Package ‘contourforest’

January 20, 2026

Type Package

Title Contour-Enhanced Forest Plots for Meta-Analysis

Version 0.2.0

Description Provides functions to create contour-enhanced forest plots for meta-analysis,
supporting binary outcomes (e.g., odds ratios, risk ratios), continuous outcomes (e.g., correlations),
and prevalence estimates. Includes options for prediction intervals, customized colors, study labeling,
and contour shading to highlight regions of statistical significance. Based on 'metafor' and 'ggplot2'.

License MIT + file LICENSE

Encoding UTF-8

RoxygenNote 7.3.2

Imports ggplot2, dplyr, metafor, stringr, grid

Depends R (>= 4.0)

NeedsCompilation no

Author Umar Hussain [aut, cre],
Muhammad Abdullah Kamran [aut],
Fayez Hussain Niazi [aut]

Maintainer Umar Hussain <`drumarhussain@gmail.com`>

Repository CRAN

Date/Publication 2026-01-20 09:20:02 UTC

Contents

`bcg` *BCG Vaccine Trials Dataset*

Description

This dataset contains summary data from 13 BCG vaccine studies, including the number of events in treatment and control groups, total sample sizes, and subgroup classification.

Usage

`bcg()`

Value

A data frame with 13 rows and 6 variables:

Study Character. Name and year of the study.

events_t Numeric. Number of events (e.g., TB cases) in the treatment (BCG) group.

n_t Numeric. Total number of participants in the treatment group.

events_c Numeric. Number of events in the control group.

n_c Numeric. Total number of participants in the control group.

subgroup Character. Type of study or subgroup classification ("random", "alternate", or "systematic").

`dat1` *Hypothetical dataset: GAD-7 Anxiety Scores by Socioeconomic Status*

Description

GAD-7 scores (mean ± SD) for high SES (control) vs low SES (treatment) groups across 6 studies.

Usage

`dat1`

Format

A data frame with 6 rows and 8 variables:

Study Study name or year

mean_c Mean GAD-7 score in high SES (control) group

sd_c Standard deviation of GAD-7 scores in high SES (control) group

n_c Sample size in high SES (control) group

mean_t Mean GAD-7 score in low SES (treatment) group

sd_t Standard deviation of GAD-7 scores in low SES (treatment) group

n_t Sample size in low SES (treatment) group

subgroup Geographical subgroup of the study (e.g., Asia, Europe)

Source

Hypothetical data

`forest_bin` *Contour-Enhanced Binary Outcome Forest Plot*

Description

Generates a contour-enhanced forest plot for binary outcome data (e.g., odds ratios, risk ratios), with study-level effects, confidence intervals, pooled effect, prediction interval, and heterogeneity statistics.

Usage

```
forest_bin(
  dat,
  measure = "OR",
  method = "REML",
  xlab = "",
  title = NULL,
  model = "Random-effects",
  estimator = "REML",
  nc_col = "n_c",
  ne_col = "n_t",
  event_c_col = "events_c",
  event_t_col = "events_t",
  diamond.col = "red",
  study.col = "blue",
  CI.col = "blue",
  Pred.Inter.col = "black",
  square.size = 10,
  contour_fill = c("gray95", "gray80", "gray60", "gray40"),
```

```
  text_size = 3.5,
  xlim = c(-1.7, 3.5),
  pred = TRUE,
  xpos = list(EventsT = -0.9, EventsC = -0.3, Effect = 2.6, Weight = 3.1),
  study_x = -1.8,
  hetero_x = -1.7,
  tlim = c(0, 2.3),
  truncate_PI = FALSE,
  contour_left_min = c(0, 0.5, 0.67, 0.83),
  contour_left_max = c(0.5, 0.67, 0.83, 1),
  contour_right_min = c(1, 1.2, 1.5, 2),
  contour_right_max = c(1.2, 1.5, 2, 2.5)
)
```

Arguments

`dat`	Data frame containing study-level binary outcome data.
`measure`	Character. Effect measure ("OR" for odds ratio, "RR" for risk ratio, etc.).
`method`	Character. Method for meta-analysis heterogeneity estimation (default "REML").
`xlab`	Character. Label for the x-axis.
`title`	Character. Plot title. If NULL, a default title is generated.
`model`	Character. Meta-analysis model ("Random-effects" or "Fixed-effects").
`estimator`	Character. Estimator used in the meta-analysis (default "REML").
`nc_col`	Character. Column name for control group sample sizes.
`ne_col`	Character. Column name for treatment group sample sizes.
`event_c_col`	Character. Column name for number of events in control group.
`event_t_col`	Character. Column name for number of events in treatment group.
`diamond.col`	Color of the pooled effect polygon.
`study.col`	Color of the study-level effect points.
`CI.col`	Color of the study-level confidence interval lines.
`Pred.Inter.col`	Color of the prediction interval line.
`square.size`	Numeric. Maximum size of study-level effect squares.
`contour_fill`	Vector of colors for contour shading levels.
`text_size`	Numeric. Base size of plot text.
`xlim`	Numeric vector of length 2. Limits of the x-axis.
`pred`	Logical. Whether to show the prediction interval.
`xpos`	List of numeric positions for text labels (EventsT, EventsC, Effect, Weight).
`study_x`	Numeric. X-position for study names.
`hetero_x`	Numeric. X-position for heterogeneity text.
`tlim`	Numeric vector of length 2. Limits for truncating study confidence intervals.
`truncate_PI`	Logical. Whether to truncate the prediction interval to `tlim`.

`contour_left_min`	Numeric vector. Minimum x-values for left-side contour shading.
`contour_left_max`	Numeric vector. Maximum x-values for left-side contour shading.
`contour_right_min`	Numeric vector. Minimum x-values for right-side contour shading.
`contour_right_max`	Numeric vector. Maximum x-values for right-side contour shading.

Value

A `ggplot2` object of the forest plot.

Examples

```
forest_bin(
  dat = bcg(),
  measure = "OR",
  xlab = "Odds Ratio",
  title = "BCG Vaccine Meta-analysis",
  tlim = c(0, 2.3),
  contour_left_min = c(0,0.3,0.5,0.7),
  contour_left_max = c(0.3,0.5,0.7,1),
  contour_right_min = c(1,1.2,1.5,1.8),
  contour_right_max = c(1.2,1.5,1.8,2.5)
)
```

`forest_bin_subgroup` *Subgroup Forest Plot for Binary Outcome Meta-analysis*

Description

Generates a contour-enhanced forest plot for binary outcome data, with optional subgroup analysis. This function calculates risk ratios (or other measures) and displays study-specific effect sizes, pooled subgroup effects, overall pooled effect, and heterogeneity statistics (I^2, tau^2).

Usage

```
forest_bin_subgroup(
  dat,
  subgroup = NULL,
  measure = "RR",
  method = "REML",
  nc_col = "n_c",
  ne_col = "n_t",
  event_c_col = "events_c",
  event_t_col = "events_t",
  xlab = "Risk Ratio (RR)",
```

```
  title = "Subgroup Forest Plot",
  diamond.col = "red",
  overall.col = "darkgreen",
  study.col = "blue",
  CI.col = "blue",
  Pred.Inter.col = "black",
  square.size = 8,
  Pred.Int.size = 2,
  xlim = c(-2, 3.5),
  tlim = c(0, 2.3),
  text_size = 3.5,
  xpos = list(EventsT = -1, EventsC = -0.4, Effect = 2.5, Weight = 3.2),
  study_x = -1.8,
  val_x = 2.6,
  contour_left_min = c(0, 0.5, 0.67, 0.83),
  contour_left_max = c(0.5, 0.67, 0.83, 1),
  contour_right_min = c(1, 1.2, 1.5, 2),
  contour_right_max = c(1.2, 1.5, 2, 2.5),
  pred = TRUE
)
```

Arguments

`dat`	A data frame containing study-level data. Must include columns for treatment and control events and sample sizes, and optionally a `subgroup` column.
`subgroup`	Column name in `dat` specifying subgroup membership (character or factor). Defaults to NULL (no subgroups).
`measure`	Effect measure to use. Default is "RR" (risk ratio).
`method`	Method for random-effects meta-analysis. Default is "REML".
`nc_col`	Character. Column name for control group sample sizes.
`ne_col`	Character. Column name for treatment group sample sizes.
`event_c_col`	Character. Column name for number of events in control group.
`event_t_col`	Character. Column name for number of events in treatment group.
`xlab`	Label for the x-axis. Default is "Risk Ratio (RR)".
`title`	Plot title. Default is "Subgroup Forest Plot".
`diamond.col`	Color for subgroup pooled effect diamonds. Default is "red".
`overall.col`	Color for overall pooled effect diamond. Default is "darkgreen".
`study.col`	Color for individual study points. Default is "blue".
`CI.col`	Color for study confidence interval bars. Default is "blue".
`Pred.Inter.col`	Color for prediction interval bars. Default is "black".
`square.size`	Maximum size of study points. Default is 8.
`Pred.Int.size`	Thickness of prediction interval line. Default is 2.
`xlim`	Numeric vector of length 2 giving x-axis limits. Default is c(-2, 3.5).

`tlim`	Numeric vector of length 2 for truncating study CIs. Default is c(0, 2.3).
`text_size`	Base text size for labels. Default is 3.5.
`xpos`	List of x-axis positions for EventsT, EventsC, Effect, and Weight labels. Default is list(EventsT=-1, EventsC=-0.4, Effect=2.5, Weight=3.2).
`study_x`	X position for study names. Default is -1.8.
`val_x`	X position for pooled effect labels. Default is 2.6.
`contour_left_min`	Numeric vector defining left contour minimum values. Default is c(0, 0.5, 0.67, 0.83).
`contour_left_max`	Numeric vector defining left contour maximum values. Default is c(0.5, 0.67, 0.83, 1).
`contour_right_min`	Numeric vector defining right contour minimum values. Default is c(1, 1.2, 1.5, 2).
`contour_right_max`	Numeric vector defining right contour maximum values. Default is c(1.2, 1.5, 2, 2.5).
`pred`	Logical indicating whether to show the prediction interval. Default is TRUE.

Value

A `ggplot` object representing the contour-enhanced subgroup forest plot.

Examples

```
# Load example dataset
data <- bcg()

# Generate subgroup forest plot
forest_bin_subgroup(
  dat = bcg(),
  tlim = c(0, 2.3),
  contour_left_min  = c(0, 0.3, 0.5, 0.7),
  contour_left_max  = c(0.3, 0.5, 0.7, 1),
  contour_right_min = c(1, 1.2, 1.5, 1.8),
  contour_right_max = c(1.2, 1.5, 1.8, 2.4)
)
```

`forest_cont` *Contour-enhanced Forest Plot for Continuous Outcomes*

Description

Creates a forest plot for continuous outcomes (MD or SMD) with optional contour shading, prediction interval, and annotated study-level means, effect sizes, and weights.

Usage

```
forest_cont(
  dat,
  measure = "SMD",
  method = "REML",
  sort = c("effect", "none"),
  xlab = "",
  title = NULL,
  model = "Random-effects",
  estimator = "REML",
  m_c_col = "mean_c",
  sd_c_col = "sd_c",
  n_c_col = "n_c",
  m_t_col = "mean_t",
  sd_t_col = "sd_t",
  n_t_col = "n_t",
  diamond.col = "red",
  study.col = "blue",
  CI.col = "blue",
  Pred.Inter.col = "black",
  contour_left_min = c(-0.8, -0.5, -0.2, 0),
  contour_left_max = c(-0.5, -0.2, 0, 0.2),
  contour_right_min = c(0, 0.2, 0.5, 0.8),
  contour_right_max = c(0.2, 0.5, 0.8, 1),
  square.size = 10,
  contour_fill = c("gray95", "gray80", "gray60", "gray40"),
  text_size = 3.5,
  pred = TRUE,
  study_x = NULL,
  treatment_x = NULL,
  control_x = NULL,
  effect_x = NULL,
  weight_x = NULL,
  PredInt_x = NULL,
  xlim = NULL,
  hetero_x = -8
)
```

Arguments

`dat`	Data frame containing study-level data. Must include treatment and control means, SDs, sample sizes, and study labels.
`measure`	Effect size measure: `"MD"` (mean difference) or `"SMD"` (standardized mean difference). Default is `"SMD"`.
`method`	Meta-analysis method for `rma()` (e.g., `"REML"`). Default is `"REML"`.
`sort`	Logical. If `TRUE`, the studies will be sorted by effect size before plotting.
`xlab`	Label for the x-axis.

`title`	Plot title. If `NULL`, a default title including measure is used.
`model`	Model description for heterogeneity annotation. Default `"Random-effects"`.
`estimator`	Estimator for heterogeneity. Default `"REML"`.
`m_c_col`	Column name for control group means. Default `"mean_c"`.
`sd_c_col`	Column name for control group SDs. Default `"sd_c"`.
`n_c_col`	Column name for control group sample sizes. Default `"n_c"`.
`m_t_col`	Column name for treatment group means. Default `"mean_t"`.
`sd_t_col`	Column name for treatment group SDs. Default `"sd_t"`.
`n_t_col`	Column name for treatment group sample sizes. Default `"n_t"`.
`diamond.col`	Color for the pooled effect diamond. Default `"red"`.
`study.col`	Color for study effect points. Default `"blue"`.
`CI.col`	Color for study confidence intervals. Default `"blue"`.
`Pred.Inter.col`	Color for prediction interval. Default `"black"`.
`contour_left_min`	Numeric vector specifying the left-side minimum x-axis boundaries for contour shading bands (values less than the null effect).
`contour_left_max`	Numeric vector specifying the left-side maximum x-axis boundaries for contour shading bands (values less than or equal to the null effect).
`contour_right_min`	Numeric vector specifying the right-side minimum x-axis boundaries for contour shading bands (values greater than or equal to the null effect).
`contour_right_max`	Numeric vector specifying the right-side maximum x-axis boundaries for contour shading bands (values greater than the null effect).
`square.size`	Size of study points. Default `10`.
`contour_fill`	Vector of four colors for contour shading. Default `c("gray95","gray80","gray60","gray40")`.
`text_size`	Size of annotated text. Default `3.5`.
`pred`	Logical; whether to show prediction interval. Default `TRUE`.
`study_x`	X-position for study labels. Default computed automatically.
`treatment_x`	X-position for treatment means. Default computed automatically.
`control_x`	X-position for control means. Default computed automatically.
`effect_x`	X-position for effect sizes. Default computed automatically.
`weight_x`	X-position for weights. Default computed automatically.
`PredInt_x`	X-position for prediction interval label. Default computed automatically.
`xlim`	X-axis limits. Default computed automatically.
`hetero_x`	X-position for heterogeneity annotation. Default `-8`.

Value

A `ggplot2` object representing the forest plot.

Examples

```
forest_cont(
  dat1,
  measure = "MD",
  xlab = "Mean Difference",
  study_x = -9,
  sort = "effect",
  hetero_x = -12,
  treatment_x = -7,
  control_x = -5,
  effect_x = 5.5,
  weight_x = 10,
  PredInt_x = 7
)

forest_cont(
  dat1,
  measure = "SMD",
  xlab = "Standardized Mean Difference",
  hetero_x = -9.9,
  study_x = -7,
  sort = "effect",
  treatment_x = -5,
  control_x = -3,
  effect_x = 2.5,
  weight_x = 4,
  PredInt_x = 4
)
forest_cont(
dat1,
study.col = "darkgreen",
CI.col = "black",
diamond.col = "red",
Pred.Inter.col = "black",
measure = "SMD",
sort = "effect",
xlab = "Standardized Mean Difference",
contour_fill = c("gray90","gray70","gray50", "gray30"),
hetero_x = -9.9,
study_x = -7,
square.size = 9,
treatment_x = -5,
control_x = -3.2,
text_size = 4,
effect_x = 2.5,
weight_x = 5.8,
PredInt_x = 3
)
```

`forest_cont_subgroup` *Forest Plot for Subgroup Meta-Analysis*

Description

Creates a detailed forest plot for subgroup meta-analysis, including study-level effect sizes, subgroup pooled effects, heterogeneity statistics, overall pooled effect, and prediction intervals.

Usage

```
forest_cont_subgroup(
  dat,
  m_t_col = "mean_t",
  sd_t_col = "sd_t",
  n_t_col = "n_t",
  m_c_col = "mean_c",
  sd_c_col = "sd_c",
  n_c_col = "n_c",
  subgroup_col = "subgroup",
  study_col = "Study",
  measure = "SMD",
  method = "REML",
  xlab = NULL,
  xlim = NULL,
  model = "RE",
  title = "Subgroup Forest Plot",
  diamond.col = "red",
  overall.col = "darkgreen",
  study.col = "blue",
  CI.col = "blue",
  Pred.Inter.col = "black",
  square.size = 5,
  Pred.Int.size = 1.5,
  text_size = 3.5,
  pred = TRUE,
 xpos = list(Study = NULL, MeanT = NULL, MeanC = NULL, Effect = NULL, Weight = NULL,
   PredInt = NULL, Hetero = NULL)
)
```

Arguments

`dat`	A data frame containing the study-level data. Use `dat1` included in the package for examples.
`m_t_col`	Name of the column for treatment group means.
`sd_t_col`	Name of the column for treatment group standard deviations.
`n_t_col`	Name of the column for treatment group sample sizes.
`m_c_col`	Name of the column for control group means.
`sd_c_col`	Name of the column for control group standard deviations.
`n_c_col`	Name of the column for control group sample sizes.
`subgroup_col`	Name of the column indicating subgroup membership.

`study_col`	Name of the column with study labels.
`measure`	Effect size measure: "SMD" (standardized mean difference) or "MD" (mean difference).
`method`	Method for meta-analysis: "REML" (default) or "FE".
`xlab`	Label for the x-axis.
`xlim`	Limits for the x-axis as a numeric vector of length 2.
`model`	Random-effects ("RE") or fixed-effects ("FE") model for pooled estimates.
`title`	Plot title.
`diamond.col`	Color for subgroup pooled effect diamonds.
`overall.col`	Color for the overall pooled effect diamond.
`study.col`	Color for study-level points.
`CI.col`	Color for confidence intervals of individual studies.
`Pred.Inter.col`	Color for the overall prediction interval.
`square.size`	Maximum size of study-level effect squares.
`Pred.Int.size`	Line thickness for prediction interval.
`text_size`	Base text size for annotations.
`pred`	Logical; if TRUE, display overall prediction interval.
`xpos`	numeric vector of x-axis positions for annotations

Value

A ggplot object representing the subgroup forest plot.

Examples

```
# Using the built-in dataset dat1
forest_cont_subgroup(dat1)
```

`forest_corr` *Forest Plot for Correlation Coefficients*

Description

Creates a contour-enhanced forest plot for correlation coefficients from multiple studies. Applies Fisher's Z transformation for meta-analysis and displays study-level correlations with 95% confidence intervals, pooled correlation, weights, and heterogeneity statistics.

Usage

```
forest_corr(
  dat,
  r_col = "r",
  n_col = "n",
  study_col = "Study",
  xlab = "Correlation (r)",
  title = "Correlation Forest Plot",
  xlim = c(-2.5, 1.5),
  diamond.col = "red",
  study.col = "blue",
  CI.col = "blue",
  square.size = 6,
  text_size = 3.5,
  xpos_study = -1.3,
  xpos_n = -1.1,
  xpos_ci = 1.2,
  xpos_weight = 1.45,
  xpos_pooled_label = NULL,
  xpos_pooled_value = NULL,
  contour_breaks = c(-1, -0.5, -0.3, -0.1, 0, 0.1, 0.3, 0.5, 1),
  contour_colors = c("gray70", "gray50", "gray30", "gray10", "gray70", "gray50",
    "gray30", "gray10")
)
```

Arguments

`dat`	Data frame containing study-level correlation data.
`r_col`	Character. Name of the column containing correlation coefficients. Default is `"r"`.
`n_col`	Character. Name of the column containing sample sizes. Default is `"n"`.
`study_col`	Character. Name of the column containing study labels. Default is `"Study"`.
`xlab`	Character. Label for the x-axis. Default is `"Correlation (r)"`.
`title`	Character. Plot title. Default is `"Correlation Forest Plot"`.
`xlim`	Numeric vector of length 2. Limits for the x-axis. Default is `c(-2.5,1.5)`.
`diamond.col`	Color for the pooled effect diamond. Default is `"red"`.
`study.col`	Color for the study points. Default is `"blue"`.
`CI.col`	Color for the horizontal confidence intervals. Default is `"blue"`.
`square.size`	Numeric. Size of the squares representing study effect sizes. Default is `6`.
`text_size`	Numeric. Size of text annotations. Default is `3.5`.
`xpos_study`	Numeric. X-position for study labels. Default is `-1.3`.
`xpos_n`	Numeric. X-position for sample size labels. Default is `-1.1`.
`xpos_ci`	Numeric. X-position for correlation (95% CI) labels. Default is `1.2`.
`xpos_weight`	Numeric. X-position for study weight labels. Default is `1.45`.

`xpos_pooled_label`	Numeric. X-position for the pooled effect label. Default is calculated automatically.
`xpos_pooled_value`	Numeric. X-position for the pooled effect value. Default is calculated automatically.
`contour_breaks`	Numeric vector. Breakpoints for contour shading along the x-axis. Default is `c(-1, -0.5, -0.3,-0.1, 0, 0.1, 0.3, 0.5, 1)`.
`contour_colors`	Character vector. Colors corresponding to contour breaks. Default is `c("gray70","gray50","gray30", "gray10", "gray70", "gray50","gray30","gray10")`.

Value

A `ggplot` object representing the correlation forest plot.

Examples

```
## Not run:
dat <- data.frame(
  Study = c("Smith 2010","Jones 2012","Lee 2015","Kim 2018"),
  r = c(0.2, 0.35, -0.1, 0.5),
  n = c(50, 120, 80, 60)
)
forest_corr(dat)

## End(Not run)
```

`forest_prev` *Prevalence Forest Plot*

Description

Generates a forest plot for prevalence data with study-level estimates, confidence intervals, weights, and pooled prevalence. Supports contour shading for prevalence ranges.

Usage

```
forest_prev(
  dat,
  events_col = "events",
  n_col = "n",
  study_col = "Study",
  xlab = "Prevalence (%)",
  title = "Prevalence Forest Plot",
  xlim = c(-25, 140),
  diamond.col = "red",
  study.col = "blue",
```

```
  CI.col = "blue",
  square.size = 7,
  text_size = 3.5,
  xpos_study = -12,
  xpos_events = -5,
  xpos_prev = 50,
  xpos_weight = 55,
  xpos_pooled_label = NULL,
  xpos_pooled_value = NULL,
  contour_breaks = c(0, 5, 10, 25, 50),
  contour_colors = c("gray90", "gray70", "gray50", "gray30"),
  legend_title = "Prevalence"
)
```

Arguments

`dat`	A data frame containing study-level prevalence data.
`events_col`	Name of the column containing the number of events.
`n_col`	Name of the column containing the total sample size.
`study_col`	Name of the column with study labels.
`xlab`	Label for the x-axis. Default is `"Prevalence (%)"`.
`title`	Plot title.
`xlim`	Numeric vector of length 2 specifying x-axis limits.
`diamond.col`	Color of the pooled prevalence diamond.
`study.col`	Color of the study points.
`CI.col`	Color of the confidence intervals.
`square.size`	Size of the study-level squares.
`text_size`	Base text size for labels and annotations.
`xpos_study`	X-axis position for study labels.
`xpos_events`	X-axis position for event counts.
`xpos_prev`	X-axis position for prevalence values.
`xpos_weight`	X-axis position for study weights.
`xpos_pooled_label`	X-axis position for pooled label (optional; defaults relative to pooled prevalence).
`xpos_pooled_value`	X-axis position for pooled value (optional; defaults relative to pooled prevalence).
`contour_breaks`	Numeric vector defining contour thresholds.
`contour_colors`	Colors for contour shading.
`legend_title`	Title for the contour legend.

Value

A ggplot object representing the prevalence forest plot.

Examples

```
dat <- data.frame(
 Study = c("Bazargani et al. 2015", "Nandhra et al. 2015", "Rai 2015", "Romano et al. 2011"),
  events = c(25, 109, 24, 9),
  n = c(454, 757, 380, 100)
)

forest_prev(
  dat = dat,
  title = "Prevalence Forest Plot",
  xlim = c(-25, 80),
  xpos_study = -12,
  xpos_events = -5,
  xpos_prev = 40,
  xpos_weight = 52,
  contour_breaks = c(0,5,10,25,35),
  contour_colors = c("gray90","gray70","gray50","gray30"),
  legend_title = "Prevalence (%)"
)
```

Index