

# Package ‘contourforest’

May 8, 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

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**Repository** CRAN

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

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bcg	<i>BCG Vaccine Trials Dataset</i>
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**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").

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dat1	<i>Hypothetical dataset: GAD-7 Anxiety Scores by Socioeconomic Status</i>
------	---

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**Description**

GAD-7 scores (mean  $\pm$  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

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

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 <code>c(0, 2.3)</code> .
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 <code>list(EventsT=-1, EventsC=-0.4, Effect=2.5, Weight=3.2)</code> .
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 <code>c(0, 0.5, 0.67, 0.83)</code> .
contour_left_max	Numeric vector defining left contour maximum values. Default is <code>c(0.5, 0.67, 0.83, 1)</code> .
contour_right_min	Numeric vector defining right contour minimum values. Default is <code>c(1, 1.2, 1.5, 2)</code> .
contour_right_max	Numeric vector defining right contour maximum values. Default is <code>c(1.2, 1.5, 2, 2.5)</code> .
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  
)
```

**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**

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

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

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