Package 'see'

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Type Package

Title Model Visualisation Toolbox for 'easystats' and 'ggplot2'

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Description Provides plotting utilities supporting packages in the 'easystats' ecosystem (<https://github.com/easystats/easystats>) and some extra themes, geoms, and scales for 'ggplot2'. Color scales are based on <https://materialui.co/>.
References: Lüdecke et al. (2021) <doi:10.21105/joss.03393>.

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URL https://easystats.github.io/see/

BugReports https://github.com/easystats/see/issues

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`add_plot_attributes` *Complete figure with its attributes*

Description

The `data_plot()` function usually stores information (such as title, axes labels, etc.) as attributes, while `add_plot_attributes()` adds this information to the plot.

Usage

```
add_plot_attributes(x)
```

Arguments

x	An object.

Examples

```
library(rstanarm)
library(bayestestR)
library(see)
library(ggplot2)

model <- suppressWarnings(stan_glm(
  Sepal.Length ~ Petal.Width + Species + Sepal.Width,
  data = iris,
  chains = 2, iter = 200, refresh = 0
))

result <- bayestestR::hdi(model, ci = c(0.5, 0.75, 0.9, 0.95))
data <- data_plot(result, data = model)

p <- ggplot(
  data,
  aes(x = x, y = y, height = height, group = y, fill = fill)
```

```
) +
  ggridges::geom_ridgeline_gradient()

p
p + add_plot_attributes(data)
```

`bluebrown_colors` *Extract blue-brown colors as hex codes*

Description

Can be used to get the hex code of specific colors from the blue-brown color palette. Use `bluebrown_colors()` to see all available colors.

Usage

```
bluebrown_colors(...)
```

Arguments

`...`	Character names of colors.

Value

A character vector with color-codes.

Examples

```
bluebrown_colors()

bluebrown_colors("blue", "brown")
```

`coord_radar` *Radar coordinate system*

Description

Add a radar coordinate system useful for radar charts.

Usage

```
coord_radar(theta = "x", start = 0, direction = 1, ...)
```

Arguments

theta	variable to map angle to (x or y)
start	Offset of starting point from 12 o'clock in radians. Offset is applied clockwise or anticlockwise depending on value of direction.
direction	1, clockwise; -1, anticlockwise
...	Other arguments to be passed to ggproto.

Examples

```
library(ggplot2)

# Create a radar/spider chart with ggplot:
data(iris)
data <- aggregate(iris[-5], list(Species = iris$Species), mean)
data <- datawizard::data_to_long(
  data,
  c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width")
)

ggplot(data, aes(x = name, y = value, color = Species, group = Species)) +
  geom_polygon(fill = NA, linewidth = 2) +
  coord_radar(start = -pi / 4)
```

---

data_plot *Prepare objects for plotting or plot objects*

Description

data_plot() extracts and transforms an object for plotting, while plot() visualizes results of functions from different packages in easystats-project. See the documentation for your object's class:

- bayestestR::bayesfactor_models()
- bayestestR::bayesfactor_parameters()
- bayestestR::equivalence_test()
- bayestestR::estimate_density()
- bayestestR::hdi()
- bayestestR::p_direction()
- bayestestR::p_significance()
- bayestestR::si()
- effectsize::effectsize()
- modelbased::estimate_contrasts()
- parameters::compare_parameters()

- parameters::describe_distribution()
- parameters::model_parameters()
- parameters::principal_components()
- parameters::n_clusters()
- parameters::n_factors()
- parameters::simulate_parameters()
- performance::check_collinearity()
- performance::check_heteroscedasticity()
- performance::check_homogeneity()
- performance::check_normality()
- performance::check_outliers()
- performance::compare_performance()
- performance::performance_roc()
- performance::check_predictions()

Usage

```
data_plot(x, ...)

## S3 method for class 'compare_performance'
data_plot(x, data = NULL, ...)
```

Arguments

x	An object.
...	Arguments passed to or from other methods.
data	The original data used to create this object. Can be a statistical model.

Details

`data_plot()` is in most situation not needed when the purpose is plotting, since most `plot()`-functions in **see** internally call `data_plot()` to prepare the data for plotting.

Many `plot()`-functions have a `data`-argument that is needed when the data or model for plotting can't be retrieved via `data_plot()`. In such cases, `plot()` gives an error and asks for providing data or models.

Most `plot()`-functions work out-of-the-box, i.e. you don't need to do much more than calling `plot(<object>)` (see 'Examples'). Some plot-functions allow to specify arguments to modify the transparency or color of geoms, these are shown in the 'Usage' section.

See Also

Package-Vignettes

Examples

```
library(bayestestR)
library(rstanarm)

model <<- suppressWarnings(stan_glm(
  Sepal.Length ~ Petal.Width * Species,
  data = iris,
  chains = 2, iter = 200, refresh = 0
))

x <- rope(model, verbose = FALSE)
plot(x)

x <- hdi(model)
plot(x) + theme_modern()

x <- p_direction(model, verbose = FALSE)
plot(x)

model <<- suppressWarnings(stan_glm(
  mpg ~ wt + gear + cyl + disp,
  chains = 2,
  iter = 200,
  refresh = 0,
  data = mtcars
))
x <- equivalence_test(model, verbose = FALSE)
plot(x)
```

---

flat_colors *Extract Flat UI colors as hex codes*

Description

Can be used to get the hex code of specific colors from the Flat UI color palette. Use `flat_colors()` to see all available colors.

Usage

```
flat_colors(...)
```

Arguments

...	Character names of colors.

Value

A character vector with color-codes.

Examples

```
flat_colors()

flat_colors("dark red", "teal")
```

`geom_binomdensity` *Add dot-densities for binary* `y` *variables*

Description

Add dot-densities for binary `y` variables

Usage

```
geom_binomdensity(data, x, y, scale = "auto", ...)
```

Arguments

`data`	A dataframe.
`x, y`	Characters corresponding to the `x` and `y` axis. Note that `y` must be a variable with two unique values.
`scale`	Character specifying method of scaling the dot-densities. Can be: `'auto'` (corresponding to the square root of the proportion), `'proportion'`, `'density'` or a custom list with values for each factor level (see examples).
`...`	Other arguments passed to `ggdist::geom_dots`.

Examples

```
library(ggplot2)
library(see)

data <- iris[1:100, ]

ggplot() +
  geom_binomdensity(data,
    x = "Sepal.Length",
    y = "Species",
    fill = "red",
    color = NA
  )

# Different scales
data[1:70, "Species"] <- "setosa" # Create unbalanced proportions

ggplot() +
  geom_binomdensity(data, x = "Sepal.Length", y = "Species", scale = "auto")
ggplot() +
  geom_binomdensity(data, x = "Sepal.Length", y = "Species", scale = "density")
```

```
ggplot() +
  geom_binomdensity(data, x = "Sepal.Length", y = "Species", scale = "proportion")
ggplot() +
  geom_binomdensity(
    data,
    x = "Sepal.Length", y = "Species",
    scale = list("setosa" = 0.4, "versicolor" = 0.6)
  )
```

`geom_from_list` *Create ggplot2 geom(s) from a list*

Description

These helper functions are built on top of `ggplot2::layer()` and can be used to add geom(s), whose type and content are specified as a list.

Usage

```
geom_from_list(x, ...)

geoms_from_list(x, ...)
```

Arguments

`x`	A list containing: • a geom type (e.g. `geom = "point"`), • a list of aesthetics (e.g. `aes = list(x = "mpg", y = "wt")`), • some data (e.g. `data = mtcars`), • and some other parameters. For `geoms_from_list()` ("geoms" with an "s"), the input must be a list of lists, ideally named `"l1"`, `"l2"`, `"l3"`, etc.
`...`	Additional arguments passed to `ggplot2::layer()`.

Examples

```
library(ggplot2)

# Example 1 (basic geoms and labels) --------------------------
l1 <- list(
  geom = "point",
  data = mtcars,
  aes = list(x = "mpg", y = "wt", size = "hp", color = "hp"),
  show.legend = c("size" = FALSE)
)
l2 <- list(
  geom = "labs",
```

```
  title = "A Title"
)

ggplot() +
  geom_from_list(l1) +
  geom_from_list(l2)

ggplot() +
  geoms_from_list(list(l1 = l1, l2 = l2))

# Example 2 (Violin, boxplots, ...) --------------------------
l1 <- list(
  geom = "violin",
  data = iris,
  aes = list(x = "Species", y = "Sepal.Width")
)
l2 <- list(
  geom = "boxplot",
  data = iris,
  aes = list(x = "Species", y = "Sepal.Width")
)
l3 <- list(
  geom = "jitter",
  data = iris,
  width = 0.1,
  aes = list(x = "Species", y = "Sepal.Width")
)

ggplot() +
  geom_from_list(l1) +
  geom_from_list(l2) +
  geom_from_list(l3)

# Example 3 (2D density) -------------------------
ggplot() +
  geom_from_list(list(
    geom = "density_2d", data = iris,
    aes = list(x = "Sepal.Width", y = "Petal.Length")
  ))
ggplot() +
  geom_from_list(list(
    geom = "density_2d_filled", data = iris,
    aes = list(x = "Sepal.Width", y = "Petal.Length")
  ))
ggplot() +
  geom_from_list(list(
    geom = "density_2d_polygon", data = iris,
    aes = list(x = "Sepal.Width", y = "Petal.Length")
  ))
ggplot() +
  geom_from_list(list(
    geom = "density_2d_raster", data = iris,
    aes = list(x = "Sepal.Width", y = "Petal.Length"),
```

```
    contour = FALSE
  ))

# Example 4 (facet and coord flip) --------------------------

ggplot(iris, aes(x = Sepal.Length, y = Petal.Width)) +
  geom_point() +
  geom_from_list(list(geom = "hline", yintercept = 2)) +
  geom_from_list(list(geom = "coord_flip")) +
  geom_from_list(list(geom = "facet_wrap", facets = "~ Species", scales = "free"))

# Example 5 (theme and scales) -------------------------
ggplot(iris, aes(x = Sepal.Length, y = Petal.Width, color = Species)) +
  geom_point() +
  geom_from_list(list(geom = "scale_color_viridis_d", option = "inferno")) +
  geom_from_list(list(geom = "theme", legend.position = "top"))

ggplot(iris, aes(x = Sepal.Length, y = Petal.Width, color = Species)) +
  geom_point() +
  geom_from_list(list(geom = "scale_color_material_d", palette = "rainbow")) +
  geom_from_list(list(geom = "theme_void"))

# Example 5 (Smooths and side densities) --------------------------

ggplot(iris, aes(x = Sepal.Length, y = Petal.Width)) +
  geom_from_list(list(geom = "point")) +
  geom_from_list(list(geom = "smooth", color = "red")) +
 geom_from_list(list(aes = list(x = "Sepal.Length"), geom = "ggside::geom_xsidedensity")) +
  geom_from_list(list(geom = "ggside::scale_xsidey_continuous", breaks = NULL))
```

`geom_point2` *Better looking points*

Description

The `*_borderless` geoms (and their shortcuts ending in `2`, such as `geom_point2` or `geom_point_borderless`) render points without an outline stroke by default. This prevents harsh edges and yields a smoother, cleaner look, especially when using transparency.

In contrast, the `*_halo` variants feature a border that automatically matches the plot's background color. This creates a subtle visual separation (a "halo" effect) that keeps overlapping points distinct.

Usage

```
geom_point2(..., stroke = 0, shape = 16)

geom_jitter2(..., size = 2, stroke = 0, shape = 16)

geom_pointrange2(..., stroke = 0)
```

```
geom_count2(..., stroke = 0)

geom_count_borderless(..., stroke = 0)

geom_point_borderless(..., stroke = 0, shape = 16)

geom_jitter_borderless(..., size = 2, stroke = 0, shape = 16)

geom_pointrange_borderless(..., stroke = 0)

geom_point_halo(...)

geom_jitter_halo(...)

geom_count_halo(...)

geom_pointrange_halo(...)
```

Arguments

`...`	Other arguments to be passed to `ggplot2::geom_point()`, `ggplot2::geom_jitter()`, `ggplot2::geom_pointrange()`, or `ggplot2::geom_count()`.
`stroke`	Stroke thickness.
`shape`	Shape of points.
`size`	Size of points.

Note

The color aesthetics for the `*_halo()` functions is `"fill"`, not `"color"`. See 'Examples'.

Examples

```
library(ggplot2)
library(see)

normal <- ggplot(iris, aes(x = Petal.Width, y = Sepal.Length)) +
  geom_point(size = 8, alpha = 0.3) +
  theme_modern()

new <- ggplot(iris, aes(x = Petal.Width, y = Sepal.Length)) +
  geom_point2(size = 8, alpha = 0.3) +
  theme_modern()

plots(normal, new, n_columns = 2)

ggplot(iris, aes(x = Petal.Width, y = Sepal.Length, color = Species)) +
  geom_point_borderless(size = 4) +
  theme_modern()
```

```
theme_set(theme_abyss())
ggplot(iris, aes(x = Petal.Width, y = Sepal.Length, color = Species)) +
  geom_point_borderless(size = 4)

# add "halo" effect - note that the aesthetics is "fill", not "color"
theme_set(theme_abyss())
ggplot(iris, aes(x = Petal.Width, y = Sepal.Length, fill = Species)) +
  geom_point_halo(size = 12)
```

`geom_poolpoint` *Pool ball points*

Description

Points labelled with the observation name.

Usage

```
geom_poolpoint(
  label,
  size_text = 3.88,
  size_background = size_text * 2,
  size_point = size_text * 3.5,
  ...
)

geom_pooljitter(
  label,
  size_text = 3.88,
  size_background = size_text * 2,
  size_point = size_text * 3.5,
  jitter = 0.1,
  ...
)
```

Arguments

`label`	Label to add inside the points.
`size_text`	Size of text.
`size_background`	Size of the white background circle.
`size_point`	Size of the ball.
`...`	Other arguments to be passed to `geom_point`.
`jitter`	Width and height of position jitter.

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Petal.Width, y = Sepal.Length, color = Species)) +
  geom_poolpoint(label = rownames(iris)) +
  scale_color_flat_d() +
  theme_modern()


ggplot(iris, aes(x = Petal.Width, y = Sepal.Length, color = Species)) +
  geom_pooljitter(label = rownames(iris)) +
  scale_color_flat_d() +
  theme_modern()
```

---

geom_violindot *Half-violin Half-dot plot*

Description

Create a half-violin half-dot plot, useful for visualising the distribution and the sample size at the same time. The half violins are drawn with `ggdist::stat_slab()` and the dots with `ggdist::geom_dots()`, so this function needs the **ggdist** package (version 3.3.3 or later). When groups are dodged, as with `fill` mapped to a second variable, each half violin takes the right half of its dodge cell (the upper half in a horizontal plot, see `geom_violinhalf()`), and, with the default `position_dots`, its dots go in the other half. The dots stay in that half when the half violin is flipped, so they overlap it.

Usage

```
geom_violindot(
  mapping = NULL,
  data = NULL,
  trim = TRUE,
  scale = c("area", "count", "width"),
  show.legend = NA,
  inherit.aes = TRUE,
  dots_size = 0.7,
  dots_color = NULL,
  dots_fill = NULL,
  binwidth = NA,
  position_dots = ggplot2::position_nudge(x = -0.025, y = 0),
  interval = FALSE,
  ...,
  size_dots = dots_size,
  color_dots = dots_color,
  fill_dots = dots_fill
)
```

Arguments

mapping	Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data	The data to be displayed in this layer. There are three options: If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot(). A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).
trim	If TRUE (default), trim the tails of the half violins to the range of the data. If FALSE, extend the tails as ggplot2::geom_violin() does.
scale	If "area" (default), all half violins have the same area (before trimming the tails). If "count", areas are scaled proportionally to the number of observations. If "width", all half violins have the same maximum width.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display. To include legend keys for all levels, even when no data exists, use TRUE. If NA, all levels are shown in legend, but unobserved levels are omitted.
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. annotation_borders().
binwidth	The bin width of the dots. The default, NA, lets ggdist::geom_dots() choose a bin width that fits the dots into the space beside each half violin. A number sets a fixed bin width, in the units of the value axis. Dodged groups leave the dots less room, so a fixed bin width can make them overflow it, with a warning from ggdist.
position_dots	Position adjustment for dots, either as a string, or the result of a call to a position adjustment function. The default nudges the dots by x = -0.025 (-0.06 with interval = TRUE). In a vertical plot, this moves them toward smaller x, away from the half violin, and in a dodged cell the nudge is at most half the room beside the half violin. In a horizontal plot, it moves them along the value axis. The default also dodges the dots with their half violins. A position that you set is used as given, so the dots are not dodged unless that position dodges them.
interval	Logical. If TRUE, add the median and the 66% and 95% quantile intervals of each group, drawn with ggdist::stat_slabinterval() without the slab, as in ggdist::stat_pointinterval(). Default is FALSE.
...	Other arguments passed to geom_violinhalf() and to ggdist::geom_dots(). The arguments of the density, the layout, and the interval (flip, stat, bw, kernel, bounds, drop, adjust, n, density, side, normalize, justification, fill_type, limits, p_limits, expand, breaks, outline_bars, slab_type,

.width, point_interval, show_point, show_interval, fatten_point, arrow, and the point_ and interval_ aesthetics) go to the half violins only. colour does not reach the dots when color_dots is set, and fill does not reach them when fill_dots is set. As for the half violins, a width (or height) is the width of a whole violin, so the dots take half of it. An argument named position matches position_dots. The dots of groups with fewer than two observations are still drawn.

size_dots, dots_size
: Size adjustment for dots, passed to the dotsize argument of ggdist::geom_dots().

color_dots, dots_color
: Color adjustment for dots.

fill_dots, dots_fill
: Fill adjustment for dots.

Value

A list of ggplot2 layers.

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_violindot() +
  theme_modern()

# The dots adapt to the scale of the data
ggplot(iris, aes(x = Species, y = Sepal.Length * 1000, fill = Species)) +
  geom_violindot(interval = TRUE) +
  theme_modern()
```

---

geom_violinhalf *Half-violin plot*

Description

Create a half-violin plot. The half violins are drawn with ggdist::stat_slab(), so this function needs the **ggdist** package (version 3.3.3 or later). By default, each half violin is at most 0.45 times the spacing of the categorical axis wide (0.45 units on a discrete axis), as before. When groups are dodged, as with fill mapped to a second variable, each group takes half of its dodge cell, from the cell's centre toward its side, as in see 0.14.

Usage

```
geom_violinhalf(
  mapping = NULL,
  data = NULL,
  stat = "ydensity",
  position = "dodge",
  trim = TRUE,
  flip = FALSE,
  scale = c("area", "count", "width"),
  show.legend = NA,
  inherit.aes = TRUE,
  interval = FALSE,
  ...
)
```

Arguments

mapping	Set of aesthetic mappings created by aes(). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data	The data to be displayed in this layer. There are three options: If NULL, the default, the data is inherited from the plot data as specified in the call to ggplot(). A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See fortify() for which variables will be created. A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).
stat	Kept for backward compatibility. The density is always computed by ggdist::stat_slab(), and any value other than "ydensity" or ggplot2::StatYdensity is ignored with a warning.
position	A position adjustment to use on the data for this layer. This can be used in various ways, including to prevent overplotting and improving the display. The position argument accepts the following: • The result of calling a position function, such as position_jitter(). This method allows for passing extra arguments to the position. • A string naming the position adjustment. To give the position as a string, strip the function name of the position_ prefix. For example, to use position_jitter(), give the position as "jitter". • For more information and other ways to specify the position, see the layer position documentation.
trim	If TRUE (default), trim the tails of the half violins to the range of the data. If FALSE, extend the tails as ggplot2::geom_violin() does.
flip	Should the half-violin plot switch directions? By default, this is FALSE and each half violin extends to the right of its position (up, in a horizontal plot), with its

flat side on the left. If `flip = TRUE`, all half violins extend to the left (down). Optionally, a numeric vector can be supplied indicating which specific geoms should be flipped. See examples for more details.

`scale` If `"area"` (default), all half violins have the same area (before trimming the tails). If `"count"`, areas are scaled proportionally to the number of observations. If `"width"`, all half violins have the same maximum width.

`show.legend` logical. Should this layer be included in the legends? `NA`, the default, includes if any aesthetics are mapped. `FALSE` never includes, and `TRUE` always includes. It can also be a named logical vector to finely select the aesthetics to display. To include legend keys for all levels, even when no data exists, use `TRUE`. If `NA`, all levels are shown in legend, but unobserved levels are omitted.

`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. `annotation_borders()`.

`interval` Logical. If `TRUE`, add the median and the 66% and 95% quantile intervals of each group, drawn with `ggdist::stat_slabinterval()` without the slab, as in `ggdist::stat_pointinterval()`. Default is `FALSE`.

`...` Other arguments passed to `ggdist::stat_slab()`, such as `colour`, `fill`, `alpha`, or `adjust`. As in `ggplot2::geom_violin()`:

- `bw` sets the bandwidth of the density (default `"nrd0"`): a number, or one of `"nrd0"`, `"nrd"`, `"ucv"`, `"bcv"`, `"SJ"`, or `"dpi"`.
- `kernel` sets the kernel (default `"gaussian"`).
- `bounds` sets known bounds of the data, which must contain all values.
- `width` (or `height`, in a horizontal plot) is the width of a whole violin, so each half violin is half as wide.

`drop` has no effect. The half violins of groups with fewer than two observations, or with all values equal, are not drawn, with a warning, but they keep their space when dodged, and their intervals are drawn. `.width`, `point_interval`, `show_point`, `show_interval`, `fatten_point`, `arrow`, and the `point_` and `interval_` aesthetics, such as `point_size`, go to the interval.

Value

A ggplot2 layer, or a list of two layers if `interval = TRUE`.

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_violinhalf() +
  theme_modern() +
  scale_fill_material_d()

# To flip all half-violin geoms, use `flip = TRUE`:
ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
```

```
  geom_violinhalf(flip = TRUE) +
  theme_modern() +
  scale_fill_material_d()

# To flip the half-violin geoms for the first and third groups only
# by passing a numeric vector
ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_violinhalf(flip = c(1, 3)) +
  theme_modern() +
  scale_fill_material_d()

# To add the median and quantile intervals
ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_violinhalf(interval = TRUE) +
  theme_modern() +
  scale_fill_material_d()
```

`golden_ratio` *Golden Ratio*

Description

Returns the golden ratio (1.618034...). Useful to easily obtain golden proportions, for instance for a horizontal figure, if you want its height to be 8, you can set its width to be `golden_ratio(8)`.

Usage

```
golden_ratio(x = 1)
```

Arguments

`x`	A number to be multiplied by the golden ratio. The default (`x = 1`) returns the value of the golden ratio.

Examples

```
golden_ratio()
golden_ratio(10)
```

material_colors *Extract material design colors as hex codes*

Description

Can be used to get the hex code of specific colors from the material design color palette. Use `material_colors()` to see all available colors.

Usage

```
material_colors(...)
```

Arguments

`...`	Character names of colors.

Value

A character vector with color-codes.

Examples

```
material_colors()

material_colors("indigo", "lime")
```

metro_colors *Extract Metro colors as hex codes*

Description

Can be used to get the hex code of specific colors from the Metro color palette. Use `metro_colors()` to see all available colors.

Usage

```
metro_colors(...)
```

Arguments

`...`	Character names of colors.

Value

A character vector with color-codes.

Examples

```
metro_colors()

metro_colors("dark red", "teal")
```

`okabeito_colors` *Extract Okabe-Ito colors as hex codes*

Description

Can be used to get the hex code of specific colors from the Okabe-Ito palette. Use `okabeito_colors()` to see all available colors.

Usage

```
okabeito_colors(..., original_names = FALSE, black_first = FALSE, amber = TRUE)

oi_colors(..., original_names = FALSE, black_first = FALSE, amber = TRUE)
```

Arguments

`...`	Character names of colors.
`original_names`	Logical. Should the colors be named using the original names used by Okabe and Ito (2008), such as "vermillion" (`TRUE`), or simplified names, such as "red" (`FALSE`, default)? Only used if no colors are specified (to see all available colors).
`black_first`	Logical. Should black be first (`TRUE`) or last (`FALSE`, default) in the color palette? Only used if no colors are specified (to see all available colors).
`amber`	If amber color should replace yellow in the palette.

Value

A character vector with color-codes.

Examples

```
okabeito_colors()

okabeito_colors(c("red", "light blue", "orange"))

okabeito_colors(original_names = TRUE)

okabeito_colors(black_first = TRUE)
```

palette_bluebrown *Blue-brown design color palette*

Description

The palette based on blue-brown colors.

Usage

```
palette_bluebrown(palette = "contrast", reverse = FALSE, ...)
```

Arguments

palette	Character name of palette. Depending on the color scale, can be one of "full", "ice", "rainbow", "complement", "contrast", "light" (for dark themes), "black_first", full_original, or black_first_original. The latter three options are especially for the Okabe-Ito color palette. The default is NULL and either "contrast" or "gradient" is used (depending on whether discrete is TRUE or FALSE), which are the two scale useful for discrete or gradient color scales, respectively.
reverse	Boolean indicating whether the palette should be reversed.
...	Additional arguments to pass to colorRampPalette().

Details

This function is usually not called directly, but from within scale_color_bluebrown().

palette_colorhex *Color palettes from color-hex.com.*

Description

This function downloads a requested color palette from color-hex.com. This website provides a large number of user-submitted color palettes.

Usage

```
palette_colorhex(palette = 1014416, reverse = FALSE, ...)
```

Arguments

palette	The numeric code for a palette at color-hex.com. For example, 1014416 for the Josiah color palette (number 1014416).
reverse	Boolean indicating whether the palette should be reversed.
...	Additional arguments to pass to colorRampPalette().

Details

This function is usually not called directly, but from within `scale_color_colorhex()`.

Note

The default Josiah color palette (number 1014416) is available without an internet connection. All other color palettes require an internet connection to download and access.

---

palette_flat *Flat UI color palette*

Description

The palette based on Flat UI.

Usage

```
palette_flat(palette = "contrast", reverse = FALSE, ...)
```

Arguments

`palette`	Character name of palette. Depending on the color scale, can be one of `"full"`, `"ice"`, `"rainbow"`, `"complement"`, `"contrast"`, `"light"` (for dark themes), `"black_first"`, `full_original`, or `black_first_original`. The latter three options are especially for the Okabe-Ito color palette. The default is `NULL` and either `"contrast"` or `"gradient"` is used (depending on whether `discrete` is `TRUE` or `FALSE`), which are the two scale useful for discrete or gradient color scales, respectively.
`reverse`	Boolean indicating whether the palette should be reversed.
`...`	Additional arguments to pass to `colorRampPalette()`.

Details

This function is usually not called directly, but from within `scale_color_flat()`.

palette_material *Material design color palette*

Description

The palette based on material design colors.

Usage

```
palette_material(palette = "contrast", reverse = FALSE, ...)
```

Arguments

palette	Character name of palette. Depending on the color scale, can be one of "full", "ice", "rainbow", "complement", "contrast", "light" (for dark themes), "black_first", full_original, or black_first_original. The latter three options are especially for the Okabe-Ito color palette. The default is NULL and either "contrast" or "gradient" is used (depending on whether discrete is TRUE or FALSE), which are the two scale useful for discrete or gradient color scales, respectively.
reverse	Boolean indicating whether the palette should be reversed.
...	Additional arguments to pass to colorRampPalette().

Details

This function is usually not called directly, but from within scale_color_material().

palette_metro *Metro color palette*

Description

The palette based on Metro colors.

Usage

```
palette_metro(palette = "complement", reverse = FALSE, ...)
```

Arguments

palette	Character name of palette. Depending on the color scale, can be one of "full", "ice", "rainbow", "complement", "contrast", "light" (for dark themes), "black_first", full_original, or black_first_original. The latter three options are especially for the Okabe-Ito color palette. The default is NULL and either "contrast" or "gradient" is used (depending on whether discrete is TRUE or FALSE), which are the two scale useful for discrete or gradient color scales, respectively.
reverse	Boolean indicating whether the palette should be reversed.
...	Additional arguments to pass to colorRampPalette().

Details

This function is usually not called directly, but from within scale_color_metro().

---

palette_okabeito *Okabe-Ito color palette*

Description

The palette based proposed by Okabe and Ito (2008).

Usage

```
palette_okabeito(palette = "full_amber", reverse = FALSE, order = 1:9, ...)

palette_oi(palette = "full_amber", reverse = FALSE, order = 1:9, ...)
```

Arguments

palette	Character name of palette. Depending on the color scale, can be one of "full", "ice", "rainbow", "complement", "contrast", "light" (for dark themes), "black_first", full_original, or black_first_original. The latter three options are especially for the Okabe-Ito color palette. The default is NULL and either "contrast" or "gradient" is used (depending on whether discrete is TRUE or FALSE), which are the two scale useful for discrete or gradient color scales, respectively.
reverse	Boolean indicating whether the palette should be reversed.
order	A vector of numbers from 1 to 9 indicating the order of colors to use (default: 1:9)
...	Additional arguments to pass to colorRampPalette().

Details

This function is usually not called directly, but from within scale_color_material().

References

Okabe, M., & Ito, K. (2008). Color universal design (CUD): How to make figures and presentations that are friendly to colorblind people. https://jfly.uni-koeln.de/color/#pallet (Original work published 2002)

`palette_pizza` *Pizza color palette*

Description

The palette based on authentic neapolitan pizzas.

Usage

```
palette_pizza(palette = "margherita", reverse = FALSE, ...)
```

Arguments

`palette`	Pizza type. Can be `"margherita"` (default), `"margherita crust"`, `"diavola"` or `"diavola crust"`.
`reverse`	Boolean indicating whether the palette should be reversed.
`...`	Additional arguments to pass to `colorRampPalette()`.

Details

This function is usually not called directly, but from within `scale_color_pizza()`.

`palette_see` *See design color palette*

Description

See design color palette

Usage

```
palette_see(palette = "contrast", reverse = FALSE, ...)
```

Arguments

palette	Character name of palette. Depending on the color scale, can be one of "full", "ice", "rainbow", "complement", "contrast", "light" (for dark themes), "black_first", full_original, or black_first_original. The latter three options are especially for the Okabe-Ito color palette. The default is NULL and either "contrast" or "gradient" is used (depending on whether discrete is TRUE or FALSE), which are the two scale useful for discrete or gradient color scales, respectively.
reverse	Boolean indicating whether the palette should be reversed.
...	Additional arguments to pass to colorRampPalette().

Details

This function is usually not called directly, but from within scale_color_see().

---

palette_social *Social color palette*

Description

The palette based Social colors.

Usage

```
palette_social(palette = "complement", reverse = FALSE, ...)
```

Arguments

palette	Character name of palette. Depending on the color scale, can be one of "full", "ice", "rainbow", "complement", "contrast", "light" (for dark themes), "black_first", full_original, or black_first_original. The latter three options are especially for the Okabe-Ito color palette. The default is NULL and either "contrast" or "gradient" is used (depending on whether discrete is TRUE or FALSE), which are the two scale useful for discrete or gradient color scales, respectively.
reverse	Boolean indicating whether the palette should be reversed.
...	Additional arguments to pass to colorRampPalette().

Details

This function is usually not called directly, but from within scale_color_social().

pizza_colors *Extract pizza colors as hex codes*

Description

Extract pizza colors as hex codes

Usage

```
pizza_colors(...)
```

Arguments

...	Character names of pizza ingredients.

Value

A character vector with color-codes.

plot.datawizard_tables *Plot tabulated data.*

Description

Plot tabulated data.

Usage

```
## S3 method for class 'datawizard_tables'
plot(
  x,
  label_values = TRUE,
  show_na = "if_any",
  na_label = "(Missing)",
  error_bar = TRUE,
  ci = 0.95,
  color_fill = "#87CEFA",
  color_error_bar = "#607B8B",
  ...
)

## S3 method for class 'datawizard_table'
plot(
  x,
  label_values = TRUE,
```

```
  show_na = "if_any",
  na_label = "(Missing)",
  error_bar = TRUE,
  ci = 0.95,
  color_fill = "#87CEFA",
  color_error_bar = "#607B8B",
  ...
)
```

Arguments

x	Object created by datawizard::data_tabulate().
label_values	Logical. Should values and percentages be displayed at the top of each bar.
show_na	Should missing values be dropped? Can be "if_any" (default) to show the missing category only if any missing values are present, "always" to always show the missing category, or "never" to never show the missing category.
na_label	The label given to missing values when they are shown.
error_bar	Logical. Should error bars be displayed? If TRUE, confidence intervals computed using the Wilson method are shown. See Brown et al. (2001) for details.
ci	Confidence Interval (CI) level. Defaults to 0.95 (95%).
color_fill	Color to use for category columns (default: "#87CEFA").
color_error_bar	Color to use for error bars (default: "#607B8B").
...	Unused

References

Brown, L. D., Cai, T. T., & Dasgupta, A. (2001). Interval estimation for a binomial proportion. *Statistical Science*, *16*(2), 101-133. doi:10.1214/ss/1009213286

---

plot.see_bayesfactor_models

Plot method for Bayes Factors for model comparison

Description

The plot() method for the bayestestR::bayesfactor_models() function. These plots visualize the **posterior probabilities** of the compared models.

Usage

```
## S3 method for class 'see_bayesfactor_models'
plot(
  x,
  n_pies = "one",
  value = "none",
  sort = FALSE,
  log = FALSE,
  prior_odds = NULL,
  ...
)
```

Arguments

x	An object.
n_pies	Number of pies. Can be "one" or "many".
value	What value to display. Can be "none", "BF", or "probability".
sort	The behavior of this argument depends on the plotting contexts. • *Plotting model parameters*: If NULL, coefficients are plotted in the order as they appear in the summary. Setting sort = "ascending" or sort = "descending" sorts coefficients in ascending or descending order, respectively. Setting sort = TRUE is the same as sort = "ascending". • *Plotting Bayes factors*: Sort pie-slices by posterior probability (descending)?
log	Logical that decides whether to display log-transformed Bayes factors.
prior_odds	An optional vector of prior odds for the models. See BayesFactor::priorOdds. As the size of the pizza slices corresponds to posterior probability (which is a function of prior probability and the Bayes Factor), custom prior_odds will change the slices' size.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(bayestestR)
library(see)

lm0 <- lm(qsec ~ 1, data = mtcars)
lm1 <- lm(qsec ~ drat, data = mtcars)
lm2 <- lm(qsec ~ wt, data = mtcars)
lm3 <- lm(qsec ~ drat + wt, data = mtcars)

result <- bayesfactor_models(lm1, lm2, lm3, denominator = lm0)
```

```
plot(result, n_pies = "one", value = "probability", sort = TRUE) +
  scale_fill_pizza(reverse = TRUE)

plot(result, n_pies = "many", value = "BF", log = TRUE) +
  scale_fill_pizza(reverse = FALSE)
```

`plot.see_bayesfactor_parameters` *Plot method for Bayes Factors for a single parameter*

Description

The `plot()` method for the `bayestestR::bayesfactor_parameters()` function.

Usage

```
## S3 method for class 'see_bayesfactor_parameters'
plot(
  x,
  size_point = 2,
  color_rope = "#0171D3",
  alpha_rope = 0.2,
  show_intercept = FALSE,
  ...
)
```

Arguments

`x`	An object.
`size_point`	Numeric specifying size of point-geoms.
`color_rope`	Character specifying color of ROPE ribbon.
`alpha_rope`	Numeric specifying transparency level of ROPE ribbon.
`show_intercept`	Logical, if `TRUE`, the intercept-parameter is included in the plot. By default, it is hidden because in many cases the intercept-parameter has a posterior distribution on a very different location, so density curves of posterior distributions for other parameters are hardly visible.
`...`	Arguments passed to or from other methods.

Value

A ggplot2-object.

plot.see_check_collinearity *Plot method for multicollinearity checks*

Description

The `plot()` method for the `performance::check_collinearity()` function.

Usage

```
## S3 method for class 'see_check_collinearity'
plot(
  x,
  data = NULL,
  theme = NULL,
  colors = c("#3aaf85", "#1b6ca8", "#cd201f"),
  size_point = 3.5,
  size_line = 0.8,
  size_title = 12,
  size_axis_title = base_size,
  base_size = 10,
  ...
)
```

Arguments

`x`	An object.
`data`	The original data used to create this object. Can be a statistical model.
`theme`	A ggplot2-theme function, e.g. `theme = theme_lucid()` or `theme = ggplot2::theme_dark()`.
`colors`	Character vector of length two, indicating the colors (in hex-format) for points and line.
`size_point`	Numeric specifying size of point-geoms.
`size_line`	Numeric value specifying size of line geoms. `linewidth` is an alias for `size_line`.
`base_size, size_axis_title, size_title`	Numeric value specifying size of axis and plot titles.
`...`	Arguments passed to or from other methods.

Details

If a term with a VIF below 2 has an upper confidence limit that is infinite or above the top of the plot, the plot has a caption. The caption says that the interval formula fails near VIF = 1, and that this is not high collinearity.

Value

A ggplot2-object.

Examples

```
library(performance)
m <- lm(mpg ~ wt + cyl + gear + disp, data = mtcars)
result <- check_collinearity(m)
result
plot(result)
```

`plot.see_check_dag` *Plot method for check DAGs*

Description

The `plot()` method for the `performance::check_dag()` function.

Usage

```
## S3 method for class 'see_check_dag'
plot(
  x,
  size_point = 20,
  size_text = 4.5,
  size_arrow = 5,
  colors = NULL,
  which = "all",
  effect = "total",
  check_colliders = TRUE,
  ...
)
```

Arguments

`x`	A `check_dag` object.
`size_point`	Numeric value specifying size of point geoms.
`size_text`	Numeric value specifying size of text elements.
`size_arrow`	Numeric value specifying size of the arrows.
`colors`	Character vector of length five, indicating the colors (in hex-format) for different types of variables, which are assigned in following order: `outcome`, `exposure`, `adjusted`, `unadjusted`, and `collider`.
`which`	Character string indicating which plot to show. Can be either `"all"`, `"current"` or `"required"`.
`effect`	Character string indicating which effect for the required model is to be estimated. Can be either `"total"` or `"direct"`.
`check_colliders`	Logical indicating whether to highlight colliders. Set to `FALSE` if the algorithm to detect colliders is very slow.
`...`	Currently not used.

Value

A ggplot2-object.

Examples

```
library(performance)
# incorrect adjustment
dag <- check_dag(
  y ~ x + b + c,
  x ~ b,
  outcome = "y",
  exposure = "x"
)
dag
plot(dag)

# plot only model with required adjustments
plot(dag, which = "required")

# collider-bias?
dag <- check_dag(
  y ~ x + c + d,
  x ~ c + d,
  b ~ x,
  b ~ y,
  outcome = "y",
  exposure = "x",
  adjusted = "c"
)
plot(dag)

# longer labels, automatic detection of outcome and exposure
dag <- check_dag(
  QoL ~ age + education + gender,
  age ~ education
)
plot(dag)
```

---

plot.see_check_distribution

Plot method for classifying the distribution of a model-family

---

Description

The `plot()` method for the `performance::check_distribution()` function.

Usage

```
## S3 method for class 'see_check_distribution'
plot(x, size_point = 2, panel = TRUE, ...)
```

Arguments

x	An object.
size_point	Numeric specifying size of point-geoms.
panel	Logical, if TRUE, plots are arranged as panels; else, single plots are returned.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(performance)
m <<- lm(mpg ~ wt + cyl + gear + disp, data = mtcars)
result <- check_distribution(m)
result
plot(result)
```

---

plot.see_check_heteroscedasticity

Plot method for (non-)constant error variance checks

Description

The plot() method for the performance::check_heteroscedasticity() function.

Usage

```
## S3 method for class 'see_check_heteroscedasticity'
plot(
  x,
  data = NULL,
  size_point = 2,
  size_line = 0.8,
  size_title = 12,
  size_axis_title = base_size,
  base_size = 10,
  theme = NULL,
  show_smooth = TRUE,
  ...
)
```

Arguments

x	An object.
data	The original data used to create this object. Can be a statistical model.
size_point	Numeric specifying size of point-geoms.
size_line	Numeric value specifying size of line geoms. linewidth is an alias for size_line.
base_size, size_axis_title, size_title	Numeric value specifying size of axis and plot titles.
theme	A ggplot2-theme function, e.g. theme = theme_lucid() or theme = ggplot2::theme_dark().
show_smooth	Logical, if FALSE, no trend line is drawn. This turns off the LOESS smoother and, for models whose fitted values take only a few distinct values, the cell means with their line and error bars. Default is TRUE.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

See Also

See also the vignette about check_model().

Examples

```
m <- lm(mpg ~ wt + cyl + gear + disp, data = mtcars)
result <- performance::check_heteroscedasticity(m)
result
plot(result, data = m) # data required for pkgdown
```

---

plot.see_check_homogeneity

Plot method for homogeneity of variances checks

Description

The plot() method for the performance::check_homogeneity() function.

Usage

```
## S3 method for class 'see_check_homogeneity'
plot(x, data = NULL, ...)
```

Arguments

x	An object.
data	The original data used to create this object. Can be a statistical model.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(performance)

model <<- lm(len ~ supp + dose, data = ToothGrowth)
result <- check_homogeneity(model)
result
plot(result)
```

`plot.see_check_model` *Plot method for checking model assumptions*

Description

The `plot()` method for the `performance::check_model()` function. Diagnostic plots for regression models.

Usage

```
## S3 method for class 'see_check_model'
plot(
  x,
  theme = NULL,
  colors = NULL,
  type = c("density", "discrete_dots", "discrete_interval", "discrete_both"),
  n_columns = 2,
  show_smooth = NULL,
  ...
)
```

Arguments

`x`	An object.
`theme`	A ggplot2-theme function, e.g. `theme = theme_lucid()` or `theme = ggplot2::theme_dark()`.
`colors`	Character vector of length two, indicating the colors (in hex-format) for points and line.
`type`	Plot type for the posterior predictive checks plot. Can be `"density"` (default), `"discrete_dots"`, `"discrete_interval"` or `"discrete_both"` (the `discrete_*` options are appropriate for models with discrete - binary, integer or ordinal etc. - outcomes).
`n_columns`	Number of columns to align plots.

show_smooth — Logical, if FALSE, no trend line is drawn in the Linearity, Homogeneity of Variance and Influential Observations panels. This turns off the LOESS smoother and, for models whose fitted values take only a few distinct values, the cell means with their line and error bars. If NULL (default), the value stored in the check_model() object is used, and TRUE if there is none. The binned residuals panel is not affected.

... — Arguments passed to or from other methods.

Details

Larger models (with many observations) may take a longer time to render. Thus, the number of data points is limited to 2000 by default. Use plot(check_model(), maximum_dots = <number>) (or check_model(maximum_dots = <number>)) to define the number of data points that should be shown in the plots.

Value

A ggplot2-object.

See Also

See also the vignette about check_model().

Examples

```
library(performance)

model <- lm(qsec ~ drat + wt, data = mtcars)
plot(check_model(model))
```

---

plot.see_check_normality

Plot method for check model for (non-)normality of residuals

Description

The plot() method for the performance::check_normality() function.

Usage

```
## S3 method for class 'see_check_normality'
plot(
  x,
  type = "qq",
  data = NULL,
  size_line = 0.8,
  size_point = 2,
```

```
  size_title = 12,
  size_axis_title = base_size,
  base_size = 10,
  alpha = 0.2,
  alpha_dot = 0.8,
  theme = NULL,
  colors = c("#3aaf85", "#1b6ca8"),
  detrend = TRUE,
  method = "ell",
  ...
)
```

Arguments

x	An object.
type	Character vector, indicating the type of plot. Options are "qq" (default) for quantile-quantile (Q-Q) plots, "pp" for probability-probability (P-P) plots, or "density" for density overlay plots.
data	The original data used to create this object. Can be a statistical model.
size_line	Numeric value specifying size of line geoms. linewidth is an alias for size_line.
size_point	Numeric specifying size of point-geoms.
base_size, size_axis_title, size_title	Numeric value specifying size of axis and plot titles.
alpha	Numeric value specifying alpha level of the confidence bands.
alpha_dot	Numeric value specifying alpha level of the point geoms.
theme	A ggplot2-theme function, e.g. theme = theme_lucid() or theme = ggplot2::theme_dark().
colors	Character vector of length two, indicating the colors (in hex-format) for points and line.
detrend	Logical that decides if Q-Q and P-P plots should be de-trended (also known as *worm plots*).
method	The method used for estimating the qq/pp bands. Default to "ell" (equal local levels / simultaneous testing - recommended). Can also be one of "pointwise" or "boot" for pointwise confidence bands, or "ks" or "ts" for simultaneous testing. See qqplotr::stat_qq_band() for details.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

See Also

See also the vignette about check_model().

Examples

```
library(performance)

m <<- lm(mpg ~ wt + cyl + gear + disp, data = mtcars)
result <- check_normality(m)
plot(result)


plot(result, type = "qq", detrend = TRUE)
```

`plot.see_check_outliers` *Plot method for checking outliers*

Description

The `plot()` method for the `performance::check_outliers()` function.

Usage

```
## S3 method for class 'see_check_outliers'
plot(
  x,
  size_text = 3.5,
  size_line = 0.8,
  size_title = 12,
  size_axis_title = base_size,
  base_size = 10,
  alpha_dot = 0.8,
  theme = NULL,
  colors = c("#3aaf85", "#1b6ca8", "#cd201f"),
  rescale_distance = FALSE,
  type = "dots",
  elbow_threshold = NULL,
  show_labels = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

`x`	An object.
`size_text`	Numeric value specifying size of text labels.
`size_line`	Numeric value specifying size of line geoms. `linewidth` is an alias for `size_line`.
`base_size, size_axis_title, size_title`	Numeric value specifying size of axis and plot titles.

alpha_dot — Numeric value specifying alpha level of the point geoms.

theme — A ggplot2-theme function, e.g. theme = theme_lucid() or theme = ggplot2::theme_dark().

colors — Character vector of length two, indicating the colors (in hex-format) for points and line.

rescale_distance — Logical. If TRUE, distance values are rescaled to a range from 0 to 1. This is mainly due to better catch the differences between distance values.

type — Character vector, indicating the type of plot. Options are:

- "dots" (default) for a scatterplot of leverage (hat) values versus residuals, with Cook's Distance contours for evaluating influential points.
- "scree" for a scree-style plot highlighting "elbow outliers" (based on sudden increases in distance; see details).
- "bars" for a bar chart of (rescaled) outlier statistic values for each data point.
- "count" for a "histogram"-style plot of outlier, where bins represent the outliers' distance values.

type = "dots" is only used for outlier plots of fitted models; for outlier plots of raw data values, type should be one of the other options.

elbow_threshold — Optional scalar specifying the minimum jump in distance (between adjacent sorted observations) used to detect the elbow point. If supplied, all observations following the first jump greater than this value are flagged as outliers. If NULL (default), the largest jump is used automatically. Higher values yield more conservative outlier detection.

show_labels — Logical. If TRUE, text labels are displayed.

verbose — Logical. If TRUE (default), prints a summary list of outliers.

... — Arguments passed to or from other methods.

Details

When using type = "scree", the function will provide a scree-style distance plot that highlights two types of outliers. Observations exceeding the specified threshold are shown in warm colors, while observations following the largest jump ("elbow", or the specified cut-off value) in the sorted distances are shown in cool colors. Elbow outliers are defined based on sudden increases in distance, analogous to inflection points in scree plots.

Value

A ggplot2-object.

References

The scree plot implementation was inspired by a visualization approach developed by Prof. Marina Doucerain (Université du Québec à Montréal).

Examples

```
library(performance)
data(mtcars)
mt1 <- mtcars[, c(1, 3, 4)]
mt1$ID <- row.names(mt1)
mt2 <- rbind(
  mt1,
  data.frame(
    mpg = c(37, 48), disp = c(300, 400), hp = c(110, 120),
    ID = c("JZ", "GP")
  )
)
model <- lm(disp ~ mpg + hp, data = mt2)
plot(check_outliers(model))
plot(check_outliers(mt2$mpg, method = "zscore"), type = "bars")

plot(check_outliers(mt2[-3], method = "mahalanobis", ID = "ID"))
```

---

plot.see_check_priors *Plot method for prior predictive checks*

Description

The `plot()` method for the `performance::check_priors()` function. For details, see *Lüdecke et al. 2026*.

Usage

```
## S3 method for class 'see_check_priors'
plot(
  x,
  size_point = 2,
  size_boxplot = 0.4,
  size_title = 12,
  size_axis_title = base_size,
  base_size = 10,
  alpha_dot = 0.15,
  alpha_boxplot = 0.35,
  theme = NULL,
  ...
)
```

Arguments

`x`	An object.
`size_point`	Numeric specifying size of point-geoms.

size_boxplot	Numeric value specifying size of boxplot geoms.
base_size, size_axis_title, size_title	Numeric value specifying size of axis and plot titles.
alpha_dot	Numeric value specifying alpha level of the point geoms.
alpha_boxplot	Numeric value specifying alpha of boxplot geoms.
theme	A ggplot2-theme function, e.g. theme = theme_lucid() or theme = ggplot2::theme_dark().
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

References

Lüdecke D, Makowski AC, Klein J, Ben-Shachar MS and Makowski D (2026) Choosing informative priors in Bayesian regression models: a simulation study and tutorial using Stan and R. Front. Psychol. 17:1856582. doi:10.3389/fpsyg.2026.1856582

Examples

```
## Not run:
library(performance)
# model with correctly defined priors. outcome is binary, prior
# predictive checks indicate the predicted probability mass based
# on the prior distributions - the resulting pattern aligns with
# our real-world assumptions
model <- insight::download_model("stan_prior_checks_1")
plot(performance::check_priors(model, "mmse"))

# model with default (weakly informative) priors, which is poorly
# calibrated. It pushes probability mass almost exclusively to the
# extremes of 0 and 1, leaving the plausible middle range largely
# unsupported
model <- insight::download_model("stan_prior_checks_2")
plot(performance::check_priors(model, "mmse"))

## End(Not run)
```

---

plot.see_compare_parameters

Plot method for comparison of model parameters

Description

The plot() method for the parameters::compare_parameters() function.

Usage

```
## S3 method for class 'see_compare_parameters'
plot(
  x,
  show_intercept = FALSE,
  size_point = 0.8,
  size_text = NA,
  dodge_position = 0.8,
  sort = NULL,
  n_columns = NULL,
  show_labels = FALSE,
  ...
)
```

Arguments

x	An object.
show_intercept	Logical, if TRUE, the intercept-parameter is included in the plot. By default, it is hidden because in many cases the intercept-parameter has a posterior distribution on a very different location, so density curves of posterior distributions for other parameters are hardly visible.
size_point	Numeric specifying size of point-geoms.
size_text	Numeric value specifying size of text labels.
dodge_position	Numeric value specifying the amount of "dodging" (spacing) between geoms.
sort	The behavior of this argument depends on the plotting contexts. • *Plotting model parameters*: If NULL, coefficients are plotted in the order as they appear in the summary. Setting sort = "ascending" or sort = "descending" sorts coefficients in ascending or descending order, respectively. Setting sort = TRUE is the same as sort = "ascending". • *Plotting Bayes factors*: Sort pie-slices by posterior probability (descending)?
n_columns	For models with multiple components (like fixed and random, count and zero-inflated), defines the number of columns for the panel-layout. If NULL, a single, integrated plot is shown.
show_labels	Logical. If TRUE, text labels are displayed.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
data(iris)
lm1 <- lm(Sepal.Length ~ Species, data = iris)
lm2 <- lm(Sepal.Length ~ Species + Petal.Length, data = iris)
```

```
lm3 <- lm(Sepal.Length ~ Species * Petal.Length, data = iris)
result <- parameters::compare_parameters(lm1, lm2, lm3)
plot(result)
```

`plot.see_compare_performance` *Plot method for comparing model performances*

Description

The `plot()` method for the `performance::compare_performance()` function.

Usage

```
## S3 method for class 'see_compare_performance'
plot(x, size_line = 1, ...)
```

Arguments

`x`	An object.
`size_line`	Numeric value specifying size of line geoms. `linewidth` is an alias for `size_line`.
`...`	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(performance)
data(iris)
lm1 <- lm(Sepal.Length ~ Species, data = iris)
lm2 <- lm(Sepal.Length ~ Species + Petal.Length, data = iris)
lm3 <- lm(Sepal.Length ~ Species * Petal.Length, data = iris)
result <- compare_performance(lm1, lm2, lm3)
result
plot(result)
```

plot.see_dw_groupmeans *Plot method for grouped means.*

Description

The `plot()` method for the `datawizard::means_by_group()` function.

Usage

```
## S3 method for class 'see_dw_groupmeans'
plot(x, title = "", ci = TRUE, caption = TRUE, flip = TRUE, ...)
```

Arguments

`x`	An object returned `datawizard::means_by_group()`.
`title`	String, can be used to specify a plot title.
`ci`	Logical, indicating if the confidence intervals should be included in the graph.
`caption`	Logical, indicating if a caption summarizing the anova results for the analysis should be included.
`flip`	Logical. If `TRUE` (the default), the groups are on the vertical axis. If `FALSE`, the groups are on the horizontal axis.
`...`	Currently not used.

Details

Produces a faceted plot when there is more than one means-table.

By default, the plot uses `ggplot2::coord_flip()`, so the groups are on the vertical axis and the means are on the horizontal axis. Use `flip = FALSE` to show the groups on the horizontal axis.

Examples

```
## Not run:
group_means_object <-  datawizard::means_by_group(iris$Sepal.Width, iris$Species)
plot(group_means_object, title = "group means", ci = FALSE, caption = FALSE)

group_means_object <- datawizard::means_by_group(
  iris,
  c("Sepal.Width", "Petal.Width"),
  "Species"
)
plot(group_means_object, title = "group means")

## End(Not run)
```

plot.see_effectsize_table

Plot method for effect size tables

Description

The `plot()` method for the `effectsize::effectsize()` function.

Usage

```
## S3 method for class 'see_effectsize_table'
plot(x, ...)
```

Arguments

`x`	An object.
`...`	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(effectsize)
m <- aov(mpg ~ factor(am) * factor(cyl), data = mtcars)
result <- eta_squared(m)
plot(result)
```

plot.see_equivalence_test_effectsize

Plot method for (conditional) equivalence testing

Description

The `plot()` method for the `bayestestR::equivalence_test()` function.

Usage

```
## S3 method for class 'see_equivalence_test_effectsize'
plot(x, ...)

## S3 method for class 'see_equivalence_test'
plot(
  x,
  color_rope = "#0171D3",
```

```
  alpha_rope = 0.2,
  show_intercept = FALSE,
  n_columns = 1,
  ...
)

## S3 method for class 'see_equivalence_test_lm'
plot(
  x,
  size_point = 0.7,
  color_rope = "#0171D3",
  alpha_rope = 0.2,
  show_intercept = FALSE,
  n_columns = 1,
  ...
)
```

Arguments

x	An object.
...	Arguments passed to or from other methods.
color_rope	Character specifying color of ROPE ribbon.
alpha_rope	Numeric specifying transparency level of ROPE ribbon.
show_intercept	Logical, if TRUE, the intercept-parameter is included in the plot. By default, it is hidden because in many cases the intercept-parameter has a posterior distribution on a very different location, so density curves of posterior distributions for other parameters are hardly visible.
n_columns	For models with multiple components (like fixed and random, count and zero-inflated), defines the number of columns for the panel-layout. If NULL, a single, integrated plot is shown.
size_point	Numeric specifying size of point-geoms.

Value

A ggplot2-object.

Examples

```
library(effectsize)
m <- aov(mpg ~ factor(am) * factor(cyl), data = mtcars)
result <- eta_squared(m)
plot(result)
```

plot.see_estimate_contrasts

Plot method for estimating contrasts

Description

The `plot()` method for the `modelbased::estimate_contrasts()` function.

Usage

```
## S3 method for class 'see_estimate_contrasts'
plot(x, data = NULL, show_data = FALSE, ...)
```

Arguments

`x`	An object.
`data`	The estimated means, obtained with `modelbased::estimate_means()`.
`show_data`	Logical. If `TRUE`, the plot draws the raw data of the model as jittered points behind the lighthouses. The raw data come from `insight::get_data()` for the model stored in `x`, not from `data`. A response that is logical or a factor with two levels is drawn as 0 and 1, with `TRUE` or the second level as 1. A response `log(y)`, `log2(y)`, or `log10(y)`, with `y` a column of the data, is drawn as the raw data of `y` if both the contrasts and the means were estimated with `transform = TRUE`. Means without the `transform` attribute, such as a plain data frame, then give an error. Ratio contrasts are drawn with the raw data. The plot stops with an error in these cases: • `show_data` is not a single `TRUE` or `FALSE`. • `x` is the output of `data_plot()`, or it does not carry its model, or the model data cannot be retrieved. • The response is a `cbind()` of successes and failures in a binomial model. • The model transforms the response, for example `log(y)`, and the contrasts and means are not back-transformed log contrasts and means as above. • The `predict` of the contrasts or of the estimated means is not one of `"prediction"`, `"response"`, `"expectation"`, `"invlink(link)"`, and `"inverse_link"`, for example `predict = "link"`. Means without this information, such as a plain data frame, are taken to be on the same scale as the contrasts. • The model data lack the response or a contrasted or `by` variable. • The estimated means do not include each value in the data of the contrasted and `by` variables, or each combination of their values. For example, a numeric `by` variable has values that the means were not estimated at. Data at factor or character `by` levels that the contrasts lack are left out instead.
`...`	Arguments passed to or from other methods.

Details

If you estimate the contrasts with by, the plot draws each contrast from the estimated means of its own by level. The plot then has one panel per level, or combination of levels, of the by variables. The estimated means must include the contrasted variables and the by variables, and no other variables that split their rows further, except the Response column of ordinal and multinomial models. If the means have no row for the levels of a contrast, the plot does not draw that contrast and gives a warning. The plot shows only the by levels, or combinations of levels, that appear in the contrasts. It leaves out the means of other by levels, and with show_data = TRUE their raw data, and gives no warning for them. For a numeric by variable, show_data = TRUE leaves out the raw data only at values that the means hold. Data at other values still give the error described under show_data. A by variable named PANEL, ROW, COL, SCALE_X, or SCALE_Y, which ggplot2 reserves for facets, works too. The facet strips show its levels.

For ordinal and multinomial models, such as MASS::polr() and mclogit::mblogit(), the means have one row per response category, in the column Response. The contrasts have the columns Response1 and Response2. The plot then has one panel per response category, or per combination of category and by levels. Each panel shows the means of that category and the contrasts whose Response1 and Response2 are both that category. The plot does not draw contrasts between two categories, and it gives no warning for them.

If you contrast two or more variables jointly, for example with contrast = c("am", "cyl"), the x axis shows their combinations of levels, such as "auto, 4". The first variable changes slowest along the axis. For three or more variables, each label shows one level per line.

If you contrast one numeric variable at unevenly spaced values, such as contrast = "wt=c(2,2.5,4)", the x axis is continuous and keeps their spacing, with breaks at those values. Evenly spaced values, such as 1, 2, and 3, and two values or fewer keep an axis with one evenly spaced position per value.

The plot takes the estimates from the column of the means that their coef_name attribute names. For means without this attribute, such as a plain data frame, it takes the first of the columns Median, Mean, MAP, Coefficient, Probability, Proportion, and Rate. If the means have none of these columns, the plot stops with an error.

Each lighthouse starts at the estimated mean of Level1 of a contrast. For a difference, the lighthouse at Level2 spans that mean minus the bounds of the confidence interval. Contrasts with a Ratio column, from comparison = ratio ~ pairwise, are ratios of the means, so the lighthouse at Level2 spans that mean divided by the bounds of the interval. Bayesian ratio contrasts have no Ratio column, so the plot reads the left side of their comparison formula, ratio, and draws them as ratios too. If the interval of a ratio includes 0, the plot does not draw that contrast and gives a warning. The contrasts must have the columns CI_low and CI_high.

Contrasts estimated with transform = TRUE are back-transformed to the scale of the response. With the default backend, if the model response is log(y), log(y, base = b), log2(y), or log10(y), these contrasts are ratios of the back-transformed means, and the plot draws them as ratios. If insight::find_transformation() reports the transformation "identity", as it does for an untransformed response and for scale(y), the plot draws them as differences. For other transformations, such as sqrt(y), and for transformations that insight::find_transformation() does not recognize, the plot stops with an error. With backend = "emmeans", which sets transform = TRUE by default, the contrasts are differences of the back-transformed means, and the plot draws them as differences. The plot draws ratio contrasts estimated with transform = TRUE as ratios if insight::find_transformation() reports the transformation "identity". For other transformations, it stops with an error, because for a transformed response they are not ratios of the

back-transformed means.

The contrasts and the means must be on the same scale. The plot stops with an error if both record a `predict` value and the two differ. The `predict` values `"response"`, `"inverse_link"`, and `"invlink(link)"` count as the same scale. With `backend = "emmeans"`, modelbased records the link scale as `predict = "none"`, which counts as `"link"`. For a model with an identity link, a response that `insight::find_transformation()` reports as `"identity"`, and no zero-inflation or hurdle part, such as `lm(y ~ x)`, `"link"` and `"none"` count as the response scale. The plot also stops with an error if both record a `transform` value and the two differ. If neither value is a `transform` function and `insight::find_transformation()` reports the transformation `"identity"`, the plot does not stop. Contrasts and means estimated with the same `transform` function also differ, because modelbased records the function on the contrasts and `transform = TRUE` on the means, so the plot stops.

Interpreting Lighthouse Plots

Lighthouse plots display both estimated marginal means and the uncertainty around their pairwise differences (contrasts) in a single visual:

- **Means and Error Bars:** The points and vertical line ranges display the estimated marginal means for each level along with their individual confidence intervals.
- **Lighthouse Beams (Projected Uncertainty):** The shaded polygonal bands ("beams") represent the pairwise contrasts. A beam originates at the point estimate of a reference level and projects toward the comparison level. At the target level, the vertical span of the beam represents the confidence interval of the estimated difference, anchored at the reference mean.
- **Interpretation:** The vertical span of the projected beam at the target level corresponds to the confidence interval of the estimated difference, evaluated *relative* to the reference point estimate. Intuitively, it answers: *"If the reference level is at value Y, where do we expect the comparison level to be based on the estimated contrast?"*
- **Reading Significance:** Because the beam illustrates the confidence interval of the difference, zero difference corresponds to a horizontal line from the reference point. If both edges of the beam tilt in the same direction (both rising or both falling), the confidence interval does not include zero (the difference is statistically significant). If one edge rises while the other falls, the beam straddles the horizontal line, indicating that a difference of zero remains plausible.

Value

A ggplot2-object.

Examples

```
library(modelbased)

model <- lm(Sepal.Width ~ Species, data = iris)
contrasts <- estimate_contrasts(model)
means <- estimate_means(model)
plot(contrasts, means)

# with the raw data as jittered points
plot(contrasts, means, show_data = TRUE)
```

```
# contrasts of `am` within each level of `cyl`, one panel per level
d <- mtcars
d$cyl <- factor(d$cyl)
d$am <- factor(d$am, labels = c("auto", "manual"))
model <- lm(mpg ~ cyl * am, data = d)
contrasts <- estimate_contrasts(model, contrast = "am", by = "cyl")
means <- estimate_means(model, by = c("cyl", "am"))
plot(contrasts, means)

# joint contrasts of `am` and `cyl`, on an axis of combined levels
contrasts <- estimate_contrasts(model, contrast = c("am", "cyl"))
plot(contrasts, means)
```

`plot.see_estimate_density` *Plot method for density estimation of posterior samples*

Description

The `plot()` method for the `bayestestR::estimate_density()` function.

Usage

```
## S3 method for class 'see_estimate_density'
plot(
  x,
  stack = TRUE,
  show_intercept = FALSE,
  n_columns = 1,
  priors = FALSE,
  alpha_priors = 0.4,
  alpha_posteriors = 0.7,
  size_line = 0.9,
  size_point = 2,
  centrality = "median",
  ci = 0.95,
  ...
)
```

Arguments

`x`	An object.
`stack`	Logical. If `TRUE`, densities are plotted as stacked lines. Else, densities are plotted for each parameter among each other.

show_intercept	Logical, if TRUE, the intercept-parameter is included in the plot. By default, it is hidden because in many cases the intercept-parameter has a posterior distribution on a very different location, so density curves of posterior distributions for other parameters are hardly visible.
n_columns	For models with multiple components (like fixed and random, count and zero-inflated), defines the number of columns for the panel-layout. If NULL, a single, integrated plot is shown.
priors	Logical. If TRUE, prior distributions are simulated (using bayestestR::simulate_prior()) and added to the plot.
alpha_priors	Numeric value specifying alpha for the prior distributions.
alpha_posteriors	Numeric value specifying alpha for the posterior distributions.
size_line	Numeric value specifying size of line geoms. linewidth is an alias for size_line.
size_point	Numeric specifying size of point-geoms.
centrality	Character specifying the point-estimate (centrality index) to compute. Can be "median", "mean" or "MAP".
ci	Numeric value of probability of the CI (between 0 and 1) to be estimated. Default to 0.95.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(rstanarm)
library(bayestestR)
set.seed(123)
m <<- suppressWarnings(stan_glm(Sepal.Length ~ Petal.Width * Species, data = iris, refresh = 0))
result <- estimate_density(m)
plot(result)
```

---

plot.see_hdi *Plot method for uncertainty or credible intervals*

Description

The plot() method for the bayestestR::hdi() and related function.

Usage

```
## S3 method for class 'see_hdi'
plot(
  x,
  data = NULL,
  show_intercept = FALSE,
  show_zero = TRUE,
  show_title = TRUE,
  n_columns = 1,
  ...
)
```

Arguments

x	An object.
data	The original data used to create this object. Can be a statistical model.
show_intercept	Logical, if TRUE, the intercept-parameter is included in the plot. By default, it is hidden because in many cases the intercept-parameter has a posterior distribution on a very different location, so density curves of posterior distributions for other parameters are hardly visible.
show_zero	Logical. If TRUE, will add a vertical (dotted) line at 0.
show_title	Logical. If TRUE, will show the title of the plot.
n_columns	For models with multiple components (like fixed and random, count and zero-inflated), defines the number of columns for the panel-layout. If NULL, a single, integrated plot is shown.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(rstanarm)
library(bayestestR)
set.seed(123)
m <- suppressWarnings(stan_glm(Sepal.Length ~ Petal.Width * Species, data = iris, refresh = 0))
result <- bayestestR::hdi(m)
result
plot(result)
```

plot.see_n_factors *Plot method for numbers of clusters to extract or factors to retain*

Description

The plot() method for the parameters::n_factors() and parameters::n_clusters()

Usage

```
## S3 method for class 'see_n_factors'
plot(x, data = NULL, type = c("bar", "line", "area"), size = 1, ...)
```

Arguments

x	An object.
data	The original data used to create this object. Can be a statistical model.
type	Character vector, indicating the type of plot. Options are three different shapes to illustrate the degree of consensus between dimensionality methods for each number of factors; "bar" (default) for a bar chart, "line" for a horizontal point and line chart, or "area" for an area chart (frequency polygon).
size	Depending on type, a numeric value specifying size of bars, lines, or segments.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
data(mtcars)
result <- parameters::n_factors(mtcars, type = "PCA")
result

plot(result) # type = "bar" by default
plot(result, type = "line")
plot(result, type = "area")
```

plot.see_parameters_brms_meta *Plot method for Model Parameters from Bayesian Meta-Analysis*

Description

The `plot()` method for the `parameters::model_parameters()` function when used with brms-meta-analysis models.

Usage

```
## S3 method for class 'see_parameters_brms_meta'
plot(
  x,
  size_point = 2,
  size_line = 0.8,
  size_text = 3.5,
  alpha_posteriors = 0.7,
  alpha_rope = 0.15,
  color_rope = "cadetblue",
  normalize_height = TRUE,
  show_labels = TRUE,
  ...
)
```

Arguments

`x`	An object.
`size_point`	Numeric specifying size of point-geoms.
`size_line`	Numeric value specifying size of line geoms. `linewidth` is an alias for `size_line`.
`size_text`	Numeric value specifying size of text labels.
`alpha_posteriors`	Numeric value specifying alpha for the posterior distributions.
`alpha_rope`	Numeric specifying transparency level of ROPE ribbon.
`color_rope`	Character specifying color of ROPE ribbon.
`normalize_height`	Logical. If `TRUE`, height of mcmc-areas is "normalized", to avoid overlap. In certain cases when the range of a posterior distribution is narrow for some parameters, this may result in very flat mcmc-areas. In such cases, set `normalize_height = FALSE`.
`show_labels`	Logical. If `TRUE`, text labels are displayed.
`...`	Arguments passed to or from other methods.

Details

Colors of density areas and errorbars: To change the colors of the density areas, use `scale_fill_manual()` with named color-values, e.g. `scale_fill_manual(values = c("Study" = "blue", "Overall" = "green"))`. To change the color of the error bars, use `scale_color_manual(values = c("Errorbar" = "red"))`.

Show or hide estimates and CI: Use `show_labels = FALSE` to hide the textual output of estimates and credible intervals.

Value

A ggplot2-object.

Examples

```
library(parameters)
library(brms)
library(metafor)
data(dat.bcg)

dat <- escalc(
  measure = "RR",
  ai = tpos,
  bi = tneg,
  ci = cpos,
  di = cneg,
  data = dat.bcg
)
dat$author <- make.unique(dat$author)

# model
set.seed(123)
priors <- c(
  prior(normal(0, 1), class = Intercept),
  prior(cauchy(0, 0.5), class = sd)
)
model <- suppressWarnings(
  brm(yi | se(vi) ~ 1 + (1 | author), data = dat, refresh = 0, silent = 2)
)

# result
mp <- model_parameters(model)
plot(mp)
```

plot.see_parameters_distribution *Plot method for describing distributions of vectors*

Description

The `plot()` method for the `parameters::describe_distribution()` function.

Usage

```
## S3 method for class 'see_parameters_distribution'
plot(
  x,
  dispersion = FALSE,
  alpha_dispersion = 0.3,
  color_dispersion = "#3498db",
  dispersion_style = c("ribbon", "curve"),
  size_bar = 0.7,
  highlight = NULL,
  color_highlight = NULL,
  ...
)
```

Arguments

`x`	An object.
`dispersion`	Logical. If `TRUE`, a range of dispersion for each variable to the plot will be added.
`alpha_dispersion`	Numeric value specifying the transparency level of dispersion ribbon.
`color_dispersion`	Character specifying the color of dispersion ribbon.
`dispersion_style`	Character describing the style of dispersion area. `"ribbon"` for a ribbon, `"curve"` for a normal-curve.
`size_bar`	Size of bar geoms.
`highlight`	A vector with names of categories in `x` that should be highlighted.
`color_highlight`	A vector of color values for highlighted categories. The remaining (non-highlighted) categories will be filled with a lighter grey.
`...`	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(parameters)
set.seed(333)
x <- sample(1:100, 1000, replace = TRUE)
result <- describe_distribution(x)
result
plot(result)
```

`plot.see_parameters_model` *Plot method for model parameters*

Description

The `plot()` method for the `parameters::model_parameters()` function.

Usage

```
## S3 method for class 'see_parameters_model'
plot(
  x,
  show_intercept = FALSE,
  size_point = 0.8,
  size_text = NA,
  sort = NULL,
  n_columns = NULL,
  type = c("forest", "funnel"),
  weight_points = TRUE,
  show_labels = FALSE,
  show_estimate = TRUE,
  show_interval = TRUE,
  show_density = FALSE,
  show_direction = TRUE,
  log_scale = FALSE,
  ...
)

## S3 method for class 'see_parameters_sem'
plot(
  x,
  data = NULL,
  component = c("regression", "correlation", "loading"),
  type = component,
  threshold_coefficient = NULL,
  threshold_p = NULL,
  ci = TRUE,
  size_point = 22,
```

```
  ...
)
```

Arguments

x	An object.
show_intercept	Logical, if TRUE, the intercept-parameter is included in the plot. By default, it is hidden because in many cases the intercept-parameter has a posterior distribution on a very different location, so density curves of posterior distributions for other parameters are hardly visible.
size_point	Numeric specifying size of point-geoms.
size_text	Numeric value specifying size of text labels.
sort	The behavior of this argument depends on the plotting contexts. • *Plotting model parameters*: If NULL, coefficients are plotted in the order as they appear in the summary. Setting sort = "ascending" or sort = "descending" sorts coefficients in ascending or descending order, respectively. Setting sort = TRUE is the same as sort = "ascending". • *Plotting Bayes factors*: Sort pie-slices by posterior probability (descending)?
n_columns	For models with multiple components (like fixed and random, count and zero-inflated), defines the number of columns for the panel-layout. If NULL, a single, integrated plot is shown.
type	Character indicating the type of plot. Only applies for model parameters from meta-analysis objects (e.g. **metafor**).
weight_points	Logical. If TRUE, for meta-analysis objects, point size will be adjusted according to the study-weights.
show_labels	Logical. If TRUE, text labels are displayed.
show_estimate	Should the point estimate of each parameter be shown? (default: TRUE)
show_interval	Should the compatibility interval(s) of each parameter be shown? (default: TRUE)
show_density	Should the compatibility density (i.e., posterior, bootstrap, or confidence density) of each parameter be shown? (default: FALSE)
show_direction	Should the "direction" of coefficients (e.g., positive or negative coefficients) be highlighted using different colors? (default: TRUE)
log_scale	Should exponentiated coefficients (e.g., odds-ratios) be plotted on a log scale? (default: FALSE)
...	Arguments passed to or from other methods.
data	The original data used to create this object. Can be a statistical model.
component	Character indicating which component of the model should be plotted.
threshold_coefficient	Numeric, threshold at which value coefficients will be displayed.
threshold_p	Numeric, threshold at which value p-values will be displayed.
ci	Logical, whether confidence intervals should be added to the plot.

Value

A ggplot2-object.

Note

By default, coefficients and their confidence intervals are colored depending on whether they show a "positive" or "negative" association with the outcome. E.g., in case of linear models, colors simply distinguish positive or negative coefficients. For logistic regression models that are shown on the odds ratio scale, colors distinguish odds ratios above or below 1. Use `show_direction = FALSE` to disable this feature and only show a one-colored forest plot.

Examples

```
library(parameters)
m <- lm(mpg ~ wt + cyl + gear + disp, data = mtcars)
result <- model_parameters(m)
result
plot(result)
```

---

plot.see_parameters_pca

Plot method for principal component analysis

Description

The `plot()` method for the `parameters::principal_components()` function.

Usage

```
## S3 method for class 'see_parameters_pca'
plot(
  x,
  type = "bar",
  size_text = 3.5,
  color_text = "black",
  colors = c("#cd201f", "#ffffff", "#0077B5"),
  size = 1,
  show_labels = TRUE,
  arrow_end_gap = 0.07,
  factor_node_size = c(25, 35),
  margins = c(0.3, 0.3),
  names_factors = NULL,
  fill_variables = "#738b8d",
  fill_factors = "#2C3E50",
  ...
)
```

Arguments

x	An object.
type	Character vector, indicating the type of plot. Options are different shapes to represent component loadings; "bar" (default) for a horizontal bar chart, "line" for a horizontal point and line chart, or "graph" for a graph.
size_text	Numeric value specifying size of text labels.
color_text	Character specifying color of text labels.
colors	Character vector of length three, indicating the colors for low (negative), mid (close to zero), and high (positive) values.
size	Depending on type, a numeric value specifying size of bars, lines, or segments.
show_labels	Logical. If TRUE, text labels are displayed.
arrow_end_gap	Numeric. Specifies the distance between the tip of the edge arrow and the variable node. Adjusting this value prevents the arrow from overlapping or clipping into the variable label. Default is 0.07 (measured in 'snpc' units). This argument is only used if type = "graph".
factor_node_size	Numeric vector of length 2. Determines the minimum and maximum size of the circular factor nodes. Factor nodes are scaled internally based on the proportion of variance they explain. This argument is only used if type = "graph".
margins	Numeric vector of length 2. Adds extra space to the left and right edges of the plot canvas (using ggplot2::expansion). This is particularly useful to prevent long variable labels on the edges from being cut off. This argument is only used if type = "graph".
names_factors	Named character vector. Allows providing custom labels for the factor nodes. The names of the vector must match the original factor names generated by the model (e.g., c("Component 1" = "Extraversion", "Component 2" = "Neuroticism")). This argument is only used if type = "graph".
fill_variables	Character vector. Specifies the fill color for the variable nodes (rectangular labels). Can be a single color hex/name (applied to all variables), a vector of colors matching the exact number of variables, or a named vector to map specific colors to specific variables. This argument is only used if type = "graph".
fill_factors	Character vector. Specifies the fill color for the factor nodes (circular points). Similar to fill_variables, this accepts a single color, a vector of matching length, or a named vector for precise mapping. This argument is only used if type = "graph".
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(parameters)
data(mtcars)
```

```
result <- principal_components(mtcars[, 1:7], n = "all", threshold = 0.2)
result
plot(result)
```

`plot.see_parameters_simulate` *Plot method for simulated model parameters*

Description

The `plot()` method for the `parameters::simulate_parameters()` function.

Usage

```
## S3 method for class 'see_parameters_simulate'
plot(
  x,
  data = NULL,
  stack = TRUE,
  show_intercept = FALSE,
  n_columns = NULL,
  normalize_height = FALSE,
  size_line = 0.9,
  alpha_posteriors = 0.7,
  centrality = "median",
  ci = 0.95,
  ...
)
```

Arguments

`x`	An object.
`data`	The original data used to create this object. Can be a statistical model.
`stack`	Logical. If `TRUE`, densities are plotted as stacked lines. Else, densities are plotted for each parameter among each other.
`show_intercept`	Logical, if `TRUE`, the intercept-parameter is included in the plot. By default, it is hidden because in many cases the intercept-parameter has a posterior distribution on a very different location, so density curves of posterior distributions for other parameters are hardly visible.
`n_columns`	For models with multiple components (like fixed and random, count and zero-inflated), defines the number of columns for the panel-layout. If `NULL`, a single, integrated plot is shown.

normalize_height
: Logical. If TRUE, height of density-areas is "normalized", to avoid overlap. In certain cases when the range of a distribution of simulated draws is narrow for some parameters, this may result in very flat density-areas. In such cases, set normalize_height = FALSE.

size_line
: Numeric value specifying size of line geoms. linewidth is an alias for size_line.

alpha_posteriors
: Numeric value specifying alpha for the posterior distributions.

centrality
: Character specifying the point-estimate (centrality index) to compute. Can be "median", "mean" or "MAP".

ci
: Numeric value of probability of the CI (between 0 and 1) to be estimated. Default to 0.95.

...
: Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(parameters)
m <<- lm(mpg ~ wt + cyl + gear, data = mtcars)
result <- simulate_parameters(m)
result
plot(result)
```

---

plot.see_performance_roc

Plot method for ROC curves

Description

The plot() method for the performance::performance_roc() function.

Usage

```
## S3 method for class 'see_performance_roc'
plot(x, ...)
```

Arguments

x
: An object.

...
: Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(performance)
data(iris)
set.seed(123)
iris$y <- rbinom(nrow(iris), size = 1, .3)

folds <- sample(nrow(iris), size = nrow(iris) / 8, replace = FALSE)
test_data <- iris[folds, ]
train_data <- iris[-folds, ]

model <- glm(y ~ Sepal.Length + Sepal.Width, data = train_data, family = "binomial")
result <- performance_roc(model, new_data = test_data)
result
plot(result)
```

---

plot.see_performance_simres

Plot method for check model for (non-)normality of residuals

Description

The `plot()` method for the `performance::check_residuals()` resp. `performance::simulate_residuals()` function.

Usage

```
## S3 method for class 'see_performance_simres'
plot(
  x,
  size_line = 0.8,
  size_point = 2,
  size_title = 12,
  size_axis_title = base_size,
  base_size = 10,
  alpha = 0.2,
  alpha_dot = 0.8,
  theme = NULL,
  colors = c("#3aaf85", "#1b6ca8"),
  detrend = FALSE,
  transform = NULL,
  ...
)
```

Arguments

`x`	An object.
`size_line`	Numeric value specifying size of line geoms. `linewidth` is an alias for `size_line`.

size_point	Numeric specifying size of point-geoms.
base_size, size_axis_title, size_title	Numeric value specifying size of axis and plot titles.
alpha	Numeric value specifying alpha level of the confidence bands.
alpha_dot	Numeric value specifying alpha level of the point geoms.
theme	A ggplot2-theme function, e.g. theme = theme_lucid() or theme = ggplot2::theme_dark().
colors	Character vector of length two, indicating the colors (in hex-format) for points and line.
detrend	Logical that decides if Q-Q and P-P plots should be de-trended (also known as *worm plots*).
transform	Function to transform the residuals. If NULL (default), no transformation is applied and uniformly distributed residuals are expected. See argument quantileFuntion in ?DHARMa:::residuals.DHARMa for more details.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

See Also

See also the vignette about check_model().

Examples

```
data(Salamanders, package = "glmmTMB")
model <- glmmTMB::glmmTMB(
  count ~ mined + spp + (1 | site),
  family = poisson(),
  data = Salamanders
)
simulated_residuals <- performance::simulate_residuals(model)
plot(simulated_residuals)

# or
simulated_residuals <- performance::simulate_residuals(model)
result <- performance::check_residuals(simulated_residuals)
plot(result)
```

`plot.see_point_estimate` *Plot method for point estimates of posterior samples*

Description

The `plot()` method for the `bayestestR::point_estimate()`.

Usage

```
## S3 method for class 'see_point_estimate'
plot(
  x,
  data = NULL,
  size_point = 2,
  size_text = 3.5,
  panel = TRUE,
  show_labels = TRUE,
  show_intercept = FALSE,
  priors = FALSE,
  alpha_priors = 0.4,
  ...
)
```

Arguments

`x`	An object.
`data`	The original data used to create this object. Can be a statistical model.
`size_point`	Numeric specifying size of point-geoms.
`size_text`	Numeric value specifying size of text labels.
`panel`	Logical, if `TRUE`, plots are arranged as panels; else, single plots are returned.
`show_labels`	Logical. If `TRUE`, the text labels for the point estimates (i.e. *"Mean"*, *"Median"* and/or *"MAP"*) are shown. You may set `show_labels = FALSE` in case of overlapping labels, and add your own legend or footnote to the plot.
`show_intercept`	Logical, if `TRUE`, the intercept-parameter is included in the plot. By default, it is hidden because in many cases the intercept-parameter has a posterior distribution on a very different location, so density curves of posterior distributions for other parameters are hardly visible.
`priors`	Logical. If `TRUE`, prior distributions are simulated (using `bayestestR::simulate_prior()`) and added to the plot.
`alpha_priors`	Numeric value specifying alpha for the prior distributions.
`...`	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(rstanarm)
library(bayestestR)
set.seed(123)
m <<- suppressWarnings(stan_glm(Sepal.Length ~ Petal.Width * Species, data = iris, refresh = 0))
result <- point_estimate(m, centrality = "median")
result
plot(result)
```

---

plot.see_p_direction *Plot method for probability of direction*

Description

The `plot()` method for the `bayestestR::p_direction()` function.

Usage

```
## S3 method for class 'see_p_direction'
plot(
  x,
  data = NULL,
  show_intercept = FALSE,
  priors = FALSE,
  alpha_priors = 0.4,
  n_columns = 1,
  ...
)
```

Arguments

`x`	An object.
`data`	The original data used to create this object. Can be a statistical model.
`show_intercept`	Logical, if `TRUE`, the intercept-parameter is included in the plot. By default, it is hidden because in many cases the intercept-parameter has a posterior distribution on a very different location, so density curves of posterior distributions for other parameters are hardly visible.
`priors`	Logical. If `TRUE`, prior distributions are simulated (using `bayestestR::simulate_prior()`) and added to the plot.
`alpha_priors`	Numeric value specifying alpha for the prior distributions.

n_columns	For models with multiple components (like fixed and random, count and zero-inflated), defines the number of columns for the panel-layout. If NULL, a single, integrated plot is shown.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(rstanarm)
library(bayestestR)
set.seed(123)
m <<- suppressWarnings(stan_glm(Sepal.Length ~ Petal.Width * Species, data = iris, refresh = 0))
result <- p_direction(m)
plot(result)
```

---

plot.see_p_function *Plot method for plotting p-functions (aka consonance functions)*

Description

The plot() method for the parameters::p_function().

Usage

```
## S3 method for class 'see_p_function'
plot(
  x,
  colors = c("black", "#1b6ca8"),
  size_point = 1.2,
  size_line = c(0.7, 0.9),
  size_text = 3,
  alpha_line = 0.15,
  show_labels = TRUE,
  n_columns = NULL,
  show_intercept = FALSE,
  ...
)
```

Arguments

x	An object returned by parameters::p_function().
colors	Character vector of length two, indicating the colors (in hex-format) used when only one parameter is plotted, resp. when panels are plotted as facets.

size_point	Numeric specifying size of point-geoms.
size_line	Numeric value specifying size of line geoms. linewidth is an alias for size_line.
size_text	Numeric value specifying size of text labels.
alpha_line	Numeric value specifying alpha of lines indicating the emphasized compatibility interval levels (see ?parameters::p_function).
show_labels	Logical. If TRUE, text labels are displayed.
n_columns	For models with multiple components (like fixed and random, count and zero-inflated), defines the number of columns for the panel-layout. If NULL, a single, integrated plot is shown.
show_intercept	Logical, if TRUE, the intercept-parameter is included in the plot. By default, it is hidden because in many cases the intercept-parameter has a posterior distribution on a very different location, so density curves of posterior distributions for other parameters are hardly visible.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(parameters)
model <- lm(Sepal.Length ~ Species + Sepal.Width + Petal.Length, data = iris)
result <- p_function(model)
plot(result, n_columns = 2, show_labels = FALSE)

result <- p_function(model, keep = "Sepal.Width")
plot(result)
```

---

plot.see_p_significance

Plot method for practical significance

Description

The plot() method for the bayestestR::p_significance() function.

Usage

```
## S3 method for class 'see_p_significance'
plot(
  x,
  data = NULL,
  show_intercept = FALSE,
  priors = FALSE,
  alpha_priors = 0.4,
```

```
  n_columns = 1,
  ...
)
```

Arguments

x	An object.
data	The original data used to create this object. Can be a statistical model.
show_intercept	Logical, if TRUE, the intercept-parameter is included in the plot. By default, it is hidden because in many cases the intercept-parameter has a posterior distribution on a very different location, so density curves of posterior distributions for other parameters are hardly visible.
priors	Logical. If TRUE, prior distributions are simulated (using bayestestR::simulate_prior()) and added to the plot.
alpha_priors	Numeric value specifying alpha for the prior distributions.
n_columns	For models with multiple components (like fixed and random, count and zero-inflated), defines the number of columns for the panel-layout. If NULL, a single, integrated plot is shown.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(rstanarm)
library(bayestestR)
set.seed(123)
m <<- suppressWarnings(stan_glm(Sepal.Length ~ Petal.Width * Species, data = iris, refresh = 0))
result <- p_significance(m)
plot(result)
```

---

plot.see_rope *Plot method for Region of Practical Equivalence*

Description

The plot() method for the bayestestR::rope().

Usage

```
## S3 method for class 'see_rope'
plot(
  x,
  data = NULL,
  alpha_rope = 0.5,
  color_rope = "cadetblue",
  show_intercept = FALSE,
  n_columns = 1,
  ...
)
```

Arguments

x	An object.
data	The original data used to create this object. Can be a statistical model.
alpha_rope	Numeric specifying transparency level of ROPE ribbon.
color_rope	Character specifying color of ROPE ribbon.
show_intercept	Logical, if TRUE, the intercept-parameter is included in the plot. By default, it is hidden because in many cases the intercept-parameter has a posterior distribution on a very different location, so density curves of posterior distributions for other parameters are hardly visible.
n_columns	For models with multiple components (like fixed and random, count and zero-inflated), defines the number of columns for the panel-layout. If NULL, a single, integrated plot is shown.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(rstanarm)
library(bayestestR)
set.seed(123)
m <<- suppressWarnings(stan_glm(Sepal.Length ~ Petal.Width * Species, data = iris, refresh = 0))
result <- rope(m)
result
plot(result)
```

plot.see_si *Plot method for support intervals*

Description

The `plot()` method for the `bayestestR::si()`.

Usage

```
## S3 method for class 'see_si'
plot(
  x,
  color_si = "#0171D3",
  alpha_si = 0.2,
  show_intercept = FALSE,
  support_only = FALSE,
  ...
)
```

Arguments

x	An object.
color_si	Character specifying color of SI ribbon.
alpha_si	Numeric value specifying Transparency level of SI ribbon.
show_intercept	Logical, if TRUE, the intercept-parameter is included in the plot. By default, it is hidden because in many cases the intercept-parameter has a posterior distribution on a very different location, so density curves of posterior distributions for other parameters are hardly visible.
support_only	Logical. Decides whether to plot only the support data, or show the "raw" prior and posterior distributions? Only applies when plotting `bayestestR::si()`.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

Examples

```
library(rstanarm)
library(bayestestR)
set.seed(123)
m <<- suppressWarnings(stan_glm(Sepal.Length ~ Petal.Width * Species, data = iris, refresh = 0))
result <- si(m, verbose = FALSE)
result
plot(result)
```

plots *Multiple plots side by side*

Description

A wrapper around *patchwork* to plot multiple figures side by side on the same page.

Usage

```
plots(
  ...,
  n_rows = NULL,
  n_columns = NULL,
  guides = NULL,
  tags = FALSE,
  tag_prefix = NULL,
  tag_suffix = NULL,
  tag_sep = NULL,
  title = NULL,
  subtitle = NULL,
  caption = NULL,
  theme = NULL
)
```

Arguments

`...`	Multiple ggplots or a list containing ggplot objects
`n_rows`	Number of rows to align plots.
`n_columns`	Number of columns to align plots.
`guides`	A string specifying how guides should be treated in the layout. `'collect'` will collect shared guides across plots, removing duplicates. `'keep'` will keep guides alongside their plot. `'auto'` will inherit from a higher patchwork level (if any). See `patchwork::plot_layout()` for details.
`tags`	Add tags to your subfigures. Can be `NULL` to omit (default) or a character vector containing tags for each plot. Automatic tags can also be generated with `'1'` for Arabic numerals, `'A'` for uppercase Latin letters, `'a'` for lowercase Latin letters, `'I'` for uppercase Roman numerals, and `'i'` for lowercase Roman numerals. For backwards compatibility, can also be `FALSE` (equivalent to `NULL`), `NA` (equivalent to `NULL`), or `TRUE` (equivalent to `'A'`).
`tag_prefix, tag_suffix`	Text strings that should appear before or after the tag.
`tag_sep`	Text string giving the separator to use between different tag levels.
`title, subtitle, caption`	Text strings to use for the various plot annotations to add to the composed patchwork.

theme — A ggplot theme specification to use for the plot. Only elements related to titles, caption, and tags, as well as plot margin and background, are used.

Details

See the *patchwork* documentation for more advanced control of plot layouts.

Examples

```
library(ggplot2)
library(see)

p1 <- ggplot(mtcars, aes(x = disp, y = mpg)) +
  geom_point()
p2 <- ggplot(mtcars, aes(x = mpg)) +
  geom_density()
p3 <- ggplot(mtcars, aes(x = factor(cyl))) +
  geom_bar() +
  scale_x_discrete("cyl")

plots(p1, p2)
plots(p1, p2, n_columns = 2, tags = "A")
plots(
  p1, p2, p3,
  n_columns = 1, tags = c("Fig. 1", "Fig. 2", "Fig. 3"),
  title = "The surprising truth about mtcars"
)
```

---

print.see_performance_pp_check

Plot method for posterior predictive checks

Description

The `plot()` method for the `performance::check_predictions()` function.

Usage

```
## S3 method for class 'see_performance_pp_check'
print(
  x,
  size_line = 0.5,
  size_point = 2,
  size_bar = 0.7,
  size_axis_title = base_size,
  size_title = 12,
  base_size = 10,
  alpha_line = 0.15,
```

```
  theme = NULL,
  colors = unname(social_colors(c("green", "blue"))),
  type = "density",
  x_limits = NULL,
  ...
)

## S3 method for class 'see_performance_pp_check'
plot(
  x,
  size_line = 0.5,
  size_point = 2,
  size_bar = 0.7,
  size_axis_title = base_size,
  size_title = 12,
  base_size = 10,
  alpha_line = 0.15,
  theme = NULL,
  colors = unname(social_colors(c("green", "blue"))),
  type = "density",
  x_limits = NULL,
  ...
)
```

Arguments

x	An object.
size_line	Numeric value specifying size of line geoms. linewidth is an alias for size_line.
size_point	Numeric specifying size of point-geoms.
size_bar	Size of bar geoms.
base_size, size_axis_title, size_title	Numeric value specifying size of axis and plot titles.
alpha_line	Numeric value specifying alpha of lines indicating yrep.
theme	A ggplot2-theme function, e.g. theme = theme_lucid() or theme = ggplot2::theme_dark().
colors	Character vector of length two, indicating the colors (in hex-format) for points and line.
type	Plot type for the posterior predictive checks plot. Can be "density" (default), "discrete_dots", "discrete_interval" or "discrete_both" (the discrete_* options are appropriate for models with discrete - binary, integer or ordinal etc. - outcomes).
x_limits	Numeric vector of length 2 specifying the limits of the x-axis. If not NULL, will zoom in the x-axis to the specified limits.
...	Arguments passed to or from other methods.

Value

A ggplot2-object.

See Also

See also the vignette about check_model().

Examples

```
library(performance)

model <- lm(Sepal.Length ~ Species * Petal.Width + Petal.Length, data = iris)
check_predictions(model)

# dot-plot style for count-models
d <- iris
d$poisson_var <- rpois(150, 1)
model <- glm(
  poisson_var ~ Species + Petal.Length + Petal.Width,
  data = d,
  family = poisson()
)
out <- check_predictions(model)
plot(out, type = "discrete_dots")
```

---

scale_color_bluebrown *Blue-brown color palette*

Description

A blue-brown color palette. Use scale_color_bluebrown_d() for *discrete* categories and scale_color_bluebrown_c() for a *continuous* scale.

Usage

```
scale_color_bluebrown(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_bluebrown_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_bluebrown_c(
```

```
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_bluebrown(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_bluebrown_c(
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_bluebrown_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_fill_bluebrown(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_bluebrown_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_bluebrown_c(
```

```
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)
```

Arguments

palette	Character name of palette. Depending on the color scale, can be one of "full", "ice", "rainbow", "complement", "contrast", "light" (for dark themes), "black_first", full_original, or black_first_original. The latter three options are especially for the Okabe-Ito color palette. The default is NULL and either "contrast" or "gradient" is used (depending on whether discrete is TRUE or FALSE), which are the two scale useful for discrete or gradient color scales, respectively.
discrete	Boolean indicating whether color aesthetic is discrete or not.
reverse	Boolean indicating whether the palette should be reversed.
aesthetics	A vector of names of the aesthetics that this scale should be applied to (e.g., c('color', 'fill')).
...	Additional arguments to pass to colorRampPalette().

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_boxplot() +
  theme_modern() +
  scale_fill_bluebrown_d()
```

---

scale_color_colorhex *Color palettes from color-hex*

Description

This function creates color scales based on palettes from color-hex.com. This website provides a large number of user-submitted color palettes. The function downloads a requested color palette from color-hex.com. and creates a {ggplot2} color scale from the provided hex codes.

Use scale_color_colorhex_d for *discrete* categories and scale_color_colorhex_c for a *continuous* scale.

Usage

```
scale_color_colorhex(
  palette = 1014416,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_colorhex_d(
  palette = 1014416,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_colorhex_c(
  palette = 1014416,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_colorhex(
  palette = 1014416,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_colorhex_c(
  palette = 1014416,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_colorhex_d(
  palette = 1014416,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)
```

```
scale_fill_colorhex(
  palette = 1014416,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_colorhex_d(
  palette = 1014416,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_colorhex_c(
  palette = 1014416,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)
```

Arguments

palette	The numeric code for a palette at color-hex.com. For example, `1014416` for the Josiah color palette (number 1014416).
discrete	Boolean indicating whether color aesthetic is discrete or not.
reverse	Boolean indicating whether the palette should be reversed.
aesthetics	A vector of names of the aesthetics that this scale should be applied to (e.g., `c('color', 'fill')`).
...	Additional arguments to pass to `colorRampPalette()`.

Note

The default Josiah color palette (number 1014416) is available without an internet connection. All other color palettes require an internet connection to download and access.

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Species, y = Sepal.Length, color = Species)) +
  geom_boxplot() +
  theme_modern() +
  scale_color_colorhex_d(palette = 1014416)
```

```
ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_violin() +
  theme_modern() +
  scale_fill_colorhex_d(palette = 1014416)

ggplot(iris, aes(x = Petal.Length, y = Petal.Width, color = Sepal.Length)) +
  geom_point() +
  theme_modern() +
  scale_color_colorhex_c(palette = 1014416)
```

`scale_color_flat` *Flat UI color palette*

Description

The palette based on Flat UI. Use `scale_color_flat_d` for *discrete* categories and `scale_color_flat_c` for a *continuous* scale, or use the `discrete` argument in `scale_color_flat()`.

Usage

```
scale_color_flat(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_flat_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_flat_c(
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_flat(
  palette = NULL,
  discrete = TRUE,
```

```
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_flat_c(
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_flat_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_fill_flat(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_flat_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_flat_c(
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)
```

Arguments

palette	Character name of palette. Depending on the color scale, can be one of "full", "ice", "rainbow", "complement", "contrast", "light" (for dark themes),

	"black_first", full_original, or black_first_original. The latter three options are especially for the Okabe-Ito color palette. The default is NULL and either "contrast" or "gradient" is used (depending on whether discrete is TRUE or FALSE), which are the two scale useful for discrete or gradient color scales, respectively.
discrete	Boolean indicating whether color aesthetic is discrete or not.
reverse	Boolean indicating whether the palette should be reversed.
aesthetics	A vector of names of the aesthetics that this scale should be applied to (e.g., c('color', 'fill')).
...	Additional arguments passed to discrete_scale() when discrete is TRUE or to scale_color_gradientn() when discrete is FALSE.

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_boxplot() +
  theme_modern() +
  scale_fill_flat()

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_violin() +
  theme_modern() +
  scale_fill_flat(palette = "ice")

ggplot(iris, aes(x = Petal.Length, y = Petal.Width, color = Sepal.Length)) +
  geom_point() +
  theme_modern() +
  scale_color_flat(discrete = FALSE)
```

---

scale_color_material *Material design color palette*

Description

The palette based on material design colors. Use scale_color_material_d() for *discrete* categories and scale_color_material_c() for a *continuous* scale, or use the discrete argument in scale_color_material().

Usage

```
scale_color_material(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
```

```
  aesthetics = "color",
  ...
)

scale_color_material_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_material_c(
  palette = "contrast",
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_material(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_material_c(
  palette = "contrast",
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_material_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_fill_material(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
```

```
  aesthetics = "fill",
  ...
)

scale_fill_material_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_material_c(
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)
```

Arguments

palette	Character name of palette. Depending on the color scale, can be one of "full", "ice", "rainbow", "complement", "contrast", "light" (for dark themes), "black_first", full_original, or black_first_original. The latter three options are especially for the Okabe-Ito color palette. The default is NULL and either "contrast" or "gradient" is used (depending on whether discrete is TRUE or FALSE), which are the two scale useful for discrete or gradient color scales, respectively.
discrete	Boolean indicating whether color aesthetic is discrete or not.
reverse	Boolean indicating whether the palette should be reversed.
aesthetics	A vector of names of the aesthetics that this scale should be applied to (e.g., c('color', 'fill')).
...	Additional arguments to pass to colorRampPalette().

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_boxplot() +
  theme_modern() +
  scale_fill_material()

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_violin() +
  theme_modern() +
  scale_fill_material(palette = "ice")
```

```
ggplot(iris, aes(x = Petal.Length, y = Petal.Width, color = Sepal.Length)) +
  geom_point() +
  theme_modern() +
  scale_color_material(discrete = FALSE)
```

`scale_color_metro` *Metro color palette*

Description

The palette based on Metro Metro colors. Use `scale_color_metro_d` for *discrete* categories and `scale_color_metro_c` for a *continuous* scale, or use the `discrete` argument in `scale_color_metro()`.

Usage

```
scale_color_metro(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_metro_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_metro_c(
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_metro(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)
```

```
scale_colour_metro_c(
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_metro_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_fill_metro(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_metro_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_metro_c(
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)
```

Arguments

palette	Character name of palette. Depending on the color scale, can be one of "full", "ice", "rainbow", "complement", "contrast", "light" (for dark themes), "black_first", full_original, or black_first_original. The latter three options are especially for the Okabe-Ito color palette. The default is NULL and either "contrast" or "gradient" is used (depending on whether discrete is TRUE or FALSE), which are the two scale useful for discrete or gradient color

	scales, respectively.
`discrete`	Boolean indicating whether color aesthetic is discrete or not.
`reverse`	Boolean indicating whether the palette should be reversed.
`aesthetics`	A vector of names of the aesthetics that this scale should be applied to (e.g., `c('color', 'fill')`).
`...`	Additional arguments to pass to `colorRampPalette()`.

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_boxplot() +
  theme_modern() +
  scale_fill_metro()

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_violin() +
  theme_modern() +
  scale_fill_metro(palette = "ice")

ggplot(iris, aes(x = Petal.Length, y = Petal.Width, color = Sepal.Length)) +
  geom_point() +
  theme_modern() +
  scale_color_metro(discrete = FALSE)
```

---

scale_color_okabeito *Okabe-Ito color palette*

Description

The Okabe-Ito color palette was proposed by Okabe and Ito (2008) as a qualitative color palette that is accessible to people with a variety of forms of color vision deficiency. In addition to being accessible, it includes 9 vivid colors that are readily nameable and include colors that correspond to major primary and secondary colors (e.g., red, yellow, blue).

Usage

```
scale_color_okabeito(
  palette = "full",
  reverse = FALSE,
  order = 1:9,
  aesthetics = "color",
  ...
)
```

```
scale_fill_okabeito(
  palette = "full",
  reverse = FALSE,
  order = 1:9,
  aesthetics = "fill",
  ...
)

scale_colour_okabeito(
  palette = "full",
  reverse = FALSE,
  order = 1:9,
  aesthetics = "color",
  ...
)

scale_colour_oi(
  palette = "full",
  reverse = FALSE,
  order = 1:9,
  aesthetics = "color",
  ...
)

scale_color_oi(
  palette = "full",
  reverse = FALSE,
  order = 1:9,
  aesthetics = "color",
  ...
)

scale_fill_oi(
  palette = "full",
  reverse = FALSE,
  order = 1:9,
  aesthetics = "fill",
  ...
)
```

Arguments

palette	Character name of palette. Depending on the color scale, can be one of "full", "ice", "rainbow", "complement", "contrast", "light" (for dark themes), "black_first", full_original, or black_first_original. The latter three options are especially for the Okabe-Ito color palette. The default is NULL and either "contrast" or "gradient" is used (depending on whether discrete is TRUE or FALSE), which are the two scale useful for discrete or gradient color scales, respectively.

reverse	Boolean indicating whether the palette should be reversed.
order	A vector of numbers from 1 to 9 indicating the order of colors to use (default: 1:9)
aesthetics	A vector of names of the aesthetics that this scale should be applied to (e.g., c('color', 'fill')).
...	Additional arguments to pass to colorRampPalette().

Details

The Okabe-Ito palette is included in the base R grDevices::palette.colors(). These functions make this palette easier to use with *ggplot2*.

The original Okabe-Ito palette's "yellow" color is "#F0E442". This color is very bright and often does not show up well on white backgrounds (see here) for a discussion of this issue). Accordingly, by default, this function uses a darker more "amber" color for "yellow" ("#F5C710"). This color is the "yellow" color used in base R >4.0's default color palette. The palettes "full" and "black_first" use this darker yellow color. For the original yellow color suggested by Okabe and Ito ("#F0E442"), use palettes "full_original" or "black_first_original".

The Okabe-Ito palette is only available as a discrete palette. For color-accessible continuous variables, consider the viridis palettes.

References

Okabe, M., & Ito, K. (2008). Color universal design (CUD): How to make figures and presentations that are friendly to colorblind people. https://jfly.uni-koeln.de/color/#pallet (Original work published 2002)

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_boxplot() +
  theme_modern() +
  scale_fill_okabeito()

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_violin() +
  theme_modern() +
  scale_fill_oi(palette = "black_first")

# for the original brighter yellow color suggested by Okabe and Ito
ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_violin() +
  theme_modern() +
  scale_fill_oi(palette = "full")

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_violin() +
```

```
  theme_modern() +
  scale_fill_oi(order = c(1, 5, 6, 2, 4, 3, 7))
```

`scale_color_pizza` *Pizza color palette*

Description

The palette based on authentic neapolitan pizzas. Use `scale_color_pizza_d()` for *discrete* categories and `scale_color_pizza_c()` for a *continuous* scale.

Usage

```
scale_color_pizza(
  palette = "margherita",
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_pizza_d(
  palette = "margherita",
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_pizza_c(
  palette = "margherita",
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_pizza(
  palette = "margherita",
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_pizza_c(
  palette = "margherita",
```

```
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_pizza_d(
  palette = "margherita",
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_fill_pizza(
  palette = "margherita",
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_pizza_d(
  palette = "margherita",
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_pizza_c(
  palette = "margherita",
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)
```

Arguments

palette	Pizza type. Can be "margherita" (default), "margherita crust", "diavola" or "diavola crust".
discrete	Boolean indicating whether color aesthetic is discrete or not.
reverse	Boolean indicating whether the palette should be reversed.
aesthetics	A vector of names of the aesthetics that this scale should be applied to (e.g., c('color', 'fill')).
...	Additional arguments to pass to colorRampPalette().

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_boxplot() +
  theme_modern() +
  scale_fill_pizza_d()

ggplot(iris, aes(x = Petal.Length, y = Petal.Width, color = Sepal.Length)) +
  geom_point() +
  theme_modern() +
  scale_color_pizza_c()
```

---

scale_color_see *See color palette*

Description

The See color palette. Use `scale_color_see_d()` for *discrete* categories and `scale_color_see_c()` for a *continuous* scale, or use the `discrete` argument in `scale_color_see()`.

Usage

```
scale_color_see(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_see_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_see_c(
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)
```

```
scale_colour_see(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_see_c(
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_see_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_fill_see(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_see_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_see_c(
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)
```

Arguments

palette	Character name of palette. Depending on the color scale, can be one of "full", "ice", "rainbow", "complement", "contrast", "light" (for dark themes), "black_first", full_original, or black_first_original. The latter three options are especially for the Okabe-Ito color palette. The default is NULL and either "contrast" or "gradient" is used (depending on whether discrete is TRUE or FALSE), which are the two scale useful for discrete or gradient color scales, respectively.
discrete	Boolean indicating whether color aesthetic is discrete or not.
reverse	Boolean indicating whether the palette should be reversed.
aesthetics	A vector of names of the aesthetics that this scale should be applied to (e.g., c('color', 'fill')).
...	Additional arguments to pass to colorRampPalette().

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_boxplot() +
  theme_modern() +
  scale_fill_see()

ggplot(iris, aes(x = Sepal.Length, y = Sepal.Width, colour = Species)) +
  geom_point() +
  theme_abyss() +
  scale_colour_see(palette = "light")

ggplot(iris, aes(x = Petal.Length, y = Petal.Width, color = Sepal.Length)) +
  geom_point() +
  theme_modern() +
  scale_color_see(discrete = FALSE)
```

---

scale_color_social *Social color palette*

Description

The palette based Social colors. Use scale_color_social_d for *discrete* categories and scale_color_social_c for a *continuous* scale, or use the discrete argument in scale_color_social().

Usage

```
scale_color_social(
  palette = NULL,
  discrete = TRUE,
```

```
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_social_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_color_social_c(
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_social(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_social_c(
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_colour_social_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "color",
  ...
)

scale_fill_social(
  palette = NULL,
  discrete = TRUE,
```

```
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_social_d(
  palette = NULL,
  discrete = TRUE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)

scale_fill_social_c(
  palette = NULL,
  discrete = FALSE,
  reverse = FALSE,
  aesthetics = "fill",
  ...
)
```

Arguments

palette	Character name of palette. Depending on the color scale, can be one of "full", "ice", "rainbow", "complement", "contrast", "light" (for dark themes), "black_first", full_original, or black_first_original. The latter three options are especially for the Okabe-Ito color palette. The default is NULL and either "contrast" or "gradient" is used (depending on whether discrete is TRUE or FALSE), which are the two scale useful for discrete or gradient color scales, respectively.
discrete	Boolean indicating whether color aesthetic is discrete or not.
reverse	Boolean indicating whether the palette should be reversed.
aesthetics	A vector of names of the aesthetics that this scale should be applied to (e.g., c('color', 'fill')).
...	Additional arguments to pass to colorRampPalette().

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_boxplot() +
  theme_modern() +
  scale_fill_social()

ggplot(iris, aes(x = Species, y = Sepal.Length, fill = Species)) +
  geom_violin() +
  theme_modern() +
```

```
  scale_fill_social(palette = "ice")

ggplot(iris, aes(x = Petal.Length, y = Petal.Width, color = Sepal.Length)) +
  geom_point() +
  theme_modern() +
  scale_color_social(discrete = FALSE)
```

---

see_colors *Extract See colors as hex codes*

Description

Can be used to get the hex code of specific colors from the See color palette. Use `see_colors()` to see all available colors.

Usage

```
see_colors(...)
```

Arguments

`...`	Character names of colors.

Value

A character vector with color-codes.

Examples

```
see_colors()

see_colors("indigo", "lime")
```

---

social_colors *Extract Social colors as hex codes*

Description

Can be used to get the hex code of specific colors from the Social color palette. Use `social_colors()` to see all available colors.

Usage

```
social_colors(...)
```

Arguments

`...`	Character names of colors.

Value

A character vector with color-codes.

Examples

```
social_colors()

social_colors("dark red", "teal")
```

`theme_abyss` *Abyss theme*

Description

A deep dark blue theme for ggplot.

Usage

```
theme_abyss(
  base_size = 11,
  base_family = "",
  plot.title.size = 1.35 * base_size,
  plot.title.face = "plain",
  plot.title.space = 1.8 * base_size,
  plot.title.position = "plot",
  legend.position = "right",
  axis.title.space = 1.8 * base_size,
  axis.text.space = base_size,
  legend.title.size = 1.2 * base_size,
  legend.text.size = 1.1 * base_size,
  axis.title.size = 1.2 * base_size,
  axis.title.face = "plain",
  axis.text.size = 1.1 * base_size,
  axis.text.angle = NULL,
  tags.size = 1.35 * base_size,
  tags.face = "bold",
  ...
)
```

Arguments

`base_size`	base font size, given in pts.
`base_family`	base font family
`plot.title.size`	Title size in pts. Can be "none".
`plot.title.face`	Title font face ("plain", "italic", "bold", "bold.italic").

`plot.title.space`
: Title spacing.

`plot.title.position`
: Alignment of the plot title/subtitle and caption. The setting for plot.title.position applies to both the title and the subtitle. A value of "panel" (the default) means that titles and/or caption are aligned to the plot panels. A value of "plot" means that titles and/or caption are aligned to the entire plot (minus any space for margins and plot tag).

`legend.position`
: the default position of legends ("none", "left", "right", "bottom", "top", "inside")

`axis.title.space`
: Axis title spacing.

`axis.text.space`
: Axis text spacing, i.e. spacing between axis and the related labels.

`legend.title.size`
: Legend elements text size in pts.

`legend.text.size`
: Legend elements text size in pts. Can be "none".

`axis.title.size`
: Axis title text size in pts.

`axis.title.face`
: Axis font face ("plain", "italic", "bold", "bold.italic").

`axis.text.size` Axis text size in pts.

`axis.text.angle`
: Rotate the x axis labels.

`tags.size` Tags text size in pts.

`tags.face` Tags font face ("plain", "italic", "bold", "bold.italic").

`...` Further arguments passed to `ggplot2::theme()`.

Note

Base elements like plot borders, titles etc. are scaling with `base_size`, i.e. when `base_size` is increased, all other relevant elements are increased in proportion to the base size, to ensure proper scaling of the plot. Set arguments for the related elements explicitly to define custom sizes.

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Sepal.Width, y = Sepal.Length)) +
  geom_point(color = "white") +
  theme_abyss()
```

`theme_azurelight` *Azurelight theme*

Description

A light-blue, clear theme for ggplot with reduced usage of panel grids.

Usage

```
theme_azurelight(
  base_size = 11,
  base_family = "",
  plot.title.size = 1.35 * base_size,
  plot.title.face = "plain",
  plot.title.space = 1.8 * base_size,
  plot.title.position = "plot",
  legend.position = "right",
  axis.title.space = 1.8 * base_size,
  axis.text.space = base_size,
  legend.title.size = 1.2 * base_size,
  legend.text.size = 1.1 * base_size,
  axis.title.size = 1.2 * base_size,
  axis.title.face = "plain",
  axis.text.size = 1.1 * base_size,
  axis.text.angle = NULL,
  tags.size = 1.35 * base_size,
  tags.face = "bold",
  ...
)
```

Arguments

`base_size`	base font size, given in pts.
`base_family`	base font family
`plot.title.size`	Title size in pts. Can be "none".
`plot.title.face`	Title font face ("plain", "italic", "bold", "bold.italic").
`plot.title.space`	Title spacing.
`plot.title.position`	Alignment of the plot title/subtitle and caption. The setting for plot.title.position applies to both the title and the subtitle. A value of "panel" (the default) means that titles and/or caption are aligned to the plot panels. A value of "plot" means that titles and/or caption are aligned to the entire plot (minus any space for margins and plot tag).

`legend.position`
: the default position of legends ("none", "left", "right", "bottom", "top", "inside")

`axis.title.space`
: Axis title spacing.

`axis.text.space`
: Axis text spacing, i.e. spacing between axis and the related labels.

`legend.title.size`
: Legend elements text size in pts.

`legend.text.size`
: Legend elements text size in pts. Can be "none".

`axis.title.size`
: Axis title text size in pts.

`axis.title.face`
: Axis font face ("plain", "italic", "bold", "bold.italic").

`axis.text.size` Axis text size in pts.

`axis.text.angle`
: Rotate the x axis labels.

`tags.size` Tags text size in pts.

`tags.face` Tags font face ("plain", "italic", "bold", "bold.italic").

`...` Further arguments passed to `ggplot2::theme()`.

Note

Base elements like plot borders, titles etc. are scaling with `base_size`, i.e. when `base_size` is increased, all other relevant elements are increased in proportion to the base size, to ensure proper scaling of the plot. Set arguments for the related elements explicitly to define custom sizes.

Examples

```
library(ggplot2)
library(see)

data(iris)

ggplot(iris, aes(Sepal.Length, Sepal.Width, colour = Species)) +
  geom_point2(size = 2.5) +
  scale_color_social() +
  theme_azurelight()
```

`theme_blackboard` *Blackboard dark theme*

Description

A modern, sleek and dark theme for ggplot.

Usage

```
theme_blackboard(
  base_size = 11,
  base_family = "",
  plot.title.size = 1.35 * base_size,
  plot.title.face = "plain",
  plot.title.space = 1.8 * base_size,
  plot.title.position = "plot",
  legend.position = "right",
  axis.title.space = 1.8 * base_size,
  axis.text.space = base_size,
  legend.title.size = 1.2 * base_size,
  legend.text.size = 1.1 * base_size,
  axis.title.size = 1.2 * base_size,
  axis.title.face = "plain",
  axis.text.size = 1.1 * base_size,
  axis.text.angle = NULL,
  tags.size = 1.35 * base_size,
  tags.face = "bold",
  ...
)
```

Arguments

`base_size`	base font size, given in pts.
`base_family`	base font family
`plot.title.size`	Title size in pts. Can be "none".
`plot.title.face`	Title font face ("plain", "italic", "bold", "bold.italic").
`plot.title.space`	Title spacing.
`plot.title.position`	Alignment of the plot title/subtitle and caption. The setting for plot.title.position applies to both the title and the subtitle. A value of "panel" (the default) means that titles and/or caption are aligned to the plot panels. A value of "plot" means that titles and/or caption are aligned to the entire plot (minus any space for margins and plot tag).

legend.position
: the default position of legends ("none", "left", "right", "bottom", "top", "inside")

axis.title.space
: Axis title spacing.

axis.text.space
: Axis text spacing, i.e. spacing between axis and the related labels.

legend.title.size
: Legend elements text size in pts.

legend.text.size
: Legend elements text size in pts. Can be "none".

axis.title.size
: Axis title text size in pts.

axis.title.face
: Axis font face ("plain", "italic", "bold", "bold.italic").

axis.text.size
: Axis text size in pts.

axis.text.angle
: Rotate the x axis labels.

tags.size
: Tags text size in pts.

tags.face
: Tags font face ("plain", "italic", "bold", "bold.italic").

...
: Further arguments passed to `ggplot2::theme()`.

Note

Base elements like plot borders, titles etc. are scaling with `base_size`, i.e. when `base_size` is increased, all other relevant elements are increased in proportion to the base size, to ensure proper scaling of the plot. Set arguments for the related elements explicitly to define custom sizes.

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Sepal.Width, y = Sepal.Length)) +
  geom_point(color = see_colors("lime")) +
  theme_blackboard()
```

---

theme_lucid *Lucid theme*

Description

A light, clear theme for ggplot.

Usage

```
theme_lucid(
  base_size = 11,
  base_family = "",
  plot.title.size = 1.1 * base_size,
  plot.title.face = "plain",
  plot.title.space = 1.35 * base_size,
  plot.title.position = "plot",
  legend.position = "right",
  axis.title.space = 0.9 * base_size,
  axis.text.space = base_size,
  legend.title.size = base_size,
  legend.text.size = 0.9 * base_size,
  axis.title.size = base_size,
  axis.title.face = "plain",
  axis.text.size = 0.9 * base_size,
  axis.text.angle = NULL,
  tags.size = base_size,
  tags.face = "plain",
  ...
)
```

Arguments

base_size	base font size, given in pts.
base_family	base font family
plot.title.size	Title size in pts. Can be "none".
plot.title.face	Title font face ("plain", "italic", "bold", "bold.italic").
plot.title.space	Title spacing.
plot.title.position	Alignment of the plot title/subtitle and caption. The setting for plot.title.position applies to both the title and the subtitle. A value of "panel" (the default) means that titles and/or caption are aligned to the plot panels. A value of "plot" means that titles and/or caption are aligned to the entire plot (minus any space for margins and plot tag).
legend.position	the default position of legends ("none", "left", "right", "bottom", "top", "inside")
axis.title.space	Axis title spacing.
axis.text.space	Axis text spacing, i.e. spacing between axis and the related labels.
legend.title.size	Legend elements text size in pts.

`legend.text.size`
: Legend elements text size in pts. Can be "none".

`axis.title.size`
: Axis title text size in pts.

`axis.title.face`
: Axis font face ("plain", "italic", "bold", "bold.italic").

`axis.text.size`
: Axis text size in pts.

`axis.text.angle`
: Rotate the x axis labels.

`tags.size`
: Tags text size in pts.

`tags.face`
: Tags font face ("plain", "italic", "bold", "bold.italic").

`...`
: Further arguments passed to `ggplot2::theme()`.

Note

Base elements like plot borders, titles etc. are scaling with `base_size`, i.e. when `base_size` is increased, all other relevant elements are increased in proportion to the base size, to ensure proper scaling of the plot. Set arguments for the related elements explicitly to define custom sizes.

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Sepal.Width, y = Sepal.Length)) +
  geom_point() +
  scale_color_metro() +
  theme_lucid()
```

---

theme_modern *The easystats' minimal theme*

Description

A modern, sleek and elegant theme for ggplot.

Usage

```
theme_modern(
  base_size = 11,
  base_family = "",
  plot.title.size = 1.35 * base_size,
  plot.title.face = "plain",
  plot.title.space = 1.8 * base_size,
  plot.title.position = "plot",
  legend.position = "right",
```

```
  axis.title.space = 1.8 * base_size,
  axis.text.space = base_size,
  legend.title.size = 1.2 * base_size,
  legend.text.size = 1.1 * base_size,
  axis.title.size = 1.2 * base_size,
  axis.title.face = "plain",
  axis.text.size = 1.1 * base_size,
  axis.text.angle = NULL,
  tags.size = 1.35 * base_size,
  tags.face = "bold",
  show.ticks = FALSE,
  ...
)
```

Arguments

base_size	base font size, given in pts.
base_family	base font family
plot.title.size	Title size in pts. Can be "none".
plot.title.face	Title font face ("plain", "italic", "bold", "bold.italic").
plot.title.space	Title spacing.
plot.title.position	Alignment of the plot title/subtitle and caption. The setting for plot.title.position applies to both the title and the subtitle. A value of "panel" (the default) means that titles and/or caption are aligned to the plot panels. A value of "plot" means that titles and/or caption are aligned to the entire plot (minus any space for margins and plot tag).
legend.position	the default position of legends ("none", "left", "right", "bottom", "top", "inside")
axis.title.space	Axis title spacing.
axis.text.space	Axis text spacing, i.e. spacing between axis and the related labels.
legend.title.size	Legend elements text size in pts.
legend.text.size	Legend elements text size in pts. Can be "none".
axis.title.size	Axis title text size in pts.
axis.title.face	Axis font face ("plain", "italic", "bold", "bold.italic").
axis.text.size	Axis text size in pts.

axis.text.angle	Rotate the x axis labels.
tags.size	Tags text size in pts.
tags.face	Tags font face ("plain", "italic", "bold", "bold.italic").
show.ticks	Logical, if TRUE, adds inner tick marks to the plot and slightly increases the padding between axis and the related labels.
...	Further arguments passed to ggplot2::theme().

Note

Base elements like plot borders, titles etc. are scaling with base_size, i.e. when base_size is increased, all other relevant elements are increased in proportion to the base size, to ensure proper scaling of the plot. Set arguments for the related elements explicitly to define custom sizes.

Examples

```
library(ggplot2)
library(see)

ggplot(iris, aes(x = Sepal.Width, y = Sepal.Length, color = Species)) +
  geom_point() +
  scale_color_see() +
  theme_modern()

# for a slightly better orientation, tick marks can be added
ggplot(iris, aes(x = Sepal.Width, y = Sepal.Length, color = Species)) +
  geom_point() +
  scale_color_see() +
  theme_modern(show.ticks = TRUE)
```

---

theme_radar *Themes for radar plots*

Description

theme_radar() is a light, clear theme for ggplot radar-plots, while theme_radar_dark() is a dark variant of theme_radar().

Usage

```
theme_radar(
  base_size = 11,
  base_family = "",
  plot.title.size = 12,
  plot.title.face = "plain",
  plot.title.space = 15,
  plot.title.position = "plot",
```

```
  legend.position = "right",
  axis.title.space = 15,
  legend.title.size = 11,
  legend.text.size = 10,
  axis.title.size = 11,
  axis.title.face = "plain",
  axis.text.size = 10,
  axis.text.angle = NULL,
  tags.size = 11,
  tags.face = "plain"
)

theme_radar_dark(
  base_size = 11,
  base_family = "",
  plot.title.size = 12,
  plot.title.face = "plain",
  plot.title.space = 15,
  legend.position = "right",
  axis.title.space = 15,
  legend.title.size = 11,
  legend.text.size = 10,
  axis.title.size = 11,
  axis.title.face = "plain",
  axis.text.size = 10,
  axis.text.angle = NULL,
  tags.size = 11,
  tags.face = "plain"
)
```

Arguments

base_size	base font size, given in pts.
base_family	base font family
plot.title.size	Title size in pts. Can be "none".
plot.title.face	Title font face ("plain", "italic", "bold", "bold.italic").
plot.title.space	Title spacing.
plot.title.position	Alignment of the plot title/subtitle and caption. The setting for plot.title.position applies to both the title and the subtitle. A value of "panel" (the default) means that titles and/or caption are aligned to the plot panels. A value of "plot" means that titles and/or caption are aligned to the entire plot (minus any space for margins and plot tag).
legend.position	the default position of legends ("none", "left", "right", "bottom", "top", "inside")

`axis.title.space`
: Axis title spacing.

`legend.title.size`
: Legend elements text size in pts.

`legend.text.size`
: Legend elements text size in pts. Can be "none".

`axis.title.size`
: Axis title text size in pts.

`axis.title.face`
: Axis font face ("plain", "italic", "bold", "bold.italic").

`axis.text.size`
: Axis text size in pts.

`axis.text.angle`
: Rotate the x axis labels.

`tags.size`
: Tags text size in pts.

`tags.face`
: Tags font face ("plain", "italic", "bold", "bold.italic").

See Also

`coord_radar()`

Examples

```
library(ggplot2)

data <- datawizard::reshape_longer(
  aggregate(iris[-5], list(Species = iris$Species), mean),
  c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width")
)

ggplot(
  data,
  aes(
    x = name,
    y = value,
    color = Species,
    group = Species,
    fill = Species
  )
) +
  geom_polygon(linewidth = 1, alpha = 0.1) +
  coord_radar() +
  theme_radar()
```

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