

Package ‘utile.visuals’

May 2, 2020

Title Create Visuals for Publication

Version 0.2.5

Description A small set of functions for making visuals for publication in ggplot2. Includes minimalist themes with transparent backgrounds and a suite of tools for building Kaplan-Meier curves with risk tables.

License LGPL (>= 2)

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

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

Encoding UTF-8

LazyData TRUE

Depends R (>= 3.4.0)

Imports dplyr, ggplot2, gridExtra, purrr

Suggests survival, broom, grid

RoxygenNote 7.1.0

NeedsCompilation no

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Repository CRAN

Date/Publication 2020-05-01 22:40:02 UTC

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append_table*Append a ggplot2 table to the bottom of a ggplot2 plot*

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

<code>plot</code>	Required. <code>ggplot2::ggplot()</code> object. If a legend is present, it will be extracted.
<code>table</code>	Required. <code>ggplot2::ggplot</code> object. If a legend is present, it will be removed and ignored.
<code>plot.height</code>	Optional. Numeric. Height of plot relative to table. Defaults to 1.
<code>table.height</code>	Optional. Numeric. Height of table relative to plot. Defaults to 0.1.
<code>plot.width</code>	Optional. Numeric. Width of plot relative to legend. Ignored if no legend present in plot. Defaults to 1.
<code>extract.legend</code>	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.
<code>legend.width</code>	Optional. Numeric. Width of legend relative to plot. Ignored if no legend present in plot or ' <code>extract.legend</code> '=FALSE. Defaults 0.2.
<code>legend.offset</code>	Optional. Numeric. Vertical offset of legend. Used to raise or lower. Ignored if no legend present in plot or ' <code>extract.legend</code> '=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_black()

# 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_black()

# 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

Occasionally when tidy'd survfit data is graphed in `ggplot2::geom_step()`, the KM curve will not connect with the origin of the plot. This tool appends data connecting the lines to the origin.

Usage

```
connect_origin(data)
```

Arguments

data	Required. <code>tibble::tibble()</code> object. <code>survival::survfit</code> data that has been tidy'd with <code>broom::tidy()</code> .
------	--

Value

A tibble containing the original data with appended points that connect the curve with to the plot origin.

Note

Adapted from the `survminer` package created by Alboukadel Kassambara.

Examples

```
library(survival)
library(broom) # tidy() model data

# 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)
fit_data <- tidy(fit)

connect_origin(fit_data)
```

Description

Produces a step function confidence interval for survival curves. Essentially the `geom_step()` for confidence intervals which `ggplot2` elects not to provide.

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. All the other miscellaneous 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)

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_black()
```

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_black()
```

theme_black	<i>Minimalist black theme for ggplot2</i>
-------------	---

Description

A ggplot2 theme which removes most background elements and makes all text/lines black.

Usage

```
theme_black(  
  base_size = 11,  
  base_family = "",  
  base_line_size = base_size/22,  
  base_rect_size = base_size/22  
)
```

Arguments

base_size	Optional. Numeric. Base font size. Defaults to 11.
base_family	Optional. Numeric. Base font family. Defaults to ?.
base_line_size	Optional. Numeric. Base line element size. Defaults to base_size/22.
base_rect_size	Optional. Numeric. Base rectangle element size. Defaults to base_size/22.

Note

Recommend exporting as PNG or TIFF to preserve background transparency.

theme_risk_black	<i>Minimalist black risk table theme for ggplot2</i>
------------------	--

Description

Ggplot2 theme which removes most background elements and makes all text/lines black.

Usage

```
theme_risk_black(  
  base_size = 10,  
  base_family = "",  
  base_line_size = base_size/22,  
  base_rect_size = base_size/22  
)
```

Arguments

`base_size` Optional. Numeric. Base font size. Defaults to 10.
`base_family` Optional. Numeric. Base font family. Defaults to ?.
`base_line_size` Optional. Numeric. Base line element size. Defaults to `base_size/22`.
`base_rect_size` Optional. Numeric. Base rectangle element size. Defaults to `base_size/22`.

Note

Recommend exporting as PNG or TIFF to preserve background transparency.

`theme_risk_white` *Minimalist white risk table theme for ggplot2*

Description

Ggplot2 theme which removes most background elements and makes all text/lines white.

Usage

```
theme_risk_white(  
  base_size = 10,  
  base_family = "",  
  base_line_size = base_size/22,  
  base_rect_size = base_size/22  
)
```

Arguments

`base_size` Optional. Numeric. Base font size. Defaults to 10.
`base_family` Optional. Numeric. Base font family. Defaults to ?.
`base_line_size` Optional. Numeric. Base line element size. Defaults to `base_size/22`.
`base_rect_size` Optional. Numeric. Base rectangle element size. Defaults to `base_size/22`.

Note

Recommend exporting as PNG or TIFF to preserve background transparency.

theme_white	<i>Minimalist white theme for ggplot2</i>
-------------	---

Description

A ggplot2 theme which removes most background elements and makes all text/lines white.

Usage

```
theme_white(  
  base_size = 11,  
  base_family = "",  
  base_line_size = base_size/22,  
  base_rect_size = base_size/22  
)
```

Arguments

`base_size` Optional. Numeric. Base font size. Defaults to 11.
`base_family` Optional. Numeric. Base font family. Defaults to ?.
`base_line_size` Optional. Numeric. Base line element size. Defaults to `base_size/22`.
`base_rect_size` Optional. Numeric. Base rectangle element size. Defaults to `base_size/22`.

Note

Recommend exporting as PNG or TIFF to preserve background transparency.

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