Package 'tidyplots'

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Title Tidy Plots for Scientific Papers

Version 0.2.0

Description The goal of 'tidyplots' is to streamline the creation of publication-ready plots for scientific papers. It allows to gradually add, remove and adjust plot components using a consistent and intuitive syntax.

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Encoding UTF-8

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Imports cli, dplyr, forcats, ggbeeswarm, ggplot2 (>= 3.5.0), ggpubr, ggrastr, ggrepel, glue, Hmisc, htmltools, lifecycle, patchwork, purrr, rlang, scales, stringr, tidyr, tidyselect

Depends R (>= 2.10)

LazyData true

URL https://github.com/jbengler/tidyplots, https://jbengler.github.io/tidyplots/

BugReports https://github.com/jbengler/tidyplots/issues

Suggests knitr, rmarkdown, testthat (>= 3.0.0), vdiffr

VignetteBuilder knitr

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NeedsCompilation no

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Contents

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add *Add ggplot2 code to a tidyplot*

Description

Add ggplot2 code to a tidyplot

Usage

```
add()
```

Value

A `tidyplot` object.

Examples

```
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add(ggplot2::geom_point())
```

add_areastack_absolute *Add area stack*

Description

Add area stack

Usage

```
add_areastack_absolute(
  plot,
  linewidth = 0.25,
  alpha = 0.4,
  reverse = FALSE,
  replace_na = FALSE,
  ...
)

add_areastack_relative(
  plot,
  linewidth = 0.25,
  alpha = 0.4,
  reverse = FALSE,
  replace_na = FALSE,
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
linewidth	Thickness of the line in points (pt). Typical values range between 0.25 and 1.
alpha	A number between 0 and 1 for the opacity of an object. A value of 0 is completely transparent, 1 is completely opaque.
reverse	Whether the order should be reversed or not. Defaults to FALSE, meaning not reversed.
replace_na	Whether to replace count = NA with count = 0.
...	Arguments passed on to the geom function.

Value

A tidyplot object.

Examples

```
# for a `count` provide `x` and `color`
# `count` of the data points in each `energy_type` category
energy %>%
  tidyplot(x = year, color = energy_type) %>%
  add_areastack_absolute()

energy %>%
  tidyplot(x = year, color = energy_type) %>%
  add_areastack_relative()

# for a `sum` provide `x`, `y` and `color`
# `sum` of `power` in each `energy_type` category
energy %>%
  tidyplot(x = year, y = power, color = energy_type) %>%
  add_areastack_absolute()

energy %>%
  tidyplot(x = year, y = power, color = energy_type) %>%
  add_areastack_relative()

# Flip x and y-axis
energy %>%
  tidyplot(x = power, y = year, color = energy_type) %>%
  add_areastack_absolute(orientation = "y")

energy %>%
  tidyplot(x = power, y = year, color = energy_type) %>%
  add_areastack_relative(orientation = "y")
```

---

add_barstack_absolute *Add bar stack*

Description

Add bar stack

Usage

```
add_barstack_absolute(plot, width = 0.8, reverse = FALSE, ...)

add_barstack_relative(plot, width = 0.8, reverse = FALSE, ...)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
width	Width of the plot area. Defaults to 50.

reverse	Whether the order should be reversed or not. Defaults to FALSE, meaning not reversed.
...	Arguments passed on to the geom function.

Value

A tidyplot object.

Examples

```
# for a `count` only provide `color`
# `count` of the data points in each `energy_type` category
energy %>%
  tidyplot(color = energy_type) %>%
  add_barstack_absolute()

energy %>%
  tidyplot(color = energy_type) %>%
  add_barstack_relative()

# for a `sum` provide `color` and `y`
# `sum` of `power` in each `energy_type` category
energy %>%
  tidyplot(y = power, color = energy_type) %>%
  add_barstack_absolute()

energy %>%
  tidyplot(y = power, color = energy_type) %>%
  add_barstack_relative()

# Include variable on second axis
energy %>%
  tidyplot(x = year, y = power, color = energy_type) %>%
  add_barstack_absolute()

energy %>%
  tidyplot(x = year, y = power, color = energy_type) %>%
  add_barstack_relative()

# Flip x and y-axis
energy %>%
  tidyplot(x = power, y = year, color = energy_type) %>%
  add_barstack_absolute(orientation = "y")

energy %>%
  tidyplot(x = power, y = year, color = energy_type) %>%
  add_barstack_relative(orientation = "y")
```

add_boxplot *Add boxplot*

Description

Add boxplot

Usage

```
add_boxplot(
  plot,
  dodge_width = NULL,
  alpha = 0.3,
  saturation = 1,
  show_whiskers = TRUE,
  show_outliers = TRUE,
  box_width = 0.6,
  whiskers_width = 0.8,
  outlier.size = 0.5,
  coef = 1.5,
  outlier.shape = 19,
  outlier.alpha = 1,
  linewidth = 0.25,
  preserve = "total",
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
dodge_width	For adjusting the distance between grouped objects. Defaults to 0.8 for plots with at least one discrete axis and 0 for plots with two continuous axes.
alpha	A number between 0 and 1 for the opacity of an object. A value of 0 is completely transparent, 1 is completely opaque.
saturation	A number between 0 and 1 for the color saturation of an object. A value of 0 is completely desaturated (white), 1 is the original color.
show_whiskers	Whether to show boxplot whiskers. Defaults to TRUE.
show_outliers	Whether to show outliers. Defaults to TRUE.
box_width	Width of the boxplot. Defaults to 0.6.
whiskers_width	Width of the whiskers. Defaults to 0.8.
outlier.size	Size of the outliers. Defaults to 0.5.
coef	Length of the whiskers as multiple of IQR. Defaults to 1.5.
outlier.shape	Shape of the outliers. Defaults to 19.
outlier.alpha	Opacity of the outliers. Defaults to 1.

linewidth	Thickness of the line in points (pt). Typical values range between 0.25 and 1.
preserve	Should dodging preserve the "total" width of all elements at a position, or the width of a "single" element?
...	Arguments passed on to the geom function.

Value

A tidyplot object.

Examples

```
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_boxplot()

# Changing arguments:
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_boxplot(show_whiskers = FALSE)

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_boxplot(show_outliers = FALSE)

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_boxplot(box_width = 0.2)

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_boxplot(whiskers_width = 0.2)
```

---

add_count_bar *Add count*

Description

Add count

Usage

```
add_count_bar(
  plot,
  dodge_width = NULL,
  width = 0.6,
  saturation = 1,
  preserve = "total",
  ...
```

```
)

add_count_dash(
  plot,
  dodge_width = NULL,
  width = 0.6,
  linewidth = 0.25,
  preserve = "total",
  ...
)

add_count_dot(plot, dodge_width = NULL, size = 2, preserve = "total", ...)

add_count_value(
  plot,
  dodge_width = NULL,
  accuracy = 0.1,
  scale_cut = NULL,
  fontsize = 7,
  extra_padding = 0.15,
  vjust = NULL,
  hjust = NULL,
  preserve = "total",
  ...
)

add_count_line(
  plot,
  group,
  dodge_width = NULL,
  linewidth = 0.25,
  preserve = "total",
  ...
)

add_count_area(
  plot,
  group,
  dodge_width = NULL,
  linewidth = 0.25,
  preserve = "total",
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
dodge_width	For adjusting the distance between grouped objects. Defaults to 0.8 for plots

	with at least one discrete axis and `0` for plots with two continuous axes.
`width`	Width of the plot area. Defaults to `50`.
`saturation`	A `number` between `0` and `1` for the color saturation of an object. A value of `0` is completely desaturated (white), `1` is the original color.
`preserve`	Should dodging preserve the `"total"` width of all elements at a position, or the width of a `"single"` element?
`...`	Arguments passed on to the `geom` function.
`linewidth`	Thickness of the line in points (pt). Typical values range between `0.25` and `1`.
`size`	A `number` representing the size of the plot symbol. Typical values range between `1` and `3`.
`accuracy`	A number to round to. Use (e.g.) `0.01` to show 2 decimal places of precision. If `NULL`, the default, uses a heuristic that should ensure breaks have the minimum number of digits needed to show the difference between adjacent values. Applied to rescaled data.
`scale_cut`	Scale cut function to be applied. See `scales::cut_short_scale()` and friends.
`fontsize`	Font size in points. Defaults to `7`.
`extra_padding`	Extra padding to create space for the value label.
`vjust`	Vertical position adjustment of the value label.
`hjust`	Horizontal position adjustment of the value label.
`group`	Variable in the dataset to be used for grouping.

Value

A `tidyplot` object.

Examples

```
dinosaurs %>%
  tidyplot(x = time_lived, color = time_lived) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_count_bar()

dinosaurs %>%
  tidyplot(x = time_lived, color = time_lived) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_count_dash()

dinosaurs %>%
  tidyplot(x = time_lived, color = time_lived) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_count_dot()

dinosaurs %>%
  tidyplot(x = time_lived, color = time_lived) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_count_value()
```

```
dinosaurs %>%
  tidyplot(x = time_lived) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_count_line()

dinosaurs %>%
  tidyplot(x = time_lived) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_count_area()

# Combination
dinosaurs %>%
  tidyplot(x = time_lived) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_count_bar(alpha = 0.4) %>%
  add_count_dash() %>%
  add_count_dot() %>%
  add_count_value() %>%
  add_count_line()

# Changing arguments: alpha
# Makes objects transparent
dinosaurs %>%
  tidyplot(x = time_lived, color = time_lived) %>%
  theme_minimal_y() %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_count_bar(alpha = 0.4)

# Changing arguments: saturation
# Reduces fill color saturation without making the object transparent
dinosaurs %>%
  tidyplot(x = time_lived, color = time_lived) %>%
  theme_minimal_y() %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_count_bar(saturation = 0.3)

# Changing arguments: accuracy
dinosaurs %>%
  tidyplot(x = time_lived, color = time_lived) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_count_value(accuracy = 1)

# Changing arguments: fontsize
dinosaurs %>%
  tidyplot(x = time_lived, color = time_lived) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_count_value(fontsize = 10)

# Changing arguments: color
dinosaurs %>%
  tidyplot(x = time_lived, color = time_lived) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
```

```
  add_count_value(color = "black")
```

`add_curve_fit` *Add curve fit*

Description

Add curve fit

Usage

```
add_curve_fit(
  plot,
  dodge_width = NULL,
  method = "loess",
  linewidth = 0.25,
  alpha = 0.4,
  preserve = "total",
  ...
)
```

Arguments

`plot`	A `tidyplot` generated with the function `tidyplot()`.
`dodge_width`	For adjusting the distance between grouped objects. Defaults to `0.8` for plots with at least one discrete axis and `0` for plots with two continuous axes.
`method`	Smoothing method (function) to use, accepts either `NULL` or a character vector, e.g. `"lm"`, `"glm"`, `"gam"`, `"loess"` or a function, e.g. `MASS::rlm` or `mgcv::gam`, `stats::lm`, or `stats::loess`. `"auto"` is also accepted for backwards compatibility. It is equivalent to `NULL`. For `method = NULL` the smoothing method is chosen based on the size of the largest group (across all panels). `stats::loess()` is used for less than 1,000 observations; otherwise `mgcv::gam()` is used with `formula = y ~ s(x, bs = "cs")` with `method = "REML"`. Somewhat anecdotally, `loess` gives a better appearance, but is $O(N^2)$ in memory, so does not work for larger datasets. If you have fewer than 1,000 observations but want to use the same `gam()` model that `method = NULL` would use, then set `method = "gam", formula = y ~ s(x, bs = "cs")`.
`linewidth`	Thickness of the line in points (pt). Typical values range between `0.25` and `1`.
`alpha`	A `number` between `0` and `1` for the opacity of an object. A value of `0` is completely transparent, `1` is completely opaque.
`preserve`	Should dodging preserve the `"total"` width of all elements at a position, or the width of a `"single"` element?
`...`	Arguments passed on to `ggplot2::geom_smooth()`.

Value

A tidyplot object.

Examples

```
time_course %>%
  tidyplot(x = day, y = score, color = treatment) %>%
  add_curve_fit()

# Changing arguments
time_course %>%
  tidyplot(x = day, y = score, color = treatment) %>%
  add_curve_fit(linewidth = 1)

time_course %>%
  tidyplot(x = day, y = score, color = treatment) %>%
  add_curve_fit(alpha = 0.8)

# Remove confidence interval
time_course %>%
  tidyplot(x = day, y = score, color = treatment) %>%
  add_curve_fit(se = FALSE)
```

---

add_data_labels *Add data labels*

Description

Add data labels

Usage

```
add_data_labels(
  plot,
  label,
  data = all_rows(),
  fontsize = 7,
  background = FALSE,
  background_color = "#FFFFFF",
  background_alpha = 0.6,
  label_position = c("below", "above", "left", "right", "center"),
  ...
)

add_data_labels_repel(
  plot,
  label,
```

```
  data = all_rows(),
  fontsize = 7,
  segment.size = 0.2,
  box.padding = 0.2,
  max.overlaps = Inf,
  background = FALSE,
  background_color = "#FFFFFF",
  background_alpha = 0.6,
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
label	Variable in the dataset to be used for the text label.
data	The data to be displayed in this layer. There are three options: • If all_rows() (the default) the complete dataset is displayed. • A function to subset the plot data. See filter_rows() and friends. • A data.frame to override the plot data.
fontsize	Font size in points. Defaults to 7.
background	Whether to include semitransparent background box behind the labels to improve legibility. Defaults to FALSE.
background_color	Hex color of the background box. Defaults to "#FFFFFF" for white.
background_alpha	Opacity of the background box. Defaults to 0.6.
label_position	Position of the label in relation to the data point. Can be one of c("below", "above", "left", "right", "center").
...	Arguments passed on to the geom function.
segment.size	Thickness of the line connecting the label with the data point. Defaults to 0.2.
box.padding	Amount of padding around bounding box, as unit or number. Defaults to 0.25. (Default unit is lines, but other units can be specified by passing unit(x, "units")).
max.overlaps	Exclude text labels when they overlap too many other things. For each text label, we count how many other text labels or other data points it overlaps, and exclude the text label if it has too many overlaps. Defaults to 10.

Details

- add_data_labels_repel() uses ggrepel::geom_text_repel(). Check there and in ggrepel examples for additional arguments.
- add_data_labels() and add_data_labels_repel() support data subsetting. See Advanced plotting.

Value

A tidyplot object.

Examples

```
# Create plot and increase padding to make more space for labels
p <-
  animals %>%
  dplyr::slice_head(n = 5) %>%
  tidyplot(x = weight, y = speed) %>%
  theme_ggplot2() %>%
  add_data_points() %>%
  adjust_padding(all = 0.3)

# Default label position is `below` the data point
p %>% add_data_labels(label = animal)

# Alternative label positions
p %>% add_data_labels(label = animal, label_position = "above")

p %>% add_data_labels(label = animal, label_position = "right")

p %>% add_data_labels(label = animal, label_position = "left")

# Include white background box
p %>% add_data_labels(label = animal, background = TRUE)

p %>% add_data_labels(label = animal, background = TRUE,
  background_color = "pink")

# Black labels
p %>% add_data_labels(label = animal, color = "black")

# Use repelling data labels
p %>% add_data_labels_repel(label = animal, color = "black")

p %>% add_data_labels_repel(label = animal, color = "black",
  background = TRUE)

p %>% add_data_labels_repel(label = animal, color = "black",
  background = TRUE, min.segment.length = 0)
```

`add_data_points` *Add data points*

Description

Add data points

Usage

```
add_data_points(
```

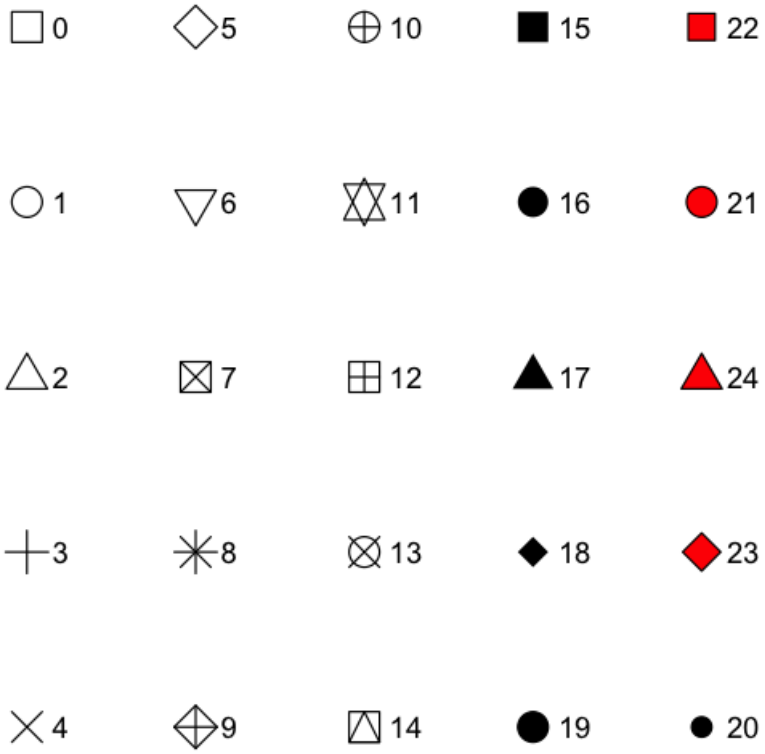
```
  plot,
  data = all_rows(),
  shape = 19,
  size = 1,
  white_border = FALSE,
  dodge_width = NULL,
  preserve = "total",
  rasterize = FALSE,
  rasterize_dpi = 300,
  ...
)

add_data_points_jitter(
  plot,
  data = all_rows(),
  shape = 19,
  size = 1,
  white_border = FALSE,
  dodge_width = NULL,
  jitter_width = 0.2,
  jitter_height = 0,
  preserve = "total",
  rasterize = FALSE,
  rasterize_dpi = 300,
  ...
)

add_data_points_beeswarm(
  plot,
  data = all_rows(),
  shape = 19,
  size = 1,
  white_border = FALSE,
  cex = 3,
  corral = "wrap",
  corral.width = 0.5,
  dodge_width = NULL,
  preserve = "total",
  rasterize = FALSE,
  rasterize_dpi = 300,
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
data	The data to be displayed in this layer. There are three options: • If all_rows() (the default) the complete dataset is displayed.

- A `function` to subset the plot data. See `filter_rows()` and friends.
- A `data.frame` to override the plot data.

`shape` An `integer` between `0` and `24`, representing the shape of the plot symbol.



`size` A `number` representing the size of the plot symbol. Typical values range between `1` and `3`.

`white_border` Whether to include a white border around data points. Defaults to `FALSE`.

`dodge_width` For adjusting the distance between grouped objects. Defaults to `0.8` for plots with at least one discrete axis and `0` for plots with two continuous axes.

`preserve` Should dodging preserve the `"total"` width of all elements at a position, or the width of a `"single"` element?

`rasterize` If `FALSE` (the default) the layer will be constructed of vector shapes. If `TRUE` the layer will be rasterized to a pixel image. This can be useful when plotting many individual objects (1,000 or more) compromises the performance of the generated PDF file.

`rasterize_dpi` The resolution in dots per inch (dpi) used for rastering the layer if `rasterize` is `TRUE`. The default is `300` dpi.

`...` Arguments passed on to the `geom` function.

`jitter_width` Amount of random noise to be added to the horizontal position of the of the data points. This can be useful to deal with overplotting. Typical values range between `0` and `1`.

jitter_height	Amount of random noise to be added to the vertical position of the of the data points. This can be useful to deal with overplotting. Typical values range between 0 and 1.
cex	Scaling for adjusting point spacing (see beeswarm::swarmx()). Values between 1 (default) and 3 tend to work best.
corral	string. Method used to adjust points that would be placed to wide horizontally, default is "none". See details below.
corral.width	numeric. Width of the corral, default is 0.9.

Details

- add_data_points_beeswarm() is based on ggbeeswarm::geom_beeswarm(). Check there for additional arguments.
- add_data_points() and friends support rasterization. See examples and Advanced plotting.
- add_data_points() and friends support data subsetting. See examples and Advanced plotting.

Value

A tidyplot object.

Examples

```
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_jitter()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm()

# Changing arguments
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_jitter(jitter_width = 1)

animals %>%
  tidyplot(x = weight, y = size) %>%
  add_data_points(white_border = TRUE)

animals %>%
  tidyplot(x = weight, y = size) %>%
  add_data_points(alpha = 0.4)

# Rasterization
animals %>%
```

```
  tidyplot(x = weight, y = size) %>%
  add_data_points(rasterize = TRUE, rasterize_dpi = 50)

# Data subsetting
animals %>%
  tidyplot(x = weight, y = size) %>%
  add_data_points() %>%
  add_data_points(data = filter_rows(size > 300), color = "red")
```

`add_heatmap` *Add heatmap*

Description

Add heatmap

Usage

```
add_heatmap(
  plot,
  scale = c("none", "row", "column"),
  rotate_labels = 90,
  rasterize = FALSE,
  rasterize_dpi = 300,
  ...
)
```

Arguments

`plot`	A `tidyplot` generated with the function `tidyplot()`.
`scale`	Whether to compute row z scores for `"row"` or `"column"`. Defaults to `"none"`.
`rotate_labels`	Degree to rotate the x-axis labels. Defaults to `90`.
`rasterize`	If `FALSE` (the default) the layer will be constructed of vector shapes. If `TRUE` the layer will be rasterized to a pixel image. This can be useful when plotting many individual objects (1,000 or more) compromises the performance of the generated PDF file.
`rasterize_dpi`	The resolution in dots per inch (dpi) used for rastering the layer if `rasterize` is `TRUE`. The default is `300` dpi.
`...`	Arguments passed on to the `geom` function.

Details

- `add_heatmap()` supports rasterization. See examples and Advanced plotting.

Value

A `tidyplot` object.

Examples

```
climate %>%
  tidyplot(x = month, y = year, color = max_temperature) %>%
  add_heatmap()

# Calculate row-wise z score
climate %>%
  tidyplot(x = month, y = year, color = max_temperature) %>%
  add_heatmap(scale = "row")

# Calculate column-wise z score
climate %>%
  tidyplot(x = month, y = year, color = max_temperature) %>%
  add_heatmap(scale = "column")

# Rasterize heatmap
climate %>%
  tidyplot(x = month, y = year, color = max_temperature) %>%
  add_heatmap(rasterize = TRUE, rasterize_dpi = 20)
```

---

add_histogram *Add histogram*

Description

Add histogram

Usage

```
add_histogram(plot, binwidth = NULL, bins = NULL, ...)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
binwidth	The width of the bins. Can be specified as a numeric value or as a function that calculates width from unscaled x. Here, "unscaled x" refers to the original x values in the data, before application of any scale transformation. When specifying a function along with a grouping structure, the function will be called once per group. The default is to use the number of bins in bins, covering the range of the data. You should always override this value, exploring multiple widths to find the best to illustrate the stories in your data. The bin width of a date variable is the number of days in each time; the bin width of a time variable is the number of seconds.
bins	Number of bins. Overridden by binwidth. Defaults to 30.
...	Arguments passed on to the geom function.

Value

A tidyplot object.

Examples

```
energy %>%
  tidyplot(x = power) %>%
  add_histogram()

energy %>%
  tidyplot(x = power, color = energy_type) %>%
  add_histogram()
```

---

add_line *Add line or area*

Description

add_line() and add_area() connect individual data points, which is rarely needed. In most cases, you are probably looking for add_sum_line(), add_mean_line(), add_sum_area() or add_mean_area().

Usage

```
add_line(
  plot,
  group,
  dodge_width = NULL,
  linewidth = 0.25,
  preserve = "total",
  ...
)

add_area(
  plot,
  group,
  dodge_width = NULL,
  linewidth = 0.25,
  alpha = 0.4,
  preserve = "total",
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
group	Variable in the dataset to be used for grouping.
dodge_width	For adjusting the distance between grouped objects. Defaults to 0.8 for plots with at least one discrete axis and 0 for plots with two continuous axes.
linewidth	Thickness of the line in points (pt). Typical values range between 0.25 and 1.
preserve	Should dodging preserve the "total" width of all elements at a position, or the width of a "single" element?
...	Arguments passed on to the geom function.
alpha	A number between 0 and 1 for the opacity of an object. A value of 0 is completely transparent, 1 is completely opaque.

Value

A tidyplot object.

Examples

```
# Paired data points
study %>%
  tidyplot(x = treatment, y = score, color = group) %>%
  reorder_x_axis_labels("A", "C", "B", "D") %>%
  add_data_points() %>%
  add_line(group = participant, color = "grey")

study %>%
  tidyplot(x = treatment, y = score) %>%
  reorder_x_axis_labels("A", "C", "B", "D") %>%
  add_data_points() %>%
  add_area(group = participant)
```

---

add_mean_bar *Add mean*

Description

Add mean

Usage

```
add_mean_bar(
  plot,
  dodge_width = NULL,
  width = 0.6,
  saturation = 1,
```

```
  preserve = "total",
  ...
)

add_mean_dash(
  plot,
  dodge_width = NULL,
  width = 0.6,
  linewidth = 0.25,
  preserve = "total",
  ...
)

add_mean_dot(plot, dodge_width = NULL, size = 2, preserve = "total", ...)

add_mean_value(
  plot,
  dodge_width = NULL,
  accuracy = 0.1,
  scale_cut = NULL,
  fontsize = 7,
  extra_padding = 0.15,
  vjust = NULL,
  hjust = NULL,
  preserve = "total",
  ...
)

add_mean_line(
  plot,
  group,
  dodge_width = NULL,
  linewidth = 0.25,
  preserve = "total",
  ...
)

add_mean_area(
  plot,
  group,
  dodge_width = NULL,
  linewidth = 0.25,
  preserve = "total",
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().

dodge_width	For adjusting the distance between grouped objects. Defaults to 0.8 for plots with at least one discrete axis and 0 for plots with two continuous axes.
width	Width of the plot area. Defaults to 50.
saturation	A number between 0 and 1 for the color saturation of an object. A value of 0 is completely desaturated (white), 1 is the original color.
preserve	Should dodging preserve the "total" width of all elements at a position, or the width of a "single" element?
...	Arguments passed on to the geom function.
linewidth	Thickness of the line in points (pt). Typical values range between 0.25 and 1.
size	A number representing the size of the plot symbol. Typical values range between 1 and 3.
accuracy	A number to round to. Use (e.g.) 0.01 to show 2 decimal places of precision. If NULL, the default, uses a heuristic that should ensure breaks have the minimum number of digits needed to show the difference between adjacent values. Applied to rescaled data.
scale_cut	Scale cut function to be applied. See scales::cut_short_scale() and friends.
fontsize	Font size in points. Defaults to 7.
extra_padding	Extra padding to create space for the value label.
vjust	Vertical position adjustment of the value label.
hjust	Horizontal position adjustment of the value label.
group	Variable in the dataset to be used for grouping.

Value

A tidyplot object.

Examples

```
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_dash()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_dot()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_value()

study %>%
  tidyplot(x = treatment, y = score) %>%
```

```
  add_mean_line()

study %>%
  tidyplot(x = treatment, y = score) %>%
  add_mean_area()

# Combination
study %>%
  tidyplot(x = treatment, y = score) %>%
  add_mean_bar(alpha = 0.4) %>%
  add_mean_dash() %>%
  add_mean_dot() %>%
  add_mean_value() %>%
  add_mean_line()

# Changing arguments: alpha
# Makes objects transparent
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  theme_minimal_y() %>%
  add_mean_bar(alpha = 0.4)

# Changing arguments: saturation
# Reduces fill color saturation without making the object transparent
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  theme_minimal_y() %>%
  add_mean_bar(saturation = 0.3)

# Changing arguments: accuracy
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_value(accuracy = 0.01)

# Changing arguments: fontsize
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_value(fontsize = 10)

# Changing arguments: color
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_value(color = "black")
```

`add_median_bar` *Add median*

Description

Add median

Usage

```
add_median_bar(
  plot,
  dodge_width = NULL,
  width = 0.6,
  saturation = 1,
  preserve = "total",
  ...
)

add_median_dash(
  plot,
  dodge_width = NULL,
  width = 0.6,
  linewidth = 0.25,
  preserve = "total",
  ...
)

add_median_dot(plot, dodge_width = NULL, size = 2, preserve = "total", ...)

add_median_value(
  plot,
  dodge_width = NULL,
  accuracy = 0.1,
  scale_cut = NULL,
  fontsize = 7,
  extra_padding = 0.15,
  vjust = NULL,
  hjust = NULL,
  preserve = "total",
  ...
)

add_median_line(
  plot,
  group,
  dodge_width = NULL,
  linewidth = 0.25,
  preserve = "total",
  ...
)

add_median_area(
  plot,
  group,
  dodge_width = NULL,
  linewidth = 0.25,
```

```
  preserve = "total",
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
dodge_width	For adjusting the distance between grouped objects. Defaults to 0.8 for plots with at least one discrete axis and 0 for plots with two continuous axes.
width	Width of the plot area. Defaults to 50.
saturation	A number between 0 and 1 for the color saturation of an object. A value of 0 is completely desaturated (white), 1 is the original color.
preserve	Should dodging preserve the "total" width of all elements at a position, or the width of a "single" element?
...	Arguments passed on to the geom function.
linewidth	Thickness of the line in points (pt). Typical values range between 0.25 and 1.
size	A number representing the size of the plot symbol. Typical values range between 1 and 3.
accuracy	A number to round to. Use (e.g.) 0.01 to show 2 decimal places of precision. If NULL, the default, uses a heuristic that should ensure breaks have the minimum number of digits needed to show the difference between adjacent values. Applied to rescaled data.
scale_cut	Scale cut function to be applied. See scales::cut_short_scale() and friends.
fontsize	Font size in points. Defaults to 7.
extra_padding	Extra padding to create space for the value label.
vjust	Vertical position adjustment of the value label.
hjust	Horizontal position adjustment of the value label.
group	Variable in the dataset to be used for grouping.

Value

A tidyplot object.

Examples

```
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_median_bar()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_median_dash()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_median_dot()
```

```
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_median_value()

study %>%
  tidyplot(x = treatment, y = score) %>%
  add_median_line()

study %>%
  tidyplot(x = treatment, y = score) %>%
  add_median_area()

# Combination
study %>%
  tidyplot(x = treatment, y = score) %>%
  add_median_bar(alpha = 0.4) %>%
  add_median_dash() %>%
  add_median_dot() %>%
  add_median_value() %>%
  add_median_line()

# Changing arguments: alpha
# Makes objects transparent
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  theme_minimal_y() %>%
  add_median_bar(alpha = 0.4)

# Changing arguments: saturation
# Reduces fill color saturation without making the object transparent
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  theme_minimal_y() %>%
  add_median_bar(saturation = 0.3)

# Changing arguments: accuracy
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_median_value(accuracy = 0.01)

# Changing arguments: fontsize
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_median_value(fontsize = 10)

# Changing arguments: color
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_median_value(color = "black")
```

add_pie *Add pie or donut chart*

Description

Add pie or donut chart

Usage

```
add_pie(plot, width = 1, reverse = FALSE, ...)

add_donut(plot, width = 1, reverse = FALSE, ...)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
width	Width of the plot area. Defaults to 50.
reverse	Whether the order should be reversed or not. Defaults to FALSE, meaning not reversed.
...	Arguments passed on to the geom function.

Value

A tidyplot object.

Examples

```
# for a `count` only provide `color`
# `count` of the data points in each `energy_type` category
energy %>%
  tidyplot(color = energy_type) %>%
  add_pie()

energy %>%
  tidyplot(color = energy_type) %>%
  add_donut()

# for a `sum` provide `color` and `y`
# `sum` of `power` in each `energy_type` category
energy %>%
  tidyplot(y = power, color = energy_type) %>%
  add_pie()

energy %>%
  tidyplot(y = power, color = energy_type) %>%
  add_donut()
```

`add_reference_lines` *Add reference lines*

Description

Add reference lines

Usage

```
add_reference_lines(
  plot,
  x = NULL,
  y = NULL,
  linetype = "dashed",
  linewidth = 0.25,
  ...
)
```

Arguments

`plot`	A `tidyplot` generated with the function `tidyplot()`.
`x`	Numeric values where the reference lines should meet the x-axis. For example, `x = 4` or `x = c(2,3,4)`.
`y`	Numeric values where the reference lines should meet the y-axis. For example, `y = 4` or `y = c(2,3,4)`.
`linetype`	Either an integer (0-6) or a name (0 = blank, 1 = solid, 2 = dashed, 3 = dotted, 4 = dotdash, 5 = longdash, 6 = twodash).
`linewidth`	Thickness of the line in points (pt). Typical values range between `0.25` and `1`.
`...`	Arguments passed on to the `geom` function.

Value

A `tidyplot` object.

Examples

```
animals %>%
  tidyplot(x = weight, y = speed) %>%
   add_reference_lines(x = 4000, y = c(100, 200)) %>%
   add_data_points()

animals %>%
  tidyplot(x = weight, y = speed) %>%
   add_reference_lines(x = 4000, y = c(100, 200), linetype = "dotdash") %>%
   add_data_points()
```

`add_sem_errorbar` *Add error bar*

Description

- `add_sem_errorbar()` adds the standard error of mean.
- `add_range_errorbar()` adds the range from smallest to largest value.
- `add_sd_errorbar()` adds the standard deviation.
- `add_ci95_errorbar()` adds the 95% confidence interval.

Usage

```
add_sem_errorbar(
  plot,
  dodge_width = NULL,
  width = 0.4,
  linewidth = 0.25,
  preserve = "total",
  ...
)

add_range_errorbar(
  plot,
  dodge_width = NULL,
  width = 0.4,
  linewidth = 0.25,
  preserve = "total",
  ...
)

add_sd_errorbar(
  plot,
  dodge_width = NULL,
  width = 0.4,
  linewidth = 0.25,
  preserve = "total",
  ...
)

add_ci95_errorbar(
  plot,
  dodge_width = NULL,
  width = 0.4,
  linewidth = 0.25,
  preserve = "total",
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
dodge_width	For adjusting the distance between grouped objects. Defaults to 0.8 for plots with at least one discrete axis and 0 for plots with two continuous axes.
width	Width of the plot area. Defaults to 50.
linewidth	Thickness of the line in points (pt). Typical values range between 0.25 and 1.
preserve	Should dodging preserve the "total" width of all elements at a position, or the width of a "single" element?
...	Arguments passed on to the geom function.

Value

A tidyplot object.

Examples

```
# Standard error of the mean
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_sem_errorbar()

# Range from minimum to maximum value
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_range_errorbar()

# Standard deviation
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_sd_errorbar()

# 95% confidence interval
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_ci95_errorbar()

# Changing arguments: error bar width
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_sem_errorbar(width = 0.8)

# Changing arguments: error bar line width
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
```

```
add_sem_errorbar(linewidth = 1)
```

---

add_sem_ribbon *Add ribbon*

Description

- add_sem_ribbon() adds the standard error of mean.
- add_range_ribbon() adds the range from smallest to largest value.
- add_sd_ribbon() adds the standard deviation.
- add_ci95_ribbon() adds the 95% confidence interval.

Usage

```
add_sem_ribbon(plot, dodge_width = NULL, alpha = 0.4, color = NA, ...)

add_range_ribbon(plot, dodge_width = NULL, alpha = 0.4, color = NA, ...)

add_sd_ribbon(plot, dodge_width = NULL, alpha = 0.4, color = NA, ...)

add_ci95_ribbon(plot, dodge_width = NULL, alpha = 0.4, color = NA, ...)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
dodge_width	For adjusting the distance between grouped objects. Defaults to 0.8 for plots with at least one discrete axis and 0 for plots with two continuous axes.
alpha	A number between 0 and 1 for the opacity of an object. A value of 0 is completely transparent, 1 is completely opaque.
color	A hex color for the stroke color. For example, "#FFFFFF" for white.
...	Arguments passed on to the geom function.

Value

A tidyplot object.

Examples

```
# Standard error of the mean
time_course %>%
  tidyplot(x = day, y = score, color = treatment) %>%
  add_mean_line() %>%
  add_sem_ribbon()

# Range from minimum to maximum value
```

```
time_course %>%
  tidyplot(x = day, y = score, color = treatment) %>%
  add_mean_line() %>%
  add_range_ribbon()

# Standard deviation
time_course %>%
  tidyplot(x = day, y = score, color = treatment) %>%
  add_mean_line() %>%
  add_sd_ribbon()

# 95% confidence interval
time_course %>%
  tidyplot(x = day, y = score, color = treatment) %>%
  add_mean_line() %>%
  add_ci95_ribbon()

# Changing arguments: alpha
time_course %>%
  tidyplot(x = day, y = score, color = treatment) %>%
  add_mean_line() %>%
  add_sem_ribbon(alpha = 0.7)
```

`add_sum_bar` *Add sum*

Description

Add sum

Usage

```
add_sum_bar(
  plot,
  dodge_width = NULL,
  width = 0.6,
  saturation = 1,
  preserve = "total",
  ...
)

add_sum_dash(
  plot,
  dodge_width = NULL,
  width = 0.6,
  linewidth = 0.25,
  preserve = "total",
  ...
```

```
)

add_sum_dot(plot, dodge_width = NULL, size = 2, preserve = "total", ...)

add_sum_value(
  plot,
  dodge_width = NULL,
  accuracy = 0.1,
  scale_cut = NULL,
  fontsize = 7,
  extra_padding = 0.15,
  vjust = NULL,
  hjust = NULL,
  preserve = "total",
  ...
)

add_sum_line(
  plot,
  group,
  dodge_width = NULL,
  linewidth = 0.25,
  preserve = "total",
  ...
)

add_sum_area(
  plot,
  group,
  dodge_width = NULL,
  linewidth = 0.25,
  preserve = "total",
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
dodge_width	For adjusting the distance between grouped objects. Defaults to 0.8 for plots with at least one discrete axis and 0 for plots with two continuous axes.
width	Width of the plot area. Defaults to 50.
saturation	A number between 0 and 1 for the color saturation of an object. A value of 0 is completely desaturated (white), 1 is the original color.
preserve	Should dodging preserve the "total" width of all elements at a position, or the width of a "single" element?
...	Arguments passed on to the geom function.
linewidth	Thickness of the line in points (pt). Typical values range between 0.25 and 1.

size	A number representing the size of the plot symbol. Typical values range between 1 and 3.
accuracy	A number to round to. Use (e.g.) 0.01 to show 2 decimal places of precision. If NULL, the default, uses a heuristic that should ensure breaks have the minimum number of digits needed to show the difference between adjacent values. Applied to rescaled data.
scale_cut	Scale cut function to be applied. See scales::cut_short_scale() and friends.
fontsize	Font size in points. Defaults to 7.
extra_padding	Extra padding to create space for the value label.
vjust	Vertical position adjustment of the value label.
hjust	Horizontal position adjustment of the value label.
group	Variable in the dataset to be used for grouping.

Value

A tidyplot object.

Examples

```
spendings %>%
  tidyplot(x = category, y = amount, color = category) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_sum_bar()

spendings %>%
  tidyplot(x = category, y = amount, color = category) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_sum_dash()

spendings %>%
  tidyplot(x = category, y = amount, color = category) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_sum_dot()

spendings %>%
  tidyplot(x = category, y = amount, color = category) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_sum_value()

spendings %>%
  tidyplot(x = category, y = amount) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_sum_line()

spendings %>%
  tidyplot(x = category, y = amount) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_sum_area()
```

```
# Combination
spendings %>%
  tidyplot(x = category, y = amount) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_median_bar(alpha = 0.4) %>%
  add_median_dash() %>%
  add_median_dot() %>%
  add_median_value() %>%
  add_median_line()

# Changing arguments: alpha
# Makes objects transparent
spendings %>%
  tidyplot(x = category, y = amount, color = category) %>%
  theme_minimal_y() %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_sum_bar(alpha = 0.4)

# Changing arguments: saturation
# Reduces fill color saturation without making the object transparent
spendings %>%
  tidyplot(x = category, y = amount, color = category) %>%
  theme_minimal_y() %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_sum_bar(saturation = 0.3)

# Changing arguments: accuracy
spendings %>%
  tidyplot(x = category, y = amount, color = category) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_sum_value(accuracy = 1)

# Changing arguments: fontsize
spendings %>%
  tidyplot(x = category, y = amount, color = category) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_sum_value(fontsize = 10)

# Changing arguments: color
spendings %>%
  tidyplot(x = category, y = amount, color = category) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_sum_value(color = "black")

# Changing arguments: extra_padding
spendings %>%
  tidyplot(x = category, y = amount, color = category) %>%
  adjust_x_axis(rotate_labels = TRUE) %>%
  add_sum_value(extra_padding = 0.5)
```

add_test_pvalue *Add statistical test*

Description

Add statistical test

Usage

```
add_test_pvalue(
  plot,
  padding_top = 0.15,
  method = "t.test",
  p.adjust.method = "none",
  ref.group = NULL,
  label = "{format_p_value(p.adj, 0.0001)}",
  label.size = 7/ggplot2::.pt,
  step.increase = 0.15,
  vjust = -0.25,
  bracket.nudge.y = 0.1,
  hide.ns = FALSE,
  p.adjust.by = "panel",
 symnum.args = list(cutpoints = c(0, 0.001, 0.01, 0.05, Inf), symbols = c("***", "**",
    "*", "ns")),
  hide_info = FALSE,
  ...
)

add_test_asterisks(
  plot,
  padding_top = 0.1,
  method = "t.test",
  p.adjust.method = "none",
  ref.group = NULL,
  label = "p.adj.signif",
  label.size = 10/ggplot2::.pt,
  step.increase = 0.2,
  vjust = 0.3,
  bracket.nudge.y = 0.15,
  hide.ns = TRUE,
  p.adjust.by = "panel",
 symnum.args = list(cutpoints = c(0, 0.001, 0.01, 0.05, Inf), symbols = c("***", "**",
    "*", "ns")),
  hide_info = FALSE,
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
padding_top	Extra padding above the data points to accommodate the statistical comparisons.
method	a character string indicating which method to be used for pairwise comparisons. Default is "wilcox_test". Allowed methods include pairwise comparisons methods implemented in the rstatix R package. These methods are: "wilcox_test", "t_test", "sign_test","dunn_test", "emmeans_test", "tukey_hsd", "games_howell_test".
p.adjust.method	method for adjusting p values (see p.adjust). Has impact only in a situation, where multiple pairwise tests are performed; or when there are multiple grouping variables. Ignored when the specified method is "tukey_hsd" or "games_howell_test" because they come with internal p adjustment method. Allowed values include "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". If you don't want to adjust the p value (not recommended), use p.adjust.method = "none".
ref.group	a character string or a numeric value specifying the reference group. If specified, for a given grouping variable, each of the group levels will be compared to the reference group (i.e. control group). ref.group can be also "all". In this case, each of the grouping variable levels is compared to all (i.e. basemean). Allowed values can be: • **numeric value**: specifying the rank of the reference group. For example, use ref.group = 1 when the first group is the reference; use ref.group = 2 when the second group is the reference, and so on. This works for all situations, including i) when comparisons are performed between x-axis groups and ii) when comparisons are performed between legend groups. • **character value**: For example, you can use ref.group = "ctrl" instead of using the numeric rank value of the "ctrl" group. • **"all"**: In this case, each of the grouping variable levels is compared to all (i.e. basemean).
label	character string specifying label. Can be: • the column containing the label (e.g.: label = "p" or label = "p.adj"), where p is the p-value. Other possible values are "p.signif", "p.adj.signif", "p.format", "p.adj.format". • an expression that can be formatted by the glue() package. For example, when specifying label = "Wilcoxon, p = \{p\}", the expression {p} will be replaced by its value. • a combination of plotmath expressions and glue expressions. You may want some of the statistical parameter in italic; for example:label = "Wilcoxon,italic(p)= {p}" .
label.size	change the size of the label text
step.increase	numeric vector with the increase in fraction of total height for every additional comparison to minimize overlap.

vjust	move the text up or down relative to the bracket.
bracket.nudge.y	Vertical adjustment to nudge brackets by (in fraction of the total height). Useful to move up or move down the bracket. If positive value, brackets will be moved up; if negative value, brackets are moved down.
hide.ns	can be logical value (TRUE or FALSE) or a character vector ("p.adj" or "p").
p.adjust.by	possible value is one of c("group", "panel"). Default is "group": for a grouped data, if pairwise test is performed, then the p-values are adjusted for each group level independently. P-values are adjusted by panel when p.adjust.by = "panel".
symnum.args	a list of arguments to pass to the function symnum for symbolic number coding of p-values. For example, symnum.args <- list(cutpoints = c(0, 0.0001, 0.001, 0.01, 0.05, Inf), symbols = c("****", "***", "**", "*", "ns")). In other words, we use the following convention for symbols indicating statistical significance: • ns: p > 0.05 • *: p <= 0.05 • **: p <= 0.01 • ***: p <= 0.001 • ****: p <= 0.0001
hide_info	Whether to hide details about the statistical testing as caption. Defaults to FALSE.
...	Arguments passed on to ggpubr::geom_pwc().

Details

- add_test_pvalue() and add_test_asterisks() use ggpubr::geom_pwc(). Check there for additional arguments.

Value

A tidyplot object.

Examples

```
study %>%
  tidyplot(x = dose, y = score, color = group) %>%
  add_mean_dash() %>%
  add_sem_errorbar() %>%
  add_data_points() %>%
  add_test_pvalue()

# Change stat methods
study %>%
  tidyplot(x = dose, y = score, color = group) %>%
  add_mean_dash() %>%
  add_sem_errorbar() %>%
  add_data_points() %>%
```

```
  add_test_pvalue(method = "wilcoxon", p.adjust.method = "BH")

# Define reference group to test against
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_dash() %>%
  add_sem_errorbar() %>%
  add_data_points() %>%
  add_test_pvalue(ref.group = "A")

# hide non-significant p values
gene_expression %>%
  # filter to one gene
  dplyr::filter(external_gene_name == "Apol6") %>%
  # start plotting
  tidyplot(x = condition, y = expression, color = sample_type) %>%
  add_mean_dash() %>%
  add_sem_errorbar() %>%
  add_data_points() %>%
  add_test_pvalue(hide.ns = TRUE)

# Adjust top padding for statistical comparisons
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_dash() %>%
  add_sem_errorbar() %>%
  add_data_points() %>%
  add_test_pvalue(padding_top = 0.08)

# Hide stats information
study %>%
  tidyplot(x = dose, y = score, color = group) %>%
  add_mean_dash() %>%
  add_sem_errorbar() %>%
  add_data_points() %>%
  add_test_pvalue(hide_info = TRUE)
```

`add_title` *Add plot title or caption*

Description

Add plot title or caption

Usage

```
add_title(plot, title = ggplot2::waiver())

add_caption(plot, caption = ggplot2::waiver())
```

Arguments

plot	A tidyplot generated with the function tidyplot().
title	Title of the plot.
caption	Caption of the plot.

Details

- add_title() and add_caption() support plotmath expressions to include special characters. See examples and Advanced plotting.

Value

A tidyplot object.

Examples

```
study %>%
  tidyplot(x = treatment, y = score) %>%
  add_data_points_beeswarm() %>%
  add_title("This is my title")

study %>%
  tidyplot(x = treatment, y = score) %>%
  add_data_points_beeswarm() %>%
  add_caption("This is the fine print in the caption")

# Plotmath expression
study %>%
  tidyplot(x = treatment, y = score) %>%
  add_data_points_beeswarm() %>%
  add_title("$H[2]*O~and~E==m*c^{2}$")
```

---

add_violin *Add violin plot*

Description

Add violin plot

Usage

```
add_violin(
  plot,
  dodge_width = NULL,
  alpha = 0.3,
  saturation = 1,
  draw_quantiles = NULL,
```

```
  trim = FALSE,
  linewidth = 0.25,
  scale = "width",
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
dodge_width	For adjusting the distance between grouped objects. Defaults to 0.8 for plots with at least one discrete axis and 0 for plots with two continuous axes.
alpha	A number between 0 and 1 for the opacity of an object. A value of 0 is completely transparent, 1 is completely opaque.
saturation	A number between 0 and 1 for the color saturation of an object. A value of 0 is completely desaturated (white), 1 is the original color.
draw_quantiles	If not(NULL) (default), draw horizontal lines at the given quantiles of the density estimate.
trim	If TRUE (default), trim the tails of the violins to the range of the data. If FALSE, don't trim the tails.
linewidth	Thickness of the line in points (pt). Typical values range between 0.25 and 1.
scale	if "area" (default), all violins have the same area (before trimming the tails). If "count", areas are scaled proportionally to the number of observations. If "width", all violins have the same maximum width.
...	Arguments passed on to the geom function.

Value

A tidyplot object.

Examples

```
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_violin()

# Changing arguments:
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_violin(saturation = 0.6)

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_violin(draw_quantiles = c(0.25, 0.5, 0.75))

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_violin(trim = TRUE)
```

```
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_violin(linewidth = 1)
```

`adjust_colors` *Adjust colors*

Description

Adjust colors

Usage

```
adjust_colors(
  plot,
  new_colors = NULL,
  saturation = 1,
  labels = tidyplot_parse_labels(),
  downsample = c("evenly", "first", "last", "middle"),
  ...
)
```

Arguments

`plot`	A `tidyplot` generated with the function `tidyplot()`.
`new_colors`	A character vector of new hex colors to use. Can be a named character vector of hex colors to assign certain data labels to specific colors.
`saturation`	A `number` between `0` and `1` for the color saturation of an object. A value of `0` is completely desaturated (white), `1` is the original color.
`labels`	One of: • `NULL` for no labels • `waiver()` for the default labels computed by the transformation object • A character vector giving labels (must be same length as `breaks`) • An expression vector (must be the same length as breaks). See ?plotmath for details. • A function that takes the breaks as input and returns labels as output. Also accepts rlang lambda function notation.
`downsample`	If too many colors are provided, whether to downsample `evenly`, or use the `first`, the `last` or the `middle` colors of the color vector. Defaults to `evenly`.
`...`	Arguments passed on to the ggplot2 `scale` function.

Value

A `tidyplot` object.

See Also

colors_discrete_friendly(), colors_continuous_viridis(), colors_diverging_blue2brown(), and new_color_scheme()

Examples

```
# Plot without adjustments
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Provide hex colors
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_colors(new_colors = c("#644296","#F08533","#3B78B0", "#D1352C"))

# Provide discrete color scheme
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_colors(new_colors = colors_discrete_seaside)

# Provide named vector
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_colors(new_colors = c(
    "A" = "pink",
    "B" = "purple",
    "C" = "grey",
    "D" = "blue"))

# Provide continuous color scheme
climate %>%
  tidyplot(x = month, y = year, color = max_temperature) %>%
  add_heatmap() %>%
  adjust_colors(new_colors = colors_continuous_turbo)
```

---

adjust_font *Adjust font*

Description

Adjust font

Usage

```
adjust_font(plot, fontsize = 7, family = NULL, face = NULL, color = "black")
```

Arguments

plot	A tidyplot generated with the function tidyplot().
fontsize	Font size in points. Defaults to 7.
family	Font family
face	Font face ("plain", "italic", "bold", "bold.italic")
color	A hex color for the stroke color. For example, "#FFFFFF" for white.

Value

A tidyplot object.

Examples

```
# Plot without adjustments
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Increase font size
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_font(fontsize = 16)

# Change font family
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_font(family = "mono")

# Change font face
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
```

```
adjust_font(face = "bold")
```

`adjust_legend_title` *Adjust legend*

Description

Adjust legend

Usage

```
adjust_legend_title(
  plot,
  title = ggplot2::waiver(),
  fontsize = NULL,
  family = NULL,
  face = NULL,
  color = "black",
  ...
)

adjust_legend_position(plot, position = "right")
```

Arguments

`plot`	A `tidyplot` generated with the function `tidyplot()`.
`title`	Legend title.
`fontsize`	Font size in points. Defaults to 7.
`family`	Font family
`face`	Font face ("plain", "italic", "bold", "bold.italic")
`color`	A hex color for the stroke color. For example, `"#FFFFFF"` for white.
`...`	Arguments passed on to `ggplot2::element_text()`.
`position`	The position of the legend. Can be one of `c("right", "left", "bottom", "top", "none")`. Defaults to `"right"`.

Details

- The `title` argument of `adjust_legend_title()` supports plotmath expressions to include special characters. See examples and Advanced plotting.

Value

A `tidyplot` object.

Examples

```
# Plot without adjustments
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# New title
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_legend_title("My new legend title")

# New title with plotmath expression
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_legend_title("$E==m*c^{2}$")

# Alternative legend positions
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_legend_position("left")

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_legend_position("top")

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_legend_position("bottom")

# `position = "none"` hides the legend
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
```

```
  adjust_legend_position("none")
```

---

adjust_padding *Adjust plot area padding*

Description

Adjust plot area padding

Usage

```
adjust_padding(
  plot,
  top = NA,
  right = NA,
  bottom = NA,
  left = NA,
  all = NA,
  force_continuous = FALSE,
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
top	Extra space between the data points and the top. Defaults to NA, which does not change the padding.
right	Extra space between the data points and the right. Defaults to NA, which does not change the padding.
bottom	Extra space between the data points and the bottom. Defaults to NA, which does not change the padding.
left	Extra space between the data points and the left. Defaults to NA, which does not change the padding.
all	Extra space around the data pointst. Overwrites top, right, bottom, left if set. Defaults to NA, which does not change the padding.
force_continuous	Whether to force the axis to be continuous. Defaults to FALSE.
...	Arguments passed on to the geom function.

Value

A tidyplot object.

Examples

```
# Plot without adjustments
animals %>%
  tidyplot(x = weight, y = size, color = family) %>%
  add_data_points() %>%
  adjust_padding()

# Increase plot area padding
animals %>%
  tidyplot(x = weight, y = size, color = family) %>%
  add_data_points() %>%
  adjust_padding(all = 0.2)

animals %>%
  tidyplot(x = weight, y = size, color = family) %>%
  add_data_points() %>%
  adjust_padding(top = 0.8)

animals %>%
  tidyplot(x = weight, y = size, color = family) %>%
  add_data_points() %>%
  adjust_padding(bottom = 0.8)

animals %>%
  tidyplot(x = weight, y = size, color = family) %>%
  add_data_points() %>%
  adjust_padding(right = 0.8)

animals %>%
  tidyplot(x = weight, y = size, color = family) %>%
  add_data_points() %>%
  adjust_padding(left = 0.8)
```

---

adjust_size *Adjust plot area size*

Description

Adjust plot area size

Usage

```
adjust_size(plot, width = 50, height = 50, unit = "mm")
```

Arguments

plot	A tidyplot generated with the function tidyplot().
width	Width of the plot area. Defaults to 50.

height	Height of the plot area. Defaults to 50.
unit	Unit of the plot area width and height. Defaults to mm.

Value

A tidyplot object.

Examples

```
# Plot without adjustments
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm(shape = 1) %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Resize to 20 x 20 mm
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm(shape = 1) %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_size(width = 20, height = 20)

# Resize to 4 x 4 cm
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm(shape = 1) %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_size(width = 4, height = 4, unit = "cm")

# Remove absolute dimensions and take all available space. This is the ggplot2 default.
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm(shape = 1) %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_size(width = NA, height = NA)
```

---

adjust_theme_details *Adjust theme details*

Description

This function is a wrapper around ggplot2::theme(). To use the required theme helper functions ggplot2::element_blank(), ggplot2::element_rect(), ggplot2::element_line(), and ggplot2::element_text() you need to either load the ggplot2 package via library(ggplot2) or use the ggplot2:: prefix as shown above.

Usage

```
adjust_theme_details(plot, ...)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
...	Arguments passed on to the geom function.

Value

A tidyplot object.

Examples

```
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm() %>%
  add_mean_bar(alpha = 0.4) %>%
  adjust_theme_details(plot.background = ggplot2::element_rect(fill = "#FFEBFF"))
```

---

adjust_title *Adjust titles and caption*

Description

Adjust titles and caption

Usage

```
adjust_title(
  plot,
  title = ggplot2::waiver(),
  fontsize = NULL,
  family = NULL,
  face = NULL,
  color = "black",
  ...
)

adjust_x_axis_title(
  plot,
  title = ggplot2::waiver(),
  fontsize = NULL,
  family = NULL,
  face = NULL,
  color = "black",
```

```
  ...
)

adjust_y_axis_title(
  plot,
  title = ggplot2::waiver(),
  fontsize = NULL,
  family = NULL,
  face = NULL,
  color = "black",
  ...
)

adjust_caption(
  plot,
  caption = ggplot2::waiver(),
  fontsize = NULL,
  family = NULL,
  face = NULL,
  color = "black",
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
title	Plot or axes title.
fontsize	Font size in points. Defaults to 7.
family	Font family
face	Font face ("plain", "italic", "bold", "bold.italic")
color	A hex color for the stroke color. For example, "#FFFFFF" for white.
...	Arguments passed on to ggplot2::element_text().
caption	Plot caption.

Details

Adjust the plot title, axis titles and caption

- All functions support plotmath expressions to include special characters. See examples and Advanced plotting.

Value

A tidyplot object.

Examples

```
# Plot without adjustments
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Adjust description
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_title("This is my fantastic plot title") %>%
  adjust_x_axis_title("Treatment group") %>%
  adjust_y_axis_title("Disease score") %>%
  adjust_legend_title("Legend title") %>%
  adjust_caption("Here goes the caption")

# Plotmath expressions
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  adjust_title("$H[2]*O$") %>%
  adjust_x_axis_title("$H[2]*O$") %>%
  adjust_y_axis_title("$H[2]*O$") %>%
  adjust_legend_title("$H[2]*O$") %>%
  adjust_caption("$H[2]*O$")
```

---

adjust_x_axis *Adjust axes*

Description

Adjust axes

Usage

```
adjust_x_axis(
  plot,
  title = ggplot2::waiver(),
  breaks = ggplot2::waiver(),
  labels = ggplot2::waiver(),
  limits = NULL,
  padding = c(NA, NA),
```

```
  rotate_labels = FALSE,
  transform = "identity",
  cut_short_scale = FALSE,
  force_continuous = FALSE,
  ...
)

adjust_y_axis(
  plot,
  title = ggplot2::waiver(),
  breaks = ggplot2::waiver(),
  labels = ggplot2::waiver(),
  limits = NULL,
  padding = c(NA, NA),
  rotate_labels = FALSE,
  transform = "identity",
  cut_short_scale = FALSE,
  force_continuous = FALSE,
  ...
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
title	Axis title.
breaks	One of: • NULL for no breaks • waiver() for the default breaks computed by the transformation object • A numeric vector of positions • A function that takes the limits as input and returns breaks as output (e.g., a function returned by scales::extended_breaks()). Note that for position scales, limits are provided after scale expansion. Also accepts rlang lambda function notation.
labels	One of: • NULL for no labels • waiver() for the default labels computed by the transformation object • A character vector giving labels (must be same length as breaks) • An expression vector (must be the same length as breaks). See ?plotmath for details. • A function that takes the breaks as input and returns labels as output. Also accepts rlang lambda function notation.
limits	Axis limits. For example, with limits = c(20, 90) the axis starts at 20 and ends at 90.
padding	Extra space between the data points and the axes. Defaults to c(NA, NA), which does not change the padding.

`rotate_labels` Whether to rotate axis labels. If `TRUE` is set to 45 degrees. You can also provide custom degree values, for example, `rotate_labels = 90`. Defaults to `FALSE`.

`transform` For continuous scales, the name of a transformation object or the object itself. Built-in transformations include "asn", "atanh", "boxcox", "date", "exp", "hms", "identity", "log", "log10", "log1p", "log2", "logit", "modulus", "probability", "probit", "pseudo_log", "reciprocal", "reverse", "sqrt" and "time".

A transformation object bundles together a transform, its inverse, and methods for generating breaks and labels. Transformation objects are defined in the scales package, and are called `transform_<name>`. If transformations require arguments, you can call them from the scales package, e.g. `scales::transform_boxcox(p = 2)`. You can create your own transformation with `scales::new_transform()`.

`cut_short_scale` Whether to shorten axis labels using `K` for thousand, `M` for million, and so on. Defaults to `FALSE`.

`force_continuous` Whether to force the axis to be continuous. Defaults to `FALSE`.

`...` Arguments passed on to ggplot2 `scale` function.

Details

- The `title` argument of `adjust_x_axis()` and `adjust_y_axis()` supports plotmath expressions to include special characters. See examples and Advanced plotting.

Value

A `tidyplot` object.

Examples

```
# Plot without adjustments
animals %>%
  tidyplot(x = weight, y = size, color = family) %>%
  add_data_points()

# New titles
animals %>%
  tidyplot(x = weight, y = size, color = family) %>%
  add_data_points() %>%
  adjust_x_axis(title = "My new x-axis title") %>%
  adjust_y_axis(title = "My new y-axis title")

# New titles with plotmath expressions
animals %>%
  tidyplot(x = weight, y = size, color = family) %>%
  add_data_points() %>%
  adjust_x_axis(title = "$H[2]*O$") %>%
  adjust_y_axis(title = "$E==m*c^{2}$")

# Axes limits
animals %>%
```

```
  tidyplot(x = weight, y = size, color = family) %>%
  add_data_points() %>%
  adjust_x_axis(limits = c(-1000, 4000)) %>%
  adjust_y_axis(limits = c(-200, 600))

# Rotate labels
animals %>%
  tidyplot(x = weight, y = size, color = family) %>%
  add_data_points() %>%
  adjust_x_axis(rotate_labels = 90) %>%
  adjust_y_axis(rotate_labels = 90)

# Increase plot area padding
animals %>%
  tidyplot(x = weight, y = size, color = family) %>%
  add_data_points() %>%
  adjust_x_axis(padding = c(0.2, 0.2)) %>%
  adjust_y_axis(padding = c(0.2, 0.2))

# Scale transformation
animals %>%
  tidyplot(x = weight, y = size, color = family) %>%
  add_data_points() %>%
  adjust_x_axis(transform = "log10") %>%
  adjust_y_axis(transform = "log2")
```

`all_rows` *Subset data rows*

Description

Subset data rows

Usage

```
all_rows()

filter_rows(..., .by = NULL)

max_rows(order_by, n, by = NULL, with_ties = TRUE, na_rm = FALSE)

min_rows(order_by, n, by = NULL, with_ties = TRUE, na_rm = FALSE)

first_rows(n, by = NULL)

last_rows(n, by = NULL)

sample_rows(n, by = NULL)
```

Arguments

...	<data-masking> Expressions that return a logical value, and are defined in terms of the variables in .data. If multiple expressions are included, they are combined with the & operator. Only rows for which all conditions evaluate to TRUE are kept.
.by, by	**[Experimental]** <tidy-select> Optionally, a selection of columns to group by for just this operation, functioning as an alternative to group_by(). For details and examples, see ?dplyr_by.
order_by	<data-masking> Variable or function of variables to order by. To order by multiple variables, wrap them in a data frame or tibble.
n	The number of rows to select. If not are supplied, n = 1 will be used. If n is greater than the number of rows in the group, the result will be silently truncated to the group size. A negative value of n will be subtracted from the group size. For example, n = -2 with a group of 5 rows will select 5 - 2 = 3 rows.
with_ties	Should ties be kept together? The default, TRUE, may return more rows than you request. Use FALSE to ignore ties, and return the first n rows.
na_rm	Should missing values in order_by be removed from the result? If FALSE, NA values are sorted to the end (like in dplyr::arrange()), so they will only be included if there are insufficient non-missing values to reach n.

Value

A function to achieve the desired data subsetting.

Examples

```
# Highlight all animals
animals %>%
 tidyplot(x = weight, y = size) %>%
 add_data_points() %>%
 add_data_points(data = all_rows(),
  color = "red", shape = 1, size = 3)

# Highlight 3 animals with the highest weight
animals %>%
 tidyplot(x = weight, y = size) %>%
 add_data_points() %>%
 add_data_points(data = max_rows(weight, n = 3),
  color = "red", shape = 1, size = 3)

# Highlight 3 animals with the lowest weight
animals %>%
 tidyplot(x = weight, y = size) %>%
 add_data_points() %>%
 add_data_points(data = min_rows(weight, n = 3),
  color = "red", shape = 1, size = 3)
```

```
# Highlight the first 3 animals in the dataset
animals %>%
 tidyplot(x = weight, y = size) %>%
 add_data_points() %>%
 add_data_points(data = first_rows(n = 3),
  color = "red", shape = 1, size = 3)

# Highlight the last 3 animals in the dataset
animals %>%
 tidyplot(x = weight, y = size) %>%
 add_data_points() %>%
 add_data_points(data = last_rows(n = 3),
  color = "red", shape = 1, size = 3)

# Highlight 3 random animals
animals %>%
 tidyplot(x = weight, y = size) %>%
 add_data_points() %>%
 add_data_points(data = sample_rows(n = 3),
  color = "red", shape = 1, size = 3)
```

`animals` *Animals data*

Description

Animals data

Usage

```
animals
```

Format

A data frame.

Source

ChatGPT-3.5, *Caution: The accuracy of the data has not been verified.*

Examples

```
dplyr::glimpse(animals)
```

as_tidyplot *Convert ggplot to tidyplot*

Description

Convert ggplot to tidyplot

Usage

```
as_tidyplot(gg, width = 50, height = 50, dodge_width = NULL)
```

Arguments

gg	A ggplot.
width	Width of the plot area. Defaults to 50.
height	Height of the plot area. Defaults to 50.
dodge_width	For adjusting the distance between grouped objects. Defaults to 0.8 for plots with at least one discrete axis and 0 for plots with two continuous axes.

Value

A tidyplot object.

Examples

```
gg <-
  study %>%
  ggplot2::ggplot(ggplot2::aes(x = treatment, y = score, color = treatment)) +
  ggplot2::geom_point()

gg

gg %>% as_tidyplot()
```

climate *Climate data*

Description

Climate data

Usage

```
climate
```

Format

A data frame.

Source

National Oceanic and Atmospheric Administration, Temperature data, weather station Hamburg Fuhlsbüttel, Germany

Examples

```
dplyr::glimpse(climate)
```

---

colors_continuous_viridis

Continuous color schemes

Description

For more information about the use of color schemes in tidyplots, check out this article: Color schemes

Usage

```
colors_continuous_viridis

colors_continuous_magma

colors_continuous_inferno

colors_continuous_plasma

colors_continuous_cividis

colors_continuous_rocket

colors_continuous_mako

colors_continuous_turbo

colors_continuous_bluepinkyellow
```

Format

An object of class `tidycolor` (inherits from `character`) of length 265.

An object of class `tidycolor` (inherits from `character`) of length 265.

An object of class `tidycolor` (inherits from `character`) of length 265.

An object of class `tidycolor` (inherits from `character`) of length 265.

An object of class `tidycolor` (inherits from `character`) of length 265.

An object of class `tidycolor` (inherits from `character`) of length 265.

An object of class `tidycolor` (inherits from `character`) of length 265.

An object of class `tidycolor` (inherits from `character`) of length 265.

An object of class `tidycolor` (inherits from `character`) of length 11.

Details

Color schemes can be conveniently previewed by using the print method of the `tidycolor` class. This will send a html preview to the RStudio Viewer pane.

`colors_continuous_viridis`

`colors_continuous_magma`

`colors_continuous_inferno`

`colors_continuous_plasma`

`colors_continuous_cividis`

`colors_continuous_rocket`

`colors_continuous_mako`

`colors_continuous_turbo`

`colors_continuous_bluepinkyellow`

`colors_discrete_friendly`

Discrete color schemes

Description

For more information about the use of color schemes in tidyplots, check out this article: Color schemes

Usage

```
colors_discrete_friendly

colors_discrete_seaside

colors_discrete_apple

colors_discrete_friendly_long

colors_discrete_okabeito

colors_discrete_ibm

colors_discrete_metro

colors_discrete_candy

colors_discrete_alger
```

Format

An object of class `tidycolor` (inherits from `character`) of length 6.

An object of class `tidycolor` (inherits from `character`) of length 5.

An object of class `tidycolor` (inherits from `character`) of length 7.

An object of class `tidycolor` (inherits from `character`) of length 7.

An object of class `tidycolor` (inherits from `character`) of length 7.

An object of class `tidycolor` (inherits from `character`) of length 5.

An object of class `tidycolor` (inherits from `character`) of length 5.

An object of class `tidycolor` (inherits from `character`) of length 5.

An object of class `tidycolor` (inherits from `character`) of length 5.

Details

The signature theme of tidyplots `colors_discrete_friendly` was adapted from the Okabe & Ito color palette that was designed to work well for people with color vision deficiency.

Color schemes can be conveniently previewed by using the print method of the `tidycolor` class. This will send a html preview to the RStudio Viewer pane.

```
colors_discrete_friendly

colors_discrete_seaside

colors_discrete_apple

colors_discrete_friendly_long
```

colors_discrete_okabeito

colors_discrete_ibm

colors_discrete_metro

colors_discrete_candy

colors_discrete_alger

---

colors_diverging_blue2red
Diverging color schemes

Description

For more information about the use of color schemes in tidyplots, check out this article: Color schemes

Usage

colors_diverging_blue2red

colors_diverging_blue2brown

colors_diverging_BuRd

colors_diverging_BuYlRd

colors_diverging_spectral

colors_diverging_icefire

Format

An object of class tidycolor (inherits from character) of length 17.

An object of class tidycolor (inherits from character) of length 17.

An object of class tidycolor (inherits from character) of length 11.

An object of class tidycolor (inherits from character) of length 11.

An object of class tidycolor (inherits from character) of length 96.

An object of class tidycolor (inherits from character) of length 96.

Details

Color schemes can be conveniently previewed by using the print method of the `tidycolor` class. This will send a html preview to the RStudio Viewer pane.

`colors_diverging_blue2red`

`colors_diverging_blue2brown`

`colors_diverging_BuRd`

`colors_diverging_BuYlRd`

`colors_diverging_spectral`

`colors_diverging_icefire`

`dinosaurs` *Dinosaurs data*

Description

Dinosaurs data

Usage

```
dinosaurs
```

Format

A data frame.

Source

ChatGPT-3.5, *Caution: The accuracy of the data has not been verified.*

Examples

```
dplyr::glimpse(dinosaurs)
```

distributions *Distributions data*

Description

Distributions data

Usage

```
distributions
```

Format

A data frame.

Source

tidyplots package

Examples

```
dplyr::glimpse(distributions)
```

energy *Energy data*

Description

Energy data

Usage

```
energy
```

Format

A data frame.

Source

Energy-Charts, Energy production data, Germany

Examples

```
dplyr::glimpse(energy)
```

energy_week *Energy week data*

Description

Energy week data

Usage

```
energy_week
```

Format

A data frame.

Source

Energy-Charts, Energy production data, Germany

Examples

```
dplyr::glimpse(energy_week)
```

eu_countries *EU countries data*

Description

EU countries data

Usage

```
eu_countries
```

Format

A data frame.

Source

ChatGPT-3.5, *Caution: The accuracy of the data has not been verified.*

Examples

```
dplyr::glimpse(eu_countries)
```

flip_plot *Flip x and y-axis*

Description

[Superseded]

This function is superseded because in many cases, `flip_plot()` can easily be replaced by swapping the `x` and `y` axis. Some plot components additionally require to set the `orientation` argument to `"y"`.

Usage

```
flip_plot(plot, ...)
```

Arguments

`plot`	A `tidyplot` generated with the function `tidyplot()`.
`...`	Arguments passed on to `ggplot2::coord_flip()`.

Value

A `tidyplot` object.

Examples

```
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  flip_plot()

energy %>%
  tidyplot(x = year, y = power, color = energy_type) %>%
  add_barstack_absolute() %>%
  flip_plot()

# Better solutions without `flip_plot()`
study %>%
  tidyplot(x = score, y = treatment, color = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

energy %>%
  tidyplot(x = power, y = year, color = energy_type) %>%
  add_barstack_absolute(orientation = "y")
```

format_number *Format numbers or p values*

Description

Format numbers or p values

Usage

```
format_number(x, accuracy = 0.1, big.mark = ",", scale_cut = NULL, ...)

format_p_value(x, accuracy = 1e-04)
```

Arguments

x	A number to format.
accuracy	A number to round to. Use (e.g.) 0.01 to show 2 decimal places of precision. If NULL, the default, uses a heuristic that should ensure breaks have the minimum number of digits needed to show the difference between adjacent values. Applied to rescaled data.
big.mark	Character used between every 3 digits to separate thousands.
scale_cut	Named numeric vector that allows you to rescale large (or small) numbers and add a prefix. Built-in helpers include: • cut_short_scale(): [10^3, 10^6) = K, [10^6, 10^9) = M, [10^9, 10^12) = B, [10^12, Inf) = T. • cut_long_scale(): [10^3, 10^6) = K, [10^6, 10^12) = M, [10^12, 10^18) = B, [10^18, Inf) = T. • cut_si(unit): uses standard SI units. If you supply a vector c(a = 100, b = 1000), absolute values in the range [0, 100) will not be rescaled, absolute values in the range [100, 1000) will be divided by 100 and given the suffix "a", and absolute values in the range [1000, Inf) will be divided by 1000 and given the suffix "b". If the division creates an irrational value (or one with many digits), the cut value below will be tried to see if it improves the look of the final label.
...	Arguments passed on to scales::number scale A scaling factor: x will be multiplied by scale before formatting. This is useful if the underlying data is very small or very large. style_positive A string that determines the style of positive numbers: • "none" (the default): no change, e.g. 1. • "plus": preceded by +, e.g. +1. • "space": preceded by a Unicode "figure space", i.e., a space equally as wide as a number or +. Compared to "none", adding a figure space can ensure numbers remain properly aligned when they are left- or right-justified.

style_negative A string that determines the style of negative numbers:

- "hyphen" (the default): preceded by a standard hypen -, e.g. -1.
- "minus", uses a proper Unicode minus symbol. This is a typographical nicety that ensures - aligns with the horizontal bar of the the horizontal bar of +.
- "parens", wrapped in parentheses, e.g. (1).

Value

Formatted number as character string.

Examples

```
format_number(232342.3443)

format_number(232342.3443, accuracy = 0.01)

format_number(232342.3443, accuracy = 1, big.mark = "")

format_p_value(0.03445553)

format_p_value(0.0003445553)

format_p_value(0.00003445553)
```

---

gene_expression *RNA-Seq expression data*

Description

RNA-Seq expression data

Usage

```
gene_expression
```

Format

A data frame.

Source

Bassoon proteinopathy drives neurodegeneration in multiple sclerosis, Nature Neuroscience

GSE104899, Gene Expression Omnibus

Examples

```
dplyr::glimpse(gene_expression)
```

new_color_scheme *New color scheme*

Description

For more information about the use of color schemes in tidyplots, check out this article: Color schemes

Usage

```
new_color_scheme(x, name = "Untitled color scheme", reverse = FALSE)
```

Arguments

x	Character vector of hex colors. For example x = c("#FF00FF", "#00FFFF").
name	Name of the custom color scheme.
reverse	Whether the order should be reversed or not. Defaults to FALSE, meaning not reversed.

Value

A tidyplot object.

Examples

```
new_color_scheme(c("#ECA669","#E06681","#8087E2","#E2D269"))

new_color_scheme(c("#ECA669","#E06681","#8087E2","#E2D269"),
  name = "my_custom_color_scheme")
```

remove_legend *Remove legend or legend title*

Description

Remove legend or legend title

Usage

```
remove_legend(plot)

remove_legend_title(plot)
```

Arguments

plot	A tidyplot generated with the function tidyplot().

Value

A tidyplot object.

Examples

```
# Before removing
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar()

# After removing
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar() %>%
  remove_legend_title()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar() %>%
  remove_legend()
```

---

remove_padding *Remove plot area padding*

Description

Remove plot area padding

Usage

```
remove_padding(plot, force_continuous = FALSE)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
force_continuous	Whether to force the axis to be continuous. Defaults to FALSE.

Value

A tidyplot object.

Examples

```
# Before removing
animals %>%
  tidyplot(x = weight, y = speed, color = family) %>%
  add_data_points()

# After removing
animals %>%
  tidyplot(x = weight, y = speed, color = family) %>%
  add_data_points() %>%
  remove_padding()
```

---

remove_title *Remove plot title or caption*

Description

Remove plot title or caption

Usage

```
remove_title(plot)

remove_caption(plot)
```

Arguments

plot	A tidyplot generated with the function tidyplot().

Value

A tidyplot object.

Examples

```
# Before removing
animals %>%
  tidyplot(x = weight, y = speed, color = family) %>%
  add_data_points() %>%
  add_title("Name of the plot") %>%
  add_caption("This is the caption")

# After removing
animals %>%
  tidyplot(x = weight, y = speed, color = family) %>%
  add_data_points() %>%
  add_title("Name of the plot") %>%
  add_caption("This is the caption") %>%
```

```
  remove_title()

animals %>%
  tidyplot(x = weight, y = speed, color = family) %>%
  add_data_points() %>%
  add_title("Name of the plot") %>%
  add_caption("This is the caption") %>%
  remove_caption()
```

`remove_x_axis` *Remove x-axis or parts of it*

Description

Remove x-axis or parts of it

Usage

```
remove_x_axis(plot)

remove_x_axis_line(plot)

remove_x_axis_ticks(plot)

remove_x_axis_labels(plot)

remove_x_axis_title(plot)
```

Arguments

`plot`	A `tidyplot` generated with the function `tidyplot()`.

Value

A `tidyplot` object.

Examples

```
# Before removing
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar()

# After removing
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar() %>%
  remove_x_axis_line()
```

```
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar() %>%
  remove_x_axis_ticks()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar() %>%
  remove_x_axis_labels()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar() %>%
  remove_x_axis_title()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar() %>%
  remove_x_axis()
```

`remove_y_axis` *Remove y-axis or parts of it*

Description

Remove y-axis or parts of it

Usage

```
remove_y_axis(plot)

remove_y_axis_line(plot)

remove_y_axis_ticks(plot)

remove_y_axis_labels(plot)

remove_y_axis_title(plot)
```

Arguments

`plot`	A `tidyplot` generated with the function `tidyplot()`.

Value

A `tidyplot` object.

Examples

```
# Before removing
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar()

# After removing
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar() %>%
  remove_y_axis_line()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar() %>%
  remove_y_axis_ticks()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar() %>%
  remove_y_axis_labels()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar() %>%
  remove_y_axis_title()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar() %>%
  remove_y_axis()
```

---

rename_x_axis_labels *Rename axis or color labels*

Description

Rename axis or color labels

Usage

```
rename_x_axis_labels(plot, new_names)

rename_y_axis_labels(plot, new_names)

rename_color_labels(plot, new_names)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
new_names	Named character vector in the format c("old1" = "new1", "old2" = "new2").

Value

A tidyplot object.

Examples

```
# Before adjustments
study %>%
  tidyplot(x = treatment, y = score) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Rename x-axis labels
study %>%
  tidyplot(x = treatment, y = score) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  rename_x_axis_labels(new_names = c(
    "A" = "This",
    "B" = "is",
    "C" = "totally",
    "D" = "new"))

# Before adjustments
study %>%
  tidyplot(x = score, y = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Rename y-axis labels
study %>%
  tidyplot(x = score, y = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  rename_y_axis_labels(new_names = c(
    "A" = "This",
    "B" = "is",
    "C" = "totally",
    "D" = "new"))

# Before adjustment
study %>%
  tidyplot(x = group, y = score, color = dose) %>%
  add_data_points() %>%
```

```
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Rename color labels
study %>%
  tidyplot(x = group, y = score, color = dose) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  rename_color_labels(new_names = c(
    "high" = "Sky high",
    "low" = "Deep low"))
```

`reorder_x_axis_labels` *Reorder axis or color labels*

Description

Reorder axis or color labels

Usage

```
reorder_x_axis_labels(plot, ...)

reorder_y_axis_labels(plot, ...)

reorder_color_labels(plot, ...)
```

Arguments

`plot`	A `tidyplot` generated with the function `tidyplot()`.
`...`	Arguments passed on to `forcats::fct_relevel()`.

Value

A `tidyplot` object.

Examples

```
# Before adjustments
study %>%
  tidyplot(x = treatment, y = score) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Reorder x-axis labels
study %>%
```

```
  tidyplot(x = treatment, y = score) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  reorder_x_axis_labels("D", "B", "A")

# Before adjustments
study %>%
  tidyplot(x = score, y = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Reorder y-axis labels
study %>%
  tidyplot(x = score, y = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  reorder_y_axis_labels("D", "B", "A")

# Before adjustment
study %>%
  tidyplot(x = group, y = score, color = dose) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Reorder color labels
study %>%
  tidyplot(x = group, y = score, color = dose) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  reorder_color_labels("low")
```

`reverse_x_axis_labels` *Reverse axis or color labels*

Description

Reverse axis or color labels

Usage

```
reverse_x_axis_labels(plot)

reverse_y_axis_labels(plot)

reverse_color_labels(plot)
```

Arguments

plot	A tidyplot generated with the function tidyplot().

Value

A tidyplot object.

Examples

```
# Before adjustments
study %>%
  tidyplot(x = treatment, y = score) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Reverse x-axis labels
study %>%
  tidyplot(x = treatment, y = score) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  reverse_x_axis_labels()

# Before adjustments
study %>%
  tidyplot(x = score, y = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Reverse y-axis labels
study %>%
  tidyplot(x = score, y = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  reverse_y_axis_labels()

# Before adjustment
study %>%
  tidyplot(x = group, y = score, color = dose) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Reverse color labels
study %>%
  tidyplot(x = group, y = score, color = dose) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
```

```
reverse_color_labels()
```

`save_plot` *Save plots to file*

Description

This function takes a plot or list of plots and writes them to a (multipage) file.

Usage

```
save_plot(
  plot = ggplot2::last_plot(),
  filename,
  width = NA,
  height = NA,
  units = c("mm", "cm", "in"),
  multiple_files = FALSE,
  bg = "transparent",
  ...
)
```

Arguments

`plot`	Plot to save, defaults to last plot displayed.
`filename`	File name to create on disk.
`width, height`	Dimensions of the graphic device to save the plot. Defaults to `NA`. In case of `NA`, the dimensions are inferred from the incoming `plot` object (see Details).
`units`	Units of length. Defaults to `"mm"`.
`multiple_files`	Whether to save multiple pages as individual files.
`bg`	Background colour. If `NULL`, uses the `plot.background` fill value from the plot theme.
`...`	Other arguments passed on to the graphics device function, as specified by `device`.

Details

Handling of file dimensions. Output file dimensions are determined according the the following precedence.

1. The `width` and `height` arguments.
2. Dimensions inferred from the incoming `plot` object with absolute dimensions.
3. System default device dimensions.

Value

A tidyplot object.

Examples

```
# Save plot to file
study %>%
  tidyplot(treatment, score) %>%
  add_data_points() %>%
  save_plot("single_plot.pdf")

# Save intermediate stages to file
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  add_data_points_beeswarm() %>%
  save_plot("before.pdf") %>%
  adjust_colors(colors_discrete_seaside) %>%
  save_plot("after.pdf")



# Save multipage PDF file
gene_expression %>%
  .[1:160,] %>%
  tidyplot(group, expression, color = sample_type) %>%
  add_data_points() %>%
  split_plot(by = external_gene_name, nrow = 2, ncol = 2) %>%
  save_plot("multipage_plot.pdf")

# Save multiple PDF files
gene_expression %>%
  .[1:160,] %>%
  tidyplot(group, expression, color = sample_type) %>%
  add_data_points() %>%
  split_plot(by = external_gene_name, nrow = 2, ncol = 2) %>%
  save_plot("plot.pdf", multiple_files = TRUE)
```

---

sort_x_axis_labels *Sort axis or color labels*

Description

Sort axis or color labels

Usage

```
sort_x_axis_labels(plot, ..., .fun = NULL, .reverse = FALSE)

sort_y_axis_labels(plot, ..., .fun = NULL, .reverse = FALSE)

sort_color_labels(plot, ..., .fun = NULL, .reverse = FALSE)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
...	Optional variables to use for sorting.
.fun	Override the function used for sorting. Is automatically determined from the plot.
.reverse	Whether the order should be reversed or not. Defaults to FALSE, meaning not reversed.

Value

A tidyplot object.

Examples

```
# Before adjustments
study %>%
  tidyplot(x = treatment, y = score) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Sort x-axis labels by score
study %>%
  tidyplot(x = treatment, y = score) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  sort_x_axis_labels()

# Before adjustments
study %>%
  tidyplot(x = score, y = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Sort y-axis labels by score
study %>%
  tidyplot(x = score, y = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
```

```
  sort_y_axis_labels()

# Before adjustment
study %>%
  tidyplot(x = group, y = score, color = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar()

# Sort color labels by score
study %>%
  tidyplot(x = group, y = score, color = treatment) %>%
  add_data_points() %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  sort_color_labels()
```

---

spendings *Spending data*

Description

Spending data

Usage

```
spendings
```

Format

A data frame.

Source

tidyplots package

Examples

```
dplyr::glimpse(spendings)
```

split_plot *Split plot into multiple subplots*

Description

Split plot into multiple subplots

Usage

```
split_plot(
  plot,
  by,
  ncol = NULL,
  nrow = NULL,
  byrow = NULL,
  widths = 30,
  heights = 25,
  guides = "collect",
  tag_level = NULL,
  design = NULL,
  unit = "mm"
)
```

Arguments

plot	A tidyplot generated with the function tidyplot().
by	Variable that should be used for splitting.
ncol, nrow	The number of columns and rows per page.
byrow	Analogous to byrow in matrix(). If FALSE the plots will be filled in in column-major order
widths, heights	The relative widths and heights of each column and row in the grid. Will get repeated to match the dimensions of the grid. The special value of NA/-1null will behave as 1null unless a fixed aspect plot is inserted in which case it will allow the dimension to expand or contract to match the aspect ratio of the content
guides	A string specifying how guides should be treated in the layout. 'collect' will collect guides below to the given nesting level, removing duplicates. 'keep' will stop collection at this level and let guides be placed alongside their plot. auto will allow guides to be collected if a upper level tries, but place them alongside the plot if not. If you modify default guide "position" with theme(legend.position=...) while also collecting guides you must apply that change to the overall patchwork (see example).
tag_level	A string ('keep' or 'new') to indicate how auto-tagging should behave. See plot_annotation().
design	Specification of the location of areas in the layout. Can either be specified as a text string or by concatenating calls to area() together. See the examples for further information on use.

unit Unit of length. Defaults to "mm".

Value

A tidyplot object.

Examples

```
# Before splitting
energy %>%
  dplyr::filter(year %in% c(2005, 2010, 2015, 2020)) %>%
  tidyplot(y = power, color = energy_source) %>%
  add_donut()

# Split by year
energy %>%
  dplyr::filter(year %in% c(2005, 2010, 2015, 2020)) %>%
  tidyplot(y = power, color = energy_source) %>%
  add_donut() %>%
  split_plot(by = year)

# Change dimensions of subplots
energy %>%
  dplyr::filter(year %in% c(2005, 2010, 2015, 2020)) %>%
  tidyplot(y = power, color = energy_source) %>%
  add_donut() %>%
  split_plot(by = year, widths = 15, heights = 15)

# Spread plots across multiple pages
energy %>%
  dplyr::filter(year %in% c(2005, 2010, 2015, 2020)) %>%
  tidyplot(y = power, color = energy_source) %>%
  add_donut() %>%
  split_plot(by = year, ncol = 2, nrow = 1)
```

---

study *Study data*

Description

Study data

Usage

```
study
```

Format

A data frame.

Source

tidyplots package

Examples

```
dplyr::glimpse(study)
```

`theme_tidyplot` *Themes*

Description

Themes

Usage

```
theme_tidyplot(plot, fontsize = 7)

theme_ggplot2(plot, fontsize = 7)

theme_minimal_xy(plot, fontsize = 7)

theme_minimal_x(plot, fontsize = 7)

theme_minimal_y(plot, fontsize = 7)
```

Arguments

`plot`	A `tidyplot` generated with the function `tidyplot()`.
`fontsize`	Font size in points. Defaults to 7.

Value

A `tidyplot` object.

Examples

```
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_sem_errorbar() %>%
  add_mean_dash() %>%
  theme_tidyplot()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_sem_errorbar() %>%
```

```
  add_mean_dash() %>%
  theme_ggplot2()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_sem_errorbar() %>%
  add_mean_dash() %>%
  theme_minimal_xy()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_sem_errorbar() %>%
  add_mean_dash() %>%
  theme_minimal_x()

study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points() %>%
  add_sem_errorbar() %>%
  add_mean_dash() %>%
  theme_minimal_y()
```

`tidyplot` *Create a new tidyplot*

Description

Create a new tidyplot

Usage

```
tidyplot(data, ..., width = 50, height = 50, dodge_width = NULL)
```

Arguments

`data`	A tidy `data.frame` to use for plotting.
`...`	Mappings for the `x` axis, `y` axis and `color`, see examples. Additional argument are passed to `ggplot2::aes()`.
`width`	Width of the plot area. Defaults to `50`.
`height`	Height of the plot area. Defaults to `50`.
`dodge_width`	For adjusting the distance between grouped objects. Defaults to `0.8` for plots with at least one discrete axis and `0` for plots with two continuous axes.

Value

A `tidyplot` object.

Examples

```
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_data_points_beeswarm()

study %>%
  tidyplot(x = group, y = score, color = dose) %>%
  add_mean_bar()

# Change plot area size
study %>%
  tidyplot(x = treatment, y = score, color = treatment,
    width = 35, height = 35) %>%
  add_data_points_beeswarm()

# Change dodge_width
study %>%
  tidyplot(x = group, y = score, color = dose, dodge_width = 0.3) %>%
  add_mean_bar()
```

---

time_course *Time course data*

Description

Time course data

Usage

```
time_course
```

Format

A data frame.

Source

tidyplots package

Examples

```
dplyr::glimpse(time_course)
```

`view_plot` *View plot on screen*

Description

View plot on screen

Usage

```
view_plot(plot, data = all_rows(), title = ggplot2::waiver(), ...)
```

Arguments

`plot`	A `tidyplot` generated with the function `tidyplot()`.
`data`	The data to be displayed in this layer. There are three options: • If `all_rows()` (the default) the complete dataset is displayed. • A `function` to subset the plot data. See `filter_rows()` and friends. • A `data.frame` to override the plot data.
`title`	Plot title.
`...`	Arguments passed on to `print()`.

Details

- `view_plot()` supports data subsetting. See examples and Advanced plotting.

Value

A `tidyplot` object.

Examples

```
# View intermediate stages on screen
study %>%
  tidyplot(x = treatment, y = score, color = treatment) %>%
  add_mean_bar(alpha = 0.4) %>%
  add_sem_errorbar() %>%
  add_data_points_beeswarm() %>%
  view_plot(title = "Before changing color scheme") %>%
  adjust_colors(colors_discrete_seaside) %>%
  view_plot(title = "After changing color scheme")

# View data subsets on screen
gene_expression %>%
  tidyplot(x = condition, y = expression, color = sample_type) %>%
  add_mean_dash() %>%
  add_sem_errorbar() %>%
  add_data_points_beeswarm() %>%
```

```
view_plot(data = filter_rows(external_gene_name == "Apol6"),
  title = "Apol6") %>%
view_plot(data = filter_rows(external_gene_name == "Bsn"),
  title = "Bsn")
```

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