

Package: ggforestplotR (via r-universe)

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Title Publication-Ready Forest Plots with 'ggplot2'

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Description Transform model coefficients into flexible forest plots using 'ggplot2'. Provides helpers to standardize coefficient data from a range of modelling workflows and render publication-ready forest plots with a consistent interface.

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add_forest_table	<i>Add a summary table to a forest plot</i>
------------------	---

Description

Compose a summary table onto a forest plot.

Usage

```
add_forest_table(
  plot = NULL,
  position = c("left", "right"),
  show_terms = TRUE,
  show_n = NULL,
  show_events = NULL,
  show_estimate = TRUE,
  show_p = FALSE,
  columns = NULL,
  term_header = "Term",
  n_header = "N",
  events_header = "Events",
  estimate_label = NULL,
  p_header = "P-value",
  column_labels = NULL,
  digits = NULL,
  estimate_digits = NULL,
  interval_digits = NULL,
  p_digits = NULL,
  estimate_fmt = NULL,
  ci_fmt = NULL,
  text_size = NULL,
  header_text_size = NULL,
  header_fontface = "bold",
  header_family = NULL,
  striped_rows = NULL,
  stripe_fill = NULL,
  stripe_colour = NULL,
  stripe_alpha = NULL,
```

```

    grid_lines = FALSE,
    grid_line_colour = "black",
    grid_line_size = 0.3,
    grid_line_linetype = 1
  )

```

Arguments

plot	A plot created by <code>ggforestplot()</code> . Leave as NULL to use + <code>add_forest_table(...)</code> syntax.
position	Whether to place the table on the left or right of the forest plot.
show_terms	Deprecated. Whether to show the term column in the table. Use <code>columns</code> instead.
show_n	Deprecated. Whether to show the N column. Use <code>columns</code> instead.
show_events	Deprecated. Whether to show the Events column. Use <code>columns</code> instead.
show_estimate	Deprecated. Whether to show the formatted estimate and confidence interval column. Use <code>columns</code> instead.
show_p	Deprecated. Whether to display the p-value column. Use <code>columns</code> instead.
columns	Optional explicit columns to display in the side table, in the order they should appear. Accepts built-in names such as "term", "n", "events", "estimate", "ci", and "p", arbitrary original dataframe columns, or positions corresponding to the built-in columns. "conf.low" and "conf.high" are accepted as aliases for "ci". When supplied, this overrides the default <code>show_*</code> column selection.
term_header	Header text for the term column.
n_header	Header text for the N column.
events_header	Header text for the Events column.
estimate_label	Header label for the estimate column. Defaults to the model-derived label when available.
p_header	Header text for the p-value column.
column_labels	Optional named vector used to relabel table column headers. Names should match values supplied to <code>columns</code> after column resolution, such as "term", "estimate", "ci", "p", or an arbitrary original dataframe column.
digits	Deprecated. Number of digits used when formatting estimates and p-values. Defaults to 2. Use <code>estimate_digits</code> , <code>interval_digits</code> , and <code>p_digits</code> for separate control.
estimate_digits	Number of digits used for point estimates.
interval_digits	Number of digits used for confidence interval bounds.
p_digits	Number of digits used for p-values.
estimate_fmt	Format string for the estimate column. Use <code>{estimate}</code> , <code>{conf.low}</code> , and <code>{conf.high}</code> as placeholders. The shorthand <code>{conf.low, conf.high}</code> is also supported. Defaults to " <code>{estimate} ({conf.low}, {conf.high})</code> ", or " <code>{estimate}</code> " when <code>columns</code> includes "ci".

<code>ci_fmt</code>	Format string for the confidence interval column when columns includes "ci". Use {conf.low} and {conf.high} as placeholders. The shorthand {conf.low, conf.high} is also supported. Defaults to "{conf.low}, {conf.high}".
<code>text_size</code>	Text size for table contents. Defaults to 3.2.
<code>header_text_size</code>	Header text size for table column labels. Defaults to 11.
<code>header_fontface</code>	Font face used for table column labels. Defaults to "bold".
<code>header_family</code>	Optional font family used for table column labels.
<code>striped_rows</code>	Whether to draw alternating row stripes behind the table. Defaults to the stripe setting used in <code>ggforestplot()</code> .
<code>stripe_fill</code>	Fill colour used for striped rows. Defaults to the stripe fill used in <code>ggforestplot()</code> .
<code>stripe_colour</code>	Outline colour for striped rows. Defaults to the stripe outline used in <code>ggforestplot()</code> .
<code>stripe_alpha</code>	Transparency for striped rows. Defaults to the stripe alpha used in <code>ggforestplot()</code> .
<code>grid_lines</code>	Whether to draw black horizontal grid lines in the table.
<code>grid_line_colour</code>	Colour used for the table grid lines.
<code>grid_line_size</code>	Line width used for the table grid lines.
<code>grid_line_linetype</code>	Line type used for the table grid lines.

Value

A patchwork-composed plot containing the forest plot and side table, or a ggplot add-on object when `plot = NULL`.

Examples

```

coefs <- data.frame(
  term = c("Age", "BMI", "Treatment"),
  estimate = c(0.3, -0.2, 0.4),
  conf.low = c(0.1, -0.4, 0.2),
  conf.high = c(0.5, 0.0, 0.6),
  sample_size = c(120, 115, 98),
  p_value = c(0.012, 0.031, 0.004)
)

p <- ggforestplot(coefs, n = "sample_size", p.value = "p_value")
add_forest_table(
  p,
  position = "left",
  columns = c("term", "n", "estimate", "p"),
  estimate_label = "Beta"
)

ggforestplot(coefs, n = "sample_size", p.value = "p_value") +
  add_forest_table(
    position = "right",
  
```

```
    columns = c("term", "n", "estimate", "p"),
    estimate_label = "Beta"
  )
```

add_split_table	<i>Add split tables around a forest plot</i>
-----------------	--

Description

Compose split table blocks around a forest plot so that summary data appear on both sides of the plotting panel.

Usage

```
add_split_table(  
  plot = NULL,  
  show_terms = TRUE,  
  show_n = NULL,  
  show_events = NULL,  
  show_estimate = TRUE,  
  show_p = FALSE,  
  left_columns = NULL,  
  right_columns = NULL,  
  term_header = "Term",  
  n_header = "N",  
  events_header = "Events",  
  estimate_label = NULL,  
  p_header = "P-value",  
  column_labels = NULL,  
  digits = NULL,  
  estimate_digits = NULL,  
  interval_digits = NULL,  
  p_digits = NULL,  
  estimate_fmt = NULL,  
  ci_fmt = NULL,  
  text_size = NULL,  
  header_text_size = NULL,  
  header_fontface = "bold",  
  header_family = NULL,  
  striped_rows = NULL,  
  stripe_fill = NULL,  
  stripe_colour = NULL,  
  stripe_alpha = NULL,  
  left_width = NULL,  
  plot_width = NULL,  
  right_width = NULL  
)
```

Arguments

plot	A plot created by <code>ggforestplot()</code> . Leave as NULL to use + <code>add_split_table(...)</code> syntax.
show_terms	Whether to include the term column in the default left-side selection when <code>left_columns</code> is not supplied.
show_n	Whether to include the N column in the default left-side selection when <code>left_columns</code> is not supplied. Defaults to TRUE when the underlying plot data include an n column.
show_events	Whether to include the Events column in the default left-side selection when <code>left_columns</code> is not supplied. Defaults to TRUE when the underlying plot data include an events column.
show_estimate	Whether to include the formatted estimate and confidence interval column in the default right-side selection when <code>right_columns</code> is not supplied.
show_p	Whether to include the p-value column in the default right-side selection when <code>right_columns</code> is not supplied.
left_columns	Optional explicit columns to place on the left side of the forest plot. Accepts built-in names such as "term", "n", "events", "estimate", "ci", and "p", arbitrary original dataframe columns, or positions corresponding to the built-in columns. "conf.low" and "conf.high" are accepted as aliases for "ci".
right_columns	Optional explicit columns to place on the right side of the forest plot. Accepts built-in names such as "estimate", "ci", and "p", arbitrary original dataframe columns, or positions corresponding to the built-in columns. "conf.low" and "conf.high" are accepted as aliases for "ci".
term_header	Header text for the term column.
n_header	Header text for the N column.
events_header	Header text for the Events column.
estimate_label	Header label for the estimate column. Defaults to the model-derived label when available.
p_header	Header text for the p-value column.
column_labels	Optional named vector used to relabel table column headers. Names should match values supplied to <code>left_columns</code> or <code>right_columns</code> after column resolution, such as "term", "estimate", "ci", "p", or an arbitrary original dataframe column.
digits	Deprecated. Number of digits used when formatting estimates and p-values. Defaults to 2. Use <code>estimate_digits</code> , <code>interval_digits</code> , and <code>p_digits</code> for separate control.
estimate_digits	Number of digits used for point estimates.
interval_digits	Number of digits used for confidence interval bounds.
p_digits	Number of digits used for p-values.

estimate_fmt	Format string for the estimate column. Use {estimate}, {conf.low}, and {conf.high} as placeholders. The shorthand {conf.low, conf.high} is also supported. Defaults to "{estimate} ({conf.low}, {conf.high})", or "{estimate}" when table columns include "ci".
ci_fmt	Format string for the confidence interval column when table columns include "ci". Use {conf.low} and {conf.high} as placeholders. The shorthand {conf.low, conf.high} is also supported. Defaults to "{(conf.low), (conf.high)}".
text_size	Text size for table contents. Defaults to 3.2.
header_text_size	Header text size for table column labels. Defaults to 11.
header_fontface	Font face used for table column labels. Defaults to "bold".
header_family	Optional font family used for table column labels.
striped_rows	Whether to draw alternating row stripes behind the split table layout. Defaults to the stripe setting used in <code>ggforestplot()</code> .
stripe_fill	Fill colour used for striped rows. Defaults to the stripe fill used in <code>ggforestplot()</code> .
stripe_colour	Outline colour for striped rows. Defaults to the stripe outline used in <code>ggforestplot()</code> .
stripe_alpha	Transparency for striped rows. Defaults to the stripe alpha used in <code>ggforestplot()</code> .
left_width	Optional width allocated to the left table block. By default this is derived from the number of displayed left-side columns relative to <code>plot_width</code> .
plot_width	Optional width allocated to the forest plot panel. Defaults to 2.5.
right_width	Optional width allocated to the right table block. By default this is derived from the number of displayed right-side columns relative to <code>plot_width</code> .

Value

A patchwork-composed plot containing a left table, the forest plot, and a right table, or a `ggplot` add-on object when `plot = NULL`.

Examples

```

coefs <- data.frame(
  term = c("Age", "BMI", "Treatment"),
  estimate = c(0.3, -0.2, 0.4),
  conf.low = c(0.1, -0.4, 0.2),
  conf.high = c(0.5, 0.0, 0.6),
  sample_size = c(120, 115, 98),
  p_value = c(0.012, 0.031, 0.004)
)

p <- ggforestplot(coefs, n = "sample_size", p.value = "p_value")
add_split_table(
  p,
  left_columns = c("term", "n"),
  right_columns = c("estimate", "p"),
  estimate_label = "HR"
)

```

```
ggforestplot(coefs, n = "sample_size", p.value = "p_value") +
  add_split_table(
    left_columns = c(1, 2),
    right_columns = c(4, 5),
    estimate_label = "HR"
  )
```

as_forest_data

Standardize coefficient data for forest plots

Description

Standardizes a coefficient table into the internal forest-plot data structure used throughout ggforestplotR.

Usage

```
as_forest_data(
  data,
  term,
  estimate,
  conf.low,
  conf.high,
  label = term,
  term_labels = NULL,
  group = NULL,
  grouping = NULL,
  separate_groups = NULL,
  n = NULL,
  events = NULL,
  p.value = NULL,
  exponentiate = FALSE,
  sort_terms = c("none", "descending", "ascending")
)
```

Arguments

data	A data frame containing coefficient estimates and intervals.
term	Column name holding the model term identifier.
estimate	Column name holding the point estimate.
conf.low	Column name holding the lower confidence bound.
conf.high	Column name holding the upper confidence bound.
label	Optional column name used for the displayed row label.
term_labels	Optional named vector used to relabel displayed terms. Names should match values in the term column and values are the labels to display.
group	Optional column name used for color-grouping multiple estimates per row.

grouping	Optional column name used to split rows into grouped plot sections.
separate_groups	Optional column name used to identify labeled variable blocks that can be outlined with separator lines.
n	Optional column name holding sample sizes or other N labels for table helpers.
events	Optional column name holding event counts or event labels for table helpers.
p.value	Optional column name holding p-values.
exponentiate	Logical; if TRUE, require positive values for estimates and intervals.
sort_terms	How to sort rows: "none", "descending", or "ascending".

Value

A standardized data frame ready for `ggforestplot()` and the table composition helpers. Original dataframe columns are retained for table helpers so they can be displayed with `add_forest_table(columns = ...)`.

Examples

```
raw <- data.frame(
  variable = c("Age", "BMI", "Treatment"),
  beta = c(0.10, -0.08, 0.34),
  lower = c(0.02, -0.16, 0.12),
  upper = c(0.18, 0.00, 0.56)
)

as_forest_data(
  data = raw,
  term = "variable",
  estimate = "beta",
  conf.low = "lower",
  conf.high = "upper"
)
```

ggforestplot

Draw a ggplot2 forest plot

Description

Builds a forest plot from standardized coefficient data or directly from a fitted model.

Usage

```
ggforestplot(
  data,
  term = "term",
  estimate = "estimate",
  conf.low = "conf.low",
```

```

  conf.high = "conf.high",
  label = term,
  term_labels = NULL,
  group = NULL,
  facet = NULL,
  facet_stripe_position = c("left", "right"),
  grouping = NULL,
  grouping_stripe_position = NULL,
  separate_groups = NULL,
  n = NULL,
  events = NULL,
  p.value = NULL,
  exponentiate = NULL,
  sort_terms = c("none", "descending", "ascending"),
  point_size = 2.3,
  point_shape = 19,
  linewidth = 0.5,
  line_size = NULL,
  staple_width = 0.2,
  dodge_width = 0.6,
  separate_lines = FALSE,
  separator_line_linetype = 2,
  separator_line_colour = "black",
  separator_line_size = 0.4,
  striped_rows = FALSE,
  stripe_fill = "grey95",
  stripe_colour = NA,
  stripe_alpha = 1,
  ref_line = NULL,
  ref_label = NULL,
  ref_linetype = 2,
  ref_color = "grey60"
)

```

Arguments

<code>data</code>	Either a tidy coefficient data frame or a model object supported by <code>broom::tidy()</code> .
<code>term</code>	Column name holding the model term identifiers.
<code>estimate</code>	Column name holding the point estimates.
<code>conf.low</code>	Column name holding the lower confidence bounds.
<code>conf.high</code>	Column name holding the upper confidence bounds.
<code>label</code>	Optional column name used for the displayed row labels.
<code>term_labels</code>	Optional named vector used to relabel displayed terms. Names should match values in the term column and values are the labels to display.
<code>group</code>	Optional column name used for color-grouping estimates.
<code>facet</code>	Optional column name used to split rows into faceted plot sections. If this column is a factor, its levels control facet order.

facet_strip_position	Positioning for facet strip labels.
grouping	Deprecated. Use facet instead.
grouping_strip_position	Deprecated. Use facet_strip_position instead.
separate_groups	Optional column name used to identify labeled variable blocks that can be outlined with grid lines.
n	Optional column name holding sample sizes or other N labels for table helpers.
events	Optional column name holding event counts or event labels for table helpers.
p.value	Optional column name holding p-values.
exponentiate	Logical; if TRUE, transform the estimates and draw the axis on the log scale with the reference line at 1. For model objects, NULL uses the canonical scale when it can be inferred, such as hazard ratios for Cox models.
sort_terms	How to sort rows: "none", "descending", or "ascending".
point_size	Point size for coefficient markers.
point_shape	Shape used for coefficient markers.
linewidth	Line width for confidence intervals.
line_size	Deprecated. Use linewidth instead.
staple_width	Width of the terminal staples on confidence interval lines.
dodge_width	Horizontal dodging used for grouped estimates.
separate_lines	Logical; if TRUE, draw grid lines around each labeled block identified by separate_groups.
separator_line_linetype	Line type used for separator lines.
separator_line_colour	Colour used for separator lines.
separator_line_size	Line width used for separator lines.
striped_rows	Logical; if TRUE, shade alternating rows.
stripe_fill	Fill color used for shaded rows.
stripe_colour	Border color for shaded rows.
stripe_alpha	Transparency for shaded rows.
ref_line	Numeric x-value where the reference line is drawn, or NULL to hide it. When omitted, defaults to 0 for additive effects and 1 for exponentiated effects.
ref_label	Optional label drawn alongside the reference line.
ref_linetype	Line type for the reference line.
ref_color	Color for the reference line.

Value

A ggplot object. Use standard ggplot2 functions such as `ggplot2::labs()` for plot labels, and add composition helpers after styling the main plot.

Examples

```

coefs <- data.frame(
  term = c("Age", "BMI", "Treatment"),
  estimate = c(0.10, -0.08, 0.34),
  conf.low = c(0.02, -0.16, 0.12),
  conf.high = c(0.18, 0.00, 0.56)
)

ggforestplot(coefs)

ggforestplot(coefs, striped_rows = TRUE, point_shape = 17)

```

tidy_forest_model	<i>Tidy a model object for forest plotting</i>
-------------------	--

Description

Uses `broom::tidy()` to convert a fitted model into forest-plot data.

Usage

```

tidy_forest_model(
  model,
  conf.int = TRUE,
  conf.level = 0.95,
  exponentiate = NULL,
  intercept = FALSE,
  term_labels = NULL,
  sort_terms = c("none", "descending", "ascending")
)

```

Arguments

<code>model</code>	A fitted model object supported by <code>broom::tidy()</code> .
<code>conf.int</code>	Logical; if TRUE, request confidence intervals from <code>broom::tidy()</code> .
<code>conf.level</code>	Confidence level for intervals.
<code>exponentiate</code>	Logical; passed through to <code>broom::tidy()</code> .
<code>intercept</code>	Logical; if FALSE, drop the intercept term.
<code>term_labels</code>	Optional named vector used to relabel displayed terms. Names should match model term names and values are the labels to display.
<code>sort_terms</code>	How to sort rows: "none", "descending", or "ascending".

Value

A standardized coefficient data frame ready for `ggforestplot()`.

Examples

```
if (requireNamespace("broom", quietly = TRUE)) {  
  fit <- lm(mpg ~ wt + hp + qsec, data = mtcars)  
  tidy_forest_model(fit)  
  
  set.seed(123)  
  logit_data <- data.frame(  
    age = rnorm(250, mean = 62, sd = 8),  
    bmi = rnorm(250, mean = 28, sd = 4),  
    treatment = factor(rbinom(250, 1, 0.45), labels = c("Control", "Treatment"))  
  )  
  linpred <- -9 + 0.09 * logit_data$age + 0.11 * logit_data$bmi +  
    0.9 * (logit_data$treatment == "Treatment")  
  logit_data$event <- rbinom(250, 1, plogis(linpred))  
  logit_fit <- glm(event ~ age + bmi + treatment, data = logit_data, family = binomial())  
  
  tidy_forest_model(logit_fit, exponentiate = TRUE)  
}
```

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