

# Package ‘modelbased’

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**Type** Package

**Title** Estimation of Model-Based Predictions, Contrasts and Means

**Version** 0.5.0

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**URL** <https://easystats.github.io/modelbased/>

**BugReports** <https://github.com/easystats/modelbased/issues>

**Description** Implements a general interface for model-based estimations for a wide variety of models (see support list of insight; Lüdecke, Waggoner & Makowski (2019) <doi:10.21105/joss.01412>), used in the computation of marginal means, contrast analysis and predictions.

**Imports** insight (>= 0.11.0), bayestestR (>= 0.8.0), parameters (>= 0.10.0), emmeans (>= 1.4.4), graphics, stats, utils

**Suggests** brms, coda, dplyr, effectsize, ganimate, gamm4, ggplot2, glmmTMB, knitr, lme4, logspline, Matrix, MASS, merTools, mgcv, rmarkdown, rstanarm, see, testthat,

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---

as.numeric\_ifnumeric *Convert to Numeric if Possible*

---

**Description**

Tries to convert vector to numeric if possible. Otherwise, leaves it as is.

**Usage**

```
as.numeric_ifnumeric(x)
```

**Arguments**

x                    A vector to be converted.

**Value**

Numeric

**Examples**

```
as.numeric_ifnumeric(c("1", "2"))
as.numeric_ifnumeric(c("1", "2", "A"))
```

---

estimate\_contrasts      *Estimate contrasts between factor levels*

---

## Description

Contrast analysis. See the documentation for your object's class:

- [Frequentist models](#)
- [Bayesian models](#)

## Usage

```
estimate_contrasts(
  model,
  levels = NULL,
  fixed = NULL,
  modulate = NULL,
  transform = "none",
  length = 10,
  standardize = TRUE,
  standardize_robust = FALSE,
  ...
)
```

## Arguments

model	A statistical model.
levels	A character vector or formula specifying the names of the predictors over which to estimate means or contrasts.
fixed	A character vector indicating the names of the predictors to be "fixed" (i.e., maintained), so that the estimation is made at these values.
modulate	A character vector indicating the names of a numeric variable along which the means or the contrasts will be estimated. Adjust its length using length.
transform	Can be "none" (default for contrasts), "response" (default for means), "mu", "unlink", "log". "none" will leave the values on scale of the linear predictors. "response" will transform them on scale of the response variable. Thus for a logistic model, "none" will give estimations expressed in log-odds (probabilities on logit scale) and "response" in terms of probabilities.
length	Length of the spread numeric variables.
standardize	If TRUE, adds standardized differences or coefficients.
standardize_robust	Robust standardization through MAD (Median Absolute Deviation, a robust estimate of SD) instead of regular SD.
...	Arguments passed to or from other methods.

**Value**

A data frame of estimated contrasts.

---

estimate\_contrasts.lm *Estimate contrasts*

---

**Description**

Estimate contrasts

**Usage**

```
## S3 method for class 'lm'
estimate_contrasts(
  model,
  levels = NULL,
  fixed = NULL,
  modulate = NULL,
  transform = "none",
  length = 10,
  standardize = TRUE,
  standardize_robust = FALSE,
  ci = 0.95,
  adjust = "holm",
  ...
)
```

**Arguments**

model	A Bayesian model.
levels	A character vector or formula specifying the names of the predictors over which to estimate means or contrasts.
fixed	A character vector indicating the names of the predictors to be "fixed" (i.e., maintained), so that the estimation is made at these values.
modulate	A character vector indicating the names of a numeric variable along which the means or the contrasts will be estimated. Adjust its length using length.
transform	Can be "none" (default for contrasts), "response" (default for means), "mu", "unlink", "log". "none" will leave the values on scale of the linear predictors. "response" will transform them on scale of the response variable. Thus for a logistic model, "none" will give estimations expressed in log-odds (probabilities on logit scale) and "response" in terms of probabilities.
length	Length of the spread numeric variables.
standardize	If TRUE, adds standardized differences or coefficients.

standardize_robust	Robust standardization through MAD (Median Absolute Deviation, a robust estimate of SD) instead of regular SD.
ci	Credible Interval (CI) level. Default to 0.89 (89%). See <a href="#">ci</a> for further details.
adjust	The p-values adjustment method for multi-comparisons. Can be one of "holm" (default), "tukey", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr" or "none". See the p-value adjustment section in the <code>emmeans::test</code> documentation.
...	Arguments passed to or from other methods.

**Value**

A dataframe of estimated contrasts.

**Examples**

```
library(modelbased)

model <- lm(Sepal.Width ~ Species, data = iris)
estimate_contrasts(model)

model <- lm(Sepal.Width ~ Species * Petal.Width, data = iris)
estimate_contrasts(model)
estimate_contrasts(model, fixed = "Petal.Width")
estimate_contrasts(model, modulate = "Petal.Width", length = 4)
estimate_contrasts(model, levels = "Petal.Width", length = 4)

if (require("lme4")) {
  data <- iris
  data$Petal.Length_factor <- ifelse(data$Petal.Length < 4.2, "A", "B")

  model <- lmer(Sepal.Width ~ Species + (1 | Petal.Length_factor), data = data)
  estimate_contrasts(model)
}
```

---

```
estimate_contrasts.stanreg
```

*Estimate contrasts*

---

**Description**

Estimate contrasts

**Usage**

```
## S3 method for class 'stanreg'
estimate_contrasts(
  model,
```

```

levels = NULL,
fixed = NULL,
modulate = NULL,
transform = "none",
length = 10,
standardize = TRUE,
standardize_robust = FALSE,
centrality = "median",
ci = 0.95,
ci_method = "hdi",
test = c("pd", "rope"),
rope_range = "default",
rope_ci = 1,
...
)

```

### Arguments

model	A Bayesian model.
levels	A character vector or formula specifying the names of the predictors over which to estimate means or contrasts.
fixed	A character vector indicating the names of the predictors to be "fixed" (i.e., maintained), so that the estimation is made at these values.
modulate	A character vector indicating the names of a numeric variable along which the means or the contrasts will be estimated. Adjust its length using <code>length</code> .
transform	Can be "none" (default for contrasts), "response" (default for means), "mu", "unlink", "log". "none" will leave the values on scale of the linear predictors. "response" will transform them on scale of the response variable. Thus for a logistic model, "none" will give estimations expressed in log-odds (probabilities on logit scale) and "response" in terms of probabilities.
length	Length of the spread numeric variables.
standardize	If TRUE, adds standardized differences or coefficients.
standardize_robust	Robust standardization through MAD (Median Absolute Deviation, a robust estimate of SD) instead of regular SD.
centrality	The point-estimates (centrality indices) to compute. Character (vector) or list with one or more of these options: "median", "mean", "MAP" or "all".
ci	Credible Interval (CI) level. Default to 0.89 (89%). See <a href="#">ci</a> for further details.
ci_method	The type of index used for Credible Interval. Can be "HDI" (default, see <a href="#">hdi</a> ), "ETI" (see <a href="#">eti</a> ) or "SI" (see <a href="#">si</a> ).
test	The indices of effect existence to compute. Character (vector) or list with one or more of these options: "p_direction" (or "pd"), "rope", "p_map", "equivalence_test" (or "equitest"), "bayesfactor" (or "bf") or "all" to compute all tests. For each "test", the corresponding <b>bayestestR</b> function is called (e.g. <a href="#">rope</a> or <a href="#">p_direction</a> ) and its results included in the summary output.

rope_range	ROPE's lower and higher bounds. Should be a list of two values (e.g., $c(-0.1, 0.1)$ ) or "default". If "default", the bounds are set to $x \pm 0.1 \times SD(\text{response})$ .
rope_ci	The Credible Interval (CI) probability, corresponding to the proportion of HDI, to use for the percentage in ROPE.
...	Arguments passed to or from other methods.

**Value**

A data frame of estimated contrasts.

**Examples**

```
library(modelbased)

data <- mtcars
data$cyl <- as.factor(data$cyl)
data$am <- as.factor(data$am)
## Not run:
if (require("rstanarm")) {
  model <- stan_glm(mpg ~ cyl * am, data = data, refresh = 0)
  estimate_contrasts(model)
  estimate_contrasts(model, fixed = "am")

  model <- stan_glm(mpg ~ cyl * wt, data = data, refresh = 0)
  estimate_contrasts(model)
  estimate_contrasts(model, fixed = "wt")
  estimate_contrasts(model, modulate = "wt", length = 4)
  estimate_contrasts(model, levels = "wt", length = 4)

  model <- stan_glm(Sepal.Width ~ Species + Petal.Width + Petal.Length, data = iris, refresh = 0)
  estimate_contrasts(model, fixed = "Petal.Width", modulate = "Petal.Length", test = "bf")
}

if (require("brms")) {
  model <- brm(mpg ~ cyl * am, data = data, refresh = 0)
  estimate_contrasts(model)
}

## End(Not run)
```

---

estimate\_means

*Estimate average value of response variable at each factor levels*

---

**Description**

See the documentation for your object's class:

- [Frequentist models](#)
- [Bayesian models](#)

**Usage**

```
estimate_means(
  model,
  levels = NULL,
  fixed = NULL,
  modulate = NULL,
  transform = "response",
  length = 10,
  ...
)
```

**Arguments**

model	A statistical model.
levels	A character vector or formula specifying the names of the predictors over which to estimate means or contrasts.
fixed	A character vector indicating the names of the predictors to be "fixed" (i.e., maintained), so that the estimation is made at these values.
modulate	A character vector indicating the names of a numeric variable along which the means or the contrasts will be estimated. Adjust its length using length.
transform	Can be "none" (default for contrasts), "response" (default for means), "mu", "unlink", "log". "none" will leave the values on scale of the linear predictors. "response" will transform them on scale of the response variable. Thus for a logistic model, "none" will give estimations expressed in log-odds (probabilities on logit scale) and "response" in terms of probabilities.
length	Length of the spread numeric variables.
...	Arguments passed to or from other methods.

**Value**

A dataframe of estimated marginal means.

---

estimate\_means.lm      *Estimate marginal means*

---

**Description**

Estimate marginal means

**Usage**

```
## S3 method for class 'lm'
estimate_means(
  model,
  levels = NULL,
  fixed = NULL,
  modulate = NULL,
  transform = "response",
  length = 10,
  ci = 0.95,
  ...
)
```

**Arguments**

model	A Bayesian model.
levels	A character vector or formula specifying the names of the predictors over which to estimate means or contrasts.
fixed	A character vector indicating the names of the predictors to be "fixed" (i.e., maintained), so that the estimation is made at these values.
modulate	A character vector indicating the names of a numeric variable along which the means or the contrasts will be estimated. Adjust its length using length.
transform	Can be "none" (default for contrasts), "response" (default for means), "mu", "unlink", "log". "none" will leave the values on scale of the linear predictors. "response" will transform them on scale of the response variable. Thus for a logistic model, "none" will give estimations expressed in log-odds (probabilities on logit scale) and "response" in terms of probabilities.
length	Length of the spread numeric variables.
ci	Confidence Interval (CI) level. Default to 0.95 (95%).
...	Arguments passed to or from other methods.

**Value**

A data frame of estimated marginal means.

**Examples**

```
library(modelbased)

model <- lm(Petal.Length ~ Sepal.Width * Species, data = iris)

estimate_means(model)
estimate_means(model, fixed = "Sepal.Width")
estimate_means(model, levels = c("Species", "Sepal.Width"), length = 2)
estimate_means(model, levels = "Species=c('versicolor', 'setosa')")
estimate_means(model, levels = "Sepal.Width=c(2, 4)")
estimate_means(model, levels = c("Species", "Sepal.Width=0"))
```

```

estimate_means(model, modulate = "Sepal.Width", length = 5)
estimate_means(model, modulate = "Sepal.Width=c(2, 4)")
## Not run:
if (require("lme4")) {
  data <- iris
  data$Petal.Length_factor <- ifelse(data$Petal.Length < 4.2, "A", "B")

  model <- lmer(Petal.Length ~ Sepal.Width + Species + (1 | Petal.Length_factor), data = data)
  estimate_means(model)
  estimate_means(model, modulate = "Sepal.Width", length = 3)
}

## End(Not run)

```

---

```
estimate_means.stanreg
```

*Estimate marginal means*

---

## Description

Estimate marginal means

## Usage

```

## S3 method for class 'stanreg'
estimate_means(
  model,
  levels = NULL,
  fixed = NULL,
  modulate = NULL,
  transform = "response",
  length = 10,
  centrality = "median",
  ci = 0.95,
  ci_method = "hdi",
  ...
)

```

## Arguments

model	A Bayesian model.
levels	A character vector or formula specifying the names of the predictors over which to estimate means or contrasts.
fixed	A character vector indicating the names of the predictors to be "fixed" (i.e., maintained), so that the estimation is made at these values.
modulate	A character vector indicating the names of a numeric variable along which the means or the contrasts will be estimated. Adjust its length using length.

transform	Can be "none" (default for contrasts), "response" (default for means), "mu", "unlink", "log". "none" will leave the values on scale of the linear predictors. "response" will transform them on scale of the response variable. Thus for a logistic model, "none" will give estimations expressed in log-odds (probabilities on logit scale) and "response" in terms of probabilities.
length	Length of the spread numeric variables.
centrality	The point-estimates (centrality indices) to compute. Character (vector) or list with one or more of these options: "median", "mean", "MAP" or "all".
ci	Credible Interval (CI) level. Default to 0.89 (89%). See <a href="#">ci</a> for further details.
ci_method	The type of index used for Credible Interval. Can be "HDI" (default, see <a href="#">hdi</a> ), "ETI" (see <a href="#">eti</a> ) or "SI" (see <a href="#">si</a> ).
...	Arguments passed to or from other methods.

### Value

A dataframe of estimated marginal means.

### Examples

```
library(modelbased)

data <- mtcars
data$cyl <- as.factor(data$cyl)
data$am <- as.factor(data$am)

if (require("rstanarm")) {
  model <- stan_glm(mpg ~ cyl * am, data = data, refresh = 0)
  estimate_means(model)

  model <- stan_glm(mpg ~ cyl * wt, data = data, refresh = 0)
  estimate_means(model)
  estimate_means(model, modulate = "wt")
  estimate_means(model, fixed = "wt")
}

if (require("brms")) {
  model <- brm(mpg ~ cyl * am, data = data, refresh = 0)
  estimate_means(model)
}
```

## Description

See the documentation for your object's class:

- [Bayesian models \(stanreg and brms\)](#)
- [Frequentist models](#)

`estimate_link` is a shortcut to `estimate_response` with `data = "grid"`. `estimate_response` would be used in the context of generating actual predictions for the existing or new data, whereas `estimate_link` is more relevant in the context of visualisation and plotting.

## Usage

```
estimate_response(
  model,
  data = NULL,
  transform = "response",
  include_smooth = TRUE,
  include_random = FALSE,
  length = 25,
  preserve_range = TRUE,
  ...
)
```

```
estimate_link(
  model,
  data = "grid",
  transform = "response",
  include_smooth = TRUE,
  include_random = FALSE,
  length = 25,
  preserve_range = TRUE,
  ...
)
```

## Arguments

<code>model</code>	A statistical model.
<code>data</code>	A data frame with model's predictors to estimate the response. If <code>NULL</code> , the model's data is used. If <code>"grid"</code> , the model matrix is obtained (through <a href="#">visualisation_matrix</a> ).
<code>transform</code>	Can be <code>"none"</code> (default for contrasts), <code>"response"</code> (default for means), <code>"mu"</code> , <code>"unlink"</code> , <code>"log"</code> . <code>"none"</code> will leave the values on scale of the linear predictors. <code>"response"</code> will transform them on scale of the response variable. Thus for a logistic model, <code>"none"</code> will give estimations expressed in log-odds (probabilities on logit scale) and <code>"response"</code> in terms of probabilities.
<code>include_smooth</code>	Should the smooth terms (in General Additive Models - GAM) be included?
<code>include_random</code>	Should it take the random effects into account? Can be <code>TRUE</code> , <code>FALSE</code> or a formula indicating which group-level parameters to condition on when making predictions. The data argument may include new levels of the grouping factors that

were specified when the model was estimated, in which case the resulting posterior predictions marginalize over the relevant variables (see `posterior_predict.stanreg`).

length Passed to `visualisation_matrix` if `data = "grid"`.

preserve\_range Passed to `visualisation_matrix` if `data = "grid"`.

... Arguments passed to or from other methods.

### Value

A data frame of predicted values.

---

`estimate_response.glm` *Generates predictions for Frequentist models*

---

### Description

Generates predictions for Frequentist models

### Usage

```
## S3 method for class 'glm'
estimate_response(
  model,
  data = NULL,
  transform = "response",
  include_smooth = TRUE,
  include_random = TRUE,
  length = 25,
  preserve_range = TRUE,
  predict = "response",
  ci = 0.95,
  ...
)

## S3 method for class 'glm'
estimate_link(
  model,
  data = "grid",
  transform = "response",
  include_smooth = TRUE,
  include_random = FALSE,
  length = 25,
  preserve_range = TRUE,
  predict = "link",
  ci = 0.95,
  ...
)
```

**Arguments**

model	A statistical model.
data	A data frame with model's predictors to estimate the response. If NULL, the model's data is used. If "grid", the model matrix is obtained (through <a href="#">visualisation_matrix</a> ).
transform	Can be "none" (default for contrasts), "response" (default for means), "mu", "unlink", "log". "none" will leave the values on scale of the linear predictors. "response" will transform them on scale of the response variable. Thus for a logistic model, "none" will give estimations expressed in log-odds (probabilities on logit scale) and "response" in terms of probabilities.
include_smooth	Should the smooth terms (in General Additive Models - GAM) be included?
include_random	Should it take the random effects into account? Can be TRUE, FALSE or a formula indicating which group-level parameters to condition on when making predictions. The data argument may include new levels of the grouping factors that were specified when the model was estimated, in which case the resulting posterior predictions marginalize over the relevant variables (see <code>posterior_predict.stanreg</code> ).
length	Passed to <a href="#">visualisation_matrix</a> if data = "grid".
preserve_range	Passed to <a href="#">visualisation_matrix</a> if data = "grid".
predict	Can be "response" (default) or "link". The former predicts the the outcome per se, while the latter predicts the link function (i.e., the regression "line"), equivalent to estimating the fit. In other words, <code>estimate_response(model, predict="link")</code> is equivalent to <code>estimate_link(model)</code> .
ci	Credible Interval (CI) level. Default to 0.89 (89%). See <a href="#">ci</a> for further details.
...	Arguments passed to or from other methods.

**Value**

A dataframe of predicted values.

**Examples**

```
library(modelbased)

model <- lm(Sepal.Width ~ Species * Petal.Length, data = iris)
estimate_response(model)
estimate_link(model)

if (require("lme4")) {
  model <- lmer(Sepal.Width ~ Petal.Length + (1 | Species), data = iris)
  estimate_response(model)
  estimate_link(model)
}
```

---

```
estimate_response.stanreg
```

*Generates predictions for Bayesian models*

---

## Description

Generates predictions for Bayesian models

## Usage

```
## S3 method for class 'stanreg'
estimate_response(
  model,
  data = NULL,
  transform = "response",
  include_smooth = TRUE,
  include_random = TRUE,
  length = 25,
  preserve_range = TRUE,
  predict = "response",
  keep_draws = FALSE,
  draws = NULL,
  seed = NULL,
  centrality = "median",
  ci = 0.95,
  ci_method = "hdi",
  ...
)
```

```
## S3 method for class 'stanreg'
estimate_link(
  model,
  data = "grid",
  transform = "response",
  include_smooth = TRUE,
  include_random = FALSE,
  length = 25,
  preserve_range = TRUE,
  predict = "link",
  keep_draws = FALSE,
  draws = NULL,
  seed = NULL,
  centrality = "median",
  ci = 0.95,
  ci_method = "hdi",
  ...
)
```

```

## S3 method for class 'data.frame'
estimate_response(
  model,
  data = NULL,
  transform = "response",
  include_smooth = TRUE,
  include_random = FALSE,
  length = 25,
  preserve_range = TRUE,
  predict = "link",
  keep_draws = FALSE,
  draws = NULL,
  seed = NULL,
  centrality = "median",
  ci = 0.95,
  ci_method = "hdi",
  ...
)

## S3 method for class 'data.frame'
estimate_link(
  model,
  data = "grid",
  transform = "response",
  include_smooth = TRUE,
  include_random = FALSE,
  length = 25,
  preserve_range = TRUE,
  predict = "link",
  keep_draws = FALSE,
  draws = NULL,
  seed = NULL,
  centrality = "median",
  ci = 0.95,
  ci_method = "hdi",
  ...
)

```

### Arguments

model	A statistical model.
data	A data frame with model's predictors to estimate the response. If NULL, the model's data is used. If "grid", the model matrix is obtained (through <a href="#">visualisation_matrix</a> ).
transform	Can be "none" (default for contrasts), "response" (default for means), "mu", "unlink", "log". "none" will leave the values on scale of the linear predictors. "response" will transform them on scale of the response variable. Thus for a logistic model, "none" will give estimations expressed in log-odds (probabilities

	on logit scale) and "response" in terms of probabilities.
include_smooth	Should the smooth terms (in General Additive Models - GAM) be included?
include_random	Should it take the random effects into account? Can be TRUE, FALSE or a formula indicating which group-level parameters to condition on when making predictions. The data argument may include new levels of the grouping factors that were specified when the model was estimated, in which case the resulting posterior predictions marginalize over the relevant variables (see <code>posterior_predict.stanreg</code> ).
length	Passed to <code>visualisation_matrix</code> if <code>data = "grid"</code> .
preserve_range	Passed to <code>visualisation_matrix</code> if <code>data = "grid"</code> .
predict	Can be "response" (default) or "link". The former predicts the the outcome per se, while the latter predicts the link function (i.e., the regression "line"), equivalent to estimating the fit. In other words, <code>estimate_response(model, predict="link")</code> is equivalent to <code>estimate_link(model)</code> .
keep_draws	If FALSE, will summarise the posterior the obtained distributions. If TRUE, will keep all prediction iterations (draws).
draws	An integer indicating the number of draws to return. The default and maximum number of draws is the size of the posterior sample contained in the model.
seed	An optional seed to use.
centrality	The point-estimates (centrality indices) to compute. Character (vector) or list with one or more of these options: "median", "mean", "MAP" or "all".
ci	Credible Interval (CI) level. Default to 0.89 (89%). See <code>ci</code> for further details.
ci_method	The type of index used for Credible Interval. Can be "HDI" (default, see <code>hdi</code> ), "ETI" (see <code>eti</code> ) or "SI" (see <code>si</code> ).
...	Arguments passed to or from other methods.

## Value

A dataframe of predicted values.

## Examples

```
library(modelbased)

if (require("rstanarm") && require("brms")) {
  model <- stan_glm(Sepal.Width ~ Species * Petal.Length, data = iris)
  estimate_response(model)
  estimate_link(model)

  model <- stan_glmer(Sepal.Width ~ Petal.Length + (1 | Species), data = iris)
  estimate_response(model)
  estimate_link(model)

  library(brms)
  model <- brms::brm(Sepal.Width ~ Petal.Length, data = iris)
  estimate_response(model)
  estimate_link(model)
}
```

---

estimate_slopes	<i>Estimate the slopes of a numeric predictor (over different factor levels)</i>
-----------------	--

---

## Description

See the documentation for your object's class:

- [Frequentist models](#)
- [Bayesian models \(stanreg and brms\)](#)

## Usage

```
estimate_slopes(
  model,
  trend = NULL,
  levels = NULL,
  transform = "response",
  standardize = TRUE,
  standardize_robust = FALSE,
  ci = 0.95,
  ...
)

## S3 method for class 'glmmTMB'
estimate_slopes(
  model,
  trend = NULL,
  levels = NULL,
  transform = "response",
  standardize = TRUE,
  standardize_robust = FALSE,
  ci = 0.95,
  component = c("conditional", "zero_inflated", "zi"),
  ...
)
```

## Arguments

model	A Bayesian model.
trend	A character vector indicating the name of the numeric variable for which to compute the slopes.
levels	A character vector indicating the variables over which the slope will be computed. If NULL (default), it will select all the remaining predictors.
transform	Can be "none" (default for contrasts), "response" (default for means), "mu", "unlink", "log". "none" will leave the values on scale of the linear predictors. "response" will transform them on scale of the response variable. Thus for a

	logistic model, "none" will give estimations expressed in log-odds (probabilities on logit scale) and "response" in terms of probabilities.
standardize	If TRUE, adds standardized differences or coefficients.
standardize_robust	Robust standardization through MAD (Median Absolute Deviation, a robust estimate of SD) instead of regular SD.
ci	Credible Interval (CI) level. Default to 0.89 (89%). See <a href="#">ci</a> for further details.
...	Arguments passed to or from other methods.
component	A character vector indicating the model component for which estimation is requested. Only applies to models from <b>glmmTMB</b> . Use "conditional" for the count-model or "zero_inflate" or "zi" for the zero-inflation model.

**Value**

A data frame of slopes.

---

estimate\_slopes.lm      *Estimate the slopes of a numeric predictor (over different factor levels)*

---

**Description**

Estimate the slopes of a numeric predictor (over different factor levels)

**Usage**

```
## S3 method for class 'lm'
estimate_slopes(
  model,
  trend = NULL,
  levels = NULL,
  transform = "response",
  standardize = TRUE,
  standardize_robust = FALSE,
  ci = 0.95,
  ...
)
```

**Arguments**

model	A Bayesian model.
trend	A character vector indicating the name of the numeric variable for which to compute the slopes.
levels	A character vector indicating the variables over which the slope will be computed. If NULL (default), it will select all the remaining predictors.

transform	Can be "none" (default for contrasts), "response" (default for means), "mu", "unlink", "log". "none" will leave the values on scale of the linear predictors. "response" will transform them on scale of the response variable. Thus for a logistic model, "none" will give estimations expressed in log-odds (probabilities on logit scale) and "response" in terms of probabilities.
standardize	If TRUE, adds standardized differences or coefficients.
standardize_robust	Robust standardization through MAD (Median Absolute Deviation, a robust estimate of SD) instead of regular SD.
ci	Credible Interval (CI) level. Default to 0.89 (89%). See <a href="#">ci</a> for further details.
...	Arguments passed to or from other methods.

### Examples

```
library(modelbased)

model <- lm(Sepal.Width ~ Species * Petal.Length, data = iris)
estimate_slopes(model)
```

---

```
estimate_slopes.stanreg
```

*Estimate the slopes of a numeric predictor (over different factor levels)*

---

### Description

Estimate the slopes of a numeric predictor (over different factor levels)

### Usage

```
## S3 method for class 'stanreg'
estimate_slopes(
  model,
  trend = NULL,
  levels = NULL,
  transform = "response",
  standardize = TRUE,
  standardize_robust = FALSE,
  ci = 0.95,
  centrality = "median",
  ci_method = "hdi",
  test = c("pd", "rope"),
  rope_range = "default",
  rope_ci = 1,
  ...
)
```

**Arguments**

model	A Bayesian model.
trend	A character vector indicating the name of the numeric variable for which to compute the slopes.
levels	A character vector indicating the variables over which the slope will be computed. If NULL (default), it will select all the remaining predictors.
transform	Can be "none" (default for contrasts), "response" (default for means), "mu", "unlink", "log". "none" will leave the values on scale of the linear predictors. "response" will transform them on scale of the response variable. Thus for a logistic model, "none" will give estimations expressed in log-odds (probabilities on logit scale) and "response" in terms of probabilities.
standardize	If TRUE, adds standardized differences or coefficients.
standardize_robust	Robust standardization through MAD (Median Absolute Deviation, a robust estimate of SD) instead of regular SD.
ci	Credible Interval (CI) level. Default to 0.89 (89%). See <a href="#">ci</a> for further details.
centrality	The point-estimates (centrality indices) to compute. Character (vector) or list with one or more of these options: "median", "mean", "MAP" or "all".
ci_method	The type of index used for Credible Interval. Can be "HDI" (default, see <a href="#">hdi</a> ), "ETI" (see <a href="#">eti</a> ) or "SI" (see <a href="#">si</a> ).
test	The indices of effect existence to compute. Character (vector) or list with one or more of these options: "p_direction" (or "pd"), "rope", "p_map", "equivalence_test" (or "equitest"), "bayesfactor" (or "bf") or "all" to compute all tests. For each "test", the corresponding <b>bayestestR</b> function is called (e.g. <a href="#">rope</a> or <a href="#">p_direction</a> ) and its results included in the summary output.
rope_range	ROPE's lower and higher bounds. Should be a list of two values (e.g., <code>c(-0.1, 0.1)</code> ) or "default". If "default", the bounds are set to $x \pm 0.1 * SD(\text{response})$ .
rope_ci	The Credible Interval (CI) probability, corresponding to the proportion of HDI, to use for the percentage in ROPE.
...	Arguments passed to or from other methods.

**Examples**

```
library(modelbased)

if (require("rstanarm")) {
  model <- stan_glm(Sepal.Width ~ Species * Petal.Length, data = iris)
  estimate_slopes(model)
}
```

---

 estimate\_smooth

*Describe the smooth term (for GAMs) or non-linear predictors*


---

### Description

This function summarise the smooth term trend in terms of linear segments. Using the aproximative derivative, it separates a non-linear vector into quasi-linear segments (in which the trend is either positive or negative). Each of this segment its characterised by its beginning, end, size (in proportion, relative to the total size) trend (the linear regression coefficient) and linearity (the R2 of the linear regression).

### Usage

```
estimate_smooth(
  model,
  smooth = NULL,
  levels = NULL,
  length = 200,
  transform = "response",
  ...
)
```

### Arguments

model	A Bayesian model.
smooth	A character indicating the name of the "smooth" term.
levels	A character vector indicating the variables over which the slope will be computed. If NULL (default), it will select all the remaining predictors.
length	Passed to <a href="#">visualisation_matrix</a> if data = "grid".
transform	Can be "none" (default for contrasts), "response" (default for means), "mu", "unlink", "log". "none" will leave the values on scale of the linear predictors. "response" will transform them on scale of the response variable. Thus for a logistic model, "none" will give estimations expressed in log-odds (probabilities on logit scale) and "response" in terms of probabilities.
...	Arguments passed to or from other methods.

### Details

See the documentation for your object's class:

- [Bayesian models \(stanreg and brms\)](#)

### Value

A dataframe of linear description of non-linear terms.

---

 estimate\_smooth.stanreg

*Describe the smooth term (for GAMs) or non-linear predictors*


---

## Description

Describe the smooth term (for GAMs) or non-linear predictors

## Usage

```
## S3 method for class 'stanreg'
estimate_smooth(
  model,
  smooth = NULL,
  levels = NULL,
  length = 200,
  transform = "response",
  centrality = "median",
  ...
)
```

## Arguments

model	A Bayesian model.
smooth	A character indicating the name of the "smooth" term.
levels	A character vector indicating the variables over which the slope will be computed. If NULL (default), it will select all the remaining predictors.
length	Passed to <a href="#">visualisation_matrix</a> if data = "grid".
transform	Can be "none" (default for contrasts), "response" (default for means), "mu", "unlink", "log". "none" will leave the values on scale of the linear predictors. "response" will transform them on scale of the response variable. Thus for a logistic model, "none" will give estimations expressed in log-odds (probabilities on logit scale) and "response" in terms of probabilities.
centrality	The point-estimates (centrality indices) to compute. Character (vector) or list with one or more of these options: "median", "mean", "MAP" or "all".
...	Arguments passed to or from other methods.

## Examples

```
library(modelbased)

if (require("rstanarm")) {
  model <- stan_gamm4(Sepal.Width ~ s(Petal.Length), data = iris)
  estimate_smooth(model)

  model <- stan_glm(Sepal.Width ~ poly(Petal.Length, 2), data = iris)
```

```

estimate_smooth(model)

model <- stan_gamm4(Sepal.Width ~ Species + s(Petal.Length), data = iris)
estimate_smooth(model)

model <- stan_glm(Sepal.Width ~ Species * poly(Petal.Length, 2), data = iris)
estimate_smooth(model)
estimate_smooth(model, levels = "Species")
}

```

---

find\_inversions      *Find points of inversion*

---

### Description

Find points of inversion of a curve.

### Usage

```
find_inversions(x)
```

### Arguments

x                    A numeric vector.

### Value

Vector of inversion points.

### Examples

```

x <- sin(seq(0, 4 * pi, length.out = 100))
plot(x, type = "b")
find_inversions(x)

```

---

reshape\_draws      *Reshape estimations with Bayesian posterior draws to long format*

---

### Description

Reshape data.frame of estimations with Bayesian posterior draws to long format.

### Usage

```
reshape_draws(draws)
```

**Arguments**

`draws` data.frame containing posterior draws obtained from `estimate_response` or `estimate_link`.

**Value**

Data frame of reshaped draws in long format.

**Examples**

```
if (require("rstanarm")) {
  model <- stan_glm(Sepal.Width ~ Species * Petal.Length, data = iris)
  estimates <- estimate_response(model, keep_draws = TRUE, draws = 200)
  reshape_draws(estimates)
}
```

---

 smoothing

*Smoothing a vector or a time series*


---

**Description**

Smoothing a vector or a time series. For data.frames, the function will smooth all numeric variables stratified by factor levels (i.e., will smooth within each factor level combination).

**Usage**

```
smoothing(x, method = "loess", strength = 0.25, ...)
```

**Arguments**

`x` A numeric vector.

`method` Can be "loess" (default) or "smooth". A loess smoothing can be slow.

`strength` This argument only applies to `smooth_method = "loess"`. Degree of smoothing passed to `span` (see [loess](#)).

`...` Arguments passed to or from other methods.

**Value**

A smoothed vector or data frame.

**Examples**

```
x <- sin(seq(0, 4 * pi, length.out = 100)) + rnorm(100, 0, 0.2)
plot(x, type = "l")
lines(smoothing(x, method = "smooth"), type = "l", col = "blue")
lines(smoothing(x, method = "loess"), type = "l", col = "red")

x <- sin(seq(0, 4 * pi, length.out = 10000)) + rnorm(10000, 0, 0.2)
plot(x, type = "l")
lines(smoothing(x, method = "smooth"), type = "l", col = "blue")
lines(smoothing(x, method = "loess"), type = "l", col = "red")
```

---

visualisation\_matrix *Create a reference grid*

---

**Description**

Create a reference matrix, useful for visualisation, with evenly spread and combined values.

**Usage**

```
visualisation_matrix(
  x,
  target = "all",
  length = 10,
  factors = "reference",
  numerics = "mean",
  preserve_range = FALSE,
  standardize = FALSE,
  standardize_robust = FALSE,
  reference = x,
  na.rm = TRUE,
  ...
)
```

**Arguments**

x	An object from which to construct the reference grid.
target	Can be "all" or list of characters indicating columns of interest. Can also contain assignments (e.g., target = "Sepal.Length = 2" or target = c("Sepal.Length = 2", "Species = 'setosa'")) - note the usage of single and double quotes to assign strings within strings). The remaining variables will be fixed.
length	Length of numeric target variables.
factors	Type of summary for factors. Can be "combination" (include all unique values), "reference" (set at the reference level) or "mode" (set at the most common level).
numerics	Type of summary for numeric values. Can be "combination" (include all unique values), any function ("mean", "median", ...) or a value (e.g., numerics = 0).

preserve_range	In the case of combinations between numeric variables and factors, setting preserve_range = TRUE removes observations where the value of the numeric variable is originally not present in the range of its factor level.
standardize	The numeric target value is spread as deviations from the mean, with the central value being the mean (or the median if standardize_robust is TRUE). For instance, if x is a vector of mean 1 and SD 2.5, and a standardized grid is required of length 3, the result will be c(Mean-1*SD, Mean, Mean+1*SD), i.e., c(-1.5, 1, 3.5). Each value represents deviations (in terms of SD or MAD) from the central value. This needs the length argument to be an even integer, so that the central value represent the mean.
standardize_robust	Standardization based on median and MAD (a robust equivalent of the SD).
reference	The reference vector from which to compute the mean and SD.
na.rm	Remove NaNs.
...	Arguments passed to or from other methods.

**Value**

Reference grid data frame.

**Examples**

```
library(modelbased)

visualisation_matrix(iris, target = "Sepal.Length")
visualisation_matrix(iris, target = "Sepal.Length", factors = "combinations")
visualisation_matrix(iris, target = c("Sepal.Length", "Species"), length = 3)
visualisation_matrix(iris, target = c("Sepal.Length", "Species"), numerics = 0)
visualisation_matrix(iris, target = c("Sepal.Length = 3", "Species"))
visualisation_matrix(iris, target = c("Sepal.Length = c(3, 1)", "Species = 'setosa'"))
visualisation_matrix(iris, target = "Sepal.Length", standardize = TRUE, length = 3)
```

---

zero\_crossings      *Find zero crossings of a vector*

---

**Description**

Find zero crossings of a vector, i.e., indices when the numeric variable crosses 0.

**Usage**

```
zero_crossings(x)
```

**Arguments**

x                      A numeric vector.

**Value**

Vector of zero crossings.

**See Also**

Based on the `uniroot.all` function from the `rootSolve` package.

**Examples**

```
x <- sin(seq(0, 4 * pi, length.out = 100))  
plot(x)  
zero_crossings(x)
```

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