Density distribution
ggdensity(gene_citation, x = "citation_index", y = ".count.", xlab = "Number of citation", ylab = "Number of genes", fill = "lightgray", color = "black", label = "gene", label.select = key.gns, repel = TRUE, font.label = list(color= "citation_index"), xticks.by = 20, # Break x ticks by 20 gradient.cols = c("blue", "red"), legend = "bottom", legend.title = "" # Hide legend title)
```

### geom_exec

**Execute ggplot2 functions**

**Description**

A helper function used by ggpubr functions to execute any geom_* functions in ggplot2. Useful only when you want to call a geom_* function without carrying about the arguments to put in aes().

**Usage**

```r
geom_exec(geomfunc = NULL, data = NULL, position = NULL, ...)
```
**get_breaks**

**Arguments**

- **geomfunc**: a ggplot2 function (e.g.: geom_point)
- **data**: a data frame to be used for mapping
- **position**: Position adjustment, either as a string, or the result of a call to a position adjustment function.
- **...**: arguments accepted by the function

**Value**

return a plot if geomfunc!=Null or a list(option, mapping) if geomfunc = NULL.

**Examples**

```r
## Not run:
ggplot() + geom_exec(geom_point, data = mtcars,
  x = "mpg", y = "wt", size = "cyl", color = "cyl")
## End(Not run)
```

---

**get_breaks**

**Easy Break Creation for Numeric Axes**

**Description**

Creates breaks for numeric axes to be used in the functions `scale_x_continuous()` and `scale_y_continuous()`. Can be used to increase the number of x and y ticks by specifying the option `n`. It’s also possible to control axis breaks by specifying a step between ticks. For example, if by = 5, a tick mark is shown on every 5.

**Usage**

`get_breaks(n = NULL, by = NULL, from = NULL, to = NULL)`

**Arguments**

- **n**: number of breaks.
- **by**: number: the step between breaks.
- **from**: the starting value of breaks. By default, 0 is used for positive variables
- **to**: the end values of breaks. This corresponds generally to the maximum limit of the axis.

**Value**

a break function
Examples

# Generate 5 breaks for a variable x
get_breaks(n = 5)(x = 1:100)

# Generate breaks using an increasing step
get_breaks(by = 10)(x = 1:100)

# Combine with ggplot scale_xx functions
library(ggplot2)

# Create a basic plot
p <- ggscatter(mtcars, x = "wt", y = "mpg")
p

# Increase the number of ticks
p +
  scale_x_continuous(breaks = get_breaks(n = 10)) +
  scale_y_continuous(breaks = get_breaks(n = 10))

# Set ticks according to a specific step, starting from 0
p + scale_x_continuous(
  breaks = get_breaks(by = 1.5, from = 0),
  limits = c(0, 6)
) +
  scale_y_continuous(
    breaks = get_breaks(by = 10, from = 0),
    limits = c(0, 40)
  )

get_coord

Checks and Returns Data Coordinates from Multiple Input Options

Description

Checks and returns selected coordinates from multiple input options, which can be either data (x-y) coordinates or npc (normalized parent coordinates).

Helper function internally used in ggpubr function to guess the type of coordinates specified by the user. For example, in the function stat_cor(), users can specify either the option label.x (data coordinates) or label.x.npc (npc coordinates); those coordinates are passed to get_coord(), which will make some checking and then return a unique coordinates for the label position.

Usage

get_coord(
  group = 1L,
  data.ranges = NULL,
  coord = NULL,
)
get_coord

npc = "left",
step = 0.1,
margin.npc = 0.05
)

Arguments

- `group` integer `ggplot`'s group id. Used to shift coordinates to avoid overlaps.
- `data.ranges` a numeric vector of length 2 containing the data ranges (minimum and the maximum). Should be specified only when `coord = NULL` and `npc` is specified. Used to convert `npc` to data coordinates. Considered only when the argument `npc` is specified.
- `coord` data coordinates (i.e., either x or y coordinates).
- `npc` numeric (in [0-1]) or character vector of coordinates. If character, should be one of c('right', 'left', 'bottom', 'top', 'center', 'centre', 'middle'). Note that, the `data.ranges`, `step` and `margin.npc`, arguments are considered only when `npc` is specified. The option `npc` is ignored when the argument `coord` is specified.
- `step` numeric value in [0-1]. The step size for shifting coordinates in `npc` units. Considered as horizontal step for x-axis and vertical step for y-axis. For y-axis, the step value can be negative to reverse the order of groups.
- `margin.npc` numeric [0-1] The margin added towards the nearest plotting area edge when converting character coordinates into `npc`.

Value

a numeric vector representing data coordinates.

See Also

- `as_npc`, `npc_to_data_coord`.

Examples

- If `npc` is specified, it is converted into data coordinates
  ```r
  get_coord(data.ranges = c(2, 20), npc = "left")
  get_coord(data.ranges = c(2, 20), npc = 0.1)
  ```

- When `coord` is specified, no transformation is performed because this is assumed to be a data coordinate
  ```r
  get_coord(coord = 5)
  ```

- For grouped plots
  ```r
  res_top <- get_coord(
      data.ranges = c(4.2, 36.4), group = c(1, 2, 3),
      npc = "top", step = -0.1, margin.npc = 0
  )
  res_top
  ```
**get_legend**  
*Extract Legends from a ggplot object*

**Description**

Extract the legend labels from a ggplot object.

**Usage**

```r
get_legend(p, position = NULL)
```

**Arguments**

- `p`:
  - an object of class `ggplot` or a list of `ggplots`. If `p` is a list, only the first legend is returned.

- `position`:
  - character specifying legend position. Allowed values are one of c("top", "bottom", "left", "right", "none"). To remove the legend use `legend = "none"`.

**Value**

an object of class `gtable`.

**Examples**

```r
# Create a scatter plot
p <- ggscatter(iris, x = "Sepal.Length", y = "Sepal.Width",
               color = "Species", palette = "jco",
               ggtheme = theme_minimal())

# Extract the legend. Returns a gtable
leg <- get_legend(p)

# Convert to a ggplot and print
as_ggplot(leg)
```

**get_palette**  
*Generate Color Palettes*

**Description**

Generate a palette of k colors from ggsci palettes, RColorBrewer palettes and custom color palettes. Useful to extend RColorBrewer and ggsci to support more colors.
get_palette

Usage

get_palette(palette = "default", k)

Arguments

palette   Color palette. Allowed values include:

- **Grey color palettes**: "grey" or "gray"
- **RColorBrewer palettes**, see brewer.pal and details section. Examples of palette names include: "RdBu", "Blues", "Dark2", "Set2", ...
- **Custom color palettes**. For example, palette = c("#00AFBB", "#E7B800", "#FC4E07");
- **ggsci scientific journal palettes**, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".

k     the number of colors to generate.

Details

**RColorBrewer palettes**: To display all available color palettes, type this in R:RColorBrewer::display.brewer.all().

Color palette names include:

- **Sequential palettes**, suited to ordered data that progress from low to high. Palette names include: Blues BuGn BuPu GnBu Greens Greys Oranges OrRd PuBu PuBuGn PuRd Purples RdPu Reds YlGn YlGnBu YlOrBr YlOrRd.
- **Diverging palettes**: Gradient colors. Names include: BrBG PiYG PRGn PuOr RdBu RdGy RdYlBu RdYlGn Spectral.
- **Qualitative palettes**: Best suited to representing nominal or categorical data. Names include: Accent, Dark2, Paired, Pastel1, Pastel2, Set1, Set2, Set3.

Value

Returns a vector of color palettes.

Examples

```r
data("iris")
iris$Species2 <- factor(rep(c(1:10), each = 15))

# Generate a gradient of 10 colors
ggscatter(iris, x = "Sepal.Length", y = "Petal.Length",
color = "Species2",
palette = get_palette(c("#00AFBB", "#E7B800", "#FC4E07"), 10))

# Scatter plot with default color palette
ggscatter(iris, x = "Sepal.Length", y = "Petal.Length",
color = "Species")

# RColorBrewer color palettes
ggscatter(iris, x = "Sepal.Length", y = "Petal.Length",
```
color = "Species", palette = get_palette("Dark2", 3))

# ggsci color palettes
ggscatter(iris, x = "Sepal.Length", y = "Petal.Length",
          color = "Species", palette = get_palette("npg", 3))

# Custom color palette
ggscatter(iris, x = "Sepal.Length", y = "Petal.Length",
          color = "Species",
          palette = c("#00AFBB", "#E7B800", "#FC4E07"))

# Or use this
ggscatter(iris, x = "Sepal.Length", y = "Petal.Length",
          color = "Species",
          palette = get_palette(c("#00AFBB", "#FC4E07"), 3))

ggadd

Add Summary Statistics or a Geom onto a ggplot

Description

Add summary statistics or a geometry onto a ggplot.

Usage

ggadd(
  p,
  add = NULL,
  color = "black",
  fill = "white",
  group = 1,
  width = 1,
  shape = 19,
  size = NULL,
  alpha = 1,
  jitter = 0.2,
  binwidth = NULL,
  dotsize = size,
  linetype = 1,
  show.legend = NA,
  error.plot = "pointrange",
  ci = 0.95,
  data = NULL,
  position = position_dodge(0.8),
)
Arguments

- **p**: a ggplot
- **add**: character vector specifying other plot elements to be added. Allowed values are one or the combination of: "none", "dotplot", "jitter", "boxplot", "point", "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", "median", "median_iqr", "median_hilow", "median_q1q3", "median_mad", "median_range".
- **color**: point or outline color.
- **fill**: fill color. Used only when error.plot = "crossbar".
- **group**: grouping variable. Allowed values are 1 (for one group) or a character vector specifying the name of the grouping variable. Used only for adding statistical summary per group.
- **width**: numeric value between 0 and 1 specifying bar or box width. Example width = 0.8. Used only when error.plot is one of c("crossbar", "errorbar").
- **shape**: point shape. Allowed values can be displayed using the function `show_point_shapes()`.
- **size**: numeric value in [0-1] specifying point and line size.
- **alpha**: numeric value specifying fill color transparency. Value should be in [0, 1], where 0 is full transparency and 1 is no transparency.
- **jitter**: a numeric value specifying the amount of jittering. Used only when add contains "jitter".
- **binwidth**: numeric value specifying bin width. Use value between 0 and 1 when you have a strong dense dotplot. For example binwidth = 0.2. Used only when add contains "dotplot".
- **dotsize**: as size but applied only to dotplot.
- **linetype**: line type.
- **show.legend**: logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
- **error.plot**: plot type used to visualize error. Allowed values are one of c("pointrange", "linerange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linerange", "lower_linerange"). Default value is "pointrange".
- **ci**: the percent range of the confidence interval (default is 0.95).
- **data**: a data.frame to be displayed. If NULL, the default, the data is inherited from the plot data as specified in the call to `ggplot`.
- **position**: position adjustment, either as a string, or the result of a call to a position adjustment function. Used to adjust position for multiple groups.
- **p_geom**: the geometry of the main plot. Ex: p_geom = "geom_line". If NULL, the geometry is extracted from p. Used only by `ggline()`.
Examples

```r
# Basic violin plot
data("ToothGrowth")
p <- ggviolin(ToothGrowth, x = "dose", y = "len", add = "none")

# Add mean +/- SD and jitter points
p %>% ggadd(c("mean_sd", "jitter"), color = "dose")

# Add box plot
p %>% ggadd(c("boxplot", "jitter"), color = "dose")
```

---

**ggarrange**

Arrange multiple ggplots

**Description**

Arrange multiple ggplots on the same page. Wrapper around `plot_grid()`. Can arrange multiple ggplots over multiple pages, compared to the standard `plot_grid()`. Can also create a common unique legend for multiple plots.

**Usage**

```r
ggarrange(
  ...,
  plotlist = NULL,
  ncol = NULL,
  nrow = NULL,
  labels = NULL,
  label.x = 0,
  label.y = 1,
  hjust = -0.5,
  vjust = 1.5,
  font.label = list(size = 14, color = "black", face = "bold", family = NULL),
  align = c("none", "h", "v", "hv"),
  widths = 1,
  heights = 1,
  legend = NULL,
  common.legend = FALSE,
  legend.grob = NULL
)
```

**Arguments**

- `...`: list of plots to be arranged into the grid. The plots can be either ggplot2 plot objects or arbitrary gtables.
- `plotlist` (optional) list of plots to display.
ggarrange

ncol (optional) number of columns in the plot grid.
nrow (optional) number of rows in the plot grid.
labels (optional) list of labels to be added to the plots. You can also set labels="AUTO" to auto-generate upper-case labels or labels="auto" to auto-generate lower-case labels.
label.x (optional) Single value or vector of x positions for plot labels, relative to each subplot. Defaults to 0 for all labels. (Each label is placed all the way to the left of each plot.)
label.y (optional) Single value or vector of y positions for plot labels, relative to each subplot. Defaults to 1 for all labels. (Each label is placed all the way to the top of each plot.)
hjust Adjusts the horizontal position of each label. More negative values move the label further to the right on the plot canvas. Can be a single value (applied to all labels) or a vector of values (one for each label). Default is -0.5.
vjust Adjusts the vertical position of each label. More positive values move the label further down on the plot canvas. Can be a single value (applied to all labels) or a vector of values (one for each label). Default is 1.5.
font.label a list of arguments for customizing labels. Allowed values are the combination of the following elements: size (e.g.: 14), face (e.g.: "plain", "bold", "italic", "bold.italic"), color (e.g.: "red") and family. For example font.label = list(size = 14, face = "bold", color ="red").
align (optional) Specifies whether graphs in the grid should be horizontally ("h") or vertically ("v") aligned. Options are "none" (default), "hv" (align in both directions), "h", and "v".
widths (optional) numerical vector of relative columns widths. For example, in a two-column grid, widths = c(2, 1) would make the first column twice as wide as the second column.
heights same as widths but for column heights.
legend character specifying legend position. Allowed values are one of c("top", "bottom", "left", "right", "none"). To remove the legend use legend = "none".
common.legend logical value. Default is FALSE. If TRUE, a common unique legend will be created for arranged plots.
legend.grob a legend grob as returned by the function get_legend(). If provided, it will be used as the common legend.

Value

return an object of class ggarrange, which is a ggplot or a list of ggplot.

Author(s)

Alboukadel Kassambara <alboukadel.kassambara@gmail.com>

See Also

annotate_figure()
Examples

data("ToothGrowth")
df <- ToothGrowth
df$dose <- as.factor(df$dose)

# Create some plots
# ::::::::::::::::::::::::::::::::::::::::::::::::::
# Box plot
bxp <- ggboxplot(df, x = "dose", y = "len",
                 color = "dose", palette = "jco")
# Dot plot
dp <- ggdotplot(df, x = "dose", y = "len",
                color = "dose", palette = "jco")
# Density plot
dens <- ggdensity(df, x = "len", fill = "dose", palette = "jco")

# Arrange
# ::::::::::::::::::::::::::::::::::::::::::::::::::
ggarrange(bxp, dp, dens, ncol = 2, nrow = 2)
# Use a common legend for multiple plots
ggarrange(bxp, dp, common.legend = TRUE)

---

**ggballoonplot**  
**Ballon plot**

Description

Plot a graphical matrix where each cell contains a dot whose size reflects the relative magnitude of the corresponding component. Useful to visualize contingency table formed by two categorical variables.

Usage

```r
ggballoonplot(
  data,
  x = NULL,  
  y = NULL,  
  size = "value",  
  facet.by = NULL,  
  size.range = c(1, 10),  
  shape = 21,  
  color = "black",  
  fill = "gray",  
  show.label = FALSE,  
  font.label = list(size = 12, color = "black"),  
  rotate.x.text = TRUE,
)```

ggtheme = theme_minimal(),
...
)

Arguments

data a data frame. Can be:

- a standard contingency table formed by two categorical variables: a data frame with row names and column names. The categories of the first variable are columns and the categories of the second variable are rows.
- a stretched contingency table: a data frame containing at least three columns corresponding, respectively, to (1) the categories of the first variable, (2) the categories of the second variable, (3) the frequency value. In this case, you should specify the argument x and y in the function ggballoonplot().

x, y the column names specifying, respectively, the first and the second variable forming the contingency table. Required only when the data is a stretched contingency table.

size point size. By default, the points size reflects the relative magnitude of the value of the corresponding cell (size = "value"). Can be also numeric (size = 4).

facet.by character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.

size.range a numeric vector of length 2 that specifies the minimum and maximum size of the plotting symbol. Default values are size.range = c(1, 10).

shape points shape. The default value is 21. Alternative values include 22, 23, 24, 25.

color point border line color.

fill point fill color. Default is "lightgray". Considered only for points 21 to 25.

show.label logical. If TRUE, show the data cell values as point labels.

font.label a vector of length 3 indicating respectively the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of point labels. For example font.label = c(14, "bold", "red"). To specify only the size and the style, use font.label = c(14, "plain").

rotate.x.text logical. If TRUE (default), rotate the x axis text.

ggtheme function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....

Examples

# Define color palette
my.cols <- c("#0D0887FF", "#6A00A8FF", "#B12A90FF", 
"#E16462FF", "#FCA636FF", "#F0F921FF")

# Standard contingency table
# Read a contingency table: housetasks
# Repartition of 13 housetasks in the couple
data <- read.delim(
  system.file("demo-data/housetasks.txt", package = "ggpubr"),
  row.names = 1
)
data

data

# Basic ballon plot
ggballoonplot(data)

# Change color and fill
ggballoonplot(data, color = "#0073C2FF", fill = "#0073C2FF")

# Change color according to the value of table cells
ggballoonplot(data, fill = "value")+
scale_fill_gradientn(colors = my_cols)

# Change the plotting symbol shape
ggballoonplot(data, fill = "value", shape = 23)+
gradient_fill(c("blue", "white", "red"))

# Set points size to 8, but change fill color by values
# Sow labels
ggballoonplot(data, fill = "value", color = "lightgray",
  size = 10, show.label = TRUE)+
gradient_fill(c("blue", "white", "red"))

# Streched contingency table

# Create an Example Data Frame Containing Car x Color data
carnames <- c("bmw","renault","mercedes","seat")
carcolors <- c("red","white","silver","green")
datavals <- round(rnorm(16, mean=100, sd=60),1)
car_data <- data.frame(Car = rep(carnames,4),
  Color = rep(carcolors, c(4,4,4,4) ),
  Value=datavals )
car_data
car_data

ggballoonplot(car_data, x = "Car", y = "Color",
  size = "Value", fill = "Value") +
scale_fill_gradientn(colors = my_cols) +
guides(size = FALSE)

# Grouped frequency table

data("Titanic")
```r
dframe <- as.data.frame(Titanic)
head(dframe)
gballoonplot(
  dframe, x = "Class", y = "Sex",
  size = "Freq", fill = "Freq",
  facet.by = c("Survived", "Age"),
  ggtheme = theme_bw()
)+
  scale_fill_gradientn(colors = my_cols)

# Hair and Eye Color of Statistics Students
data(HairEyeColor)
gballoonplot( as.data.frame(HairEyeColor),
  x = "Hair", y = "Eye", size = "Freq",
  ggtheme = theme_gray()) %>%
  facet("Sex")
```

---

**ggbarplot**

**Bar plot**

**Description**

Create a bar plot.

**Usage**

```r
ggbarplot(
  data,
  x,
  y,
  combine = FALSE,
  merge = FALSE,
  color = "black",
  fill = "white",
  palette = NULL,
  size = NULL,
  width = NULL,
  title = NULL,
  xlab = NULL,
  ylab = NULL,
  facet.by = NULL,
  panel.labs = NULL,
  short.panel.labs = TRUE,
  select = NULL,
  remove = NULL,
  order = NULL,
)```
Arguments

data  a data frame
x, y  x and y variables for drawing.
combine  logical value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of y variables.
merge  logical or character value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, merge multiple y variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If merge = "flip", then y variables are used as x tick labels and the x variable is used as grouping variable.
color, fill  outline and fill colors.
palette  the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
size  Numeric value (e.g.: size = 1). change the size of points and outlines.
width  numeric value between 0 and 1 specifying box width.
title  plot main title.
xlab  character vector specifying x axis labels. Use xlab = FALSE to hide xlab.
ylab  character vector specifying y axis labels. Use ylab = FALSE to hide ylab.
facet.by  character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
panel.labs  a list of one or two character vectors to modify facet panel labels. For example, panel.labs = list(sex = c("Male", "Female")) specifies the labels for the "sex"
variable. For two grouping variables, you can use for example panel.labs =
list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2" ) ).

short.panel.labs
logical value. Default is TRUE. If TRUE, create short labels for panels by omit-
tting variable names; in other words panels will be labelled only by variable
grouping levels.

select character vector specifying which items to display.

remove character vector specifying which items to remove from the plot.

order character vector specifying the order of items.

add character vector for adding another plot element (e.g.: dot plot or error bars). Allowed values are one or the combination of: "none", "dotplot", "jitter", "box-
plot", "point", "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", "me-
dian", "median_iqr", "median_hilow", "median_q1q3", "median_mad", "me-
dian_range"; see ?desc_statby for more details.

add.params parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: add.params
= list(color = "red").

error.plot plot type used to visualize error. Allowed values are one of c("pointrange", "lin-
erange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange",
"lower_pointrange", "upper_linerange", "lower_linerange"). Default value is
"pointrange" or "errorbar". Used only when add != "none" and add contains
one "mean_*" or "med_*" where "*" = sd, se, ....

classic() theme_classic(), theme_void(), ....

... other arguments to be passed to be passed to ggpar().
Details

The plot can be easily customized using the function `ggpar()`. Read `?ggpar` for changing:

- main title and axis labels: `main`, `xlab`, `ylab`
- axis limits: `xlim`, `ylim` (e.g. `ylim = c(0, 30)`)
- axis scales: `xscale`, `yscale` (e.g. `yscale = "log2"`)
- color palettes: `palette = "Dark2"` or `palette = c("gray", "blue", "red")`
- legend title, labels and position: `legend = "right"`
- plot orientation: `orientation = c("vertical", "horizontal", "reverse")`

See Also

`ggpar`, `ggline`

Examples

```r
# Data
df <- data.frame(dose=c("D0.5", "D1", "D2"),
  len=c(4.2, 10, 29.5))
print(df)

# Basic plot with label outside
# +++++++++++++++++++++++++++
ggbarplot(df, x = "dose", y = "len",
  label = TRUE, label.pos = "out")

# Change width
ggbarplot(df, x = "dose", y = "len", width = 0.5)

# Change the plot orientation: horizontal
ggbarplot(df, "dose", "len", orientation = "horiz")

# Change the default order of items
ggbarplot(df, "dose", "len",
  order = c("D2", "D1", "D0.5"))

# Change colors
# +++++++++++++++++++++++++++
# Change fill and outline color
# add labels inside bars
ggbarplot(df, "dose", "len",
  fill = "steelblue", color = "steelblue",
  label = TRUE, lab.pos = "in", lab.col = "white")

# Change colors by groups: dose
# Use custom color palette
ggbarplot(df, "dose", "len", color = "dose",
  palette = c("#00AFBB", "#E7B800", "#FC4E07"))
```
# Change fill and outline colors by groups
```r
ggbarplot(df, "dose", "len",
    fill = "dose", color = "dose",
    palette = c("#00AFBB", "#E7B800", "#FC4E07"))
```

# Plot with multiple groups
# +++++++++++++++++++++

# Create some data
```r
df2 <- data.frame(supp=rep(c("VC", "OJ"), each=3),
    dose=rep(c("D0.5", "D1", "D2"),2),
    len=c(6.8, 15, 33, 4.2, 10, 29.5))
```
```r
print(df2)
```
# Plot "len" by "dose" and change color by a second group: "supp"
# Add labels inside bars
```r
ggbarplot(df2, "dose", "len",
    fill = "supp", color = "supp", palette = "Paired",
    label = TRUE, lab.col = "white", lab.pos = "in")
```
# Change position: Interleaved (dodged) bar plot
```r
ggbarplot(df2, "dose", "len",
    fill = "supp", color = "supp", palette = "Paired",
    label = TRUE,
    position = position_dodge(0.9))
```

# Add points and errors
# ++++++++++++++++++++++++++

# Data: ToothGrowth data set we'll be used.
```r
df3 <- ToothGrowth
head(df3, 10)
```
# It can be seen that for each group we have
# different values
```r
ggbarplot(df3, x = "dose", y = "len")
```
# Visualize the mean of each group
```r
ggbarplot(df3, x = "dose", y = "len",
    add = "mean")
```
# Add error bars: mean_se
# (other values include: mean_sd, mean_ci, median_iqr, ....)
# Add labels
```r
ggbarplot(df3, x = "dose", y = "len",
    add = "mean_se", label = TRUE, lab.vjust = -1.6)
```
# Use only "upper_errorbar"
```r
ggbarplot(df3, x = "dose", y = "len",
    add = "mean_se", error.plot = "upper_errorbar")
```
# Change error.plot to "pointrange"
ggbarplot(df3, x = "dose", y = "len",
          add = "mean_se", error.plot = "pointrange")

# Add jitter points and errors (mean_se)
ggbarplot(df3, x = "dose", y = "len",
          add = c("mean_se", "jitter"))

# Add dot and errors (mean_se)
ggbarplot(df3, x = "dose", y = "len",
          add = c("mean_se", "dotplot"))

# Multiple groups with error bars and jitter point
ggbarplot(df3, x = "dose", y = "len", color = "supp",
          add = "mean_se", palette = c("#00AFBB", "#E7B800"),
          position = position_dodge())

ggboxplot  

**Box plot**

**Description**

Create a box plot with points. Box plots display a group of numerical data through their quartiles.

**Usage**

ggboxplot(
  data,
  x,
  y,
  combine = FALSE,
  merge = FALSE,
  color = "black",
  fill = "white",
  palette = NULL,
  title = NULL,
  xlab = NULL,
  ylab = NULL,
  bxp.errorbar = FALSE,
  bxp.errorbar.width = 0.4,
  facet.by = NULL,
  panel.labs = NULL,
  short.panel.labs = TRUE,
  linetype = "solid",
  size = NULL,
  width = 0.7,
notch = FALSE,
outlier.shape = 19,
select = NULL,
remove = NULL,
order = NULL,
add = "none",
add.params = list(),
error.plot = "pointrange",
label = NULL,
font.label = list(size = 11, color = "black"),
label.select = NULL,
repel = FALSE,
label.rectangle = FALSE,
ggtheme = theme_pubr(),
... 
)

Arguments

data a data frame
x character string containing the name of x variable.
y character vector containing one or more variables to plot
combine logical value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of y variables.
merge logical or character value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, merge multiple y variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If merge = "flip", then y variables are used as x tick labels and the x variable is used as grouping variable.
color outline color.
fill fill color.
palette the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "hpg","aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
title plot main title.
xlab character vector specifying x axis labels. Use xlab = FALSE to hide xlab.
ylab character vector specifying y axis labels. Use ylab = FALSE to hide ylab.
bxp.errorbar logical value. If TRUE, shows error bars of box plots.
bxp.errorbar.width numeric value specifying the width of box plot error bars. Default is 0.4.
facet.by character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
panel.labs a list of one or two character vectors to modify facet panel labels. For example, `panel.labs = list(sex = c("Male", "Female"))` specifies the labels for the "sex" variable. For two grouping variables, you can use for example `panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))`.

short.panel.labs logical value. Default is TRUE. If TRUE, create short labels for panels by omitting variable names; in other words panels will be labelled only by variable grouping levels.

linetype line types.

size Numeric value (e.g.: size = 1). change the size of points and outlines.

width numeric value between 0 and 1 specifying box width.

notch If FALSE (default) make a standard box plot. If TRUE, make a notched box plot. Notches are used to compare groups; if the notches of two boxes do not overlap, this suggests that the medians are significantly different.

outlier.shape point shape of outlier. Default is 19. To hide outlier, specify `outlier.shape = NA`. When jitter is added, then outliers will be automatically hidden.

select character vector specifying which items to display.

remove character vector specifying which items to remove from the plot.

order character vector specifying the order of items.

add character vector for adding another plot element (e.g.: dot plot or error bars). Allowed values are one or the combination of: "none", "dotplot", "jitter", "boxplot", "point", "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", "median", "median_iqr", "median_hilow", "median_q1q3", "median_mad", "median_range"; see ?desc_statby for more details.

add.params parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: `add.params = list(color = "red")`.

error.plot plot type used to visualize error. Allowed values are one of c("pointrange", "linerange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linerange", "lower_linerange"). Default value is "pointrange" or "errorbar". Used only when add != "none" and add contains one "mean_" or "med_" where "_" = sd, se, ....

label the name of the column containing point labels. Can be also a character vector with length = nrow(data).

font.label a list which can contain the combination of the following elements: the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of labels. For example `font.label = list(size = 14, face = "bold", color ="red")`. To specify only the size and the style, use `font.label = list(size = 14, face = "plain")`.

label.select can be of two formats:

- a character vector specifying some labels to show.
- a list containing one or the combination of the following components:
  - top.up and top.down: to display the labels of the top up/down points.
    For example, `label.select = list(top.up = 10, top.down = 4)`.
criteria: to filter, for example, by x and y variables values, use this:
label.select = list(criteria = "y > 2 & y < 5 & x %in% c('A', 'B')").

- repel: a logical value, whether to use ggrepel to avoid overplotting text labels or not.
- label.rectangle: a logical value. If TRUE, add rectangle underneath the text, making it easier to read.

- ggtheme: function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....

- ... other arguments to be passed to geom_boxplot, ggpar and facet.

Details

The plot can be easily customized using the function ggpar(). Read ?ggpar for changing:

- main title and axis labels: main, xlab, ylab
- axis limits: xlim, ylim (e.g.: ylim = c(0, 30))
- axis scales: xscale, yscale (e.g.: yscale = "log2")
- color palettes: palette = "Dark2" or palette = c("gray", "blue", "red")
- legend title, labels and position: legend = "right"
- plot orientation: orientation = c("vertical", "horizontal", "reverse")

Suggestions for the argument "add"

Suggested values are one of c("dotplot", "jitter").

See Also

ggpar, ggviolin, ggdotplot and ggstripchart.

Examples

# Load data
data("ToothGrowth")
df <- ToothGrowth

# Basic plot
# +++++++++++++++++++++++++++++++
# width: change box plots width
ggboxplot(df, x = "dose", y = "len", width = 0.8)

# Change orientation: horizontal
ggboxplot(df, "dose", "len", orientation = "horizontal")

# Notched box plot
ggboxplot(df, x = "dose", y = "len", notch = TRUE)
# Add dots
# ++++++++++++++++++++++++++
ggboxplot(df, x = "dose", y = "len",
          add = "dotplot")

# Add jitter points and change the shape by groups
ggboxplot(df, x = "dose", y = "len",
          add = "jitter", shape = "dose")

# Select and order items
# ++++++++++++++++++++++++++++++
# Select which items to display: "0.5" and "2"
ggboxplot(df, "dose", "len",
          select = c("0.5", "2"))

# Change the default order of items
ggboxplot(df, "dose", "len",
          order = c("2", "1", "0.5"))

# Change colors
# +++++++++++++++++++++++++++
# Change outline and fill colors
ggboxplot(df, "dose", "len",
          color = "black", fill = "gray")

# Change outline colors by groups: dose
# Use custom color palette
# Add jitter points and change the shape by groups
ggboxplot(df, "dose", "len",
          color = "dose", palette = c("#00AFBB", "#E7B800", "#FC4E07"),
          add = "jitter", shape = "dose")

# Change fill color by groups: dose
ggboxplot(df, "dose", "len",
          fill = "dose", palette = c("#00AFBB", "#E7B800", "#FC4E07"))

# Box plot with multiple groups
# ++++++++++++++++++++++++++++++
# fill or color box plot by a second group: "supp"
ggboxplot(df, "dose", "len", color = "supp",
          palette = c("#00AFBB", "#E7B800"))

---

**ggdensity**  
*Density plot*
Description

Create a density plot.

Usage

```r
ggdensity(
  data,
  x,
  y = "density",
  combine = FALSE,
  merge = FALSE,
  color = "black",
  fill = NA,
  palette = NULL,
  size = NULL,
  linetype = "solid",
  alpha = 0.5,
  title = NULL,
  xlab = NULL,
  ylab = NULL,
  facet.by = NULL,
  panel.labs = NULL,
  short.panel.labs = TRUE,
  add = c("none", "mean", "median"),
  add.params = list(linetype = "dashed"),
  rug = FALSE,
  label = NULL,
  font.label = list(size = 11, color = "black"),
  label.select = NULL,
  repel = FALSE,
  label.rectangle = FALSE,
  ggtheme = theme_pubr(),
  ...)
```

Arguments

data a data frame

x variable to be drawn.

y one of "density" or "count".

combine logical value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of y variables.

merge logical or character value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, merge multiple y variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If merge = "flip", then y variables are used as x tick labels and the x variable is used as grouping variable.
color, fill
density line color and fill color.

palette
the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".

size
Numeric value (e.g.: size = 1). change the size of points and outlines.

linetype
line type. See show_line_types.

alpha
numeric value specifying fill color transparency. Value should be in [0, 1], where 0 is full transparency and 1 is no transparency.

title
plot main title.

xlab
character vector specifying x axis labels. Use xlab = FALSE to hide xlab.

ylab
character vector specifying y axis labels. Use ylab = FALSE to hide ylab.

facet.by
character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.

panel.labs
a list of one or two character vectors to modify facet panel labels. For example, panel.labs = list(xlab = c("Male", "Female")) specifies the labels for the "sex" variable. For two grouping variables, you can use for example panel.labs = list(xlab = c("Male", "Female"), ylab = c("Obs", "Lev", "Lev2").

short.panel.labs
logical value. Default is TRUE. If TRUE, create short labels for panels by omitting variable names; in other words panels will be labelled only by variable grouping levels.

add
allowed values are one of "mean" or "median" (for adding mean or median line, respectively).

add.params
parameters (color, size, linetype) for the argument 'add'; e.g.: add.params = list(color = "red").

rug
logical value. If TRUE, add marginal rug.

label
the name of the column containing point labels. Can be also a character vector with length = nrow(data).

font.label
a list which can contain the combination of the following elements: the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of labels. For example font.label = list(size = 14, face = "bold", color = "red"). To specify only the size and the style, use font.label = list(size = 14, face = "plain").

label.select
can be of two formats:

- a character vector specifying some labels to show.
- a list containing one or the combination of the following components:
  - top.up and top.down: to display the labels of the top up/down points. For example, label.select = list(top.up = 10, top.down = 4).
  - criteria: to filter, for example, by x and y variables values, use this: label.select = list(criteria = "\'y\' > 2 & \'y\' < 5 & \'x\' %in% c(\'A\', \'B\')").
**ggdensity**

- repel: a logical value, whether to use ggrepel to avoid overplotting text labels or not.
- label.rectangle: logical value. If TRUE, add rectangle underneath the text, making it easier to read.
- ggtheme: function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ...
- ... other arguments to be passed to `geom_density` and `ggpar`.

**Details**

The plot can be easily customized using the function `ggpar()`. Read `?ggpar` for changing:

- main title and axis labels: `main`, `xlab`, `ylab`
- axis limits: `xlim`, `ylim` (e.g.: `ylim = c(0, 30)`)  
- axis scales: `xscale`, `yscale` (e.g.: `yscale = "log2"`)
- color palettes: `palette = "Dark2"` or `palette = c("gray", "blue", "red")`
- legend title, labels and position: `legend = "right"`  
- plot orientation: `orientation = c("vertical", "horizontal", "reverse")`

**See Also**

`gghistogram` and `ggpar`.

**Examples**

```r
# Create some data format
set.seed(1234)
wdata = data.frame(
  sex = factor(rep(c("F", "M"), each=200)),
  weight = c(rnorm(200, 55), rnorm(200, 58)))
head(wdata, 4)

# Basic density plot
# Add mean line and marginal rug
ggdensity(wdata, x = "weight", fill = "lightgray",
  add = "mean", rug = TRUE)

# Change outline colors by groups ("sex")
# Use custom palette
ggdensity(wdata, x = "weight",
  add = "mean", rug = TRUE,
  color = "sex", palette = c("#00AFBB", "#E7B800"))

# Change outline and fill colors by groups ("sex")
# Use custom palette
ggdensity(wdata, x = "weight",
  add = "mean", rug = TRUE,
  color = "sex", palette = c("#00AFBB", "#E7B800"))
```

ggdonutchart

Donut chart

Description
Create a donut chart.

Usage

```r
ggdonutchart(
data, 
  x, 
  label = x, 
  lab.pos = c("out", "in"), 
  lab.adjust = 0, 
  lab.font = c(4, "bold", "black"), 
  font.family = "", 
  color = "black", 
  fill = "white", 
  palette = NULL, 
  size = NULL, 
  ggtheme = theme_pubr(), 
  ... 
)
```

Arguments

data a data frame

x variable containing values for drawing.

label variable specifying the label of each slice.

lab.pos character specifying the position for labels. Allowed values are "out" (for outside) or "in" (for inside).

lab.adjust numeric value, used to adjust label position when lab.pos = "in". Increase or decrease this value to see the effect.

lab.font a vector of length 3 indicating respectively the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of label font. For example `lab.font = c(4, "bold", "red")`.

font.family character vector specifying font family.

color, fill outline and fill colors.
The plot can be easily customized using the function `ggpar()`. Read `?ggpar` for changing:

- main title and axis labels: `main`, `xlab`, `ylab`
- axis limits: `xlim`, `ylim` (e.g.: `ylim = c(0, 30)`)
- axis scales: `xscale`, `yscale` (e.g.: `yscale = "log2"`)
- color palettes: palette = "Dark2" or palette = c("gray", "blue", "red")
- legend title, labels and position: `legend = "right"`
- plot orientation : `orientation = c("vertical", "horizontal", "reverse")`

See Also

- `ggpar`, `ggsave`

Examples

```r
# Data: Create some data
# ++++++++++++++++++++++++++++++++++++++++

df <- data.frame(
  group = c("Male", "Female", "Child"),
  value = c(25, 25, 50))

head(df)

# Basic pie charts
# ++++++++++++++++++++++++++++++++++++++++
ggdonutchart(df, "value", label = "group")

# Change color
# ++++++++++++++++++++++++++++++++++++++++
# Change fill color by group
```
# set line color to white
# Use custom color palette  
ggdonutchart(df, "value", label = "group",
        fill = "group", color = "white",
        palette = c("#00AFBB" ,"#E7B800" ,"#FC4E07") )

# Change label
# ++++++++++++++++++++++++++++++++

# Show group names and value as labels
labs <- paste0(df$group, " (", df$value, ")")
ggdonutchart(df, "value", label = labs,  
fill = "group", color = "white",
        palette = c("#00AFBB" ,"#E7B800" ,"#FC4E07"))

# Change the position and font color of labels
ggdonutchart(df, "value", label = labs,  
lab.pos = "in", lab.font = "white",
fill = "group", color = "white",
        palette = c("#00AFBB" ,"#E7B800" ,"#FC4E07"))

---

**gdotchart**

*Cleveland’s Dot Plots*

### Description

Draw a Cleveland dot plot.

### Usage

```r

ggdotchart(  
data,
        x,
        y,
        group = NULL,
        combine = FALSE,
        color = "black",
        palette = NULL,
        shape = 19,
        size = NULL,
        dot.size = size,
        sorting = c("ascending", "descending", "none"),
        add = c("none", "segment"),
        add.params = list(),
        x.text.col = TRUE,
```
rotate = FALSE,
title = NULL,
xlab = NULL,
ylab = NULL,
facet.by = NULL,
panel.labs = NULL,
short.panel.labs = TRUE,
select = NULL,
remove = NULL,
order = NULL,
label = NULL,
font.label = list(size = 11, color = "black"),
label.select = NULL,
repel = FALSE,
label.rectangle = FALSE,
position = "identity",
ggtheme = theme_pubr(),
...
)

theme_cleveland(rotate = TRUE)

Arguments

data a data frame
x, y x and y variables for drawing.
group an optional column name indicating how the elements of x are grouped.
combine logical value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of y variables.
color, size points color and size.
palette the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
shape point shape. See show_point_shapes.
dot.size numeric value specifying the dot size.
sorting a character vector for sorting into ascending or descending order. Allowed values are one of "descending", "ascending" and "none". Partial match are allowed (e.g. sorting = "desc" or "asc"). Default is "descending".
add character vector for adding another plot element (e.g.: dot plot or error bars). Allowed values are one or the combination of: "none", "dotplot", "jitter", "boxplot", "point", "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", "median", "median_iqr", "median_hilow", "median_q1q3", "median_nmad", "median_range"; see ?desc_statby for more details.
add.params parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: add.params = list(color = "red").

x.text.col logical. If TRUE (default), x axis texts are colored by groups.

rotate logical value. If TRUE, rotate the graph by setting the plot orientation to horizontal.

title plot main title.

xlab character vector specifying x axis labels. Use xlab = FALSE to hide xlab.

ylab character vector specifying y axis labels. Use ylab = FALSE to hide ylab.

facet.by character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.

panel.labs a list of one or two character vectors to modify facet panel labels. For example, panel.labs = list(sex = c("Male", "Female")) specifies the labels for the "sex" variable. For two grouping variables, you can use for example panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2") )

short.panel.labs logical value. Default is TRUE. If TRUE, create short labels for panels by omitting variable names; in other words panels will be labelled only by variable grouping levels.

select character vector specifying which items to display.

remove character vector specifying which items to remove from the plot.

order character vector specifying the order of items.

label the name of the column containing point labels.

font.label a list which can contain the combination of the following elements: the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of labels. For example font.label = list(size = 14, face = "bold", color = "red"). To specify only the size and the style, use font.label = list(size = 14, face = "plain").

label.select can be of two formats:
  • a character vector specifying some labels to show.
  • a list containing one or the combination of the following components:
    – top. up and top. down: to display the labels of the top up/down points.
      For example, label.select = list(top. up = 10, top. down = 4).
    – criteria: to filter, for example, by x and y variables values, use this:
      label.select = list(criteria = "y > 2 & y < 5 & x %in% c('A', 'B')").

repel a logical value, whether to use ggrepel to avoid overplotting text labels or not.

label.rectangle logical value. If TRUE, add rectangle underneath the text, making it easier to read.

position Position adjustment, either as a string, or the result of a call to a position adjustment function.

ggtheme function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....

... other arguments to be passed to geom_point and ggpar.
Details

The plot can be easily customized using the function ggpar(). Read ?ggpar for changing:

- main title and axis labels: main, xlab, ylab
- axis limits: xlim, ylim (e.g.: ylim = c(0, 30))
- axis scales: xscale, yscale (e.g.: yscale = "log2")
- color palettes: palette = "Dark2" or palette = c("gray", "blue", "red")
- legend title, labels and position: legend = "right"
- plot orientation : orientation = c("vertical", "horizontal", "reverse")

See Also

ggpar

Examples

# Load data
data("mtcars")
df <- mtcars
df$cyl <- as.factor(df$cyl)
df$name <- rownames(df)
head(df[, c("wt", "mpg", "cyl")], 3)

# Basic plot
ggdotchart(df, x = "name", y = "mpg",
ggtheme = theme_bw())

# Change colors by group cyl
ggdotchart(df, x = "name", y = "mpg",
group = "cyl", color = "cyl",
palette = c(quotesingle.Var, #999999, "#E69F00", "#56B4E9"),
rotate = TRUE,
sorting = "descending",
ggtheme = theme_bw(),
y.text.col = TRUE )

# Plot with multiple groups
# +++++++++++++++++++++
# Create some data
df2 <- data.frame(supp=rep(c("VC", "OJ"), each=3),
dose = rep(c("D0.5", "D1", "D2"),2),
len = c(6.8, 15, 33, 4.2, 10, 29.5))
print(df2)

ggdotchart(df2, x = "dose", y = "len",
color = "supp", size = 3,
add = "segment",
add.params = list(color = "lightgray", size = 1.5),
position = position_dodge(0.3),
ggdotplot

**Dot plot**

**Description**

Create a dot plot.

**Usage**

```r
ggdotplot(
  data,
  x,
  y,
  combine = FALSE,
  merge = FALSE,
  color = "black",
  fill = "lightgray",
  palette = NULL,
  title = NULL,
  xlab = NULL,
  ylab = NULL,
  facet.by = NULL,
  panel.labs = NULL,
  short.panel.labs = TRUE,
  size = NULL,
  binwidth = NULL,
  select = NULL,
  remove = NULL,
  order = NULL,
  add = "mean_se",
  add.params = list(),
  error.plot = "pointrange",
  label = NULL,
  font.label = list(size = 11, color = "black"),
  label.select = NULL,
  repel = FALSE,
  label.rectangle = FALSE,
  ggtheme = theme_pubr(),
  ...
)
```

```r
pal <- ggplot2::scale_fill_manual(values = c("#4f817e", "#c9947d", "#e26b3e", "#f44236"))
ggtheme = theme_pubr()
```
Arguments

- **data**: a data frame
- **x**: character string containing the name of x variable.
- **y**: character vector containing one or more variables to plot
- **combine**: logical value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of y variables.
- **merge**: logical or character value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, merge multiple y variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If merge = "flip", then y variables are used as x tick labels and the x variable is used as grouping variable.
- **color**: outline color.
- **fill**: fill color.
- **palette**: the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggscl R package, e.g.: "npg", "aaas", "lancet", "jco", "ucsgb", "uchicago", "simpsons" and "rickandmorty".
- **title**: plot main title.
- **xlab**: character vector specifying x axis labels. Use xlab = FALSE to hide xlab.
- **ylab**: character vector specifying y axis labels. Use ylab = FALSE to hide ylab.
- **facet.by**: character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
- **panel.labs**: a list of one or two character vectors to modify facet panel labels. For example, panel.labs = list(sex = c("Male", "Female")) specifies the labels for the "sex" variable. For two grouping variables, you can use for example panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2")
- **short.panel.labs**: logical value. Default is TRUE. If TRUE, create short labels for panels by omitting variable names; in other words panels will be labelled only by variable grouping levels.
- **size**: numeric value (e.g.: size = 1). change the size of points and outlines.
- **binwidth**: numeric value specifying bin width. use value between 0 and 1 when you have a strong dense dotplot. For example binwidth = 0.2.
- **select**: character vector specifying which items to display.
- **remove**: character vector specifying which items to remove from the plot.
- **order**: character vector specifying the order of items.
- **add**: character vector for adding another plot element (e.g.: dot plot or error bars). Allowed values are one or the combination of: "none", "dotplot", "jitter", "boxplot", "point", "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", "median", "median_iqr", "median_hilow", "median_q1q3", "median_q1q3", "median_range": see ?desc_statby for more details.
add.params: parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: add.params = list(color = "red").

error.plot: plot type used to visualize error. Allowed values are one of c("pointrange", "linerange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linerange", "lower_linerange"). Default value is "pointrange" or "errorbar". Used only when add != "none" and add contains one "mean_*" or "med_*" where "_*" = sd, se, ....

label: the name of the column containing point labels. Can be also a character vector with length = nrow(data).

font.label: a list which can contain the combination of the following elements: the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of labels. For example font.label = list(size = 14, face = "bold", color = "red"). To specify only the size and the style, use font.label = list(size = 14, face = "plain").

label.select: can be of two formats:
- a character vector specifying some labels to show.
- a list containing one or the combination of the following components:
  - top.up and top.down: to display the labels of the top up/down points. For example, label.select = list(top.up = 10, top.down = 4).
  - criteria: to filter, for example, by x and y variabes values, use this: label.select = list(criteria = "y > 2 & y < 5 & x %in% c("A", "B")").

repel: a logical value, whether to use ggrepel to avoid overplotting text labels or not.

label.rectangle: logical value. If TRUE, add rectangle underneath the text, making it easier to read.

ggtheme: function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....

Details
The plot can be easily customized using the function ggpar(). Read ?ggpar for changing:
- main title and axis labels: main, xlab, ylab
- axis limits: xlim, ylim (e.g.: ylim = c(0, 30))
- axis scales: xscale, yscale (e.g.: yscale = "log2")
- color palettes: palette = "Dark2" or palette = c("gray", "blue", "red")
- legend title, labels and position: legend = "right"
- plot orientation : orientation = c("vertical", "horizontal", "reverse")

See Also

ggpar, ggviolin, ggboxplot and ggstripchart.
Examples

# Load data
data("ToothGrowth")
df <- ToothGrowth

# Basic plot with summary statistics : mean_sd
# +++++++++++++++++++++++++++
ggdotplot(df, x = "dose", y = "len",
    add = "mean_sd")

# Change error.plot to "crossbar"
ggdotplot(df, x = "dose", y = "len",
    add = "mean_sd", add.params = list(width = 0.5),
    error.plot = "crossbar")

# Add box plot
ggdotplot(df, x = "dose", y = "len",
    add = "boxplot")

# Add violin + mean_sd
ggdotplot(df, x = "dose", y = "len",
    add = c("violin", "mean_sd"))

# Change colors
# +++++++++++++++++++++++++++
# Change fill and outline colors by groups: dose
# Use custom color palette
ggdotplot(df, "dose", "len",
    add = "boxplot",
    color = "dose", fill = "dose",
    palette = c("#00AFBB", "#E7B800", "#FC4E07"))

# Plot with multiple groups
# +++++++++++++++++++++++
# Change color by a second group : "supp"
ggdotplot(df, "dose", "len", fill = "supp", color = "supp",
    palette = c("#00AFBB", "#E7B800"))

---

ggecdf

Empirical cumulative density function

Description

Empirical Cumulative Density Function (ECDF).
Usage

ggecdf(
    data,
    x,
    combine = FALSE,
    merge = FALSE,
    color = "black",
    palette = NULL,
    size = NULL,
    linetype = "solid",
    title = NULL,
    xlab = NULL,
    ylab = NULL,
    facet.by = NULL,
    panel.labs = NULL,
    short.panel.labs = TRUE,
    ggtheme = theme_pubr(),
    ...
)

Arguments

data a data frame
x variable to be drawn.
combine logical value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of y variables.
merge logical or character value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, merge multiple y variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If merge = "flip", then y variables are used as x tick labels and the x variable is used as grouping variable.
color line and point color.
palette the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
size line and point size.
linetype line type. See show_line_types.
title plot main title.
xlab character vector specifying x axis labels. Use xlab = FALSE to hide xlab.
ylab character vector specifying y axis labels. Use ylab = FALSE to hide ylab.
facet.by character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
panel.labs  a list of one or two character vectors to modify facet panel labels. For example, panel.labs = list(sex = c("Male", "Female")) specifies the labels for the "sex" variable. For two grouping variables, you can use for example panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2" )).

short.panel.labs  logical value. Default is TRUE. If TRUE, create short labels for panels by omitting variable names; in other words panels will be labelled only by variable grouping levels.

ggtheme  function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....

... other arguments to be passed to stat_ecdf and ggpar.

Details

The plot can be easily customized using the function ggpar(). Read ?ggpar for changing:

- main title and axis labels: main, xlab, ylab
- axis limits: xlim, ylim (e.g.: ylim = c(0, 30))
- axis scales: xscale, yscale (e.g.: yscale = "log2")
- color palettes: palette = "Dark2" or palette = c("gray", "blue", "red")
- legend title, labels and position: legend = "right"
- plot orientation : orientation = c("vertical", "horizontal", "reverse")

See Also

ggpar

Examples

# Create some data format
set.seed(1234)
wdata = data.frame(
    sex = factor(rep(c("F", "M"), each=200)),
    weight = c(rnorm(200, 55), rnorm(200, 58)))

head(wdata, 4)

# Basic ECDF plot
ggecdf(wdata, x = "weight")

# Change colors and linetype by groups ("sex")
# Use custom palette
ggecdf(wdata, x = "weight",
    color = "sex", linetype = "sex",
    palette = c("#00AFBB", "#E7B800"))
ggerrorplot  Visualizing Error

Description
Visualizing error.

Usage

```r
ggerrorplot(
  data,
  x,
  y,
  desc_stat = "mean_se",
  numeric.x.axis = FALSE,
  combine = FALSE,
  merge = FALSE,
  color = "black",
  fill = "white",
  palette = NULL,
  size = NULL,
  width = NULL,
  title = NULL,
  xlab = NULL,
  ylab = NULL,
  facet.by = NULL,
  panel.labs = NULL,
  short.panel.labs = TRUE,
  select = NULL,
  remove = NULL,
  order = NULL,
  add = "none",
  add.params = list(),
  error.plot = "pointrange",
  ci = 0.95,
  position = position_dodge(),
  ggtheme = theme_pubr(),
  ...
)
```

Arguments

- **data** a data frame
- **x, y** x and y variables for drawing.
- **desc_stat** descriptive statistics to be used for visualizing errors. Default value is "mean_se". Allowed values are one of , "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", 

"median", "median_iqr", "median_hilow", "median_q1q3", "median_mad", "median_range"; see `desc_statby` for more details.

**numeric.x.axis**
logical. If TRUE, x axis will be treated as numeric. Default is FALSE.

**combine**
logical value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of y variables.

**merge**
logical or character value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, merge multiple y variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If merge = "flip", then y variables are used as x tick labels and the x variable is used as grouping variable.

**color, fill**
outline and fill colors.

**palette**
the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".

**size**
Numeric value (e.g.: size = 1). change the size of points and outlines.

**width**
umberic value between 0 and 1 specifying box width.

**title**
plot main title.

**xlab**
character vector specifying x axis labels. Use xlab = FALSE to hide xlab.

**ylab**
character vector specifying y axis labels. Use ylab = FALSE to hide ylab.

**facet.by**
character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.

**panel.labs**
a list of one or two character vectors to modify facet panel labels. For example, panel.labs = list(sex = c("Male", "Female")) specifies the labels for the "sex" variable. For two grouping variables, you can use for example panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))

**short.panel.labs**
logical value. Default is TRUE. If TRUE, create short labels for panels by omitting variable names; in other words panels will be labelled only by variable grouping levels.

**select**
character vector specifying which items to display.

**remove**
character vector specifying which items to remove from the plot.

**order**
character vector specifying the order of items. Considered only when x axis is a factor variable.

**add**
character vector for adding another plot element (e.g.: dot plot or error bars). Allowed values are one or the combination of: "none", "dotplot", "jitter", "boxplot", "point", "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", "median", "median_iqr", "median_hilow", "median_q1q3", "median_mad", "median_range"; see `desc_statby` for more details.

**add.params**
parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: add.params = list(color = "red").
error.plot  plot type used to visualize error. Allowed values are one of c("pointrange", "linerange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linerange", "lower_linerange"). Default value is "pointrange" or "errorbar". Used only when add != "none" and add contains one "mean_*" or "med_*" where "*" = sd, se, ....

ci  the percent range of the confidence interval (default is 0.95).

position  Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

ggtheme  function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....

...  other arguments to be passed to be passed to ggpar().

Details

The plot can be easily customized using the function ggpar(). Read ?ggpar for changing:

- main title and axis labels: main, xlab, ylab
- axis limits: xlim, ylim (e.g.: ylim = c(0, 30))
- axis scales: xscale, yscale (e.g.: yscale = "log2")
- color palettes: palette = "Dark2" or palette = c("gray", "blue", "red")
- legend title, labels and position: legend = "right"
- plot orientation: orientation = c("vertical", "horizontal", "reverse")

See Also

ggpar, ggline

Examples

# Data: ToothGrowth data set we'll be used.
df<- ToothGrowth
head(df, 10)

# Plot mean_se
ggerrorplot(df, x = "dose", y = "len")

# Change desc_stat to mean_sd
# (other values include: mean_sd, mean_ci, median_iqr, ....)
# Add labels
ggerrorplot(df, x = "dose", y = "len",
desc_stat = "mean_sd")

# Change error.plot to "errorbar" and add mean point
# Visualize the mean of each group
ggenerrorplot(df, x = "dose", y = "len",
               add = "mean", error.plot = "errorbar")

# Horizontal plot
ggenerrorplot(df, x = "dose", y = "len",
               add = "mean", error.plot = "errorbar",
               orientation = "horizontal")

# Change error.plot to "crossbar"
ggenerrorplot(df, x = "dose", y = "len",
               error.plot = "crossbar", width = 0.5)

# Add jitter points and errors (mean_se)
ggenerrorplot(df, x = "dose", y = "len",
               add = "jitter")

# Add dot and errors (mean_se)
ggenerrorplot(df, x = "dose", y = "len",
               add = "dotplot")

# Multiple groups with error bars and jitter point
ggenerrorplot(df, x = "dose", y = "len",
               color = "supp", palette = "Paired",
               error.plot = "pointrange",
               position = position_dodge(0.5))

---

ggexport

Export ggplots

Description

Export ggplots

Usage

ggexport(
    ..., plotlist = NULL, filename = NULL,
    ncol = NULL, nrow = NULL, width = 480,
    height = 480, pointsize = 12,
    res = NA, verbose = TRUE
)
Arguments

plotlist (optional) list of plots to display.
filename File name to create on disk.
ncol (optional) number of columns in the plot grid.
nrow (optional) number of rows in the plot grid.
width, height plot width and height, respectively (example, width = 800, height = 800). Applied only to raster plots: "png", "jpeg", "jpg", "bmp" and "tiff".
pointsize the default pointsize of plotted text (example, pointsize = 8). Used only for raster plots.
res the resolution in ppi (example, res = 250). Used only for raster plots.
verbose logical. If TRUE, show message.

Author(s)

Alboukadel Kassambara <alboukadel.kassambara@gmail.com>

Examples

```r
## Not run:
require("magrittr")

# Load data
data("ToothGrowth")
df <- ToothGrowth
df$dose <- as.factor(df$dose)

# Box plot
bxp <- ggboxplot(df, x = "dose", y = "len",
color = "dose", palette = "jco")
# Dot plot
dp <- ggdotplot(df, x = "dose", y = "len",
color = "dose", palette = "jco")
# Density plot
dens <- ggdensity(df, x = "len", fill = "dose", palette = "jco")

# Export to pdf
ggarrange(bxp, dp, dens, ncol = 2) %>%
ggexport(filename = "test.pdf")

# Export to png

ggarrange(bxp, dp, dens, ncol = 2) %>%
ggexport(filename = "test.png")

## End(Not run)
```
Description

Create a histogram plot.

Usage

gghistogram(
  data,
  x,
  y = "count",
  combine = FALSE,
  merge = FALSE,
  weight = NULL,
  color = "black",
  fill = NA,
  palette = NULL,
  size = NULL,
  linetype = "solid",
  alpha = 0.5,
  bins = NULL,
  binwidth = NULL,
  title = NULL,
  xlab = NULL,
  ylab = NULL,
  facet.by = NULL,
  panel.labs = NULL,
  short.panel.labs = TRUE,
  add = c("none", "mean", "median"),
  add.params = list(linetype = "dashed"),
  rug = FALSE,
  add_density = FALSE,
  label = NULL,
  font.label = list(size = 11, color = "black"),
  label.select = NULL,
  repel = FALSE,
  label.rectangle = FALSE,
  position = position_identity(),
  ggtheme = theme_pubr(),
  ...
)

Arguments

data a data frame
x variable to be drawn.
y one of "density" or "count".
combine logical value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of y variables.
merge logical or character value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, merge multiple y variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If merge = "flip", then y variables are used as x tick labels and the x variable is used as grouping variable.
weight a variable name available in the input data for creating a weighted histogram.
color, fill histogram line color and fill color.
palette the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
size Numeric value (e.g.: size = 1). change the size of points and outlines.
linetype line type. See show_line_types.
alpha numeric value specifying fill color transparency. Value should be in [0, 1], where 0 is full transparency and 1 is no transparency.
bins Number of bins. Defaults to 30.
binwidth numeric value specifying bin width. use value between 0 and 1 when you have a strong dense dotplot. For example binwidth = 0.2.
title plot main title.
xlab character vector specifying x axis labels. Use xlab = FALSE to hide xlab.
ylab character vector specifying y axis labels. Use ylab = FALSE to hide ylab.
facet.by character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
panel.labs a list of one or two character vectors to modify facet panel labels. For example, panel.labs = list(sex = c("Male", "Female")) specifies the labels for the "sex" variable. For two grouping variables, you can use for example panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2") ).
short.panel.labs logical value. Default is TRUE. If TRUE, create short labels for panels by omitting variable names; in other words panels will be labelled only by variable grouping levels.
add allowed values are one of "mean" or "median" (for adding mean or median line, respectively).
add.params parameters (color, size, linetype) for the argument 'add'; e.g.: add.params = list(color = "red").
rug logical value. If TRUE, add marginal rug.
add_density logical value. If TRUE, add density curves.

label the name of the column containing point labels. Can be also a character vector with length = nrow(data).

font.label a list which can contain the combination of the following elements: the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of labels. For example font.label = list(size = 14, face = "bold", color = "red"). To specify only the size and the style, use font.label = list(size = 14, face = "plain").

label.select can be of two formats:

• a character vector specifying some labels to show.
• a list containing one or the combination of the following components:
  – top.up and top.down: to display the labels of the top up/down points. For example, label.select = list(top.up = 10, top.down = 4).
  – criteria: to filter, for example, by x and y variables values, use this: label.select = list(criteria = "y > 2 & y < 5 & x %in% c('A', 'B')").

repel a logical value, whether to use ggrepel to avoid overplotting text labels or not.

label.rectangle logical value. If TRUE, add rectangle underneath the text, making it easier to read.

position Position adjustment, either as a string, or the result of a call to a position adjustment function. Allowed values include "identity", "stack", "dodge".

ggtheme function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....

... other arguments to be passed to geom_histogram and ggpar.

Details

The plot can be easily customized using the function ggpar(). Read ?ggpar for changing:

• main title and axis labels: main, xlab, ylab
• axis limits: xlim, ylim (e.g.: ylim = c(0, 30))
• axis scales: xscale, yscale (e.g.: yscale = "log2")
• color palettes: palette = "Dark2" or palette = c("gray", "blue", "red")
• legend title, labels and position: legend = "right"
• plot orientation: orientation = c("vertical", "horizontal", "reverse")

See Also

ggdensity and ggpar
Examples

```r
# Create some data format
set.seed(1234)
wdata = data.frame(
    sex = factor(rep(c("F", "M"), each=200)),
    weight = c(rnorm(200, 55), rnorm(200, 58)))

head(wdata, 4)

# Basic density plot
# Add mean line and marginal rug
gghistogram(wdata, x = "weight", fill = "lightgray",
            add = "mean", rug = TRUE)

# Change outline colors by groups ("sex")
# Use custom color palette
gghistogram(wdata, x = "weight",
            add = "mean", rug = TRUE,
            color = "sex", palette = c("#00AFBB", "#E7B800"))

# Change outline and fill colors by groups ("sex")
# Use custom color palette
gghistogram(wdata, x = "weight",
            add = "mean", rug = TRUE,
            color = "sex", fill = "sex",
            palette = c("#00AFBB", "#E7B800"))

# Combine histogram and density plots
gghistogram(wdata, x = "weight",
            add = "mean", rug = TRUE,
            fill = "sex", palette = c("#00AFBB", "#E7B800"),
            add_density = TRUE)

# Weighted histogram
gghistogram(iris, x = "Sepal.Length", weight = "Petal.Length")
```

---

**ggline**

*Line plot*

**Description**

Create a line plot.

**Usage**

```r
ggline(data, 
    ...
)```

Arguments

data a data frame
x, y x and y variables for drawing.
group grouping variable to connect points by line. Allowed values are 1 (for one line, one group) or a character vector specifying the name of the grouping variable (case of multiple lines).
numeric.x.axis logical. If TRUE, x axis will be treated as numeric. Default is FALSE.
combine logical value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot
of y variables.

merge logical or character value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, merge multiple y variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If merge = "flip", then y variables are used as x tick labels and the x variable is used as grouping variable.

color line colors.

palette the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".

linetype line type.

plot_type plot type. Allowed values are one of "b" for both line and point; "l" for line only; and "p" for point only. Default is "b".

size Numeric value (e.g.: size = 1). change the size of points and outlines.

shape point shapes.

stroke point stroke. Used only for shapes 21-24 to control the thickness of points border.

point.size point size.

point.color point color.

title plot main title.

xlab character vector specifying x axis labels. Use xlab = FALSE to hide xlab.

ylab character vector specifying y axis labels. Use ylab = FALSE to hide ylab.

facet.by character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.

panel.labs a list of one or two character vectors to modify facet panel labels. For example, panel.labs = list(sex = c("Male", "Female")) specifies the labels for the "sex" variable. For two grouping variables, you can use for example panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2")) .

short.panel.labs logical value. Default is TRUE. If TRUE, create short labels for panels by omitting variable names; in other words panels will be labelled only by variable grouping levels.

select character vector specifying which items to display.

remove character vector specifying which items to remove from the plot.

order character vector specifying the order of items.

add character vector for adding another plot element (e.g.: dot plot or error bars). Allowed values are one or the combination of: "none", "dotplot", "jitter", "boxplot", "point", "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", "median", "median_iqr", "median_hilow", "median_q1q3", "median_q1q3", "median_range": see ?desc_statby for more details.
**ggline**

add.params parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: `add.params = list(color = "red")`.

error.plot plot type used to visualize error. Allowed values are one of `c("pointrange", "linerange","crossbar","errorbar","upper_errorbar","lower_errorbar","upper_pointrange", "lower_pointrange","upper_linerange","lower_linerange")`. Default value is "pointrange" or "errorbar". Used only when `add != "none"` and `add` contains one "mean_*" or "med_*" where "*" = sd, se, ....

label the name of the column containing point labels. Can be also a character vector with length = nrow(data).

font.label a list which can contain the combination of the following elements: the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of labels. For example `font.label = list(size = 14, face = "bold", color = "red")`. To specify only the size and the style, use `font.label = list(size = 14, face = "plain")`.

label.select can be of two formats:

- a character vector specifying some labels to show.
- a list containing one or the combination of the following components:
  - `top.up` and `top.down`: to display the labels of the top up/down points. For example, `label.select = list(top.up = 10, top.down = 4)`.
  - `criteria`: to filter, for example, by x and y variables values, use this: `label.select = list(criteria = "y < 2 & y > 5 & x %in% c('A', 'B')")`.

repel a logical value, whether to use ggrepel to avoid overplotting text labels or not.

label.rectangle logical value. If TRUE, add rectangle underneath the text, making it easier to read.

show.line.label logical value. If TRUE, shows line labels.

position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

ggtheme function, ggplot2 theme name. Default value is `theme_pubr()`. Allowed values include ggplot2 official themes: `theme_gray()`, `theme_bw()`, `theme_minimal()`, `theme_classic()`, `theme_void()`, ....

Details

The plot can be easily customized using the function `ggpar()`. Read `ggpar` for changing:

- main title and axis labels: `main`, `xlab`, `ylab`
- axis limits: `xlim`, `ylim` (e.g.: `ylim = c(0, 30)`)  
- axis scales: `xscale`, `yscale` (e.g.: `yscale = "log2"`) 
- color palettes: `palette = "Dark2"` or `palette = c("gray", "blue", "red")`
- legend title, labels and position: `legend = "right"`
- plot orientation: `orientation = c("vertical", "horizontal", "reverse")`
See Also

ggpar, ggbarplot

Examples

# Data
df <- data.frame(dose=c("D0.5", "D1", "D2"),
  len=c(4.2, 10, 29.5))
print(df)

# Basic plot
# ++++++++++++++++++++++++++
ggline(df, x = "dose", y = "len")

# Plot with multiple groups
# +++++++++++++++++++++++

# Create some data
df2 <- data.frame(supp=rep(c("VC", "OJ"), each=3),
  dose=rep(c("D0.5", "D1", "D2"),2),
  len=c(6.8, 15, 33, 4.2, 10, 29.5))
print(df2)

# Plot "len" by "dose" and
# Change line types and point shapes by a second groups: "supp"
ggline(df2, "dose", "len",
  linetype = "supp", shape = "supp")

# Change colors
# ++++++++++++++++++++++

# Change color by group: "supp"
# Use custom color palette
ggline(df2, "dose", "len",
  linetype = "supp", shape = "supp",
  color = "supp", palette = c("#00AFBB", "#E7B800"))

# Add points and errors
# ++++++++++++++++++++++++

# Data: ToothGrowth data set we'll be used.
df3 <- ToothGrowth
head(df3, 10)

# It can be seen that for each group we have
# different values
ggline(df3, x = "dose", y = "len")

# Visualize the mean of each group
ggline(df3, x = "dose", y = "len",
       add = "mean")

# Add error bars: mean_se
# (other values include: mean_sd, mean_ci, median_iqr, ....)
# Add labels
ggline(df3, x = "dose", y = "len", add = "mean_se")

# Change error.plot to "pointrange"
ggline(df3, x = "dose", y = "len",
       add = "mean_se", error.plot = "pointrange")

# Add jitter points and errors (mean_se)
ggline(df3, x = "dose", y = "len",
       add = c("mean_se", "jitter"))

# Add dot and errors (mean_se)
ggline(df3, x = "dose", y = "len",
       add = c("mean_se", "dotplot"), color = "steelblue")

# Add violin and errors (mean_se)
ggline(df3, x = "dose", y = "len",
       add = c("mean_se", "violin"), color = "steelblue")

# Multiple groups with error bars
# ++++++++++++++++++++++

ggline(df3, x = "dose", y = "len", color = "supp",
       add = "mean_se", palette = c("#00AFBB", "#E7B800"))

# Add jitter

ggline(df3, x = "dose", y = "len", color = "supp",
       add = c("mean_se", "jitter"), palette = c("#00AFBB", "#E7B800"))

# Add dot plot

ggline(df3, x = "dose", y = "len", color = "supp",
       add = c("mean_se", "dotplot"), palette = c("#00AFBB", "#E7B800"))

---

**ggmaplot**

MA-plot from means and log fold changes

**Description**

Make MA-plot which is a scatter plot of log2 fold changes (M, on the y-axis) versus the average expression signal (A, on the x-axis). $M = \log_2(x/y)$ and $A = (\log_2(x) + \log_2(y))/2 = \log_2(xy)^{1/2}$, where x and y are respectively the mean of the two groups being compared.
Usage

ggmaplot(
  data,
  fdr = 0.05,
  fc = 1.5,
  genenames = NULL,
  detection_call = NULL,
  size = NULL,
  alpha = 1,
  font.label = c(12, "plain", "black"),
  label.rectangle = FALSE,
  palette = c("#B31B21", "#1465AC", "darkgray"),
  top = 15,
  select.top.method = c("padj", "fc"),
  label.select = NULL,
  main = NULL,
  xlab = "Log2 mean expression",
  ylab = "Log2 fold change",
  ggtheme = theme_classic(),
  ...
)

Arguments

data an object of class DESeqResults, get_diff, DE_Results, matrix or data frame containing the columns baseMean (or baseMeanLog2), log2FoldChange, and padj. Rows are genes.

Two possible formats are accepted for the input data:

  1/ baseMean | log2FoldChange | padj. This is a typical output from DESeq2 pipeline. Here, we’ll use log2(baseMean) as the x-axis variable.

  2/ baseMeanLog2 | log2FoldChange | padj. Here, baseMeanLog2 is assumed to be the mean of logged values; so we’ll use it as the x-axis variable without any transformation. This is the real A in MA plot. In other words, it is the average of two log-scales values: $A = (\log2(x) + \log2(y))/2 = \log2(xy)^{1/2}$

Terminology:

  • baseMean: the mean expression of genes in the two groups.
  • log2FoldChange: the log2 fold changes of group 2 compared to group 1
  • padj: the adjusted p-value of the used statistical test.

fdr Accepted false discovery rate for considering genes as differentially expressed.

fc the fold change threshold. Only genes with a fold change >= fc and padj <= fdr are considered as significantly differentially expressed.

genenames a character vector of length nrow(data) specifying gene names corresponding to each row. Used for point labels.
detection_call a numeric vector with length = nrow(data), specifying if the genes is expressed (value = 1) or not (value = 0). For example detection_call = c(1, 1, 0, 1, 0, 1). Default is NULL. If detection_call column is available in data, it will be used.

size points size.

alpha numeric value between 0 and 1 specifying point alpha for controlling transparency. For example, use alpha = 0.5.

font.label a vector of length 3 indicating respectively the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of point labels. For example font.label = c(14, "bold", "red").

label.rectangle logical value. If TRUE, add rectangle underneath the text, making it easier to read.

palette the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".

top the number of top genes to be shown on the plot. Use top = 0 to hide to gene labels.

select.top.method methods to be used for selecting top genes. Allowed values include "padj" and "fc" for selecting by adjusted p values or fold changes, respectively.

label.select character vector specifying some labels to show.

main plot main title.

xlab character vector specifying x axis labels. Use xlab = FALSE to hide xlab.

ylab character vector specifying y axis labels. Use ylab = FALSE to hide ylab.

ggtheme function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....

... other arguments to be passed to ggpar.

Value

returns a ggplot.

Examples

data(diff_express)

# Default plot
ggmaplot(diff_express, main = expression("Group 1" %->% "Group 2"),
    fdr = 0.05, fc = 2, size = 0.4,
    palette = c("#B31B21", "#1F78B4", "darkgray"),
    genenames = as.vector(diff_express$name),
    legend = "top", top = 20,
    font.label = c("bold", 11),

font.legend = "bold",
font.main = "bold",
ggtheme = ggplot2::theme_minimal()

# Add rectangle around labels
ggmaplot(diff_express, main = expression("Group 1" %->% "Group 2"),
    fdr = 0.05, fc = 2, size = 0.4,
    palette = c("#B31B21", "#1465AC", "darkgray"),
    genenames = as.vector(diff_express$name),
    legend = "top", top = 20,
    font.label = c("bold", 11), label.rectangle = TRUE,
    font.legend = "bold",
    font.main = "bold",
    ggtheme = ggplot2::theme_minimal()
)

# Select specific genes to show
# set top = 0, then specify genes using label.select argument
ggmaplot(diff_express, main = expression("Group 1" %->% "Group 2"),
    fdr = 0.05, fc = 2, size = 0.4,
    genenames = as.vector(diff_express$name),
    ggtheme = ggplot2::theme_minimal(),
    top = 0, label.select = c("BUB1", "CD83")
)

---

ggpaired  
Plot Paired Data

Description
Plot paired data.

Usage
```r
ggpaired(
  data,
  cond1,
  cond2,
  x = NULL,
  y = NULL,
  id = NULL,
  color = "black",
  fill = "white",
  palette = NULL,
  width = 0.5,
  point.size = 1.2,
  line.size = 0.5,
  line.color = "black",
  linetype = "solid",
  font.legend = "bold",
  font.main = "bold",
  ggtheme = ggplot2::theme_minimal()
)
```
title = NULL,
  xlab = "Condition",
  ylab = "Value",
  facet.by = NULL,
  panel.labs = NULL,
  short.panel.labs = TRUE,
  label = NULL,
  font.label = list(size = 11, color = "black"),
  label.select = NULL,
  repel = FALSE,
  label.rectangle = FALSE,
  ggtheme = theme_pubr(),
  ...
)

Arguments

data a data frame
cond1 variable name corresponding to the first condition.
cond2 variable name corresponding to the second condition.
x, y x and y variables, where x is a grouping variable and y contains values for each
group. Considered only when cond1 and cond2 are missing.
id variable name corresponding to paired samples' id. Used to connect paired
points with lines.
color points and box plot colors. To color by conditions, use color = "condition".
fill box plot fill color. To change fill color by conditions, use fill = "condition".
palette the color palette to be used for coloring or filling by groups. Allowed values
include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues",
...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes
from ggscl R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago",
"simpsons" and "rickandmorty".
width box plot width.
point.size, line.size point and line size, respectively.
line.color line color.
linetype line type.
title plot main title.
xlab character vector specifying x axis labels. Use xlab = FALSE to hide xlab.
ylab character vector specifying y axis labels. Use ylab = FALSE to hide ylab.
facet.by character vector, of length 1 or 2, specifying grouping variables for faceting the
plot into multiple panels. Should be in the data.
panel.labs a list of one or two character vectors to modify facet panel labels. For example,
panel.labs = list(sex = c("Male", "Female")) specifies the labels for the "sex"
variable. For two grouping variables, you can use for example panel.labs =
list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2")) .
short.panel.labs

logical value. Default is TRUE. If TRUE, create short labels for panels by omitting variable names; in other words panels will be labelled only by variable grouping levels.

label

the name of the column containing point labels. Can be also a character vector with length = nrow(data).

font.label

a list which can contain the combination of the following elements: the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of labels. For example font.label = list(size = 14, face = "bold", color ="red"). To specify only the size and the style, use font.label = list(size = 14, face = "plain").

label.select

can be of two formats:

- a character vector specifying some labels to show.
- a list containing one or the combination of the following components:
  - top.up and top.down: to display the labels of the top up/down points. For example, label.select = list(top.up = 10, top.down = 4).
  - criteria: to filter, for example, by x and y variables values, use this: label.select = list(criteria = "y > 2 & y < 5 & x %in% c('A', 'B')").

repel

a logical value, whether to use ggrepel to avoid overplotting text labels or not.

label.rectangle

logical value. If TRUE, add rectangle underneath the text, making it easier to read.

ggtheme

function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....

... other arguments to be passed to be passed to ggpar().

Examples

# Example 1

before <-c(200.1, 190.9, 192.7, 213, 241.4, 196.9, 172.2, 185.5, 205.2, 193.7)
after <-c(392.9, 393.2, 345.1, 393, 434, 427.9, 422, 383.9, 392.3, 352.2)
d <- data.frame(before = before, after = after)
ggpaired(d, cond1 = "before", cond2 = "after", fill = "condition", palette = "jco")

# Example 2

ggpaired(ToothGrowth, x = "supp", y = "len", color = "supp", line.color = "gray", line.size = 0.4, palette = "npg")
ggpar

Graphical parameters

Description

Graphical parameters

Usage

ggpar(
  p,
  palette = NULL,
  gradient.cols = NULL,
  main = NULL,
  submain = NULL,
  caption = NULL,
  xlab = NULL,
  ylab = NULL,
  title = NULL,
  subtitle = NULL,
  font.main = NULL,
  font.submain = NULL,
  font.x = NULL,
  font.y = NULL,
  font.caption = NULL,
  font.title = NULL,
  font.subtitle = NULL,
  font.family = "",
  xlim = NULL,
  ylim = NULL,
  xscale = c("none", "log2", "log10", "sqrt"),
  yscale = c("none", "log2", "log10", "sqrt"),
  format.scale = FALSE,
  legend = NULL,
  legend.title = NULL,
  font.legend = NULL,
  ticks = TRUE,
  tickslab = TRUE,
  font.tickslab = NULL,
  font.xtickslab = font.tickslab,
  font.ytickslab = font.tickslab,
  x.text.angle = NULL,
  y.text.angle = NULL,
  xtickslab.rt = x.text.angle,
  ytickslab.rt = y.text.angle,
  xticks.by = NULL,
  yticks.by = NULL,
rotate = FALSE,
orientation = c("vertical", "horizontal", "reverse"),
ggtheme = NULL,
...
)

Arguments

p     an object of class ggplot or a list of ggplots
palette the color palette to be used for coloring or filling by groups. Allowed values include 'grey' for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty". Can be also a numeric vector of length(groups); in this case a basic color palette is created using the function palette.
gradient.cols vector of colors to use for n-colour gradient. Allowed values include brewer and ggsci color palettes.
main, title plot main title.
submain, subtitle plot subtitle.
caption plot caption.
xlab character vector specifying x axis labels. Use xlab = FALSE to hide xlab.
ylab character vector specifying y axis labels. Use ylab = FALSE to hide ylab.
font.main, font.submain, font.caption, font.x, font.y a vector of length 3 indicating respectively the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of main title, subtitle, caption, xlab and ylab, respectively. For example font.x = c(14, "bold", "red"). Use font.x = 14, to change only font size; or use font.x = "bold", to change only font face.
font.title, font.subtitle alias of font.submain and font.submain, respectively.
font.family character vector specifying font family.
xlim, ylim a numeric vector of length 2, specifying x and y axis limits (minimum and maximum), respectively. e.g.: ylim = c(0, 50).
xscale, yscale x and y axis scale, respectively. Allowed values are one of c("none", "log2", "log10", "sqrt"); e.g.: yscale="log2".
format.scale logical value. If TRUE, axis tick mark labels will be formatted when xscale or yscale = "log2" or "log10".
legend character specifying legend position. Allowed values are one of c("top", "bottom", "left", "right", "none"). To remove the legend use legend = "none". Legend position can be also specified using a numeric vector c(x, y); see details section.
legend.title, e.g.: legend.title = "Species". Can be also a list, legend.title = list(color = "Species", linetype = "Species", shape = "Species").
font.legend logical value. Default is TRUE. If FALSE, hide axis tick marks.

font.tickslab logical value. Default is TRUE. If FALSE, hide axis tick labels.

font.tickslab, font.xtickslab, font.ytickslab Font style (size, face, color) for tick labels, e.g.: c(14, "bold", "red").

x.text.angle, y.text.angle Numeric value specifying the rotation angle of x and y axis tick labels, respectively. Default value is NULL. For vertical x axis texts use x.text.angle = 90.

xticklab.rt, yticklab.rt Same as x.text.angle and y.text.angle, respectively. Will be deprecated in the near future.

xticks.by, yticks.by numeric value controlling x and y axis breaks, respectively. For example, if yticks.by = 5, a tick mark is shown on every 5. Default value is NULL.

rotate logical value. If TRUE, rotate the graph by setting the plot orientation to horizontal.

orientation change the orientation of the plot. Allowed values are one of c( "vertical", "horizontal", "reverse"). Partial match is allowed.

ggtheme function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(),....

Examples

# Load data
data("ToothGrowth")

df <- ToothGrowth

# Basic box plot
# ++++++++++++++++++++++++++++
p <- ggboxplot(df, x = "dose", y = "len")

# Change the plot orientation: horizontal
ggpar(p, orientation = "horiz")

# Change main title and axis labels
# ++++++++++++++++++++++++++++++
ggpar(p,
  main = "Plot of length \n by dose",
  xlab = "Dose (mg)", ylab = "Length")

# Title font styles: 'plain', 'italic', 'bold', 'bold.italic'
ggpar(p,
  main = "Length by dose",
font.main = c(14, "bold.italic", "red"),
font.x = c(14, "bold", "#2E9FDF"),
font.y = c(14, "bold", "#E7B800"))

# Hide axis labels
ggpar(p, xlab = FALSE, ylab = FALSE)

# Change colors
# ++++++++++++++++++++++++
# Change outline colors by groups: dose
p2 <- ggboxplot(df, "dose", "len", color = "dose")
p2

# Use custom color palette
ggpar(p2, palette = c("#00AFBB", "#E7B800", "#FC4E07"))

# Use brewer palette
ggpar(p2, palette = "Dark2")

# Use grey palette
ggpar(p2, palette = "grey")

# Use scientific journal palette from ggsci package
ggpar(p2, palette = "npg") # nature

# Axis ticks, limits, scales
# +++++++++++++++++++++++++
# Axis ticks labels and rotation
# ggpar(p,
# font.tickslab = c(14,"bold", "#993333"),
# xtickslab.rt = 45, ytickslab.rt = 45)
# Hide axis ticks and tick labels
# ggpar(p, ticks = FALSE, tickslab = FALSE)

# Axis limits
ggpar(p, ylim = c(0, 50))

# Axis scale
ggpar(p, yscale = "log2")

# Format axis scale
# ggpar(p, yscale = "log2", format.scale = TRUE)

# Legends
# ++++++++++++++++++++++
# Change legend position and title
ggpar(p2,
# legend = "right", legend.title = "Dose (mg)",
# font.legend = c(10, "bold", "red"))
ggparagraph

Draw a Paragraph of Text

Description

Draw a paragraph of text. Splits a long text into multiple lines (by inserting line breaks) so that the output will fit within the current viewport.

Usage

ggparagraph(
  text,
  color = NULL,
  size = NULL,
  face = NULL,
  family = NULL,
  lineheight = NULL
)

## S3 method for class 'splitText'
drawDetails(x, recording)

Arguments

text the text to plot.

color font color, example: color = "black"

size font size, example: size = 12

face font face. Allowed values are one of "plain", "italic", "bold", "bold.italic".

family font family

lineheight Line height, example: lineheight = 2.

x a grid grob

recording a logical value indicating whether a grob is being added to the display list or redrawn from the display list.

Author(s)

Alboukadel Kassambara <alboukadel.kassambara@gmail.com>

Examples

# Density plot
density.p <- ggdensity(iris, x = "Sepal.Length",
  fill = "Species", palette = "jco")

# Text plot
text <- paste("iris data set gives the measurements in cm",

"of the variables sepal length and width",
"and petal length and width, respectively."
"for 50 flowers from each of 3 species of iris."
"The species are Iris setosa, versicolor, and virginica.")

```r
text.p <- ggparagraph(text, face = "italic", size = 12)
```

# Arrange the plots on the same page
```r
ggarrange(density.p, text.p,
  ncol = 1, nrow = 2,
  heights = c(1, 0.3))
```

---

**ggpie**

*Pie chart*

**Description**

Create a pie chart.

**Usage**

```r
ggpie(
  data,
  x,
  label = x,
  lab.pos = c("out", "in"),
  lab.adjust = 0,
  lab.font = c(4, "bold", "black"),
  font.family = "",
  color = "black",
  fill = "white",
  palette = NULL,
  size = NULL,
  ggtheme = theme_pubr(),
  ...
)
```

**Arguments**

- `data`: a data frame
- `x`: variable containing values for drawing.
- `label`: variable specifying the label of each slice.
- `lab.pos`: character specifying the position for labels. Allowed values are "out" (for outside) or "in" (for inside).
- `lab.adjust`: numeric value, used to adjust label position when `lab.pos = "in"`. Increase or decrease this value to see the effect.
lab.font

A vector of length 3 indicating respectively the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of label font. For example `lab.font = c(4, "bold", "red")`.

font.family

A character vector specifying font family.

color, fill

The color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorthy".

size

A numeric value (e.g.: size = 1). Change the size of points and outlines.

ggtheme

A function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ... etc.

... other arguments to be passed to be passed to ggpar().

Details

The plot can be easily customized using the function ggpar(). Read ?ggpar for changing:

- main title and axis labels: main, xlab, ylab
- axis limits: xlim, ylim (e.g.: ylim = c(0, 30))
- axis scales: xscale,yscale (e.g.: yscale = "log2")
- color palettes: palette = "Dark2" or palette = c("gray", "blue", "red")
- legend title, labels and position: legend = "right"
- plot orientation: orientation = c("vertical", "horizontal", "reverse")

See Also

ggpar, ggline

Examples

```r
# Data: Create some data
# +++++++++++++++++++++++++++++++

df <- data.frame(
    group = c("Male", "Female", "Child"),
    value = c(25, 25, 50))

head(df)

# Basic pie charts
# +++++++++++++++++++++++++++++++
```
ggpie(df, "value", label = "group")

# Change color
# ++++++++++++++++++++++++++++++++

# Change fill color by group
# set line color to white
# Use custom color palette
ggpie(df, "value", label = "group",
      fill = "group", color = "white",
      palette = c("#00AFBB", "#E7B800", "#FC4E07") )

# Change label
# ++++++++++++++++++++++++++++++++

# Show group names and value as labels
labs <- paste0(df$group, " (", df$value, ")")

ggpie(df, "value", label = labs,
      fill = "group", color = "white",
      palette = c("#00AFBB", "#E7B800", "#FC4E07") )

# Change the position and font color of labels

ggpie(df, "value", label = labs,
      lab.pos = "in", lab.font = "white",
      fill = "group", color = "white",
      palette = c("#00AFBB", "#E7B800", "#FC4E07") )

---

ggpubr General Arguments Description

Description

ggpubr General Arguments Description

Arguments

data a data frame

x character string containing the name of x variable.

y character vector containing one or more variables to plot

combine logical value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of y variables.
merge  logical or character value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, merge multiple y variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If merge = "flip", then y variables are used as x tick labels and the x variable is used as grouping variable.

color  outline color.

fill  fill color.

palette  the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorta".

linetype  line types.

size  Numeric value (e.g.: size = 1). change the size of points and outlines.

select  character vector specifying which items to display.

remove  character vector specifying which items to remove from the plot.

order  character vector specifying the order of items.

add  character vector for adding another plot element (e.g.: dot plot or error bars). Allowed values are one or the combination of: "none", "dotplot", "jitter", "boxplot", "point", "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", "median", "median_iqr", "median_mad", "median_range"; see ?desc.statby for more details.

add.params  parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: add.params = list(color = "red").

error.plot  plot type used to visualize error. Allowed values are one of c("pointrange", "linerange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linerange", "lower_linerange"). Default value is "pointrange" or "errorbar". Used only when add != "none" and add contains one "mean_*" or "med_*" where "+*" = sd, se, ....

font.label  a list which can contain the combination of the following elements: the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of labels. For example font.label = list(size = 14, face = "bold", color ="red"). To specify only the size and the style, use font.label = list(size = 14, face = "plain").

title  plot main title.

xlab  character vector specifying x axis labels. Use xlab = FALSE to hide xlab.

ylab  character vector specifying y axis labels. Use ylab = FALSE to hide ylab.

ggtheme  function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....
**ggpubr_options**

*Global Options for GGPlot*

**Description**

Displays allowed global options in ggpubr.

**Usage**

```r
ggpubr_options()
```

**Examples**

```r
ggpubr_options()
```

---

**ggqqplot**

*QQ Plots*

**Description**

Quantile-Quantile plot.

**Usage**

```r
ggqqplot(
data, x, combine = FALSE, merge = FALSE, color = "black", palette = NULL, size = NULL, shape = NULL, add = c("qqline", "none"), add.params = list(linetype = "solid"), conf.int = TRUE, conf.int.level = 0.95, title = NULL, xlab = NULL, ylab = NULL, facet.by = NULL, panel.labs = NULL, short.panel.labs = TRUE, ggtheme = theme_pubr(), ...)
```

...
Arguments

data
- a data frame

x
- variable to be drawn.

combine
- logical value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of y variables.

merge
- logical or character value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, merge multiple y variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If merge = "flip", then y variables are used as x tick labels and the x variable is used as grouping variable.

color
- point color.

palette
- the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".

size
- point size.

shape
- point shape.

add
- character vector. Allowed values are one of "none" and "qqline" (for addingqqline).

add.params
- parameters (color, size, linetype) for the argument 'add'; e.g.: add.params = list(color = "red").

conf.int
- logical value. If TRUE, confidence interval is added.

conf.int.level
- the confidence level. Default value is 0.95.

title
- plot main title.

xlab
- character vector specifying x axis labels. Use xlab = FALSE to hide xlab.

ylab
- character vector specifying y axis labels. Use ylab = FALSE to hide ylab.

facet.by
- character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.

panel.labs
- a list of one or two character vectors to modify facet panel labels. For example, panel.labs = list(sex = c("Male", "Female")) specifies the labels for the "sex" variable. For two grouping variables, you can use for example panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2") ).

short.panel.labs
- logical value. Default is TRUE. If TRUE, create short labels for panels by omitting variable names; in other words panels will be labelled only by variable grouping levels.

ggtheme
- function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....

other arguments to be passed to ggpar.
ggscatter

Details

The plot can be easily customized using the function ggpar(). Read ?ggpar for changing:

- main title and axis labels: main, xlab, ylab
- axis limits: xlim, ylim (e.g.: ylim = c(0, 30))
- axis scales: xscale, yscale (e.g.: yscale = "log2")
- color palettes: palette = "Dark2" or palette = c("gray", "blue", "red")
- legend title, labels and position: legend = "right"
- plot orientation: orientation = c("vertical", "horizontal", "reverse")

See Also

ggpar

Examples

# Create some data format
set.seed(1234)
wdata = data.frame(
  sex = factor(rep(c("F", "M"), each=200)),
  weight = c(rnorm(200, 55), rnorm(200, 58)))

head(wdata, 4)

# Basic QQ plot
ggqqplot(wdata, x = "weight")

# Change colors and shape by groups ("sex")
# Use custom palette
ggqqplot(wdata, x = "weight",
  color = "sex", palette = c("#00AFBB", "#E7B800"))

---

ggscatter

Scatter plot

Description

Create a scatter plot.

Usage

ggscatter(
  data,
  x,
  y,
  combine = FALSE,
Arguments

data  a data frame
x, y  x and y variables for drawing.
combine  logical value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of y variables.
merge  logical or character value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, merge multiple y variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If merge = "flip", then y variables are used as x tick labels and the x variable is used as grouping variable.
color, fill  point colors.
palette  the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
shape  point shape. See show_point_shapes.
size  Numeric value (e.g.: size = 1). change the size of points and outlines.
point  logical value. If TRUE, show points.
rug  logical value. If TRUE, add marginal rug.
title  plot main title.

xlab  character vector specifying x axis labels. Use xlab = FALSE to hide xlab.
ylab  character vector specifying y axis labels. Use ylab = FALSE to hide ylab.
facet.by  character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.

panel.labs  a list of one or two character vectors to modify facet panel labels. For example, panel.labs = list(sex = c("Male", "Female")) specifies the labels for the "sex" variable. For two grouping variables, you can use for example panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2")).

short.panel.labs  logical value. Default is TRUE. If TRUE, create short labels for panels by omitting variable names; in other words panels will be labelled only by variable grouping levels.

add  allowed values are one of "none", "reg.line" (for adding linear regression line) or "loess" (for adding local regression fitting).

add.params  parameters (color, size, linetype) for the argument 'add'; e.g.: add.params = list(color = "red").

conf.int  logical value. If TRUE, adds confidence interval.

conf.int.level  Level controlling confidence region. Default is 95%. Used only when add != "none" and conf.int = TRUE.
fullrange should the fit span the full range of the plot, or just the data. Used only when add != "none".
ellipse logical value. If TRUE, draws ellipses around points.
ellipse.size the size of the concentration ellipse in normal probability.
ellipse.type Character specifying frame type. Possible values are "convex", "confidence" or types supported by **stat_ellipse()** including one of c("t", "norm", "euclid") for plotting concentration ellipses.
  • "convex": plot convex hull of a set of points.
  • "confidence": plot confidence ellipses around group mean points as **FactoMineR::coord.ellipse()**.
  • "t": assumes a multivariate t-distribution.
  • "norm": assumes a multivariate normal distribution.
  • "euclid": draws a circle with the radius equal to level, representing the euclidean distance from the center. This ellipse probably won’t appear circular unless **coord_fixed()** is applied.
ellipse.alpha Alpha for ellipse specifying the transparency level of fill color. Use alpha = 0 for no fill color.
ellipse.border.remove logical value. If TRUE, remove ellipse border lines.
mean.point logical value. If TRUE, group mean points are added to the plot.
mean.point.size numeric value specifying the size of mean points.
star.plot logical value. If TRUE, a star plot is generated.
star.plot.lty, star.plot.lwd line type and line width (size) for star plot, respectively.
label the name of the column containing point labels. Can be also a character vector with length = nrow(data).
font.label a vector of length 3 indicating respectively the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of point labels. For example **font.label = c(14, "bold", "red")**. To specify only the size and the style, use **font.label = c(14, "plain")**.
font.family character vector specifying font family.
label.select character vector specifying some labels to show.
repel a logical value, whether to use ggrepel to avoid overplotting text labels or not.
label.rectangle logical value. If TRUE, add rectangle underneath the text, making it easier to read.
parse If TRUE, the labels will be parsed into expressions and displayed as described in ?plotmath.
cor.coef logical value. If TRUE, correlation coefficient with the p-value will be added to the plot.
cor.coef.args a list of arguments to pass to the function **stat_cor** for customizing the displayed correlation coefficients. For example: **cor.coef.args = list(method = "pearson", label.x.npc = "right", label.y.npc = "top")**.
cor.method method for computing correlation coefficient. Allowed values are one of "pearson", "kendall", or "spearman".

cor.coef.coord numeric vector, of length 2, specifying the x and y coordinates of the correlation coefficient. Default values are NULL.

cor.coef.size correlation coefficient text font size.

ggp a ggplot. If not NULL, points are added to an existing plot.

show.legend.text logical. Should text be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.

ggtheme function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....

... other arguments to be passed to geom_point and ggpar.

Details

The plot can be easily customized using the function ggpar(). Read ?ggpar for changing:

• main title and axis labels: main, xlab, ylab
• axis limits: xlim, ylim (e.g.: ylim = c(0, 30))
• axis scales: xscale, yscale (e.g.: yscale = "log2")
• color palettes: palette = "Dark2" or palette = c("gray", "blue", "red")
• legend title, labels and position: legend = "right"
• plot orientation : orientation = c("vertical", "horizontal", "reverse")

See Also

stat_cor, stat_stars, stat_conf_ellipse and ggpar.

Examples

# Load data
data("mtcars")
df <- mtcars
df$cyl <- as.factor(df$cyl)
head(df[, c("wt", "mpg", "cyl")], 3)

# Basic plot
# +++++++++++++++++++++++++++
ggscatter(df, x = "wt", y = "mpg",
    color = "black", shape = 21, size = 3, # Points color, shape and size
    add = "reg.line", # Add regressin line
    add.params = list(color = "blue", fill = "lightgray"), # Customize reg. line
    conf.int = TRUE, # Add confidence interval
    cor.coef = TRUE, # Add correlation coefficient. see ?stat_cor
    cor.coef.args = list(method = "pearson", label.x = 3, label.sep = "\n")
)
# loess method: local regression fitting
ggscatter(df, x = "wt", y = "mpg",
         add = "loess", conf.int = TRUE)

# Control point size by continuous variable values ("qsec")
ggscatter(df, x = "wt", y = "mpg",
         color = "#00AFBB", size = "qsec")

# Change colors
# ++++++++++++++++++++++++++
# Use custom color palette
# Add marginal rug
ggscatter(df, x = "wt", y = "mpg", color = "cyl",
          palette = c("#00AFBB", "#E7B800", "#FC4E07") )

# Add group ellipses and mean points
# Add stars
# +++++++++++++++
ggscatter(df, x = "wt", y = "mpg",
          color = "cyl", shape = "cyl",
          palette = c("#00AFBB", "#E7B800", "#FC4E07"),
          ellipse = TRUE, mean.point = TRUE,
          star.plot = TRUE)

# Textual annotation
# ++++++++++++++++++
# df$name <- rownames(df)
# ggscatter(df, x = "wt", y = "mpg",
#          color = "cyl", palette = c("#00AFBB", "#E7B800", "#FC4E07"),
#          label = "name", repel = TRUE)

ggscatterhist

Scatter Plot with Marginal Histograms

Description

Create a scatter plot with marginal histograms, density plots or box plots.

Usage

ggscatterhist(
  data,
```r
x, y, group = NULL, color = "black", fill = NA, palette = NULL, shape = 19, size = 2, linetype = "solid", bins = 30, margin.plot = c("density", "histogram", "boxplot"), margin.params = list(), margin.ggtheme = theme_void(), margin.space = FALSE, main.plot.size = 2, margin.plot.size = 1, title = NULL, xlab = NULL, ylab = NULL, legend = "top", ggtheme = theme_pubr(), print = TRUE,
... )

## S3 method for class 'ggscatterhist'
print(
  x, margin.space = FALSE, main.plot.size = 2, margin.plot.size = 1, title = NULL, legend = "top",
  ...
)

Arguments

data a data frame
x an object of class ggscatterhist.
y x and y variables for drawing.

group a grouping variable. Change points color and shape by groups if the options color and shape are missing. Should be also specified when you want to create a marginal box plot that is grouped.
color point colors.
fill point colors.
```
palette the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".

shape point shape. See show_point_shapes.

size Numeric value (e.g.: size = 1). change the size of points and outlines.

linetype line type ("solid", "dashed", ...)

bins Number of histogram bins. Defaults to 30. Pick a better value that fit to your data.

margin.plot the type of the marginal plot. Default is "hist".

margin.params parameters to be applied to the marginal plots.

margin.ggtheme the theme of the marginal plot. Default is theme_void().

margin.space logical value. If TRUE, adds space between the main plot and the marginal plot.

main.plot.size the width of the main plot. Default is 2.

margin.plot.size the width of the marginal plot. Default is 1.

title plot main title.

xlab character vector specifying x axis labels. Use xlab = FALSE to hide xlab.

ylab character vector specifying y axis labels. Use ylab = FALSE to hide ylab.

legend specify the legend position. Allowed values include: "top", "bottom", "left", "right".

ggtheme the theme to be used for the scatter plot. Default is theme_pubr().

print logical value. If TRUE (default), print the plot.

... other arguments passed to the function ggscatter().

Value an object of class ggscatterhist, which is list of ggplots, including the following elements:

- sp: main scatter plot;
- xplot: marginal x-axis plot;
- yplot: marginal y-axis plot.

User can modify each of plot before printing.

Examples

# Basic scatter plot with marginal density plot
ggscatterhist(iris, x = "Sepal.Length", y = "Sepal.Width", color = "#00AFBB", margin:params = list(fill = "lightgray"))
# Grouped data
ggscatterhist(
  iris, x = "Sepal.Length", y = "Sepal.Width",
  color = "Species", size = 3, alpha = 0.6,
  palette = c("#00AFBB", "#E7B800", "#FC4E07"),
  margin.params = list(fill = "Species", color = "black", size = 0.2)
)

# Use boxplot as marginal
ggscatterhist(
  iris, x = "Sepal.Length", y = "Sepal.Width",
  color = "Species", size = 3, alpha = 0.6,
  palette = c("#00AFBB", "#E7B800", "#FC4E07"),
  margin.plot = "boxplot",
  ggtheme = theme_bw()
)

# Add vertical and horizontal line to a gscatterhist
plots <- gscatterhist(iris, x = "Sepal.Length", y = "Sepal.Width", print = FALSE)
plots$sp <- plots$sp +
  geom_hline(yintercept = 3, linetype = "dashed", color = "blue") +
  geom_vline(xintercept = 6, linetype = "dashed", color = "red")
plots

---

## ggstripchart

### Stripcharts

**Description**

Create a stripchart, also known as one dimensional scatter plots. These plots are suitable compared to box plots when sample sizes are small.

**Usage**

```r
ggstripchart(
  data,
  x,
  y,
  combine = FALSE,
  merge = FALSE,
  color = "black",
  fill = "white",
  palette = NULL,
  title = NULL,
  xlab = NULL,
  ylab = NULL,
  facet.by = NULL,
```
Arguments

data
x
y
combine
merge
color
fill
palette
title
xlab
ylab
facet.by

a data frame
character string containing the name of x variable.
character vector containing one or more variables to plot
logical value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of y variables.
logical or character value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, merge multiple y variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If merge = "flip", then y variables are used as x tick labels and the x variable is used as grouping variable.
outline color.
fill color.
the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
plot main title.
character vector specifying x axis labels. Use xlab = FALSE to hide xlab.
character vector specifying y axis labels. Use ylab = FALSE to hide ylab.
character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
ggstripchart

panel.labs  a list of one or two character vectors to modify facet panel labels. For example, `panel.labs = list(sex = c("Male", "Female"))` specifies the labels for the "sex" variable. For two grouping variables, you can use for example `panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))`.

short.panel.labs  logical value. Default is TRUE. If TRUE, create short labels for panels by omitting variable names; in other words panels will be labelled only by variable grouping levels.

shape  point shape

size  Numeric value (e.g.: size = 1). change the size of points and outlines.

select  character vector specifying which items to display.

remove  character vector specifying which items to remove from the plot.

order  character vector for adding another plot element (e.g.: dot plot or error bars). Allowed values are one or the combination of: "none", "dotplot", "jitter", "boxplot", "point", "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", "median", "median_iqr", "median_hilow", "median_q1q3", "median_mad", "median_range"; see ?desc_statby for more details.

add.params  parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: `add.params = list(color = "red")`.

error.plot  plot type used to visualize error. Allowed values are one of c("pointrange", "linerange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linerange", "lower_linerange"). Default value is "pointrange" or "errorbar". Used only when `add != "none"` and add contains one "mean_*" or "med_*" where "*" = sd, se, ....

label  the name of the column containing point labels. Can be also a character vector with length = nrow(data).

font.label  a list which can contain the combination of the following elements: the size (e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color (e.g.: "red") of labels. For example `font.label = list(size = 14, face = "bold", color = "red")`. To specify only the size and the style, use `font.label = list(size = 14, face = "plain")`.

label.select  can be of two formats:

  • a character vector specifying some labels to show.
  • a list containing one or the combination of the following components:
    – top. up and top. down: to display the labels of the top up/down points.
      For example, `label.select = list(top.up = 10, top.down = 4)`.
    – criteria: to filter, for example, by x and y variables values, use this:\n      `label.select = list(criteria = "x \> 2 & y \< 5 & x %in% c('A', 'B')")`.

repel  a logical value, whether to use ggrepel to avoid overplotting text labels or not.

label.rectangle  logical value. If TRUE, add rectangle underneath the text, making it easier to read.
ggstripchart

jitter the amount of jitter.
position position adjustment, either as a string, or the result of a call to a position adjustment function. Used to adjust position for multiple groups.
ggtheme function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....

... other arguments to be passed to geom_jitter, ggpar and facet.

Details

The plot can be easily customized using the function ggpar(). Read ?ggpar for changing:

- main title and axis labels: main, xlab, ylab
- axis limits: xlim, ylim (e.g.: ylim = c(0, 30))
- axis scales: xscale, yscale (e.g.: yscale = "log2")
- color palettes: palette = "Dark2" or palette = c("gray", "blue", "red")
- legend title, labels and position: legend = "right"
- plot orientation : orientation = c("vertical", "horizontal", "reverse")

See Also
ggpar, ggviolin, ggdotplot and ggboxplot.

Examples

# Load data
data("ToothGrowth")
df <- ToothGrowth

# Basic plot with summary statistics: mean_se
# +++++++++++++++++++++++++++
# Change point shapes by groups: "dose"
ggstripchart(df, x = "dose", y = "len",
shape = "dose", size = 3,
add = "mean_se")

# Use mean_sd
# Change error.plot to "crossbar"
ggstripchart(df, x = "dose", y = "len",
shape = "dose", size = 3,
add = "mean_sd", add.params = list(width = 0.5),
error.plot = "crossbar")

# Add summary statistics
# +++++++++++++++++++++++++++

# Add box plot
ggstripchart(df, x = "dose", y = "len",
shape = "dose", add = "boxplot")

# Add violin + mean_sd
ggstripchart(df, x = "dose", y = "len",
shape = "dose", add = c("violin", "mean_sd"))

# Change colors
# +++++++++++++++++++++++++
# Change colors by groups: dose
# Use custom color palette
ggstripchart(df, "dose", "len", shape = "dose",
color = "dose", palette = c("#00AFBB", "#E7B800", "#FC4E07"),
add = "mean_sd")

# Plot with multiple groups
# ++++++++ ++++++++++++++++++++
# Change shape and color by a second group : "supp"
ggstripchart(df, "dose", "len", shape = "supp",
color = "supp", palette = c("#00AFBB", "#E7B800"))

# Adjust point position
ggstripchart(df, "dose", "len", shape = "supp",
color = "supp", palette = c("#00AFBB", "#E7B800"),
position = position_dodge(0.8) )

# You can also use position_jitterdodge()
# but fill aesthetic is required
ggstripchart(df, "dose", "len", shape = "supp",
color = "supp", palette = c("#00AFBB", "#E7B800"),
position = position_jitterdodge() )

# Add boxplot
ggstripchart(df, "dose", "len", shape = "supp",
color = "supp", palette = c("#00AFBB", "#E7B800"),
add = "boxplot", add.params = list(color = "black") )

---

ggsummarytable  
**GGPLOT with Summary Stats Table Under the Plot**

**Description**

Create a ggplot with summary stats (n, median, mean, iqr) table under the plot. Read more: How to Create a Beautiful Plots in R with Summary Statistics Labels.
Usage

ggsummarytable(
  data,
  x,
  y,
  digits = 0,
  size = 3,
  color = "black",
  palette = NULL,
  facet.by = NULL,
  labeller = "label_value",
  position = "identity",
  ggtheme = theme_pubr(),
  ...
)

ggsummarystats(
  data,
  x,
  y,
  summaries = c("n", "median", "iqr"),
  gfunc = ggboxplot,
  color = "black",
  fill = "white",
  palette = NULL,
  facet.by = NULL,
  free.panels = FALSE,
  labeller = "label_value",
  heights = c(0.8, 0.2),
  digits = 0,
  table.font.size = 3,
  ggtheme = theme_pubr(),
  ...
)

## S3 method for class 'ggsummarystats'
print(x, heights = c(0.8, 0.2), ...)

## S3 method for class 'ggsummarystats_list'
print(x, heights = c(0.8, 0.2), legend = NULL, ...)

Arguments

data a data frame
x a list of ggsummarystats.
y character vector containing one or more variables to plot
digits integer indicating the number of decimal places (round) to be used.
size

Numeric value (e.g.: size = 1). change the size of points and outlines.

color

outline color.

palette

the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".

facet.by

character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.

labeller

Character vector. An alternative to the argument short.panel.labs. Possible values are one of "label_both" (panel labelled by both grouping variable names and levels) and "label_value" (panel labelled with only grouping levels).

position

Position adjustment, either as a string, or the result of a call to a position adjustment function.

ggtheme

function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....

... other arguments passed to the function ggpar(), facet() or ggarrange() when printing the plot.

summaries

summary stats to display in the table. Possible values are those returned by the function get_summary_stats(), including: "n", "min", "max", "median", "q1", "q2", "q3", "mad", "mean", "sd", "se", "ci".

ggfunc

a ggpubr function, including: ggboxplot, ggviolin, ggdotplot, ggbarplot, ggline, etc. Can be any other ggplot function that accepts the following arguments data, x, color, fill, palette, ggtheme, facet.by.

fill

fill color.

free.panels

logical. If TRUE, create free plot panels when the argument facet.by is specified.

heights

a numeric vector of length 2, specifying the heights of the main and the summary table, respectively.

table.font.size

the summary table font size.

legend

character specifying legend position. Allowed values are one of c("top", "bottom", "left", "right", "none"). To remove the legend use legend = "none".

Functions

- ggsummarytable: Create a table of summary stats
- ggsummarystats: Create a ggplot with a summary stat table under the plot.

Examples

# Data preparation
#:::::::::::::::::::::::::::::::::::::::::::::::::
data("ToothGrowth")
df <- ToothGrowth
df$dose <- as.factor(df$dose)
# Add random QC column
set.seed(123)
qc <- rep(c("pass", "fail"), 30)
df$qc <- as.factor(sample(qc, 60))
# Inspect the data
head(df)

# Basic summary stats
#::::::::::::::::::::::::::::::::::::::::::::::::
# Compute summary statistics
summary.stats <- df %>%
  group_by(dose) %>%
ggsummarystats(type = "common")
summary.stats

# Visualize summary table
ggsummarytable(
  summary.stats, x = "dose", y = c("n", "median", "iqr"),
ggtheme = theme_bw()
)

# Create plots with summary table under the plot
#::::::::::::::::::::::::::::::::::::::::::::::::
# Basic plot
ggsummarystats(
  df, x = "dose", y = "len",
ggfunc = ggboxplot, add = "jitter"
)

# Color by groups
ggsummarystats(
  df, x = "dose", y = "len",
ggfunc = ggbarplot, add = "jitter",
  color = "dose", palette = "npg"
)

# Create a barplot
ggsummarystats(
  df, x = "dose", y = "len",
ggfunc = ggbarplot, add = c("jitter", "median_iqr"),
  color = "dose", palette = "npg"
)

# Facet
#::::::::::::::::::::::::::::::::::::::::::::::::
# Specify free.panels = TRUE for free panels
ggsummarystats(
  df, x = "dose", y = "len",
ggfunc = ggboxplot, add = "jitter",
  free.panels = TRUE
)
ggtext

Text

Description

Add text to a plot.

Usage

```r
ggtext(
  data,
  x = NULL,
  y = NULL,
  label = NULL,
  color = "black",
  palette = NULL,
  size = 11,
  face = "plain",
  family = "",
  show.legend = NA,
  label.select = NULL,
  repel = FALSE,
  label.rectangle = FALSE,
  parse = FALSE,
  grouping.vars = NULL,
  position = "identity",
  ggp = NULL,
  ggtheme = theme_pubr(),
  ...
)
```

Arguments

data
  a data frame

x, y
  x and y variables for drawing.

label
  the name of the column containing point labels. Can be also a character vector with length = nrow(data).

color
  text font color.
palette  the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "hpg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".

size text font size.

face text font style. Allowed values are one of c("plain", "bold", "italic", "bold.italic").

family character vector specifying font family.

show.legend logical. Should text be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.

label.select can be of two formats:
- a character vector specifying some labels to show.
- a list containing one or the combination of the following components:
  - top.up and top.down: to display the labels of the top up/down points. For example, label.select = list(top.up = 10, top.down = 4).
  - criteria: to filter, for example, by x and y variables values, use this:
    label.select = list(criteria = "x > 2 & y < 5 & x %in% c('A', 'B')").

repel a logical value, whether to use ggrepel to avoid overplotting text labels or not.

label.rectangle logical value. If TRUE, add rectangle underneath the text, making it easier to read.

parse If TRUE, the labels will be parsed into expressions and displayed as described in ?plotmath.

grouping.vars grouping variables to sort the data by, when the user wants to display the top n up/down labels.

position Position adjustment, either as a string, or the result of a call to a position adjustment function.

gg a ggplot. If not NULL, points are added to an existing plot.

ggtheme function, ggplot2 theme name. Default value is theme_pubr(). Allowed values include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(), theme_classic(), theme_void(), ....

... other arguments to be passed to ggpar.

Details

The plot can be easily customized using the function ggpar(). Read ?ggpar for changing:

- main title and axis labels: main, xlab, ylab
- axis limits: xlim, ylim (e.g.: ylim = c(0, 30))
- axis scales: xscale, yscale (e.g.: yscale = "log2")
- color palettes: palette = "Dark2" or palette = c("gray", "blue", "red")
- legend title, labels and position: legend = "right"
See Also

ggpar

Examples

# Load data
data("mtcars")
.df <- mtcars
df$cyl <- as.factor(df$cyl)
df$name <- rownames(df)
head(df[, c("wt", "mpg", "cyl")], 3)

# Textual annotation
# +++++++++++++++++
ggtext(df, x = "wt", y = "mpg",
color = "cyl", palette = c("#00AFBB", "#E7B800", "#FC4E07"),
label = "name", repel = TRUE)

# Add rectangle around label
ggtext(df, x = "wt", y = "mpg",
color = "cyl", palette = c("#00AFBB", "#E7B800", "#FC4E07"),
label = "name", repel = TRUE, label.rectangle = TRUE)

---

ggtexttable

**Draw a Textual Table**

Description

Draw a textual table.

- `ggtexttable()`: draw a textual table.
- `ttheme()`: customize table theme.
- `rownames_style()`, `colnames_style()`, `tbody_style()`: helper functions to customize the table row names, column names and body.
- `table_cell_font()`: access to a table cell for changing the text font (size and face).
- `table_cell_bg()`: access to a table cell for changing the background (fill, color, linewidth).
- `tab_cell_crossout()`: cross out a table cell.
- `tab_ncol()`, `tab_nrow()`: returns, respectively, the number of columns and rows in a ggtexttable.
- `tab_add_hline()`: Creates horizontal lines or separators at the top or the bottom side of a given specified row.
- `tab_add_vline()`: Creates vertical lines or separators at the right or the left side of a given specified column.
- `tab_add_border()`, `tbody_add_border()`, `thead_add_border()`: Add borders to table; tbody is for table body and thead is for table head.
- `tab_add_title()`, `tab_add_footnote()`: Add title, subtitle and footnote to a table.
Usage

ggtexttable(x,
  rows = rownames(x),
  cols = colnames(x),
  vp = NULL,
  theme = ttheme(),
  ...)


ttheme(
  base_style = "default",
  base_size = 11,
  base_colour = "black",
  padding = unit(c(4, 4), "mm"),
  colnames.style = colnames_style(size = base_size),
  rownames.style = rownames_style(size = base_size),
  tbody.style = tbody_style(size = base_size)
)


colnames_style(
  color = "black",
  face = "bold",
  size = 12,
  fill = "grey80",
  linewidth = 1,
  linecolor = "white",
  parse = FALSE,
  ...
)


rownames_style(
  color = "black",
  face = "italic",
  size = 12,
  fill = NA,
  linewidth = 1,
  linecolor = "white",
  parse = FALSE,
  ...
)

tbody_style(
  color = "black",
  face = "plain",
  size = 12,
  fill = c("grey95", "grey90"),
  linewidth = 1,
linecolor = "white",
parse = FALSE,
...
)

table_cell_font(tab, row, column, face = NULL, size = NULL, color = NULL)

table_cell_bg(
  tab,
  row,
  column,
  fill = NULL,
  color = NULL,
  linewidth = NULL,
  alpha = NULL
)

tab_cell_crossout(
  tab,
  row,
  column,
  linetype = 1,
  linewidth = 1,
  linecolor = "black",
  reduce.size.by = 0
)

tab_ncol(tab)


tab_nrow(tab)

tab_add_hline(
  tab,
  at.row = 2:tab_nrow(tab),
  row.side = c("bottom", "top"),
  from.column = 1,
  to.column = tab_ncol(tab),
  linetype = 1,
  linewidth = 1,
  linecolor = "black"
)

tab_add_vline(
  tab,
  at.column = 2:tab_ncol(tab),
  column.side = c("left", "right"),
  from.row = 1,
  to.row = tab_nrow(tab),

linetype = 1,
linewidth = 1,
linecolor = "black"
)

tab_add_border(
  tab,
  from.row = 2,
  to.row = tab_nrow(tab),
  from.column = 1,
  to.column = tab_ncol(tab),
  linetype = 1,
  linewidth = 1,
  linecolor = "black"
)

tbody_add_border(
  tab,
  from.row = 2,
  to.row = tab_nrow(tab),
  from.column = 1,
  to.column = tab_ncol(tab),
  linetype = 1,
  linewidth = 1,
  linecolor = "black"
)

thead_add_border(
  tab,
  from.row = 1,
  to.row = 1,
  from.column = 1,
  to.column = tab_ncol(tab),
  linetype = 1,
  linewidth = 1,
  linecolor = "black"
)

tab_add_title(
  tab,
  text,
  face = NULL,
  size = NULL,
  color = NULL,
  family = NULL,
  padding = unit(1.5, "line"),
  just = "left",
hjust = NULL,
vjust = NULL
)

tab_add_footnote(
  tab,
  text,
  face = NULL,
  size = NULL,
  color = NULL,
  family = NULL,
  padding = unit(1.5, "line"),
  just = "right",
  hjust = NULL,
  vjust = NULL
)

Arguments

- **x**: a data.frame or matrix.
- **rows**: optional vector to specify row names
- **cols**: optional vector to specify column names
- **vp**: optional viewport
- **theme**: a list, as returned by the function ttheme(), defining the parameters of the table theme. Allowed values include one of ttheme() and ttheme_clean().
- **...**: extra parameters for text justification, e.g.: hjust and x. Default is "centre" for the body and header, and "right" for the row names. Left justification: hjust = 0, x = 0.1. Right justification: hjust = 1, x = 0.9.
- **base_style**: character string the table style/theme. The available themes are illustrated in the ggtexttable-theme.pdf file. Allowed values include one of c("default", "blank", "classic", "minimal", "light", "lBlack", "lBlue", "lRed", "lGreen", "lViolet", "lCyan", "lOrange", "lBlackWhite", "lBlueWhite", "lRedWhite", "lGreenWhite", "lVioletWhite", "lCyanWhite", "lOrangeWhite", "mBlack", "mBlue", "mRed", "mGreen", "mViolet", "mCyan", "mOrange", "mBlackWhite", "mBlueWhite", "mRedWhite", "mGreenWhite", "mVioletWhite", "mCyanWhite", "mOrangeWhite"). Note that, l = "light"; m = "medium".
- **base_size**: default font size
- **base_colour**: default font colour
- **padding**: length-2 unit vector specifying the horizontal and vertical padding of text within each cell
- **colnames.style**: a list, as returned by the function colnames_style(), defining the style of the table column names. Considered only when base_size = "default".
- **rownames.style**: a list, as returned by the function rownames_style(), defining the style of the table row names. Considered only when base_size = "default".
- **tbody.style**: a list, as returned by the function tbody_style(), defining the style of the table body. Considered only when base_size = "default".
color, face, size

text font color, face and size, respectively. Allowed values for face include c("plain", "bold", "italic", "bold.italic").

fill

background color.

linewidth, linecolor

line width and color, respectively.

parse

logical, default behaviour for parsing text as plotmath

tab

an object from ggtexttable or from gridExtra::tableGrob().

row, column

an integer specifying the row and the column numbers for the cell of interest.

alpha

numeric value specifying fill color transparency. Value should be in [0, 1], where 0 is full transparency and 1 is no transparency.

linetype

line type

reduce.size.by

Numeric value in [0, 1] to reduce the size by.

at.row

a numeric vector of row indexes; for example at.row = c(1, 2).

row.side

row side to which the horizontal line should be added. Can be one of c("bottom", "top").

from.column

integer indicating the column from which to start drawing the horizontal line.

to.column

integer indicating the column to which the horizontal line should end.

at.column

a numeric vector of column indexes; for example at.column = c(1, 2).

column.side

column side to which the vertical line should be added. Can be one of c("left", "right").

from.row

integer indicating the row from which to start drawing the horizontal line.

to.row

integer indicating the row to which the vertical line should end.

text

text to be added as title or footnote.

family

font family

just

The justification of the text relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". For numeric values, 0 means left (bottom) alignment and 1 means right (top) alignment.

hjust

A numeric vector specifying horizontal justification. If specified, overrides the just setting.

vjust

A numeric vector specifying vertical justification. If specified, overrides the just setting.

Value

an object of class ggplot.
Examples

# data
df <- head(iris)

# Default table
# Remove row names using rows = NULL
print_ggtexttable(df, rows = NULL)

# Blank theme
print_ggtexttable(df, rows = NULL, theme = ttheme("blank"))

# light theme
print_ggtexttable(df, rows = NULL, theme = ttheme("light"))

# Column names border only
print_ggtexttable(df, rows = NULL, theme = ttheme("blank")) %>%
  tab_add_hline(at.row = 1:2, row.side = "top", linewidth = 2)

# classic theme
print_ggtexttable(df, rows = NULL, theme = ttheme("classic"))

# minimal theme
print_ggtexttable(df, rows = NULL, theme = ttheme("minimal"))

# Medium blue (mBlue) theme
print_ggtexttable(df, rows = NULL, theme = ttheme("mBlue"))

# Customize the table as you want
print_ggtexttable(df, rows = NULL,
  theme = ttheme(
    colnames.style = colnames_style(color = "white", fill = "#8cc257"),
    tbody.style = tbody_style(color = "black", fill = c("#e8f3de", "#d3e8bb"))
  )
)

# Use RColorBrewer palette
# Provide as many fill color as there are rows in the table body, here nrow = 6
print_ggtexttable(df,
  theme = ttheme(
    colnames.style = colnames_style(fill = "white"),
    tbody.style = tbody_style(fill = get_palette("RdBu", 6))
  )
)

# Text justification
#::::::::::::::::::::::::::::::::::::::::::::::
# Default is "centre" for the body and header, and "right" for the row names.
# Left justification: hjust=0, x=0.1
# Right justification: hjust=1, x=0.9
tbody.style = tbody_style(color = "black",
  fill = c("#e8f3de", "#d3e8bb"), hjust=1, x=0.9)
ggtexttable(head(iris), rows = NULL,
  theme = ttheme(
    colnames.style = colnames_style(color = "white", fill = "#8cc257"),
    tbody.style = tbody.style
  )
)

# Access and modify the font and
# the background of table cells
# :::::::::::::::::::::::::::::::::::::::::::::::::
tab <- ggtexttable(head(iris), rows = NULL,
  theme = ttheme("classic"))
tab <- table_cell_font(tab, row = 3, column = 2,
  face = "bold")
tab <- table_cell_bg(tab, row = 4, column = 3, linewidth = 5,
  fill="darkolivegreen1", color = "darkolivegreen4")
tab

# Change table cells background and font for column 3,
# Spaning from row 2 to the last row in the data
tab <- ggtexttable(df, rows = NULL, theme = ttheme("classic"))
tab %>%
  table_cell_bg(row = 2:tab_nrow(tab), column = 3, fill = "darkblue") %>%
  table_cell_font(row = 2:tab_nrow(tab), column = 3, face = "italic", color = "white")

# Add separators and borders
# :::::::::::::::::::::::::::::::::::::::::::::::::::
# Table with blank theme
tab <- ggtexttable(df, theme = ttheme("blank"), rows = NULL)
# Add horizontal and vertical lines
tab %>%
  tab_add_hline(at.row = c(1, 2), row.side = "top", linewidth = 3, linetype = 1) %>%
  tab_add_hline(at.row = c(7), row.side = "bottom", linewidth = 3, linetype = 1) %>%
  tab_add_vline(at.column = 2:tab_ncol(tab), column.side = "left", from.row = 2, linetype = 2)

# Add borders to table body and header
# Cross out some cells
  tab %>%
  tbody_add_border() %>%
  thead_add_border() %>%
  tab_cell_crossout(
    row = c(2, 4), column = 3, linecolor = "red",
    reduce.size.by = 0.6
  )

# Add titles and footnote
# :::::::::::::::::::::::::::::::::::::::::::::::::::
# Add titles and footnote
# Wrap subtitle into multiple lines using strwrap()
main.title <- "Edgar Anderson's Iris Data"
subtitle <- paste0(
  "This famous (Fisher's or Anderson's) iris data set gives the measurements",
  " in centimeters of the variables sepal length and width and petal length and width,"
"respectively, for 50 flowers from each of 3 species of iris."
"The species are Iris setosa, versicolor, and virginica."

```r
tab <- ggtexttable(head(iris), theme = ttheme("light"))
tab %>%
  tab_add_title(text = subtitle, face = "plain", size = 10) %>%
  tab_add_title(text = main.title, face = "bold", padding = unit(0.1, "line")) %>%
  tab_add_footnote(text = "*Table created using ggpubr", size = 10, face = "italic")
```

---

**ggviolin**

**Violin plot**

Description

Create a violin plot with error bars. Violin plots are similar to box plots, except that they also show the kernel probability density of the data at different values.

Usage

```r
ggviolin(
  data,
  x,
  y,
  combine = FALSE,
  merge = FALSE,
  color = "black",
```
Arguments

- **data**: a data frame
- **x**: character string containing the name of x variable.
- **y**: character vector containing one or more variables to plot
- **combine**: logical value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of y variables.
- **merge**: logical or character value. Default is FALSE. Used only when y is a vector containing multiple variables to plot. If TRUE, merge multiple y variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If merge = "flip", then y variables are used as x tick labels and the x variable is used as grouping variable.
- **color**: outline color.
- **fill**: fill color.
- **palette**: the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues",...

```r
fill = "white",
palette = NULL,
alpha = 1,
title = NULL,
xlab = NULL,
ylab = NULL,
facet.by = NULL,
panel.labs = NULL,
short.panel.labs = TRUE,
linetype = "solid",
trim = FALSE,
size = NULL,
width = 1,
draw_quantiles = NULL,
select = NULL,
remove = NULL,
order = NULL,
add = "mean_se",
add.params = list(),
error.plot = "pointrange",
label = NULL,
font.label = list(size = 11, color = "black"),
label.select = NULL,
repel = FALSE,
label.rectangle = FALSE,
position = position_dodge(0.8),
ggtheme = theme_pubr(),
...)
```
...; or custom color palette e.g. `c("blue", "red")`; and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".

`alpha` color transparency. Values should be between 0 and 1.

`title` plot main title.

`xlab` character vector specifying x axis labels. Use `xlab = FALSE` to hide xlab.

`ylab` character vector specifying y axis labels. Use `ylab = FALSE` to hide ylab.

`facet.by` character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.

`panel.labs` a list of one or two character vectors to modify facet panel labels. For example, `panel.labs = list(sex = c("Male", "Female"))` specifies the labels for the "sex" variable. For two grouping variables, you can use for example `panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))`.

`short.panel.labs` logical value. Default is TRUE. If TRUE, create short labels for panels by omitting variable names; in other words panels will be labelled only by variable grouping levels.

`linetype` line types.

`trim` If TRUE (default), trim the tails of the violins to the range of the data. If FALSE, don’t trim the tails.

`size` Numeric value (e.g.: `size = 1`). change the size of points and outlines.

`width` violin width.

`draw_quantiles` If not(NULL) (default), draw horizontal lines at the given quantiles of the density estimate.

`select` character vector specifying which items to display.

`remove` character vector specifying which items to remove from the plot.

`order` character vector specifying the order of items.

`add` character vector for adding another plot element (e.g.: dot plot or error bars). Allowed values are one or the combination of: "none", "dotplot", "jitter", "boxplot", "point", "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", "median", "median_iqr", "median_hilow", "median_q1q3", "median_sd", "median_range"; see ?desc_statby for more details.

`add.params` parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: `add.params = list(color = "red")`.

`error.plot` plot type used to visualize error. Allowed values are one of c("pointrange", "linerange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linerange", "lower_linerange"). Default value is "pointrange" or "errorbar". Used only when add != "none" and add contains one "mean_*" or "med_*" where ";*" = sd, se, ....

`label` the name of the column containing point labels. Can be also a character vector with length = nrow(data).
font.label  a list which can contain the combination of the following elements: the size
(e.g.: 14), the style (e.g.: "plain", "bold", "italic", "bold.italic") and the color
(e.g.: "red") of labels. For example font.label = list(size = 14, face = "bold",
color = "red"). To specify only the size and the style, use font.label = list(size =
14, face = "plain").

label.select can be of two formats:

• a character vector specifying some labels to show.
• a list containing one or the combination of the following components:
  – top. up and top. down: to display the labels of the top up/down points.
    For example, label.select = list(top. up = 10, top. down = 4).
  – criteria: to filter, for example, by x and y variables values, use this:
    label.select = list(criteria = "y > 2 & y < 5 & x %in% c('A',
'B'))

repel  a logical value, whether to use ggrepel to avoid overplotting text labels or not.

label.rectangle  logical value. If TRUE, add rectangle underneath the text, making it easier to
read.

position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to
use position_jitter), or the result of a call to a position adjustment function.
Use the latter if you need to change the settings of the adjustment.

ggtheme function, ggplot2 theme name. Default value is theme_pubr(). Allowed values
include ggplot2 official themes: theme_gray(), theme_bw(), theme_minimal(),
theme_classic(), theme_void(), ...

... other arguments to be passed to geom_violin, ggpar and facet.

Details

The plot can be easily customized using the function ggpar(). Read ?ggpar for changing:

• main title and axis labels: main, xlab, ylab
• axis limits: xlim, ylim (e.g.: ylim = c(0, 30))
• axis scales: xscale, yscale (e.g.: yscale = "log2")
• color palettes: palette = "Dark2" or palette = c("gray", "blue", "red")
• legend title, labels and position: legend = "right"
• plot orientation: orientation = c("vertical", "horizontal", "reverse")

See Also

ggpar

Examples

# Load data
data("ToothGrowth")
df <- ToothGrowth
# Basic plot
# +++++++++++++++++++++++++++
ggviolin(df, x = "dose", y = "len")
# Change the plot orientation: horizontal
ggviolin(df, "dose", "len", orientation = "horiz")

# Add summary statistics
# ++++++++++++++++++++++++++
# Draw quantiles
ggviolin(df, "dose", "len", add = "none",
        draw_quantiles = 0.5)

# Add box plot
ggviolin(df, x = "dose", y = "len",
        add = "boxplot")

ggviolin(df, x = "dose", y = "len",
        add = "dotplot")

# Add jitter points and
# change point shape by groups ("dose")
ggviolin(df, x = "dose", y = "len",
        add = "jitter", shape = "dose")

# Add mean_sd + jittered points
ggviolin(df, x = "dose", y = "len",
        add = c("jitter", "mean_sd"))

# Change error.plot to "crossbar"
ggviolin(df, x = "dose", y = "len",
        add = "mean_sd", error.plot = "crossbar")

# Change colors
# ++++++++++++++++++++++++++
# Change outline and fill colors
ggviolin(df, "dose", "len",
        color = "black", fill = "gray")

# Change outline colors by groups: dose
# Use custom color palette and add boxplot
ggviolin(df, "dose", "len", color = "dose",
        palette = c("#00AFBB", "#E7B800", "#FC4E07"),
        add = "boxplot")

# Change fill color by groups: dose
# add boxplot with white fill color
ggviolin(df, "dose", "len", fill = "dose",
        palette = c("#00AFBB", "#E7B800", "#FC4E07"),
        add = "boxplot", add.params = list(fill = "white"))
# Plot with multiple groups
# +++++++++++++++++++++
# fill or color box plot by a second group : "supp"

```r
ggviolin(df, "dose", "len", color = "supp",
         palette = c("#00AFBB", "#E7B800"), add = "boxplot")
```

---

### Description

Change gradient color.

- `gradient_color()`: Change gradient color.
- `gradient_fill()`: Change gradient fill.

### Usage

```r
gradient_color(palette)
gradient_fill(palette)
```

#### Arguments

- `palette` the color palette to be used for coloring or filling by groups. Allowed values include "grey" for grey color palettes; brewer palettes e.g. "RdBu", "Blues", ...; or custom color palette e.g. c("blue", "red"); and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorthy". Can be also a numeric vector; in this case a basic color palette is created using the function `palette`.

### See Also

`set_palette`.

### Examples

```r
df <- mtcars
p <- ggscatter(df, x = "wt", y = "mpg",
               color = "mpg")

# Change gradient color
# Use one custom color
p + gradient_color("red")

# Two colors
p + gradient_color(c("blue", "red"))
```
# Three colors
p + gradient_color(c("blue", "white", "red"))

# Use RColorBrewer palette
p + gradient_color("RdYlBu")

# Use ggsci color palette
p + gradient_color("npg")

grids

Add Grids to a ggplot

Description
Add grids to ggplot.

Usage
grids(axis = c("xy", "x", "y"), color = "grey92", size = NULL, linetype = NULL)

Arguments
axis axis for which grid should be added. Allowed values include c("xy", "x", "y").
color grid line color.
size numeric value specifying grid line size.
linetype line type. An integer (0:8), a name (blank, solid, dashed, dotted, dotdash, long-dash, twodash). See show_line_types.

Examples
# Load data
data("ToothGrowth")

# Basic plot
p <- ggboxplot(ToothGrowth, x = "dose", y = "len")
p

# Add border
p + grids(linetype = "dashed")
npc_to_data_coord

Convert NPC to Data Coordinates

Description
Convert NPC (Normalized Parent Coordinates) into data coordinates.

Usage

npc_to_data_coord(npc, data.ranges)

Arguments

npc               a numeric vector. Each value should be in [0-1]

data.ranges       a numeric vector of length 2 containing the data ranges (minimum and the maximum)

Value

a numeric vector representing data coordinates.

See Also

as_npc, get_coord.

Examples

npc_to_data_coord(npc = c(0.2, 0.95), data.ranges = c(1, 20))
as_npc(c("top", "right")) %>%
  npc_to_data_coord(data.ranges = c(1, 20))

rotate

Rotate a ggplot Horizontally

Description
Rotate a ggplot to create horizontal plots. Wrapper around coord_flip.

Usage

rotate(...)

Arguments

... other arguments to pass to coord_flip.
Examples

# Load data
data("ToothGrowth")
df <- ToothGrowth

# Basic plot
p <- ggboxplot(df, x = "dose", y = "len",
               color = "dose", palette = "jco")
p

# Create horizontal plots
p + rotate()

rotate_axis_text

Rotate Axes Text

Description

Rotate the x-axis text (tick mark labels).

• rotate_x_text(): Rotate x axis text.
• rotate_y_text(): Rotate y axis text.

Usage

rotate_x_text(angle = 90, hjust = NULL, vjust = NULL, ...)

rotate_y_text(angle = 90, hjust = NULL, vjust = NULL, ...)

Arguments

angle numeric value specifying the rotation angle. Default is 90 for vertical x-axis text.

hjust horizontal justification (in [0, 1]).

tjust vertical justification (in [0, 1]).

... other arguments to pass to the function element_text().

Examples

# Load data
data("ToothGrowth")
df <- ToothGrowth

# Basic plot
p <- ggboxplot(df, x = "dose", y = "len")
p

# Vertical x axis text
p + rotate_x_text()

# Set rotation angle to 45
rremove

p + rotate_x_text(45)
p + rotate_y_text(45)

rremove  Remove a ggplot Component

Description
Remove a specific component from a ggplot.

Usage
rremove(object)

Arguments

object character string specifying the plot components. Allowed values include:
  • "grid" for both x and y grids
  • "x.grid" for x axis grids
  • "y.grid" for y axis grids
  • "axis" for both x and y axes
  • "x.axis" for x axis
  • "y.axis" for y axis
  • "xlab", or "x.title" for x axis label
  • "ylab", or "y.title" for y axis label
  • "xlab", "xy.label" or "axis.title" for both x and y axis labels
  • "x.text" for x axis texts (x axis tick labels)
  • "y.text" for y axis texts (y axis tick labels)
  • "xy.text" or "axis.text" for both x and y axis texts
  • "ticks" for both x and y ticks
  • "x.ticks" for x ticks
  • "y.ticks" for y ticks
  • "legend.title" for the legend title
  • "legend" for the legend

Examples

# Load data
data("ToothGrowth")

# Basic plot
p <- ggboxplot(ToothGrowth, x = "dose", y = "len",
               ggtheme = theme_gray())
p
```r
# Remove all grids
p + rremove("grid")

# Remove only x grids
p + rremove("x.grid")
```

---

**set_palette**

Set Color Palette

**Description**
- `change_palette()`, `set_palette()`: Change both color and fill palettes.
- `color_palette()`: change color palette only.
- `fill_palette()`: change fill palette only.

**Usage**

```r
set_palette(p, palette)
change_palette(p, palette)
color_palette(palette = NULL, ...)
fill_palette(palette = NULL, ...)
```

**Arguments**

- `p`: a ggplot
- `palette`: Color palette. Allowed values include:
  - **Grey color palettes**: "grey" or "gray";
  - **RColorBrewer palettes**, see `brewer.pal` and details section. Examples of palette names include: "RdBu", "Blues", "Dark2", "Set2", ...;
  - **Custom color palettes**. For example, `palette = c("#00AFBB", ","#E7B800", ","#FC4E07")`;
  - **ggsci scientific journal palettes**, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
- `...`: other arguments passed to ggplot2 `scale_color_xxx()` and `scale_fill_xxx()` functions.

**See Also**

`get_palette`. 
Examples

# Load data
data("ToothGrowth")
df <- ToothGrowth

# Basic plot
p <- ggboxplot(df, x = "dose", y = "len",
               color = "dose")
p

# Change the color palette
set_palette(p, "jco")

show_line_types

show_line_types  Line types available in R

Description

Show line types available in R.

Usage

show_line_types()

Value

a ggplot.

See Also

ggpar and ggline.

Examples

show_line_types()+
theme_minimal()
show_point_shapes  Point shapes available in R

Description
Show point shapes available in R.

Usage
show_point_shapes()

Value
a ggplot.

See Also
ggpar and ggline.

Examples
show_point_shapes()+
theme_minimal()

stat_anova_test  Add Anova Test P-values to a GGPlot

Description
Adds automatically one-way and two-way ANOVA test p-values to a ggplot, such as box blots, dot plots and stripcharts.

Usage
stat_anova_test(
mapping = NULL,
data = NULL,
method = c("one_way", "one_way_repeated", "two_way", "two_way_repeated",
           "two_way_mixed"),
wid = NULL,
group.by = NULL,
type = NULL,
effect.size = "ges",
error = NULL,
correction = c("auto", "GG", "HF", "none"),
label = "{method}, p = {p.format}",
Arguments

mapping
Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

data
The data to be displayed in this layer. There are three options:
If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

method
ANOVA test methods. Possible values are one of c("one_way", "one_way_repeated", "two_way", "two_way_repeated", "two_way_mixed").

wid
(factor) column name containing individuals/subjects identifier. Should be unique per individual. Required only for repeated measure tests ("one_way_repeated", "two_way_repeated", "friedman_test", etc).

group.by
(optional) character vector specifying the grouping variable; it should be used only for grouped plots. Possible values are:
- "x.var": Group by the x-axis variable and perform the test between legend groups. In other words, the p-value is compute between legend groups at each x position
- "legend.var": Group by the legend variable and perform the test between x-axis groups. In other words, the test is performed between the x-groups for each legend level.

type
the type of sums of squares for ANOVA. Allowed values are either 1, 2 or 3. type = 2 is the default because this will yield identical ANOVA results as type = 1 when data are balanced but type = 2 will additionally yield various assumption
tests where appropriate. When the data are unbalanced the type = 3 is used by popular commercial softwares including SPSS.

**effect.size**

the effect size to compute and to show in the ANOVA results. Allowed values can be either "ges" (generalized eta squared) or "pes" (partial eta squared) or both. Default is "ges".

**error**

(optional) for a linear model, an lm model object from which the overall error sum of squares and degrees of freedom are to be calculated. Read more in `Anova()` documentation.

**correction**

character. Used only in repeated measures ANOVA test to specify which correction of the degrees of freedom should be reported for the within-subject factors. Possible values are:

- "GG": applies Greenhouse-Geisser correction to all within-subjects factors even if the assumption of sphericity is met (i.e., Mauchly’s test is not significant, p > 0.05).
- "HF": applies Hyunh-Feldt correction to all within-subjects factors even if the assumption of sphericity is met,
- "none": returns the ANOVA table without any correction and
- "auto": apply automatically GG correction to only within-subjects factors violating the sphericity assumption (i.e., Mauchly’s test p-value is significant, p <= 0.05).

**label**

character string specifying label. Can be:

- the column containing the label (e.g.: `label = "p"` or `label = "p.adj"`), where `p` is the p-value. Other possible values are "p.signif", "p.adj.signif", "p.format", "p.adj.format".
- an expression that can be formatted by the `glue()` package. For example, when specifying `label = "Anova, p = \{p\}"`, the expression `{p}` will be replaced by its value.
- a combination of plotmath expressions and glue expressions. You may want some of the statistical parameter in italic; for example: `label = "Anova, italic(p) = \{p\}"`.
- a constant: `label = "as_italic": display statistical parameters in italic; label = "as_detailed": detailed plain text; label = "as_detailed_expression" or label = "as_detailed_italic": detailed plotmath expression. Statistical parameters will be displayed in italic.

**label.x.npc, label.y.npc**

can be numeric or character vector of the same length as the number of groups and/or panels. If too short they will be recycled.

- If numeric, value should be between 0 and 1. Coordinates to be used for positioning the label, expressed in "normalized parent coordinates".
- If character, allowed values include: i) one of c('right', 'left', 'center', 'centre', 'middle') for x-axis; ii) and one of c('bottom', 'top', 'center', 'centre', 'middle') for y-axis.

**label.x, label.y**

numeric Coordinates (in data units) to be used for absolute positioning of the label. If too short they will be recycled.
**step.increase**

numeric value in with the increase in fraction of total height for every additional comparison to minimize overlap. The step value can be negative to reverse the order of groups.

**p.adjust.method**

method for adjusting p values (see `p.adjust`). Has impact only in a situation, where multiple pairwise tests are performed; or when there are multiple grouping variables. Allowed values include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". If you don’t want to adjust the p value (not recommended), use `p.adjust.method = "none"`.

**significance**

a list of arguments specifying the significance cutpoints and symbols. For example, `significance <- list(cutpoints = c(0, 0.0001, 0.001, 0.01, 0.05, Inf), symbols = c("****", "***", ",**", ",*", "ns")).

In other words, we use the following convention for symbols indicating statistical significance:

- **ns**: p > 0.05
- *: p <= 0.05
- **: p <= 0.01
- ***: p <= 0.001
- ****: p <= 0.0001

**geom**

The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. "point" rather than "geom_point")

**position**

Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

**na.rm**

If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.

**show.legend**

logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

**inherit.aes**

If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

**parse**

If TRUE, the labels will be parsed into expressions and displayed as described in `?plotmath`.

**...**

other arguments to pass to `geom_text`, such as:

- `hjust`: horizontal justification of the text. Move the text left or right and
- `vjust`: vertical justification of the text. Move the text up or down.

**Computed variables**

- **DFn**: Degrees of Freedom in the numerator (i.e. DF effect).
- **DFd**: Degrees of Freedom in the denominator (i.e., DF error).
• ges: Generalized Eta-Squared measure of effect size. Computed only when the option effect.size = "ges".
• pes: Partial Eta-Squared measure of effect size. Computed only when the option effect.size = "pes".
• F: F-value.
• p: p-value.
• p.adj: Adjusted p-values.
• p.signif: P-value significance.
• p.adj.signif: Adjusted p-value significance.
• p.format: Formated p-value.
• p.adj.format: Formated adjusted p-value.
• n: number of samples.

Examples

# Data preparation

# Transform `dose` into factor variable
df <- ToothGrowth
df$dose <- as.factor(df$dose)
# Add individuals id
df$id <- rep(1:10, 6)
# Add a random grouping variable
set.seed(123)
df$group <- sample(factor(rep(c("grp1", "grp2", "grp3"), 20)))
df$len <- ifelse(df$group == "grp2", df$len+2, df$len)
df$len <- ifelse(df$group == "grp3", df$len+7, df$len)
head(df, 3)

# Basic boxplot

# Create a basic boxplot
# Add 5% and 10% space to the plot bottom and the top, respectively
bxp <- ggboxplot(df, x = "dose", y = "len") +
  scale_y_continuous(expand = expansion(mult = c(0.05, 0.1)))

# Add the p-value to the boxplot
bxp + stat_anova_test()

## Not run:
# Change the label position
# Using coordinates in data units
bxp + stat_anova_test(label.x = "1", label.y = 10, hjust = 0)

## End(Not run)

# Format the p-value differently
custom_p_format <- function(p) {

rstatix::p_format(p, accuracy = 0.0001, digits = 3, leading.zero = FALSE)
}

bxp + stat_anova_test(
  label = "Anova, italic(p) = {custom_p_format(p)}(p.signif)"
)

# Show a detailed label in italic
bxp + stat_anova_test(label = "as_detailed_italic")

# Faceted plots
# Create a ggplot facet
bxp <- ggboxplot(df, x = "dose", y = "len", facet.by = "supp") +
  scale_y_continuous(expand = expansion(mult = c(0.05, 0.1)))
# Add p-values
bxp + stat_anova_test()

# Grouped plots
bxp2 <- ggboxplot(df, x = "group", y = "len", color = "dose", palette = "npg")
# For each x-position, computes tests between legend groups
bxp2 + stat_anova_test(aes(group = dose), label = "p = {p.format}(p.signif)"
)
# For each legend group, computes tests between x variable groups
bxp2 + stat_anova_test(aes(group = dose, color = dose), group.by = "legend.var")

## Not run:
# Two-way ANOVA: Independent measures
# Visualization: box plots with p-values
# Two-way interaction p-values between x and legend (group) variables
bxp3 <- ggboxplot(
  df, x = "supp", y = "len",
  color = "dose", palette = "jco"
)
bxp3 + stat_anova_test(aes(group = dose), method = "two_way")

# One-way repeated measures ANOVA
# Two-way repeated measures ANOVA
# df$id <- as.factor(rep(1:10, 6))
ggboxplot(df, x = "dose", y = "len", color = "supp", palette = "jco") +
  stat_anova_test(aes(group = supp), method = "two_way_repeated", wid = "id")

# Two-way repeated measures ANOVA
# df$id <- as.factor(rep(1:10, 3))
ggboxplot(df, x = "dose", y = "len") +
  stat_anova_test(aes(group = dose), method = "one_way_repeated", wid = "id")
# Grouped one-way repeated measures ANOVA

ggboxplot(df, x = "dose", y = "len", color = "supp", palette = "jco") +
  stat_anova_test(aes(group = supp, color = supp),
    method = "one_way_repeated", wid = "id", group.by = "legend.var")

## End(Not run)

---

**stat_bracket**  
*Add Brackets with Labels to a GGPlot*

**Description**

add brackets with label annotation to a ggplot. Helpers for adding p-value or significance levels to a plot.

**Usage**

```r
stat_bracket(
  mapping = NULL,
  data = NULL,
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  label = NULL,
  type = c("text", "expression"),
  y.position = NULL,
  xmin = NULL,
  xmax = NULL,
  step.increase = 0,
  step.group.by = NULL,
  tip.length = 0.03,
  bracket.nudge.y = 0,
  bracket.shorten = 0,
  size = 0.3,
  label.size = 3.88,
  family = ",",
  vjust = 0,
  ...
)
```

```r
geom_bracket(
  mapping = NULL,
  data = NULL,
  stat = "bracket",
  position = "identity",
  na.rm = FALSE,
  
```
show.legend = NA,
inherit.aes = TRUE,
label = NULL,
type = c("text", "expression"),
y.position = NULL,
xmin = NULL,
xmax = NULL,
step.increase = 0,
step.group.by = NULL,
tip.length = 0.03,
bracket.nudge.y = 0,
bracket.shorten = 0,
size = 0.3,
label.size = 3.88,
family = "",
vjust = 0,
coord.flip = FALSE,
...
)

Arguments

mapping

Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data

The data to be displayed in this layer. There are three options:

If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().

A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created.

A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).

position

Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

na.rm

If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.

show.legend

logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes

If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

label

character vector with alternative label, if not null test is ignored
type: the label type. Can be one of "text" and "expression" (for parsing plotmath expression).
y.position: numeric vector with the y positions of the brackets
xmin: numeric vector with the positions of the left sides of the brackets
xmax: numeric vector with the positions of the right sides of the brackets
step.increase: numeric vector with the increase in fraction of total height for every additional comparison to minimize overlap.
step.group.by: a variable name for grouping brackets before adding step.increase. Useful to group bracket by facet panel.
tip.length: numeric vector with the fraction of total height that the bar goes down to indicate the precise column
bracket.nudge.y: Vertical adjustment to nudge brackets by. Useful to move up or move down the bracket. If positive value, brackets will be moved up; if negative value, brackets are moved down.
bracket.shorten: a small numeric value in [0-1] for shortening the width of bracket.
size: change the width of the lines of the bracket
label.size: change the size of the label text
family: change the font used for the text
vjust: move the text up or down relative to the bracket
...: other arguments passed on to layer. These are often aesthetics, used to set an aesthetic to a fixed value, like color = "red" or size = 3. They may also be parameters to the paired geom/stat.
stat: The statistical transformation to use on the data for this layer, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")
coord.flip: logical. If TRUE, flip x and y coordinates so that horizontal becomes vertical, and vertical, horizontal. When adding the p-values to a horizontal ggplot (generated using coord_flip()), you need to specify the option coord.flip = TRUE.

Examples

df <- ToothGrowth
df$dose <- factor(df$dose)

# Add bracket with labels
ggboxplot(df, x = "dose", y = "len") +
geom_bracket(
  xmin = "0.5", xmax = "1", y.position = 30,
  label = "t-test, p < 0.05"
)

# Customize bracket tip.length tip.length
ggboxplot(df, x = "dose", y = "len") +
stat_central_tendency

Add Central Tendency Measures to a GGPlot

Description

Add central tendency measures (mean, median, mode) to density and histogram plots created using ggplots.
Note that, normally, the mode is used for categorical data where we wish to know which is the most common category. Therefore, we can have have two or more values that share the highest frequency. This might be problematic for continuous variable.

For continuous variable, we can consider using mean or median as the measures of the central tendency.

**Usage**

```
stat_central_tendency(
  mapping = NULL,
  data = NULL,
  geom = c("line", "point"),
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  type = c("mean", "median", "mode"),
  ...
)
```

**Arguments**

- **mapping**: Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

- **data**: The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

- **geom**: The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. "point" rather than "geom_point")

- **position**: Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

- **na.rm**: If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.

- **show.legend**: logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
stat_chull

### Description

Plot convex hull of a set of points.

### Examples

```r
# Simple density plot
data(mtcars)
ggdensity(mtcars, x = "mpg", fill = "red") +
  scale_x_continuous(limits = c(-1, 50)) +
  stat_central_tendency(type = "mean", linetype = "dashed")

# Color by groups
data(iris)
ggdensity(iris, "Sepal.Length", color = "Species") +
  stat_central_tendency(aes(color = Species), type = "median", linetype = 2)

# Use geom = "point" for central tendency
data(iris)
ggdensity(iris, "Sepal.Length", color = "Species") +
  stat_central_tendency(
    aes(color = Species), type = "median",
    geom = "point", size = 4
  )

# Facet
ggdensity(iris, "Sepal.Length", facet.by = "Species") +
  stat_central_tendency(type = "mean", color = "red", linetype = 2) +
  stat_central_tendency(type = "median", color = "blue", linetype = 2)
```

### stat_chull

Plot convex hull of a set of points.

### Parameters

- **inherit.aes**
  
  If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

- **type**
  
  the type of central tendency measure to be used. Possible values include: "mean", "median", "mode".

- **...**
  
  other arguments to pass to `geom_line`.

### See Also

- `ggdensity`
Usage

```r
stat_chull(
  mapping = NULL,
  data = NULL,
  geom = "path",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)
```

Arguments

- **mapping**: Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.
- **data**: The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).
- **geom**: The geometric object to use to display the data, either as a `ggproto` `Geom` subclass or as a string naming the geom stripped of the `geom_` prefix (e.g. "point" rather than "geom_point")
- **position**: Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
- **na.rm**: If `FALSE`, the default, missing values are removed with a warning. If `TRUE`, missing values are silently removed.
- **show.legend**: logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
- **inherit.aes**: If `FALSE`, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.
- **...**: Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

See Also

- `ggpar`, `ggscatter`
Examples

```r
# Load data
data("mtcars")
df <- mtcars
df$cyl <- as.factor(df$cyl)

# scatter plot with convex hull
ggscatter(df, x = "wt", y = "mpg", color = "cyl")+
  stat_chull(aes(color = cyl))

ggscatter(df, x = "wt", y = "mpg", color = "cyl")+
  stat_chull(aes(color = cyl, fill = cyl), alpha = 0.1, geom = "polygon")
```

---

**stat_compare_means**  
*Add Mean Comparison P-values to a ggplot*

Description

Add mean comparison p-values to a ggplot, such as box plots, dot plots and stripcharts.

Usage

```r
stat_compare_means(
  mapping = NULL,
  data = NULL,
  method = NULL,
  paired = FALSE,
  method.args = list(),
  ref.group = NULL,
  comparisons = NULL,
  hide.ns = FALSE,
  label.sep = ", ",
  label = NULL,
  label.x.npc = "left",
  label.y.npc = "top",
  label.x = NULL,
  label.y = NULL,
  vjust = 0,
  tip.length = 0.03,
  bracket.size = 0.3,
  step.increase = 0,
  symnum.args = list(),
  geom = "text",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
)```
stat_compare_means

```r

inherit.aes = TRUE,
...
)
```

**Arguments**

- **mapping**: Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

- **data**: The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

- **method**: a character string indicating which method to be used for comparing means.

- **paired**: a logical indicating whether you want a paired test. Used only in `t.test` and in `wilcox.test`.

- **method.args**: a list of additional arguments used for the test method. For example one might use `method.args = list(alternative = "greater")` for wilcoxon test.

- **ref.group**: a character string specifying the reference group. If specified, for a given grouping variable, each of the group levels will be compared to the reference group (i.e. control group).
  - `ref.group` can be also `.all.`. In this case, each of the grouping variable levels is compared to all (i.e. basemean).

- **comparisons**: A list of length-2 vectors. The entries in the vector are either the names of 2 values on the x-axis or the 2 integers that correspond to the index of the groups of interest, to be compared.

- **hide.ns**: logical value. If TRUE, hide ns symbol when displaying significance levels.

- **label.sep**: a character string to separate the terms. Default is ", ", to separate the correlation coefficient and the p.value.

- **label**: character string specifying label type. Allowed values include "p.signif" (shows the significance levels), "p.format" (shows the formatted p value).

- **label.x.npc, label.y.npc**: can be numeric or character vector of the same length as the number of groups and/or panels. If too short they will be recycled.
  - If numeric, value should be between 0 and 1. Coordinates to be used for positioning the label, expressed in "normalized parent coordinates".
  - If character, allowed values include: i) one of c("right", "left", "center", "centre", "middle") for x-axis; ii) and one of c( "bottom", "top", "center", "centre", "middle") for y-axis.
label.x, label.y

numeric Coordinates (in data units) to be used for absolute positioning of the label. If too short they will be recycled.

vjust

move the text up or down relative to the bracket.

tip.length

numeric vector with the fraction of total height that the bar goes down to indicate the precise column. Default is 0.03. Can be of same length as the number of comparisons to adjust specifically the tip length of each comparison. For example tip.length = c(0.01, 0.03).

If too short they will be recycled.

bracket.size

Width of the lines of the bracket.

step.increase

numeric vector with the increase in fraction of total height for every additional comparison to minimize overlap.

symnum.args

a list of arguments to pass to the function symnum for symbolic number coding of p-values. For example, symnum.args <- list(cutpoints = c(0, 0.0001, 0.001, 0.01, 0.05, Inf), symbols = c("****", "***", "**", ",", "ns")).

In other words, we use the following convention for symbols indicating statistical significance:

- ns: p > 0.05
- *: p <= 0.05
- **: p <= 0.01
- ***: p <= 0.001
- ****: p <= 0.0001

geom

The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. "point" rather than "geom_point")

position

Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

na.rm

If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.

show.legend

logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes

If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

...

other arguments to pass to geom_text or geom_label.

See Also

cmpare_means
Examples

# Load data
data("ToothGrowth")
head(ToothGrowth)

# Two independent groups
#:::::::::::::::::::::::::::::::::::::::::::::::::
p <- ggboxplot(ToothGrowth, x = "supp", y = "len",
    color = "supp", palette = "npg", add = "jitter")

# Add p-value
p + stat_compare_means()
# Change method
p + stat_compare_means(method = "t.test")

# Paired samples
#:::::::::::::::::::::::::::::::::::::::::::::::::
ggpaired(ToothGrowth, x = "supp", y = "len",
    color = "supp", line.color = "gray", line.size = 0.4,
    palette = "npg")+
stat_compare_means(paired = TRUE)

# More than two groups
#:::::::::::::::::::::::::::::::::::::::::::::::::
# Pairwise comparisons: Specify the comparisons you want
my_comparisons <- list( c("0.5", "1"), c("1", "2"), c("0.5", "2") )
ggboxplot(ToothGrowth, x = "dose", y = "len",
    color = "dose", palette = "npg")+
stat_compare_means(comparisons = my_comparisons, label.y = c(29, 35, 40))+
stat_compare_means(label.y = 45) # Add global Anova p-value

# Multiple pairwise test against a reference group
ggboxplot(ToothGrowth, x = "dose", y = "len",
    color = "dose", palette = "npg")+
stat_compare_means(method = "anova", label.y = 40) # Add global p-value
stat_compare_means(aes(label = after_stat(p.signif)),
    method = "t.test", ref.group = "0.5")

# Multiple grouping variables
#:::::::::::::::::::::::::::::::::::::::::::::::::
# Box plot faceted by "dose"
p <- ggboxplot(ToothGrowth, x = "supp", y = "len",
    color = "supp", palette = "npg",
    add = "jitter",
    facet.by = "dose", short.panel.labs = FALSE)
# Use only p.format as label. Remove method name.
p + stat_compare_means(
    aes(label = paste0("p = ", after_stat(p.format)))))
StatConfEllipse

Plot confidence ellipses.

Description
Plot confidence ellipses around barycenters. The method for computing confidence ellipses has been modified from FactoMineR::coord.ellipse().

Usage
stat_conf_ellipse(
  mapping = NULL,
  data = NULL,
  geom = "path",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  level = 0.95,
  npoint = 100,
  bary = TRUE,
  ...
)

Arguments

mapping Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().
A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).

geom The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. "point" rather than "geom_point")

position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

na.rm If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend: logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes: If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

level: confidence level used to construct the ellipses. By default, 0.95.

npoint: number of points used to draw the ellipses.

bary: logical value. If TRUE, the coordinates of the ellipse around the barycentre of individuals are calculated.

...: Other arguments passed on to `layer()`. These are often aesthetics, used to set an aesthetic to a fixed value, like `colour = "red"` or `size = 3`. They may also be parameters to the paired geom/stat.

See Also

`stat_conf_ellipse`

Examples

```r
# Load data
data("mtcars")
df <- mtcars
df$cyl <- as.factor(df$cyl)

# scatter plot with confidence ellipses
ggscatter(df, x = "wt", y = "mpg", color = "cyl")+
  stat_conf_ellipse(aes(color = cyl))

ggscatter(df, x = "wt", y = "mpg", color = "cyl")+
  stat_conf_ellipse(aes(color = cyl, fill = cyl), alpha = 0.1, geom = "polygon")
```

Description

Add correlation coefficients with p-values to a scatter plot. Can be also used to add ‘R2’.

Usage

```r
stat_cor(
  mapping = NULL,
  data = NULL,
  method = "pearson",
  alternative = "two.sided",
  ...)
```
cor.coef.name = c("R", "rho", "tau"),
label.sep = ", ",
label.x.npc = "left",
label.y.npc = "top",
label.x = NULL,
label.y = NULL,
output.type = "expression",
digits = 2,
r.digits = digits,
p.digits = digits,
r.accuracy = NULL,
p.accuracy = NULL,
geom = "text",
position = "identity",
na.rm = FALSE,
show.legend = NA,
inherit.aes = TRUE,
...
)

Arguments

mapping Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data The data to be displayed in this layer. There are three options:
  - If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().
  - A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).
method a character string indicating which correlation coefficient (or covariance) is to be computed. One of "pearson" (default), "kendall", or "spearman".
alternative a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
cor.coef.name character. Can be one of "R" (pearson coef), "rho" (spearman coef) and "tau" (kendall coef). Uppercase and lowercase are allowed.
label.sep a character string to separate the terms. Default is ", ", to separate the correlation coefficient and the p.value.
label.x.npc, label.y.npc can be numeric or character vector of the same length as the number of groups and/or panels. If too short they will be recycled.
  - If numeric, value should be between 0 and 1. Coordinates to be used for positioning the label, expressed in "normalized parent coordinates".
- If character, allowed values include: i) one of c('right', 'left', 'center', 'centre', 'middle') for x-axis; ii) and one of c('bottom', 'top', 'center', 'centre', 'middle') for y-axis.

If too short they will be recycled.

**label.x, label.y**

numeric Coordinates (in data units) to be used for absolute positioning of the label. If too short they will be recycled.

**output.type**

character One of "expression", "latex", "tex" or "text".

**digits, r.digits, p.digits**

integer indicating the number of decimal places (round) or significant digits (signif) to be used for the correlation coefficient and the p-value, respectively.

**r.accuracy**

a real value specifying the number of decimal places of precision for the correlation coefficient. Default is NULL. Use (e.g.) 0.01 to show 2 decimal places of precision. If specified, then r.digits is ignored.

**p.accuracy**

a real value specifying the number of decimal places of precision for the p-value. Default is NULL. Use (e.g.) 0.0001 to show 4 decimal places of precision. If specified, then p.digits is ignored.

**geom**

The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_prefix (e.g. "point" rather than "geom_point")

**position**

Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

**na.rm**

If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.

**show.legend**

logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

**inherit.aes**

If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

... other arguments to pass to geom_text or geom_label.

**Computed variables**

- **r** correlation coefficient
- **rr** correlation coefficient squared
- **r.label** formatted label for the correlation coefficient
- **rr.label** formatted label for the squared correlation coefficient
- **p.label** label for the p-value
- **label** default label displayed by stat_cor()

**See Also**

ggscatter
Examples

```r
# Load data
data(mtcars)
df <- mtcars
df$cyl <- as.factor(df$cyl)

# Scatter plot with correlation coefficient
sp <- ggscatter(df, x = "wt", y = "mpg",
    add = "reg.line", # Add regression line
    add.params = list(color = "blue", fill = "lightgray"), # Customize reg. line
    conf.int = TRUE # Add confidence interval
)
# Add correlation coefficient
sp + stat_cor(method = "pearson", label.x = 3, label.y = 30)

# Specify the number of decimal places of precision for p and r
# Using 3 decimal places for the p-value and
# 2 decimal places for the correlation coefficient (r)
sp + stat_cor(p.accuracy = 0.001, r.accuracy = 0.01)

# Show only the r.label but not the p.label
sp + stat_cor(aes(label = ..r.label..), label.x = 3)

# Use R2 instead of R
ggscatter(df, x = "wt", y = "mpg", add = "reg.line") +
    stat_cor(
        aes(label = paste(..rr.label.., ..p.label.., sep = "\", "\")),
        label.x = 3
    )

# Color by groups and facet
sp <- ggscatter(df, x = "wt", y = "mpg",
    color = "cyl", palette = "jco",
    add = "reg.line", conf.int = TRUE)
sp + stat_cor(aes(color = cyl), label.x = 3)
```

stat_friedman_test  Add Friedman Test P-values to a GGPLOT

Description

Add automatically Friedman test p-values to a ggplot, such as box plots, dot plots and stripcharts.

Usage

```r
stat_friedman_test(
    mapping = NULL,
```
data = NULL,
wid = NULL,
group.by = NULL,
label = "{method}, p = {p.format}",
label.x.npc = "left",
label.y.npc = "top",
label.x = NULL,
label.y = NULL,
step.increase = 0.1,
p.adjust.method = "holm",
significance = list(),
geom = "text",
position = "identity",
na.rm = FALSE,
show.legend = FALSE,
inherit.aes = TRUE,
parse = FALSE,
...
)

Arguments

mapping  Set of aesthetic mappings created by \texttt{aes()}. If specified and \texttt{inherit.aes = TRUE} (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data  The data to be displayed in this layer. There are three options:
If \texttt{NULL}, the default, the data is inherited from the plot data as specified in the call to \texttt{ggplot()}. A \texttt{data.frame}, or other object, will override the plot data. All objects will be fortified to produce a data frame. See \texttt{fortify()} for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a \texttt{data.frame}, and will be used as the layer data. A function can be created from a formula (e.g. \texttt{~ head(.x, 10)}).

wid  (factor) column name containing individuals/subjects identifier. Should be unique per individual. Required only for repeated measure tests ("one_way_repeated", "two_way_repeated", "friedman_test", etc).

label  (optional) character vector specifying the grouping variable; it should be used only for grouped plots. Possible values are:
- "x.var": Group by the x-axis variable and perform the test between legend groups. In other words, the p-value is compute between legend groups at each x position
- "legend.var": Group by the legend variable and perform the test between x-axis groups. In other words, the test is performed between the x-groups for each legend level.

label  the column containing the label (e.g.: label = "p" or label = "p.adj"), where p is the p-value. Can be also an expression that can be formatted by the \texttt{glue()}
For example, when specifying `label = "t-test, p = \{p\}"`, the expression `{p}` will be replaced by its value.

`label.x.npc` can be numeric or character vector of the same length as the number of groups and/or panels. If too short they will be recycled.

- If numeric, value should be between 0 and 1. Coordinates to be used for positioning the label, expressed in "normalized parent coordinates".
- If character, allowed values include: i) one of c('right', 'left', 'center', 'centre', 'middle') for x-axis; ii) and one of c('bottom', 'top', 'center', 'centre', 'middle') for y-axis.

`label.y.npc` can be numeric or character vector of the same length as the number of groups and/or panels. If too short they will be recycled.

- If numeric, value should be between 0 and 1. Coordinates to be used for positioning the label, expressed in "normalized parent coordinates".
- If character, allowed values include: i) one of c('right', 'left', 'center', 'centre', 'middle') for x-axis; ii) and one of c('bottom', 'top', 'center', 'centre', 'middle') for y-axis.

`label.x` numeric Coordinates (in data units) to be used for absolute positioning of the label. If too short they will be recycled.

`label.y` numeric Coordinates (in data units) to be used for absolute positioning of the label. If too short they will be recycled.

`step.increase` numeric vector with the increase in fraction of total height for every additional comparison to minimize overlap.

`p.adjust.method` method for adjusting p values (see `p.adjust`). Has impact only in a situation, where multiple pairwise tests are performed; or when there are multiple grouping variables. Allowed values include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". If you don't want to adjust the p value (not recommended), use `p.adjust.method = "none"`.

`significance` a list of arguments specifying the significance cutpoints and symbols. For example, `significance <- list(cutpoints = c(0, 0.0001, 0.001, 0.01, 0.05, Inf), symbols = c("****", "***", "**", "+", "ns"))`. In other words, we use the following convention for symbols indicating statistical significance:

- ns: p > 0.05
- *: p <= 0.05
- **: p <= 0.01
- ***: p <= 0.001
- ****: p <= 0.0001

`geom` The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the `geom_` prefix (e.g. "point" rather than "geom_point")

`position` Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use `position_jitter`), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
na.rm  If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.

show.legend  logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes  If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

parse  If TRUE, the labels will be parsed into expressions and displayed as described in ?plotmath.

...  other arguments passed to the function geom_bracket() or geom_text()

Computed variables

- statistic: the value of the test statistic (Chi-squared).
- df: the degrees of freedom of the approximate chi-squared distribution of the test statistic.
- p: p-value.
- p.adj: Adjusted p-values.
- p.signif: P-value significance.
- p.adj.signif: Adjusted p-value significance.
- p.format: Formated p-value.
- p.adj.format: Formated adjusted p-value.
- n: number of samples.

Examples

# Data preparation
#%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
# Transform `dose` into factor variable
df <- ToothGrowth
df$dose <- as.factor(df$dose)
df$id <- as.factor(c(rep(1:10, 3), rep(11:20, 3)))
# Add a random grouping variable
set.seed(123)
df$group <- sample(factor(rep(c("grp1", "grp2", "grp3"), 20)))
df<len <- ifelse(df$group == "grp2", df<len+2, df<len)
df<len <- ifelse(df$group == "grp3", df<len+7, df<len)
head(df, 3)

# Basic boxplot
#%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
# Create a basic boxplot
# Add 5% and 10% space to the plot bottom and the top, respectively
bxp <- ggboxplot(df, x = "dose", y = "len") +
    scale_y_continuous(expand = expansion(mult = c(0.05, 0.1)))
stat_kruskal_test

# Add the p-value to the boxplot
bxp + stat_friedman_test(aes(wid = id))

# Change the label position
# Using coordinates in data units
bxp + stat_friedman_test(aes(wid = id), label.x = "1", label.y = 10, hjust = 0)

# Format the p-value differently
custom_p_format <- function(p) {
  rstatix::p_format(p, accuracy = 0.0001, digits = 3, leading.zero = FALSE)
}
bxp + stat_friedman_test(aes(wid = id),
  label = "Friedman test, italic(p) = {custom_p_format(p)}{p.signif}"
)

# Show a detailed label in italic
bxp + stat_friedman_test(aes(wid = id), label = "as_detailed_italic")

# Faceted plots
#%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
# Create a ggplot facet
df$id <- rep(1:10,6)
wx <- ggboxplot(df, x = "dose", y = "len", facet.by = "supp") +
  scale_y_continuous(expand = expansion(mult = c(0.05, 0.1)))
# Add p-values
bxp + stat_friedman_test(aes(wid = id))

# Grouped plots
#%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
df$id <- rep(1:10,6)
wx <- ggboxplot(df, x = "dose", y = "len", color = "supp", palette = "jco")

# For each legend group, computes tests within x variable groups
bxp + stat_friedman_test(aes(wid = id, group = supp, color = supp), within = "x")

# For each x-position, computes tests within legend variable groups
bxp + stat_friedman_test(aes(wid = id, group = supp, color = supp),
  within = "group", label = "p = {p.format}"}

stat_kruskal_test
Add Kruskal-Wallis Test P-values to a GGPlot

Description

Add Kruskal-Wallis test p-values to a ggplot, such as box plots, dot plots and stripcharts.
Usage

```r
stat_kruskal_test(
  mapping = NULL,
  data = NULL,
  group.by = NULL,
  label = "{method}, p = {p.format}",
  label.x.npc = "left",
  label.y.npc = "top",
  label.x = NULL,
  label.y = NULL,
  step.increase = 0.1,
  p.adjust.method = "holm",
  significance = list(),
  geom = "text",
  position = "identity",
  na.rm = FALSE,
  show.legend = FALSE,
  inherit.aes = TRUE,
  parse = FALSE,
  ...
)
```

Arguments

- **mapping**: Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.

- **data**: The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

- **group.by**: (optional) character vector specifying the grouping variable; it should be used only for grouped plots. Possible values are:
  - "x.var": Group by the x-axis variable and perform the test between legend groups. In other words, the p-value is compute between legend groups at each x position.
  - "legend.var": Group by the legend variable and perform the test between x-axis groups. In other words, the test is performed between the x-groups for each legend level.

- **label**: the column containing the label (e.g.: `label = "p"` or `label = "p.adj"`), where `p` is the p-value. Can be also an expression that can be formatted by the `glue()`
package. For example, when specifying `label = "t-test, p = \{p\}"`, the expression `{p}` will be replaced by its value.

- **label.x.npc** can be numeric or character vector of the same length as the number of groups and/or panels. If too short they will be recycled.
  - If numeric, value should be between 0 and 1. Coordinates to be used for positioning the label, expressed in "normalized parent coordinates".
  - If character, allowed values include: i) one of c('right', 'left', 'center', 'centre', 'middle') for x-axis; ii) and one of c( 'bottom', 'top', 'center', 'centre', 'middle') for y-axis.

- **label.y.npc** can be numeric or character vector of the same length as the number of groups and/or panels. If too short they will be recycled.
  - If numeric, value should be between 0 and 1. Coordinates to be used for positioning the label, expressed in "normalized parent coordinates".
  - If character, allowed values include: i) one of c('right', 'left', 'center', 'centre', 'middle') for x-axis; ii) and one of c( 'bottom', 'top', 'center', 'centre', 'middle') for y-axis.

- **label.x** numeric Coordinates (in data units) to be used for absolute positioning of the label. If too short they will be recycled.
- **label.y** numeric Coordinates (in data units) to be used for absolute positioning of the label. If too short they will be recycled.
- **step.increase** numeric vector with the increase in fraction of total height for every additional comparison to minimize overlap.
- **p.adjust.method** method for adjusting p values (see `p.adjust`). Has impact only in a situation, where multiple pairwise tests are performed; or when there are multiple grouping variables. Allowed values include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". If you don’t want to adjust the p value (not recommended), use p.adjust.method = "none".
- **significance** a list of arguments specifying the significance cutpoints and symbols. For example, `significance <- list(cutpoints = c(0, 0.0001, 0.001, 0.01, 0.05, Inf), symbols = c("****", "***", "**", "+", "ns"))`. In other words, we use the following convention for symbols indicating statistical significance:
  - ns: p > 0.05
  - *: p <= 0.05
  - **: p <= 0.01
  - ***: p <= 0.001
  - ****: p <= 0.0001
- **geom** The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. "point" rather than "geom_point")
- **position** Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
na.rm If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.

show.legend logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

parse If TRUE, the labels will be parsed into expressions and displayed as described in ?plotmath.

... other arguments passed to the function geom_bracket() or geom_text()

Computed variables

- statistic: the Kruskal-Wallis rank sum chi-squared statistic used to compute the p-value.
- p: p-value.
- p.adj: Adjusted p-values.
- p.signif: P-value significance.
- p.adj.signif: Adjusted p-value significance.
- p.format: Formated p-value.
- p.adj.format: Formated adjusted p-value.
- n: number of samples.

Examples

# Data preparation
#%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
# Transform `dose` into factor variable
df <- ToothGrowth
df$dose <- as.factor(df$dose)
# Add a random grouping variable
set.seed(123)
df$group <- sample(factor(rep(c("grp1", "grp2", "grp3"), 20)))
df$len <- ifelse(df$group == "grp2", df$len+2, df$len)
df$len <- ifelse(df$group == "grp3", df$len+7, df$len)
head(df, 3)

# Basic boxplot
#%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
# Create a basic boxplot
# Add 5% and 10% space to the plot bottom and the top, respectively
bxp <- ggboxplot(df, x = "dose", y = "len") +
  scale_y_continuous(expand = expansion(mult = c(0.05, 0.1)))

# Add the p-value to the boxplot
bxp + stat_kruskal_test()
stat_mean

# Change the label position
# Using coordinates in data units
bxp + stat_kruskal_test(label.x = "1", label.y = 10, hjust = 0)

# Format the p-value differently
custom_p_format <- function(p) {
  rstatix::p_format(p, accuracy = 0.0001, digits = 3, leading.zero = FALSE)
}

bxp + stat_kruskal_test(
  label = "Kruskal-Wallis, italic(p) = {custom_p_format(p)}{p.signif}"
)

# Show a detailed label in italic
bxp + stat_kruskal_test(label = "as_detailed_italic")

# Faceted plots
# Create a ggplot facet
bxp <- ggboxplot(df, x = "dose", y = "len", facet.by = "supp") +
  scale_y_continuous(expand = expansion(mult = c(0.05, 0.1)))
  # Add p-values
  bxp + stat_kruskal_test()

# Grouped plots
bxp2 <- ggboxplot(df, x = "group", y = "len", color = "dose", palette = "npg")

# For each x-position, computes tests between legend groups
bxp2 + stat_kruskal_test(aes(group = dose), label = "p = {p.format}{p.signif}"
)

# For each legend group, computes tests between x variable groups
bxp2 + stat_kruskal_test(aes(group = dose, color = dose), group.by = "legend.var")

---

**stat_mean**  
**Draw group mean points**

**Description**

Draw the mean point of each group.

**Usage**

```
stat_mean(
  mapping = NULL,
  data = NULL,
  geom = "point",
)```
position = "identity",
na.rm = FALSE,
show.legend = NA,
inherit.aes = TRUE,
...
)

Arguments

mapping    Set of aesthetic mappings created by \texttt{aes()}. If specified and \texttt{inherit.aes = TRUE} (the default), it is combined with the default mapping at the top level of the plot. You must supply \texttt{mapping} if there is no plot mapping.
data       The data to be displayed in this layer. There are three options:
           If \texttt{NULL}, the default, the data is inherited from the plot data as specified in the call to \texttt{ggplot()}. A \texttt{data.frame}, or other object, will override the plot data. All objects will be fortified to produce a data frame. See \texttt{fortify()} for which variables will be created.
           A function will be called with a single argument, the plot data. The return value must be a \texttt{data.frame}, and will be used as the layer data. A function can be created from a \texttt{formula} (e.g. \texttt{~ head(.x, 10)}).
geom       The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. "point" rather than "geom_point")
positional adjustment, either as a string naming the adjustment (e.g. "jitter" to use \texttt{position_jitter}), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.
nan.rms     If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.
show.legend logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.
inherit.aes If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. \texttt{borders()}.

See Also

stat_conf_ellipse, stat_chull and \texttt{ggscatter}

Examples

# Load data
data("mtcars")
df <- mtcars
df$cyl <- as.factor(df$cyl)
# Scatter plot with ellipses and group mean points
```r
ggscatter(df, x = "wt", y = "mpg",
    color = "cyl", shape = "cyl", ellipse = TRUE)+
  stat_mean(aes(color = cyl, shape = cyl), size = 4)
```

---

### Description

Overlay normal density plot (with the same mean and SD) to the density distribution of 'x'. This is useful for visually inspecting the degree of deviance from normality.

### Usage

```r
stat_overlay_normal_density(
  mapping = NULL,
  data = NULL,
  geom = "line",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...
)
```

### Arguments

- **mapping**: Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

- **data**: The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).

- **geom**: The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. "point" rather than "geom_point")
position

Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

na.rm

If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.

show.legend

logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes

If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders()...

See Also

ggdensity

Examples

# Simple density plot
data("mtcars")
ggdensity(mtcars, x = "mpg", fill = "red") +
  scale_x_continuous(limits = c(-1, 50)) +
  stat_overlay_normal_density(color = "red", linetype = "dashed")

# Color by groups
data(iris)
ggdensity(iris, "Sepal.Length", color = "Species") +
  stat_overlay_normal_density(aes(color = Species), linetype = "dashed")

# Facet
ggdensity(iris, "Sepal.Length", facet.by = "Species") +
  stat_overlay_normal_density(color = "red", linetype = "dashed")

---

**stat_pvalue_manual**

Add Manually P-values to a ggplot

Description

Add manually p-values to a ggplot, such as box blots, dot plots and stripcharts. Frequently asked questions are available on Datanovia ggpubr FAQ page, for example:

- How to Add P-Values onto Basic GGPlots
- How to Add Adjusted P-values to a Multi-Panel GGPlot
- How to Add P-values to GGPlot Facets
• How to Add P-Values Generated Elsewhere to a GG PLOT
• How to Add P-Values onto a Grouped GG PLOT using the GG PUBL R Package
• How to Create Stacked Bar Plots with Error Bars and P-values
• How to Add P-Values onto Horizontal GG PLOTS

Usage

stat_pvalue_manual(
  data, label = NULL, y.position = "y.position", xmin = "group1", xmax = "group2", x = NULL, size = 3.88, label.size = size, bracket.size = 0.3, bracket.nudge.y = 0, bracket.shorten = 0, color = "black", linetype = 1, tip.length = 0.03, remove.bracket = FALSE, step.increase = 0, step.group.by = NULL, hide.ns = FALSE, vjust = 0, coord.flip = FALSE, position = "identity", ...
)

Arguments

data a data frame containing statistical test results. The expected default format should contain the following columns: group1 | group2 | p | y.position | etc. group1 and group2 are the groups that have been compared. p is the resulting p-value. y.position is the y coordinates of the p-values in the plot.

label the column containing the label (e.g.: label = "p" or label = "p.adj"), where p is the p-value. Can be also an expression that can be formatted by the \texttt{glue()} package. For example, when specifying label = "t-test, p = \{p\}", the expression \{p\} will be replaced by its value.

y.position column containing the coordinates (in data units) to be used for absolute positioning of the label. Default value is "y.position". Can be also a numeric vector.

xmin column containing the position of the left sides of the brackets. Default value is "group1".
xmax (optional) column containing the position of the right sides of the brackets. Default value is "group2". If NULL, the p-values are plotted as a simple text.

x x position of the p-value. Should be used only when you want plot the p-value as text (without brackets).

size, label.size size of label text.

bracket.size Width of the lines of the bracket.

bracket.nudge.y Vertical adjustment to nudge brackets by. Useful to move up or move down the bracket. If positive value, brackets will be moved up; if negative value, brackets are moved down.

bracket.shorten a small numeric value in [0-1] for shortening the with of bracket.

color text and line color. Can be variable name in the data for coloring by groups.

linetype linetype. Can be variable name in the data for changing linetype by groups.

tip.length numeric vector with the fraction of total height that the bar goes down to indicate the precise column. Default is 0.03.

remove.bracket logical, if TRUE, brackets are removed from the plot. Considered only in the situation, where comparisons are performed against reference group or against "all".

step.increase numeric vector with the increase in fraction of total height for every additional comparison to minimize overlap.

step.group.by a variable name for grouping brackets before adding step.increase. Useful to group bracket by facet panel.

hide.ns can be logical value or a character vector.

• Case when logical value. If TRUE, hide ns symbol when displaying significance levels. Filter is done by checking the column p.adj.signif, p.signif, p.adj and p.

• Case when character value. Possible values are "p" or "p.adj", for filtering out non significant.

vjust move the text up or down relative to the bracket. Can be also a column name available in the data.

coord.flip logical. If TRUE, flip x and y coordinates so that horizontal becomes vertical, and vertical, horizontal. When adding the p-values to a horizontal ggplot (generated using coord_flip()), you need to specify the option coord.flip = TRUE.

position position adjustment, either as a string, or the result of a call to a position adjustment function.

... other arguments passed to the function geom_bracket() or geom_text()

See Also

stat_compare_means
Examples

# T-test
stat.test <- compare_means(
  len ~ dose, data = ToothGrowth,
  method = "t.test"
)
stat.test

# Create a simple box plot
p <- ggboxplot(ToothGrowth, x = "dose", y = "len")
p

# Perform a t-test between groups
stat.test <- compare_means(
  len ~ dose, data = ToothGrowth,
  method = "t.test"
)
stat.test

# Add manually p-values from stat.test data
# First specify the y.position of each comparison
stat.test <- stat.test %>%
  mutate(y.position = c(29, 35, 39))
p + stat_pvalue_manual(stat.test, label = "p.adj")

# Customize the label with glue expression
# (https://github.com/tidyverse/glue)
p + stat_pvalue_manual(stat.test, label = "p = {p.adj}"

# Grouped bar plots
#%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
ToothGrowth$dose <- as.factor(ToothGrowth$dose)
# Comparisons against reference
stat.test <- compare_means(
  len ~ dose, data = ToothGrowth, group.by = "supp",
  method = "t.test", ref.group = "0.5"
)
stat.test

# Plot
bp <- ggbarplot(ToothGrowth, x = "supp", y = "len",
  fill = "dose", palette = "jco",
  add = "mean_sd", add.params = list(group = "dose"),
  position = position_dodge(0.8))
bp + stat_pvalue_manual(
  stat.test, x = "supp", y.position = 33,
  label = "p.signif",
  position = position_dodge(0.8))
Add Pairwise Comparisons P-values to a GGPlot

Description

add pairwise comparison p-values to a ggplot such as box plots, dot plots and stripcharts.

Usage

stat_pwc(
  mapping = NULL,
  data = NULL,
  method = "wilcox_test",
  method.args = list(),
  ref.group = NULL,
  label = "p.format",
  y.position = NULL,
  group.by = NULL,
  dodge = 0.8,
  bracket.nudge.y = 0.05,
  bracket.shorten = 0,
  bracket.group.by = c("x.var", "legend.var"),
  step.increase = 0.12,
  tip.length = 0.03,
  size = 0.3,
  label.size = 3.88,
  family = "",
  vjust = 0,
  hjust = 0.5,
  p.adjust.method = "holm",
  p.adjust.by = c("group", "panel"),
  symnum.args = list(),
  hide.ns = FALSE,
  remove.bracket = FALSE,
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  parse = FALSE,
  ...
)

geom_pwc(
  mapping = NULL,
  data = NULL,
  stat = "pwc",
  method = "wilcox_test",
  ...
method.args = list(),
ref.group = NULL,
label = "p.format",
y.position = NULL,
group.by = NULL,
dodge = 0.8,
stack = FALSE,
step.increase = 0.12,
tip.length = 0.03,
bracket.nudge.y = 0.05,
bracket.shorten = 0,
bracket.group.by = c("x.var", "legend.var"),
size = 0.3,
lable.size = 3.88,
family = "",
vjust = 0,
hjust = 0.5,
p.adjust.method = "holm",
p.adjust.by = c("group", "panel"),
synumm.args = list(),
hide.ns = FALSE,
remove.bracket = FALSE,
position = "identity",
na.rm = FALSE,
show.legend = NA,
inherit.aes = TRUE,
parse = FALSE,
...)

Arguments

mapping Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot().
A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).

method a character string indicating which method to be used for pairwise comparisons. Default is "wilcox_test". Allowed methods include pairwise comparisons methods implemented in the rstatix R package. These methods are:
"wilcoxon_test", "t_test", "sign_test", "dunn_test", "emmeans_test", "tukey_hsd", "games_howell_test".

method.args

a list of additional arguments used for the test method. For example one might use method.args = list(alternative = "greater") for wilcoxon test.

ref.group

a character string or a numeric value specifying the reference group. If specified, for a given grouping variable, each of the group levels will be compared to the reference group (i.e. control group). ref.group can be also "all". In this case, each of the grouping variable levels is compared to all (i.e. basemean).

Allowed values can be:

• numeric value: specifying the rank of the reference group. For example, use ref.group = 1 when the first group is the reference; use ref.group = 2 when the second group is the reference, and so on. This works for all situations, including i) when comparisons are performed between x-axis groups and ii) when comparisons are performed between legend groups.

• character value: For example, you can use ref.group = "ctrl" instead of using the numeric rank value of the "ctrl" group.

• "all": In this case, each of the grouping variable levels is compared to all (i.e. basemean).

label

character string specifying label. Can be:

• the column containing the label (e.g.: label = "p" or label = "p.adj"), where p is the p-value. Other possible values are "p.signif", "p.adj.signif", "p.format", "p.adj.format".

• an expression that can be formatted by the glue() package. For example, when specifying label = "Wilcoxon, p = \{p\}", the expression \{p\} will be replaced by its value.

• a combination of plotmath expressions and glue expressions. You may want some of the statistical parameter in italic; for example: label = "Wilcoxon, italic(p)=\{p\}".

y.position

numeric vector with the y positions of the brackets.

group.by

(optional) character vector specifying the grouping variable; it should be used only for grouped plots. Possible values are:

• "x.var": Group by the x-axis variable and perform the test between legend groups. In other words, the p-value is compute between legend groups at each x position.

• "legend.var": Group by the legend variable and perform the test between x-axis groups. In other words, the test is performed between the x-groups for each legend level.

dodge

dodge width for grouped ggplot/test. Default is 0.8. It’s used to dodge the brackets position when group.by = "legend.var".

bracket.nudge.y

Vertical adjustment to nudge brackets by (in fraction of the total height). Useful to move up or move down the bracket. If positive value, brackets will be moved up; if negative value, brackets are moved down.
bracket_shorten: a small numeric value in [0-1] for shortening the width of bracket.

bracket_group_by: (optional); a variable name for grouping brackets before adding step.increase. Useful for grouped plots. Possible values include "x.var" and "legend.var".

step.increase: numeric vector with the increase in fraction of total height for every additional comparison to minimize overlap.

tip.length: numeric vector with the fraction of total height that the bar goes down to indicate the precise column/value.

size: change the width of the lines of the bracket.

label.size: change the size of the label text.

family: change the font used for the text.

vjust: move the text up or down relative to the bracket.

hjust: move the text left or right relative to the bracket.

p.adjust.method: method for adjusting p values (see `p.adjust`). Has impact only in a situation, where multiple pairwise tests are performed; or when there are multiple grouping variables. Ignored when the specified method is "tukey_hsd" or "games_howell_test" because they come with internal p adjustment method. Allowed values include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". If you don't want to adjust the p value (not recommended), use p.adjust.method = "none".

p.adjust.by: possible value is one of c("group", "panel"). Default is "group": for a grouped data, if pairwise test is performed, then the p-values are adjusted for each group level independently. P-values are adjusted by panel when p.adjust.by = "panel".

symnum.args: a list of arguments to pass to the function symnum for symbolic number coding of p-values. For example, symnum.args <- list(cutpoints = c(0, 0.0001, 0.001, 0.01, 0.05, Inf), symbols = c("****", "***", "**", ",", "ns")). In other words, we use the following convention for symbols indicating statistical significance:

- **ns**: p > 0.05
- */**: p <= 0.05
- ***/**: p <= 0.01
- ********: p <= 0.001

hide.ns: can be logical value (TRUE or FALSE) or a character vector ("p.adj" or "p").

remove.bracket: logical, if TRUE, brackets are removed from the plot.

Case when logical value. If TRUE, hide ns symbol when displaying significance levels. Filter is done by checking the column p.adj.signif, p.signif, p.adj and p.

Case when character value. Possible values are "p" or "p.adj", for filtering out non significant.
position

Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

na.rm

If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.

show.legend

logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes

If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

parse

logical for parsing plotmath expression.

... other arguments passed on to layer. These are often aesthetics, used to set an aesthetic to a fixed value, like color = "red" or size = 3. They may also be parameters to the paired geom/stat.

stat

The statistical transformation to use on the data for this layer, either as a ggproto Geom subclass or as a string naming the stat stripped of the stat_ prefix (e.g. "count" rather than "stat_count")

stack

logical value. Default is FALSE; should be set to TRUE for stacked bar plots or line plots. If TRUE, then the brackets are automatically removed and the dodge value is set to zero.

Examples

df <- ToothGrowth
df$dose <- factor(df$dose)

# Data preparation
#%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
# Transform `dose` into factor variable
df <- ToothGrowth
df$dose <- as.factor(df$dose)
# Add a random grouping variable
df$group <- factor(rep(c("grp1", "grp2"), 30))
head(df, 3)

# Two groups by x position
#%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
# Create a box plot
# Add 10% spaces between the p-value labels and the plot border
bxp <- ggboxplot(
  df, x = "dose", y = "len",
  color = "supp", palette = c("#00AFBB", "#E7B800")
) +
scale_y_continuous(expand = expansion(mult = c(0.05, 0.10)))
# Add p-values onto the box plots
# label can be "p.format" or "p.adj.format"
bxp + geom_pwc(
  aes(group = supp), tip.length = 0,
  method = "t_test", label = "p.format"
)

# Show adjusted p-values and significance levels
# Hide ns (non-significant)
bxp + geom_pwc(
  aes(group = supp), tip.length = 0,
  method = "t_test", label = "p.adj.format\{p.adj.signif\}",
  p.adjust.method = "bonferroni", p.adjust.by = "panel",
  hide.ns = TRUE
)

# Complex cases

# 1. Add p-values of OJ vs VC at each dose group
bxp.complex <- bxp +
  geom_pwc(
    aes(group = supp), tip.length = 0,
    method = "t_test", label = "p.adj.format",
    p.adjust.method = "bonferroni", p.adjust.by = "panel"
  )

# 2. Add pairwise comparisons between dose levels
# Nudge up the brackets by 20% of the total height
bxp.complex <- bxp.complex +
  geom_pwc(
    method = "t_test", label = "p.adj.format",
    p.adjust.method = "bonferroni",
    bracket.nudge.y = 0.2
  )

# 3. Display the plot
bxp.complex

# Three groups by x position

# Simple plots

# Box plots with p-values
bxp <- ggboxplot(
  df, x = "supp", y = "len", fill = "dose",
  palette = "npg"
)

bxp +
  geom_pwc(
    aes(group = dose), tip.length = 0,
    method = "t_test", label = "p.adj.format",
    bracket.nudge.y = -0.08
  )
stat_regline_equation

Description

Add regression line equation and R^2 to a ggplot. Regression model is fitted using the function `lm`.

Usage

```r
stat_regline_equation(
  mapping = NULL,
  data = NULL,
  formula = y ~ x,
  label.x.npc = "left",
  label.y.npc = "top",
  label.x = NULL,
  label.y = NULL,
  output.type = "expression",
  geom = "text",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  ...)
```

Arguments

`mapping` Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data
The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).

formula
a formula object

label.x.npc, label.y.npc
can be numeric or character vector of the same length as the number of groups and/or panels. If too short they will be recycled.
  • If numeric, value should be between 0 and 1. Coordinates to be used for positioning the label, expressed in "normalized parent coordinates".
  • If character, allowed values include: i) one of c('right', 'left', 'center', 'centre', 'middle') for x-axis; ii) and one of c('bottom', 'top', 'center', 'centre', 'middle') for y-axis.
If too short they will be recycled.

label.x, label.y
numeric Coordinates (in data units) to be used for absolute positioning of the label. If too short they will be recycled.

output.type
character One of "expression", "latex" or "text".

geom
The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. "point" rather than "geom_point")

position
Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

na.rm
If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.

show.legend
logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes
If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. `borders()`.

... other arguments to pass to `geom_text` or `geom_label`.

Computed variables
x x position for left edge
y y position near upper edge
eq.label equation for the fitted polynomial as a character string to be parsed
**stat_regline_equation**

- **rr.label** $R^2$ of the fitted model as a character string to be parsed
- **adj.rr.label** Adjusted $R^2$ of the fitted model as a character string to be parsed
- **AIC.label** AIC for the fitted model.
- **BIC.label** BIC for the fitted model.
- **hjust** Set to zero to override the default of the "text" geom.

**References**

The source code of the function `stat_regline_equation()` is inspired from the code of the function `stat_poly_eq()` (in ggpmisc package).

**See Also**

- `ggscatter`

**Examples**

```r
# Simple scatter plot with correlation coefficient and
# regression line
#:::::::::::::::::::::::::::::::::::::::::::::::::::::::::
ggscatter(mtcars, x = "wt", y = "mpg", add = "reg.line") +
  stat_cor(label.x = 3, label.y = 34) +
  stat_regline_equation(label.x = 3, label.y = 32)

# Grouped scatter plot
#:::::::::::::::::::::::::::::::::::::::::::::::::::::::::
#iris, x = "Sepal.Length", y = "Sepal.Width",
#color = "Species", palette = "jco",
#add = "reg.line"
# facet_wrap(~Species) +
ggscatter(iris, x = "Sepal.Length", y = "Sepal.Width",
          color = "Species", palette = "jco",
          add = "reg.line"
          ) + facet_wrap(~Species) +
  stat_cor(label.y = 4.4) +
  stat_regline_equation(label.y = 4.2)

# Polynomial equation
#::::::::::::::::::::::::::::::::::::::::::::::::::::::::

# Demo data
set.seed(4321)
x <- 1:100
y <- (x + x^2 + x^3) + rnorm(length(x), mean = 0, sd = mean(x^3) / 4)
my.data <- data.frame(x, y, group = c("A", "B"),
y2 = y * c(0.5, 2), block = c("a", "a", "b", "b"))

# Fit polynomial regression line and add labels
formula <- y ~ poly(x, 3, raw = TRUE)
p <- ggplot(my.data, aes(x, y2, color = group)) +
  geom_point() +
```
Add Stars to a Scatter Plot

Description

Create a star plot by drawing segments from group centroid to each points.

Usage

```r
stat_stars(
    mapping = NULL,
    data = NULL,
    geom = "segment",
    position = "identity",
    na.rm = FALSE,
    show.legend = NA,
    inherit.aes = TRUE,
    ...
)
```

Arguments

- **mapping**: Set of aesthetic mappings created by `aes()`. If specified and `inherit.aes = TRUE` (the default), it is combined with the default mapping at the top level of the plot. You must supply `mapping` if there is no plot mapping.
- **data**: The data to be displayed in this layer. There are three options:
  - If `NULL`, the default, the data is inherited from the plot data as specified in the call to `ggplot()`.
  - A `data.frame`, or other object, will override the plot data. All objects will be fortified to produce a data frame. See `fortify()` for which variables will be created.
  - A function will be called with a single argument, the plot data. The return value must be a `data.frame`, and will be used as the layer data. A function can be created from a formula (e.g. `~ head(.x, 10)`).
- **geom**: The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. "point" rather than "geom_point")
position
Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

na.rm
If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.

show.legend
logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes
If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

... other arguments to pass to geom_segment.

See Also
ggscatter

Examples

# Load data
data("mtcars")
df <- mtcars
df$cyl <- as.factor(df$cyl)

# Scatter plot with ellipses and group mean points
ggscatter(df, x = "wt", y = "mpg",
color = "cyl", shape = "cyl",
mean.point = TRUE, ellipse = TRUE)+
stat_stars(aes(color = cyl))

stat_welch_anova_test

Add Welch One-Way ANOVA Test P-values to a GGPlot

Description

Add Welch one-way ANOVA test p-values to a ggplot, such as box plots, dot plots and stripcharts.

Usage

stat_welch_anova_test(
  mapping = NULL,
  data = NULL,
  group.by = NULL,
  label = "{method}, p = {p.format}",
  label.x.npc = "left",
  label.y.npc = "top",
)
label.x = NULL,
label.y = NULL,
step.increase = 0.1,
p.adjust.method = "holm",
significance = list(),
geom = "text",
position = "identity",
na.rm = FALSE,
show.legend = FALSE,
inherit.aes = TRUE,
parse = FALSE,
...)

Arguments

mapping Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.

data The data to be displayed in this layer. There are three options:
If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot(). An object, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created.
A function will be called with a single argument, the plot data. The return value must be a data frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).

group.by (optional) character vector specifying the grouping variable; it should be used only for grouped plots. Possible values are:

- "x.var": Group by the x-axis variable and perform the test between legend groups. In other words, the p-value is computed between legend groups at each x position
- "legend.var": Group by the legend variable and perform the test between x-axis groups. In other words, the test is performed between the x-groups for each legend level.

label the column containing the label (e.g.: label = "p" or label = "p.adj"), where p is the p-value. Can be also an expression that can be formatted by the glue() package. For example, when specifying label = "t-test, p = {p}"; the expression {p} will be replaced by its value.

label.x.npc can be numeric or character vector of the same length as the number of groups and/or panels. If too short they will be recycled.

- If numeric, value should be between 0 and 1. Coordinates to be used for positioning the label, expressed in "normalized parent coordinates".
- If character, allowed values include: i) one of c('right', 'left', 'center', 'centre', 'middle') for x-axis; ii) and one of c('bottom', 'top', 'center', 'centre', 'middle') for y-axis.
label.y.npc can be numeric or character vector of the same length as the number of groups and/or panels. If too short they will be recycled.

- If numeric, value should be between 0 and 1. Coordinates to be used for positioning the label, expressed in "normalized parent coordinates".
- If character, allowed values include: i) one of c('right', 'left', 'center', 'centre', 'middle') for x-axis; ii) and one of c('bottom', 'top', 'center', 'centre', 'middle') for y-axis.

label.x numeric Coordinates (in data units) to be used for absolute positioning of the label. If too short they will be recycled.

label.y numeric Coordinates (in data units) to be used for absolute positioning of the label. If too short they will be recycled.

step.increase numeric vector with the increase in fraction of total height for every additional comparison to minimize overlap.

p.adjust.method method for adjusting p values (see p.adjust). Has impact only in a situation, where multiple pairwise tests are performed; or when there are multiple grouping variables. Allowed values include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". If you don’t want to adjust the p value (not recommended), use p.adjust.method = "none".

significance a list of arguments specifying the significance cutpoints and symbols. For example, significance <- list(cutpoints = c(0, 0.0001, 0.001, 0.01, 0.05, Inf), symbols = c("****", "***", "**", ",", "ns").

In other words, we use the following convention for symbols indicating statistical significance:

- ns: p > 0.05
- *: p <= 0.05
- **: p <= 0.01
- ***: p <= 0.001
- ****: p <= 0.0001

geom The geometric object to use to display the data, either as a ggproto Geom subclass or as a string naming the geom stripped of the geom_ prefix (e.g. "point" rather than "geom_point")

position Position adjustment, either as a string naming the adjustment (e.g. "jitter" to use position_jitter), or the result of a call to a position adjustment function. Use the latter if you need to change the settings of the adjustment.

na.rm If FALSE (the default), removes missing values with a warning. If TRUE silently removes missing values.

show.legend logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn’t inherit behaviour from the default plot specification, e.g. borders().

parse If TRUE, the labels will be parsed into expressions and displayed as described in ?plotmath.

... other arguments passed to the function geom_bracket() or geom_text()
Computed variables

- statistic: the value of the test statistic (F-value)
- DFn: Degrees of Freedom in the numerator (i.e. DF effect)
- DFd: Degrees of Freedom in the denominator (i.e., DF error)
- p: p-value.
- p.adj: Adjusted p-values.
- p.signif: P-value significance.
- p.adj.signif: Adjusted p-value significance.
- p.format: Formated p-value.
- p.adj.format: Formated adjusted p-value.
- n: number of samples.

Examples

# Data preparation

```r
# Transform 'dose' into factor variable
df <- ToothGrowth
df$dose <- as.factor(df$dose)
# Add a random grouping variable
set.seed(123)
df$group <- sample(factor(rep(c("grp1", "grp2", "grp3"), 20)))
df$len <- ifelse(df$group == "grp2", df$len+2, df$len)
df$len <- ifelse(df$group == "grp3", df$len+7, df$len)
head(df, 3)
```

# Basic boxplot

```r
# Create a basic boxplot
bxp <- ggboxplot(df, x = "dose", y = "len") +
  scale_y_continuous(expand = expansion(mult = c(0.05, 0.1)))
# Add the p-value to the boxplot
bxp + stat_welch_anova_test()
# Change the label position
# Using coordinates in data units
bxp + stat_welch_anova_test(label.x = "1", label.y = 10, hjust = 0)
# Format the p-value differently
custom_p_format <- function(p) {
  rstatix::p_format(p, accuracy = 0.0001, digits = 3, leading.zero = FALSE)
}
bxp + stat_welch_anova_test(
  label = "Welch Anova, italic(p) = {custom_p_format(p)}{p.signif}"}
```
# Show a detailed label in italic
bxp + stat_welch_anova_test(label = "as_detailed_italic")

# Faceted plots
# Create a ggplot facet
bxp <- ggboxplot(df, x = "dose", y = "len", facet.by = "supp") +
  scale_y_continuous(expand = expansion(mult = c(0.05, 0.1)))
# Add p-values
bxp + stat_welch_anova_test()

# Grouped plots
# For each x-position, computes tests between legend groups
bxp2 <- ggboxplot(df, x = "group", y = "len", color = "dose", palette = "npg")
# For each legend group, computes tests between x variable groups
bxp2 + stat_welch_anova_test(aes(group = dose), label = "p = {p.format}{p.signif}")

bxp2 + stat_welch_anova_test(aes(group = dose, color = dose), group.by = "legend.var")

---

text_grob

Create a Text Graphical object

**Description**

Create easily a customized text grob (graphical object). Wrapper around `textGrob`.

**Usage**

```r
text_grob(
  label,
  just = "centre",
  hjust = NULL,
  vjust = NULL,
  rot = 0,
  color = "black",
  face = "plain",
  size = NULL,
  lineheight = NULL,
  family = NULL,
  ...
)
```
Arguments

label A character or expression vector. Other objects are coerced by `as.graphicsAnnot`.

just The justification of the text relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". For numeric values, 0 means left (bottom) alignment and 1 means right (top) alignment.

hjust A numeric vector specifying horizontal justification. If specified, overrides the just setting.

vjust A numeric vector specifying vertical justification. If specified, overrides the just setting.

rot The angle to rotate the text.

color text font color.

face font face. Allowed values include one of "plain", "bold", "italic", "bold.italic".

size font size (e.g.: size = 12)

lineheight line height (e.g.: lineheight = 2).

family font family.

... other arguments passed to `textGrob`.

Value

a text grob.

Examples

text <- paste("iris data set gives the measurements in cm",
               "of the variables sepal length and width",
               "and petal length and width, respectively",
               "for 50 flowers from each of 3 species of iris.",
               "The species are Iris setosa, versicolor, and virginica."
               , sep = "\n")

# Create a text grob
tgrob <- text_grob(text, face = "italic", color = "steelblue")
# Draw the text
as_ggplot(tgrob)
Description

- **theme_pubr()**: Create a publication ready theme
- **theme_pubclean()**: a clean theme without axis lines, to direct more attention to the data.
- **labs_pubr()**: Format only plot labels to a publication ready style
- **theme_classic2()**: Create a classic theme with axis lines.
- **clean_theme()**: Remove axis lines, ticks, texts and titles.
- **clean_table_theme()**: Clean the the theme of a table, such as those created by `ggsummarytable()`.

Usage

```r
theme_pubr(
  base_size = 12,
  base_family = "",
  border = FALSE,
  margin = TRUE,
  legend = c("top", "bottom", "left", "right", "none"),
  x.text.angle = 0
)
```

```r
theme_pubclean(base_size = 12, base_family = "", flip = FALSE)
```

```r
labs_pubr(base_size = 14, base_family = "")
```

```r
theme_classic2(base_size = 12, base_family = "")
```

```r
clean_theme()
```

```r
clean_table_theme()
```

Arguments

- **base_size**: base font size
- **base_family**: base font family
- **border**: logical value. Default is FALSE. If TRUE, add panel border.
- **margin**: logical value. Default is TRUE. If FALSE, reduce plot margin.
- **legend**: character specifying legend position. Allowed values are one of c("top", "bottom", "left", "right", "none"). Default is "top" side position. To remove the legend use legend = "none". Legend position can be also specified using a numeric vector c(x, y). In this case it is possible to position the legend inside the plotting area. x and y are the coordinates of the legend box. Their values should be between 0 and 1. c(0,0) corresponds to the "bottom left" and c(1,1) corresponds to the "top right" position. For instance use legend = c(0.8, 0.2).
- **x.text.angle**: Rotation angle of x axis tick labels. Default value is 0. Use 90 for vertical text.
- **flip**: logical. If TRUE, grid lines are added to y axis instead of x axis.
Examples

```r
p <- ggplot(mtcars, aes(x = wt, y = mpg)) +
  geom_point(aes(color = gear))

# Default plot
p

# Use theme_pubr()
p + theme_pubr()

# Format labels
p + labs_pubr()
```

---

### theme_transparent

Create a ggplot with Transparent Background

**Description**

Create a ggplot with transparent background.

**Usage**

```r
theme_transparent(base_size = 12, base_family = "")
```

**Arguments**

- `base_size`: base font size
- `base_family`: base font family

**See Also**

- `theme_pubr`

**Examples**

```r
# Create a scatter plot
sp <- ggscatter(iris, x = "Sepal.Length", y = "Sepal.Width",
                color = "Species", palette = "jco",
                size = 3, alpha = 0.6)

sp

# Transparent theme
sp + theme_transparent()
```
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