Package ‘ggeffects’

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Type Package
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Title Create Tidy Data Frames of Marginal Effects for 'ggplot' from Model Outputs
Version 1.1.0
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Description Compute marginal effects and adjusted predictions from statistical models and returns the result as tidy data frames. These data frames are ready to use with the 'ggplot2'-package. Effects and predictions can be calculated for many different models. Interaction terms, splines and polynomial terms are also supported. The main functions are ggpredict(), ggemmeans() and ggeffect(). There is a generic plot()-method to plot the results using 'ggplot2'.
License GPL-3
Depends R (>= 3.4)
Imports graphics, insight (>= 0.13.0), MASS, sjlabelled (>= 1.1.2), stats
Suggests AER, aod, betareg, brms, clubSandwich, effects (>= 4.1-2), emmeans (>= 1.4.1), gam, gamlss, gamm4, gee, geepack, ggplot2, GLMMAdaptive, glmTMB (>= 1.0.0), gridExtra, haven, htr, knitr, lme4, logistf, magrittr, margins, Matrix, mice, MCMCglmm, mgcv, nlme, ordinal, parameters, prediction, pscl, quantreg, rmarkdown, rms, robustbase, rstanarm, rstantools, sandwich, see, sjstats, sjmisc (>= 2.8.2), survey, survival, testthat, VGAM
URL https://strengejacke.github.io/ggeffects/
BugReports https://github.com/strengejacke/ggeffects/issues/
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NeedsCompilation no
Description

This function extracts the raw data points (i.e. the data that was used to fit the model) and "averages" (i.e. "collapses") the response variable over the levels of the grouping factor given in collapse.by. Only works with mixed models.

Usage

\[
\text{collapse_by_group}(\text{grid}, \text{model}, \text{collapse.by = NULL, residuals = FALSE})
\]

Arguments

- **grid**: A data frame representing the data grid, or an object of class ggeffects, as returned by `ggpredict()` and others.
- **model**: The model for which to compute partial residuals. The data grid `grid` should match to predictors in the model.
- **collapse.by**: Name of the (random effects) grouping factor. Data is collapsed by the levels of this factor.
residuals Logical, if TRUE, collapsed partial residuals instead of raw data by the levels of the grouping factor.

Value

A data frame with raw data points, averaged over the levels of the given grouping factor from the random effects. The group level of the random effect is saved in the column "random".

Examples

```r
library(ggeffects)
if (require("lme4", quietly = TRUE)) {
  data(efc)
  efc$e15relat <- as.factor(efc$e15relat)
  efc$c161sex <- as.factor(efc$c161sex)
  levels(efc$c161sex) <- c("male", "female")
  model <- lmer(neg_c_7 ~ c161sex + (1 | e15relat), data = efc)
  me <- ggpredict(model, terms = "c161sex")
  head(attributes(me)$rawdata)
  collapse_by_group(me, model, "e15relat")
}
```

efc Sample dataset from the EUROFAMCARE project

Description

A SPSS sample data set, imported with the sjlabelled::read_spss() function.

Examples

```r
# Attach EFC-data
data(efc)

# Show structure
str(efc)

# show first rows
head(efc)
```

fish Sample data set

Description

A sample data set, used in tests and some examples.
**get_title**

*Get titles and labels from data*

**Description**

Get variable and value labels from ggeffects-objects. Functions like `ggpredict()` or `ggeffect()` save information on variable names and value labels as additional attributes in the returned data frame. This is especially helpful for labelled data (see sjlabelled), since these labels can be used to set axis labels and titles.

**Usage**

```r
get_title(x, case = NULL)
get_x_title(x, case = NULL)
get_y_title(x, case = NULL)
get_legend_title(x, case = NULL)
get_legend_labels(x, case = NULL)
get_x_labels(x, case = NULL)
get_complete_df(x, case = NULL)
```

**Arguments**

- `x` An object of class ggeffects, as returned by any ggeffects-function; for `get_complete_df()`, must be a list of ggeffects-objects.
- `case` Desired target case. Labels will automatically converted into the specified character case. See `?sjlabelled::convert_case` for more details on this argument.

**Value**

The titles or labels as character string, or NULL, if variables had no labels; `get_complete_df()` returns the input list `x` as single data frame, where the grouping variable indicates the predicted values for each term.

**Examples**

```r
if (require("sjmisc", quietly = TRUE) &
   require("ggplot2", quietly = TRUE) &
   require("effects", quietly = TRUE)) {
  data(efc)
  efc$c172code <- to_factor(efc$c172code)
  fit <- lm(barthtot ~ c12hour + neg_c_7 + c161sex + c172code, data = efc)
  ```
```r
mydf <- ggpredict(fit, terms = c("c12hour", "c161sex", "c172code"))

ggplot(mydf, aes(x = x, y = predicted, colour = group)) +
  stat_smooth(method = "lm") +
  facet_wrap(~facet, ncol = 2) +
  labs(
    x = get_x_title(mydf),
    y = get_y_title(mydf),
    colour = get_legend_title(mydf)
  )

# adjusted predictions, a list of data frames (one data frame per term)
eff <- ggeffect(fit)
eff
g_get_complete_df(eff)

# adjusted predictions for education only, and get x-axis-labels
mydat <- eff[["c172code"]]

```
ggeffect

back.transform = TRUE,
interval = "confidence",
...
)

ggpredict(
  model,
  terms,
  ci.lvl = 0.95,
  type = "fe",
  typical = "mean",
  condition = NULL,
  back.transform = TRUE,
  ppd = FALSE,
  vcov.fun = NULL,
  vcov.type = NULL,
  vcov.args = NULL,
  interval = "confidence",
  ...
)

Arguments

model A fitted model object, or a list of model objects. Any model that supports common methods like predict(), family() or model.frame() should work. For ggeffect(), any model that is supported by effects should work, and for ggemmeans(), all models supported by emmeans should work.

terms Character vector (or a formula) with the names of those terms from model, for which predictions should be displayed. At least one term is required to calculate effects for certain terms, maximum length is four terms, where the second to fourth term indicate the groups, i.e. predictions of first term are grouped at the values or levels of the remaining terms. If terms is missing or NULL, adjusted predictions for each model term are calculated. It is also possible to define specific values for terms, at which adjusted predictions should be calculated (see 'Details'). All remaining covariates that are not specified in terms are held constant (see 'Details'). See also arguments condition and typical.

ci.lvl Numeric, the level of the confidence intervals. For ggpredict(), use ci.lvl = NA, if confidence intervals should not be calculated (for instance, due to computation time). Typically, confidence intervals based on the standard errors as returned by the predict() function are returned, assuming normal distribution (i.e. +/- 1.96 * SE). See introduction of this vignette for more details.

... For ggpredict(), further arguments passed down to predict(); for ggeffect(), further arguments passed down to effects::Effect(); and for ggemmeans(), further arguments passed down to emmeans::emmeans(). If type = "sim", ... may also be used to set the number of simulation, e.g. nsim = 500.

type Character, only applies for survival models, mixed effects models and/or models with zero-inflation. Note: For brmsfit-models with zero-inflation component,
there is no type = "zero_inflated" nor type = "zi_random"; predicted values for MixMod-models from GLMMadaptive with zero-inflation component always condition on the zero-inflation part of the model (see 'Details').

"fixed" (or "fe" or "count") Predicted values are conditioned on the fixed effects or conditional model only (for mixed models: predicted values are on the population-level and confidence intervals are returned). For instance, for models fitted with zeroinfl from pscl, this would return the predicted mean from the count component (without zero-inflation). For models with zero-inflation component, this type calls predict(..., type = "link") (however, predicted values are back-transformed to the response scale).

"random" (or "re") This only applies to mixed models, and type = "random" does not condition on the zero-inflation component of the model. type = "random" still returns population-level predictions, however, unlike type = "fixed", intervals also consider the uncertainty in the variance parameters (the mean random effect variance, see Johnson et al. 2014 for details) and hence can be considered as prediction intervals. For models with zero-inflation component, this type calls predict(..., type = "link") (however, predicted values are back-transformed to the response scale).

To get predicted values for each level of the random effects groups, add the name of the related random effect term to the terms-argument (for more details, see this vignette).

"zero_inflated" (or "fe.zi" or "zi") Predicted values are conditioned on the fixed effects and the zero-inflation component. For instance, for models fitted with zeroinfl from pscl, this would return the predicted response \( \mu(1-p) \) and for glmmTMB, this would return the expected value \( \mu(1-p) \) without conditioning on random effects (i.e. random effect variances are not taken into account for the confidence intervals). For models with zero-inflation component, this type calls predict(..., type = "response"). See 'Details'.

"zi_random" (or "re.zi" or "zero_inflated_random") Predicted values are conditioned on the zero-inflation component and take the random effects uncertainty into account. For models fitted with glmmTMB(), hurdle() or zeroinfl(), this would return the expected value \( \mu(1-p) \). For glmmTMB, prediction intervals also consider the uncertainty in the random effects variances. This type calls predict(..., type = "response"). See 'Details'.

"zi_prob" (or "zi.prob") Predicted zero-inflation probability. For glmmTMB models with zero-inflation component, this type calls predict(..., type = "zlink"); models from pscl call predict(..., type = "zero") and for GLMMadaptive, predict(..., type = "zero_part") is called.

"simulate" (or "sim") Predicted values and confidence resp. prediction intervals are based on simulations, i.e. calls to simulate(). This type of prediction takes all model uncertainty into account, including random effects variances. Currently supported models are objects of class lm, glm, glmmTMB, wbm, MixMod and merMod. See ... for details on number of simulations.
"survival" and "cumulative_hazard" (or "surv" and "cumhaz") Applies only to coxph-objects from the survival-package and calculates the survival probability or the cumulative hazard of an event.

**typical** Character vector, naming the function to be applied to the covariates over which the effect is "averaged". The default is "mean". See ?sjmisc::typical_value for options.

**condition** Named character vector, which indicates covariates that should be held constant at specific values. Unlike typical, which applies a function to the covariates to determine the value that is used to hold these covariates constant, condition can be used to define exact values, for instance condition = c(covariate1 = 20, covariate2 = 5). See 'Examples'.

**back.transform** Logical, if TRUE (the default), predicted values for log- or log-log transformed responses will be back-transformed to original response-scale.

**interval** Type of interval calculation, can either be "confidence" (default) or "prediction". May be abbreviated. Unlike confidence intervals, prediction intervals include the residual variance (sigma^2). This argument is ignored for mixed models, as interval = "prediction" is equivalent to type = "random" (and interval = "confidence" is equivalent to type = "fixed"). Note that prediction intervals are not available for all models, but only for models that work with insight::get_sigma().

**ppd** Logical, if TRUE, predictions for Stan-models are based on the posterior predictive distribution (rstantools::posterior_predict()). If FALSE (the default), predictions are based on posterior draws of the linear predictor (rstantools::posterior_linpred()).

**vcov.fun** String, indicating the name of the vcov*()-function from the sandwich or clubSandwich-package, e.g. vcov.fun = "vcovCL", which is used to compute (cluster) robust standard errors for predictions. If NULL, standard errors (and confidence intervals) for predictions are based on the standard errors as returned by the predict()-function. Note that probably not all model objects that work with ggpredict() are also supported by the sandwich or clubSandwich-package.

**vcov.type** Character vector, specifying the estimation type for the robust covariance matrix estimation (see ?sandwich::vcovHC or ?clubSandwich::vcovCR for details).

**vcov.args** List of named vectors, used as additional arguments that are passed down to vcov.fun.

**Details**

**Supported Models:** A list of supported models can be found at https://github.com/strengejacke/ggeffects. Support for models varies by function, i.e. although ggpredict(), ggemmeans() and ggeffect() support most models, some models are only supported exclusively by one of the three functions.

**Difference between ggpredict() and ggeffect() or ggemmeans:** ggpredict() calls predict(), while ggeffect() calls effects::Effect() and ggemmeans() calls emmeans::emmeans() to compute predicted values. Thus, effects returned by ggpredict() can be described as conditional effects (i.e. these are conditioned on certain (reference) levels of factors), while ggemmeans() and ggeffect() return marginal means, since the effects are "marginalized" (or "averaged") over
the levels of factors. Therefore, ggpredict() and ggeffect() resp. ggemmeans() differ in how factors are held constant: ggpredict() uses the reference level, while ggeffect() and ggemmeans() compute a kind of "average" value, which represents the proportions of each factor's category. Use condition to set a specific level for factors in ggemmeans(), so factors are not averaged over their categories, but held constant at a given level.

**Marginal Effects and Adjusted Predictions at Specific Values:** Specific values of model terms can be specified via the terms-argument. Indicating levels in square brackets allows for selecting only specific groups or values resp. value ranges. Term name and the start of the levels in brackets must be separated by a whitespace character, e.g. `terms = c("age","education [1,3]")`. Numeric ranges, separated with colon, are also allowed: `terms = c("education","age [30:60]")`. The stepsize for range can be adjusted using 'by', e.g. `terms = "age [30:60 by=5]"`.

The terms-argument also supports the same shortcuts as the values-argument in values_at(). So `terms = "age [meansd]"` would return predictions for the values one standard deviation below the mean age, the mean age and one SD above the mean age. `terms = "age [quart2]"` would calculate predictions at the value of the lower, median and upper quartile of age.

Furthermore, it is possible to specify a function name. Values for predictions will then be transformed, e.g. `terms = "income [exp]"`. This is useful when model predictors were transformed for fitting the model and should be back-transformed to the original scale for predictions. It is also possible to define own functions (see this vignette).

Instead of a function, it is also possible to define the name of a variable with specific values, e.g. to define a vector `v = c(1000,2000,3000)` and then use `terms = "income [v]"`.

You can take a random sample of any size with `sample=n`, e.g `terms = "income [sample=8]"`, which will sample eight values from all possible values of the variable income. This option is especially useful for plotting predictions at certain levels of random effects group levels, where the group factor has many levels that can be completely plotted. For more details, see this vignette.

Finally, numeric vectors for which no specific values are given, a "pretty range" is calculated (see pretty_range), to avoid memory allocation problems for vectors with many unique values. If a numeric vector is specified as second or third term (i.e. if this vector represents a grouping structure), representative values (see values_at) are chosen (unless other values are specified). If all values for a numeric vector should be used to compute predictions, you may use e.g. `terms = "age [all]"`. See also package vignettes.

To create a pretty range that should be smaller or larger than the default range (i.e. if no specific values would be given), use the n-tag, e.g. `terms="age [n=5]"` or `terms="age [n=12]"`. Larger values for n return a larger range of predicted values.

**Holding covariates at constant values:** For ggpredict(), expand.grid() is called on all unique combinations of model.frame(model)[,terms] and used as newdata-argument for predict(). In this case, all remaining covariates that are not specified in terms are held constant: Numeric values are set to the mean (unless changed with the condition or typical-argument), factors are set to their reference level (may also be changed with condition) and character vectors to their mode (most common element).
$\text{ggeffect()}$ and $\text{ggemmeans()}$, by default, set remaining numeric covariates to their mean value, while for factors, a kind of "average" value, which represents the proportions of each factor's category, is used. For $\text{ggemmeans()}$, use condition to set a specific level for factors so that these are not averaged over their categories, but held constant at the given level.

**Bayesian Regression Models:** $\text{ggpredict()}$ also works with Stan-models from the rstanarm or brms-package. The predicted values are the median value of all drawn posterior samples. The confidence intervals for Stan-models are Bayesian predictive intervals. By default (i.e. ppd = FALSE), the predictions are based on rstantools::posterior_linpred() and hence have some limitations: the uncertainty of the error term is not taken into account. The recommendation is to use the posterior predictive distribution (rstantools::posterior_predict()).

**Zero-Inflated and Zero-Inflated Mixed Models with brms:** Models of class brmsfit always condition on the zero-inflation component, if the model has such a component. Hence, there is no type = "zero_inflated" nor type = "zi_random" for brmsfit-models, because predictions are based on draws of the posterior distribution, which already account for the zero-inflation part of the model.

**Zero-Inflated and Zero-Inflated Mixed Models with glmmTMB:** If model is of class glmmTMB, hurdle, zeroinfl or zerotrunc, simulations from a multivariate normal distribution (see MASS::mvrnorm) are drawn to calculate $\mu \ast (1 - p)$. Confidence intervals are then based on quantiles of these results. For type = "zi_random", prediction intervals also take the uncertainty in the random-effect parameters into account (see also Brooks et al. 2017, pp.391-392 for details).

An alternative for models fitted with glmmTMB that take all model uncertainties into account are simulations based on simulate(), which is used when type = "sim" (see Brooks et al. 2017, pp.392-393 for details).

**MixMod-models from GLMMadaptive:** Predicted values for the fixed effects component (type = "fixed" or type = "zero_inflated") are based on predict(...,type = "mean_subject"), while predicted values for random effects components (type = "random" or type = "zi_random") are calculated with predict(...,type = "subject_specific") (see ?GLMMadaptive::predict.MixMod for details). The latter option requires the response variable to be defined in the newdata-argument of predict(), which will be set to its typical value (see ?sjmisc::typical_value).

Value

A data frame (with ggeffects class attribute) with consistent data columns:

- **x** the values of the first term in `terms`, used as x-position in plots.
- **predicted** the predicted values of the response, used as y-position in plots.
- **std.error** the standard error of the predictions. *Note that the standard errors are always on the link-scale, and not back-transformed for non-Gaussian models!*
- **conf.low** the lower bound of the confidence interval for the predicted values.
- **conf.high** the upper bound of the confidence interval for the predicted values.
- **group** the grouping level from the second term in `terms`, used as grouping-aesthetics in plots.
- **facet** the grouping level from the third term in `terms`, used to indicate facets in plots.
The estimated marginal means (predicted values) are always on the response scale!

For proportional odds logistic regression (see ?MASS::polr) resp. cumulative link models (e.g., see ?ordinal::clm), an additional column response.level is returned, which indicates the grouping of predictions based on the level of the model’s response.

Note that for convenience reasons, the columns for the intervals are always named conf.low and conf.high, even though for Bayesian models credible or highest posterior density intervals are returned.

**Note**

**Multinomial Models:** polr-, clm-models, or more generally speaking, models with ordinal or multinominal outcomes, have an additional column response.level, which indicates with which level of the response variable the predicted values are associated.

**Printing Results:** The print()-method gives a clean output (especially for predictions by groups), and indicates at which values covariates were held constant. Furthermore, the print()-method has the arguments digits and n to control number of decimals and lines to be printed, and an argument x.lab to print factor-levels instead of numeric values if x is a factor.

**Limitations:** The support for some models, for example from package MCMCglmm, is rather experimental and may fail for certain models. If you encounter any errors, please file an issue at https://github.com/strengejacke/ggeffects/issues.

**References**


**Examples**

```r
library(sjlabelled)
data(efc)
fit <- lm(barthtot ~ c12hour + neg_c_7 + c161sex + c172code, data = efc)
ggpredict(fit, terms = "c12hour")
ggpredict(fit, terms = c("c12hour", "c172code"))
ggpredict(fit, terms = c("c12hour", "c172code", "c161sex"))

# specified as formula
ggpredict(fit, terms = ~ c12hour + c172code + c161sex)

# only range of 40 to 60 for variable 'c12hour'
ggpredict(fit, terms = "c12hour [40:60]")

# using "summary()" shows that covariate "neg_c_7" is held constant at a value of 11.84 (its mean value). To use a
# different value, use "condition"
ggpredict(fit, terms = "c12hour [40:60]", condition = c(neg_c_7 = 20))

# to plot ggeffects-objects, you can use the 'plot()-function.  
# the following examples show how to build your ggplot by hand.

# plot predicted values, remaining covariates held constant
library(ggplot2)
mydf <- ggpredict(fit, terms = "c12hour")
ggplot(mydf, aes(x, predicted)) +
  geom_line() +
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high), alpha = .1)

# three variables, so we can use facets and groups
mydf <- ggpredict(fit, terms = c("c12hour", "c161sex", "c172code"))
ggplot(mydf, aes(x = x, y = predicted, colour = group)) +
  stat_smooth(method = "lm", se = FALSE) +
  facet_wrap(~ facet, ncol = 2)

# select specific levels for grouping terms
mydf <- ggpredict(fit, terms = c("c12hour", "c172code [1,3]", "c161sex"))
ggplot(mydf, aes(x = x, y = predicted, colour = group)) +
  stat_smooth(method = "lm", se = FALSE) +
  facet_wrap(~ facet) +
  labs(
    y = get_y_title(mydf),
    x = get_x_title(mydf),
    colour = get_legend_title(mydf)
  )

# level indication also works for factors with non-numeric levels
# and in combination with numeric levels for other variables
data(efc)
efc$c172code <- as_label(efc$c172code)
fit <- lm(barthtot ~ c12hour + neg_c_7 + c161sex + c172code, data = efc)
ggpredict(fit, terms = c("c12hour",
  "c172code [low level of education, high level of education]",
  "c161sex [1]"))

# use categorical value on x-axis, use axis-labels, add error bars
dat <- ggpredict(fit, terms = c("c172code", "c161sex"))
ggplot(dat, aes(x, predicted, colour = group)) +
  geom_point(position = position_dodge(.1)) +
  geom_errorbar(
    aes(ymin = conf.low, ymax = conf.high),
    position = position_dodge(.1)
  ) +
  scale_x_discrete(breaks = 1:3, labels = get_x_labels(dat))

# 3-way-interaction with 2 continuous variables
data(efc)
# make categorical
efc$c161sex <- as_factor(efc$c161sex)
fit <- lm(neg_c_7 ~ c12hour * barthtot * c161sex, data = efc)
# select only levels 30, 50 and 70 from continuous variable Barthel-Index
dat <- ggpredict(fit, terms = c("c12hour", "barthtot [30,50,70]", "c161sex"))
ggplot(dat, aes(x = x, y = predicted, colour = group)) +
  stat_smooth(method = "lm", se = FALSE, fullrange = TRUE) +
  facet_wrap(~facet) +
  labs(
    colour = get_legend_title(dat),
    x = get_x_title(dat),
    y = get_y_title(dat),
    title = get_title(dat)
)

# or with ggeffects' plot-method
plot(dat, ci = FALSE)

# predictions for polynomial terms
data(efc)
fit <- glm(
  tot_sc_e ~ c12hour + e42dep + e17age + I(e17age^2) + I(e17age^3),
  data = efc,
  family = poisson()
)
ggeffect(fit, terms = "e17age")

---

### lung2

**Sample data set**

A sample data set, used in tests and examples for survival models. This dataset is originally included in the `survival` package, but for convenience reasons it is also available in this package.

---

### new_data

**Create a data frame from all combinations of predictor values**

Create a data frame for the "newdata"-argument that contains all combinations of values from the terms in questions. Similar to `expand.grid()`. The `terms`-argument accepts all shortcuts for representative values as in `ggpredict()`.

**Usage**

```r
new_data(model, terms, typical = "mean", condition = NULL)
data_grid(model, terms, typical = "mean", condition = NULL)
```
### Arguments

- **model**: A fitted model object.
- **terms**: Character vector with the names of those terms from `model` for which all combinations of values should be created.
- **typical**: Character vector, naming the function to be applied to the covariates over which the effect is "averaged". The default is "mean". See ?sjmisc::typical_value for options.
- **condition**: Named character vector, which indicates covariates that should be held constant at specific values. Unlike `typical`, which applies a function to the covariates to determine the value that is used to hold these covariates constant, `condition` can be used to define exact values, for instance `condition = c(covariate1 = 20, covariate2 = 5)`. See 'Examples'.

### Value

A data frame containing one row for each combination of values of the supplied variables.

### Examples

```r
data(efc)
fit <- lm(barthtot ~ c12hour + neg_c_7 + c161sex + c172code, data = efc)
new_data(fit, c("c12hour [meansd]", "c161sex"))

nd <- new_data(fit, c("c12hour [meansd]", "c161sex"))
pr <- predict(fit, type = "response", newdata = nd)
nd$predicted <- pr
nd

# compare to
ggpredict(fit, c("c12hour [meansd]", "c161sex"))
```

---

### Description

A generic plot-method for `ggeffects`-objects.

### Usage

```r
# S3 method for class 'ggeffects'
plot(
  x,
  ci = TRUE,
  ci.style = c("ribbon", "errorbar", "dash", "dot"),
  facets,
```

---

### plot

**Plot ggeffects-objects**

A generic plot-method for `ggeffects`-objects.
add.data = FALSE,
limit.range = FALSE,
residuals = FALSE,
residuals.line = FALSE,
collapse.group = FALSE,
colors = "Set1",
alpha = 0.15,
dodge = 0.25,
use.theme = TRUE,
dot.alpha = 0.35,
jitter = 0.2,
log.y = FALSE,
case = NULL,
show.legend = TRUE,
show.title = TRUE,
show.x.title = TRUE,
show.y.title = TRUE,
dot.size = NULL,
line.size = NULL,
connect.lines = FALSE,
grids, one.plot = TRUE,
rawdata,
residuals.type,

theme_ggeffects(base_size = 11, base_family = "")

show_pals()

Arguments

x  An object of class ggeffects, as returned by the functions from this package.

Ci  Logical, if TRUE, confidence bands (for continuous variables at x-axis) resp. error bars (for factors at x-axis) are plotted.

Ci.style  Character vector, indicating the style of the confidence bands. May be either "ribbon", "errorbar", "dash" or "dot", to plot a ribbon, error bars, or dashed or dotted lines as confidence bands.

Facets, Grid  Logical, defaults to TRUE, if x has a column named facet, and defaults to FALSE, if x has no such column. Set facets = TRUE to wrap the plot into facets even for grouping variables (see 'Examples'). grid is an alias for facets.

Add.data, Rawdata  Logical, if TRUE, a layer with raw data from response by predictor on the x-axis, plotted as point-geoms, is added to the plot.

Limit.range  Logical, if TRUE, limits the range of the prediction bands to the range of the data.
residuals Logical, if TRUE, a layer with partial residuals is added to the plot. See vignette "Effect Displays with Partial Residuals" from effects for more details on partial residual plots.

residuals.line Logical, if TRUE, a loess-fit line is added to the partial residuals plot. Only applies if residuals is TRUE.

collapse.group For mixed effects models, name of the grouping variable of random effects. If collapse.group = TRUE, data points "collapsed" by the first random effect groups are added to the plot. Else, if collapse.group is a name of a group factor, data is collapsed by that specific random effect. See collapse_by_group for further details.

colors Character vector with color values in hex-format, valid color value names (see demo("colors")) or a name of a ggeffects-color-palette. Following options are valid for colors:

- If not specified, the color brewer palette "Set1" will be used.
- If "gs", a greyscale will be used.
- If "bw", the plot is black/white and uses different line types to distinguish groups.
- There are some pre-defined color-palettes in this package that can be used, e.g. colors = "metro". See show_pals() to show all available palettes.
- Else specify own color values or names as vector (e.g. colors = c("#f00000", "#00ff00").

alpha Alpha value for the confidence bands.

dodge Value for offsetting or shifting error bars, to avoid overlapping. Only applies, if a factor is plotted at the x-axis (in such cases, the confidence bands are replaced by error bars automatically), or if ci.style = "errorbars".

use.theme Logical, if TRUE, a slightly tweaked version of ggplot's minimal-theme, theme_ggeffects(), is applied to the plot. If FALSE, no theme-modifications are applied.

dot.alpha Alpha value for data points, when add.data = TRUE.

jitter Numeric, between 0 and 1. If not NULL and add.data = TRUE, adds a small amount of random variation to the location of data points dots, to avoid overplotting. Hence the points don't reflect exact values in the data. May also be a numeric vector of length two, to add different horizontal and vertical jittering. For binary outcomes, raw data is not jittered by default to avoid that data points exceed the axis limits.

log.y Logical, if TRUE, the y-axis scale is log-transformed. This might be useful for binomial models with predicted probabilities on the y-axis.

case Desired target case. Labels will automatically converted into the specified character case. See ?sjlabelled::convert_case for more details on this argument.

show.legend Logical, shows or hides the plot legend.

show.title Logical, shows or hides the plot title.

show.x.title Logical, shows or hides the plot title for the x-axis.

show.y.title Logical, shows or hides the plot title for the y-axis.

dot.size Numeric, size of the point geoms.
line.size       Numeric, size of the line geoms.
connect.lines  Logical, if TRUE and plot has point-geoms with error bars (this is usually the case when the x-axis is discrete), points of same groups will be connected with a line.
one.plot       Logical, if TRUE and x has a panel column (i.e. when four terms were used), a single, integrated plot is produced.
residuals.type Deprecated. Formally was the residual type. Now is always “working”.
...            Further arguments passed down to ggplot::scale_y*, to control the appearance of the y-axis.
base_size      Base font size.
base_family    Base font family.

Details
For proportional odds logistic regression (see ?MASS::polr) or cumulative link models in general, plots are automatically faceted by response.level, which indicates the grouping of predictions based on the level of the model’s response.

Value
A ggplot2-object.

Partial Residuals
For **generalized linear models** (glmns), residualized scores are computed as \( \text{inv.link}(\text{link}(Y) + r) \) where \( Y \) are the predicted values on the response scale, and \( r \) are the *working* residuals.

For (generalized) linear **mixed models**, the random effect are also partialled out.

Note
Load library(ggplot2) and use theme_set(theme_ggeffects()) to set the ggeffects-theme as default plotting theme. You can then use further plot-modifiers from sjPlot, like legend_style() or font_size() without losing the theme-modifications.

There are pre-defined colour palettes in this package. Use show_pals() to show all available colour palettes.

Examples
library(sjlabelled)
data(efc)
ecf$c172code <- as_label(efc$c172code)
fit <- lm(barthtot ~ c12hour + neg_c_7 + c161sex + c172code, data = efc)

dat <- ggpredict(fit, terms = "c12hour")
plot(dat)
# facet by group, use pre-defined color palette
dat <- ggpredict(fit, terms = c("c12hour", "c172code"))
plot(dat, facet = TRUE, colors = "hero")

# don't use facets, b/w figure, w/o confidence bands
dat <- ggpredict(fit, terms = c("c12hour", "c172code"))
plot(dat, colors = "bw", ci = FALSE)

# factor at x axis, plot exact data points and error bars
dat <- ggpredict(fit, terms = c("c172code", "c161sex"))
plot(dat)

# for three variables, automatic facetting
dat <- ggpredict(fit, terms = c("c12hour", "c172code", "c161sex"))
plot(dat)

# show all color palettes
show_pals()

---

pool_predictions 

**Pool Predictions or Estimated Marginal Means**

**Description**

This function "pools" (i.e. combines) multiple ggeffects objects, in a similar fashion as mice::pool().

**Usage**

```r
pool_predictions(x, ...)
```

**Arguments**

- `x` A list of ggeffects objects, as returned by `ggpredict`, `ggemmeans` or `ggeffect`.
- `...` Currently not used.

**Details**

Averaging of parameters follows Rubin's rules (Rubin, 1987, p. 76).

**Value**

A data frame with pooled predictions.

**References**

pretty_range

Examples

# example for multiple imputed datasets
if (require("mice")) {
  data("nhanes2")
  imp <- mice(nhanes2, printFlag = FALSE)
  predictions <- lapply(1:5, function(i) {
    m <- lm(bmi ~ age + hyp + chl, data = complete(imp, action = i))
    ggpredict(m, "age")
  })
  pool_predictions(predictions)
}

pretty_range

Create a pretty sequence over a range of a vector

Description

Creates an evenly spaced, pretty sequence of numbers for a range of a vector.

Usage

pretty_range(x, n = NULL, length = NULL)

Arguments

x  
A numeric vector.

n  
Numeric value, indicating the size of how many values are used to create a pretty sequence. If x has a large value range (> 100), n could be something between 1 to 5. If x has a rather small amount of unique values, n could be something between 10 to 20. If n = NULL, pretty_range() automatically tries to find a pretty sequence.

length  
Integer value, as alternative to n, defines the number of intervals to be returned.

Value

A numeric vector with a range corresponding to the minimum and maximum values of x. If x is missing, a function, pre-programmed with n and length is returned. See examples.

Examples

data(iris)
# pretty range for vectors with decimal points
pretty_range(iris$Petal.Length)

# pretty range for large range, increasing by 50
pretty_range(1:1000)

# increasing by 20
residualize_over_grid

Compute partial residuals from a data grid

Description
This function computes partial residuals based on a data grid, where the data grid is usually a data frame from all combinations of factor variables or certain values of numeric vectors. This data grid is usually used as newdata argument in predict(), and can be created with new_data.

Usage
residualize_over_grid(grid, model, ...)

## S3 method for class 'data.frame'
residualize_over_grid(grid, model, pred_name, type, ...)

## S3 method for class 'ggeffects'
residualize_over_grid(grid, model, protect_names = TRUE, ...)

Arguments
grid A data frame representing the data grid, or an object of class ggeffects, as returned by ggpredict() and others.
model The model for which to compute partial residuals. The data grid grid should match to predictors in the model.
... Currently not used.
pred_name The name of the focal predictor, for which partial residuals are computed.
type Deprecated. Formally was the residual type. Now is always "working".
protect_names Logical, if TRUE, preserves column names from the ggeffects objects that is used as grid.

Value
A data frame with residuals for the focal predictor.
Partial Residuals

For generalized linear models (glms), residualized scores are computed as \( \text{inv.link}(\text{link}(Y) + r) \) where \( Y \) are the predicted values on the response scale, and \( r \) are the working residuals.

For (generalized) linear mixed models, the random effect are also partialled out.

References


Examples

```r
library(ggeffects)
set.seed(1234)
x <- rnorm(200)
z <- rnorm(200)
# quadratic relationship
y <- 2 * x + x^2 + 4 * z + rnorm(200)
d <- data.frame(x, y, z)
model <- lm(y ~ x + z, data = d)
pr <- ggpredict(model, c("x [all]", "z"))
head(residualize_over_grid(pr, model))
```

values_at

Calculate representative values of a vector

Description

This function calculates representative values of a vector, like minimum/maximum values or lower, median and upper quartile etc., which can be used for numeric vectors to plot marginal effects at these representative values.

Usage

```r
values_at(x, values = "meansd")
representative_values(x, values = "meansd")
```

Arguments

- **x**: A numeric vector.
- **values**: Character vector, naming a pattern for which representative values should be calculated.
"minmax" (default) minimum and maximum values (lower and upper bounds) of the moderator are used to plot the interaction between independent variable and moderator.

"meansd" uses the mean value of the moderator as well as one standard deviation below and above mean value to plot the effect of the moderator on the independent variable.

"zeromax" is similar to the "minmax" option, however, 0 is always used as minimum value for the moderator. This may be useful for predictors that don’t have an empirical zero-value, but absence of moderation should be simulated by using 0 as minimum.

"quart" calculates and uses the quartiles (lower, median and upper) of the moderator value, including minimum and maximum value.

"quart2" calculates and uses the quartiles (lower, median and upper) of the moderator value, excluding minimum and maximum value.

"all" uses all values of the moderator variable. Note that this option only applies to type = "eff", for numeric moderator values.

Value

A numeric vector of length two or three, representing the required values from \( x \), like minimum/maximum value or mean and +/- 1 SD. If \( x \) is missing, a function, pre-programmed with \( n \) and \( length \) is returned. See examples.

Examples

```r
data(efc)
values_at(efc$c12hour)
values_at(efc$c12hour, "quart2")

mean_sd <- values_at(values = "meansd")
mean_sd(efc$c12hour)
```
Arguments

object: An object of class "ggeffects", as returned by ggpredict().
vcov.fun: String, indicating the name of the vcov*()-function from the sandwich or clubSandwich-package, e.g. vcov.fun = "vcovCL", which is used to compute (cluster) robust standard errors for predictions. If NULL, standard errors (and confidence intervals) for predictions are based on the standard errors as returned by the predict()-function. Note that probably not all model objects that work with ggpredict() are also supported by the sandwich or clubSandwich-package.
vcov.type: Character vector, specifying the estimation type for the robust covariance matrix estimation (see ?sandwich::vcovHC or ?clubSandwich::vcovCR for details).
vcov.args: List of named vectors, used as additional arguments that are passed down to vcov.fun.

Details

The returned matrix has as many rows (and columns) as possible combinations of predicted values from the ggpredict() call. For example, if there are two variables in the terms-argument of ggpredict() with 3 and 4 levels each, there will be 3*4 combinations of predicted values, so the returned matrix has a 12x12 dimension. In short, nrow(object) is always equal to nrow(vcov(object)). See also 'Examples'.

Value

The variance-covariance matrix for the predicted values from object.

Examples

data(efc)
model <- lm(barthtot ~ c12hour + neg_c_7 + c161sex + c172code, data = efc)
result <- ggpredict(model, c("c12hour [meansd]", "c161sex"))

vcov(result)

# compare standard errors
sqrt(diag(vcov(result)))
as.data.frame(result)

# only two predicted values, no further terms
# vcov() returns a 2x2 matrix
result <- ggpredict(model, "c161sex")
vcov(result)

# 2 levels for c161sex multiplied by 3 levels for c172code
# result in 6 combinations of predicted values
# thus vcov() returns a 6x6 matrix
result <- ggpredict(model, c("c161sex", "c172code"))
vcov(result)
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