

Package ‘utile.visuals’

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Title Create Visuals for Publication

Version 0.3.3

Description A set of functions to aid in the production of visuals in ggplot2.

License LGPL (>= 2)

URL <https://efinite.github.io/utile.visuals/>

BugReports <https://github.com/efinite/utile.visuals/issues>

Encoding UTF-8

Depends R (>= 3.4.0)

Imports dplyr, ggplot2 (>= 0.3.4), gridExtra, purrr

Suggests survival, broom, grid

RoxygenNote 7.2.3

NeedsCompilation no

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append_table	<i>Append a ggplot2 table to the bottom of a ggplot2 plot</i>
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Description

Aligns axes and combines a ggplot2 plot and table into a single plot. Can handle legends.

Usage

```
append_table(
  plot = NULL,
  table = NULL,
  plot.height = 1,
  table.height = 0.1,
  plot.width = 1,
  extract.legend = TRUE,
  legend.width = 0.2,
  legend.offset = -15
)
```

Arguments

plot	Required. ggplot2::ggplot() object. If a legend is present, it will be extracted.
table	Required. ggplot2::ggplot object. If a legend is present, it will be removed and ignored.
plot.height	Optional. Numeric. Height of plot relative to table. Defaults to 1.
table.height	Optional. Numeric. Height of table relative to plot. Defaults to 0.1.
plot.width	Optional. Numeric. Width of plot relative to legend. Ignored if no legend present in plot. Defaults to 1.
extract.legend	Optional. Logical. Indicates whether to extract the legend from the plot and reinsert it adjacent to the final combined plot. May be undesired if legend already embedded within the plot area. Defaults to TRUE.
legend.width	Optional. Numeric. Width of legend relative to plot. Ignored if no legend present in plot or 'extract.legend'=FALSE. Defaults 0.2.
legend.offset	Optional. Numeric. Vertical offset of legend. Used to raise or lower. Ignored if no legend present in plot or 'extract.legend'=FALSE. Defaults to -15.

Value

A ggplot2 tableGrob object. Use grid::grid.draw() to open in RStudio viewer. Works with ggplot2::ggsave() out of the box.

Note

To ensure proper alignment, double check that both plots use the same scale and breaks!

Examples

```
library(survival)
library(ggplot2)
library(broom) # tidy() model data
library(grid) # grid.draw() finished plot

# Data with group names specified
data_diabetic <- diabetic
data_diabetic$trt <- as.factor(data_diabetic$trt)
levels(data_diabetic$trt) <- c('None', 'Laser')

# Survival Model
fit <- survfit(Surv(time, status) ~ trt, data = data_diabetic)

# Kaplan Meier (KM) Plot
plot_km <- ggplot(
  data = tidy(fit),
  mapping = aes(x = time, y = estimate)
) +
  geom_step(aes(color = strata)) +
  geom_stepconfint(aes(ymin = conf.low, ymax = conf.high, fill = strata), alpha = 0.3) +
  coord_cartesian(c(0, 50)) + # Note scale set here!
  scale_x_continuous(expand = c(0.02,0)) +
  labs(x = 'Time', y = 'Freedom From Event') +
  scale_color_manual(
    values = c('#d83641', '#1A45A7'),
    name = 'Treatment',
    labels = c('Laser', 'None'),
    aesthetics = c('colour', 'fill')) +
  theme_basic()

# Risk Table
tbl_risk <- ggrisktable(fit, c(0, 10, 20, 30, 40, 50)) +
  coord_cartesian(c(0, 50)) +
  scale_x_continuous(expand = c(0.02,0)) +
  theme_risk()

# Combine KM plot and risk table
plot_cmbd <- append_table(
  plot = plot_km,
  table = tbl_risk
)

# Draw in RStudio viewer
grid.newpage()
grid.draw(plot_cmbd)
```

Description

Produces a step function confidence interval for survival curves.

Usage

```
geom_stepconfint(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  na.rm = FALSE,
  ...
)
```

Arguments

mapping	Aesthetic mappings with aes() function. Like geom_ribbon(), you must provide columns for x, ymin (lower limit), ymax (upper limit).
data	The data to be displayed in this layer. Can inherit from ggplot parent.
stat	The statistical transformation to use on the data for this layer, as a string. Defaults to 'identity'.
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
na.rm	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
...	Optional. Any other ggplot geom_ribbon() arguments.

Note

Adapted from the survminer package <<https://github.com/kassambara/survminer>>.

Examples

```
library(survival)
library(broom)
library(ggplot2)

fit <- survfit(Surv(time, status) ~ trt, data = diabetic)
fit <- survfit0(fit) # connect origin

ggplot(
  data = tidy(fit),
  mapping = aes(x = time, y = estimate)
) +
  geom_step(aes(color = strata)) +
  geom_stepconfint(aes(ymin = conf.low, ymax = conf.high, fill = strata), alpha = 0.3) +
  coord_cartesian(c(0, 50)) +
  scale_x_continuous(expand = c(0.02, 0)) +
  labs(x = 'Time', y = 'Freedom From Event') +
```

```
scale_color_manual(  
  values = c('#d83641', '#1A45A7'),  
  name = 'Treatment',  
  labels = c('None', 'Laser'),  
  aesthetics = c('colour', 'fill')) +  
theme_basic()
```

ggrisktable*Create a ggplot2 table showing the number at risk*

Description

A simple wrapper function which calculates the numbers at risk for a survival model and a given set of time points then creates a ggplot2 table with them.

Usage

```
ggrisktable(  
  fit = NULL,  
  times = NULL,  
  text.color = "black",  
  strata.order = NULL  
)
```

Arguments

<code>fit</code>	Required. <code>survival::survfit()</code> object.
<code>times</code>	Required. Numeric. One or more time points to calculate the number at risk for.
<code>text.color</code>	Optional. Character. Color of text within table. Defaults to 'black'.
<code>strata.order</code>	Optional. Character. Ordered names of strata factor levels.

Value

An unformatted ggplot2 table showing the number at risk.

Examples

```
library(survival)  
  
fit <- survfit(Surv(time, status) ~ trt, data = diabetic)  
  
ggrisktable(  
  fit = fit,  
  times = c(0, 10, 20, 30, 40, 50),  
  strata.order = c('0', '1')  
) + theme_risk()
```

panel_border *Add a panel border to a ggplot2 plot*

Description

A simple ggplot2 theme which replaces the axis lines with a bordered panel.

Usage

```
panel_border(base_size = 12, base_color = NULL)
```

Arguments

base_size A numeric. Base size. Used to calculate line size and spacing.
base_color A character. Base color for lines.

Note

This should be placed after the primary theme for the plot.

Examples

```
library(ggplot2)

ggplot(datasets::mtcars, aes(x = wt, y = hp, color = as.factor(cyl))) +
  geom_point() +
  facet_wrap(~as.logical(am)) +
  theme_basic() +
  panel_border()
```

theme_basic *Minimalist theme for ggplot2*

Description

A minimalist ggplot2 theme which removes most background elements and lines.

Usage

```
theme_basic(
  base_size = 12,
  base_family = NULL,
  base_color = "black",
  base_line_size = base_size/12,
  base_rect_size = base_size/12
)
```

Arguments

base_size A numeric. Base font size.
base_family A numeric. Base font family.
base_color A character. Base color for lines and text.
base_line_size A numeric. Base line element size.
base_rect_size A numeric. Base rectangle element size.

Note

Recommend exporting as PNG or TIFF to preserve background transparency.

Examples

```
library(ggplot2)

ggplot(datasets::mtcars, aes(x = wt, y = hp, color = as.factor(cyl))) +
  geom_point() +
  theme_basic()
```

theme_risk

Minimalist risk table theme for ggplot2

Description

A minimalist ggplot2 theme which removes most background elements and lines.

Usage

```
theme_risk(
  base_size = 12,
  base_family = NULL,
  base_color = "black",
  base_line_size = base_size/12,
  base_rect_size = base_size/12
)
```

Arguments

base_size A numeric. Base font size.
base_family A numeric. Base font family.
base_color A character. Base color for lines and text.
base_line_size A numeric. Base line element size.
base_rect_size A numeric. Base rectangle element size.

Note

Recommend exporting as PNG or TIFF to preserve background transparency.

See Also

[ggrisktable](#)

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