

Package ‘ggpubr’

August 22, 2017

Type Package

Title 'ggplot2' Based Publication Ready Plots

Version 0.1.5

Date 2017-08-21

Description 'ggplot2' is an excellent and flexible package 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.

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LazyData TRUE

Depends R (>= 3.1.0), ggplot2, magrittr

Imports ggrepel, grid, ggsci, stats, utils, tidyr, purrr, dplyr(>= 0.7.1), cowplot, ggsignif, scales, gridExtra

Suggests grDevices, knitr, RColorBrewer, gtable

URL <http://www.sthda.com/english/rpkgs/ggpubr>

BugReports <https://github.com/kassambara/ggpubr/issues>

RoxygenNote 6.0.1

Collate 'utilities_color.R' 'utilities_base.R' 'desc_statby.R'
'utilities.R' 'add_summary.R' 'annotate_figure.R' 'as_ggplot.R'
'axis_scale.R' 'background_image.R' 'bgcolor.R' 'border.R'
'compare_means.R' 'diff_express.R' 'facet.R' 'font.R'
'gene_citation.R' 'geom_exec.R' 'get_legend.R' 'get_palette.R'
'ggadd.R' 'ggarrange.R' 'ggpar.R' 'ggbarplot.R' 'ggboxplot.R'
'ggdensity.R' 'stat_conf_ellipse.R' 'stat_chull.R'
'ggdotchart.R' 'ggdotplot.R' 'ggecdf.R' 'ggerrorplot.R'
'ggexport.R' 'gghistogram.R' 'ggline.R' 'ggmapplot.R'
'ggpaired.R' 'ggparagraph.R' 'ggpie.R' 'ggpubr_args.R'
'ggqqplot.R' 'utilities_label.R' 'stat_cor.R' 'stat_stars.R'
'ggscatter.R' 'ggstripchart.R' 'ggtext.R' 'ggtexttable.R'

'ggviolin.R' 'gradient_color.R' 'grids.R' 'rotate.R'
 'rotate_axis_text.R' 'remove.R' 'set_palette.R'
 'show_line_types.R' 'show_point_shapes.R'
 'stat_compare_means.R' 'stat_mean.R' 'text_grob.R'
 'theme_pubr.R' 'theme_transparent.R'

NeedsCompilation no

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Repository CRAN

Date/Publication 2017-08-22 07:13:13 UTC

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add_summary	<i>Add Summary Statistics onto a ggplot.</i>
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Description

add summary statistics onto a ggplot.

Usage

```
add_summary(p, fun = "mean_se", error.plot = "pointrange",
  color = "black", fill = "white", width = NULL, shape = 19, size = 1,
  data = NULL, position = position_dodge(0.8))
```

```
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_mad(x, error.limit = "both")
```

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

Arguments

<code>p</code>	a <code>ggplot</code> on which you want to add summary statistics.
<code>fun</code>	a function that is given the complete data and should return a data frame with variables <code>ymin</code> , <code>y</code> , and <code>ymax</code> . Allowed values are one of: "mean", "mean_se", "mean_sd", "mean_ci", "mean_range", "median", "median_iqr", "median_mad", "median_range".
<code>error.plot</code>	plot type used to visualize error. Allowed values are one of <code>c("pointrange", "linerange", "crossbar")</code> . Default value is "pointrange".
<code>color</code>	point or outline color.
<code>fill</code>	fill color. Used only when <code>error.plot = "crossbar"</code> .
<code>width</code>	numeric value between 0 and 1 specifying bar or box width. Example <code>width = 0.8</code> . Used only when <code>error.plot</code> is one of <code>c("crossbar", "errorbar")</code> .
<code>shape</code>	point shape. Allowed values can be displayed using the function <code>show_point_shapes()</code> .
<code>size</code>	numeric value in [0-1] specifying point and line size.
<code>data</code>	a <code>data.frame</code> to be displayed. If <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <code>ggplot</code> .
<code>position</code>	position adjustment, either as a string, or the result of a call to a position adjustment function. Used to adjust position for multiple groups.
<code>x</code>	a numeric vector.
<code>error.limit</code>	allowed values are one of ("both", "lower", "upper", "none") specifying whether to plot the lower and/or the upper limits of error interval.
<code>ci</code>	the percent range of the confidence interval (default is 0.95).

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_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

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

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

annotate_figure	<i>Annotate Arranged Figure</i>
-----------------	---------------------------------

Description

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

Usage

```
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", "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: \n ToothGrowth data set", color = "blue",
    hjust = 1, x = 1, face = "italic", size = 10),
  left = text_grob("Figure arranged using ggpubr", color = "green", rot = 90),
  right = "I'm done, thanks :-)",
  fig.lab = "Figure 1", fig.lab.face = "bold"
)

```

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)
```

axis_scale

*Change Axis Scale: log2, log10 and more***Description**

Change axis scale.

- xscale: change x axis scale.
- yscale: change y axis scale.

Usage

```
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)
```

background_image *Add Background Image to ggplot2*

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
img.file <- system.file(file.path("images", "background-image.png"),
                        package = "ggpubr")
img <- 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")
p

# 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). Sess [show_line_types](#).

Examples

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

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

# Add border
p + border()
```

compare_means

*Comparison of Means***Description**

Performs one or multiple mean comparisons.

Usage

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

Arguments

formula	a formula of the form $x \sim \text{group}$ 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, <code>formula = TP53 ~ cancer_group</code> . It's also possible to perform the test for multiple response variables at the same time. For example, <code>formula = c(TP53, PTEN) ~ cancer_group</code> .
data	a data.frame containing the variables in the formula.
method	the type of test. Default is wilcox.test . Allowed values include: <ul style="list-style-type: none"> • 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). <code>ref.group</code> can be also <code>".all."</code> . In this case, each of the grouping variable levels is compared to all (i.e. basemean).


```

# 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")

```

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, sd²

Examples

```
# 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

```
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

```
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](#)

Usage

```
facet(p, facet.by, nrow = NULL, ncol = NULL, scales = "fixed",
      short.panel.labs = TRUE, 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, ...)
```

Arguments

<code>p</code>	a <code>ggplot</code>
<code>facet.by</code>	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
<code>nrow</code> , <code>ncol</code>	Number of rows and columns in the panel. Used only when the data is faceted by one grouping variable.
<code>scales</code>	should axis scales of panels be fixed ("fixed", the default), free ("free"), or free in one dimension ("free_x", "free_y").
<code>short.panel.labs</code>	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.
<code>panel.labs</code>	a list of one or two character vectors to modify facet panel labels. For example, <code>panel.labs = list(sex = c("Male", "Female"))</code> specifies the labels for the "sex" variable. For two grouping variables, you can use for example <code>panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))</code> .
<code>panel.labs.background</code>	a list to customize the background of panel labels. Should contain the combination of the following elements: <ul style="list-style-type: none"> • <code>color</code>, <code>linetype</code>, <code>size</code>: background line color, type and size • <code>fill</code>: background fill color. For example, <code>panel.labs.background = list(color = "blue", fill = "pink", linetype = "dashed", size = 0.5)</code> .
<code>panel.labs.font</code>	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.
<code>panel.labs.font.x</code> , <code>panel.labs.font.y</code>	same as <code>panel.labs.font</code> but for only x and y direction, respectively.
<code>...</code>	not used

Examples

```
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")
)

```

font

*Change the Appearance of Titles and Axis Labels***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

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

Arguments

object	character string specifying the plot components. Allowed values include: <ul style="list-style-type: none"> • "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 • "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.
...	other arguments to pass to the function <code>element_text()</code> .

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

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

Format

A data frame with 66 rows and 2 columns.

gene gene names

citation_index mean citation index

Examples

```

data(gene_citation)

# Some key genes of interest to be highlighted
key.gns <- c("MYC", "PRDM1", "CD69", "IRF4", "CASP3", "BCL2L1", "MYB", "BACH2", "BIM1", "PTEN",
            "KRAS", "FOXP1", "IGF1R", "KLF4", "CDK6", "CCND2", "IGF1", "TNFAIP3", "SMAD3", "SMAD7",
            "BMP2", "RB1", "IGF2R", "ARNT")
# 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(). Basic users of ggpubr don't need this function.

Usage

```
geom_exec(geomfunc = NULL, data = NULL, position = NULL, ...)
```

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

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

## End(Not run)
```

`get_legend`*Extract Legends from a ggplot object*

Description

Extract the legend labels from a ggplot object.

Usage

```
get_legend(p)
```

Arguments

`p` an object of class `ggplot`.

Value

an object of class `gtable`.

Examples

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

# 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.

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", "uc-scgb", "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

```

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", width = 1,
  shape = 19, size = NULL, alpha = 1, jitter = 0.2, binwidth = NULL,
  dotsize = size, error.plot = "pointrange", data = NULL,
  position = position_dodge(0.8), p_geom = "")

```

Arguments

<code>p</code>	a <code>ggplot</code>
<code>add</code>	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_mad", "median_range".
<code>color</code>	point or outline color.
<code>fill</code>	fill color. Used only when <code>error.plot = "crossbar"</code> .
<code>width</code>	numeric value between 0 and 1 specifying bar or box width. Example <code>width = 0.8</code> . Used only when <code>error.plot</code> is one of <code>c("crossbar", "errorbar")</code> .
<code>shape</code>	point shape. Allowed values can be displayed using the function <code>show_point_shapes()</code> .
<code>size</code>	numeric value in [0-1] specifying point and line size.
<code>alpha</code>	numeric value specifying fill color transparency. Value should be in [0, 1], where 0 is full transparency and 1 is no transparency.
<code>jitter</code>	a numeric value specifying the amount of jittering. Used only when <code>add</code> contains "jitter".
<code>binwidth</code>	numeric value specifying bin width. use value between 0 and 1 when you have a strong dense dotplot. For example <code>binwidth = 0.2</code> . Used only when <code>add</code> contains "dotplot".
<code>dotsize</code>	as <code>size</code> but applied only to dotplot.
<code>error.plot</code>	plot type used to visualize error. Allowed values are one of <code>c("pointrange", "linerrange", "crossbar")</code> . Default value is "pointrange".
<code>data</code>	a <code>data.frame</code> to be displayed. If <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to <code>ggplot</code> .
<code>position</code>	position adjustment, either as a string, or the result of a call to a position adjustment function. Used to adjust position for multiple groups.
<code>p_geom</code>	the geometry of the main plot. Ex: <code>p_geom = "geom_line"</code> . If <code>NULL</code> , the geometry is extracted from <code>p</code> . Used only by <code>ggline()</code> .

Examples

```
# 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

```
ggarrange(..., plotlist = NULL, ncol = NULL, nrow = NULL, labels = NULL,
  align = c("none", "h", "v", "hv"), widths = 1, heights = 1,
  legend = NULL, common.legend = FALSE)
```

Arguments

<code>...</code>	list of plots to be arranged into the grid. The plots can be either ggplot2 plot objects or arbitrary gtables.
<code>plotlist</code>	(optional) list of plots to display.
<code>ncol</code>	(optional) number of columns in the plot grid.
<code>nrow</code>	(optional) number of rows in the plot grid.
<code>labels</code>	(optional) list of labels to be added to the plots. You can also set <code>labels="AUTO"</code> to auto-generate upper-case labels or <code>labels="auto"</code> to auto-generate lower-case labels.
<code>align</code>	(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".
<code>widths</code>	(optional) numerical vector of relative columns widths. For example, in a two-column grid, <code>widths = c(2, 1)</code> would make the first column twice as wide as the second column.
<code>heights</code>	same as <code>widths</code> but for column heights.
<code>legend</code>	character specifying legend position. Allowed values are one of <code>c("top", "bottom", "left", "right", "none")</code> . To remove the legend use <code>legend = "none"</code> .
<code>common.legend</code>	logical value. Default is FALSE. If TRUE, a common unique legend will be created for arranged plots.

Value

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

Author(s)

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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)
```

ggbarplot

Bar plot

Description

Create a bar plot.

Usage

```
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, add = "none", add.params = list(),
  error.plot = "errorbar", label = FALSE, lab.col = "black",
  lab.size = 4, lab.pos = c("out", "in"), lab.vjust = NULL,
  lab.hjust = NULL, sort.val = c("none", "desc", "asc"),
  sort.by.groups = TRUE, top = Inf, position = position_stack(),
  ggtheme = theme_pubr(), ...)
```


Arguments

<code>data</code>	a data frame
<code>x, y</code>	x and y variables for drawing.
<code>combine</code>	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.
<code>merge</code>	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 <code>merge = "flip"</code> , then y variables are used as x tick labels and the x variable is used as grouping variable.
<code>color, fill</code>	outline and fill colors.
<code>palette</code>	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. <code>c("blue", "red")</code> ; and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmarty".
<code>size</code>	Numeric value (e.g.: <code>size = 1</code>). change the size of points and outlines.
<code>width</code>	numeric value between 0 and 1 specifying box width.
<code>title</code>	plot main title.
<code>xlab</code>	character vector specifying x axis labels. Use <code>xlab = FALSE</code> to hide xlab.
<code>ylab</code>	character vector specifying y axis labels. Use <code>ylab = FALSE</code> to hide ylab.
<code>facet.by</code>	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
<code>panel.labs</code>	a list of one or two character vectors to modify facet panel labels. For example, <code>panel.labs = list(sex = c("Male", "Female"))</code> specifies the labels for the "sex" variable. For two grouping variables, you can use for example <code>panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))</code> .
<code>short.panel.labs</code>	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.
<code>select</code>	character vector specifying which items to display.
<code>remove</code>	character vector specifying which items to remove from the plot.
<code>order</code>	character vector specifying the order of items.
<code>add</code>	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 <code>?desc_statby</code> for more details.
<code>add.params</code>	parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: <code>add.params = list(color = "red")</code> .

<code>error.plot</code>	plot type used to visualize error. Allowed values are one of <code>c("pointrange", "linrange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linrange", "lower_linrange")</code> . Default value is "pointrange" or "errorbar". Used only when <code>add != "none"</code> and <code>add</code> contains one "mean_*" or "med_*" where "*" = sd, se,
<code>label</code>	specify whether to add labels on the bar plot. Allowed values are: <ul style="list-style-type: none"> • logical value: If TRUE, y values is added as labels on the bar plot • character vector: Used as text labels; must be the same length as y.
<code>lab.col</code> , <code>lab.size</code>	text color and size for labels.
<code>lab.pos</code>	character specifying the position for labels. Allowed values are "out" (for outside) or "in" (for inside). Ignored when <code>lab.vjust != NULL</code> .
<code>lab.vjust</code>	numeric, vertical justification of labels. Provide negative value (e.g.: -0.4) to put labels outside the bars or positive value to put labels inside (e.g.: 2).
<code>lab.hjust</code>	numeric, horizontal justification of labels.
<code>sort.val</code>	a string specifying whether the value should be sorted. Allowed values are "none" (no sorting), "asc" (for ascending) or "desc" (for descending).
<code>sort.by.groups</code>	logical value. If TRUE the data are sorted by groups. Used only when <code>sort.val != "none"</code> .
<code>top</code>	a numeric value specifying the number of top elements to be shown.
<code>position</code>	Position adjustment, either as a string, or the result of a call to a position adjustment function.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
<code>...</code>	other arguments to be passed to be passed to <code>ggpar()</code> .

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
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
ggbarplot(df, "dose", "len",
  fill = "dose", color = "dose",
  palette = c("#00AFBB", "#E7B800", "#FC4E07"))

# 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 color by a second group: "supp"

```

```

# Add labels inside bars
ggbarplot(df2, "dose", "len",
  fill = "supp", color = "supp", palette = "Paired",
  label = TRUE, lab.col = "white", lab.pos = "in")

# Change position: Interleaved (dodged) bar plot
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.
df3 <- ToothGrowth
head(df3, 10)

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

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

# Add error bars: mean_se
# (other values include: mean_sd, mean_ci, median_iqr, ...)
# Add labels
ggbarplot(df3, x = "dose", y = "len",
  add = "mean_se", label = TRUE, lab.vjust = -1.6)

# Use only "upper_errorbar"
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, facet.by = NULL, panel.labs = NULL,
  short.panel.labs = TRUE, linetype = "solid", size = NULL, width = 0.7,
  notch = FALSE, 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

<code>data</code>	a data frame
<code>x</code>	character string containing the name of x variable.
<code>y</code>	character vector containing one or more variables to plot
<code>combine</code>	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.
<code>merge</code>	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 <code>merge = "flip"</code> , then y variables are used as x tick labels and the x variable is used as grouping variable.
<code>color</code>	outline color.
<code>fill</code>	fill color.
<code>palette</code>	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. <code>c("blue", "red")</code> ; and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
<code>title</code>	plot main title.
<code>xlab</code>	character vector specifying x axis labels. Use <code>xlab = FALSE</code> to hide xlab.
<code>ylab</code>	character vector specifying y axis labels. Use <code>ylab = FALSE</code> to hide ylab.

<code>facet.by</code>	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
<code>panel.labs</code>	a list of one or two character vectors to modify facet panel labels. For example, <code>panel.labs = list(sex = c("Male", "Female"))</code> specifies the labels for the "sex" variable. For two grouping variables, you can use for example <code>panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))</code> .
<code>short.panel.labs</code>	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.
<code>linetype</code>	line types.
<code>size</code>	Numeric value (e.g.: <code>size = 1</code>). change the size of points and outlines.
<code>width</code>	numeric value between 0 and 1 specifying box width.
<code>notch</code>	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.
<code>select</code>	character vector specifying which items to display.
<code>remove</code>	character vector specifying which items to remove from the plot.
<code>order</code>	character vector specifying the order of items.
<code>add</code>	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 <code>?desc_statby</code> for more details.
<code>add.params</code>	parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: <code>add.params = list(color = "red")</code> .
<code>error.plot</code>	plot type used to visualize error. Allowed values are one of <code>c("pointrange", "linerrange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linerrange", "lower_linerrange")</code> . Default value is "pointrange" or "errorbar". Used only when <code>add != "none"</code> and <code>add</code> contains one "mean_*" or "med_*" where "*" = sd, se,
<code>label</code>	the name of the column containing point labels. Can be also a character vector with <code>length = nrow(data)</code> .
<code>font.label</code>	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 <code>font.label = list(size = 14, face = "bold", color = "red")</code> . To specify only the size and the style, use <code>font.label = list(size = 14, face = "plain")</code> .
<code>label.select</code>	can be of two formats: <ul style="list-style-type: none"> • a character vector specifying some labels to show. • a list containing one or the combination of the following components: <ul style="list-style-type: none"> – <code>top.up</code> and <code>top.down</code>: to display the labels of the top up/down points. For example, <code>label.select = list(top.up = 10, top.down = 4)</code>.

	– <code>criteria</code> : to filter, for example, by x and y variables values, use this: <code>label.select = list(criteria = "`y` > 2 & `y` < 5 & `x` %in% c('A', 'B')")</code> .
<code>repel</code>	a logical value, whether to use <code>ggrepel</code> to avoid overplotting text labels or not.
<code>label.rectangle</code>	logical value. If TRUE, add rectangle underneath the text, making it easier to read.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
...	other arguments to be passed to <code>geom_boxplot</code> , <code>ggpar</code> and <code>facet</code> .

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"))

```


Description

Create a density plot.

Usage

```
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 <code>"..density.."</code> or <code>"..count.."</code> .
combine	logical value. Default is <code>FALSE</code> . Used only when <code>y</code> is a vector containing multiple variables to plot. If <code>TRUE</code> , create a multi-panel plot by combining the plot of <code>y</code> variables.
merge	logical or character value. Default is <code>FALSE</code> . Used only when <code>y</code> is a vector containing multiple variables to plot. If <code>TRUE</code> , merge multiple <code>y</code> variables in the same plotting area. Allowed values include also <code>"asis"</code> (<code>TRUE</code>) and <code>"flip"</code> . If <code>merge = "flip"</code> , then <code>y</code> variables are used as <code>x</code> tick labels and the <code>x</code> 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 <code>"grey"</code> for grey color palettes; brewer palettes e.g. <code>"RdBu"</code> , <code>"Blues"</code> , ...; or custom color palette e.g. <code>c("blue", "red")</code> ; and scientific journal palettes from <code>ggsci</code> R package, e.g.: <code>"npg"</code> , <code>"aaas"</code> , <code>"lancet"</code> , <code>"jco"</code> , <code>"ucscgb"</code> , <code>"uchicago"</code> , <code>"simpsons"</code> and <code>"rickandmorty"</code> .
size	Numeric value (e.g.: <code>size = 1</code>). 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 <code>[0, 1]</code> , where 0 is full transparency and 1 is no transparency.
title	plot main title.
xlab	character vector specifying <code>x</code> axis labels. Use <code>xlab = FALSE</code> to hide <code>xlab</code> .
ylab	character vector specifying <code>y</code> axis labels. Use <code>ylab = FALSE</code> to hide <code>ylab</code> .
facet.by	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.

<code>panel.labs</code>	a list of one or two character vectors to modify facet panel labels. For example, <code>panel.labs = list(sex = c("Male", "Female"))</code> specifies the labels for the "sex" variable. For two grouping variables, you can use for example <code>panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))</code> .
<code>short.panel.labs</code>	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.
<code>add</code>	allowed values are one of "mean" or "median" (for adding mean or median line, respectively).
<code>add.params</code>	parameters (color, size, linetype) for the argument 'add'; e.g.: <code>add.params = list(color = "red")</code> .
<code>rug</code>	logical value. If TRUE, add marginal rug.
<code>label</code>	the name of the column containing point labels. Can be also a character vector with length = <code>nrow(data)</code> .
<code>font.label</code>	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 <code>font.label = list(size = 14, face = "bold", color = "red")</code> . To specify only the size and the style, use <code>font.label = list(size = 14, face = "plain")</code> .
<code>label.select</code>	can be of two formats: <ul style="list-style-type: none"> • a character vector specifying some labels to show. • a list containing one or the combination of the following components: <ul style="list-style-type: none"> – <code>top.up</code> and <code>top.down</code>: to display the labels of the top up/down points. For example, <code>label.select = list(top.up = 10, top.down = 4)</code>. – <code>criteria</code>: to filter, for example, by x and y variables values, use this: <code>label.select = list(criteria = "`y` > 2 & `y` < 5 & `x` %in% c('A', 'B')")</code>.
<code>repel</code>	a logical value, whether to use <code>ggrepel</code> to avoid overplotting text labels or not.
<code>label.rectangle</code>	logical value. If TRUE, add rectangle underneath the text, making it easier to read.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
...	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`, `ylob`
- 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

```
# 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", fill = "sex",
  palette = c("#00AFBB", "#E7B800"))
```

Description

Draw a Cleveland dot plot.

Usage

```
ggdotchart(data, x, y, group = NULL, combine = FALSE, color = "black",
  palette = NULL, shape = 19, size = NULL, dot.size = size,
  sorting = c("ascending", "descending"), 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,
  ggtheme = theme_pubr(), ...)
```

```
theme_cleveland(rotate = TRUE)
```

Arguments

<code>data</code>	a data frame
<code>x, y</code>	x and y variables for drawing.
<code>group</code>	an optional column name indicating how the elements of x are grouped.
<code>combine</code>	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.
<code>color, size</code>	points color and size.
<code>palette</code>	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 "rickandmarty".
<code>shape</code>	point shape. See show_point_shapes .
<code>dot.size</code>	numeric value specifying the dot size.
<code>sorting</code>	a character vector for sorting into ascending or descending order. Allowed values are one of "descending" and "ascending". Partial match are allowed (e.g. sorting = "desc" or "asc"). Default is "descending".
<code>add</code>	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 <code>?desc_statby</code> for more details.
<code>add.params</code>	parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: <code>add.params = list(color = "red")</code> .
<code>x.text.col</code>	logical. If TRUE (default), x axis texts are colored by groups.
<code>rotate</code>	logical value. If TRUE, rotate the graph by setting the plot orientation to horizontal.
<code>title</code>	plot main title.
<code>xlab</code>	character vector specifying x axis labels. Use <code>xlab = FALSE</code> to hide xlab.

<code>ylab</code>	character vector specifying y axis labels. Use <code>ylab = FALSE</code> to hide <code>ylab</code> .
<code>facet.by</code>	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
<code>panel.labs</code>	a list of one or two character vectors to modify facet panel labels. For example, <code>panel.labs = list(sex = c("Male", "Female"))</code> specifies the labels for the "sex" variable. For two grouping variables, you can use for example <code>panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))</code> .
<code>short.panel.labs</code>	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.
<code>select</code>	character vector specifying which items to display.
<code>remove</code>	character vector specifying which items to remove from the plot.
<code>order</code>	character vector specifying the order of items.
<code>label</code>	the name of the column containing point labels.
<code>font.label</code>	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 <code>font.label = list(size = 14, face = "bold", color = "red")</code> . To specify only the size and the style, use <code>font.label = list(size = 14, face = "plain")</code> .
<code>label.select</code>	can be of two formats: <ul style="list-style-type: none"> • a character vector specifying some labels to show. • a list containing one or the combination of the following components: <ul style="list-style-type: none"> – <code>top.up</code> and <code>top.down</code>: to display the labels of the top up/down points. For example, <code>label.select = list(top.up = 10, top.down = 4)</code>. – <code>criteria</code>: to filter, for example, by x and y variables values, use this: <code>label.select = list(criteria = "`y` > 2 & `y` < 5 & `x` %in% c('A', 'B')")</code>.
<code>repel</code>	a logical value, whether to use <code>ggrepel</code> to avoid overplotting text labels or not.
<code>label.rectangle</code>	logical value. If TRUE, add rectangle underneath the text, making it easier to read.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
<code>...</code>	other arguments to be passed to <code>geom_point</code> and <code>ggpar</code> .

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('#999999', '#E69F00', '#56B4E9'),
  rotate = TRUE,
  sorting = "descending",
  ggtheme = theme_bw(),
  y.text.col = TRUE )
```

ggdotplot

Dot plot

Description

Create a dot plot.

Usage

```
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(), ...)
```

Arguments

<code>data</code>	a data frame
<code>x</code>	character string containing the name of x variable.
<code>y</code>	character vector containing one or more variables to plot
<code>combine</code>	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.
<code>merge</code>	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.
<code>color</code>	outline color.
<code>fill</code>	fill color.
<code>palette</code>	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 "rickandmarty".
<code>title</code>	plot main title.
<code>xlab</code>	character vector specifying x axis labels. Use xlab = FALSE to hide xlab.
<code>ylab</code>	character vector specifying y axis labels. Use ylab = FALSE to hide ylab.
<code>facet.by</code>	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
<code>panel.labs</code>	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")).
<code>short.panel.labs</code>	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.
<code>size</code>	Numeric value (e.g.: size = 1). change the size of points and outlines.
<code>binwidth</code>	numeric value specifying bin width. use value between 0 and 1 when you have a strong dense dotplot. For example binwidth = 0.2. http://r4ds.had.co.nz/eda.html).
<code>select</code>	character vector specifying which items to display.
<code>remove</code>	character vector specifying which items to remove from the plot.
<code>order</code>	character vector specifying the order of items.
<code>add</code>	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.

<code>add.params</code>	parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: <code>add.params = list(color = "red")</code> .
<code>error.plot</code>	plot type used to visualize error. Allowed values are one of <code>c("pointrange", "lin- erange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linrange", "lower_linrange")</code> . Default value is <code>"pointrange"</code> or <code>"errorbar"</code> . Used only when <code>add != "none"</code> and <code>add</code> contains one <code>"mean_*</code> " or <code>"med_*</code> " where <code>"*" = sd, se, ...</code>
<code>label</code>	the name of the column containing point labels. Can be also a character vector with <code>length = nrow(data)</code> .
<code>font.label</code>	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 <code>font.label = list(size = 14, face = "bold", color = "red")</code> . To specify only the size and the style, use <code>font.label = list(size = 14, face = "plain")</code> .
<code>label.select</code>	can be of two formats: <ul style="list-style-type: none"> • a character vector specifying some labels to show. • a list containing one or the combination of the following components: <ul style="list-style-type: none"> – <code>top.up</code> and <code>top.down</code>: to display the labels of the top up/down points. For example, <code>label.select = list(top.up = 10, top.down = 4)</code>. – <code>criteria</code>: to filter, for example, by x and y variabes values, use this: <code>label.select = list(criteria = "`y` > 2 & `y` < 5 & `x` %in% c('A', 'B')")</code>.
<code>repel</code>	a logical value, whether to use <code>ggrepel</code> to avoid overplotting text labels or not.
<code>label.rectangle</code>	logical value. If TRUE, add rectangle underneath the text, making it easier to read.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
<code>...</code>	other arguments to be passed to <code>geom_dotplot</code> , <code>ggpar</code> and <code>facet</code> .

Details

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

- main title and axis labels: `main`, `xlab`, `ylob`
- 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

<code>data</code>	a data frame
<code>x</code>	variable to be drawn.
<code>combine</code>	logical value. Default is FALSE. Used only when <code>y</code> is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of <code>y</code> variables.
<code>merge</code>	logical or character value. Default is FALSE. Used only when <code>y</code> is a vector containing multiple variables to plot. If TRUE, merge multiple <code>y</code> variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If <code>merge = "flip"</code> , then <code>y</code> variables are used as <code>x</code> tick labels and the <code>x</code> variable is used as grouping variable.
<code>color</code>	line and point color.
<code>palette</code>	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. <code>c("blue", "red")</code> ; and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmarty".
<code>size</code>	line and point size.
<code>linetype</code>	line type. See show_line_types .
<code>title</code>	plot main title.
<code>xlab</code>	character vector specifying <code>x</code> axis labels. Use <code>xlab = FALSE</code> to hide <code>xlab</code> .
<code>ylab</code>	character vector specifying <code>y</code> axis labels. Use <code>ylab = FALSE</code> to hide <code>ylab</code> .
<code>facet.by</code>	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
<code>panel.labs</code>	a list of one or two character vectors to modify facet panel labels. For example, <code>panel.labs = list(sex = c("Male", "Female"))</code> specifies the labels for the "sex" variable. For two grouping variables, you can use for example <code>panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))</code> .
<code>short.panel.labs</code>	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.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
<code>...</code>	other arguments to be passed to <code>stat_ecdf</code> and <code>ggpar</code> .

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"))
```

Description

Visualizing error.

Usage

```
ggerrorplot(data, x, y, desc_stat = "mean_se", 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",
  position = position_dodge(), ggtheme = theme_pubr(), ...)
```

Arguments

<code>data</code>	a data frame
<code>x, y</code>	x and y variables for drawing.
<code>desc_stat</code>	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_mad", "median_range"; see desc_statby for more details.
<code>combine</code>	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.
<code>merge</code>	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 <code>merge = "flip"</code> , then y variables are used as x tick labels and the x variable is used as grouping variable.
<code>color, fill</code>	outline and fill colors.
<code>palette</code>	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. <code>c("blue", "red")</code> ; and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmarty".
<code>size</code>	Numeric value (e.g.: <code>size = 1</code>). change the size of points and outlines.
<code>width</code>	numeric value between 0 and 1 specifying box width.
<code>title</code>	plot main title.
<code>xlab</code>	character vector specifying x axis labels. Use <code>xlab = FALSE</code> to hide xlab.
<code>ylab</code>	character vector specifying y axis labels. Use <code>ylab = FALSE</code> to hide ylab.
<code>facet.by</code>	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
<code>panel.labs</code>	a list of one or two character vectors to modify facet panel labels. For example, <code>panel.labs = list(sex = c("Male", "Female"))</code> specifies the labels for the "sex" variable. For two grouping variables, you can use for example <code>panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))</code> .

<code>short.panel.labs</code>	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.
<code>select</code>	character vector specifying which items to display.
<code>remove</code>	character vector specifying which items to remove from the plot.
<code>order</code>	character vector specifying the order of items.
<code>add</code>	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 <code>?desc_statby</code> for more details.
<code>add.params</code>	parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: <code>add.params = list(color = "red")</code> .
<code>error.plot</code>	plot type used to visualize error. Allowed values are one of <code>c("pointrange", "linerrange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linerrange", "lower_linerrange")</code> . Default value is "pointrange" or "errorbar". Used only when <code>add != "none"</code> and <code>add</code> contains one "mean_*" or "med_*" where "*" = sd, se,
<code>position</code>	Position adjustment, either as a string, or the result of a call to a position adjustment function.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
<code>...</code>	other arguments to be passed to be passed to <code>ggpar()</code> .

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
ggerrorplot(df, x = "dose", y = "len",
  add = "mean", error.plot = "errorbar")

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

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

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

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

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

Description

Export ggplots

Usage

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

Arguments

...	list of plots to be arranged into the grid. The plots can be either ggplot2 plot objects, arbitrary gtables or an object of class <code>ggarrange</code> .
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)

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Examples

```
## 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)

```

gghistogram

Histogram plot

Description

Create a histogram plot.

Usage

```

gghistogram(data, x, y = "..count..", combine = FALSE, merge = FALSE,
  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,
  ggtheme = theme_pubr(), ...)

```

Arguments

data	a data frame
x	variable to be drawn.
y	one of <code>"..density.."</code> or <code>"..count.."</code> .
combine	logical value. Default is <code>FALSE</code> . Used only when <code>y</code> is a vector containing multiple variables to plot. If <code>TRUE</code> , create a multi-panel plot by combining the plot of <code>y</code> variables.
merge	logical or character value. Default is <code>FALSE</code> . Used only when <code>y</code> is a vector containing multiple variables to plot. If <code>TRUE</code> , merge multiple <code>y</code> variables in the same plotting area. Allowed values include also <code>"asis"</code> (<code>TRUE</code>) and <code>"flip"</code> . If <code>merge = "flip"</code> , then <code>y</code> variables are used as <code>x</code> tick labels and the <code>x</code> variable is used as grouping variable.
color, fill	histogram line color and fill color.
palette	the color palette to be used for coloring or filling by groups. Allowed values include <code>"grey"</code> for grey color palettes; brewer palettes e.g. <code>"RdBu"</code> , <code>"Blues"</code> , ...; or custom color palette e.g. <code>c("blue", "red")</code> ; and scientific journal palettes from <code>ggsci</code> R package, e.g.: <code>"npg"</code> , <code>"aaas"</code> , <code>"lancet"</code> , <code>"jco"</code> , <code>"ucscgb"</code> , <code>"uchicago"</code> , <code>"simpsons"</code> and <code>"rickandmorty"</code> .

<code>size</code>	Numeric value (e.g.: <code>size = 1</code>). change the size of points and outlines.
<code>linetype</code>	line type. See show_line_types .
<code>alpha</code>	numeric value specifying fill color transparency. Value should be in $[0, 1]$, where 0 is full transparency and 1 is no transparency.
<code>bins</code>	Number of bins. Defaults to 30.
<code>binwidth</code>	numeric value specifying bin width. use value between 0 and 1 when you have a strong dense dotplot. For example <code>binwidth = 0.2</code> . http://r4ds.had.co.nz/eda.html .
<code>title</code>	plot main title.
<code>xlab</code>	character vector specifying x axis labels. Use <code>xlab = FALSE</code> to hide xlab.
<code>ylab</code>	character vector specifying y axis labels. Use <code>ylab = FALSE</code> to hide ylab.
<code>facet.by</code>	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
<code>panel.labs</code>	a list of one or two character vectors to modify facet panel labels. For example, <code>panel.labs = list(sex = c("Male", "Female"))</code> specifies the labels for the "sex" variable. For two grouping variables, you can use for example <code>panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))</code> .
<code>short.panel.labs</code>	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.
<code>add</code>	allowed values are one of "mean" or "median" (for adding mean or median line, respectively).
<code>add.params</code>	parameters (color, size, linetype) for the argument 'add'; e.g.: <code>add.params = list(color = "red")</code> .
<code>rug</code>	logical value. If TRUE, add marginal rug.
<code>add_density</code>	logical value. If TRUE, add density curves.
<code>label</code>	the name of the column containing point labels. Can be also a character vector with <code>length = nrow(data)</code> .
<code>font.label</code>	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 <code>font.label = list(size = 14, face = "bold", color = "red")</code> . To specify only the size and the style, use <code>font.label = list(size = 14, face = "plain")</code> .
<code>label.select</code>	can be of two formats: <ul style="list-style-type: none"> • a character vector specifying some labels to show. • a list containing one or the combination of the following components: <ul style="list-style-type: none"> – <code>top.up</code> and <code>top.down</code>: to display the labels of the top up/down points. For example, <code>label.select = list(top.up = 10, top.down = 4)</code>. – <code>criteria</code>: to filter, for example, by x and y variables values, use this: <code>label.select = list(criteria = "`y` > 2 & `y` < 5 & `x` %in% c('A', 'B')")</code>.
<code>repel</code>	a logical value, whether to use <code>ggrepel</code> to avoid overplotting text labels or not.

<code>label.rectangle</code>	logical value. If TRUE, add rectangle underneath the text, making it easier to read.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
<code>...</code>	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

```
# 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)
```

ggline

Line plot

Description

Create a line plot.

Usage

```
ggline(data, x, y, group = 1, combine = FALSE, merge = FALSE,
  color = "black", palette = NULL, linetype = "solid",
  plot_type = c("b", "l", "p"), size = 0.5, shape = 19,
  point.size = size, point.color = color, 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 = "errorbar",
  label = NULL, font.label = list(size = 11, color = "black"),
  label.select = NULL, repel = FALSE, label.rectangle = FALSE,
  show.line.label = FALSE, ggtheme = theme_pubr(), ...)
```

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).
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.

<code>color</code>	line colors.
<code>palette</code>	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. <code>c("blue", "red")</code> ; and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
<code>linetype</code>	line type.
<code>plot_type</code>	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".
<code>size</code>	Numeric value (e.g.: <code>size = 1</code>). change the size of points and outlines.
<code>shape</code>	point shapes.
<code>point.size</code>	point size.
<code>point.color</code>	point color.
<code>title</code>	plot main title.
<code>xlab</code>	character vector specifying x axis labels. Use <code>xlab = FALSE</code> to hide xlab.
<code>ylab</code>	character vector specifying y axis labels. Use <code>ylab = FALSE</code> to hide ylab.
<code>facet.by</code>	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
<code>panel.labs</code>	a list of one or two character vectors to modify facet panel labels. For example, <code>panel.labs = list(sex = c("Male", "Female"))</code> specifies the labels for the "sex" variable. For two grouping variables, you can use for example <code>panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))</code> .
<code>short.panel.labs</code>	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.
<code>select</code>	character vector specifying which items to display.
<code>remove</code>	character vector specifying which items to remove from the plot.
<code>order</code>	character vector specifying the order of items.
<code>add</code>	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 <code>?desc_statby</code> for more details.
<code>add.params</code>	parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: <code>add.params = list(color = "red")</code> .
<code>error.plot</code>	plot type used to visualize error. Allowed values are one of <code>c("pointrange", "linrange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linrange", "lower_linrange")</code> . Default value is "pointrange" or "errorbar". Used only when <code>add != "none"</code> and <code>add</code> contains one "mean_*" or "med_*" where "*" = sd, se,
<code>label</code>	the name of the column containing point labels. Can be also a character vector with length = <code>nrow(data)</code> .

<code>font.label</code>	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 <code>font.label = list(size = 14, face = "bold", color = "red")</code> . To specify only the size and the style, use <code>font.label = list(size = 14, face = "plain")</code> .
<code>label.select</code>	can be of two formats: <ul style="list-style-type: none"> • a character vector specifying some labels to show. • a list containing one or the combination of the following components: <ul style="list-style-type: none"> – <code>top.up</code> and <code>top.down</code>: to display the labels of the top up/down points. For example, <code>label.select = list(top.up = 10, top.down = 4)</code>. – <code>criteria</code>: to filter, for example, by x and y variables values, use this: <code>label.select = list(criteria = "`y` > 2 & `y` < 5 & `x` %in% c('A', 'B')")</code>.
<code>repel</code>	a logical value, whether to use <code>ggrepel</code> to avoid overplotting text labels or not.
<code>label.rectangle</code>	logical value. If TRUE, add rectangle underneath the text, making it easier to read.
<code>show.line.label</code>	logical value. If TRUE, shows line labels.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
...	other arguments to be passed to <code>geom_dotplot</code> .

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 (on the y-axis) versus the mean expression signal (on the x-axis).

Usage

```

ggmaplot(data, fdr = 0.05, fc = 1.5, genenames = NULL,
  detection_call = NULL, size = NULL, font.label = c(12, "plain",
  "black"), label.rectangle = FALSE, palette = c("#B31B21", "#1465AC",
  "darkgray"), top = 15, select.top.method = c("padj", "fc"), 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, log2FoldChange, and padj. Rows are genes.

- 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 \geq fc and padj \leq 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.
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 <i>font.label = c(14, "bold", "red")</i> .
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.
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", "#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())

```

ggpaired

*Plot Paired Data***Description**

Plot paired data.

Usage

```

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", 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

<code>data</code>	a data frame
<code>cond1</code>	variable name corresponding to the first condition.
<code>cond2</code>	variable name corresponding to the second condition.
<code>x, y</code>	x and y variables, where x is a grouping variable and y contains values for each group. Considered only when <code>cond1</code> and <code>cond2</code> are missing.
<code>id</code>	variable name corresponding to paired samples' id. Used to connect paired points with lines.

<code>color</code>	points and box plot colors. To color by conditions, use <code>color = "condition"</code> .
<code>fill</code>	box plot fill color. To change fill color by conditions, use <code>fill = "condition"</code> .
<code>palette</code>	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. <code>c("blue", "red")</code> ; and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
<code>width</code>	box plot width.
<code>point.size</code> , <code>line.size</code>	point and line size, respectively.
<code>line.color</code>	line color.
<code>title</code>	plot main title.
<code>xlab</code>	character vector specifying x axis labels. Use <code>xlab = FALSE</code> to hide xlab.
<code>ylab</code>	character vector specifying y axis labels. Use <code>ylab = FALSE</code> to hide ylab.
<code>facet.by</code>	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
<code>panel.labs</code>	a list of one or two character vectors to modify facet panel labels. For example, <code>panel.labs = list(sex = c("Male", "Female"))</code> specifies the labels for the "sex" variable. For two grouping variables, you can use for example <code>panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))</code> .
<code>short.panel.labs</code>	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.
<code>label</code>	the name of the column containing point labels. Can be also a character vector with length = <code>nrow(data)</code> .
<code>font.label</code>	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 <code>font.label = list(size = 14, face = "bold", color = "red")</code> . To specify only the size and the style, use <code>font.label = list(size = 14, face = "plain")</code> .
<code>label.select</code>	can be of two formats: <ul style="list-style-type: none"> • a character vector specifying some labels to show. • a list containing one or the combination of the following components: <ul style="list-style-type: none"> – <code>top.up</code> and <code>top.down</code>: to display the labels of the top up/down points. For example, <code>label.select = list(top.up = 10, top.down = 4)</code>. – <code>criteria</code>: to filter, for example, by x and y variables values, use this: <code>label.select = list(criteria = "`y` > 2 & `y` < 5 & `x` %in% c('A', 'B')")</code>.
<code>repel</code>	a logical value, whether to use <code>ggrepel</code> to avoid overplotting text labels or not.
<code>label.rectangle</code>	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 [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

<code>p</code>	an object of class <code>ggplot</code> or a list of <code>ggplots</code>
<code>palette</code>	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. <code>c("blue", "red")</code> ; 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(<code>groups</code>); in this case a basic color palette is created using the function palette .
<code>gradient.cols</code>	vector of colors to use for n-colour gradient. Allowed values include brewer and ggsci color palettes.
<code>main, title</code>	plot main title.
<code>submain, subtitle</code>	plot subtitle.
<code>caption</code>	plot caption.
<code>xlab</code>	character vector specifying x axis labels. Use <code>xlab = FALSE</code> to hide <code>xlab</code> .
<code>ylab</code>	character vector specifying y axis labels. Use <code>ylab = FALSE</code> to hide <code>ylab</code> .
<code>font.main, font.submain, font.caption, font.x, font.y</code>	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, <code>xlab</code> and <code>ylab</code> , respectively. For example <code>font.x = c(14, "bold", "red")</code> . Use <code>font.x = 14</code> , to change only font size; or use <code>font.x = "bold"</code> , to change only font face.
<code>font.title, font.subtitle</code>	alias of <code>font.submain</code> and <code>font.submain</code> , respectively.
<code>font.family</code>	character vector specifying font family.
<code>xlim, ylim</code>	a numeric vector of length 2, specifying x and y axis limits (minimum and maximum), respectively. e.g.: <code>ylim = c(0, 50)</code> .
<code>xscale, yscale</code>	x and y axis scale, respectively. Allowed values are one of <code>c("none", "log2", "log10", "sqrt")</code> ; e.g.: <code>yscale="log2"</code> .
<code>format.scale</code>	logical value. If TRUE, axis tick mark labels will be formatted when <code>xscale</code> or <code>yscale = "log2"</code> or "log10".
<code>legend</code>	character specifying legend position. Allowed values are one of <code>c("top", "bottom", "left", "right", "none")</code> . To remove the legend use <code>legend = "none"</code> . Legend position can be also specified using a numeric vector <code>c(x, y)</code> ; see details section.
<code>legend.title</code>	legend title, e.g.: <code>legend.title = "Species"</code> . Can be also a list, <code>legend.title = list(color = "Spe</code>
<code>font.legend</code>	legend text font style; e.g.: <code>font.legend = c(10, "plain", "black")</code> .
<code>ticks</code>	logical value. Default is TRUE. If FALSE, hide axis tick marks.
<code>tickslab</code>	logical value. Default is TRUE. If FALSE, hide axis tick labels.
<code>font.tickslab, font.xtickslab, font.ytickslab</code>	Font style (size, face, color) for tick labels, e.g.: <code>c(14, "bold", "red")</code> .

<code>x.text.angle</code> , <code>y.text.angle</code>	Numeric value specifying the rotation angle of x and y axis tick labels, respectively. Default value is NULL. For vertical x axis texts use <code>x.text.angle = 90</code> .
<code>xtickslab.rt</code> , <code>ytickslab.rt</code>	Same as <code>x.text.angle</code> and <code>y.text.angle</code> , respectively. Will be deprecated in the near future.
<code>xticks.by</code> , <code>yticks.by</code>	numeric value controlling x and y axis breaks, respectively. For example, if <code>yticks.by = 5</code> , a tick mark is shown on every 5. Default value is NULL.
<code>rotate</code>	logical value. If TRUE, rotate the graph by setting the plot orientation to horizontal.
<code>orientation</code>	change the orientation of the plot. Allowed values are one of <code>c("vertical", "horizontal", "reverse")</code> . Partial match is allowed.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
<code>...</code>	not used

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"))

```

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.
...	other arguments passed to grob .

Author(s)

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

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

ggpie

*Pie chart***Description**

Create a pie chart.

Usage

```
ggpie(data, x, label = NULL, 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_classic(), ...)
```

Arguments

<code>data</code>	a data frame
<code>x</code>	variable containing values for drawing.
<code>label</code>	variable specifying the label of each slice.
<code>lab.pos</code>	character specifying the position for labels. Allowed values are "out" (for outside) or "in" (for inside).
<code>lab.adjust</code>	numeric value, used to adjust label position when <code>lab.pos = "in"</code> . Increase or decrease this value to see the effect.
<code>lab.font</code>	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 <code>lab.font= c(4, "bold", "red")</code> .
<code>font.family</code>	character vector specifying font family.
<code>color, fill</code>	outline and fill colors.
<code>palette</code>	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. <code>c("blue", "red")</code> ; and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
<code>size</code>	Numeric value (e.g.: <code>size = 1</code>). change the size of points and outlines.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
<code>...</code>	other arguments to be passed to be passed to <code>ggpar()</code> .

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: 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_args

*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 "rickandmorty".
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.

<code>add</code>	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 <code>?desc_statby</code> for more details.
<code>add.params</code>	parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: <code>add.params = list(color = "red")</code> .
<code>error.plot</code>	plot type used to visualize error. Allowed values are one of <code>c("pointrange", "linerrange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linerrange", "lower_linerrange")</code> . Default value is "pointrange" or "errorbar". Used only when <code>add != "none"</code> and <code>add</code> contains one "mean_*" or "med_*" where "*" = sd, se,
<code>font.label</code>	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 <code>font.label = list(size = 14, face = "bold", color = "red")</code> . To specify only the size and the style, use <code>font.label = list(size = 14, face = "plain")</code> .
<code>title</code>	plot main title.
<code>xlab</code>	character vector specifying x axis labels. Use <code>xlab = FALSE</code> to hide xlab.
<code>ylab</code>	character vector specifying y axis labels. Use <code>ylab = FALSE</code> to hide ylab.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,

ggqqplot

QQ Plots

Description

Quantile-Quantile plot.

Usage

```
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

<code>data</code>	a data frame
<code>x</code>	variable to be drawn.

<code>combine</code>	logical value. Default is FALSE. Used only when <code>y</code> is a vector containing multiple variables to plot. If TRUE, create a multi-panel plot by combining the plot of <code>y</code> variables.
<code>merge</code>	logical or character value. Default is FALSE. Used only when <code>y</code> is a vector containing multiple variables to plot. If TRUE, merge multiple <code>y</code> variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If <code>merge = "flip"</code> , then <code>y</code> variables are used as <code>x</code> tick labels and the <code>x</code> variable is used as grouping variable.
<code>color</code>	point color.
<code>palette</code>	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. <code>c("blue", "red")</code> ; and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
<code>size</code>	point size.
<code>shape</code>	point shape.
<code>add</code>	character vector. Allowed values are one of "none" and "qqline" (for adding qqline).
<code>add.params</code>	parameters (color, size, linetype) for the argument 'add'; e.g.: <code>add.params = list(color = "red")</code> .
<code>conf.int</code>	logical value. If TRUE, confidence interval is added.
<code>conf.int.level</code>	the confidence level. Default value is 0.95.
<code>title</code>	plot main title.
<code>xlab</code>	character vector specifying <code>x</code> axis labels. Use <code>xlab = FALSE</code> to hide <code>xlab</code> .
<code>ylab</code>	character vector specifying <code>y</code> axis labels. Use <code>ylab = FALSE</code> to hide <code>ylab</code> .
<code>facet.by</code>	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
<code>panel.labs</code>	a list of one or two character vectors to modify facet panel labels. For example, <code>panel.labs = list(sex = c("Male", "Female"))</code> specifies the labels for the "sex" variable. For two grouping variables, you can use for example <code>panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))</code> .
<code>short.panel.labs</code>	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.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
<code>...</code>	other arguments to be passed to <code>ggpar</code> .

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, merge = FALSE, color = "black",
  fill = "lightgray", palette = NULL, shape = 19, size = 2,
  point = TRUE, rug = FALSE, title = NULL, xlab = NULL, ylab = NULL,
  facet.by = NULL, panel.labs = NULL, short.panel.labs = TRUE,
  add = c("none", "reg.line", "loess"), add.params = list(),
  conf.int = FALSE, conf.int.level = 0.95, fullrange = FALSE,
  ellipse = FALSE, ellipse.level = 0.95, ellipse.type = "norm",
  ellipse.alpha = 0.1, ellipse.border.remove = FALSE, mean.point = FALSE,
```

```

mean.point.size = ifelse(is.numeric(size), 2 * size, size),
star.plot = FALSE, star.plot.lty = 1, star.plot.lwd = NULL,
label = NULL, font.label = c(12, "plain"), font.family = "",
label.select = NULL, repel = FALSE, label.rectangle = FALSE,
cor.coef = FALSE, cor.coeff.args = list(), cor.method = "pearson",
cor.coef.coord = c(NULL, NULL), cor.coef.size = 4, ggp = NULL,
show.legend.text = NA, ggtheme = theme_pubr(), ...)

```

Arguments

<code>data</code>	a data frame
<code>x, y</code>	x and y variables for drawing.
<code>combine</code>	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.
<code>merge</code>	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 <code>merge = "flip"</code> , then y variables are used as x tick labels and the x variable is used as grouping variable.
<code>color, fill</code>	point colors.
<code>palette</code>	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. <code>c("blue", "red")</code> ; and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmarty".
<code>shape</code>	point shape. See show_point_shapes .
<code>size</code>	Numeric value (e.g.: <code>size = 1</code>). change the size of points and outlines.
<code>point</code>	logical value. If TRUE, show points.
<code>rug</code>	logical value. If TRUE, add marginal rug.
<code>title</code>	plot main title.
<code>xlab</code>	character vector specifying x axis labels. Use <code>xlab = FALSE</code> to hide xlab.
<code>ylab</code>	character vector specifying y axis labels. Use <code>ylab = FALSE</code> to hide ylab.
<code>facet.by</code>	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
<code>panel.labs</code>	a list of one or two character vectors to modify facet panel labels. For example, <code>panel.labs = list(sex = c("Male", "Female"))</code> specifies the labels for the "sex" variable. For two grouping variables, you can use for example <code>panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))</code> .
<code>short.panel.labs</code>	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.

<code>add</code>	allowed values are one of "none", "reg.line" (for adding linear regression line) or "loess" (for adding local regression fitting).
<code>add.params</code>	parameters (color, size, linetype) for the argument 'add'; e.g.: <code>add.params = list(color = "red")</code> .
<code>conf.int</code>	logical value. If TRUE, adds confidence interval.
<code>conf.int.level</code>	Level controlling confidence region. Default is 95%. Used only when <code>add != "none"</code> and <code>conf.int = TRUE</code> .
<code>fullrange</code>	should the fit span the full range of the plot, or just the data. Used only when <code>add != "none"</code> .
<code>ellipse</code>	logical value. If TRUE, draws ellipses around points.
<code>ellipse.level</code>	the size of the concentration ellipse in normal probability.
<code>ellipse.type</code>	Character specifying frame type. Possible values are "convex", "confidence" or types supported by <code>stat_ellipse()</code> including one of <code>c("t", "norm", "euclid")</code> for plotting concentration ellipses. <ul style="list-style-type: none"> • "convex": plot convex hull of a set o points. • "confidence": plot confidence ellipses around group mean points as <code>coord_ellipse()</code> [in FactoMineR]. • "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 <code>coord_fixed()</code> is applied.
<code>ellipse.alpha</code>	Alpha for ellipse specifying the transparency level of fill color. Use <code>alpha = 0</code> for no fill color.
<code>ellipse.border.remove</code>	logical value. If TRUE, remove ellipse border lines.
<code>mean.point</code>	logical value. If TRUE, group mean points are added to the plot.
<code>mean.point.size</code>	numeric value specifying the size of mean points.
<code>star.plot</code>	logical value. If TRUE, a star plot is generated.
<code>star.plot.lty</code> , <code>star.plot.lwd</code>	line type and line width (size) for star plot, respectively.
<code>label</code>	the name of the column containing point labels. Can be also a character vector with <code>length = nrow(data)</code> .
<code>font.label</code>	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 <code>font.label = c(14, "bold", "red")</code> . To specify only the size and the style, use <code>font.label = c(14, "plain")</code> .
<code>font.family</code>	character vector specifying font family.
<code>label.select</code>	character vector specifying some labels to show.
<code>repel</code>	a logical value, whether to use <code>ggrepel</code> to avoid overplotting text labels or not.

<code>label.rectangle</code>	logical value. If TRUE, add rectangle underneath the text, making it easier to read.
<code>cor.coef</code>	logical value. If TRUE, correlation coefficient with the p-value will be added to the plot.
<code>cor.coeff.args</code>	a list of arguments to pass to the function <code>stat_cor</code> for customizing the displayed correlation coefficients. For example: <code>cor.coeff.args = list(method = "pearson", label.x</code>
<code>cor.method</code>	method for computing correlation coefficient. Allowed values are one of "pearson", "kendall", or "spearman".
<code>cor.coef.coord</code>	numeric vector, of length 2, specifying the x and y coordinates of the correlation coefficient. Default values are NULL.
<code>cor.coef.size</code>	correlation coefficient text font size.
<code>ggp</code>	a ggplot. If not NULL, points are added to an existing plot.
<code>show.legend.text</code>	logical. Should text be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
<code>...</code>	other arguments to be passed to <code>geom_point</code> and <code>ggpar</code> .

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)

```

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

```
ggstripchart(data, x, y, combine = FALSE, merge = FALSE, color = "black",
  fill = "white", palette = NULL, title = NULL, xlab = NULL,
  ylab = NULL, facet.by = NULL, panel.labs = NULL,
  short.panel.labs = TRUE, shape = 19, size = 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, jitter = 0.2,
  position = position_jitter(jitter), 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.: "npg", "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.
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")).

<code>short.panel.labs</code>	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.
<code>shape</code>	point shape
<code>size</code>	Numeric value (e.g.: <code>size = 1</code>). change the size of points and outlines.
<code>select</code>	character vector specifying which items to display.
<code>remove</code>	character vector specifying which items to remove from the plot.
<code>order</code>	character vector specifying the order of items.
<code>add</code>	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 <code>?desc_statby</code> for more details.
<code>add.params</code>	parameters (color, shape, size, fill, linetype) for the argument 'add'; e.g.: <code>add.params = list(color = "red")</code> .
<code>error.plot</code>	plot type used to visualize error. Allowed values are one of <code>c("pointrange", "linerrange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linerrange", "lower_linerrange")</code> . Default value is "pointrange" or "errorbar". Used only when <code>add != "none"</code> and <code>add</code> contains one "mean_*" or "med_*" where "*" = sd, se,
<code>label</code>	the name of the column containing point labels. Can be also a character vector with <code>length = nrow(data)</code> .
<code>font.label</code>	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 <code>font.label = list(size = 14, face = "bold", color = "red")</code> . To specify only the size and the style, use <code>font.label = list(size = 14, face = "plain")</code> .
<code>label.select</code>	can be of two formats: <ul style="list-style-type: none"> • a character vector specifying some labels to show. • a list containing one or the combination of the following components: <ul style="list-style-type: none"> – <code>top.up</code> and <code>top.down</code>: to display the labels of the top up/down points. For example, <code>label.select = list(top.up = 10, top.down = 4)</code>. – <code>criteria</code>: to filter, for example, by x and y variables values, use this: <code>label.select = list(criteria = "`y` > 2 & `y` < 5 & `x` %in% c('A', 'B')")</code>.
<code>repel</code>	a logical value, whether to use <code>ggrepel</code> to avoid overplotting text labels or not.
<code>label.rectangle</code>	logical value. If TRUE, add rectangle underneath the text, making it easier to read.
<code>jitter</code>	the amount of jitter.
<code>position</code>	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") )

```

ggtext

Text

Description

Add text to a plot.

Usage

```

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

```

Arguments

<code>data</code>	a data frame
<code>x, y</code>	x and y variables for drawing.
<code>label</code>	the name of the column containing point labels. Can be also a character vector with length = nrow(data).
<code>color</code>	text font color.
<code>palette</code>	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".
<code>size</code>	text font size.
<code>face</code>	text font style. Allowed values are one of c("plain", "bold", "italic", "bold.italic").
<code>family</code>	character vector specifying font family.
<code>label.select</code>	can be of two formats: <ul style="list-style-type: none"> • a character vector specifying some labels to show. • a list containing one or the combination of the following components: <ul style="list-style-type: none"> – <code>top.up</code> and <code>top.down</code>: to display the labels of the top up/down points. For example, <code>label.select = list(top.up = 10, top.down = 4)</code>. – <code>criteria</code>: to filter, for example, by x and y variables values, use this: <code>label.select = list(criteria = "`y` > 2 & `y` < 5 & `x` %in% c('A', 'B')")</code>.
<code>repel</code>	a logical value, whether to use <code>ggrepel</code> to avoid overplotting text labels or not.
<code>label.rectangle</code>	logical value. If TRUE, add rectangle underneath the text, making it easier to read.
<code>grouping.vars</code>	grouping variables to sort the data by, when the user wants to display the top n up/down labels.
<code>position</code>	Position adjustment, either as a string, or the result of a call to a position adjustment function.
<code>ggp</code>	a ggplot. If not NULL, points are added to an existing plot.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
<code>...</code>	other arguments to be passed to <code>ggpar</code> .

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.

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, ...)

```

Arguments

<code>x</code>	a <code>data.frame</code> or <code>matrix</code> .
<code>rows</code>	optional vector to specify row names
<code>cols</code>	optional vector to specify column names
<code>vp</code>	optional viewport
<code>theme</code>	a list, as returned by the function <code>ttheme()</code> , defining the parameters of the table theme. Allowed values include one of <code>ttheme()</code> and <code>ttheme_clean()</code> .
<code>...</code>	extra parameters for text justification, e.g.: <code>hjust</code> and <code>x</code> . Default is "centre" for the body and header, and "right" for the row names. Left justification: <code>hjust = 0</code> , <code>x = 0.1</code> . Right justification: <code>hjust = 1</code> , <code>x = 0.9</code> .
<code>base_style</code>	character string the table style/theme. The available themes are illustrated in the ggtexttable-theme.pdf file. Allowed values include one of <code>c("default", "blank", "classic", "minimal")</code> . Note that, <code>l = "light"</code> ; <code>m = "medium"</code> .
<code>base_size</code>	default font size
<code>base_colour</code>	default font colour
<code>padding</code>	length-2 unit vector specifying the horizontal and vertical padding of text within each cell
<code>colnames.style</code>	a list, as returned by the function <code>colnames_style()</code> , defining the style of the table column names. Considered only when <code>base_size = "default"</code> .
<code>rownames.style</code>	a list, as returned by the function <code>rownames_style()</code> , defining the style of the table row names. Considered only when <code>base_size = "default"</code> .
<code>tbody.style</code>	a list, as returned by the function <code>tbody_style()</code> , defining the style of the table body. Considered only when <code>base_size = "default"</code> .
<code>color, face, size</code>	text font color, face and size, respectively. Allowed values for face include <code>c("plain", "bold", "italic", "bold.italic")</code> .
<code>fill</code>	background color.
<code>linewidth, linecolor</code>	line width and color, respectively.
<code>parse</code>	logical, default behaviour for parsing text as <code>plotmath</code>

Value

an object of class `ggplot`.

Examples

```

# data
df <- head(iris)

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

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

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

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

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

# Customize the table as you want
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
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
  )
)

```

```

# Combine density plot and summary table
#::::::::::::::::::::::::::::::::::::::::::
# Density plot of "Sepal.Length"
density.p <- ggdensity(iris, x = "Sepal.Length",
                      fill = "Species", palette = "jco")

# Draw the summary table of Sepal.Length
# Descriptive statistics by groups
stable <- desc_statby(iris, measure.var = "Sepal.Length",
                    grps = "Species")
stable <- stable[, c("Species", "length", "mean", "sd")]
stable.p <- ggtexttable(stable, rows = NULL,
                      theme = ttheme("mOrange"))

# Arrange the plots on the same page
ggarrange(density.p, stable.p,
          ncol = 1, nrow = 2,
          heights = c(1, 0.5))

```

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

```

ggviolin(data, x, y, combine = FALSE, merge = FALSE, color = "black",
         fill = "white", palette = NULL, 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, 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.

<code>merge</code>	logical or character value. Default is FALSE. Used only when <code>y</code> is a vector containing multiple variables to plot. If TRUE, merge multiple <code>y</code> variables in the same plotting area. Allowed values include also "asis" (TRUE) and "flip". If <code>merge = "flip"</code> , then <code>y</code> variables are used as <code>x</code> tick labels and the <code>x</code> variable is used as grouping variable.
<code>color</code>	outline color.
<code>fill</code>	fill color.
<code>palette</code>	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. <code>c("blue", "red")</code> ; and scientific journal palettes from ggsci R package, e.g.: "npg", "aaas", "lancet", "jco", "ucscgb", "uchicago", "simpsons" and "rickandmorty".
<code>title</code>	plot main title.
<code>xlab</code>	character vector specifying <code>x</code> axis labels. Use <code>xlab = FALSE</code> to hide <code>xlab</code> .
<code>ylab</code>	character vector specifying <code>y</code> axis labels. Use <code>ylab = FALSE</code> to hide <code>ylab</code> .
<code>facet.by</code>	character vector, of length 1 or 2, specifying grouping variables for faceting the plot into multiple panels. Should be in the data.
<code>panel.labs</code>	a list of one or two character vectors to modify facet panel labels. For example, <code>panel.labs = list(sex = c("Male", "Female"))</code> specifies the labels for the "sex" variable. For two grouping variables, you can use for example <code>panel.labs = list(sex = c("Male", "Female"), rx = c("Obs", "Lev", "Lev2"))</code> .
<code>short.panel.labs</code>	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.
<code>linetype</code>	line types.
<code>trim</code>	If TRUE (default), trim the tails of the violins to the range of the data. If FALSE, don't trim the tails.
<code>size</code>	Numeric value (e.g.: <code>size = 1</code>). change the size of points and outlines.
<code>width</code>	violin width.
<code>draw_quantiles</code>	If not (NULL) (default), draw horizontal lines at the given quantiles of the density estimate.
<code>select</code>	character vector specifying which items to display.
<code>remove</code>	character vector specifying which items to remove from the plot.
<code>order</code>	character vector specifying the order of items.
<code>add</code>	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 <code>?desc_statby</code> for more details.
<code>add.params</code>	parameters (<code>color</code> , <code>shape</code> , <code>size</code> , <code>fill</code> , <code>linetype</code>) for the argument 'add'; e.g.: <code>add.params = list(color = "red")</code> .

<code>error.plot</code>	plot type used to visualize error. Allowed values are one of <code>c("pointrange", "lin- erange", "crossbar", "errorbar", "upper_errorbar", "lower_errorbar", "upper_pointrange", "lower_pointrange", "upper_linerange", "lower_linerange")</code> . Default value is "pointrange" or "errorbar". Used only when <code>add != "none"</code> and <code>add</code> contains one "mean_*" or "med_*" where "*" = sd, se,
<code>label</code>	the name of the column containing point labels. Can be also a character vector with <code>length = nrow(data)</code> .
<code>font.label</code>	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 <code>font.label = list(size = 14, face = "bold", color = "red")</code> . To specify only the size and the style, use <code>font.label = list(size = 14, face = "plain")</code> .
<code>label.select</code>	can be of two formats: <ul style="list-style-type: none"> • a character vector specifying some labels to show. • a list containing one or the combination of the following components: <ul style="list-style-type: none"> – <code>top.up</code> and <code>top.down</code>: to display the labels of the top up/down points. For example, <code>label.select = list(top.up = 10, top.down = 4)</code>. – <code>criteria</code>: to filter, for example, by x and y variabes values, use this: <code>label.select = list(criteria = "`y` > 2 & `y` < 5 & `x` %in% c('A', 'B')")</code>.
<code>repel</code>	a logical value, whether to use <code>ggrepel</code> to avoid overplotting text labels or not.
<code>label.rectangle</code>	logical value. If TRUE, add rectangle underneath the text, making it easier to read.
<code>ggtheme</code>	function, ggplot2 theme name. Default value is <code>theme_pubr()</code> . Allowed values include ggplot2 official themes: <code>theme_gray()</code> , <code>theme_bw()</code> , <code>theme_minimal()</code> , <code>theme_classic()</code> , <code>theme_void()</code> ,
...	other arguments to be passed to <code>geom_violin</code> , <code>ggpar</code> and <code>facet</code> .

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

gradient_color	<i>Set Gradient Color</i>
----------------	---------------------------

Description

Change gradient color.

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

Usage

```
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 "rickandmorty". Can be also a numeric vector; in this case a basic color palette is created using the function palette .
---------	--

See Also

[set_palette](#).

Examples

```
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 <code>c("xy", "x", "y")</code> .
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, longdash, twodash). Sess show_line_types .

Examples

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

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

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

rotate	<i>Rotate a ggplot Horizontally</i>
--------	-------------------------------------

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	<i>Rotate Axes Text</i>
------------------	-------------------------

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]).
vjust	vertical justification (in [0, 1]).
...	other arguments to pass to the function <code>element_text()</code> .

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
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: <ul style="list-style-type: none"> • "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
--------	--

- "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
- "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

# 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

```
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: <ul style="list-style-type: none"> • 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 "rickandmarty".
...	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 *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	<i>Point shapes available in R</i>
-------------------	------------------------------------

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_chull	<i>Plot convex hull of a set of points</i>
------------	--

Description

Plot convex hull of a set of points.

Usage

```
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 or aes_ . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to ggplot . A <code>data.frame</code> , 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 <code>data.frame</code> , and will be used as the layer data.
geom	The geometric object to use display the data
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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 <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.

See Also

[ggpar](#), [ggscatter](#)

Examples

```
# 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 blots, dot plots and stripcharts.

Usage

```
stat_compare_means(mapping = NULL, data = NULL, method = NULL,
  paired = FALSE, 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, geom = "text",
  position = "identity", na.rm = FALSE, show.legend = NA,
  inherit.aes = TRUE, ...)
```

Arguments

mapping	Set of aesthetic mappings created by aes or aes_ . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to ggplot . A <code>data.frame</code> , 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 <code>data.frame</code> , and will be used as the layer data.
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 .
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). <code>ref.group</code> can be also <code>".all."</code> . 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 <code>TRUE</code> , hide ns symbol when displaying significance levels.
label.sep	a character string to separate the terms. Default is <code>", "</code> , 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. <ul style="list-style-type: none"> • 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. <p>If too short they will be recycled.</p>
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.
geom	The geometric object to use display the data
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
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.
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[compare_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")+
# Add pairwise comparisons p-value
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 = ..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 = ", ..p.format..))
)

```

stat_conf_ellipse *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 or aes_ . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to ggplot . A <code>data.frame</code> , 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 <code>data.frame</code> , and will be used as the layer data.
geom	The geometric object to use display the data
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
na.rm	If <code>FALSE</code> , the default, missing values are removed with a warning. If <code>TRUE</code> , missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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 <code>TRUE</code> , 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 <code>color = "red"</code> or <code>size = 3</code> . They may also be parameters to the paired geom/stat.

See Also

[stat_conf_ellipse](#)

Examples

```
# 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")
```

stat_cor

Add Correlation Coefficients with P-values to a Scatter Plot

Description

Add correlation coefficients with p-values to a scatter plot.

Usage

```
stat_cor(mapping = NULL, data = NULL, method = "pearson",
  label.sep = ", ", label.x.npc = "left", label.y.npc = "top",
  label.x = NULL, label.y = NULL, geom = "text", position = "identity",
  na.rm = FALSE, show.legend = NA, inherit.aes = TRUE, ...)
```

Arguments

mapping	Set of aesthetic mappings created by aes or aes_ . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to ggplot . A <code>data.frame</code> , 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 <code>data.frame</code> , and will be used as the layer data.
method	a character string indicating which correlation coefficient (or covariance) is to be computed. One of "pearson" (default), "kendall", or "spearman".
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. <ul style="list-style-type: none"> • 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 <code>c('right', 'left', 'center', 'centre', 'middle')</code> for x-axis; ii) and one of <code>c('bottom', 'top', 'center', 'centre', 'middle')</code> 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.
geom	The geometric object to use display the data
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
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.
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. <code>borders</code> .
...	other arguments to pass to <code>geom_text</code> or <code>geom_label</code> .

See Also

[ggscatter](#)

Examples

```
# 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 regressin 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)

# 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_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 aes or aes_ . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to ggplot . A <code>data.frame</code> , 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 <code>data.frame</code> , and will be used as the layer data.
geom	The geometric object to use display the data
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
na.rm	If <code>FALSE</code> (the default), removes missing values with a warning. If <code>TRUE</code> silently removes missing values.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.
inherit.aes	If <code>FALSE</code> , 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_point .

See Also

[stat_conf_ellipse](#), [stat_chull](#) and [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", ellipse = TRUE)+
  stat_mean(aes(color = cyl, shape = cyl), size = 4)
```

stat_stars

*Add Stars to a Scatter Plot***Description**

Create a star plot by drawing segments from group centroid to each points.

Usage

```
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 or aes_ . If specified and <code>inherit.aes = TRUE</code> (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 <code>NULL</code> , the default, the data is inherited from the plot data as specified in the call to ggplot . A <code>data.frame</code> , 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 <code>data.frame</code> , and will be used as the layer data.
geom	The geometric object to use display the data
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
na.rm	If <code>FALSE</code> (the default), removes missing values with a warning. If <code>TRUE</code> silently removes missing values.
show.legend	logical. Should this layer be included in the legends? <code>NA</code> , the default, includes if any aesthetics are mapped. <code>FALSE</code> never includes, and <code>TRUE</code> always includes.

`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))
```

text_grob

Create a Text Graphical object

Description

Create easily a customized text grob (graphical object). Wrapper around [textGrob](#).

Usage

```
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 alignment and 1 means right 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 <code>textGrob</code> .

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)
```

 theme_pubr

Publication ready theme

Description

- **theme_pubr()**: Create a publication ready theme
- **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.

Usage

```
theme_pubr(base_size = 12, base_family = "", border = FALSE,
           margin = TRUE, legend = c("top", "bottom", "left", "right", "none"),
           x.text.angle = 0)

labs_pubr(base_size = 14, base_family = "")

theme_classic2(base_size = 12, base_family = "")

clean_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.

Examples

```
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

```
theme_transparent(base_size = 12, base_family = "")
```

Arguments

base_size	base font size
base_family	base font family

See Also

[theme_pubr](#)

Examples

```
# 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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