

Package ‘modelbased’

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Type Package

Title Estimation of Model-Based Predictions, Contrasts and Means

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Description Implements a general interface for model-based estimations for a wide variety of models (see list of supported models using the function 'insight::supported_models()'), used in the computation of marginal means, contrast analysis and predictions.

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

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

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describe_nonlinear	<i>Describe the smooth term (for GAMs) or non-linear predictors</i>
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Description

This function summarises the smooth term trend in terms of linear segments. Using the approximate 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 characterized 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

```
describe_nonlinear(data, ...)

## S3 method for class 'data.frame'
describe_nonlinear(data, x = NULL, y = NULL, ...)

estimate_smooth(data, ...)
```

Arguments

data	The data containing the link, as for instance obtained by <code>estimate_relation()</code> .
...	Other arguments to be passed to or from.
x, y	The name of the responses variable (y) predicting variable (x).

Value

A dataframe of linear description of non-linear terms.

Examples

```
library(modelbased)

# Create data
data <- data.frame(x = rnorm(200))
data$y <- data$x^2 + rnorm(200, 0, 0.5)

model <- lm(y ~ poly(x, 2), data = data)
link_data <- estimate_relation(model, length = 100)

describe_nonlinear(link_data, x = "x")
```

estimate_contrasts *Estimate Marginal Contrasts*

Description

Run a contrast analysis by estimating the differences between each level of a factor. See also other related functions such as [estimate_means\(\)](#) and [estimate_slopes\(\)](#).

Usage

```
estimate_contrasts(
  model,
  contrast = NULL,
  at = NULL,
  fixed = NULL,
  transform = "none",
  ci = 0.95,
  adjust = "holm",
  ...
)
```

Arguments

model	A statistical model.
contrast	A character vector indicating the name of the variable(s) for which to compute the contrasts.
at	The predictor variable(s) <i>at</i> which to evaluate the desired effect / mean / contrasts. Other predictors of the model that are not included here will be collapsed and "averaged" over (the effect will be estimated across them).
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.

transform	Is passed to the type argument in <code>emmeans::emmeans()</code> . See this vignette . 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.
ci	Confidence Interval (CI) level. Default to 0.95 (95%).
adjust	The p-values adjustment method for frequentist multiple 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.
...	Other arguments passed for instance to <code>visualisation_matrix()</code> .

Details

The `estimate_slopes()`, `estimate_means()` and `estimate_contrasts()` functions are forming a group, as they are all based on *marginal* estimations (estimations based on a model). All three are also built on the **emmeans** package, so reading its documentation (for instance for `emmeans::emmeans()` and `emmeans::emtrends()`) is recommended to understand the idea behind these types of procedures.

- Model-based **predictions** is the basis for all that follows. Indeed, the first thing to understand is how models can be used to make predictions (see `estimate_link()`). This corresponds to the predicted response (or "outcome variable") given specific predictor values of the predictors (i.e., given a specific data configuration). This is why the concept of `reference_grid()` is so important for direct predictions.
- **Marginal "means"**, obtained via `estimate_means()`, are an extension of such predictions, allowing to "average" (collapse) some of the predictors, to obtain the average response value at a specific predictors configuration. This is typically used when some of the predictors of interest are factors. Indeed, the parameters of the model will usually give you the intercept value and then the "effect" of each factor level (how different it is from the intercept). Marginal means can be used to directly give you the mean value of the response variable at all the levels of a factor. Moreover, it can also be used to control, or average over predictors, which is useful in the case of multiple predictors with or without interactions.
- **Marginal contrasts**, obtained via `estimate_contrasts()`, are themselves an extension of marginal means, in that they allow to investigate the difference (i.e., the contrast) between the marginal means. This is, again, often used to get all pairwise differences between all levels of a factor. It works also for continuous predictors, for instance one could also be interested in whether the difference at two extremes of a continuous predictor is significant.
- Finally, **marginal effects**, obtained via `estimate_slopes()`, are different in that their focus is not values on the response variable, but the model's parameters. The idea is to assess the effect of a predictor at a specific configuration of the other predictors. This is relevant in the case of interactions or non-linear relationships, when the effect of a predictor variable changes depending on the other predictors. Moreover, these effects can also be "averaged" over other predictors, to get for instance the "general trend" of a predictor over different factor levels.

Example: let's imagine the following model $\text{lm}(y \sim \text{condition} * x)$ where `condition` is a factor with 3 levels A, B and C and `x` a continuous variable (like age for example). One idea is to see how

this model performs, and compare the actual response y to the one predicted by the model (using `estimate_response()`). Another idea is evaluate the average mean at each of the condition's levels (using `estimate_means()`), which can be useful to visualize them. Another possibility is to evaluate the difference between these levels (using `estimate_contrasts()`). Finally, one could also estimate the effect of x averaged over all conditions, or instead within each condition (using `[estimate_slopes]`).

Value

A data frame of estimated contrasts.

Examples

```
library(modelbased)

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

# Dealing with interactions
model <- lm(Sepal.Width ~ Species * Petal.Width, data = iris)
# By default: selects first factor
estimate_contrasts(model)
# Can also run contrasts between points of numeric
estimate_contrasts(model, contrast = "Petal.Width", length = 4)
# Or both
estimate_contrasts(model, contrast = c("Species", "Petal.Width"), length = 2)
# Or with custom specifications
estimate_contrasts(model, contrast = c("Species", "Petal.Width=c(1, 2)"))
# Can fixate the numeric at a specific value
estimate_contrasts(model, fixed = "Petal.Width")
# Or modulate it
estimate_contrasts(model, at = "Petal.Width", length = 4)

# Standardized differences
estimated <- estimate_contrasts(lm(Sepal.Width ~ Species, data = iris))
effectsize::standardize(estimated)

# Other models (mixed, Bayesian, ...)
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)
}

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, at = "wt", length = 4)

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

## End(Not run)

```

estimate_expectation *Model-based response estimates and uncertainty*

Description

After fitting a model, it is useful generate model-based estimates of the response variables for different combinations of predictor values. Such estimates can be used to make inferences about relationships between variables and to make predictions about individual cases.

Model-based response estimates and uncertainty can be generated for both the conditional average response values (the regression line or expectation) and for predictions about individual cases. See below for details.

Usage

```

estimate_expectation(
  model,
  data = NULL,
  ci = 0.95,
  keep_iterations = FALSE,
  ...
)

estimate_response(...)

estimate_link(model, data = "grid", ci = 0.95, keep_iterations = FALSE, ...)

estimate_prediction(
  model,
  data = NULL,
  ci = 0.95,
  keep_iterations = FALSE,

```

```

    ...
  )

estimate_relation(
  model,
  data = "grid",
  ci = 0.95,
  keep_iterations = FALSE,
  ...
)

```

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 visualisation_matrix()).
ci	Confidence Interval (CI) level. Default to 0.95 (95%).
keep_iterations	If TRUE, will keep all iterations (draws) of bootstrapped or Bayesian models. They will be added as additional columns named iter_1, iter_2, You can reshape them to a long format by running reshape_iterations() .
...	You can add all the additional control arguments from visualisation_matrix() (used when data = "grid") and insight::get_predicted() .

Value

A data frame of predicted values and uncertainty intervals, with class "estimate_predicted". Methods for [visualisation_recipe\(\)](#) and [plot\(\)](#) are available.

Expected (average) values

The most important way that various types of response estimates differ is in terms of what quantity is being estimated and the meaning of the uncertainty intervals. The major choices are **expected values** for uncertainty in the regression line and **predicted values** for uncertainty in the individual case predictions.

Expected values refer to the fitted regression line—the estimated *average* response value (i.e., the "expectation") for individuals with specific predictor values. For example, in a linear model $y = 2 + 3x + 4z + e$, the estimated average y for individuals with $x = 1$ and $z = 2$ is 11.

For expected values, uncertainty intervals refer to uncertainty in the estimated **conditional average** (where might the true regression line actually fall)? Uncertainty intervals for expected values are also called "confidence intervals".

Expected values and their uncertainty intervals are useful for describing the relationship between variables and for describing how precisely a model has been estimated.

For generalized linear models, expected values are reported on one of two scales:

- The **link scale** refers to scale of the fitted regression line, after transformation by the link function. For example, for a logistic regression (logit binomial) model, the link scale gives expected log-odds. For a log-link Poisson model, the link scale gives the expected log-count.

- The **response scale** refers to the original scale of the response variable (i.e., without any link function transformation). Expected values on the link scale are back-transformed to the original response variable metric (e.g., expected probabilities for binomial models, expected counts for Poisson models).

Individual case predictions

In contrast to expected values, **predicted values** refer to predictions for **individual cases**. Predicted values are also called "posterior predictions" or "posterior predictive draws".

For predicted values, uncertainty intervals refer to uncertainty in the **individual response values for each case** (where might any single case actually fall)? Uncertainty intervals for predicted values are also called "prediction intervals" or "posterior predictive intervals".

Predicted values and their uncertainty intervals are useful for forecasting the range of values that might be observed in new data, for making decisions about individual cases, and for checking if model predictions are reasonable ("posterior predictive checks").

Predicted values and intervals are always on the scale of the original response variable (not the link scale).

Functions for estimating predicted values and uncertainty

`modelbased` provides 4 functions for generating model-based response estimates and their uncertainty:

- `estimate_expectation()`:
 - Generates **expected values** (conditional average) on the **response scale**.
 - The uncertainty interval is a *confidence interval*.
 - By default, values are computed using the data used to fit the model.
- `estimate_link()`:
 - Generates **expected values** (conditional average) on the **link scale**.
 - The uncertainty interval is a *confidence interval*.
 - By default, values are computed using a reference grid spanning the observed range of predictor values (see `visualisation_matrix()`).
- `estimate_prediction()`:
 - Generates **predicted values** (for individual cases) on the **response scale**.
 - The uncertainty interval is a *prediction interval*.
 - By default, values are computed using the data used to fit the model.
- `estimate_relation()`:
 - Like `estimate_expectation()`.
 - Useful for visualizing a model.
 - Generates **expected values** (conditional average) on the **response scale**.
 - The uncertainty interval is a *confidence interval*.
 - By default, values are computed using a reference grid spanning the observed range of predictor values (see `visualisation_matrix()`).

`estimate_response()` is a deprecated alias for `estimate_expectation()`.

Data for predictions

If the data = NULL, values are estimated using the data used to fit the model. If data = "grid", values are computed using a reference grid spanning the observed range of predictor values with `visualisation_matrix()`. This can be useful for model visualization. The number of predictor values used for each variable can be controlled with the length argument. data can also be a data frame containing columns with names matching the model frame (see `insight::get_data()`). This can be used to generate model predictions for specific combinations of predictor values.

Note

These functions are built on top of `insight::get_predicted()` and correspond to different specifications of its parameters. It may be useful to read its [documentation](#), in particular the description of the predict argument for additional details on the difference between expected vs. predicted values and link vs. response scales.

Additional control parameters can be used to control results from `visualisation_matrix()` (when data = "grid") and from `insight::get_predicted()` (the function used internally to compute predictions).

For plotting, check the examples in `visualisation_recipe()`. Also check out the [Vignettes](#) and [README examples](#) for various examples, tutorials and usecases.

Examples

```
library(modelbased)

# Linear Models
model <- lm(mpg ~ wt, data = mtcars)

# Get predicted and prediction interval (see insight::get_predicted)
estimate_response(model)

# Get expected values with confidence interval
pred <- estimate_relation(model)
pred

# Visualisation (see visualisation_recipe())
plot(pred)

# Standardize predictions
pred <- estimate_relation(lm(mpg ~ wt + am, data = mtcars))
z <- effectsize::standardize(pred, include_response = FALSE)
z
effectsize::unstandardize(z, include_response = FALSE)

# Logistic Models
model <- glm(vs ~ wt, data = mtcars, family = "binomial")
estimate_response(model)
estimate_relation(model)

# Mixed models
if (require("lme4")) {
```

```

model <- lmer(mpg ~ wt + (1 | gear), data = mtcars)
estimate_response(model)
estimate_relation(model)
}

# Bayesian models

if (require("rstanarm")) {
  model <- rstanarm::stan_glm(mpg ~ wt, data = mtcars, refresh = 0, iter = 200)
  estimate_response(model)
  estimate_relation(model)
}

```

estimate_grouplevel *Group-specific parameters of mixed models random effects*

Description

Extract random parameters of each individual group in the context of mixed models. Can be reshaped to be of the same dimensions as the original data, which can be useful to add the random effects to the original data.

Usage

```

estimate_grouplevel(model, type = "random", ...)

reshape_grouplevel(x, indices = "all", ...)

```

Arguments

model	A mixed model with random effects.
type	If "random" (default), the coefficients are the ones estimated natively by the model (as they are returned by, for instance, <code>lme4::ranef()</code>). They correspond to the deviation of each individual group from their fixed effect. As such, a coefficient close to 0 means that the participants' effect is the same as the population-level effect (in other words, it is "in the norm"). If "total", it will return the sum of the random effect and its corresponding fixed effects. These are known as BLUPs (Best Linear Unbiased Predictions). This argument can be used to reproduce the results given by <code>lme4::ranef()</code> and <code>coef()</code> (see <code>?coef.merMod</code>). Note that BLUPs currently don't have uncertainty indices (such as SE and CI), as these are not computable.
...	Other arguments passed to or from other methods.
x	The output of <code>estimate_grouplevel()</code> .
indices	A list containing the indices to extract.

Examples

```
# lme4 model
if (require("lme4") && require("see")) {
  model <- lmer(mpg ~ hp + (1 | carb), data = mtcars)
  random <- estimate_grouplevel(model)
  random

  # Visualize random effects
  plot(random)

  # Show group-specific effects
  estimate_grouplevel(model, deviation = FALSE)

  # Reshape to wide data so that it matches the original dataframe...
  reshaped <- reshape_grouplevel(random, indices = c("Coefficient", "SE"))

  # ... and can be easily combined
  alldata <- cbind(mtcars, reshaped)

  # Use summary() to remove duplicated rows
  summary(reshaped)

  # Compute BLUPs
  estimate_grouplevel(model, type = "total")
}

# Bayesian models

if (require("rstanarm")) {
  model <- rstanarm::stan_lmer(mpg ~ hp + (1 | carb), data = mtcars, refresh = 0)
}
```

estimate_means

Estimate Marginal Means (Model-based average at each factor level)

Description

Estimate average value of response variable at each factor levels. For plotting, check the examples in [visualisation_recipe\(\)](#). See also other related functions such as [estimate_contrasts\(\)](#) and [estimate_slopes\(\)](#).

Usage

```
estimate_means(
  model,
  at = "auto",
  fixed = NULL,
  transform = "response",
```

```

    ci = 0.95,
    ...
  )

```

Arguments

model	A statistical model.
at	The predictor variable(s) <i>at</i> which to evaluate the desired effect / mean / contrasts. Other predictors of the model that are not included here will be collapsed and "averaged" over (the effect will be estimated across them).
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.
transform	Is passed to the type argument in <code>emmeans::emmeans()</code> . See this vignette . 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.
ci	Confidence Interval (CI) level. Default to 0.95 (95%).
...	Other arguments passed for instance to <code>visualisation_matrix()</code> .

Details

The `estimate_slopes()`, `estimate_means()` and `estimate_contrasts()` functions are forming a group, as they are all based on *marginal* estimations (estimations based on a model). All three are also built on the **emmeans** package, so reading its documentation (for instance for `emmeans::emmeans()` and `emmeans::emtrends()`) is recommended to understand the idea behind these types of procedures.

- Model-based **predictions** is the basis for all that follows. Indeed, the first thing to understand is how models can be used to make predictions (see `estimate_link()`). This corresponds to the predicted response (or "outcome variable") given specific predictor values of the predictors (i.e., given a specific data configuration). This is why the concept of [reference grid\(\)](#) is so important for direct predictions.
- **Marginal "means"**, obtained via `estimate_means()`, are an extension of such predictions, allowing to "average" (collapse) some of the predictors, to obtain the average response value at a specific predictors configuration. This is typically used when some of the predictors of interest are factors. Indeed, the parameters of the model will usually give you the intercept value and then the "effect" of each factor level (how different it is from the intercept). Marginal means can be used to directly give you the mean value of the response variable at all the levels of a factor. Moreover, it can also be used to control, or average over predictors, which is useful in the case of multiple predictors with or without interactions.
- **Marginal contrasts**, obtained via `estimate_contrasts()`, are themselves at extension of marginal means, in that they allow to investigate the difference (i.e., the contrast) between the marginal means. This is, again, often used to get all pairwise differences between all levels of a factor. It works also for continuous predictors, for instance one could also be interested in whether the difference at two extremes of a continuous predictor is significant.

- Finally, **marginal effects**, obtained via `estimate_slopes()`, are different in that their focus is not values on the response variable, but the model's parameters. The idea is to assess the effect of a predictor at a specific configuration of the other predictors. This is relevant in the case of interactions or non-linear relationships, when the effect of a predictor variable changes depending on the other predictors. Moreover, these effects can also be "averaged" over other predictors, to get for instance the "general trend" of a predictor over different factor levels.

Example: let's imagine the following model $\text{lm}(y \sim \text{condition} * x)$ where `condition` is a factor with 3 levels A, B and C and `x` a continuous variable (like age for example). One idea is to see how this model performs, and compare the actual response `y` to the one predicted by the model (using `estimate_response()`). Another idea is evaluate the average mean at each of the condition's levels (using `estimate_means()`), which can be useful to visualize them. Another possibility is to evaluate the difference between these levels (using `estimate_contrasts()`). Finally, one could also estimate the effect of `x` averaged over all conditions, or instead within each condition (using `[estimate_slopes]`).

Value

A dataframe of estimated marginal means.

Examples

```
library(modelbased)

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

estimate_means(model)
estimate_means(model, fixed = "Sepal.Width")
estimate_means(model, at = c("Species", "Sepal.Width"), length = 2)
estimate_means(model, at = "Species=c('versicolor', 'setosa')")
estimate_means(model, at = "Sepal.Width=c(2, 4)")
estimate_means(model, at = c("Species", "Sepal.Width=0"))
estimate_means(model, at = "Sepal.Width", length = 5)
estimate_means(model, at = "Sepal.Width=c(2, 4)")

# Methods that can be applied to it:
means <- estimate_means(model, fixed = "Sepal.Width")
plot(means) # which runs visualisation_recipe()
effectsize::standardize(means)

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, at = "Sepal.Width", length = 3)
}
```

estimate_slopes *Estimate Marginal Effects*

Description

Estimate the slopes (i.e., the coefficient) of a predictor over or within different factor levels, or alongside a numeric variable. In other words, to assess the effect of a predictor *at* specific configurations data. Other related functions based on marginal estimations includes [estimate_contrasts\(\)](#) and [estimate_means\(\)](#).

See the **Details** section below, and don't forget to also check out the **Vignettes** and **README examples** for various examples, tutorials and usecases.

Usage

```
estimate_slopes(model, trend = NULL, at = NULL, ci = 0.95, ...)
```

Arguments

model	A statistical model.
trend	A character indicating the name of the variable for which to compute the slopes.
at	The predictor variable(s) <i>at</i> which to evaluate the desired effect / mean / contrasts. Other predictors of the model that are not included here will be collapsed and "averaged" over (the effect will be estimated across them).
ci	Confidence Interval (CI) level. Default to 0.95 (95%).
...	Other arguments passed for instance to visualisation_matrix() .

Details

The [estimate_slopes\(\)](#), [estimate_means\(\)](#) and [estimate_contrasts\(\)](#) functions are forming a group, as they are all based on *marginal* estimations (estimations based on a model). All three are also built on the **emmeans** package, so reading its documentation (for instance for [emmeans::emmeans\(\)](#) and [emmeans::emtrends\(\)](#)) is recommended to understand the idea behind these types of procedures.

- Model-based **predictions** is the basis for all that follows. Indeed, the first thing to understand is how models can be used to make predictions (see [estimate_link\(\)](#)). This corresponds to the predicted response (or "outcome variable") given specific predictor values of the predictors (i.e., given a specific data configuration). This is why the concept of [reference grid\(\)](#) is so important for direct predictions.
- **Marginal "means"**, obtained via [estimate_means\(\)](#), are an extension of such predictions, allowing to "average" (collapse) some of the predictors, to obtain the average response value at a specific predictors configuration. This is typically used when some of the predictors of interest are factors. Indeed, the parameters of the model will usually give you the intercept value and then the "effect" of each factor level (how different it is from the intercept). Marginal means can be used to directly give you the mean value of the response variable at all the levels

of a factor. Moreover, it can also be used to control, or average over predictors, which is useful in the case of multiple predictors with or without interactions.

- **Marginal contrasts**, obtained via `estimate_contrasts()`, are themselves an extension of marginal means, in that they allow to investigate the difference (i.e., the contrast) between the marginal means. This is, again, often used to get all pairwise differences between all levels of a factor. It works also for continuous predictors, for instance one could also be interested in whether the difference at two extremes of a continuous predictor is significant.
- Finally, **marginal effects**, obtained via `estimate_slopes()`, are different in that their focus is not values on the response variable, but the model's parameters. The idea is to assess the effect of a predictor at a specific configuration of the other predictors. This is relevant in the case of interactions or non-linear relationships, when the effect of a predictor variable changes depending on the other predictors. Moreover, these effects can also be "averaged" over other predictors, to get for instance the "general trend" of a predictor over different factor levels.

Example: let's imagine the following model $\text{lm}(y \sim \text{condition} * x)$ where *condition* is a factor with 3 levels A, B and C and *x* a continuous variable (like age for example). One idea is to see how this model performs, and compare the actual response *y* to the one predicted by the model (using `estimate_response()`). Another idea is to evaluate the average mean at each of the condition's levels (using `estimate_means()`), which can be useful to visualize them. Another possibility is to evaluate the difference between these levels (using `estimate_contrasts()`). Finally, one could also estimate the effect of *x* averaged over all conditions, or instead within each condition (using `estimate_slopes()`).

Value

A data.frame of class `estimate_slopes`.

Examples

```
# Get an idea of the data
if (require("ggplot2")) {
  ggplot(iris, aes(x = Petal.Length, y = Sepal.Width)) +
    geom_point(aes(color = Species)) +
    geom_smooth(color = "black", se = FALSE) +
    geom_smooth(aes(color = Species), linetype = "dotted", se = FALSE) +
    geom_smooth(aes(color = Species), method = "lm", se = FALSE)
}

# Model it
model <- lm(Sepal.Width ~ Species * Petal.Length, data = iris)
# Compute the marginal effect of Petal.Length at each level of Species
slopes <- estimate_slopes(model, trend = "Petal.Length", at = "Species")
slopes
plot(slopes)
effectsize::standardize(slopes)

if (require("mgcv")) {
  model <- mgcv::gam(Sepal.Width ~ s(Petal.Length), data = iris)
  slopes <- estimate_slopes(model, at = "Petal.Length", length = 50)
  summary(slopes)
}
```

```

plot(slopes)

model <- mgcv::gam(Sepal.Width ~ s(Petal.Length, by = Species), data = iris)
slopes <- estimate_slopes(model,
  trend = "Petal.Length",
  at = c("Petal.Length", "Species"), length = 20
)
summary(slopes)
plot(slopes)
}

```

find_inversions	<i>Find points of inversion</i>
-----------------	---------------------------------

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)

```

model_emcontrasts	<i>Easy 'emmeans' and 'emtrends'</i>
-------------------	--------------------------------------

Description

The model_emmeans function is a wrapper to facilitate the usage of emmeans::emmeans() and emmeans::emtrends(), providing a somewhat simpler and intuitive API to find the specifications and variables of interest. It is mainly made to for the developers to facilitate the organization and debugging, and end-users should rather use the estimate_* series of functions.

Usage

```

model_emcontrasts(
  model,
  contrast = NULL,
  at = NULL,
  fixed = NULL,
  transform = "none",
  ...
)

model_emmeans(
  model,
  at = "auto",
  fixed = NULL,
  transform = "response",
  levels = NULL,
  modulate = NULL,
  ...
)

model_emptrends(
  model,
  trend = NULL,
  at = NULL,
  fixed = NULL,
  levels = NULL,
  modulate = NULL,
  ...
)

```

Arguments

model	A statistical model.
contrast	A character vector indicating the name of the variable(s) for which to compute the contrasts.
at	The predictor variable(s) <i>at</i> which to evaluate the desired effect / mean / contrasts. Other predictors of the model that are not included here will be collapsed and "averaged" over (the effect will be estimated across them).
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.
transform	Is passed to the type argument in <code>emmeans::emmeans()</code> . See this vignette . 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.
...	Other arguments passed for instance to <code>visualisation_matrix()</code> .

levels, modulate

Deprecated, use at instead.

trend

A character indicating the name of the variable for which to compute the slopes.

Examples

```
# Basic usage
model <- lm(Sepal.Width ~ Species, data = iris)
model_emcontrasts(model)

# Dealing with interactions
model <- lm(Sepal.Width ~ Species * Petal.Width, data = iris)
# By default: selects first factor
model_emcontrasts(model)
# Can also run contrasts between points of numeric
model_emcontrasts(model, contrast = "Petal.Width", length = 3)
# Or both
model_emcontrasts(model, contrast = c("Species", "Petal.Width"), length = 2)
# Or with custom specifications
estimate_contrasts(model, contrast = c("Species", "Petal.Width=c(1, 2)"))
# Can fixate the numeric at a specific value
model_emcontrasts(model, fixed = "Petal.Width")
# Or modulate it
model_emcontrasts(model, at = "Petal.Width", length = 4)
model <- lm(Sepal.Length ~ Species + Petal.Width, data = iris)

# By default, 'at' is set to "Species"
model_emmeans(model)

# Overall mean (close to 'mean(iris$Sepal.Length)')
model_emmeans(model, at = NULL)

# One can estimate marginal means at several values of a 'modulate' variable
model_emmeans(model, at = "Petal.Width", length = 3)

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

model_emmeans(model)
model_emmeans(model, at = c("Species", "Petal.Length"), length = 2)
model_emmeans(model, at = c("Species", "Petal.Length = c(1, 3, 5)"), length = 2)
model <- lm(Sepal.Width ~ Species * Petal.Length, data = iris)

model_emtrends(model)
model_emtrends(model, at = "Species")
model_emtrends(model, at = "Petal.Length")
model_emtrends(model, at = c("Species", "Petal.Length"))

model <- lm(Petal.Length ~ poly(Sepal.Width, 4), data = iris)
model_emtrends(model)
model_emtrends(model, at = "Sepal.Width")
```

smoothing	<i>Smoothing a vector or a time series</i>
-----------	--

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 when 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	<i>Create a reference grid</i>
----------------------	--------------------------------

Description

Create a reference matrix, useful for visualisation, with evenly spread and combined values. `data_matrix()` is an alternative name for `visualisation_matrix()`.

Usage

```

visualisation_matrix(x, ...)

data_matrix(x, ...)

## S3 method for class 'data.frame'
visualisation_matrix(
  x,
  at = "all",
  target = NULL,
  factors = "reference",
  numerics = "mean",
  preserve_range = FALSE,
  reference = x,
  ...
)

## S3 method for class 'numeric'
visualisation_matrix(x, length = 10, range = "range", ...)

## S3 method for class 'factor'
visualisation_matrix(x, ...)

```

Arguments

x	An object from which to construct the reference grid.
...	Arguments passed to or from other methods (for instance, length or range to control the spread of numeric variables.).
at, target	Can be "all" or list of characters indicating columns of interest. Can also contain assignments (e.g., at = "Sepal.Length = 2" or at = 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. (target is the deprecated name of that argument).
factors	Type of summary for factors. Can be "reference" (set at the reference level), "mode" (set at the most common level) or "all" to keep all levels.
numerics	Type of summary for numeric values. Can be "all" (will duplicate the grid for 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 will drop the observations where the value of the numeric variable is originally not present in the range of its factor level. This leads to an unbalanced grid. Also, if you want the minimum and the maximum to closely match the actual ranges, you should increase the length argument.
reference	The reference vector from which to compute the mean and SD.
length	Length of numeric "at" variables.

range Can be one of `c("range", "iqr", "ci", "hdi", "eti")`. If "range" (default), will use the min and max of the original vector as end-points. If any other interval, will spread within the range (the default CI width is 95% but this can be changed by setting something else, e.g., `ci = 0.90`). See `IQR()` and `bayestestR::ci()`.

Value

Reference grid data frame.

Examples

```
library(modelbased)

# Add one row to change the "mode" of Species
data <- rbind(iris, iris[149, ], make.row.names = FALSE)

# Single variable is of interest; all others are "fixed"
visualisation_matrix(data, at = "Sepal.Length")
visualisation_matrix(data, at = "Sepal.Length", length = 3)
visualisation_matrix(data, at = "Sepal.Length", range = "ci", ci = 0.90)
visualisation_matrix(data, at = "Sepal.Length", factors = "mode")

# Multiple variables are of interest, creating a combination
visualisation_matrix(data, at = c("Sepal.Length", "Species"), length = 3)
visualisation_matrix(data, at = c(1, 3), length = 3)
visualisation_matrix(data, at = c("Sepal.Length", "Species"), preserve_range = TRUE)
visualisation_matrix(data, at = c("Sepal.Length", "Species"), numerics = 0)
visualisation_matrix(data, at = c("Sepal.Length = 3", "Species"))
visualisation_matrix(data, at = c("Sepal.Length = c(3, 1)", "Species = 'setosa'"))

# Standardize
vizdata <- visualisation_matrix(data, at = "Sepal.Length")
effectsize::standardize(vizdata)
```

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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