Package ‘brms’

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Description Fit Bayesian generalized (non-)linear multivariate multilevel models using 'Stan' for full Bayesian inference. A wide range of distributions and link functions are supported, allowing users to fit -- among others -- linear, robust linear, count data, survival, response times, ordinal, zero-inflated, hurdle, and even self-defined mixture models all in a multilevel context. Further modeling options include both theory-driven and data-driven non-linear terms, auto-correlation structures, censoring and truncation, meta-analytic standard errors, and quite a few more. In addition, all parameters of the response distribution can be predicted in order to perform distributional regression. Prior specifications are flexible and explicitly encourage users to apply prior distributions that actually reflect their prior knowledge. Models can easily be evaluated and compared using several methods assessing posterior or prior predictions.

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https://discourse.mc-stan.org/
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The **brms** package provides an interface to fit Bayesian generalized multivariate (non-)linear multilevel models using **Stan**, which is a C++ package for obtaining full Bayesian inference (see [https://mc-stan.org/](https://mc-stan.org/)). The formula syntax is an extended version of the syntax applied in the **lme4** package to provide a familiar and simple interface for performing regression analyses.

### Details

The main function of **brms** is **brm**, which uses formula syntax to specify a wide range of complex Bayesian models (see **brmsformula** for details). Based on the supplied formulas, data, and additional information, it writes the Stan code on the fly via **make_stancode**, prepares the data via **make_standata**, and fits the model using **Stan**.

Subsequently, a large number of post-processing methods can be applied: To get an overview on the estimated parameters, **summary** or **conditional_effects** are perfectly suited. Detailed visual analyses can be performed by applying the **pp_check** and **stanplot** methods, which both rely on the **bayesplot** package. Model comparisons can be done via **loo** and **waic**, which make use of the **loo** package as well as via **bayes_factor** which relies on the **bridgesampling** package. For a full list of methods to apply, type `methods(class = "brmsfit")`.

Because **brms** is based on **Stan**, a C++ compiler is required. The program Rtools (available on [https://cran.r-project.org/bin/windows/Rtools/](https://cran.r-project.org/bin/windows/Rtools/)) comes with a C++ compiler for Windows. On Mac, you should use Xcode. For further instructions on how to get the compilers running, see the prerequisites section at the **RStan-Getting-Started** page.

When comparing other packages fitting multilevel models to **brms**, keep in mind that the latter needs to compile models before actually fitting them, which will require between 20 and 40 seconds depending on your machine, operating system and overall model complexity.

Thus, fitting smaller models may be relatively slow as compilation time makes up the majority of the whole running time. For larger / more complex models however, fitting may take several minutes or even hours, so that the compilation time won’t make much of a difference for these models.

See **vignette**("brms_overview") and **vignette**("brms_multilevel") for a general introduction and overview of **brms**. For a full list of available vignettes, type **vignette**(package = "brms").
addition-terms

References


See Also

brm, brmsformula, brmsfamily, brmsfit

---

addition-terms  Additional Response Information

Description

Provide additional information on the response variable in brms models, such as censoring, truncation, or known measurement error. Detailed documentation on the use of each of these functions can be found in the Details section of brmsformula (under "Additional response information").

Usage

```r
resp_se(x, sigma = FALSE)
resp_weights(x, scale = FALSE)
resp_trials(x)
resp_thres(x, gr = NA)
resp_cat(x)
resp_dec(x)
resp_cens(x, y2 = NA)
resp_trunc(lb = -Inf, ub = Inf)
resp_mi(sdy = NA)
resp_index(x)
resp_rate(denom)
```
resp_subset(x)

resp_vreal(....)

resp_vint(....)

Arguments

x  A vector; Ideally a single variable defined in the data (see Details). Allowed values depend on the function: resp_se and resp_weights require positive numeric values. resp_trials, resp_thres, and resp_cat require positive integers. resp_dec requires 0 and 1, or alternatively 'lower' and 'upper'. resp_subset requires 0 and 1, or alternatively FALSE and TRUE. resp_cens requires 'left', 'none', 'right', and 'interval' (or equivalently -1, 0, 1, and 2) to indicate left, no, right, or interval censoring. resp_index does not make any requirements other than the value being unique for each observation.

sigma  Logical; Indicates whether the residual standard deviation parameter sigma should be included in addition to the known measurement error. Defaults to FALSE for backwards compatibility, but setting it to TRUE is usually the better choice.

scale  Logical; Indicates whether weights should be scaled so that the average weight equals one. Defaults to FALSE.

g  A vector of grouping indicators.

y2  A vector specifying the upper bounds in interval censoring. Will be ignored for non-interval censored observations. However, it should NOT be NA even for non-interval censored observations to avoid accidental exclusion of these observations.

1b  A numeric vector or single numeric value specifying the lower truncation bound.

ub  A numeric vector or single numeric value specifying the upper truncation bound.

sdy  Optional known measurement error of the response treated as standard deviation. If specified, handles measurement error and (completely) missing values at the same time using the plausible-values-technique.

denom  A vector of positive numeric values specifying the denominator values from which the response rates are computed.

...  For resp_vreal, vectors of real values. For resp_vint, vectors of integer values. In Stan, these variables will be named vreal1, vreal2, ..., and vint1, vint2, ..., respectively.

Details

These functions are almost solely useful when called in formulas passed to the \texttt{brms} package. Within formulas, the \texttt{resp_} prefix may be omitted. More information is given in the 'Details' section of \texttt{brmsformula} (under "Additional response information").

It is highly recommended to use a single data variable as input for \( x \) (instead of a more complicated expression) to make sure all post-processing functions work as expected.
Value

A list of additional response information to be processed further by `brms`.

See Also

`brm`, `brmsformula`

Examples

```r
## Not run:
## Random effects meta-analysis
nstudies <- 20
tureffects <- rnorm(nstudies, 0.5, 0.2)
sei <- runif(nstudies, 0.05, 0.3)
outcomes <- rnorm(nstudies, true_effects, sei)
data1 <- data.frame(outcomes, sei)
fit1 <- brm(outcomes | se(sei, sigma = TRUE) ~ 1,
            data = data1)
summary(fit1)

## Probit regression using the binomial family
n <- sample(1:10, 100, TRUE) # number of trials
success <- rbinom(100, size = n, prob = 0.4)
x <- rnorm(100)
data2 <- data.frame(n, success, x)
fit2 <- brm(success | trials(n) ~ x, data = data2,
            family = binomial("probit"))
summary(fit2)

## Survival regression modeling the time between the first
## and second recurrence of an infection in kidney patients.
fit3 <- brm(time | cens(censored) ~ age * sex + disease + (1|patient),
            data = kidney, family = lognormal())
summary(fit3)

## Poisson model with truncated counts
fit4 <- brm(count | trunc(ub = 104) ~ zBase * Trt,
            data = epilepsy, family = poisson())
summary(fit4)

## End(Not run)
```
Usage

add_criterion(x, ...)

## S3 method for class 'brmsfit'
add_criterion(
  x,
  criterion,
  model_name = NULL,
  overwrite = FALSE,
  file = NULL,
  force_save = FALSE,
  ...
)

Arguments

x An R object typically of class brmsfit.
...
Further arguments passed to the underlying functions computing the model fit criteria.
criterion Names of model fit criteria to compute. Currently supported are "loo", "waic", "kfold", "loo_subsample", "bayes_R2" (Bayesian R-squared), "loo_R2" (LOO-adjusted R-squared), and "marglik" (log marginal likelihood).
model_name Optional name of the model. If NULL (the default) the name is taken from the call to x.
overwrite Logical; Indicates if already stored fit indices should be overwritten. Defaults to FALSE.
file Either NULL or a character string. In the latter case, the fitted model object including the newly added criterion values is saved via saveRDS in a file named after the string supplied in file. The .rds extension is added automatically. If x was already stored in a file before, the file name will be reused automatically (with a message) unless overwritten by file. In any case, file only applies if new criteria were actually added via add_criterion or if force_save was set to TRUE.
force_save Logical; only relevant if file is specified and ignored otherwise. If TRUE, the fitted model object will be saved regardless of whether new criteria were added via add_criterion.

Details

Functions add_loo and add_waic are aliases of add_criterion with fixed values for the criterion argument.

Value

An object of the same class as x, but with model fit criteria added for later usage.
add_loo

Examples

```r
## Not run:
fit <- brm(count ~ Trt, data = epilepsy)
# add both LOO and WAIC at once
fit <- add_criterion(fit, c("loo", "waic"))
print(fit$criteria$loo)
print(fit$criteria$waic)

## End(Not run)
```

Description

Deprecated aliases of `add_criterion`.

Usage

```r
add_loo(x, model_name = NULL, ...)
add_waic(x, model_name = NULL, ...)
add_ic(x, ...)
## S3 method for class 'brmsfit'
add_ic(x, ic = "loo", model_name = NULL, ...)
add_ic(x, ...) <- value
```

Arguments

- `x` An R object typically of class `brmsfit`.
- `model_name` Optional name of the model. If NULL (the default) the name is taken from the call to `x`.
- `...` Further arguments passed to the underlying functions computing the model fit criteria.
- `ic, value` Names of model fit criteria to compute. Currently supported are "loo", "waic", "kfold", "R2" (R-squared), and "marglik" (log marginal likelihood).

Value

An object of the same class as `x`, but with model fit criteria added for later usage. Previously computed criterion objects will be overwritten.
add_rstan_model  
*Add compiled rstan models to brmsfit objects*

**Description**

Compile a stanmodel and add it to a brmsfit object. This enables some advanced functionality of rstan, most notably log_prob and friends, to be used with brms models fitted with other Stan backends.

**Usage**

```r
add_rstan_model(x, overwrite = FALSE)
```

**Arguments**

- **x**: A brmsfit object to be updated.
- **overwrite**: Logical. If TRUE, overwrite any existing stanmodel. Defaults to FALSE.

**Value**

A (possibly updated) brmsfit object.

---

ar  
*Set up AR(p) correlation structures*

**Description**

Set up an autoregressive (AR) term of order p in brms. The function does not evaluate its arguments – it exists purely to help set up a model with AR terms.

**Usage**

```r
ar(time = NA, gr = NA, p = 1, cov = FALSE)
```

**Arguments**

- **time**: An optional time variable specifying the time ordering of the observations. By default, the existing order of the observations in the data is used.
- **gr**: An optional grouping variable. If specified, the correlation structure is assumed to apply only to observations within the same grouping level.
- **p**: A non-negative integer specifying the autoregressive (AR) order of the ARMA structure. Default is 1.
cov  
A flag indicating whether ARMA effects should be estimated by means of residual covariance matrices. This is currently only possible for stationary ARMA effects of order 1. If the model family does not have natural residuals, latent residuals are added automatically. If FALSE (the default), a regression formulation is used that is considerably faster and allows for ARMA effects of order higher than 1 but is only available for gaussian models and some of its generalizations.

Value
An object of class 'arma_term', which is a list of arguments to be interpreted by the formula parsing functions of {brms}.

See Also
autocor-terms, arma, ma

Examples
## Not run:
data("LakeHuron")
LakeHuron <- as.data.frame(LakeHuron)
fit <- brm(x ~ ar(p = 2), data = LakeHuron)
summary(fit)
## End(Not run)
q

A non-negative integer specifying the moving average (MA) order of the ARMA structure. Default is 1.

cov

A flag indicating whether ARMA effects should be estimated by means of residual covariance matrices. This is currently only possible for stationary ARMA effects of order 1. If the model family does not have natural residuals, latent residuals are added automatically. If FALSE (the default), a regression formulation is used that is considerably faster and allows for ARMA effects of order higher than 1 but is only available for gaussian models and some of its generalizations.

Value

An object of class ‘arma_term’, which is a list of arguments to be interpreted by the formula parsing functions of brms.

See Also

autocor-terms, ar, ma,

Examples

## Not run:
data("LakeHuron")LakeHuron <- as.data.frame(LakeHuron)fit <- brm(x ~ arma(p = 2, q = 1), data = LakeHuron)summary(fit)

## End(Not run)
Arguments

- **x** A `brmsfit` object or another R object for which the methods are defined.
- **row.names**, optional
  - Unused and only added for consistency with the `as.data.frame` generic.
- **pars** Deprecated alias of `variable`. For reasons of backwards compatibility, `pars` is interpreted as a vector of regular expressions by default unless `fixed = TRUE` is specified.
- **variable** A character vector providing the variables to extract. By default, all variables are extracted.
- **draw** The draw indices to be select. Subsetting draw indices will lead to an automatic merging of chains.
- **subset** Deprecated alias of `draw`.
- **...** Further arguments to be passed to the corresponding `as_draws_*` methods as well as to `subset_draws`.

Value

A data.frame, matrix, or array containing the posterior draws.

See Also

`as_draws`, `subset_draws`
Usage

## S3 method for class 'brmsfit'
as.mcmc(
  x,
  pars = NA,
  fixed = FALSE,
  combine_chains = FALSE,
  inc_warmup = FALSE,
  ...
)

Arguments

- **x**: An R object typically of class `brmsfit`
- **pars**: Names of parameters for which posterior samples should be returned, as given by a character vector or regular expressions. By default, all posterior samples of all parameters are extracted.
- **fixed**: Indicates whether parameter names should be matched exactly (TRUE) or treated as regular expressions (FALSE). Default is FALSE.
- **combine_chains**: Indicates whether chains should be combined.
- **inc_warmup**: Indicates if the warmup samples should be included. Default is FALSE. Warmup samples are used to tune the parameters of the sampling algorithm and should not be analyzed.
- **...**: currently unused

Value

If `combine_chains = TRUE` an `mcmc` object is returned. If `combine_chains = FALSE` an `mcmc.list` object is returned.

---

### AsymLaplace

**The Asymmetric Laplace Distribution**

#### Description

Density, distribution function, quantile function and random generation for the asymmetric Laplace distribution with location `mu`, scale `sigma` and asymmetry parameter `quantile`.

#### Usage

- `dasym_laplace(x, mu = 0, sigma = 1, quantile = 0.5, log = FALSE)`
- `pasym_laplace(q, mu = 0,`
\texttt{autocor-terms}

\begin{verbatim}
    sigma = 1,
    quantile = 0.5,
    lower.tail = TRUE,
    log.p = FALSE
)

qasym_laplace(
    p,
    mu = 0,
    sigma = 1,
    quantile = 0.5,
    lower.tail = TRUE,
    log.p = FALSE
)

rasym_laplace(n, mu = 0, sigma = 1, quantile = 0.5)
\end{verbatim}

**Arguments**

- \texttt{x}, \texttt{q}
  Vector of quantiles.
- \texttt{mu}
  Vector of locations.
- \texttt{sigma}
  Vector of scales.
- \texttt{quantile}
  Asymmetry parameter corresponding to quantiles in quantile regression (hence
  the name).
- \texttt{log}
  Logical; If \texttt{TRUE}, values are returned on the log scale.
- \texttt{lower.tail}
  Logical; If \texttt{TRUE} (default), return \( P(X \leq x) \). Else, return \( P(X > x) \).
- \texttt{log.p}
  Logical; If \texttt{TRUE}, values are returned on the log scale.
- \texttt{p}
  Vector of probabilities.
- \texttt{n}
  Number of draws to sample from the distribution.

**Details**

See \texttt{vignette("brms_families")} for details on the parameterization.

---

**autocor-terms**

<table>
<thead>
<tr>
<th>Autocorrelation structures</th>
</tr>
</thead>
</table>

**Description**

Specify autocorrelation terms in \texttt{brms} models. Currently supported terms are \texttt{arma}, \texttt{ar}, \texttt{ma}, \texttt{cosy}, \texttt{unstr}, \texttt{sar}, \texttt{car}, and \texttt{fcor}. Terms can be directly specified within the formula, or passed to the \texttt{autocor} argument of \texttt{brmsformula} in the form of a one-sided formula. For deprecated ways of specifying autocorrelation terms, see \texttt{cor_brms}.
The autocor term functions are almost solely useful when called in formulas passed to the \texttt{brms} package. They do not evaluate its arguments – but exist purely to help set up a model with autocorrelation terms.

\textbf{See Also}

\texttt{brmsformula}, \texttt{acformula}, \texttt{arma}, \texttt{ar}, \texttt{ma}, \texttt{cosy}, \texttt{unstr}, \texttt{sar}, \texttt{car}, \texttt{fcor}

\textbf{Examples}

\begin{verbatim}
# specify autocor terms within the formula
y ~ x + arma(p = 1, q = 1) + car(M)

# specify autocor terms in the 'autocor' argument
bf(y ~ x, autocor = ~ arma(p = 1, q = 1) + car(M))

# specify autocor terms via 'acformula'
bf(y ~ x) + acformula(~ arma(p = 1, q = 1) + car(M))
\end{verbatim}

\textbf{autocor.brmsfit} \hspace{1cm} (Deprecated) Extract Autocorrelation Objects

\textbf{Description}

(Deprecated) Extract Autocorrelation Objects

\textbf{Usage}

\begin{verbatim}
## S3 method for class 'brmsfit'
autocor(object, resp = NULL, ...)

autocor(object, ...)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{object} \hspace{1cm} An object of class \texttt{brmsfit}.
  \item \texttt{resp} \hspace{1cm} Optional names of response variables. If specified, predictions are performed only for the specified response variables.
  \item \texttt{...} \hspace{1cm} Currently unused.
\end{itemize}

\textbf{Value}

A \texttt{cor.brms} object or a list of such objects for multivariate models. Not supported for models fitted with \texttt{brms 2.11.1} or higher.
bayes_factor.brmsfit  Bayes Factors from Marginal Likelihoods

Description

Compute Bayes factors from marginal likelihoods.

Usage

```r
## S3 method for class 'brmsfit'
bayes_factor(x1, x2, log = FALSE, ...)
```

Arguments

- `x1`: A `brmsfit` object
- `x2`: Another `brmsfit` object based on the same responses.
- `log`: Report Bayes factors on the log-scale?
- `...`: Additional arguments passed to `bridge_sampler`.

Details

Computing the marginal likelihood requires samples of all variables defined in Stan's `parameters` block to be saved. Otherwise `bayes_factor` cannot be computed. Thus, please set `save_all_pars = TRUE` in the call to `brm`, if you are planning to apply `bayes_factor` to your models.

The computation of Bayes factors based on bridge sampling requires a lot more posterior samples than usual. A good conservative rule of thumb is perhaps 10-fold more samples (read: the default of 4000 samples may not be enough in many cases). If not enough posterior samples are provided, the bridge sampling algorithm tends to be unstable, leading to considerably different results each time it is run. We thus recommend running `bayes_factor` multiple times to check the stability of the results.

More details are provided under `bridgesampling::bayes_factor`.

See Also

- `bridge_sampler`, `post_prob`

Examples

```r
## Not run:
# model with the treatment effect
fit1 <- brm(
  count ~ zAge + zBase + Trt,
  data = epilepsy, family = negbinomial(),
  prior = prior(normal(0, 1), class = b),
  save_all_pars = TRUE
)
summary(fit1)
```
# model without the treatment effect
fit2 <- brm(
  count ~ zAge + zBase,
  data = epilepsy, family = negbinomial(),
  prior = prior(normal(0, 1), class = b),
  save_all_pars = TRUE
)
summary(fit2)

# compute the bayes factor
bayes_factor(fit1, fit2)

## End(Not run)

bayes_R2.brmsfit  

**Compute a Bayesian version of R-squared for regression models**

**Description**

Compute a Bayesian version of R-squared for regression models

**Usage**

```r
## S3 method for class 'brmsfit'
bayes_R2(
  object,
  resp = NULL,
  summary = TRUE,
  robust = FALSE,
  probs = c(0.025, 0.975),
  ...
)
```

**Arguments**

- `object`: An object of class `brmsfit`.
- `resp`: Optional names of response variables. If specified, predictions are performed only for the specified response variables.
- `summary`: Should summary statistics be returned instead of the raw values? Default is `TRUE`.
- `robust`: If `FALSE` (the default) the mean is used as the measure of central tendency and the standard deviation as the measure of variability. If `TRUE`, the median and the median absolute deviation (MAD) are applied instead. Only used if `summary` is `TRUE`.
- `probs`: The percentiles to be computed by the `quantile` function. Only used if `summary` is `TRUE`.
Further arguments passed to `posterior_epred`, which is used in the computation of the R-squared values.

Details

For an introduction to the approach, see Gelman et al. (2018) and https://github.com/jgabry/bayes_R2/.

Value

If `summary = TRUE`, an M x C matrix is returned (M = number of response variables and c = `length(probs) + 2`) containing summary statistics of the Bayesian R-squared values. If `summary = FALSE`, the posterior draws of the Bayesian R-squared values are returned in an S x M matrix (S is the number of draws).

References


Examples

```r
## Not run:
fit <- brm(mpg ~ wt + cyl, data = mtcars)
summary(fit)
bayes_R2(fit)

# compute R2 with new data
nd <- data.frame(mpg = c(10, 20, 30), wt = c(4, 3, 2), cyl = c(8, 6, 4))
bayes_R2(fit, newdata = nd)
## End(Not run)
```

---

**BetaBinomial**

*The Beta-binomial Distribution*

Description

Cumulative density & mass functions, and random number generation for the Beta-binomial distribution using the following re-parameterisation of the Stan Beta-binomial definition:

- `mu = alpha * beta` mean probability of trial success.
- `phi = (1 - mu) * beta` precision or over-dispersion, component.
Usage

dbeta_binomial(x, size, mu, phi, log = FALSE)

pbeta_binomial(q, size, mu, phi, lower.tail = TRUE, log.p = FALSE)

rbeta_binomial(n, size, mu, phi)

Arguments

x, q
Vector of quantiles.

size
Vector of number of trials (zero or more).

mu
Vector of means.

phi
Vector of precisions.

log
Logical; If TRUE, values are returned on the log scale.

lower.tail
Logical; If TRUE (default), return P(X <= x). Else, return P(X > x).

log.p
Logical; If TRUE, values are returned on the log scale.

n
Number of draws to sample from the distribution.

bridge_sampler.brmsfit

Log Marginal Likelihood via Bridge Sampling

Description

Computes log marginal likelihood via bridge sampling, which can be used in the computation of
bayes factors and posterior model probabilities. The brmsfit method is just a thin wrapper around the corresponding method for stanfit objects.

Usage

## S3 method for class 'brmsfit'
bridge_sampler(samples, recompile = FALSE, ...)

Arguments

samples
A brmsfit object.

recompile
Logical, indicating whether the Stan model should be recompiled. This may be necessary if you are running bridge sampling on another machine than the one used to fit the model. No recompilation is done by default.

...
Additional arguments passed to bridge_sampler.stanfit.
**brm**

Fit Bayesian Generalized (Non-)Linear Multivariate Multilevel Models

---

**Details**

Computing the marginal likelihood requires samples of all variables defined in Stan's parameters block to be saved. Otherwise bridge_sampler cannot be computed. Thus, please set `save_pars = save_pars(all = TRUE)` in the call to brm, if you are planning to apply bridge_sampler to your models.

The computation of marginal likelihoods based on bridge sampling requires a lot more posterior draws than usual. A good conservative rule of thumb is perhaps 10-fold more draws (read: the default of 4000 draws may not be enough in many cases). If not enough posterior draws are provided, the bridge sampling algorithm tends to be unstable leading to considerably different results each time it is run. We thus recommend running bridge_sampler multiple times to check the stability of the results.

More details are provided under `bridgesampling::bridge_sampler`.

**See Also**

`bayes_factor`, `post_prob`

**Examples**

```r
## Not run:
# model with the treatment effect
fit1 <- brm(
  count ~ zAge + zBase + Trt,
  data = epilepsy, family = negbinomial(),
  prior = prior(normal(0, 1), class = b),
  save_pars = save_pars(all = TRUE)
)
summary(fit1)
bridge_sampler(fit1)

# model without the treatment effect
fit2 <- brm(
  count ~ zAge + zBase,
  data = epilepsy, family = negbinomial(),
  prior = prior(normal(0, 1), class = b),
  save_pars = save_pars(all = TRUE)
)
summary(fit2)
bridge_sampler(fit2)

## End(Not run)
```
Description

Fit Bayesian generalized (non-)linear multivariate multilevel models using Stan for full Bayesian inference. A wide range of distributions and link functions are supported, allowing users to fit – among others – linear, robust linear, count data, survival, response times, ordinal, zero-inflated, hurdle, and even self-defined mixture models all in a multilevel context. Further modeling options include non-linear and smooth terms, auto-correlation structures, censored data, meta-analytic standard errors, and quite a few more. In addition, all parameters of the response distributions can be predicted in order to perform distributional regression. Prior specifications are flexible and explicitly encourage users to apply prior distributions that actually reflect their beliefs. In addition, model fit can easily be assessed and compared with posterior predictive checks and leave-one-out cross-validation.

Usage

```r
brm(
  formula,  
data,  
family = gaussian(),  
prior = NULL,  
autocor = NULL,  
data2 = NULL,  
cov_ranef = NULL,  
sample_prior = "no",  
sparse = NULL,  
knots = NULL,  
dropUnusedLevels = TRUE,  
stanvars = NULL,  
stan_funs = NULL,  
fit = NA,  
savePars = NULL,  
save_ranef = NULL,  
save_mevars = NULL,  
save_all_pars = NULL,  
init = NULL,  
inits = NULL,  
chains = 4,  
iter = 2000,  
warmup = floor(iter/2),  
thin = 1,  
cores = getOption("mc.cores", 1),  
threads = getOption("brms.threads", NULL),  
opencl = getOption("brms.opencl", NULL),  
normalize = getOption("brms.normalize", TRUE),  
control = NULL,  
algorithm = getOption("brms.algorithm", "sampling"),  
backend = getOption("brms.backend", "rstan"),  
future = getOption("future", FALSE),  
silent = 1,
)```
seed = NA,
save_model = NULL,
stan_model_args = list(),
file = NULL,
file_refit =getOption("brms.file_refit", "never"),
empty = FALSE,
rename = TRUE,
...)

Arguments

formula An object of class formula, brmsformula, or mvbrmsformula (or one that can be coerced to that classes): A symbolic description of the model to be fitted. The details of model specification are explained in brmsformula.
data An object of class data.frame (or one that can be coerced to that class) containing data of all variables used in the model.
family A description of the response distribution and link function to be used in the model. This can be a family function, a call to a family function or a character string naming the family. Every family function has a link argument allowing to specify the link function to be applied on the response variable. If not specified, default links are used. For details of supported families see brmsfamily. By default, a linear gaussian model is applied. In multivariate models, family might also be a list of families.
prior One or more brmsprior objects created by set_prior or related functions and combined using the c method or the + operator. See also get_prior for more help.
autocor (Deprecated) An optional cor_brms object describing the correlation structure within the response variable (i.e., the 'autocorrelation'). See the documentation of cor_brms for a description of the available correlation structures. Defaults to NULL, corresponding to no correlations. In multivariate models, autocor might also be a list of autocorrelation structures. It is now recommend to specify autocorrelation terms directly within formula. See brmsformula for more details.
data2 A named list of objects containing data, which cannot be passed via argument data. Required for some objects used in autocorrelation structures to specify dependency structures as well as for within-group covariance matrices.
cov_ranef (Deprecated) A list of matrices that are proportional to the (within) covariance structure of the group-level effects. The names of the matrices should correspond to columns in data that are used as grouping factors. All levels of the grouping factor should appear as rownames of the corresponding matrix. This argument can be used, among others to model pedigrees and phylogenetic effects. It is now recommended to specify those matrices in the formula interface using the gr and related functions. See vignette("brms_phylogenetics") for more details.
sample_prior Indicate if draws from priors should be drawn additionally to the posterior draws. Options are "no" (the default), "yes", and "only". Among others, these draws can be used to calculate Bayes factors for point hypotheses via hypothesis.
Please note that improper priors are not sampled, including the default improper priors used by `brm`. See `set_prior` on how to set (proper) priors. Please also note that prior draws for the overall intercept are not obtained by default for technical reasons. See `brmsformula` how to obtain prior draws for the intercept. If `sample_prior` is set to "only", draws are drawn solely from the priors ignoring the likelihood, which allows among others to generate draws from the prior predictive distribution. In this case, all parameters must have proper priors.

**sparse**

(Deprecated) Logical; indicates whether the population-level design matrices should be treated as sparse (defaults to `FALSE`). For design matrices with many zeros, this can considerably reduce required memory. Sampling speed is currently not improved or even slightly decreased. It is now recommended to use the `sparse` argument of `brmsformula` and related functions.

**knots**

Optional list containing user specified knot values to be used for basis construction of smoothing terms. See `gamm` for more details.

**drop_unused_levels**

Should unused factors levels in the data be dropped? Defaults to `TRUE`.

**stanvars**

An optional `stanvars` object generated by function `stanvar` to define additional variables for use in `Stan`'s program blocks.

**stan_funs**

(Deprecated) An optional character string containing self-defined `Stan` functions, which will be included in the functions block of the generated `Stan` code. It is now recommended to use the `stanvars` argument for this purpose instead.

**fit**

An instance of S3 class `brmsfit` derived from a previous fit; defaults to `NA`. If `fit` is of class `brmsfit`, the compiled model associated with the fitted result is re-used and all arguments modifying the model code or data are ignored. It is not recommended to use this argument directly, but to call the `update` method, instead.

**save_pars**

An object generated by `save_pars` controlling which parameters should be saved in the model. The argument has no impact on the model fitting itself.

**save_ranef**

(Deprecated) A flag to indicate if group-level effects for each level of the grouping factor(s) should be saved (default is `TRUE`). Set to `FALSE` to save memory. The argument has no impact on the model fitting itself.

**save_mevars**

(Deprecated) A flag to indicate if draws of latent noise-free variables obtained by using `me` and `mi` terms should be saved (default is `FALSE`). Saving these draws allows to better use methods such as `predict` with the latent variables but leads to very large `R` objects even for models of moderate size and complexity.

**save_all_pars**

(Deprecated) A flag to indicate if draws from all variables defined in `Stan`'s parameters block should be saved (default is `FALSE`). Saving these draws is required in order to apply the methods `bridge_sampler`, `bayes_factor`, and `post_prob`.

**init**

Initial values for the sampler. If `NULL` (the default) or "random", Stan will randomly generate initial values for parameters in a reasonable range. If 0, all parameters are initialized to zero on the unconstrained space. This option is sometimes useful for certain families, as it happens that default random initial values cause draws to be essentially constant. Generally, setting `init = 0` is worth a try, if chains do not initialize or behave well. Alternatively, `init` can
be a list of lists containing the initial values, or a function (or function name) generating initial values. The latter options are mainly implemented for internal testing but are available to users if necessary. If specifying initial values using a list or a function then currently the parameter names must correspond to the names used in the generated Stan code (not the names used in \texttt{R}). For more details on specifying initial values you can consult the documentation of the selected backend.

\textbf{inits}  
(Deprecated) Alias of \texttt{init}.

\textbf{chains}  
Number of Markov chains (defaults to 4).

\textbf{iter}  
Number of total iterations per chain (including warmup; defaults to 2000).

\textbf{warmup}  
A positive integer specifying number of warmup (aka burnin) iterations. This also specifies the number of iterations used for stepsize adaptation, so warmup draws should not be used for inference. The number of warmup should not be larger than \texttt{iter} and the default is $\text{iter}/2$.

\textbf{thin}  
Thinning rate. Must be a positive integer. Set $\text{thin} > 1$ to save memory and computation time if \texttt{iter} is large.

\textbf{cores}  
Number of cores to use when executing the chains in parallel, which defaults to 1 but we recommend setting the \texttt{mc.cores} option to be as many processors as the hardware and RAM allow (up to the number of chains). For non-Windows OS in non-interactive \texttt{R} sessions, forking is used instead of PSOCK clusters.

\textbf{threads}  
Number of threads to use in within-chain parallelization. For more control over the threading process, threads may also be a \texttt{brmsthreads} object created by \texttt{threading}. Within-chain parallelization is experimental! We recommend its use only if you are experienced with Stan’s \texttt{reduce_sum} function and have a slow running model that cannot be sped up by any other means. Can be set globally for the current \texttt{R} session via the "\texttt{brms.threads}" option (see \texttt{options}).

\textbf{opencl}  
The platform and device IDs of the OpenCL device to use for fitting using GPU support. If you don’t know the IDs of your OpenCL device, \texttt{c(0,0)} is most likely what you need. For more details, see \texttt{opencl}. Can be set globally for the current \texttt{R} session via the "\texttt{brms.opencl}" option.

\textbf{normalize}  
Logical. Indicates whether normalization constants should be included in the Stan code (defaults to \texttt{TRUE}). Setting it to \texttt{FALSE} requires Stan version $\geq 2.25$ to work. If \texttt{FALSE}, sampling efficiency may be increased but some post processing functions such as \texttt{bridge_sampler} will not be available. Can be controlled globally for the current \texttt{R} session via the '\texttt{brms.normalize}' option.

\textbf{control}  
A named list of parameters to control the sampler’s behavior. It defaults to \texttt{NULL} so all the default values are used. The most important control parameters are discussed in the 'Details' section below. For a comprehensive overview see \texttt{stan}.

\textbf{algorithm}  
Character string naming the estimation approach to use. Options are "\texttt{sampling}" for MCMC (the default), "\texttt{meanfield}" for variational inference with independent normal distributions, "\texttt{fullrank}" for variational inference with a multivariate normal distribution, or "\texttt{fixed_param}" for sampling from fixed parameter values. Can be set globally for the current \texttt{R} session via the "\texttt{brms.algorithm}" option (see \texttt{options}).
backend  Character string naming the package to use as the backend for fitting theStan
model. Options are "rstan" (the default) or "cmdstanr". Can be set globally
for the current R session via the "brms.backend" option (see options). Details
on the rstan and cmdstanr packages are available at https://mc-stan.org/
rstan/ and https://mc-stan.org/cmdstanr/, respectively. Additionally a
"mock" backend is available to make testing brms and packages that depend on
it easier. The "mock" backend does not actually do any fitting, it only checks
the generated Stan code for correctness and then returns whatever is passed in
an additional mock_fit argument as the result of the fit.

future  Logical; If TRUE, the future package is used for parallel execution of the chains
and argument cores will be ignored. Can be set globally for the current R
session via the "future" option. The execution type is controlled via plan (see
the examples section below).

silent  Verbosity level between 0 and 2. If 1 (the default), most of the informational
messages of compiler and sampler are suppressed. If 2, even more messages
are suppressed. The actual sampling progress is still printed. Set refresh = 0 to
turn this off as well. If using backend = "rstan" you can also set open_progress
= FALSE to prevent opening additional progress bars.

seed  The seed for random number generation to make results reproducible. If NA (the
default), Stan will set the seed randomly.

save_model  Either NULL or a character string. In the latter case, the model's Stan code is
saved via cat in a text file named after the string supplied in save_model.

stan_model_args  A list of further arguments passed to rstan::stan_model for backend = "rstan"
or to cmdstanr::cmdstan_model for backend = "cmdstanr", which allows to
change how models are compiled.

file  Either NULL or a character string. In the latter case, the fitted model object is
saved via saveRDS in a file named after the string supplied in file. The .rds
extension is added automatically. If the file already exists, brm will load and
return the saved model object instead of refitting the model. Unless you specify
the file_refit argument as well, the existing files won’t be overwritten, you
have to manually remove the file in order to refit and save the model under an
existing file name. The file name is stored in the brmsfit object for later usage.

file_refit  Modifies when the fit stored via the file parameter is re-used. Can be set glob-
ally for the current R session via the "brms.file_refit" option (see options). For "never" (default) the fit is always loaded if it exists and fitting is skipped.
For "always" the model is always refitted. If set to "on_change", brms will
refit the model if model, data or algorithm as passed to Stan differ from what is
stored in the file. This also covers changes in priors, sample_prior, stanvars,
covariance structure, etc. If you believe there was a false positive, you can use
brmsfit_needs_refit to see why refit is deemed necessary. Refit will not be
triggered for changes in additional parameters of the fit (e.g., initial values, num-
ber of iterations, control arguments, ...). A known limitation is that a refit will
be triggered if within-chain parallelization is switched on/off.

empty  Logical. If TRUE, the Stan model is not created and compiled and the corre-
sponding 'fit' slot of the brmsfit object will be empty. This is useful if you
have estimated a brms-created Stan model outside of \textbf{brms} and want to feed it back into the package.

\texttt{rename}  
For internal use only.

\ldots
Further arguments passed to Stan. For backend = "rstan" the arguments are passed to \texttt{sampling} or \texttt{vb}. For backend = "cmdstanr" the arguments are passed to the \texttt{cmdstanr::sample} or \texttt{cmdstanr::variational} method.

\textbf{Details}

Fit a generalized (non-)linear multivariate multilevel model via full Bayesian inference using Stan. A general overview is provided in the vignettes \texttt{vignette("brms_overview")} and \texttt{vignette("brms_multilevel")}. For a full list of available vignettes see \texttt{vignette(package = "brms")}.

\textbf{Formula syntax of brms models}

Details of the formula syntax applied in \textbf{brms} can be found in \texttt{brmsformula}.

\textbf{Families and link functions}

Details of families supported by \textbf{brms} can be found in \texttt{brmsfamily}.

\textbf{Prior distributions}

Priors should be specified using the \texttt{set_prior} function. Its documentation contains detailed information on how to correctly specify priors. To find out on which parameters or parameter classes priors can be defined, use \texttt{get_prior}. Default priors are chosen to be non or very weakly informative so that their influence on the results will be negligible and you usually don’t have to worry about them. However, after getting more familiar with Bayesian statistics, I recommend you to start thinking about reasonable informative priors for your model parameters: Nearly always, there is at least some prior information available that can be used to improve your inference.

\textbf{Adjusting the sampling behavior of Stan}

In addition to choosing the number of iterations, warmup draws, and chains, users can control the behavior of the NUTS sampler, by using the \texttt{control} argument. The most important reason to use \texttt{control} is to decrease (or eliminate at best) the number of divergent transitions that cause a bias in the obtained posterior draws. Whenever you see the warning "There were x divergent transitions after warmup." you should really think about increasing \texttt{adapt_delta}. To do this, write \texttt{control = list(adapt_delta = <x>)} where \texttt{<x>} should usually be value between 0.8 (current default) and 1. Increasing \texttt{adapt_delta} will slow down the sampler but will decrease the number of divergent transitions threatening the validity of your posterior draws.

Another problem arises when the depth of the tree being evaluated in each iteration is exceeded. This is less common than having divergent transitions, but may also bias the posterior draws. When it happens, \textbf{Stan} will throw out a warning suggesting to increase \texttt{max_treedepth}, which can be accomplished by writing \texttt{control = list(max_treedepth = <x>)} with a positive integer \texttt{<x>} that should usually be larger than the current default of 10. For more details on the \texttt{control} argument see \texttt{stan}.

\textbf{Value}

An object of class \texttt{brmsfit}, which contains the posterior draws along with many other useful information about the model. Use \texttt{methods(class = "brmsfit")} for an overview on available methods.
Author(s)

Paul-Christian Buerkner <paul.buerkner@gmail.com>

References


See Also

brms, brmsformula, brmsfamily, brmsfit

Examples

```r
## Not run:
# Poisson regression for the number of seizures in epileptic patients
# using normal priors for population-level effects
# and half-cauchy priors for standard deviations of group-level effects
prior1 <- prior(normal(0,10), class = b) +
  prior(cauchy(0,2), class = sd)
fit1 <- brm(count ~ zAge + zBase * Trt + (1|patient),
  data = epilepsy, family = poisson(), prior = prior1)
# generate a summary of the results
summary(fit1)
# plot the MCMC chains as well as the posterior distributions
plot(fit1, ask = FALSE)
# predict responses based on the fitted model
head(predict(fit1))
# plot conditional effects for each predictor
plot(conditional_effects(fit1), ask = FALSE)
# investigate model fit
loo(fit1)
pp_check(fit1)

# Ordinal regression modeling patient's rating of inhaler instructions
# category specific effects are estimated for variable 'treat'
fit2 <- brm(rating ~ period + carry + cs(treat),
  data = inhaler, family = sratio("logit"),
  prior = set_prior("normal(0,5)"), chains = 2)
summary(fit2)
plot(fit2, ask = FALSE)
WAIC(fit2)
```
# Survival regression modeling the time between the first
# and second recurrence of an infection in kidney patients.
fit3 <- brm(time | cens(censored) ~ age * sex + disease + (1|patient),
            data = kidney, family = lognormal())
summary(fit3)
plot(fit3, ask = FALSE)
plot(conditional_effects(fit3), ask = FALSE)

# Probit regression using the binomial family
ntrials <- sample(1:10, 100, TRUE)
success <- rbinom(100, size = ntrials, prob = 0.4)
x <- rnorm(100)
data4 <- data.frame(ntrials, success, x)
fit4 <- brm(success | trials(ntrials) ~ x, data = data4,
            family = binomial("probit"))
summary(fit4)

# Non-linear Gaussian model
fit5 <- brm(
    bf(cum ~ ult * (1 - exp(- (dev/theta)^omega)),
       ult ~ 1 + (1|AY), omega ~ 1, theta ~ 1,
       nl = TRUE),
    data = loss, family = gaussian(),
    prior = c(
        prior(normal(5000, 1000), nlpar = "ult"),
        prior(normal(1, 2), nlpar = "omega"),
        prior(normal(45, 10), nlpar = "theta")
    ),
    control = list(adapt_delta = 0.9)
)
summary(fit5)
conditional_effects(fit5)

# Normal model with heterogeneous variances
data_het <- data.frame(
    y = c(rnorm(50), rnorm(50, 1, 2)),
    x = factor(rep(c("a", "b"), each = 50))
)
fit6 <- brm(bf(y ~ x, sigma ~ 0 + x), data = data_het)
summary(fit6)
plot(fit6)
conditional_effects(fit6)

# extract estimated residual SDs of both groups
sigmas <- exp(as.data.frame(fit6, variable = "^b_sigma_", regex = TRUE))
ggplot(stack(sigmas), aes(values)) +
geom_density(aes(fill = ind))
# Quantile regression predicting the 25%-quantile
fit7 <- brm(bf(y ~ x, quantile = 0.25), data = data_het, 
            family = asym_laplace())
summary(fit7)
conditional_effects(fit7)

# use the future package for more flexible parallelization
library(future)
plan(multiprocess)
fit7 <- update(fit7, future = TRUE)

# fit a model manually via rstan
scode <- make_stancode(count ~ Trt, data = epilepsy)
sdata <- make_standata(count ~ Trt, data = epilepsy)
stanfit <- rstan::stan(model_code = scode, data = sdata)
# feed the Stan model back into brms
fit8 <- brm(count ~ Trt, data = epilepsy, empty = TRUE)
fit8$fit <- stanfit
fit8 <- rename_pars(fit8)
summary(fit8)

## End(Not run)

---

**brmsfamily**  
*Special Family Functions for *brms* Models*

**Description**

Family objects provide a convenient way to specify the details of the models used by many model fitting functions. The family functions presented here are for use with *brms* only and will **not** work with other model fitting functions such as *glm* or *glmer*. However, the standard family functions as described in *family* will work with *brms*. You can also specify custom families for use in *brms* with the `custom_family` function.

**Usage**

```r
brmsfamily(
  family,
  link = NULL,
  link_sigma = "log",
  link_shape = "log",
  link_nu = "logm1",
  link_phi = "log",
  link_kappa = "log",
  link_beta = "log",
  link_zi = "logit",
)```
link_hu = "logit",
link_zoi = "logit",
link_coi = "logit",
link_disc = "log",
link_bs = "log",
link_ndt = "log",
link_bias = "logit",
link_xi = "log1p",
link_alpha = "identity",
link_quantile = "logit",
threshold = "flexible",
refcat = NULL,
bhaz = NULL)

student(link = "identity", link_sigma = "log", link_nu = "logm1")

bernoulli(link = "logit")

beta_binomial(link = "logit", link_phi = "log")

negbinomial(link = "log", link_shape = "log")

geometric(link = "log")

lognormal(link = "identity", link_sigma = "log")

shifted_lognormal(link = "identity", link_sigma = "log", link_ndt = "log")

skew_normal(link = "identity", link_sigma = "log", link_alpha = "identity")

exponential(link = "log")

weibull(link = "log", link_shape = "log")

frechet(link = "log", link_nu = "logm1")

gen_extreme_value(link = "identity", link_sigma = "log", link_xi = "log1p")

exgaussian(link = "identity", link_sigma = "log", link_beta = "log")

wiener(
  link = "identity",
  link_bs = "log",
  link_ndt = "log",
  link_bias = "logit"
)
Beta(link = "logit", link_phi = "log")
dirichlet(link = "logit", link_phi = "log", refcat = NULL)
logistic_normal(link = "identity", link_sigma = "log", refcat = NULL)
von_mises(link = "tan_half", link_kappa = "log")
asym_laplace(link = "identity", link_sigma = "log", link_quantile = "logit")
cox(link = "log", bhaz = NULL)
hurdle_poisson(link = "log")
hurdle_negbinomial(link = "log", link_shape = "log", link_hu = "logit")
hurdle_gamma(link = "log", link_shape = "log", link_hu = "logit")
hurdle_lognormal(link = "identity", link_sigma = "log", link_hu = "logit")
hurdle_cumulative(
  link = "logit",
  link_hu = "logit",
  link_disc = "log",
  threshold = "flexible"
)
zero_inflated_beta(link = "logit", link_phi = "log", link_zi = "logit")
zero_one_inflated_beta(
  link = "logit",
  link_phi = "log",
  link_zoi = "logit",
  link_coi = "logit"
)
zero_inflated_poisson(link = "log", link_zi = "logit")
zero_inflated_negbinomial(link = "log", link_shape = "log", link_zi = "logit")
zero_inflated_binomial(link = "logit", link_zi = "logit")
zero_inflated_beta_binomial(
  link = "logit",
  link_phi = "log",
  link_zi = "logit"
categorical(link = "logit", refcat = NULL)

multinomial(link = "logit", refcat = NULL)

cumulative(link = "logit", link_disc = "log", threshold = "flexible")

sratio(link = "logit", link_disc = "log", threshold = "flexible")

cratio(link = "logit", link_disc = "log", threshold = "flexible")

acat(link = "logit", link_disc = "log", threshold = "flexible")

**Arguments**

- **family**
  A character string naming the distribution family of the response variable to be used in the model. Currently, the following families are supported: gaussian, student, binomial, bernoulli, beta-binomial, poisson, negbinomial, geometric, Gamma, skew normal, lognormal, shifted lognormal, exgaussian, wiener, inverse gaussian, exponential, weibull, frechet, Beta, dirichlet, von mises, asym laplace, gen extreme value, categorical, multinomial, cumulative, cratio, sratio, acat, hurdle poisson, hurdle negbinomial, hurdle gamma, hurdle lognormal, hurdle cumulative, zero inflated binomial, zero inflated beta binomial, zero inflated beta, zero inflated negbinomial, zero inflated poisson, and zero one inflated beta.

- **link**
  A specification for the model link function. This can be a name/expression or character string. See the 'Details' section for more information on link functions supported by each family.

- **link_sigma**
  Link of auxiliary parameter sigma if being predicted.

- **link_shape**
  Link of auxiliary parameter shape if being predicted.

- **link_nu**
  Link of auxiliary parameter nu if being predicted.

- **link_phi**
  Link of auxiliary parameter phi if being predicted.

- **link_kappa**
  Link of auxiliary parameter kappa if being predicted.

- **link_beta**
  Link of auxiliary parameter beta if being predicted.

- **link_zi**
  Link of auxiliary parameter zi if being predicted.

- **link_hu**
  Link of auxiliary parameter hu if being predicted.

- **link_zoi**
  Link of auxiliary parameter zoi if being predicted.

- **link_coi**
  Link of auxiliary parameter coi if being predicted.

- **link_disc**
  Link of auxiliary parameter disc if being predicted.

- **link_bs**
  Link of auxiliary parameter bs if being predicted.

- **link_ndt**
  Link of auxiliary parameter ndt if being predicted.

- **link_bias**
  Link of auxiliary parameter bias if being predicted.

- **link_xi**
  Link of auxiliary parameter xi if being predicted.

- **link_alpha**
  Link of auxiliary parameter alpha if being predicted.
link_quantile  Link of auxiliary parameter quantile if being predicted.
threshold     A character string indicating the type of thresholds (i.e. intercepts) used in an ordinal model. "flexible" provides the standard unstructured thresholds, "equidistant" restricts the distance between consecutive thresholds to the same value, and "sum_to_zero" ensures the thresholds sum to zero.
refcat        Optional name of the reference response category used in categorical, multinomial, dirichlet and logistic_normal models. If NULL (the default), the first category is used as the reference. If NA, all categories will be predicted, which requires strong priors or carefully specified predictor terms in order to lead to an identified model.
bhaz          Currently for experimental purposes only.

Details

Below, we list common use cases for the different families. This list is not ment to be exhaustive.

- Family gaussian can be used for linear regression.
- Family student can be used for robust linear regression that is less influenced by outliers.
- Family skew_normal can handle skewed responses in linear regression.
- Families poisson, negbinomial, and geometric can be used for regression of unbounded count data.
- Families bernoulli, binomial, and beta_binomial can be used for binary regression (i.e., most commonly logistic regression).
- Families categorical and multinomial can be used for multi-logistic regression when there are more than two possible outcomes.
- Families cumulative, cratio (‘continuation ratio’), sratio (‘stopping ratio’), and acat (‘adjacent category’) leads to ordinal regression.
- Families Gamma, weibull, exponential, lognormal, frechet, inverse.gaussian, and cox (Cox proportional hazards model) can be used (among others) for time-to-event regression also known as survival regression.
- Families weibull, frechet, and gen_extreme_value (‘generalized extreme value’) allow for modeling extremes.
- Families beta, dirichlet, and logistic_normal can be used to model responses representing rates or probabilities.
- Family asym_laplace allows for quantile regression when fixing the auxiliary quantile parameter to the quantile of interest.
- Family exgaussian (‘exponentially modified Gaussian’) and shifted_lognormal are especially suited to model reaction times.
- Family wiener provides an implementation of the Wiener diffusion model. For this family, the main formula predicts the drift parameter 'delta' and all other parameters are modeled as auxiliary parameters (see brmsformula for details).
- Families hurdle_poisson, hurdle_negbinomial, hurdle_gamma, hurdle_lognormal, zero_inflated_poisson, zero_inflated_negbinomial, zero_inflated_binomial, zero_inflated_beta_binomial, zero_inflated_beta, zero_one_inflated_beta, and hurdle_cumulative allow to estimate zero-inflated and hurdle models. These models can be very helpful when there are many
zeros in the data (or ones in case of one-inflated models) that cannot be explained by the primary distribution of the response.

Below, we list all possible links for each family. The first link mentioned for each family is the default.

- Families `gaussian`, `student`, `skew_normal`, `exgaussian`, `asym_laplace`, and `gen_extreme_value` support the links (as names) `identity`, `log`, `inverse`, and `softplus`.
- Families `poisson`, `negbinomial`, `geometric`, `zero_inflated_poisson`, `zero_inflated_negbinomial`, `hurdle_poisson`, and `hurdle_negbinomial` support `log`, `identity`, `sqrt`, and `softplus`.
- Families `binomial`, `bernoulli`, `beta_binomial`, `zero_inflated_binomial`, `zero_inflated_beta`, and `zero_one_inflated_beta` support `logit`, `probit`, `probit_approx`, `cloglog`, `cauchit`, `identity`, and `log`.
- Families `cumulative`, `cratio`, `sratio`, `acat`, and `hurdle_cumulative` support `logit`, `probit`, `probit_approx`, `cloglog`, `cauchit`, `identity`, and `log`.
- Families `categorical`, `multinomial`, and `dirichlet` support `logit`.
- Families `Gamma`, `weibull`, `exponential`, `frechet`, and `hurdle_gamma` support `log`, `identity`, `inverse`, and `softplus`.
- Families `lognormal` and `hurdle_lognormal` support `identity` and `inverse`.
- Family `logistic_normal` supports `identity`.
- Family `inverse.gaussian` supports `1/mu^2`, `inverse`, `identity`, `log`, and `softplus`.
- Family `von_mises` supports `tan_half` and `identity`.
- Family `cox` supports `log`, `identity`, and `softplus` for the proportional hazards parameter.
- Family `wiener` supports `identity`, `log`, and `softplus` for the main parameter which represents the drift rate.

Please note that when calling the `Gamma` family function of the `stats` package, the default link will be `inverse` instead of `log` although the latter is the default in `brms`. Also, when using the family functions `gaussian`, `binomial`, `poisson`, and `Gamma` of the `stats` package (see `family`), special link functions such as `softplus` or `cauchit` won’t work. In this case, you have to use `brmsfamily` to specify the family with corresponding link function.

**See Also**
- `brm`, `family`, `customfamily`

**Examples**

```r
# create a family object
(fam1 <- student("log"))
# alternatively use the brmsfamily function
(fam2 <- brmsfamily("student", "log"))
# both leads to the same object
identical(fam1, fam2)
```
**brmsfit-class**

Class `brmsfit` of models fitted with the `brms` package

**Description**

Models fitted with the `brms` package are represented as a `brmsfit` object, which contains the posterior draws (samples), model formula, Stan code, relevant data, and other information.

**Details**

See `methods(class = "brmsfit")` for an overview of available methods.

**Slots**

- `formula` A `brmsformula` object.
- `data` A `data.frame` containing all variables used in the model.
- `data2` A list of data objects which cannot be passed via `data`.
- `prior` A `brmsprior` object containing information on the priors used in the model.
- `stanvars` A `stanvars` object.
- `model` The model code in Stan language.
- `ranef` A `data.frame` containing the group-level structure.
- `exclude` The names of the parameters for which draws are not saved.
- `algorithm` The name of the algorithm used to fit the model.
- `backend` The name of the backend used to fit the model.
- `threads` An object of class 'brmsthreads' created by `threading`.
- `opencl` An object of class 'brmsopencl' created by `opencl`.
- `stan_args` Named list of additional control arguments that were passed to the Stan backend directly.
- `fit` An object of class `stanfit` among others containing the posterior draws.
- `criteria` An empty list for adding model fit criteria after estimation of the model.
- `file` Optional name of a file in which the model object was stored in or loaded from.
- `version` The versions of `brms` and `rstan` with which the model was fitted.
- `family` (Deprecated) A `brmsfamily` object.
- `autocor` (Deprecated) An `cor_brms` object containing the autocorrelation structure if specified.
- `cov_ranef` (Deprecated) A list of customized group-level covariance matrices.
- `stan_funs` (Deprecated) A character string of length one or NULL.
- `data.name` (Deprecated) The name of data as specified by the user.

**See Also**

`brms`, `brm`, `brmsformula`, `brmsfamily`
**Set up a model formula for use in brms**

**Description**

Set up a model formula for use in the **brms** package allowing to define (potentially non-linear) additive multilevel models for all parameters of the assumed response distribution.

**Usage**

```r
brmsformula(
  formula,
  ..., flist = NULL,
  family = NULL,
  autocor = NULL,
  nl = NULL,
  loop = NULL,
  center = NULL,
  cmc = NULL,
  sparse = NULL,
  decomp = NULL,
  unused = NULL
)
```

**Arguments**

- `formula`: An object of class **formula** (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given in 'Details'.
- `...`: Additional **formula** objects to specify predictors of non-linear and distributional parameters. Formulas can either be named directly or contain names on their left-hand side. Alternatively, it is possible to fix parameters to certain values by passing numbers or character strings in which case arguments have to be named to provide the parameter names. See 'Details' for more information.
- `flist`: Optional list of formulas, which are treated in the same way as formulas passed via the ... argument.
- `family`: Same argument as in **brm**. If family is specified in brmsformula, it will overwrite the value specified in other functions.
- `autocor`: An optional **formula** which contains autocorrelation terms as described in **autocor-terms** or alternatively a **cor_brms** object (deprecated). If autocor is specified in brmsformula, it will overwrite the value specified in other functions.
- `nl`: Logical; Indicates whether formula should be treated as specifying a non-linear model. By default, formula is treated as an ordinary linear model formula.
loop Logical; Only used in non-linear models. Indicates if the computation of the non-linear formula should be done inside (TRUE) or outside (FALSE) a loop over observations. Defaults to TRUE.

center Logical; Indicates if the population-level design matrix should be centered, which usually increases sampling efficiency. See the 'Details' section for more information. Defaults to TRUE for distributional parameters and to FALSE for non-linear parameters.

cmc Logical; Indicates whether automatic cell-mean coding should be enabled when removing the intercept by adding 0 to the right-hand of model formulas. Defaults to TRUE to mirror the behavior of standard R formula parsing.

sparse Logical; indicates whether the population-level design matrices should be treated as sparse (defaults to FALSE). For design matrices with many zeros, this can considerably reduce required memory. Sampling speed is currently not improved or even slightly decreased.

decomp Optional name of the decomposition used for the population-level design matrix. Defaults to NULL that is no decomposition. Other options currently available are "QR" for the QR decomposition that helps in fitting models with highly correlated predictors.

unused An optional formula which contains variables that are unused in the model but should still be stored in the model’s data frame. This can be useful, for example, if those variables are required for post-processing the model.

Details

General formula structure

The formula argument accepts formulas of the following syntax:

response | aterms ~ pterms + (gterms | group)

The pterms part contains effects that are assumed to be the same across observations. We call them 'population-level' or 'overall' effects, or (adopting frequentist vocabulary) 'fixed' effects. The optional gterms part may contain effects that are assumed to vary across grouping variables specified in group. We call them 'group-level' or 'varying' effects, or (adopting frequentist vocabulary) 'random' effects, although the latter name is misleading in a Bayesian context. For more details type vignette("brms_overview") and vignette("brms_multilevel").

Group-level terms

Multiple grouping factors each with multiple group-level effects are possible. (Of course we can also run models without any group-level effects.) Instead of | you may use || in grouping terms to prevent correlations from being modeled. Equivalently, the cor argument of the gr function can be used for this purpose, for example, (1 + x | | g) is equivalent to (1 + x | gr(g, cor = FALSE)).

It is also possible to model different group-level terms of the same grouping factor as correlated (even across different formulas, e.g., in non-linear models) by using |<ID>| instead of |. All group-level terms sharing the same ID will be modeled as correlated. If, for instance, one specifies the terms (1+x|i|g) and (1+z|i|g) somewhere in the formulas passed to brmsformula, correlations between the corresponding group-level effects will be estimated. In the above example, i is not a variable in the data but just a symbol to indicate correlations between multiple group-level terms. Equivalently, the id argument of the gr function can be used as well, for example, (1 + x | gr(g, id = "i")).
If levels of the grouping factor belong to different sub-populations, it may be reasonable to assume a different covariance matrix for each of the sub-populations. For instance, the variation within the treatment group and within the control group in a randomized control trial might differ. Suppose that $y$ is the outcome, and $x$ is the factor indicating the treatment and control group. Then, we could estimate different hyper-parameters of the varying effects (in this case a varying intercept) for treatment and control group via $y \sim x + (1 | \text{gr(subject, by = x)}).$

You can specify multi-membership terms using the $\text{mm}$ function. For instance, a multi-membership term with two members could be $(1 | \text{mm(g1, g2)})$, where $g1$ and $g2$ specify the first and second member, respectively. Moreover, if a covariate $x$ varies across the levels of the grouping-factors $g1$ and $g2$, we can save the respective covariate values in the variables $x1$ and $x2$ and then model the varying effect as $(1 + \text{mmc}(x1, x2) | \text{mm(g1, g2)})$.

**Special predictor terms**

Flexible non-linear smooth terms can modeled using the $s$ and $t2$ functions in the $pterms$ part of the model formula. This allows to fit generalized additive mixed models (GAMMs) with $\text{brms}$. The implementation is similar to that used in the $\text{gamm4}$ package. For more details on this model class see $\text{gam}$ and $\text{gamm}$.

Gaussian process terms can be fitted using the $gp$ function in the $pterms$ part of the model formula. Similar to smooth terms, Gaussian processes can be used to model complex non-linear relationships, for instance temporal or spatial autocorrelation. However, they are computationally demanding and are thus not recommended for very large datasets or approximations need to be used.

The $pterms$ and $gterms$ parts may contain four non-standard effect types namely monotonic, measurement error, missing value, and category specific effects, which can be specified using terms of the form $\text{mo}(\text{predictor}), \text{me}(\text{predictor, sd_predictor}), \text{mi}(\text{predictor}), \text{and cs(<predictors>)}$, respectively. Category specific effects can only be estimated in ordinal models and are explained in more detail in the package’s main vignette (type vignette("brms_overview")). The other three effect types are explained in the following.

A monotonic predictor must either be integer valued or an ordered factor, which is the first difference to an ordinary continuous predictor. More importantly, predictor categories (or integers) are not assumed to be equidistant with respect to their effect on the response variable. Instead, the distance between adjacent predictor categories (or integers) is estimated from the data and may vary across categories. This is realized by parameterizing as follows: One parameter takes care of the direction and size of the effect similar to an ordinary regression parameter, while an additional parameter vector estimates the normalized distances between consecutive predictor categories. A main application of monotonic effects are ordinal predictors that can this way be modeled without (falsely) treating them as continuous or as unordered categorical predictors. For more details and examples see vignette("brms_monotonic").

Quite often, predictors are measured and as such naturally contain measurement error. Although most researchers are well aware of this problem, measurement error in predictors is ignored in most regression analyses, possibly because only few packages allow for modeling it. Notably, measurement error can be handled in structural equation models, but many more general regression models (such as those featured by $\text{brms}$) cannot be transferred to the SEM framework. In $\text{brms}$, effects of noise-free predictors can be modeled using the $\text{me}$ (for 'measurement error') function. If, say, $y$ is the response variable and $x$ is a measured predictor with known measurement error $\text{sdx}$, we can simply include it on the right-hand side of the model formula via $y \sim \text{me}(x, \text{sdx})$. This can easily be extended to more general formulas. If $x2$ is another measured predictor with corresponding error $\text{sdx2}$ and $z$ is a predictor without error (e.g., an experimental setting), we can
model all main effects and interactions of the three predictors in the well known manner: \( y \sim \text{me}(x, sdx) \times \text{me}(x2, sdx2) \times z \). The \text{me} function is soft deprecated in favor of the more flexible and consistent \text{mi} function (see below).

When a variable contains missing values, the corresponding rows will be excluded from the data by default (row-wise exclusion). However, quite often we want to keep these rows and instead estimate the missing values. There are two approaches for this: (a) Impute missing values before the model fitting for instance via multiple imputation (see \textbf{brm_multiple} for a way to handle multiple imputed datasets). (b) Impute missing values on the fly during model fitting. The latter approach is explained in the following. Using a variable with missing values as predictors requires two things, First, we need to specify that the predictor contains missings that should to be imputed. If, say, \( y \) is the primary response, \( x \) is a predictor with missings and \( z \) is a predictor without missings, we go for \( y \sim \text{mi}(x) + z \). Second, we need to model \( x \) as an additional response with corresponding predictors and the addition term \text{mi}(). In our example, we could write \( x | \text{mi}() \sim z \). Measurement error may be included via the \text{sdy} argument, say, \( x | \text{mi}(sdy = \text{se}) \sim z \). See \textbf{mi} for examples with real data.

**Autocorrelation terms**

Autocorrelation terms can be directly specified inside the pterms part as well. Details can be found in \textbf{autocor-terms}.

**Additional response information**

Another special of the \textbf{brms} formula syntax is the optional aterms part, which may contain multiple terms of the form \text{fun(<variable>)} separated by + each providing special information on the response variable. \text{fun} can be replaced with either \text{se}, \text{weights}, \text{subset}, \text{cens}, \text{trunc}, \text{trials}, \text{cat}, \text{dec}, \text{rate}, \text{vreal}, or \text{vint}. Their meanings are explained below (see also \textbf{addition-terms}).

For families \text{gaussian}, \text{student} and \text{skew_normal}, it is possible to specify standard errors of the observations, thus allowing to perform meta-analysis. Suppose that the variable \( y_i \) contains the effect sizes from the studies and \( se_i \) the corresponding standard errors. Then, fixed and random effects meta-analyses can be conducted using the formulas \( y_i | se(se_i) \sim 1 \) and \( y_i | se(se_i) \sim 1 + (1|\text{study}) \), respectively, where study is a variable uniquely identifying every study. If desired, meta-regression can be performed via \( y_i | se(se_i) \sim 1 + \text{mod1} + \text{mod2} + (1|\text{study}) \) or \( y_i | se(se_i) \sim 1 + \text{mod1} + \text{mod2} + (1 + \text{mod1} + \text{mod2}|\text{study}) \), where \text{mod1} and \text{mod2} represent moderator variables. By default, the standard errors replace the parameter \( \sigma \). To model \( \sigma \) in addition to the known standard errors, set argument \text{sigma} in function \text{se} to \text{TRUE}, for instance, \( y_i | se(se_i, \text{sigma} = \text{TRUE}) \sim 1 \).

For all families, weighted regression may be performed using weights in the aterms part. Internally, this is implemented by multiplying the log-posterior values of each observation by their corresponding weights. Suppose that variable \( \text{wei} \) contains the weights and that \( y_i \) is the response variable. Then, formula \( y_i | \text{weights(wei)} \sim \text{predictors} \) implements a weighted regression.

For multivariate models, \text{subset} may be used in the aterms part, to use different subsets of the data in different univariate models. For instance, if \text{sub} is a logical variable and \( y \) is the response of one of the univariate models, we may write \( y | \text{subset(sub)} \sim \text{predictors} \) so that \( y \) is predicted only for those observations for which \text{sub} evaluates to \text{TRUE}.

For log-linear models such as poisson models, \text{rate} may be used in the aterms part to specify the denominator of a response that is expressed as a rate. The numerator is given by the actual response variable and has a distribution according to the family as usual. Using \text{rate(denom)} is equivalent to adding \text{offset(log(denom))} to the linear predictor of the main parameter but the former is arguably more convenient and explicit.
With the exception of categorical and ordinal families, left, right, and interval censoring can be modeled through \( y \mid \text{cens(censored)} \sim \text{predictors} \). The censoring variable (named censored in this example) should contain the values 'left', 'none', 'right', and 'interval' (or equivalently -1, 0, 1, and 2) to indicate that the corresponding observation is left censored, not censored, right censored, or interval censored. For interval censored data, a second variable (let’s call it \( y_2 \)) has to be passed to cens. In this case, the formula has the structure \( y \mid \text{cens(censored, } y_2) \sim \text{predictors} \). While the lower bounds are given in \( y \), the upper bounds are given in \( y_2 \) for interval censored data. Intervals are assumed to be open on the left and closed on the right: \( (y, y_2) \).

With the exception of categorical and ordinal families, the response distribution can be truncated using the trunc function in the addition part. If the response variable is truncated between, say, 0 and 100, we can specify this via \( y_i \mid \text{trunc}(l_b = 0, u_b = 100) \sim \text{predictors} \). Instead of numbers, variables in the data set can also be passed allowing for varying truncation points across observations. Defining only one of the two arguments in trunc leads to one-sided truncation.

For all continuous families, missing values in the responses can be imputed within Stan by using the addition term \( \text{mi} \). This is mostly useful in combination with \( \text{mi} \) predictor terms as explained above under 'Special predictor terms'.

For families binomial and zero_inflated_binomial, addition should contain a variable indicating the number of trials underlying each observation. In lme4 syntax, we may write for instance \( \text{cbind} (\text{success}, n - \text{success}) \), which is equivalent to \( \text{success} \mid \text{trials(n)} \) in \text{brms} syntax. If the number of trials is constant across all observations, say 10, we may also write \( \text{success} \mid \text{trials(10)} \).

Please note that the \text{cbind()} syntax will not work in \text{brms} in the expected way because this syntax is reserved for other purposes.

For all ordinal families, aterms may contain a term \text{thres(number)} to specify the number thresholds (e.g., \text{thres(6)}) which should be equal to the total number of response categories - 1. If not given, the number of thresholds is calculated from the data. If different threshold vectors should be used for different subsets of the data, the \( \text{gr} \) argument can be used to provide the grouping variable (e.g., \text{thres(6, gr = item)}, if \text{item} is the grouping variable). In this case, the number of thresholds can also be a variable in the data with different values per group.

A deprecated quasi alias of \text{thres()} is \text{cat()} with which the total number of response categories (i.e., number of thresholds + 1) can be specified.

In Wiener diffusion models (family \text{wiener}) the addition term \text{dec} is mandatory to specify the (vector of) binary decisions corresponding to the reaction times. Non-zero values will be treated as a response on the upper boundary of the diffusion process and zeros will be treated as a response on the lower boundary. Alternatively, the variable passed to dec might also be a character vector consisting of 'lower' and 'upper'.

All families support the index addition term to uniquely identify each observation of the corresponding response variable. Currently, index is primarily useful in combination with the subset addition and \text{mi} terms.

For custom families, it is possible to pass an arbitrary number of real and integer vectors via the addition terms \( \text{vreal} \) and \( \text{vint} \), respectively. An example is provided in \text{vignette(‘brms_customfamilies’)}. To pass multiple vectors of the same data type, provide them separated by commas inside a single \text{vreal} or \text{vint} statement.

Multiple addition terms of different types may be specified at the same time using the + operator. For example, the formula \text{formula} = \text{yi} \mid \text{se(sei)} + \text{cens(censored)} \sim 1 \text{ implies a censored meta-analytic model.}
The addition argument `disp` (short for dispersion) has been removed in version 2.0. You may instead use the distributional regression approach by specifying `sigma ~ 1 + offset(log(xdisp))` or `shape ~ 1 + offset(log(xdisp))`, where `xdisp` is the variable being previously passed to `disp`.

**Parameterization of the population-level intercept**

By default, the population-level intercept (if incorporated) is estimated separately and not as part of population-level parameter vector `b`. As a result, priors on the intercept also have to be specified separately. Furthermore, to increase sampling efficiency, the population-level design matrix `X` is centered around its column means `X_means` if the intercept is incorporated. This leads to a temporary bias in the intercept equal to `<X_means, b>`, where `<,>` is the scalar product. The bias is corrected after fitting the model, but be aware that you are effectively defining a prior on the intercept of the centered design matrix not on the real intercept. You can turn off this special handling of the intercept by setting argument `center` to `FALSE`. For more details on setting priors on population-level intercepts, see `set_prior`.

This behavior can be avoided by using the reserved (and internally generated) variable `Intercept`. Instead of `y ~ x`, you may write `y ~ 0 + Intercept + x`. This way, priors can be defined on the real intercept, directly. In addition, the intercept is just treated as an ordinary population-level effect and thus priors defined on `b` will also apply to it. Note that this parameterization may be less efficient than the default parameterization discussed above.

**Formula syntax for non-linear models**

In `brms`, it is possible to specify non-linear models of arbitrary complexity. The non-linear model can just be specified within the `formula` argument. Suppose, that we want to predict the response `y` through the predictor `x`, where `x` is linked to `y` through `y = alpha - beta * lambda^x`, with parameters `alpha`, `beta`, and `lambda`. This is certainly a non-linear model being defined via `formula = y ~ alpha - beta * lambda^x` (addition arguments can be added in the same way as for ordinary formulas). To tell `brms` that this is a non-linear model, we set argument `nl` to `TRUE`. Now we have to specify a model for each of the non-linear parameters. Let’s say we just want to estimate those three parameters with no further covariates or random effects. Then we can pass `alpha + beta + lambda ~ 1` or equivalently (and more flexible) `alpha ~ 1, beta ~ 1, lambda ~ 1` to the ... argument. This can, of course, be extended. If we have another predictor `z` and observations nested within the grouping factor `g`, we may write for instance `alpha ~ 1, beta ~ 1 + z + (1|x), lambda ~ 1`. The formula syntax described above applies here as well. In this example, we are using `z` and `g` only for the prediction of `beta`, but we might also use them for the other non-linear parameters (provided that the resulting model is still scientifically reasonable).

By default, non-linear covariates are treated as real vectors in Stan. However, if the data of the covariates is of type `integer` in R (which can be enforced by the `as.integer` function), the Stan type will be changed to an integer array. That way, covariates can also be used for indexing purposes in Stan.

Non-linear models may not be uniquely identified and / or show bad convergence. For this reason it is mandatory to specify priors on the non-linear parameters. For instructions on how to do that, see `set_prior`. For some examples of non-linear models, see vignette("brms_nonlinear").

**Formula syntax for predicting distributional parameters**

It is also possible to predict parameters of the response distribution such as the residual standard deviation `sigma` in gaussian models or the hurdle probability `hu` in hurdle models. The syntax closely resembles that of a non-linear parameter, for instance `sigma ~ x + s(z) + (1|x|g)`. For some examples of distributional models, see vignette("brms_distreg").
Parameter \( \mu \) exists for every family and can be used as an alternative to specifying terms in \( \text{formula} \). If both \( \mu \) and \( \text{formula} \) are given, the right-hand side of \( \text{formula} \) is ignored. Accordingly, specifying terms on the right-hand side of both \( \text{formula} \) and \( \mu \) at the same time is deprecated. In future versions, \( \text{formula} \) might be updated by \( \mu \).

The following are distributional parameters of specific families (all other parameters are treated as non-linear parameters): \( \sigma \) (residual standard deviation or scale of the Gaussian, student, skew_normal, lognormal exgaussian, and asym_laplace families); \( \text{shape} \) (shape parameter of the Gamma, weibull, negbinomial, and related zero-inflated / hurdle families); \( \nu \) (degrees of freedom parameter of the student and frechet families); \( \phi \) (precision parameter of the beta and zero_inflated_beta families); \( \kappa \) (precision parameter of the von_mises family); \( \beta \) (mean parameter of the exponential component of the exgaussian family); \( \text{quantile} \) (quantile parameter of the asym_laplace family); \( \text{zi} \) (zero-inflation probability); \( \text{hu} \) (hurdle probability); \( \text{zoi} \) (zero-one-inflation probability); \( \text{coi} \) (conditional one-inflation probability); \( \text{disc} \) (discrimination) for ordinal models; \( \text{bs} \), \( \text{ndt} \), and \( \text{bias} \) (boundary separation, non-decision time, and initial bias of the wiener diffusion model). By default, distributional parameters are modeled on the log scale if they can be positive only or on the logit scale if they can only be within the unit interval.

Alternatively, one may fix distributional parameters to certain values. However, this is mainly useful when models become too complicated and otherwise have convergence issues. We thus suggest to be generally careful when making use of this option. The \( \text{quantile} \) parameter of the asym_laplace distribution is a good example where it is useful. By fixing \( \text{quantile} \), one can perform quantile regression for the specified quantile. For instance, \( \text{quantile} = 0.25 \) allows predicting the 25%-quantile. Furthermore, the \( \text{bias} \) parameter in drift-diffusion models, is assumed to be 0.5 (i.e. no bias) in many applications. To achieve this, simply write \( \text{bias} = 0.5 \). Other possible applications are the Cauchy distribution as a special case of the Student-t distribution with \( \nu = 1 \), or the geometric distribution as a special case of the negative binomial distribution with \( \text{shape} = 1 \). Furthermore, the parameter \( \text{disc} \) ("discrimination") in ordinal models is fixed to 1 by default and not estimated, but may be modeled as any other distributional parameter if desired (see examples). For reasons of identification, ‘\( \text{disc} \)’ can only be positive, which is achieved by applying the log-link.

In categorical models, distributional parameters do not have fixed names. Instead, they are named after the response categories (excluding the first one, which serves as the reference category), with the prefix ‘\( \mu \)’. If, for instance, categories are named cat1, cat2, and cat3, the distributional parameters will be named mucat2 and mucat3.

Some distributional parameters currently supported by \texttt{brmsformula} have to be positive (a negative standard deviation or precision parameter does not make any sense) or are bounded between 0 and 1 (for zero-inflated / hurdle probabilities, quantiles, or the initial bias parameter of drift-diffusion models). However, linear predictors can be positive or negative, and thus the log link (for positive parameters) or logit link (for probability parameters) are used by default to ensure that distributional parameters are within their valid intervals. This implies that, by default, effects for such distributional parameters are estimated on the log / logit scale and one has to apply the inverse link function to get to the effects on the original scale. Alternatively, it is possible to use the identity link to predict parameters on their original scale, directly. However, this is much more likely to lead to problems in the model fitting, if the parameter actually has a restricted range.

See also \texttt{brmsfamily} for an overview of valid link functions.

**Formula syntax for mixture models**

The specification of mixture models closely resembles that of non-mixture models. If not specified otherwise (see below), all mean parameters of the mixture components are predicted using the right-
hand side of formula. All types of predictor terms allowed in non-mixture models are allowed in mixture models as well.

Distributional parameters of mixture distributions have the same name as those of the corresponding ordinary distributions, but with a number at the end to indicate the mixture component. For instance, if you use family mixture(gaussian, gaussian), the distributional parameters are sigma1 and sigma2. Distributional parameters of the same class can be fixed to the same value. For the above example, we could write sigma2 = “sigma1” to make sure that both components have the same residual standard deviation, which is in turn estimated from the data.

In addition, there are two types of special distributional parameters. The first are named mu<ID>, that allow for modeling different predictors for the mean parameters of different mixture components. For instance, if you want to predict the mean of the first component using predictor x and the mean of the second component using predictor z, you can write mu1 ~ x as well as mu2 ~ z. The second are named theta<ID>, which constitute the mixing proportions. If the mixing proportions are fixed to certain values, they are internally normalized to form a probability vector. If one seeks to predict the mixing proportions, all but one of the them has to be predicted, while the remaining one is used as the reference category to identify the model. The so-called 'softmax' transformation is applied on the linear predictor terms to form a probability vector.

For more information on mixture models, see the documentation of mixture.

Formula syntax for multivariate models

Multivariate models may be specified using mvbind notation or with help of the mvbf function. Suppose that y1 and y2 are response variables and x is a predictor. Then mvbind(y1, y2) ~ x specifies a multivariate model. The effects of all terms specified at the RHS of the formula are assumed to vary across response variables. For instance, two parameters will be estimated for x, one for the effect on y1 and another for the effect on y2. This is also true for group-level effects. When writing, for instance, mvbind(y1, y2) ~ x + (1+x|g), group-level effects will be estimated separately for each response. To model these effects as correlated across responses, use the ID syntax (see above). For the present example, this would look as follows: mvbind(y1, y2) ~ x + (1+x|2|g). Of course, you could also use any value other than 2 as ID.

It is also possible to specify different formulas for different responses. If, for instance, y1 should be predicted by x and y2 should be predicted by z, we could write mvbf(y1 ~ x, y2 ~ z). Alternatively, multiple brmsformula objects can be added to specify a joint multivariate model (see ‘Examples’).

Value

An object of class brmsformula, which is essentially a list containing all model formulas as well as some additional information.

See Also

mvbrmsformula, brmsformula-helpers

Examples

# multilevel model with smoothing terms
brmsformula(y ~ x1*x2 + s(z) + (1+x1|1) + (1|g2))

# additionally predict 'sigma'
brmsformula(y ~ x1*x2 + s(z) + (1+x1|1) + (1|g2),
\[
\text{sigma} \sim x_1 + (1|g2))
\]

# use the shorter alias 'bf'
(formula1 <- brmsformula(y ~ x + (x|g)))
(formula2 <- bf(y ~ x + (x|g)))
# will be TRUE
identical(formula1, formula2)

# incorporate censoring
bf(y | cens(censor_variable) ~ predictors)

# define a simple non-linear model
bf(y ~ a_1 - a_2^x, a_1 + a_2 ~ 1, nl = TRUE)
# predict \(a_1\) and \(a_2\) differently
bf(y ~ a_1 - a_2^x, a_1 ~ 1, a_2 ~ x + (x|g), nl = TRUE)
# correlated group-level effects across parameters
bf(y ~ a_1 - a_2^x, a_1 ~ 1 + (1 | 2 | g), a_2 ~ x + (x | 2 | g), nl = TRUE)
# alternative but equivalent way to specify the above model
bf(y ~ a_1 - a_2^x, a_1 ~ 1 + (1 | gr(g, id = 2)),
a_2 ~ x + (x | gr(g, id = 2)), nl = TRUE)

# define a multivariate model
bf(mvbind(y1, y2) ~ x * z + (1|g))

# define a zero-inflated model
# also predicting the zero-inflation part
bf(y ~ x * z + (1+x|ID1|g), zi ~ x + (1|ID1|g))

# specify a predictor as monotonic
bf(y ~ mo(x) + more_predictors)
# for ordinal models only
# specify a predictor as category specific
bf(y ~ cs(x) + more_predictors)
# add a category specific group-level intercept
bf(y ~ cs(x) + (cs(1)|g))
# specify parameter 'disc'
bf(y ~ person + item, disc ~ item)

# specify variables containing measurement error
bf(y ~ me(x, sdx))

# specify predictors on all parameters of the wiener diffusion model
# the main formula models the drift rate 'delta'
bf(rt | dec(decision) ~ x, bs ~ x, ndt ~ x, bias ~ x)

# fix the bias parameter to 0.5
bf(rt | dec(decision) ~ x, bias = 0.5)

# specify different predictors for different mixture components
mix <- mixture(gaussian, gaussian)
bf(y ~ 1, mu1 ~ x, mu2 ~ z, family = mix)

# fix both residual standard deviations to the same value
bf(y ~ x, sigma2 = "sigma", family = mix)

# use the '+' operator to specify models
bf(y ~ 1) +
  nlf(sigma ~ a * exp(b * x), a ~ x) +
  lf(b ~ z + (1|g), dpar = "sigma") +
  gaussian()

# specify a multivariate model using the '+' operator
bf(y1 ~ x + (1|g)) +
  gaussian() + cor_ar(~1|g) +
  bf(y2 ~ z) + poisson()

# specify correlated residuals of a gaussian and a poisson model
form1 <- bf(y1 ~ 1 + x + (1|g), sigma = 1) + gaussian()
form2 <- bf(y2 ~ 1 + x + (1|g)) + poisson()

# model missing values in predictors
bf(bmi ~ age * mi(chl)) +
  bf(chl | mi() ~ age) +
  set_rescor(FALSE)

# model sigma as a function of the mean
bf(y ~ eta, nl = TRUE) +
  lf(eta ~ 1 + x) +
  nlf(sigma ~ tau * sqrt(eta)) +
  lf(tau ~ 1)

---

brmsformula-helpers  Linear and Non-linear formulas in brms

Description

Helper functions to specify linear and non-linear formulas for use with brmsformula.

Usage

nlf(formula, ..., flist = NULL, dpar = NULL, resp = NULL, loop = NULL)

lf(
  ...,
  flist = NULL,
  dpar = NULL,
  resp = NULL,
  center = NULL,
Arguments

formula  Non-linear formula for a distributional parameter. The name of the distributional parameter can either be specified on the left-hand side of formula or via argument dpar.

...  Additional formula objects to specify predictors of non-linear and distributional parameters. Formulas can either be named directly or contain names on their left-hand side. Alternatively, it is possible to fix parameters to certain values by passing numbers or character strings in which case arguments have to be named to provide the parameter names. See 'Details' for more information.

flist  Optional list of formulas, which are treated in the same way as formulas passed via the ... argument.

dpar  Optional character string specifying the distributional parameter to which the formulas passed via ... and flist belong.

resp  Optional character string specifying the response variable to which the formulas passed via ... and flist belong. Only relevant in multivariate models.

loop  Logical; Only used in non-linear models. Indicates if the computation of the non-linear formula should be done inside (TRUE) or outside (FALSE) a loop over observations. Defaults to TRUE.

center  Logical; Indicates if the population-level design matrix should be centered, which usually increases sampling efficiency. See the 'Details' section for more information. Defaults to TRUE for distributional parameters and to FALSE for non-linear parameters.

cmc  Logical; Indicates whether automatic cell-mean coding should be enabled when removing the intercept by adding 0 to the right-hand of model formulas. Defaults to TRUE to mirror the behavior of standard R formula parsing.

sparse  Logical; indicates whether the population-level design matrices should be treated as sparse (defaults to FALSE). For design matrices with many zeros, this can considerably reduce required memory. Sampling speed is currently not improved or even slightly decreased.

decom  Optional name of the decomposition used for the population-level design matrix. Defaults to NULL that is no decomposition. Other options currently available are "QR" for the QR decomposition that helps in fitting models with highly correlated predictors.
A one sided formula containing autocorrelation terms. All none autocorrelation terms in autocor will be silently ignored.

Logical; Indicates whether formula should be treated as specifying a non-linear model. By default, formula is treated as an ordinary linear model formula.

Logical; Indicates if residual correlation between the response variables should be modeled. Currently this is only possible in multivariate gaussian and student models. Only relevant in multivariate models.

Logical; Indicates if correlations between latent variables defined by me terms should be modeled. Defaults to TRUE.

For lf and nlf a list that can be passed to brmsformula or added to an existing brmsformula or mvbrmsformula object. For set_nl and set_rescor a logical value that can be added to an existing brmsformula or mvbrmsformula object.

# add more formulas to the model
bf(y ~ 1) +
  nlf(sigma ~ a * exp(b * x)) +
  lf(a ~ x, b ~ z + (1|g)) +
  gaussian()

# specify 'nl' later on
bf(y ~ a * inv_logit(x * b)) +
  lf(a + b ~ z) +
  set_nl(TRUE)

# specify a multivariate model
bf(y1 ~ x + (1|g)) +
  bf(y2 ~ z) +
  set_rescor(TRUE)

# add autocorrelation terms
bf(y ~ x) + acformula(~ arma(p = 1, q = 1) + car(W))

A brmshypothesis object contains posterior draws as well as summary statistics of non-linear hypotheses as returned by hypothesis.
Usage

## S3 method for class 'brmshypothesis'
print(x, digits = 2, chars = 20, ...)

## S3 method for class 'brmshypothesis'
plot(
x, 
N = 5,
ignore_prior = FALSE,
chars = 40,
colors = NULL,
theme = NULL,
ask = TRUE,
plot = TRUE,
...
)

Arguments

x An object of class brmsfit.
digits Minimal number of significant digits, see print.default.
chars Maximum number of characters of each hypothesis to print or plot. If NULL, print the full hypotheses. Defaults to 20.
... Currently ignored.
N The number of parameters plotted per page.
ignore_prior A flag indicating if prior distributions should also be plotted. Only used if priors were specified on the relevant parameters.
colors Two values specifying the colors of the posterior and prior density respectively. If NULL (the default) colors are taken from the current color scheme of the bayesplot package.
theme A theme object modifying the appearance of the plots. For some basic themes see ggtheme and theme_default.
ask Logical; indicates if the user is prompted before a new page is plotted. Only used if plot is TRUE.
plot Logical; indicates if plots should be plotted directly in the active graphic device. Defaults to TRUE.

Details

The two most important elements of a brmshypothesis object are hypothesis, which is a data.frame containing the summary estimates of the hypotheses, and samples, which is a data.frame containing the corresponding posterior draws.

See Also

hypothesis
Parse Formulas of \texttt{brms} Models

Description

Parse formulas objects for use in \texttt{brms}.

Usage

\begin{verbatim}
brmsterms(formula, ...)

## Default S3 method:
brmsterms(formula, ...)

## S3 method for class 'brmsformula'
brmsterms(formula, check_response = TRUE, resp_rhs_all = TRUE, ...)

## S3 method for class 'mvbrmsformula'
brmsterms(formula, ...)
\end{verbatim}

Arguments

\begin{itemize}
\item \texttt{formula} \hspace{1cm} An object of class \texttt{formula}, \texttt{brmsformula}, or \texttt{mvbrmsformula} (or one that can be coerced to that classes): A symbolic description of the model to be fitted. The details of model specification are explained in \texttt{brmsformula}.
\item \texttt{...} \hspace{1cm} Further arguments passed to or from other methods.
\item \texttt{check_response} Logical; Indicates whether the left-hand side of \texttt{formula} (i.e. response variables and addition arguments) should be parsed. If \texttt{FALSE}, \texttt{formula} may also be one-sided.
\item \texttt{resp_rhs_all} Logical; Indicates whether to also include response variables on the right-hand side of \texttt{formula}. \texttt{.allvars}, where \texttt{.} represents the output of \texttt{brmsterms}.
\end{itemize}

Details

This is the main formula parsing function of \texttt{brms}. It should usually not be called directly, but is exported to allow package developers making use of the formula syntax implemented in \texttt{brms}. As long as no other packages depend on this functions, it may be changed without deprecation warnings, when new features make this necessary.

Value

An object of class \texttt{brmsterms} or \texttt{mvbrmsterms} (for multivariate models), which is a list containing all required information initially stored in \texttt{formula} in an easier to use format, basically a list of formulas (not an abstract syntax tree).
**brm_multiple**

**See Also**

`brm`, `brmsformula`, `mvbrmsformula`

---

**Description**

Run the same `brms` model on multiple datasets and then combine the results into one fitted model object. This is useful in particular for multiple missing value imputation, where the same model is fitted on multiple imputed data sets. Models can be run in parallel using the `future` package.

**Usage**

```r
brm_multiple(
  formula,
  data,
  family = gaussian(),
  prior = NULL,
  data2 = NULL,
  autocor = NULL,
  cov_ranef = NULL,
  sample_prior = c("no", "yes", "only"),
  sparse = NULL,
  knots = NULL,
  stanvars = NULL,
  stan_funs = NULL,
  silent = 1,
  recompile = FALSE,
  combine = TRUE,
  fit = NA,
  algorithm =getOption("brms.algorithm", "sampling"),
  seed = NA,
  file = NULL,
  file_refit = "never",
  ...
)
```

**Arguments**

- `formula`: An object of class `formula`, `brmsformula`, or `mvbrmsformula` (or one that can be coerced to that classes): A symbolic description of the model to be fitted. The details of model specification are explained in `brmsformula`.

- `data`: A `list` of data.frames each of which will be used to fit a separate model. Alternatively, a `mids` object from the `mice` package.
family
A description of the response distribution and link function to be used in the model. This can be a family function, a call to a family function or a character string naming the family. Every family function has a link argument allowing to specify the link function to be applied on the response variable. If not specified, default links are used. For details of supported families see `brmsfamily`. By default, a linear gaussian model is applied. In multivariate models, family might also be a list of families.

prior
One or more `brmsprior` objects created by `set_prior` or related functions and combined using the `c` method or the `+` operator. See also `get_prior` for more help.

data2
A list of named lists each of which will be used to fit a separate model. Each of the named lists contains objects representing data which cannot be passed via argument data (see `brm` for examples). The length of the outer list should match the length of the list passed to the data argument.

autocor
(Deprecated) An optional `cor_brms` object describing the correlation structure within the response variable (i.e., the 'autocorrelation'). See the documentation of `cor_brms` for a description of the available correlation structures. Defaults to NULL, corresponding to no correlations. In multivariate models, autocor might also be a list of autocorrelation structures. It is now recommend to specify autocorrelation terms directly within formula. See `brmsformula` for more details.

cov_ranef
(Deprecated) A list of matrices that are proportional to the (within) covariance structure of the group-level effects. The names of the matrices should correspond to columns in data that are used as grouping factors. All levels of the grouping factor should appear as rownames of the corresponding matrix. This argument can be used, among others to model pedigrees and phylogenetic effects. It is now recommended to specify those matrices in the formula interface using the `gr` and related functions. See vignette("brms_phylogenetics") for more details.

sample_prior
Indicate if draws from priors should be drawn additionally to the posterior draws. Options are "no" (the default), "yes", and "only". Among others, these draws can be used to calculate Bayes factors for point hypotheses via `hypothesis`. Please note that improper priors are not sampled, including the default improper priors used by `brm`. See `set_prior` on how to set (proper) priors. Please also note that prior draws for the overall intercept are not obtained by default for technical reasons. See `brmsformula` how to obtain prior draws for the intercept. If `sample_prior` is set to "only", draws are drawn solely from the priors ignoring the likelihood, which allows among others to generate draws from the prior predictive distribution. In this case, all parameters must have proper priors.

sparse
(Deprecated) Logical; indicates whether the population-level design matrices should be treated as sparse (defaults to `FALSE`). For design matrices with many zeros, this can considerably reduce required memory. Sampling speed is currently not improved or even slightly decreased. It is now recommended to use the sparse argument of `brmsformula` and related functions.

knots
Optional list containing user specified knot values to be used for basis construction of smoothing terms. See `gamm` for more details.

stanvars
An optional `stanvars` object generated by function `stanvar` to define additional variables for use in Stan's program blocks.
### brm_multiple

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>stan_funs</strong></td>
<td>(Deprecated) An optional character string containing self-defined Stan functions, which will be included in the functions block of the generated Stan code. It is now recommended to use the stanvars argument for this purpose instead.</td>
</tr>
<tr>
<td><strong>silent</strong></td>
<td>Verbosity level between 0 and 2. If 1 (the default), most of the informational messages of compiler and sampler are suppressed. If 2, even more messages are suppressed. The actual sampling progress is still printed. Set <code>refresh = 0</code> to turn this off as well. If using <code>backend = &quot;rstan&quot;</code> you can also set <code>open_progress = FALSE</code> to prevent opening additional progress bars.</td>
</tr>
<tr>
<td><strong>recompile</strong></td>
<td>Logical, indicating whether the Stan model should be recompiled for every imputed data set. Defaults to <code>FALSE</code>. If <code>NULL</code>, <code>brm_multiple</code> tries to figure out internally, if recompilation is necessary, for example because data-dependent priors have changed. Using the default of no recompilation should be fine in most cases.</td>
</tr>
<tr>
<td><strong>combine</strong></td>
<td>Logical; Indicates if the fitted models should be combined into a single fitted model object via <code>combine_models</code>. Defaults to <code>TRUE</code>.</td>
</tr>
<tr>
<td><strong>fit</strong></td>
<td>An instance of S3 class <code>brmsfit_multiple</code> derived from a previous fit; defaults to <code>NA</code>. If <code>fit</code> is of class <code>brmsfit_multiple</code>, the compiled model associated with the fitted result is re-used and all arguments modifying the model code or data are ignored. It is not recommended to use this argument directly, but to call the <code>update</code> method, instead.</td>
</tr>
<tr>
<td><strong>algorithm</strong></td>
<td>Character string naming the estimation approach to use. Options are &quot;sampling&quot; for MCMC (the default), &quot;meanfield&quot; for variational inference with independent normal distributions, &quot;fullrank&quot; for variational inference with a multivariate normal distribution, or &quot;fixed_param&quot; for sampling from fixed parameter values. Can be set globally for the current R session via the &quot;brms.algorithm&quot; option (see <code>options</code>).</td>
</tr>
<tr>
<td><strong>seed</strong></td>
<td>The seed for random number generation to make results reproducible. If <code>NA</code> (the default), Stan will set the seed randomly.</td>
</tr>
<tr>
<td><strong>file</strong></td>
<td>Either <code>NULL</code> or a character string. In the latter case, the fitted model object is saved via <code>saveRDS</code> in a file named after the string supplied in <code>file</code>. The <code>.rds</code> extension is added automatically. If the file already exists, <code>brm</code> will load and return the saved model object instead of refitting the model. Unless you specify the <code>file_refit</code> argument as well, the existing files won't be overwritten, you have to manually remove the file in order to refit and save the model under an existing file name. The file name is stored in the <code>brmsfit</code> object for later usage.</td>
</tr>
<tr>
<td><strong>file_refit</strong></td>
<td>Modifies when the fit stored via the <code>file</code> parameter is re-used. Can be set globally for the current R session via the &quot;brms.file_refit&quot; option (see <code>options</code>). For &quot;never&quot; (default) the fit is always loaded if it exists and fitting is skipped. For &quot;always&quot; the model is always refitted. If set to &quot;on_change&quot;, <code>brms</code> will refit the model if model, data or algorithm as passed to Stan differ from what is stored in the file. This also covers changes in priors, sample_prior, stanvars, covariance structure, etc. If you believe there was a false positive, you can use <code>brmsfit_needs_refit</code> to see why refit is deemed necessary. Refit will not be triggered for changes in additional parameters of the fit (e.g., initial values, number of iterations, control arguments, ...). A known limitation is that a refit will be triggered if within-chain parallelization is switched on/off.</td>
</tr>
</tbody>
</table>

... Further arguments passed to `brm`. 

---

*This text was generated from the source code using a natural language processing model.*
Details

The combined model may issue false positive convergence warnings, as the MCMC chains corresponding to different datasets may not necessarily overlap, even if each of the original models did converge. To find out whether each of the original models converged, investigate \texttt{fit$rhats}, where \texttt{fit} denotes the output of \texttt{brm_multiple}.

Value

If \texttt{combine = TRUE} a \texttt{brmsfit_multiple} object, which inherits from class \texttt{brmsfit} and behaves essentially the same. If \texttt{combine = FALSE} a list of \texttt{brmsfit} objects.

Author(s)

Paul-Christian Buerkner <paul.buerkner@gmail.com>

Examples

```r
## Not run:
library(mice)
imp <- mice(nhanes2)

# fit the model using mice and \texttt{lm}
fit_imp1 <- with(lm(bmi ~ age + hyp + chl), data = imp)
summary(pool(fit_imp1))

# fit the model using \texttt{brms}
fit_imp2 <- brm_multiple(bmi ~ age + hyp + chl, data = imp, chains = 1)
summary(fit_imp2)
plot(fit_imp2, pars = "^b_")
# investigate convergence of the original models
fit_imp2$rhats

# use the future package for parallelization
library(future)
plan(multiprocess)
fit_imp3 <- brm_multiple(bmi~age+hyp+chl, data = imp, chains = 1)
summary(fit_imp3)
## End(Not run)
```

---

car  

Spatial conditional autoregressive (CAR) structures

Description

Set up an spatial conditional autoregressive (CAR) term in \texttt{brms}. The function does not evaluate its arguments – it exists purely to help set up a model with CAR terms.
Usage

car(M, gr = NA, type = "escar")

Arguments

M
Adjacent matrix of locations. All non-zero entries are treated as if the two locations are adjacent. If gr is specified, the row names of M have to match the levels of the grouping factor.

gr
An optional grouping factor mapping observations to spatial locations. If not specified, each observation is treated as a separate location. It is recommended to always specify a grouping factor to allow for handling of new data in post-processing methods.

type
Type of the CAR structure. Currently implemented are "escar" (exact sparse CAR), "esicar" (exact sparse intrinsic CAR), "icar" (intrinsic CAR), and "bym2". More information is provided in the 'Details' section.

Details

The escar and esicar types are implemented based on the case study of Max Joseph (https://github.com/mbjoseph/CARstan). The icar and bym2 type is implemented based on the case study of Mitzi Morris (https://mc-stan.org/users/documentation/case-studies/icar_stan.html).

Value

An object of class 'car_term', which is a list of arguments to be interpreted by the formula parsing functions of brms.

See Also

autocor-terms

Examples

## Not run:
# generate some spatial data
east <- north <- 1:10
Grid <- expand.grid(east, north)
K <- nrow(Grid)

# set up distance and neighbourhood matrices
distance <- as.matrix(dist(Grid))
W <- array(0, c(K, K))
W[distance == 1] <- 1

# generate the covariates and response data
x1 <- rnorm(K)
x2 <- rnorm(K)
theta <- rnorm(K, sd = 0.05)
phi <- rmulti_normal(
  1, mu = rep(0, K), Sigma = 0.4 * exp(-0.1 * distance)
eta <- x1 + x2 + phi
prob <- exp(eta) / (1 + exp(eta))
size <- rep(50, K)
y <- rbinom(n = K, size = size, prob = prob)
dat <- data.frame(y, size, x1, x2)

# fit a CAR model
fit <- brm(y | trials(size) ~ x1 + x2 + car(W),
          data = dat, data2 = list(W = W),
          family = binomial())
summary(fit)

## End(Not run)

### coef.brmsfit

#### Extract Model Coefficients

**Description**

Extract model coefficients, which are the sum of population-level effects and corresponding group-level effects

**Usage**

```r
## S3 method for class 'brmsfit'
coef(object, summary = TRUE, robust = FALSE, probs = c(0.025, 0.975), ...)
```

**Arguments**

- `object`: An object of class `brmsfit`.
- `summary`: Should summary statistics be returned instead of the raw values? Default is `TRUE`.
- `robust`: If `FALSE` (the default) the mean is used as the measure of central tendency and the standard deviation as the measure of variability. If `TRUE`, the median and the median absolute deviation (MAD) are applied instead. Only used if `summary` is `TRUE`.
- `probs`: The percentiles to be computed by the quantile function. Only used if `summary` is `TRUE`.
- `...`: Further arguments passed to `fixef.brmsfit` and `ranef.brmsfit`.

**Value**

A list of 3D arrays (one per grouping factor). If `summary` is `TRUE`, the 1st dimension contains the factor levels, the 2nd dimension contains the summary statistics (see `posterior_summary`), and the 3rd dimension contains the group-level effects. If `summary` is `FALSE`, the 1st dimension contains the posterior draws, the 2nd dimension contains the factor levels, and the 3rd dimension contains the group-level effects.
Examples

```r
## Not run:
fit <- brm(count ~ zAge + zBase * Trt + (1+Trt|visit),
  data = epilepsy, family = gaussian(), chains = 2)
## extract population and group-level coefficients separately
fixef(fit)
ranef(fit)
## extract combined coefficients
coef(fit)
## End(Not run)
```

**combine_models**

*Combine Models fitted with brms*

**Description**

Combine multiple `brmsfit` objects, which fitted the same model. This is usefully for instance when having manually run models in parallel.

**Usage**

```r
combine_models(..., mlist = NULL, check_data = TRUE)
```

**Arguments**

- `...`: One or more `brmsfit` objects.
- `mlist`: Optional list of one or more `brmsfit` objects.
- `check_data`: Logical; indicates if the data should be checked for being the same across models (defaults to `TRUE`). Setting it to `FALSE` may be useful for instance when combining models fitted on multiple imputed data sets.

**Details**

This function just takes the first model and replaces its `stanfit` object (slot `fit`) by the combined `stanfit` objects of all models.

**Value**

A `brmsfit` object.
compare_ic

Compare Information Criteria of Different Models

Description

Compare information criteria of different models fitted with waic or loo. Deprecated and will be removed in the future. Please use loo_compare instead.

Usage

compare_ic(..., x = NULL, ic = c("loo", "waic", "kfold"))

Arguments

... At least two objects returned by waic or loo. Alternatively, brmsfit objects with information criteria precomputed via add_ic may be passed, as well.

x A list containing the same types of objects as can be passed via ....

ic The name of the information criterion to be extracted from brmsfit objects. Ignored if information criterion objects are only passed directly.

Details

See loo_compare for the recommended way of comparing models with the loo package.

Value

An object of class iclist.

See Also

loo, loo_compare addCriterion

Examples

## Not run:
# model with population-level effects only
fit1 <- brm(rating ~ treat + period + carry, 
data = inhaler)
waic1 <- waic(fit1)

# model with an additional varying intercept for subjects
fit2 <- brm(rating ~ treat + period + carry + (1|subject),
data = inhaler)
waic2 <- waic(fit2)

# compare both models
compare_ic(waic1, waic2)
## Display Conditional Effects of Predictors

### Description
Display conditional effects of one or more numeric and/or categorical predictors including two-way interaction effects.

### Usage
```r
## S3 method for class 'brmsfit'
conditional_effects(
  x,
  effects = NULL,
  conditions = NULL,
  int_conditions = NULL,
  re_formula = NA,
  prob = 0.95,
  robust = TRUE,
  method = "posterior_epred",
  spaghetti = FALSE,
  surface = FALSE,
  categorical = FALSE,
  ordinal = FALSE,
  transform = NULL,
  resolution = 100,
  select_points = 0,
  too_far = 0,
  probs = NULL,
  ...
)

conditional_effects(x, ...)

## S3 method for class 'brms_conditional_effects'
plot(
  x,
  ncol = NULL,
  points =getOption("brms.plot_points", FALSE),
  rug =getOption("brms.plot_rug", FALSE),
  mean = TRUE,
  jitter_width = 0,
  stype = c("contour", "raster"),
)```
Arguments

x
An object of class \texttt{brmsfit}.

effects
An optional character vector naming effects (main effects or interactions) for which to compute conditional plots. Interactions are specified by a : between variable names. If \texttt{NULL} (the default), plots are generated for all main effects and two-way interactions estimated in the model. When specifying \texttt{effects} manually, \textit{all} two-way interactions (including grouping variables) may be plotted even if not originally modeled.

conditions
An optional \texttt{data.frame} containing variable values to condition on. Each effect defined in \texttt{effects} will be plotted separately for each row of \texttt{conditions}. Values in the \texttt{cond__} column will be used as titles of the subplots. If \texttt{cond__} is not given, the row names will be used for this purpose instead. It is recommended to only define a few rows in order to keep the plots clear. See \texttt{make_conditions} for an easy way to define conditions. If \texttt{NULL} (the default), numeric variables will be conditionalized by using their means and factors will get their first level assigned. \texttt{NA} values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.

int_conditions
An optional named \texttt{list} whose elements are vectors of values of the variables specified in \texttt{effects}. At these values, predictions are evaluated. The names of \texttt{int_conditions} have to match the variable names exactly. Additionally, the elements of the vectors may be named themselves, in which case their names appear as labels for the conditions in the plots. Instead of vectors, functions returning vectors may be passed and are applied on the original values of the corresponding variable. If \texttt{NULL} (the default), predictions are evaluated at the \texttt{mean} and at \texttt{mean + / − sd} for numeric predictors and at all categories for factor-like predictors.

re_formula
A formula containing group-level effects to be considered in the conditional predictions. If \texttt{NULL}, include all group-level effects; if \texttt{NA} (default), include no group-level effects.

prob
A value between 0 and 1 indicating the desired probability to be covered by the uncertainty intervals. The default is 0.95.
Conditional Effects (brmsfit)

**robust**
If TRUE (the default) the median is used as the measure of central tendency. If FALSE the mean is used instead.

**method**
Method used to obtain predictions. Can be set to "posterior_epred" (the default), "posterior_predict", or "posterior_linpred". For more details, see the respective function documentations.

**spaghetti**
Logical. Indicates if predictions should be visualized via spaghetti plots. Only applied for numeric predictors. If TRUE, it is recommended to set argument n_draws to a relatively small value (e.g., 100) in order to reduce computation time.

**surface**
Logical. Indicates if interactions or two-dimensional smooths should be visualized as a surface. Defaults to FALSE. The surface type can be controlled via argument stype of the related plotting method.

**categorical**
Logical. Indicates if effects of categorical or ordinal models should be shown in terms of probabilities of response categories. Defaults to FALSE.

**ordinal**
(Deprecated) Please use argument categorical. Logical. Indicates if effects in ordinal models should be visualized as a raster with the response categories on the y-axis. Defaults to FALSE.

**transform**
A function or a character string naming a function to be applied on the predicted responses before summary statistics are computed. Only allowed if method = "posterior_predict".

**resolution**
Number of support points used to generate the plots. Higher resolution leads to smoother plots. Defaults to 100. If surface is TRUE, this implies 10000 support points for interaction terms, so it might be necessary to reduce resolution when only few RAM is available.

**select_points**
Positive number. Only relevant if points or rug are set to TRUE: Actual data points of numeric variables that are too far away from the values specified in conditions can be excluded from the plot. Values are scaled into the unit interval and then points more than select_points from the values in conditions are excluded. By default, all points are used.

**too_far**
Positive number. For surface plots only: Grid points that are too far away from the actual data points can be excluded from the plot. too_far determines what is too far. The grid is scaled into the unit square and then grid points more than too_far from the predictor variables are excluded. By default, all grid points are used. Ignored for non-surface plots.

**probs**
(Deprecated) The quantiles to be used in the computation of uncertainty intervals. Please use argument prob instead.

**...**
Further arguments such as draw_ids or n_draws passed to posterior_predict or posterior_epred.

**ncol**
Number of plots to display per column for each effect. If NULL (default), ncol is computed internally based on the number of rows of conditions.

**points**
Logical. Indicates if the original data points should be added via geom_jitter. Default is FALSE. Can be controlled globally via the brms.plot.points option. Note that only those data points will be added that match the specified conditions defined in conditions. For categorical predictors, the conditions have to match exactly. For numeric predictors, argument select_points is used to determine, which points do match a condition.
rug Logical. Indicates if a rug representation of predictor values should be added via `geom_rug`. Default is FALSE. Depends on `select_points` in the same way as points does. Can be controlled globally via the `brms.plot_rug` option.

mean Logical. Only relevant for spaghetti plots. If TRUE (the default), display the mean regression line on top of the regression lines for each sample.

jitter_width Only used if `points` = TRUE: Amount of horizontal jittering of the data points. Mainly useful for ordinal models. Defaults to 0 that is no jittering.

stype Indicates how surface plots should be displayed. Either "contour" or "raster".

line_args Only used in plots of continuous predictors: A named list of arguments passed to `geom_smooth`.

cat_args Only used in plots of categorical predictors: A named list of arguments passed to `geom_point`.

errorbar_args Only used in plots of categorical predictors: A named list of arguments passed to `geom_errorbar`.

surface_args Only used in surface plots: A named list of arguments passed to `geom_contour` or `geom_raster` (depending on argument `stype`).

spaghetti_args Only used in spaghetti plots: A named list of arguments passed to `geom_smooth`.

point_args Only used if `points` = TRUE: A named list of arguments passed to `geom_jitter`.

rug_args Only used if `rug` = TRUE: A named list of arguments passed to `geom_rug`.

facet_args Only used if multiple conditions are provided: A named list of arguments passed to `facet_wrap`.

theme A `theme` object modifying the appearance of the plots. For some basic themes see `ggtheme` and `theme_default`.

ask Logical; indicates if the user is prompted before a new page is plotted. Only used if `plot` is TRUE.

plot Logical; indicates if plots should be plotted directly in the active graphic device. Defaults to TRUE.

Details

When creating `conditional_effects` for a particular predictor (or interaction of two predictors), one has to choose the values of all other predictors to condition on. By default, the mean is used for continuous variables and the reference category is used for factors, but you may change these values via argument conditions. This also has an implication for the points argument: In the created plots, only those points will be shown that correspond to the factor levels actually used in the conditioning, in order not to create the false impression of bad model fit, where it is just due to conditioning on certain factor levels.

To fully change colors of the created plots, one has to amend both `scale_colour` and `scale_fill`. See `scale_colour_grey` or `scale_colour_gradient` for more details.

Value

An object of class 'brms_conditional_effects' which is a named list with one data.frame per effect containing all information required to generate conditional effects plots. Among others, these
data.frames contain some special variables, namely `estimate__` (predicted values of the response), `se__` (standard error of the predicted response), `lower__` and `upper__` (lower and upper bounds of the uncertainty interval of the response), as well as `cond__` (used in faceting when conditions contain multiple rows).

The corresponding `plot` method returns a named list of `ggplot` objects, which can be further customized using the `ggplot2` package.

**Examples**

```r
## Not run:
fit <- brm(count ~ zAge + zBase * Trt + (1 | patient),
            data = epilepsy, family = poisson())
## plot all conditional effects
plot(conditional_effects(fit), ask = FALSE)

## change colours to grey scale
library(ggplot2)
ce <- conditional_effects(fit, "zBase:Trt")
plot(ce, plot = FALSE)[[1]] +
   scale_color_grey() +
   scale_fill_grey()

## only plot the conditional interaction effect of "zBase:Trt"
## for different values for "zAge"
conditions <- data.frame(zAge = c(-1, 0, 1))
plot(conditional_effects(fit, effects = "zBase:Trt",
                       conditions = conditions))

## also incorporate group-level effects variance over patients
## also add data points and a rug representation of predictor values
plot(conditional_effects(fit, effects = "zBase:Trt",
                        conditions = conditions, re_formula = NULL),
     points = TRUE, rug = TRUE)

## change handling of two-way interactions
int_conditions <- list(
    zBase = setNames(c(-2, 1, 0), c("b", "c", "a"))
)
conditional_effects(fit, effects = "Trt:zBase",
                    int_conditions = int_conditions)
conditional_effects(fit, effects = "Trt:zBase",
                    int_conditions = list(zBase = quantile))

## fit a model to illustrate how to plot 3-way interactions
fit3way <- brm(count ~ zAge * zBase * Trt, data = epilepsy)
conditions <- make_conditions(fit3way, "zAge")
conditional_effects(fit3way, "zBase:Trt", conditions = conditions)
## only include points close to the specified values of zAge
c <- conditional_effects(
    fit3way, "zBase:Trt", conditions = conditions,
    select_points = 0.1)
```
### conditional_smooths.brmsfit

#### Display Smooth Terms

**Description**

Display smooth s and t2 terms of models fitted with `brms`.

**Usage**

```r
## S3 method for class 'brmsfit'
conditional_smooths(
  x,
  smooths = NULL,
  int_conditions = NULL,
  prob = 0.95,
  spaghetti = FALSE,
  resolution = 100,
  too_far = 0,
  ndraws = NULL,
  draw_ids = NULL,
  nsamples = NULL,
  subset = NULL,
  probs = NULL,
  ...
)
```

**Arguments**

- `x` An object of class `brmsfit`.
- `smooths` Optional character vector of smooth terms to display. If NULL (the default) all smooth terms are shown.
- `int_conditions` An optional named list whose elements are vectors of values of the variables specified in `effects`. At these values, predictions are evaluated. The names of `int_conditions` have to match the variable names exactly. Additionally, the elements of the vectors may be named themselves, in which case their names appear as labels for the conditions in the plots. Instead of vectors, functions returning vectors may be passed and are applied on the original values of the corresponding variable. If NULL (the default), predictions are evaluated at the
mean and at mean $\pm sd$ for numeric predictors and at all categories for factor-like predictors.

prob
A value between 0 and 1 indicating the desired probability to be covered by the uncertainty intervals. The default is 0.95.

spaghetti
Logical. Indicates if predictions should be visualized via spaghetti plots. Only applied for numeric predictors. If TRUE, it is recommended to set argument ndraws to a relatively small value (e.g., 100) in order to reduce computation time.

resolution
Number of support points used to generate the plots. Higher resolution leads to smoother plots. Defaults to 100. If surface is TRUE, this implies 10000 support points for interaction terms, so it might be necessary to reduce resolution when only few RAM is available.

too_far
Positive number. For surface plots only: Grid points that are too far away from the actual data points can be excluded from the plot. too_far determines what is too far. The grid is scaled into the unit square and then grid points more than too_far from the predictor variables are excluded. By default, all grid points are used. Ignored for non-surface plots.

ndraws
Positive integer indicating how many posterior draws should be used. If NULL (the default) all draws are used. Ignored if draw_ids is not NULL.

draw_ids
An integer vector specifying the posterior draws to be used. If NULL (the default), all draws are used.

nsamples
Deprecated alias of ndraws.

subset
Deprecated alias of draw_ids.

probs
(Deprecated) The quantiles to be used in the computation of uncertainty intervals. Please use argument prob instead.

... Currently ignored.

Details
Two-dimensional smooth terms will be visualized using either contour or raster plots.

Value
For the brmsfit method, an object of class brms_conditional_effects. See conditional_effects for more details and documentation of the related plotting function.

Examples
```r
## Not run:
set.seed(0)
dat <- mgcv::gamSim(1, n = 200, scale = 2)
fit <- brm(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = dat)
# show all smooth terms
plot(conditional_smooths(fit), rug = TRUE, ask = FALSE)
# show only the smooth term s(x2)
plot(conditional_smooths(fit, smooths = "s(x2)"), ask = FALSE)
```
# fit and plot a two-dimensional smooth term
fit2 <- brm(y ~ t2(x0, x2), data = dat)
ms <- conditional_smooths(fit2)
plot(ms, stype = "contour")
plot(ms, stype = "raster")

## End(Not run)

control_params  

**Extract Control Parameters of the NUTS Sampler**

**Description**

Extract control parameters of the NUTS sampler such as `adapt_delta` or `max_treedepth`.

**Usage**

```r
control_params(x, ...)
```

## S3 method for class 'brmsfit'
control_params(x, pars = NULL, ...)

**Arguments**

- `x`: An R object
- `...`: Currently ignored.
- `pars`: Optional names of the control parameters to be returned. If `NULL` (the default) all control parameters are returned. See `stan` for more details.

**Value**

A named list with control parameter values.

cor_ar  

**(Deprecated) AR(p) correlation structure**

**Description**

This function is deprecated. Please see `ar` for the new syntax. This function is a constructor for the `cor_arma` class, allowing for autoregression terms only.

**Usage**

```r
cor_ar(formula = ~1, p = 1, cov = FALSE)
```
cor_arma

Arguments

- **formula**: A one sided formula of the form \( \sim t \), or \( \sim t \ | g \), specifying a time covariate \( t \) and, optionally, a grouping factor \( g \). A covariate for this correlation structure must be integer valued. When a grouping factor is present in `formula`, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to \( \sim 1 \), which corresponds to using the order of the observations in the data as a covariate, and no groups.

- **p**: A non-negative integer specifying the autoregressive (AR) order of the ARMA structure. Default is 1.

- **cov**: A flag indicating whether ARMA effects should be estimated by means of residual covariance matrices. This is currently only possible for stationary ARMA effects of order 1. If the model family does not have natural residuals, latent residuals are added automatically. If `FALSE` (the default) a regression formulation is used that is considerably faster and allows for ARMA effects of order higher than 1 but is only available for `gaussian` models and some of its generalizations.

Details

AR refers to autoregressive effects of residuals, which is what is typically understood as autoregressive effects. However, one may also model autoregressive effects of the response variable, which is called ARR in `brms`.

Value

An object of class `cor_arma` containing solely autoregression terms.

See Also

- `cor_arma`

Examples

```r
  cor_ar(~visit|patient, p = 2)
```

---

**Description**

This function is deprecated. Please see `arma` for the new syntax. This functions is a constructor for the `cor_arma` class, representing an autoregression-moving average correlation structure of order \( p, q \).
cor_brms

Usage

\texttt{cor_arma(formula = \sim t, p = 0, q = 0, r = 0, cov = FALSE)}

Arguments

\textbf{formula} \hspace{1cm} A one sided formula of the form \sim t, or \sim t \mid g, specifying a time covariate t and, optionally, a grouping factor g. A covariate for this correlation structure must be integer valued. When a grouping factor is present in \texttt{formula}, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to \sim 1, which corresponds to using the order of the observations in the data as a covariate, and no groups.

\textbf{p} \hspace{1cm} A non-negative integer specifying the autoregressive (AR) order of the ARMA structure. Default is 0.

\textbf{q} \hspace{1cm} A non-negative integer specifying the moving average (MA) order of the ARMA structure. Default is 0.

\textbf{r} \hspace{1cm} No longer supported.

\textbf{cov} \hspace{1cm} A flag indicating whether ARMA effects should be estimated by means of residual covariance matrices. This is currently only possible for stationary ARMA effects of order 1. If the model family does not have natural residuals, latent residuals are added automatically. If FALSE (the default) a regression formulation is used that is considerably faster and allows for ARMA effects of order higher than 1 but is only available for \texttt{gaussian} models and some of its generalizations.

Value

An object of class \texttt{cor_arma}, representing an autoregression-moving-average correlation structure.

See Also

\texttt{cor_ar, cor_ma}

Examples

\texttt{cor_arma(~ visit \mid patient, p = 2, q = 2)}

\hline
\textbf{cor_brms} & \textit{(Deprecated) Correlation structure classes for the \texttt{brms} package} \\
\hline

\textbf{Description}

Classes of correlation structures available in the \texttt{brms} package. \texttt{cor_brms} is not a correlation structure itself, but the class common to all correlation structures implemented in \texttt{brms}. 
Available correlation structures

- **cor_arma** autoregressive-moving average (ARMA) structure, with arbitrary orders for the autoregressive and moving average components
- **cor_ar** autoregressive (AR) structure of arbitrary order
- **cor_ma** moving average (MA) structure of arbitrary order
- **cor_car** Spatial conditional autoregressive (CAR) structure
- **cor_sar** Spatial simultaneous autoregressive (SAR) structure
- **cor_fixed** fixed user-defined covariance structure

See Also

- cor_arma, cor_ar, cor_ma, cor_car, cor_sar, cor_fixed

---

**cor_car** *(Deprecated) Spatial conditional autoregressive (CAR) structures*

**Description**

These function are deprecated. Please see `car` for the new syntax. These functions are constructors for the cor_car class implementing spatial conditional autoregressive structures.

**Usage**

```r
cor_car(W, formula = ~1, type = "escar")
cor_icar(W, formula = ~1)
```

**Arguments**

- **W**: Adjacency matrix of locations. All non-zero entries are treated as if the two locations are adjacent. If `formula` contains a grouping factor, the row names of `W` have to match the levels of the grouping factor.
- **formula**: An optional one-sided formula of the form `~ 1 | g`, where `g` is a grouping factor mapping observations to spatial locations. If not specified, each observation is treated as a separate location. It is recommended to always specify a grouping factor to allow for handling of new data in post-processing methods.
- **type**: Type of the CAR structure. Currently implemented are "escar" (exact sparse CAR), "esicar" (exact sparse intrinsic CAR), "icar" (intrinsic CAR), and "bym2". More information is provided in the 'Details' section.

**Details**

The escar and esicar types are implemented based on the case study of Max Joseph ([https://github.com/mbjoseph/CARstan](https://github.com/mbjoseph/CARstan)). The icar and bym2 type is implemented based on the case study of Mitzi Morris ([https://mc-stan.org/users/documentation/case-studies/icar_stan.html](https://mc-stan.org/users/documentation/case-studies/icar_stan.html)).
## Examples

```r
## Not run:
# generate some spatial data
east <- north <- 1:10
Grid <- expand.grid(east, north)
K <- nrow(Grid)

# set up distance and neighbourhood matrices
distance <- as.matrix(dist(Grid))
W <- array(0, c(K, K))
W[distance == 1] <- 1

# generate the covariates and response data
x1 <- rnorm(K)
x2 <- rnorm(K)
theta <- rnorm(K, sd = 0.05)
phi <- rmulti_normal(
  1, mu = rep(0, K), Sigma = 0.4 * exp(-0.1 * distance)
)
eta <- x1 + x2 + phi
prob <- exp(eta) / (1 + exp(eta))
size <- rep(50, K)
y <- rbinom(n = K, size = size, prob = prob)
dat <- data.frame(y, size, x1, x2)

# fit a CAR model
fit <- brm(y | trials(size) ~ x1 + x2, data = dat,
           family = binomial(), autocor = cor_car(W))
summary(fit)

## End(Not run)
```

---

**cor_cosy**

*(Deprecated)* Compound Symmetry (COSY) Correlation Structure

### Description

This function is deprecated. Please see `cosy` for the new syntax. This function is a constructor for the `cor_cosy` class, representing a compound symmetry structure corresponding to uniform correlation.

### Usage

```r
cor_cosy(formula = ~1)
```
cor_fixed

Arguments

formula A one sided formula of the form \( ~ t \), or \( ~ t | g \), specifying a time covariate \( t \) and, optionally, a grouping factor \( g \). A covariate for this correlation structure must be integer valued. When a grouping factor is present in formula, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to \( ~ 1 \), which corresponds to using the order of the observations in the data as a covariate, and no groups.

Value

An object of class `cor_cosy`, representing a compound symmetry correlation structure.

Examples

```
cor_cosy(~ visit | patient)
```

---

cor_fixed

(Deprecated) Fixed user-defined covariance matrices

Description

This function is deprecated. Please see `fcor` for the new syntax. Define a fixed covariance matrix of the response variable for instance to model multivariate effect sizes in meta-analysis.

Usage

```
cor_fixed(V)
```

Arguments

V Known covariance matrix of the response variable. If a vector is passed, it will be used as diagonal entries (variances) and covariances will be set to zero.

Value

An object of class `cor_fixed`.

Examples

```
## Not run:
dat <- data.frame(y = rnorm(3))
V <- cbind(c(0.5, 0.3, 0.2), c(0.3, 1, 0.1), c(0.2, 0.1, 0.2))
fit <- brm(y~1, data = dat, autocor = cor_fixed(V))

## End(Not run)
```
cor_ma

( Deprecated) MA(q) correlation structure

Description

This function is deprecated. Please see ma for the new syntax. This function is a constructor for the cor_arma class, allowing for moving average terms only.

Usage

cor_ma(formula = ~1, q = 1, cov = FALSE)

Arguments

formula A one sided formula of the form \( \sim t \), or \( \sim t \mid g \), specifying a time covariate \( t \) and, optionally, a grouping factor \( g \). A covariate for this correlation structure must be integer valued. When a grouping factor is present in formula, the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to \( \sim 1 \), which corresponds to using the order of the observations in the data as a covariate, and no groups.

q A non-negative integer specifying the moving average (MA) order of the ARMA structure. Default is 1.

cov A flag indicating whether ARMA effects should be estimated by means of residual covariance matrices. This is currently only possible for stationary ARMA effects of order 1. If the model family does not have natural residuals, latent residuals are added automatically. If FALSE (the default) a regression formulation is used that is considerably faster and allows for ARMA effects of order higher than 1 but is only available for gaussian models and some of its generalizations.

Value

An object of class cor_arma containing solely moving average terms.

See Also

cor_arma

Examples

cor_ma(~visit|patient, q = 2)
(Deprecated) Spatial simultaneous autoregressive (SAR) structures

Description

These functions are deprecated. Please see `sar` for the new syntax. These functions are constructors for the `cor_sar` class implementing spatial simultaneous autoregressive structures. The `lagsar` structure implements SAR of the response values:

\[ y = \rho W y + \eta + e \]

The `errorsar` structure implements SAR of the residuals:

\[ y = \eta + u, u = \rho Wu + e \]

In the above equations, \( \eta \) is the predictor term and \( e \) are independent normally or t-distributed residuals.

Usage

```r
cor_sar(W, type = c("lag", "error"))
cor_lagsar(W)
cor_errorsar(W)
```

Arguments

- `W`: An object specifying the spatial weighting matrix. Can be either the spatial weight matrix itself or an object of class `listw` or `nb`, from which the spatial weighting matrix can be computed.
- `type`: Type of the SAR structure. Either "lag" (for SAR of the response values) or "error" (for SAR of the residuals).

Details

Currently, only families `gaussian` and `student` support SAR structures.

Value

An object of class `cor_sar` to be used in calls to `brm`.

Examples

```r
## Not run:
data(oldcol, package = "spdep")
fit1 <- brm(CRIME ~ INC + HOVAL, data = COL.OLD,
            autocor = cor_lagsar(COL.nb),
            chains = 2, cores = 2)
```
cosy

Set up COSY correlation structures

description

Set up a compounds symmetry (COSY) term in brms. The function does not evaluate its arguments – it exists purely to help set up a model with COSY terms.

Usage

cosy(time = NA, gr = NA)

Arguments

time An optional time variable specifying the time ordering of the observations. By default, the existing order of the observations in the data is used.

gr An optional grouping variable. If specified, the correlation structure is assumed to apply only to observations within the same grouping level.

Value

An object of class 'cosy_term', which is a list of arguments to be interpreted by the formula parsing functions of brms.

See Also

autocor-terms

Examples

## Not run:
data("lh")
lh <- as.data.frame(lh)
fit <- brm(x ~ cosy(), data = lh)
summary(fit)

## End(Not run)
Description

Category Specific Predictors in *brms* Models

Usage

cs(expr)

Arguments

- `expr` Expression containing predictors, for which category specific effects should be estimated. For evaluation, R formula syntax is applied.

Details

For detailed documentation see `help(brmsformula)` as well as `vignette("brms_overview")`. This function is almost solely useful when called in formulas passed to the *brms* package.

See Also

`brmsformula`

Examples

```r
## Not run:
fit <- brm(rating ~ period + carry + cs(treat),
           data = inhaler, family = sratio("cloglog"),
           prior = set_prior("normal(0,5)"), chains = 2)
summary(fit)
plot(fit, ask = FALSE)
## End(Not run)
```

Description

Define custom families (i.e. response distribution) for use in *brms* models. It allows users to benefit from the modeling flexibility of *brms*, while applying their self-defined likelihood functions. All of the post-processing methods for *brmsfit* objects can be made compatible with custom families. See `vignette("brms_customfamilies")` for more details. For a list of built-in families see `brmsfamily`. 
Usage

custom_family(
  name,
  dpars = "mu",
  links = "identity",
  type = c("real", "int"),
  lb = NA,
  ub = NA,
  vars = NULL,
  loop = TRUE,
  specials = NULL,
  threshold = "flexible",
  log_lik = NULL,
  posterior_predict = NULL,
  posterior_epred = NULL,
  predict = NULL,
  fitted = NULL,
  env = parent.frame()
)

Arguments

name
  Name of the custom family.

dpars
  Names of the distributional parameters of the family. One parameter must be named "mu" and the main formula of the model will correspond to that parameter.

links
  Names of the link functions of the distributional parameters.

type
  Indicates if the response distribution is continuous ("real") or discrete ("int"). This controls if the corresponding density function will be named with <name>_lpdf or <name>_lpmf.

lb
  Vector of lower bounds of the distributional parameters. Defaults to NA that is no lower bound.

ub
  Vector of upper bounds of the distributional parameters. Defaults to NA that is no upper bound.

vars
  Names of variables that are part of the likelihood function without being distributional parameters. That is, vars can be used to pass data to the likelihood. Such arguments will be added to the list of function arguments at the end, after the distributional parameters. See stanvar for details about adding self-defined data to the generated Stan model. Addition arguments vreal and vint may be used for this purpose as well (see Examples below). See also brmsformula and addition-terms for more details.

loop
  Logical; Should the likelihood be evaluated via a loop (TRUE; the default) over observations in Stan? If FALSE, the Stan code will be written in a vectorized manner over observations if possible.

specials
  A character vector of special options to enable for this custom family. Currently for internal use only.
threshold Optional threshold type for custom ordinal families. Ignored for non-ordinal families.

log_lik Optional function to compute log-likelihood values of the model in R. This is only relevant if one wants to ensure compatibility with method log_lik.

posterior_predict Optional function to compute posterior prediction of the model in R. This is only relevant if one wants to ensure compatibility with method posterior_predict.

posterior_epred Optional function to compute expected values of the posterior predictive distribution of the model in R. This is only relevant if one wants to ensure compatibility with method posterior_epred.

predict Deprecated alias of 'posterior_predict'.

fitted Deprecated alias of 'posterior_epred'.

env An environment in which certain post-processing functions related to the custom family can be found, if there were not directly passed to custom_family. This is only relevant if one wants to ensure compatibility with the methods log_lik, posterior_predict, or posterior_epred. By default, env is the environment from which custom_family is called.

Details

The corresponding probability density or mass Stan functions need to have the same name as the custom family. That is if a family is called myfamily, then the Stan functions should be called myfamily_lpdf or myfamily_lpmf depending on whether it defines a continuous or discrete distribution.

Value

An object of class customfamily inheriting from class brmsfamily.

See Also

brmsfamily, brmsformula, stanvar

Examples

```r
## Not run:
## demonstrate how to fit a beta-binomial model
## generate some fake data
phi <- 0.7
n <- 300
z <- rnorm(n, sd = 0.2)
ntrials <- sample(1:10, n, replace = TRUE)
eta <- 1 + z
mu <- exp(eta) / (1 + exp(eta))
a <- mu * phi
b <- (1 - mu) * phi
p <- rbeta(n, a, b)
y <- rbinom(n, ntrials, p)
```
dat <- data.frame(y, z, ntrials)

# define a custom family
beta_binomial2 <- custom_family(
  "beta_binomial2", dpars = c("mu", "phi"),
  links = c("logit", "log"), lb = c(NA, 0),
  type = "int", vars = "vint1[n]"
)

# define the corresponding Stan density function
stan_density <- 
  real beta_binomial2_lpmf(int y, real mu, real phi, int N) {
    return beta_binomial_lpmf(y | N, mu * phi, (1 - mu) * phi);
  }

stanvars <- stanvar(scode = stan_density, block = "functions")

# fit the model
fit <- brm(y | vint(ntrials) ~ z, data = dat,
  family = beta_binomial2, stanvars = stanvars)
summary(fit)

# define a *vectorized* custom family (no loop over observations)
# notice also that 'vint' no longer has an observation index
beta_binomial2_vec <- custom_family(
  "beta_binomial2", dpars = c("mu", "phi"),
  links = c("logit", "log"), lb = c(NA, 0),
  type = "int", vars = "vint1", loop = FALSE
)

# define the corresponding Stan density function
stan_density_vec <- 
  real beta_binomial2_lpmf(int[] y, vector mu, real phi, int[] N) {
    return beta_binomial_lpmf(y | N, mu * phi, (1 - mu) * phi);
  }

stanvars_vec <- stanvar(scode = stan_density_vec, block = "functions")

# fit the model
fit_vec <- brm(y | vint(ntrials) ~ z, data = dat,
  family = beta_binomial2_vec, stanvars = stanvars_vec)
summary(fit_vec)

## End(Not run)

---

density_ratio

Compute Density Ratios
**Description**

Compute the ratio of two densities at given points based on draws of the corresponding distributions.

**Usage**

density_ratio(x, y = NULL, point = 0, n = 4096, ...)

**Arguments**

- **x**: Vector of draws from the first distribution, usually the posterior distribution of the quantity of interest.
- **y**: Optional vector of draws from the second distribution, usually the prior distribution of the quantity of interest. If NULL (the default), only the density of x will be evaluated.
- **point**: Numeric values at which to evaluate and compare the densities. Defaults to 0.
- **n**: Single numeric value. Influences the accuracy of the density estimation. See density for details.
- **...**: Further arguments passed to density.

**Details**

In order to achieve sufficient accuracy in the density estimation, more draws than usual are required. That is you may need an effective sample size of 10,000 or more to reliably estimate the densities.

**Value**

A vector of length equal to length(point). If y is provided, the density ratio of x against y is returned. Else, only the density of x is returned.

**Examples**

```r
x <- rnorm(10000)
y <- rnorm(10000, mean = 1)
density_ratio(x, y, point = c(0, 1))
```

---

**diagnostic-quantities**  
*Extract Diagnostic Quantities of brms Models*

**Description**

Extract quantities that can be used to diagnose sampling behavior of the algorithms applied by Stan at the back-end of brms.
Usage

```r
## S3 method for class 'brmsfit'
log_posterior(object, ...)

## S3 method for class 'brmsfit'
nuts_params(object, pars = NULL, ...)

## S3 method for class 'brmsfit'
rhat(x, pars = NULL, ...)

## S3 method for class 'brmsfit'
neff_ratio(object, pars = NULL, ...)
```

Arguments

- `object, x` A `brmsfit` object.
- `...` Arguments passed to individual methods.
- `pars` An optional character vector of parameter names. For `nuts_params` these will be NUTS sampler parameter names rather than model parameters. If `pars` is omitted all parameters are included.

Details

For more details see `bayesplot-extractors`.

Value

The exact form of the output depends on the method.

Examples

```r
## Not run:
fit <- brm(time ~ age * sex, data = kidney)

lp <- log_posterior(fit)
head(lp)

np <- nuts_params(fit)
str(np)
# extract the number of divergence transitions
sum(subset(np, Parameter == "divergent__")$Value)

head(rhat(fit))
head(neff_ratio(fit))

## End(Not run)
```
The Dirichlet Distribution

Description

Density function and random number generation for the dirichlet distribution with shape parameter vector alpha.

Usage

ddirichlet(x, alpha, log = FALSE)

rdirichlet(n, alpha)

Arguments

x Matrix of quantiles. Each row corresponds to one probability vector.
alpha Matrix of positive shape parameters. Each row corresponds to one probability vector.
log Logical; If TRUE, values are returned on the log scale.
n Number of draws to sample from the distribution.

Details

See vignette("brms_families") for details on the parameterization.

draws-brms Transform brmsfit to draws objects

Description

Transform a brmsfit object to a format supported by the posterior package.

Usage

## S3 method for class 'brmsfit'
as_draws(x, variable = NULL, regex = FALSE, inc_warmup = FALSE, ...)

## S3 method for class 'brmsfit'
as_draws_matrix(x, variable = NULL, regex = FALSE, inc_warmup = FALSE, ...)

## S3 method for class 'brmsfit'
as_draws_array(x, variable = NULL, regex = FALSE, inc_warmup = FALSE, ...)

## S3 method for class 'brmsfit'
as_draws_df(x, variable = NULL, regex = FALSE, inc_warmup = FALSE, ...)

## S3 method for class 'brmsfit'
as_draws_list(x, variable = NULL, regex = FALSE, inc_warmup = FALSE, ...)

## S3 method for class 'brmsfit'
as_draws_rvars(x, variable = NULL, regex = FALSE, inc_warmup = FALSE, ...)

Arguments

- **x**: A `brmsfit` object or another R object for which the methods are defined.
- **variable**: A character vector providing the variables to extract. By default, all variables are extracted.
- **regex**: Logical; Should variable should be treated as a (vector of) regular expressions? Any variable in `x` matching at least one of the regular expressions will be selected. Defaults to `FALSE`.
- **inc_warmup**: Should warmup draws be included? Defaults to `FALSE`.
- **...**: Arguments passed to individual methods (if applicable).

Details

To subset iterations, chains, or draws, use the `subset_draws` method after transforming the `brmsfit` to a `draws` object.

See Also

draws subset_draws

Examples

## Not run:
fit <- brm(count ~ zAge + zBase * Trt + (1|patient),
            data = epilepsy, family = poisson())

# extract posterior draws in an array format
(draws_fit <- as_draws_array(fit))
posterior::summarize_draws(draws_fit)

# extract only certain variables
as_draws_array(fit, variable = "r_patient")
as_draws_array(fit, variable = "^b_", regex = TRUE)

# extract posterior draws in a random variables format
as_draws_rvars(fit)

## End(Not run)
Index brmsfit objects

Description

Index brmsfit objects

Usage

```r
## S3 method for class 'brmsfit'
variables(x, ...)

## S3 method for class 'brmsfit'
nvariables(x, ...)

## S3 method for class 'brmsfit'
niterations(x)

## S3 method for class 'brmsfit'
nchains(x)

## S3 method for class 'brmsfit'
ndraws(x)
```

Arguments

- `x`: A `brmsfit` object or another R object for which the methods are defined.
- `...`: Arguments passed to individual methods (if applicable).

Support Functions for `emmeans`

Description

Functions required for compatibility of `brms` with `emmeans`. Users are not required to call these functions themselves. Instead, they will be called automatically by the `emmeans` function of the `emmeans` package.

Usage

```r
recover_data.brmsfit(
  object,
  data,
  resp = NULL,
  dpar = NULL,
```
nlpar = NULL,
re_formula = NA,
epred = FALSE,
...
)

emmeans.brmsfit(
  object,
  trms,
  xlev,
  grid,
  vcov.,
  resp = NULL,
  dpar = NULL,
  nlpar = NULL,
  re_formula = NA,
  epred = FALSE,
  ...
)

Arguments

object        An object of class brmsfit.
data, trms, xlev, grid, vcov.
  Arguments required by emmeans.
resp          Optional names of response variables. If specified, predictions are performed
  only for the specified response variables.
dpar          Optional name of a predicted distributional parameter. If specified, expected
  predictions of this parameters are returned.
nlpar         Optional name of a predicted non-linear parameter. If specified, expected pre-
  dictions of this parameters are returned.
re_formula    Optional formula containing group-level effects to be considered in the predic-
  tion. If NULL, include all group-level effects; if NA (default), include no group-
  level effects.
epred Logical. If TRUE compute predictions of the posterior predictive distribution’s
  mean (see posterior_epred.brmsfit) while ignoring arguments dpar and nlpar. Defaults to FALSE. If you have specified a response transformation
  within the formula, you need to set epred to TRUE for emmeans to detect this
  transformation.
...
  Additional arguments passed to emmeans.

Details

In order to ensure compatibility of most brms models with emmeans, predictions are not generated
‘manually’ via a design matrix and coefficient vector, but rather via posterior_linpred.brmsfit.
This appears to generally work well, but note that it produces an ‘.@linfct’ slot that contains the
computed predictions as columns instead of the coefficients.
Examples

```r
## Not run:
fit1 <- brm(time | cens(censored) ~ age * sex + disease + (1|patient),
data = kidney, family = lognormal())
summary(fit1)

# summarize via 'emmeans'
library(emmeans)
rg <- ref_grid(fit1)
em <- emmeans(rg, "disease")
summary(em, point.est = mean)

# obtain estimates for the posterior predictive distribution's mean
epred <- emmeans(fit1, "disease", epred = TRUE)
summary(epred, point.est = mean)

# model with transformed response variable
fit2 <- brm(log(mpg) ~ factor(cyl), data = mtcars)
summary(fit2)

# results will be on the log scale by default
emmeans(fit2, ~ cyl)
# log transform is detected and can be adjusted automatically
emmeans(fit2, ~ cyl, epred = TRUE, type = "response")

## End(Not run)
```
The patient number

The session number from 1 (first visit) to 4 (last visit)

The seizure count between two visits

The observation number, that is a unique identifier for each observation

Standardized Age

Standardized Base


## Examples

```r
## Not run:
## poisson regression without random effects.
fit1 <- brm(count ~ zAge + zBase * Trt,
            data = epilepsy, family = poisson())
summary(fit1)
plot(fit1)

## poisson regression with varying intercepts of patients
## as well as normal priors for overall effects parameters.
fit2 <- brm(count ~ zAge + zBase * Trt + (1|patient),
            data = epilepsy, family = poisson(),
            prior = set_prior("normal(0,5)"))
summary(fit2)
plot(fit2)

## End(Not run)
```

The Exponentially Modified Gaussian Distribution

Density, distribution function, and random generation for the exponentially modified Gaussian distribution with mean mu and standard deviation sigma of the gaussian component, as well as scale beta of the exponential component.
Usage

dexgaussian(x, mu, sigma, beta, log = FALSE)
pexgaussian(q, mu, sigma, beta, lower.tail = TRUE, log.p = FALSE)
rexgaussian(n, mu, sigma, beta)

Arguments

x, q  Vector of quantiles.
mu  Vector of means of the combined distribution.
sigma  Vector of standard deviations of the gaussian component.
beta  Vector of scales of the exponential component.
log  Logical; If TRUE, values are returned on the log scale.
lower.tail  Logical; If TRUE (default), return P(X <= x). Else, return P(X > x).
log.p  Logical; If TRUE, values are returned on the log scale.
n  Number of draws to sample from the distribution.

Details

See vignette("brms_families") for details on the parameterization.

dexgaussian
  Expose user-defined Stan functions

Description

Export user-defined Stan function and optionally vectorize them. For more details see expose_stan_functions.

Usage

## S3 method for class 'brmsfit'
expose_functions(x, vectorize = FALSE, env = globalenv(), ...)

Arguments

x  An object of class brmsfit.
vectorize  Logical; Indicates if the exposed functions should be vectorized via Vectorize. Defaults to FALSE.
env  Environment where the functions should be made available. Defaults to the global environment.
...  Further arguments passed to expose_stan_functions.
expp1  

*Exponential function plus one.*

### Description

Computes \( \exp(x) + 1 \).

### Usage

\[
\text{expp1}(x)
\]

### Arguments

- **x**  
  A numeric or complex vector.

### family.brmsfit

*Extract Model Family Objects*

### Description

Extract Model Family Objects

### Usage

```r
## S3 method for class 'brmsfit'
family(object, resp = NULL, ...)
```

### Arguments

- **object**  
  An object of class `brmsfit`.

- **resp**  
  Optional names of response variables. If specified, predictions are performed only for the specified response variables.

- **...**  
  Currently unused.

### Value

A `brmsfamily` object or a list of such objects for multivariate models.
Fixed residual correlation (FCOR) structures

Description

Set up a fixed residual correlation (FCOR) term in \texttt{brms}. The function does not evaluate its arguments – it exists purely to help set up a model with FCOR terms.

Usage

\texttt{fcor(M)}

Arguments

\texttt{M}  
Known correlation/covariance matrix of the response variable. If a vector is passed, it will be used as diagonal entries (variances) and correlations/covariances will be set to zero. The actual covariance matrix used in the likelihood is obtained by multiplying \texttt{M} by the square of the residual standard deviation parameter \texttt{sigma} estimated as part of the model.

Value

An object of class ‘\texttt{fcor\_term}’, which is a list of arguments to be interpreted by the formula parsing functions of \texttt{brms}.

See Also

\texttt{autocor\_terms}

Examples

```r
## Not run:
dat <- data.frame(y = rnorm(3))
V <- cbind(c(0.5, 0.3, 0.2), c(0.3, 1, 0.1), c(0.2, 0.1, 0.2))
fit <- brm(y ~ 1 + fcor(V), data = dat, data2 = list(V = V))
## End(Not run)
```
fitted.brmsfit

Expected Values of the Posterior Predictive Distribution

Description

This method is an alias of `posterior_epred.brmsfit` with additional arguments for obtaining summaries of the computed draws.

Usage

```r
## S3 method for class 'brmsfit'
fitted(
  object,
  newdata = NULL,
  re_formula = NULL,
  scale = c("response", "linear"),
  resp = NULL,
  dpar = NULL,
  nlpar = NULL,
  ndraws = NULL,
  draw_ids = NULL,
  sort = FALSE,
  summary = TRUE,
  robust = FALSE,
  probs = c(0.025, 0.975),
  ...
)
```

Arguments

- **object**: An object of class `brmsfit`.
- **newdata**: An optional data.frame for which to evaluate predictions. If NULL (default), the original data of the model is used. NA values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.
- **re_formula**: formula containing group-level effects to be considered in the prediction. If NULL (default), include all group-level effects; if NA, include no group-level effects.
- **scale**: Either "response" or "linear". If "response", results are returned on the scale of the response variable. If "linear", results are returned on the scale of the linear predictor term, that is without applying the inverse link function or other transformations.
- **resp**: Optional names of response variables. If specified, predictions are performed only for the specified response variables.
- **dpar**: Optional name of a predicted distributional parameter. If specified, expected predictions of this parameter are returned.
Optional name of a predicted non-linear parameter. If specified, expected predictions of this parameter are returned.

Positive integer indicating how many posterior draws should be used. If NULL (the default) all draws are used. Ignored if draw_ids is not NULL.

An integer vector specifying the posterior draws to be used. If NULL (the default), all draws are used.

Logical. Only relevant for time series models. Indicating whether to return predicted values in the original order (FALSE; default) or in the order of the time series (TRUE).

Should summary statistics be returned instead of the raw values? Default is TRUE.

If FALSE (the default) the mean is used as the measure of central tendency and the standard deviation as the measure of variability. If TRUE, the median and the median absolute deviation (MAD) are applied instead. Only used if summary is TRUE.

The percentiles to be computed by the quantile function. Only used if summary is TRUE.

Further arguments passed to prepare_predictions that control several aspects of data validation and prediction.

An array of predicted mean response values. If summary = FALSE the output resembles those of posterior_epred.brmsfit.

If summary = TRUE the output depends on the family: For categorical and ordinal families, the output is an N x E x C array, where N is the number of observations, E is the number of summary statistics, and C is the number of categories. For all other families, the output is an N x E matrix. The number of summary statistics E is equal to 2 + length(probs): The Estimate column contains point estimates (either mean or median depending on argument robust), while the Est.Error column contains uncertainty estimates (either standard deviation or median absolute deviation depending on argument robust). The remaining columns starting with Q contain quantile estimates as specified via argument probs.

In multivariate models, an additional dimension is added to the output which indexes along the different response variables.

See Also
posterior_epred.brmsfit

Examples
## Not run:
## fit a model
fit <- brm(rating ~ treat + period + carry + (1|subject),
           data = inhaler)

## compute expected predictions
fitted_values <- fitted(fit)
head(fitted_values)

## plot expected predictions against actual response
dat <- as.data.frame(cbind(Y = standata(fit)$Y, fitted_values))
ggplot(dat) + geom_point(aes(x = Estimate, y = Y))

## End(Not run)

---

**fixef.brmsfit**

Extract Population-Level Estimates

**Description**

Extract the population-level ('fixed') effects from a `brmsfit` object.

**Usage**

```r
## S3 method for class 'brmsfit'
fixef(
  object,
  summary = TRUE,
  robust = FALSE,
  probs = c(0.025, 0.975),
  pars = NULL,
  ...
)
```

**Arguments**

- `object` An object of class `brmsfit`.
- `summary` Should summary statistics be returned instead of the raw values? Default is `TRUE`.
- `robust` If `FALSE` (the default) the mean is used as the measure of central tendency and the standard deviation as the measure of variability. If `TRUE`, the median and the median absolute deviation (MAD) are applied instead. Only used if `summary` is `TRUE`.
- `probs` The percentiles to be computed by the `quantile` function. Only used if `summary` is `TRUE`.
- `pars` Optional names of coefficients to extract. By default, all coefficients are extracted.
- `...` Currently ignored.
**Value**

If `summary` is TRUE, a matrix returned by `posterior_summary` for the population-level effects. If `summary` is FALSE, a matrix with one row per posterior draw and one column per population-level effect.

**Examples**

```r
## Not run:
fit <- brm(time | cens(censored) ~ age + sex + disease, 
data = kidney, family = "exponential")
fixef(fit)
# extract only some coefficients
fixef(fit, pars = c("age", "sex"))
## End(Not run)
```

---

**Frechet**

**The Frechet Distribution**

**Description**

Density, distribution function, quantile function and random generation for the Frechet distribution with location `loc`, scale `scale`, and shape `shape`.

**Usage**

```r
dfrechet(x, loc = 0, scale = 1, shape = 1, log = FALSE)
pfrechet(q, loc = 0, scale = 1, shape = 1, lower.tail = TRUE, log.p = FALSE)
qfrechet(p, loc = 0, scale = 1, shape = 1, lower.tail = TRUE, log.p = FALSE)
rfrechet(n, loc = 0, scale = 1, shape = 1)
```

**Arguments**

- `x, q` Vector of quantiles.
- `loc` Vector of locations.
- `scale` Vector of scales.
- `shape` Vector of shapes.
- `log` Logical; If TRUE, values are returned on the log scale.
- `lower.tail` Logical; If TRUE (default), return P(X <= x). Else, return P(X > x).
- `log.p` Logical; If TRUE, values are returned on the log scale.
- `p` Vector of probabilities.
- `n` Number of draws to sample from the distribution.
GenExtremeValue

The Generalized Extreme Value Distribution

Details

See vignette("brms_families") for details on the parameterization.

Description

Density, distribution function, and random generation for the generalized extreme value distribution with location mu, scale sigma and shape xi.

Usage

dgen_extreme_value(x, mu = 0, sigma = 1, xi = 0, log = FALSE)

pgen_extreme_value(q, mu = 0, sigma = 1, xi = 0, lower.tail = TRUE, log.p = FALSE)

qgen_extreme_value(p, mu = 0, sigma = 1, xi = 0, lower.tail = TRUE, log.p = FALSE)

rgen_extreme_value(n, mu = 0, sigma = 1, xi = 0)

Arguments

x, q Vector of quantiles.
mu Vector of locations.
sigma Vector of scales.
xi Vector of shapes.
log Logical; If TRUE, values are returned on the log scale.
lower.tail Logical; If TRUE (default), return P(X <= x). Else, return P(X > x).
log.p Logical; If TRUE, values are returned on the log scale.
p Vector of probabilities.
n Number of draws to sample from the distribution.
**get_dpar**

*Draws of a Distributional Parameter*

**Description**

Get draws of a distributional parameter from a `brmsprep` or `mvbrmsprep` object. This function is primarily useful when developing custom families or packages depending on **brms**. This function lets callers easily handle both the case when the distributional parameter is predicted directly, via a (non-)linear predictor or fixed to a constant. See the vignette `vignette("brms_customfamilies")` for an example use case.

**Usage**

```
get_dpar(prep, dpar, i = NULL, inv_link = NULL)
```

**Arguments**

- `prep` : A `brmsprep` or `mvbrmsprep` object created by `prepare_predictions`.
- `dpar` : Name of the distributional parameter.
- `i` : The observation numbers for which predictions shall be extracted. If `NULL` (the default), all observation will be extracted. Ignored if `dpar` is not predicted.
- `inv_link` : Should the inverse link function be applied? If `NULL` (the default), the value is chosen internally. In particular, `inv_link` is `TRUE` by default for custom families.

**Value**

If the parameter is predicted and `i` is `NULL` or `length(i) > 1`, an `S x N` matrix. If the parameter it not predicted or `length(i) == 1`, a vector of length `S`. Here `S` is the number of draws and `N` is the number of observations or length of `i` if specified.

**Examples**

```r
## Not run:
posterior_predict_my_dist <- function(i, prep, ...) {
  mu <- brms:::get_dpar(prep, "mu", i = i)
  mypar <- brms:::get_dpar(prep, "mypar", i = i)
  my_rng(mu, mypar)
}

## End(Not run)
```
get_prior  

Overview on Priors for \texttt{brms} Models

Description

Get information on all parameters (and parameter classes) for which priors may be specified including default priors.

Usage

\begin{verbatim}
get_prior( 
  formula, 
  data, 
  family = gaussian(), 
  autocor = NULL, 
  data2 = NULL, 
  knots = NULL, 
  dropUnusedLevels = TRUE, 
  sparse = NULL, 
  ... 
)
\end{verbatim}

Arguments

\begin{itemize}
  \item \texttt{formula} An object of class \texttt{formula}, \texttt{brmsformula}, or \texttt{mvbrmsformula} (or one that can be coerced to that classes): A symbolic description of the model to be fitted. The details of model specification are explained in \texttt{brmsformula}.
  \item \texttt{data} An object of class \texttt{data.frame} (or one that can be coerced to that class) containing data of all variables used in the model.
  \item \texttt{family} A description of the response distribution and link function to be used in the model. This can be a family function, a call to a family function or a character string naming the family. Every family function has a \texttt{link} argument allowing to specify the link function to be applied on the response variable. If not specified, default links are used. For details of supported families see \texttt{brmsfamily}. By default, a linear gaussian model is applied. In multivariate models, \texttt{family} might also be a list of families.
  \item \texttt{autocor} (Deprecated) An optional \texttt{cor_brms} object describing the correlation structure within the response variable (i.e., the ’autocorrelation’). See the documentation of \texttt{cor_brms} for a description of the available correlation structures. Defaults to \texttt{NULL}, corresponding to no correlations. In multivariate models, autocor might also be a list of autocorrelation structures. It is now recommend to specify autocorrelation terms directly within \texttt{formula}. See \texttt{brmsformula} for more details.
  \item \texttt{data2} A named list of objects containing data, which cannot be passed via argument \texttt{data}. Required for some objects used in autocorrelation structures to specify dependency structures as well as for within-group covariance matrices.
\end{itemize}
get_refmodel.brmsfit

knots

Optional list containing user specified knot values to be used for basis construction of smoothing terms. See gamm for more details.

drop_unused_levels

Should unused factors levels in the data be dropped? Defaults to TRUE.

sparse

(Deprecated) Logical; indicates whether the population-level design matrices should be treated as sparse (defaults to FALSE). For design matrices with many zeros, this can considerably reduce required memory. Sampling speed is currently not improved or even slightly decreased. It is now recommended to use the sparse argument of brmsformula and related functions.

...

Other arguments for internal usage only.

Value

A data.frame with columns prior, class, coef, and group and several rows, each providing information on a parameter (or parameter class) on which priors can be specified. The prior column is empty except for internal default priors.

See Also

set_prior

Examples

```r
# get all parameters and parameters classes to define priors on
(prior <- get_prior(count ~ zAge + zBase * Trt + (1|patient) + (1|obs),
                    data = epilepsy, family = poisson()))

# define a prior on all population-level effects a once
prior$prior[1] <- "normal(0,10)"

# define a specific prior on the population-level effect of Trt
prior$prior[5] <- "student_t(10, 0, 5)"

# verify that the priors indeed found their way into Stan's model code
make_stancode(count ~ zAge + zBase * Trt + (1|patient) + (1|obs),
              data = epilepsy, family = poisson(),
              prior = prior)
```

---

get_refmodel.brmsfit  
Projection Predictive Variable Selection: Get Reference Model

Description

The get_refmodel.brmsfit method can be used to create the reference model structure which is needed by the projpred package for performing a projection predictive variable selection. This method is called automatically when performing variable selection via varsel or cv_varsel, so you will rarely need to call it manually yourself.
Usage

get_refmodel.brmsfit(
  object,
  newdata = NULL,
  resp = NULL,
  cvfun = NULL,
  dis = NULL,
  latent = FALSE,
  brms_seed = NULL,
  ...
)

Arguments

object An object of class brmsfit.
newdata An optional data.frame for which to evaluate predictions. If NULL (default), the original data of the model is used. NA values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.
resp Optional names of response variables. If specified, predictions are performed only for the specified response variables.
cvfun Optional cross-validation function (see get_refmodel for details). If NULL (the default), cvfun is defined internally based on kfold.brmsfit.
dis Passed to argument dis of init_refmodel, but leave this at NULL unless projpred complains about it.
latent See argument latent of extend_family. Setting this to TRUE requires a projpred version >= 2.4.0.
brms_seed A seed used to infer seeds for kfold.brmsfit and for sampling group-level effects for new levels (in multilevel models).
... Further arguments passed to init_refmodel.

Details

Note that the extract_model_data function used internally by get_refmodel.brmsfit ignores arguments wrhs and orhs. This is relevant for predict.refmodel, for example.

Value

A refmodel object to be used in conjunction with the projpred package.

Examples

```r
## Not run:
# fit a simple model
fit <- brm(count ~ zAge + zBase * Trt,
            data = epilepsy, family = poisson())
summary(fit)
```
# The following code requires the 'projpred' package to be installed:
library(projpred)

# perform variable selection without cross-validation
vs <- varsel(fit)
summary(vs)
plot(vs)

# perform variable selection with cross-validation
cv_vs <- cv_varsel(fit)
summary(cv_vs)
plot(cv_vs)

## End(Not run)

---

### gp

**Set up Gaussian process terms in brms**

**Description**

Set up a Gaussian process (GP) term in *brms*. The function does not evaluate its arguments – it exists purely to help set up a model with GP terms.

**Usage**

```r
gp(
  ..., 
  by = NA,
  k = NA,
  cov = "exp_quad",
  iso = TRUE,
  gr = TRUE,
 cmc = TRUE,
  scale = TRUE,
  c = NULL
)
```

**Arguments**

- `...` One or more predictors for the GP.
- `by` A numeric or factor variable of the same length as each predictor. In the numeric vector case, the elements multiply the values returned by the GP. In the factor variable case, a separate GP is fitted for each factor level.
- `k` Optional number of basis functions for computing approximate GPs. If NA (the default), exact GPs are computed.
- `cov` Name of the covariance kernel. By default, the exponentiated-quadratic kernel "exp_quad" is used.
iso

A flag to indicate whether an isotropic (TRUE; the default) or a non-isotropic GP should be used. In the former case, the same amount of smoothing is applied to all predictors. In the latter case, predictors may have different smoothing. Ignored if only a single predictor is supplied.

gr

Logical; Indicates if auto-grouping should be used (defaults to TRUE). If enabled, observations sharing the same predictor values will be represented by the same latent variable in the GP. This will improve sampling efficiency drastically if the number of unique predictor combinations is small relative to the number of observations.

cmc

Logical; Only relevant if by is a factor. If TRUE (the default), cell-mean coding is used for the by-factor, that is one GP per level is estimated. If FALSE, contrast GPs are estimated according to the contrasts set for the by-factor.

scale

Logical; If TRUE (the default), predictors are scaled so that the maximum Euclidean distance between two points is 1. This often improves sampling speed and convergence. Scaling also affects the estimated length-scale parameters in that they resemble those of scaled predictors (not of the original predictors) if scale is TRUE.

c

Numeric value only used in approximate GPs. Defines the multiplicative constant of the predictors’ range over which predictions should be computed. A good default could be \( c = 5/4 \) but we are still working on providing better recommendations.

Details

A GP is a stochastic process, which describes the relation between one or more predictors \( x = (x_1, ..., x_d) \) and a response \( f(x) \), where \( d \) is the number of predictors. A GP is the generalization of the multivariate normal distribution to an infinite number of dimensions. Thus, it can be interpreted as a prior over functions. The values of \( f() \) at any finite set of locations are jointly multivariate normal, with a covariance matrix defined by the covariance kernel \( k_p(x_i, x_j) \), where \( p \) is the vector of parameters of the GP:

\[
(f(x_1), ..., f(x_n) \sim MVN(0, (k_p(x_i, x_j))_{i,j=1}^n).
\]

The smoothness and general behavior of the function \( f \) depends only on the choice of covariance kernel. For a more detailed introduction to Gaussian processes, see https://en.wikipedia.org/wiki/Gaussian_process.

Below, we describe the currently supported covariance kernels:

- "exp_quad": The exponentiated-quadratic kernel is defined as \( k(x_i, x_j) = sdgp^2 \exp(-||x_i - x_j||^2/(2lscale^2)) \), where \(||.||\) is the Euclidean norm, \( sdgp \) is a standard deviation parameter, and \( lscale \) is characteristic length-scale parameter. The latter practically measures how close two points \( x_i \) and \( x_j \) have to be to influence each other substantially.

In the current implementation, "exp_quad" is the only supported covariance kernel. More options will follow in the future.

Value

An object of class 'gp_term', which is a list of arguments to be interpreted by the formula parsing functions of \texttt{brms}.
See Also

`brmsformula`

Examples

```r
## Not run:
# simulate data using the mgcv package
dat <- mgcv::gamSim(1, n = 30, scale = 2)

# fit a simple GP model
fit1 <- brm(y ~ gp(x2), dat, chains = 2)
summary(fit1)
me1 <- conditional_effects(fit1, ndraws = 200, spaghetti = TRUE)
plot(me1, ask = FALSE, points = TRUE)

# fit a more complicated GP model
fit2 <- brm(y ~ gp(x0) + x1 + gp(x2) + x3, dat, chains = 2)
summary(fit2)
me2 <- conditional_effects(fit2, ndraws = 200, spaghetti = TRUE)
plot(me2, ask = FALSE, points = TRUE)

# fit a multivariate GP model
fit3 <- brm(y ~ gp(x1, x2), dat, chains = 2)
summary(fit3)
me3 <- conditional_effects(fit3, ndraws = 200, spaghetti = TRUE)
plot(me3, ask = FALSE, points = TRUE)

# compare model fit
LOO(fit1, fit2, fit3)

# simulate data with a factor covariate
dat2 <- mgcv::gamSim(4, n = 90, scale = 2)

# fit separate gaussian processes for different levels of 'fac'
fit4 <- brm(y ~ gp(x2, by = fac), dat2, chains = 2)
summary(fit4)
plot(conditional_effects(fit4), points = TRUE)

## End(Not run)
```

---

gr

**Set up basic grouping terms in** `brms`

Description

Function used to set up a basic grouping term in `brms`. The function does not evaluate its arguments – it exists purely to help set up a model with grouping terms. `gr` is called implicitly inside the package and there is usually no need to call it directly.
Usage

```
gr(..., by = NULL, cor = TRUE, id = NA, cov = NULL, dist = "gaussian")
```

Arguments

- **...** One or more terms containing grouping factors.
- **by** An optional factor variable, specifying sub-populations of the groups. For each level of the by variable, a separate variance-covariance matrix will be fitted. Levels of the grouping factor must be nested in levels of the by variable.
- **cor** Logical. If TRUE (the default), group-level terms will be modelled as correlated.
- **id** Optional character string. All group-level terms across the model with the same id will be modeled as correlated (if cor is TRUE). See `brmsformula` for more details.
- **cov** An optional matrix which is proportional to the withon-group covariance matrix of the group-level effects. All levels of the grouping factor should appear as row-names of the corresponding matrix. This argument can be used, among others, to model pedigrees and phylogenetic effects. See vignette("brms_phylogenetics") for more details. By default, levels of the same grouping factor are modeled as independent of each other.
- **dist** Name of the distribution of the group-level effects. Currently "gaussian" is the only option.

See Also

`brmsformula`

Examples

```r
## Not run:
# model using basic lme4-style formula
fit1 <- brm(count ~ Trt + (1|patient), data = epilepsy)
summary(fit1)

# equivalent model using 'gr' which is called anyway internally
fit2 <- brm(count ~ Trt + (1|gr(patient)), data = epilepsy)
summary(fit2)

# include Trt as a by variable
fit3 <- brm(count ~ Trt + (1|gr(patient, by = Trt)), data = epilepsy)
summary(fit3)

## End(Not run)
```
horseshoe

Regularized horseshoe priors in brms

Description

Function used to set up regularized horseshoe priors and related hierarchical shrinkage priors for population-level effects in brms. The function does not evaluate its arguments – it exists purely to help set up the model.

Usage

horseshoe(
    df = 1,
    scale_global = 1,
    df_global = 1,
    scale_slab = 2,
    df_slab = 4,
    par_ratio = NULL,
    autoscale = TRUE
)

Arguments

df Degrees of freedom of student-t prior of the local shrinkage parameters. Defaults to 1.
scale_global Scale of the student-t prior of the global shrinkage parameter. Defaults to 1. In linear models, scale_global will internally be multiplied by the residual standard deviation parameter sigma.
df_global Degrees of freedom of student-t prior of the global shrinkage parameter. Defaults to 1. If df_global is greater than 1, the shape of the prior will no longer resemble a horseshoe and it may be more appropriately called an hierarchical shrinkage prior in this case.
scale_slab Scale of the Student-t slab. Defaults to 2. The original unregularized horseshoe prior is obtained by setting scale_slab to infinite, which we can approximate in practice by setting it to a very large real value.
df_slab Degrees of freedom of the student-t slab. Defaults to 4.
par_ratio Ratio of the expected number of non-zero coefficients to the expected number of zero coefficients. If specified, scale_global is ignored and internally computed as par_ratio / sqrt(N), where N is the total number of observations in the data.
autoscale Logical; indicating whether the horseshoe prior should be scaled using the residual standard deviation sigma if possible and sensible (defaults to TRUE). Autoscaling is not applied for distributional parameters or when the model does not contain the parameter sigma.
Details

The horseshoe prior is a special shrinkage prior initially proposed by Carvalho et al. (2009). It is symmetric around zero with fat tails and an infinitely large spike at zero. This makes it ideal for sparse models that have many regression coefficients, although only a minority of them is non-zero. The horseshoe prior can be applied on all population-level effects at once (excluding the intercept) by using `set_prior("horseshoe(1)")`. The 1 implies that the student-t prior of the local shrinkage parameters has 1 degrees of freedom. This may, however, lead to an increased number of divergent transition in Stan. Accordingly, increasing the degrees of freedom to slightly higher values (e.g., 3) may often be a better option, although the prior no longer resembles a horseshoe in this case. Further, the scale of the global shrinkage parameter plays an important role in amount of shrinkage applied. It defaults to 1, but this may result in too few shrinkage (Piironen & Vehtari, 2016). It is thus possible to change the scale using argument `scale_global` of the horseshoe prior, for instance `horseshoe(1, scale_global = 0.5)`. In linear models, `scale_global` will internally be multiplied by the residual standard deviation parameter `sigma`. See Piironen and Vehtari (2016) for recommendations how to properly set the global scale. The degrees of freedom of the global shrinkage prior may also be adjusted via argument `df_global`. Piironen and Vehtari (2017) recommend to specifying the ratio of the expected number of non-zero coefficients to the expected number of zero coefficients `par_ratio` rather than `scale_global` directly. As proposed by Piironen and Vehtari (2017), an additional regularization is applied that only affects non-zero coefficients. The amount of regularization can be controlled via `scale_slab` and `df_slab`. To make sure that shrinkage can equally affect all coefficients, predictors should be on the same scale. Generally, models with horseshoe priors a more likely than other models to have divergent transitions so that increasing `adapt_delta` from 0.8 to values closer to 1 will often be necessary. See the documentation of `brm` for instructions on how to increase `adapt_delta`.

Value

A character string obtained by `match.call()` with additional arguments.

References

Carvalho, C. M., Polson, N. G., & Scott, J. G. (2009). Handling sparsity via the horseshoe. In International Conference on Artificial Intelligence and Statistics (pp. 73-80).


See Also

`set_prior`

Examples

`set_prior(horseshoe(df = 3, par_ratio = 0.1))`
Description
Density and distribution functions for hurdle distributions.

Usage

dhurdle_poisson(x, lambda, hu, log = FALSE)

phurdle_poisson(q, lambda, hu, lower.tail = TRUE, log.p = FALSE)

dhurdle_negbinomial(x, mu, shape, hu, log = FALSE)

phurdle_negbinomial(q, mu, shape, hu, lower.tail = TRUE, log.p = FALSE)

dhurdle_gamma(x, shape, scale, hu, log = FALSE)

phurdle_gamma(q, shape, scale, hu, lower.tail = TRUE, log.p = FALSE)

dhurdle_lognormal(x, mu, sigma, hu, log = FALSE)

phurdle_lognormal(q, mu, sigma, hu, lower.tail = TRUE, log.p = FALSE)

Arguments

- **x**: Vector of quantiles.
- **hu**: hurdle probability
- **log**: Logical; If TRUE, values are returned on the log scale.
- **q**: Vector of quantiles.
- **lower.tail**: Logical; If TRUE (default), return P(X <= x). Else, return P(X > x).
- **log.p**: Logical; If TRUE, values are returned on the log scale.
- **mu, lambda**: location parameter
- **shape**: shape parameter
- **sigma, scale**: scale parameter

Details
The density of a hurdle distribution can be specified as follows. If $x = 0$ set $f(x) = \theta$. Else set $f(x) = (1 - \theta) \cdot g(x)/(1 - G(0))$ where $g(x)$ and $G(x)$ are the density and distribution function of the non-hurdle part, respectively.
hypothesis.brmsfit  Non-Linear Hypothesis Testing

Description

Perform non-linear hypothesis testing for all model parameters.

Usage

## S3 method for class 'brmsfit'
hypothesis(
  x,
  hypothesis,
  class = "b",
  group = "",
  scope = c("standard", "ranef", "coef"),
  alpha = 0.05,
  robust = FALSE,
  seed = NULL,
  ...
)

hypothesis(x, ...)

## Default S3 method:
hypothesis(x, hypothesis, alpha = 0.05, robust = FALSE, ...)

Arguments

x  An R object. If it is no brmsfit object, it must be coercible to a data.frame. In the latter case, the variables used in the hypothesis argument need to correspond to column names of x, while the rows are treated as representing posterior draws of the variables.

hypothesis  A character vector specifying one or more non-linear hypothesis concerning parameters of the model.

class  A string specifying the class of parameters being tested. Default is "b" for population-level effects. Other typical options are "sd" or "cor". If class = NULL, all parameters can be tested against each other, but have to be specified with their full name (see also variables)

group  Name of a grouping factor to evaluate only group-level effects parameters related to this grouping factor.

scope  Indicates where to look for the variables specified in hypothesis. If "standard", use the full parameter names (subject to the restriction given by class and group). If "coef" or "ranef", compute the hypothesis for all levels of the grouping factor given in "group", based on the output of coef.brmsfit and ranef.brmsfit, respectively.
alpha  The alpha-level of the tests (default is 0.05; see 'Details' for more information).

robust  If FALSE (the default) the mean is used as the measure of central tendency and the standard deviation as the measure of variability. If TRUE, the median and the median absolute deviation (MAD) are applied instead.

seed  A single numeric value passed to set.seed to make results reproducible.

...  Currently ignored.

Details

Among others, hypothesis computes an evidence ratio (Evid.Ratio) for each hypothesis. For a one-sided hypothesis, this is just the posterior probability (Post.Prob) under the hypothesis against its alternative. That is, when the hypothesis is of the form \( a > b \), the evidence ratio is the ratio of the posterior probability of \( a > b \) and the posterior probability of \( a < b \). In this example, values greater than one indicate that the evidence in favor of \( a > b \) is larger than evidence in favor of \( a < b \). For an two-sided (point) hypothesis, the evidence ratio is a Bayes factor between the hypothesis and its alternative computed via the Savage-Dickey density ratio method. That is the posterior density at the point of interest divided by the prior density at that point. Values greater than one indicate that evidence in favor of the point hypothesis has increased after seeing the data. In order to calculate this Bayes factor, all parameters related to the hypothesis must have proper priors and argument sample_prior of function brm must be set to "yes". Otherwise Evid.Ratio (and Post.Prob) will be NA. Please note that, for technical reasons, we cannot sample from priors of certain parameters classes. Most notably, these include overall intercept parameters (prior class "Intercept") as well as group-level coefficients. When interpreting Bayes factors, make sure that your priors are reasonable and carefully chosen, as the result will depend heavily on the priors. In particular, avoid using default priors.

The Evid.Ratio may sometimes be 0 or Inf implying very small or large evidence, respectively, in favor of the tested hypothesis. For one-sided hypotheses pairs, this basically means that all posterior draws are on the same side of the value dividing the two hypotheses. In that sense, instead of 0 or Inf, you may rather read it as Evid.Ratio smaller 1 / S or greater S, respectively, where S denotes the number of posterior draws used in the computations.

The argument alpha specifies the size of the credible interval (i.e., Bayesian confidence interval). For instance, if we tested a two-sided hypothesis and set alpha = 0.05 (5%) an, the credible interval will contain 1 - alpha = 0.95 (95%) of the posterior values. Hence, alpha * 100% of the posterior values will lie outside of the credible interval. Although this allows testing of hypotheses in a similar manner as in the frequentist null-hypothesis testing framework, we strongly argue against using arbitrary cutoffs (e.g., \( p < .05 \)) to determine the 'existence' of an effect.

Value

A brmshypothesis object.

Author(s)

Paul-Christian Buerkner <paul.buerkner@gmail.com>

See Also

brmshypothesis
Examples

```r
## Not run:
## define priors
prior <- c(set_prior("normal(0,2)", class = "b"),
           set_prior("student_t(10,0,1)", class = "sigma"),
           set_prior("student_t(10,0,1)", class = "sd"))

## fit a linear mixed effects models
fit <- brm(time ~ age + sex + disease + (1 + age|patient),
           data = kidney, family = lognormal(),
           prior = prior, sample_prior = "yes",
           control = list(adapt_delta = 0.95))

## perform two-sided hypothesis testing
(hyp1 <- hypothesis(fit, "sexfemale = age + diseasePKD"))
plot(hyp1)

(hypothesis(fit, "exp(age) - 3 = 0", alpha = 0.01))

## perform one-sided hypothesis testing
hypothesis(fit, "diseasePKD + diseaseGN - 3 < 0")

hypothesis(fit, "age < Intercept",
           class = "sd", group = "patient")

## test the amount of random intercept variance on all variance
h <- paste("sd_patient__Intercept^2 / (sd_patient__Intercept^2 +",
            "sd_patient__age^2 + sigma^2) = 0")
(hyp2 <- hypothesis(fit, h, class = NULL))
plot(hyp2)

## test more than one hypothesis at once
h <- c("diseaseGN = diseaseAN", "2 * diseaseGN - diseasePKD = 0")
(hyp3 <- hypothesis(fit, h))
plot(hyp3, ignore_prior = TRUE)

## compute hypotheses for all levels of a grouping factor
hypothesis(fit, "age = 0", scope = "coef", group = "patient")

## use the default method
dat <- as.data.frame(fit)
str(dat)
hypothesis(dat, "b_age > 0")

## End(Not run)
```

inhaler

Clarity of inhaler instructions
Description

Ezzet and Whitehead (1991) analyze data from a two-treatment, two-period crossover trial to compare 2 inhalation devices for delivering the drug salbutamol in 286 asthma patients. Patients were asked to rate the clarity of leaflet instructions accompanying each device, using a 4-point ordinal scale.

Usage

inhaler

Format

A data frame of 572 observations containing information on the following 5 variables.

subject  The subject number
rating  The rating of the inhaler instructions on a scale ranging from 1 to 4
treat  A contrast to indicate which of the two inhaler devices was used
period  A contrast to indicate the time of administration
carry  A contrast to indicate possible carry over effects

Source


Examples

```r
## Not run:
## ordinal regression with family "sratio"
fit1 <- brm(rating ~ treat + period + carry,
            data = inhaler, family = sratio(),
            prior = set_prior("normal(0,5)"))
summary(fit1)
plot(fit1)

## ordinal regression with family "cumulative"
## and random intercept over subjects
fit2 <- brm(rating ~ treat + period + carry + (1|subject),
            data = inhaler, family = cumulative(),
            prior = set_prior("normal(0,5)"))
summary(fit2)
plot(fit2)

## End(Not run)
```
InvGaussian  

The Inverse Gaussian Distribution

Description
Density, distribution function, and random generation for the inverse Gaussian distribution with location \( \mu \), and shape \( \text{shape} \).

Usage
```
dinv_gaussian(x, mu = 1, shape = 1, log = FALSE)
```
```
pinv_gaussian(q, mu = 1, shape = 1, lower.tail = TRUE, log.p = FALSE)
```
```
rinv_gaussian(n, mu = 1, shape = 1)
```

Arguments
- \( x, q \) Vector of quantiles.
- \( \mu \) Vector of locations.
- \( \text{shape} \) Vector of shapes.
- \( \log \) Logical; If TRUE, values are returned on the log scale.
- \( \text{lower.tail} \) Logical; If TRUE (default), return \( P(X \leq x) \). Else, return \( P(X > x) \).
- \( \log.p \) Logical; If TRUE, values are returned on the log scale.
- \( n \) Number of draws to sample from the distribution.

Details
See vignette("brms_families") for details on the parameterization.

inv_logit_scaled  

Scaled inverse logit-link

Description
Computes \( \text{inv_logit}(x) \times (\text{ub} - \text{lb}) + \text{lb} \)

Usage
```
inv_logit_scaled(x, lb = 0, ub = 1)
```
is.brmsfit

Arguments

x  A numeric or complex vector.

lb  Lower bound defaulting to 0.

ub  Upper bound defaulting to 1.

Value

A numeric or complex vector between lb and ub.

is.brmsfit  Checks if argument is a brmsfit object

Description

Checks if argument is a brmsfit object

Usage

is.brmsfit(x)

Arguments

x  An R object

is.brmsfit_multiple  Checks if argument is a brmsfit_multiple object

Description

Checks if argument is a brmsfit_multiple object

Usage

is.brmsfit_multiple(x)

Arguments

x  An R object
is.brmsformula

Description
Checks if argument is a `brmsformula` object

Usage
is.brmsformula(x)

Arguments
x An R object

is.brmsprior

Description
Checks if argument is a `brmsprior` object

Usage
is.brmsprior(x)

Arguments
x An R object

is.brmsterms

Description
Checks if argument is a `brmsterms` object

Usage
is.brmsterms(x)

Arguments
x An R object

See Also
brmsterms
### is.cor_brms

**Check if argument is a correlation structure**

**Description**

Check if argument is one of the correlation structures used in `brms`.

**Usage**

```r
is.cor_brms(x)
is.cor_arma(x)
is.cor_cosy(x)
is.cor_sar(x)
is.cor_car(x)
is.cor_fixed(x)
```

**Arguments**

- `x`: An R object.

### is.mvbrmsformula

**Checks if argument is a mvbrmsformula object**

**Description**

Checks if argument is a `mvbrmsformula` object

**Usage**

```r
is.mvbrmsformula(x)
```

**Arguments**

- `x`: An R object
is.mvbrmsterms Checks if argument is a mvbrmsterms object

Description
Checks if argument is a mvbrmsterms object

Usage
is.mvbrmsterms(x)

Arguments
x An R object

See Also
brmsterms

kfold.brmsfit K-Fold Cross-Validation

Description
Perform exact K-fold cross-validation by refitting the model $K$ times each leaving out one-$K$th of the original data. Folds can be run in parallel using the future package.

Usage
## S3 method for class 'brmsfit'
kfold(
  x,
  ..., 
  K = 10,
  Ksub = NULL,
  folds = NULL,
  group = NULL,
  exact_loo = NULL,
  compare = TRUE,
  resp = NULL,
  model_names = NULL,
  save_fits = FALSE,
  recompile = NULL,
  future_args = list()
)


**Arguments**

- **x**: A `brmsfit` object.
- **...**: Further arguments passed to `brm`.
- **K**: The number of subsets of equal (if possible) size into which the data will be partitioned for performing \( K \)-fold cross-validation. The model is refit \( K \) times, each time leaving out one of the \( K \) subsets. If \( K \) is equal to the total number of observations in the data then \( K \)-fold cross-validation is equivalent to exact leave-one-out cross-validation.
- **Ksub**: Optional number of subsets (of those subsets defined by \( K \)) to be evaluated. If `NULL` (the default), \( K \)-fold cross-validation will be performed on all subsets. If `Ksub` is a single integer, `Ksub` subsets (out of all \( K \)) subsets will be randomly chosen. If `Ksub` consists of multiple integers or a one-dimensional array (created via `as.array`) potentially of length one, the corresponding subsets will be used. This argument is primarily useful, if evaluation of all subsets is infeasible for some reason.
- **folds**: Determines how the subsets are being constructed. Possible values are `NULL` (the default), "stratified", "grouped", or "loo". May also be a vector of length equal to the number of observations in the data. Alters the way `group` is handled. More information is provided in the 'Details' section.
- **group**: Optional name of a grouping variable or factor in the model. What exactly is done with this variable depends on argument `folds`. More information is provided in the 'Details' section.
- **exact_loo**: Deprecated! Please use `folds = "loo"` instead.
- **compare**: A flag indicating if the information criteria of the models should be compared to each other via `loo_compare`.
- **resp**: Optional names of response variables. If specified, predictions are performed only for the specified response variables.
- **model_names**: If `NULL` (the default) will use model names derived from deparsing the call. Otherwise will use the passed values as model names.
- **save_fits**: If `TRUE`, a component `fits` is added to the returned object to store the cross-validated `brmsfit` objects and the indices of the omitted observations for each fold. Defaults to `FALSE`.
- **recompile**: Logical, indicating whether the Stan model should be recompiled. This may be necessary if you are running `reloo` on another machine than the one used to fit the model.
- **future_args**: A list of further arguments passed to `future` for additional control over parallel execution if activated.

**Details**

The `kfold` function performs exact \( K \)-fold cross-validation. First the data are partitioned into \( K \) folds (i.e. subsets) of equal (or as close to equal as possible) size by default. Then the model is refit \( K \) times, each time leaving out one of the \( K \) subsets. If \( K \) is equal to the total number of observations in the data then \( K \)-fold cross-validation is equivalent to exact leave-one-out cross-validation (to
which `loo` is an efficient approximation). The `compare_ic` function is also compatible with the objects returned by `kfold`.

The subsets can be constructed in multiple different ways:

- If both `folds` and `group` are `NULL`, the subsets are randomly chosen so that they have equal (or as close to equal as possible) size.
- If `folds` is `NULL` but `group` is specified, the data is split up into subsets, each time omitting all observations of one of the factor levels, while ignoring argument `K`.
- If `folds` = "stratified" the subsets are stratified after `group` using `loo::kfold_split_stratified`.
- If `folds` = "grouped" the subsets are split by `group` using `loo::kfold_split_grouped`.
- If `folds` = "loo" exact leave-one-out cross-validation will be performed and `K` will be ignored. Further, if `group` is specified, all observations corresponding to the factor level of the currently predicted single value are omitted. Thus, in this case, the predicted values are only a subset of the omitted ones.
- If `folds` is a numeric vector, it must contain one element per observation in the data. Each element of the vector is an integer in `1:` `K` indicating to which of the `K` folds the corresponding observation belongs. There are some convenience functions available in the `loo` package that create integer vectors to use for this purpose (see the Examples section below and also the `kfold-helpers` page).

When running `kfold` on a `brmsfit` created with the `cmdstanr` backend in a different R session, several recompilations will be triggered because by default, `cmdstanr` writes the model executable to a temporary directory. To avoid that, set option "cmdstanr_write_stan_file_dir" to a non-temporary path of your choice before creating the original `brmsfit` (see section 'Examples' below).

Value

`kfold` returns an object that has a similar structure as the objects returned by the `loo` and `waic` methods and can be used with the same post-processing functions.

See Also

`loo`, `reloo`

Examples

```r
# Not run:
fit1 <- brm(count ~ zAge + zBase * Trt + (1|patient) + (1|obs),
            data = epilepsy, family = poisson())
# throws warning about some pareto k estimates being too high
(loo1 <- loo(fit1))
# perform 10-fold cross validation
(kfold1 <- kfold(fit1, chains = 1))

# use the future package for parallelization
library(future)
plan(multiprocess)
kfold(fit1, chains = 1)
```
kfold_predict

Predictions from K-Fold Cross-Validation

Description

Compute and evaluate predictions after performing K-fold cross-validation via kfold.

Usage

kfold_predict(x, method = c("predict", "fitted"), resp = NULL, ...)

Arguments

x

Object of class 'kfold' computed by kfold. For kfold_predict to work, the fitted model objects need to have been stored via argument save_fits of kfold.

method

The method used to make predictions. Either "predict" or "fitted". See predict.brmsfit for details.

resp

Optional names of response variables. If specified, predictions are performed only for the specified response variables.

...

Further arguments passed to prepare_predictions that control several aspects of data validation and prediction.
A list with two slots named 'y' and 'yrep'. Slot y contains the vector of observed responses. Slot yrep contains the matrix of predicted responses, with rows being posterior draws and columns being observations.

See Also

kfold

Examples

```r
## Not run:
fit <- brm(count ~ zBase * Trt + (1|patient),
           data = epilepsy, family = poisson())

# perform k-fold cross validation
(kf <- kfold(fit, save_fits = TRUE, chains = 1))

# define a loss function
rmse <- function(y, yrep) {
  yrep_mean <- colMeans(yrep)
  sqrt(mean((yrep_mean - y)^2))
}

# predict responses and evaluate the loss
kfp <- kfold_predict(kf)
rmse(y = kfp$y, yrep = kfp$yrep)

## End(Not run)
```

kidney

Infections in kidney patients

Description

This dataset, originally discussed in McGilchrist and Aisbett (1991), describes the first and second (possibly right censored) recurrence time of infection in kidney patients using portable dialysis equipment. In addition, information on the risk variables age, sex and disease type is provided.

Usage

kidney
**Format**

A data frame of 76 observations containing information on the following 7 variables.

- **time**  The time to first or second recurrence of the infection, or the time of censoring
- **recur** A factor of levels 1 or 2 indicating if the infection recurred for the first or second time for this patient
- **censored** Either 0 or 1, where 0 indicates no censoring of recurrence time and 1 indicates right censoring
- **patient** The patient number
- **age**  The age of the patient
- **sex**  The sex of the patient
- **disease** A factor of levels other, GN, AN, and PKD specifying the type of disease

**Source**


**Examples**

```r
## Not run:
## performing survival analysis using the "weibull" family
fit1 <- brm(time | cens(censored) ~ age + sex + disease,
            data = kidney, family = weibull, init = "0")
summary(fit1)
plot(fit1)

## adding random intercepts over patients
fit2 <- brm(time | cens(censored) ~ age + sex + disease + (1|patient),
            data = kidney, family = weibull(), init = "0",
            prior = set_prior("cauchy(0,2)", class = "sd"))
summary(fit2)
plot(fit2)

## End(Not run)
```

**lasso**

*Set up a lasso prior in brms*

**Description**

Function used to set up a lasso prior for population-level effects in *brms*. The function does not evaluate its arguments – it exists purely to help set up the model.

**Usage**

```r
lasso(df = 1, scale = 1)
```
**Arguments**

- **df**
  Degrees of freedom of the chi-square prior of the inverse tuning parameter. Defaults to 1.

- **scale**
  Scale of the lasso prior. Defaults to 1.

**Details**

The lasso prior is the Bayesian equivalent to the LASSO method for performing variable selection (Park & Casella, 2008). With this prior, independent Laplace (i.e. double exponential) priors are placed on the population-level effects. The scale of the Laplace priors depends on a tuning parameter that controls the amount of shrinkage. In `brms`, the inverse of the tuning parameter is used so that smaller values imply more shrinkage. The inverse tuning parameter has a chi-square distribution and with degrees of freedom controlled via argument `df` of function `lasso` (defaults to 1). For instance, one can specify a lasso prior using `set_prior("lasso(1)")`. To make sure that shrinkage can equally affect all coefficients, predictors should be one the same scale. If you do not want to standardized all variables, you can adjust the general scale of the lasso prior via argument `scale`, for instance, `lasso(1, scale = 10).

**Value**

A character string obtained by `match.call()` with additional arguments.

**References**


**See Also**

`set_prior`

**Examples**

```r
set_prior(lasso(df = 1, scale = 10))
```

---

**launch_shinystan.brmsfit**

*Interface to shinystan*

**Description**

Provide an interface to `shinystan` for models fitted with `brms`

**Usage**

```r
## S3 method for class 'brmsfit'
launch_shinystan(object, rstudio = getOption("shinystan.rstudio"), ...)
```
Arguments

object A fitted model object typically of class brmsfit.
rstudio Only relevant for RStudio users. The default (rstudio=FALSE) is to launch the
app in the default web browser rather than RStudio’s pop-up Viewer. Users can
change the default to TRUE by setting the global option
options(shinystan.rstudio = TRUE).
...
Optional arguments to pass to runApp

Value

An S4 shinystan object

See Also

launch_shinystan

Examples

## Not run:
fit <- brm(rating ~ treat + period + carry + (1|subject),
         data = inhaler, family = "gaussian")
launch_shinystan(fit)
## End(Not run)
### logit_scaled

**Scaled logit-link**

**Description**

Computes logit((x - lb) / (ub - lb))

**Usage**

```r
logit_scaled(x, lb = 0, ub = 1)
```

**Arguments**

- **x**
  - A numeric or complex vector.
- **lb**
  - Lower bound defaulting to 0.
- **ub**
  - Upper bound defaulting to 1.

**Value**

A numeric or complex vector.

---

### logm1

**Logarithm with a minus one offset.**

**Description**

Computes log(x - 1).

**Usage**

```r
logm1(x, base = exp(1))
```

**Arguments**

- **x**
  - A numeric or complex vector.
- **base**
  - A positive or complex number: the base with respect to which logarithms are computed. Defaults to $e = \exp(1)$.
**Description**

Compute the Pointwise Log-Likelihood

**Usage**

```r
## S3 method for class 'brmsfit'
log_lik(
  object,
  newdata = NULL,
  re_formula = NULL,
  resp = NULL,
  ndraws = NULL,
  draw_ids = NULL,
  pointwise = FALSE,
  combine = TRUE,
  add_point_estimate = FALSE,
  cores = NULL,
  ...
)
```

**Arguments**

- `object`: A fitted model object of class `brmsfit`.
- `newdata`: An optional data.frame for which to evaluate predictions. If NULL (default), the original data of the model is used. NA values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.
- `re_formula`: formula containing group-level effects to be considered in the prediction. If NULL (default), include all group-level effects; if NA, include no group-level effects.
- `resp`: Optional names of response variables. If specified, predictions are performed only for the specified response variables.
- `ndraws`: Positive integer indicating how many posterior draws should be used. If NULL (the default) all draws are used. Ignored if `draw_ids` is not NULL.
- `draw_ids`: An integer vector specifying the posterior draws to be used. If NULL (the default), all draws are used.
- `pointwise`: A flag indicating whether to compute the full log-likelihood matrix at once (the default), or just return the likelihood function along with all data and draws required to compute the log-likelihood separately for each observation. The latter option is rarely useful when calling `log_lik` directly, but rather when computing `waic` or `loo`.
combine

Only relevant in multivariate models. Indicates if the log-likelihoods of the sub-models should be combined per observation (i.e. added together; the default) or if the log-likelihoods should be returned separately.

add_point_estimate

For internal use only. Ensures compatibility with the loo_subsample method.

cores

Number of cores (defaults to 1). On non-Windows systems, this argument can be set globally via the mc.cores option.

...

Further arguments passed to prepare_predictions that control several aspects of data validation and prediction.

Details

NA values within factors in newdata, are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.

In multilevel models, it is possible to allow new levels of grouping factors to be used in the predictions. This can be controlled via argument allow_new_levels. New levels can be sampled in multiple ways, which can be controlled via argument sample_new_levels. Both of these arguments are documented in prepare_predictions along with several other useful arguments to control specific aspects of the predictions.

Value

Usually, an S x N matrix containing the pointwise log-likelihood draws, where S is the number of draws and N is the number of observations in the data. For multivariate models and if combine is FALSE, an S x N x R array is returned, where R is the number of response variables. If pointwise = TRUE, the output is a function with a draws attribute containing all relevant data and posterior draws.

Description

Perform approximate leave-one-out cross-validation based on the posterior likelihood using the loo package. For more details see loo.

Usage

## S3 method for class 'brmsfit'

loo(
  x,
  ...,
  compare = TRUE,
  resp = NULL,
  pointwise = FALSE,
  moment_match = FALSE,
Arguments

x
A brmsfit object.

... More brmsfit objects or further arguments passed to the underlying post-processing functions. In particular, see prepare_predictions for further supported arguments.

compare A flag indicating if the information criteria of the models should be compared to each other via loo_compare.

resp Optional names of response variables. If specified, predictions are performed only for the specified response variables.

pointwise A flag indicating whether to compute the full log-likelihood matrix at once or separately for each observation. The latter approach is usually considerably slower but requires much less working memory. Accordingly, if one runs into memory issues, pointwise = TRUE is the way to go.

moment_match Logical; Indicate whether loo_moment_match should be applied on problematic observations. Defaults to FALSE. For most models, moment matching will only work if you have set save_pars = save_pars(all = TRUE) when fitting the model with brm. See loo_moment_match.brmsfit for more details.

reloo Logical; Indicate whether reloo should be applied on problematic observations. Defaults to FALSE.

k_threshold The threshold at which pareto k estimates are treated as problematic. Defaults to 0.7. Only used if argument reloo is TRUE. See pareto_k_ids for more details.

save_psis Should the “psis” object created internally be saved in the returned object? For more details see loo.

moment_match_args Optional list of additional arguments passed to loo_moment_match.

reloo_args Optional list of additional arguments passed to reloo.

model_names If NULL (the default) will use model names derived from deparsing the call. Otherwise will use the passed values as model names.

Details

See loo_compare for details on model comparisons. For brmsfit objects, LOO is an alias of loo. Use method add_criterion to store information criteria in the fitted model object for later usage.

Value

If just one object is provided, an object of class loo. If multiple objects are provided, an object of class loolist.
References


Examples

```r
## Not run:
# model with population-level effects only
fit1 <- brm(rating ~ treat + period + carry,
            data = inhaler)
(loo1 <- loo(fit1))

# model with an additional varying intercept for subjects
fit2 <- brm(rating ~ treat + period + carry + (1|subject),
            data = inhaler)
(loo2 <- loo(fit2))

# compare both models
loo_compare(loo1, loo2)

## End(Not run)
```

loo_compare.brmsfit  
Model comparison with the **loo** package

Description

For more details see `loo_compare`.

Usage

```r
## S3 method for class 'brmsfit'
loo_compare(x, ..., criterion = c("loo", "waic", "kfold"), model_names = NULL)
```

Arguments

- `x` A `brmsfit` object.
- `...` More `brmsfit` objects.
- `criterion` The name of the criterion to be extracted from `brmsfit` objects.
- `model_names` If `NULL` (the default) will use model names derived from deparsing the call. Otherwise will use the passed values as model names.
Details

All brmsfit objects should contain precomputed criterion objects. See \texttt{add_criterion} for more help.

Value

An object of class \texttt{"compare.loo"}.

Examples

```r
## Not run:
# model with population-level effects only
fit1 <- brm(rating ~ treat + period + carry,
            data = inhaler)
fit1 <- add_criterion(fit1, "waic")

# model with an additional varying intercept for subjects
fit2 <- brm(rating ~ treat + period + carry + (1|subject),
            data = inhaler)
fit2 <- add_criterion(fit2, "waic")

# compare both models
loo_compare(fit1, fit2, criterion = "waic")
## End(Not run)
```

---

\texttt{loo_model_weights.brmsfit}

\textit{Model averaging via stacking or pseudo-BMA weighting.}

Description

Compute model weights for \texttt{brmsfit} objects via stacking or pseudo-BMA weighting. For more details, see \texttt{loo::loo_model_weights}.

Usage

```
## S3 method for class 'brmsfit'
loo_model_weights(x, ..., model_names = NULL)
```

Arguments

- \texttt{x} \ A \texttt{brmsfit} object.
- \texttt{...} \ More \texttt{brmsfit} objects or further arguments passed to the underlying post-processing functions. In particular, see \texttt{prepare_predictions} for further supported arguments.
- \texttt{model_names} \ If \texttt{NULL} (the default) will use model names derived from deparsing the call. Otherwise will use the passed values as model names.
Value

A named vector of model weights.

Examples

## Not run:
# model with population-level effects only
fit1 <- brm(rating ~ treat + period + carry, 
            data = inhaler, family = "gaussian")
# model with an additional varying intercept for subjects
fit2 <- brm(rating ~ treat + period + carry + (1|subject), 
            data = inhaler, family = "gaussian")
loo_model_weights(fit1, fit2)

## End(Not run)

---

**loo_moment_match.brmsfit**

*Moment matching for efficient approximate leave-one-out cross-validation*

Description

Moment matching for efficient approximate leave-one-out cross-validation (LOO-CV). See `loo_moment_match` for more details.

Usage

```r
## S3 method for class 'brmsfit'
loo_moment_match(
  x, 
  loo, 
  k_threshold = 0.7, 
  newdata = NULL, 
  resp = NULL, 
  check = TRUE, 
  recompile = FALSE, 
  ...
)
```

Arguments

- **x** An object of class `brmsfit`.
- **loo** An object of class `loo` originally created from `x`.
- **k_threshold** The threshold at which Pareto $k$ estimates are treated as problematic. Defaults to `0.7`. See `pareto_k_ids` for more details.
newdata An optional data.frame for which to evaluate predictions. If NULL (default), the original data of the model is used. NA values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.

resp Optional names of response variables. If specified, predictions are performed only for the specified response variables.

check Logical; If TRUE (the default), some checks are performed if the loo object was generated from the brmsfit object passed to argument fit.

recompile Logical, indicating whether the Stan model should be recompiled. This may be necessary if you are running moment matching on another machine than the one used to fit the model. No recompilation is done by default.

... Further arguments passed to the underlying methods. Additional arguments initially passed to loo, for example, newdata or resp need to be passed again to loo_moment_match in order for the latter to work correctly.

Details

The moment matching algorithm requires draws of all variables defined in Stan’s parameters block to be saved. Otherwise loo_moment_match cannot be computed. Thus, please set save_pars = save_pars(all = TRUE) in the call to brm, if you are planning to apply loo_moment_match to your models.

Value

An updated object of class loo.

References


Examples

```r
## Not run:
fit1 <- brm(count ~ zAge + zBase * Trt + (1|patient),
            data = epilepsy, family = poisson(),
            save_pars = save_pars(all = TRUE))

# throws warning about some pareto k estimates being too high
(loo1 <- loo(fit1))
(mmloo1 <- loo_moment_match(fit1, loo = loo1))
```

## End(Not run)
**loo_predict.brmsfit**  
*Compute Weighted Expectations Using LOO*

**Description**
These functions are wrappers around the `E_loo` function of the `loo` package.

**Usage**
```r
## S3 method for class 'brmsfit'
loo_predict(
  object,
  type = c("mean", "var", "quantile"),
  probs = 0.5,
  psis_object = NULL,
  resp = NULL,
  ...
)

## S3 method for class 'brmsfit'
loo_linpred(
  object,
  type = c("mean", "var", "quantile"),
  probs = 0.5,
  psis_object = NULL,
  resp = NULL,
  ...
)

## S3 method for class 'brmsfit'
loo_predictive_interval(object, prob = 0.9, psis_object = NULL, ...)
```

**Arguments**
- `object`  
  An object of class `brmsfit`.
- `type`  
  The statistic to be computed on the results. Can be either "mean" (default), "var", or "quantile".
- `probs`  
  A vector of quantiles to compute. Only used if `type = quantile`.
- `psis_object`  
  An optional object returned by `psis`. If `psis_object` is missing then `psis` is executed internally, which may be time consuming for models fit to very large datasets.
- `resp`  
  Optional names of response variables. If specified, predictions are performed only for the specified response variables.
- `...`  
  Optional arguments passed to the underlying methods that is `log_lik`, as well as `posterior_predict` or `posterior_linpred`.
- `prob`  
  For `loo_predictive_interval`, a scalar in (0, 1) indicating the desired probability mass to include in the intervals. The default is `prob = 0.9` (90% intervals).
Value

loo_predict and loo_linpred return a vector with one element per observation. The only exception is if `type = "quantile"` and `length(probs) >= 2`, in which case a separate vector for each element of `probs` is computed and they are returned in a matrix with `length(probs)` rows and one column per observation.

loo_predictive_interval returns a matrix with one row per observation and two columns. `loo_predictive_interval(..., prob = p)` is equivalent to `loo_predict(..., type = "quantile", probs = c(a, 1-a))` with `a = (1 - p)/2`, except it transposes the result and adds informative column names.

Examples

```r
## Not run:
## data from help("lm")
ctl <- c(4.17,5.58,5.18,6.11,4.50,4.61,5.17,4.53,5.33,5.14)
trt <- c(4.81,4.17,4.41,3.59,5.87,3.83,6.03,4.89,4.32,4.69)
d <- data.frame(
  weight = c(ctl, trt),
  group = gl(2, 10, 20, labels = c("Ctl", "Trt"))
)
fit <- brm(weight ~ group, data = d)
loo_predictive_interval(fit, prob = 0.8)
## optionally log-weights can be pre-computed and reused
psis <- loo::psis(-log_lik(fit), cores = 2)
loo_predictive_interval(fit, prob = 0.8, psis_object = psis)
loo_predict(fit, type = "var", psis_object = psis)
## End(Not run)
```

Description

Compute a LOO-adjusted R-squared for regression models

Usage

```r
## S3 method for class 'brmsfit'
loo_R2(
  object,
  resp = NULL,
  summary = TRUE,
  robust = FALSE,
  probs = c(0.025, 0.975),
  ...
)
```
Arguments

object An object of class brmsfit.
resp Optional names of response variables. If specified, predictions are performed only for the specified response variables.
summary Should summary statistics be returned instead of the raw values? Default is TRUE.
robust If FALSE (the default) the mean is used as the measure of central tendency and the standard deviation as the measure of variability. If TRUE, the median and the median absolute deviation (MAD) are applied instead. Only used if summary is TRUE.
probs The percentiles to be computed by the quantile function. Only used if summary is TRUE.
... Further arguments passed to posterior_epred and log_lik, which are used in the computation of the R-squared values.

Value

If summary = TRUE, an M x C matrix is returned (M = number of response variables and c = length(probs) + 2) containing summary statistics of the LOO-adjusted R-squared values. If summary = FALSE, the posterior draws of the LOO-adjusted R-squared values are returned in an S x M matrix (S is the number of draws).

Examples

```r
## Not run:
fit <- brm(mpg ~ wt + cyl, data = mtcars)
summary(fit)
loo_R2(fit)

# compute R2 with new data
nd <- data.frame(mpg = c(10, 20, 30), wt = c(4, 3, 2), cyl = c(8, 6, 4))
loo_R2(fit, newdata = nd)
## End(Not run)
```

Efficient approximate leave-one-out cross-validation (LOO) using subsampling
## S3 method for class 'brmsfit'

```r
txt
```

```r
loo_subsample(x, ..., compare = TRUE, resp = NULL, model_names = NULL)
```

### Arguments

- **x**: A `brmsfit` object.
- **...**: More `brmsfit` objects or further arguments passed to the underlying post-processing functions. In particular, see `prepare_predictions` for further supported arguments.
- **compare**: A flag indicating if the information criteria of the models should be compared to each other via `loo_compare`.
- **resp**: Optional names of response variables. If specified, predictions are performed only for the specified response variables.
- **model_names**: If `NULL` (the default) will use model names derived from deparsing the call. Otherwise will use the passed values as model names.

### Details

More details can be found on `loo_subsample`.

### Examples

```r
## Not run:
# model with population-level effects only
fit1 <- brm(rating ~ treat + period + carry,
             data = inhaler)
(loo1 <- loo_subsample(fit1))

# model with an additional varying intercept for subjects
fit2 <- brm(rating ~ treat + period + carry + (1|subject),
            data = inhaler)
(loo2 <- loo_subsample(fit2))

# compare both models
loo_compare(loo1, loo2)

## End(Not run)
```

---

### Description

This dataset, discussed in Gesmann & Morris (2020), contains cumulative insurance loss payments over the course of ten years.
Usage

loss

Format

A data frame of 55 observations containing information on the following 4 variables.

- **AY**: Origin year of the insurance (1991 to 2000)
- **dev**: Deviation from the origin year in months
- **cum**: Cumulative loss payments
- **premium**: Achieved premiums for the given origin year

Source


Examples

```r
## Not run:
# non-linear model to predict cumulative loss payments
fit_loss <- brm(
  bf(cum ~ ult * (1 - exp(-(dev/theta)^omega)),
     ult ~ 1 + (1|AY), omega ~ 1, theta ~ 1,
     nl = TRUE),
  data = loss, family = gaussian(),
  prior = c(
    prior(normal(5000, 1000), nlpar = "ult"),
    prior(normal(1, 2), nlpar = "omega"),
    prior(normal(45, 10), nlpar = "theta")
  ),
  control = list(adapt_delta = 0.9)
)

# basic summaries
summary(fit_loss)
conditional_effects(fit_loss)

# plot predictions per origin year
conditions <- data.frame(AY = unique(loss$AY))
rownames(conditions) <- unique(loss$AY)
me_loss <- conditional_effects(
  fit_loss, conditions = conditions,
  re_formula = NULL, method = "predict"
)
plot(me_loss, ncol = 5, points = TRUE)

## End(Not run)
```
Set up MA(q) correlation structures

Description

Set up a moving average (MA) term of order q in brms. The function does not evaluate its arguments – it exists purely to help set up a model with MA terms.

Usage

ma(time = NA, gr = NA, q = 1, cov = FALSE)

Arguments

time: An optional time variable specifying the time ordering of the observations. By default, the existing order of the observations in the data is used.
gr: An optional grouping variable. If specified, the correlation structure is assumed to apply only to observations within the same grouping level.
q: A non-negative integer specifying the moving average (MA) order of the ARMA structure. Default is 1.
cov: A flag indicating whether ARMA effects should be estimated by means of residual covariance matrices. This is currently only possible for stationary ARMA effects of order 1. If the model family does not have natural residuals, latent residuals are added automatically. If FALSE (the default), a regression formulation is used that is considerably faster and allows for ARMA effects of order higher than 1 but is only available for gaussian models and some of its generalizations.

Value

An object of class 'arma_term', which is a list of arguments to be interpreted by the formula parsing functions of brms.

See Also

autocor-terms, arma, ar

Examples

```r
## Not run:
data("LakeHuron")
LakeHuron <- as.data.frame(LakeHuron)
fit <- brm(x ~ ma(p = 2), data = LakeHuron)
summary(fit)
## End(Not run)
```
make_conditions

Prepare Fully Crossed Conditions

Description

This is a helper function to prepare fully crossed conditions primarily for use with the conditions argument of conditional_effects. Automatically creates labels for each row in the cond__ column.

Usage

make_conditions(x, vars, ...)

Arguments

x An R object from which to extract the variables that should be part of the conditions.

vars Names of the variables that should be part of the conditions.

... Arguments passed to rows2labels.

Details

For factor like variables, all levels are used as conditions. For numeric variables, mean + (-1:1) * SD are used as conditions.

Value

A data.frame where each row indicates a condition.

See Also

conditional_effects, rows2labels

Examples

df <- data.frame(x = c("a", "b"), y = rnorm(10))
make_conditions(df, vars = c("x", "y"))
**Description**

Generate Stan code for **brms** models

**Usage**

```r
make_stancode(
    formula, data,
    family = gaussian(),
    prior = NULL,
    autocor = NULL,
    data2 = NULL,
    cov_ranef = NULL,
    sparse = NULL,
    sample_prior = "no",
    stanvars = NULL,
    stan_funs = NULL,
    knots = NULL,
    dropUnusedLevels = TRUE,
    threads =getOption("brms.threads", NULL),
    normalize =getOption("brms.normalize", TRUE),
    save_model = NULL,
    ...,
)
```

**Arguments**

- **formula**: An object of class `formula`, `brmsformula`, or `mvbrmsformula` (or one that can be coerced to that classes): A symbolic description of the model to be fitted. The details of model specification are explained in `brmsformula`.
- **data**: An object of class `data.frame` (or one that can be coerced to that class) containing data of all variables used in the model.
- **family**: A description of the response distribution and link function to be used in the model. This can be a family function, a call to a family function or a character string naming the family. Every family function has a link argument allowing to specify the link function to be applied on the response variable. If not specified, default links are used. For details of supported families see `brmsfamily`. By default, a linear gaussian model is applied. In multivariate models, family might also be a list of families.
- **prior**: One or more `brmsprior` objects created by `set_prior` or related functions and combined using the `c` method or the `+` operator. See also `get_prior` for more help.
autocor (Deprecated) An optional cor_brms object describing the correlation structure within the response variable (i.e., the 'autocorrelation'). See the documentation of cor_brms for a description of the available correlation structures. Defaults to NULL, corresponding to no correlations. In multivariate models, autocor might also be a list of autocorrelation structures. It is now recommend to specify autocorrelation terms directly within formula. See brmsformula for more details.

data2 A named list of objects containing data, which cannot be passed via argument data. Required for some objects used in autocorrelation structures to specify dependency structures as well as for within-group covariance matrices.

cov_ranef (Deprecated) A list of matrices that are proportional to the (within) covariance structure of the group-level effects. The names of the matrices should correspond to columns in data that are used as grouping factors. All levels of the grouping factor should appear as rownames of the corresponding matrix. This argument can be used, among others to model pedigrees and phylogenetic effects. It is now recommended to specify those matrices in the formula interface using the gr and related functions. See vignette("brms_phylogenetics") for more details.

sparse (Deprecated) Logical; indicates whether the population-level design matrices should be treated as sparse (defaults to FALSE). For design matrices with many zeros, this can considerably reduce required memory. Sampling speed is currently not improved or even slightly decreased. It is now recommended to use the sparse argument of brmsformula and related functions.

sample_prior Indicate if draws from priors should be drawn additionally to the posterior draws. Options are "no" (the default), "yes", and "only". Among others, these draws can be used to calculate Bayes factors for point hypotheses via hypothesis. Please note that improper priors are not sampled, including the default improper priors used by brm. See set_prior on how to set (proper) priors. Please also note that prior draws for the overall intercept are not obtained by default for technical reasons. See brmsformula how to obtain prior draws for the intercept. If sample_prior is set to "only", draws are drawn solely from the priors ignoring the likelihood, which allows among others to generate draws from the prior predictive distribution. In this case, all parameters must have proper priors.

stanvars An optional stanvars object generated by function stanvar to define additional variables for use in Stan’s program blocks.

stan_funs (Deprecated) An optional character string containing self-defined Stan functions, which will be included in the functions block of the generated Stan code. It is now recommended to use the stanvars argument for this purpose instead.

knots Optional list containing user specified knot values to be used for basis construction of smoothing terms. See gamm for more details.

drop_unused_levels Should unused factors levels in the data be dropped? Defaults to TRUE.

threads Number of threads to use in within-chain parallelization. For more control over the threading process, threads may also be a brmstthreads object created by threading. Within-chain parallelization is experimental! We recommend its use only if you are experienced with Stan's reduce_sum function and have a slow running model that cannot be sped up by any other means. Can be set globally for the current R session via the "brms.threads" option (see options).
make_standata

normalize Logical. Indicates whether normalization constants should be included in the Stan code (defaults to TRUE). Setting it to FALSE requires Stan version >= 2.25 to work. If FALSE, sampling efficiency may be increased but some post processing functions such as bridge_sampler will not be available. Can be controlled globally for the current R session via the ‘brms.normalize’ option.

save_model Either NULL or a character string. In the latter case, the model’s Stan code is saved via cat in a text file named after the string supplied in save_model.

... Other arguments for internal usage only.

Value

A character string containing the fully commented Stan code to fit a brms model.

Examples

make_stancode(rating ~ treat + period + carry + (1|subject),
              data = inhaler, family = "cumulative")

make_stancode(count ~ zAge + zBase * Trt + (1|patient),
               data = epilepsy, family = "poisson")

make_standata

Data for brms Models

Description

Generate data for brms models to be passed to Stan

Usage

make_standata(
  formula,
  data,
  family = gaussian(),
  prior = NULL,
  autocor = NULL,
  data2 = NULL,
  cov_ranef = NULL,
  sample_prior = "no",
  stanvars = NULL,
  threads =getOption("brms.threads", NULL),
  knots = NULL,
  drop_unused_levels = TRUE,
  ...
)
Arguments

**formula**
An object of class `formula`, `brmsformula`, or `mvbrmsformula` (or one that can be coerced to that classes): A symbolic description of the model to be fitted. The details of model specification are explained in `brmsformula`.

**data**
An object of class `data.frame` (or one that can be coerced to that class) containing data of all variables used in the model.

**family**
A description of the response distribution and link function to be used in the model. This can be a family function, a call to a family function or a character string naming the family. Every family function has a `link` argument allowing to specify the link function to be applied on the response variable. If not specified, default links are used. For details of supported families see `brmsfamily`. By default, a linear gaussian model is applied. In multivariate models, family might also be a list of families.

**prior**
One or more `brmsprior` objects created by `set_prior` or related functions and combined using the `c` method or the `+` operator. See also `get_prior` for more help.

**autocor**
(Deprecated) An optional `cor_brms` object describing the correlation structure within the response variable (i.e., the 'autocorrelation'). See the documentation of `cor_brms` for a description of the available correlation structures. Defaults to `NULL`, corresponding to no correlations. In multivariate models, autocor might also be a list of autocorrelation structures. It is now recommend to specify autocorrelation terms directly within formula. See `brmsformula` for more details.

**data2**
A named list of objects containing data, which cannot be passed via argument `data`. Required for some objects used in autocorrelation structures to specify dependency structures as well as for within-group covariance matrices.

**cov_ranef**
(Deprecated) A list of matrices that are proportional to the (within) covariance structure of the group-level effects. The names of the matrices should correspond to columns in `data` that are used as grouping factors. All levels of the grouping factor should appear as rownames of the corresponding matrix. This argument can be used, among others to model pedigrees and phylogenetic effects. It is now recommended to specify those matrices in the formula interface using the `gr` and related functions. See vignette("brms_phylogenetics") for more details.

**sample_prior**
Indicate if draws from priors should be drawn additionally to the posterior draws. Options are "no" (the default), "yes", and "only". Among others, these draws can be used to calculate Bayes factors for point hypotheses via `hypothesis`. Please note that improper priors are not sampled, including the default improper priors used by `brm`. See `set_prior` on how to set (proper) priors. Please also note that prior draws for the overall intercept are not obtained by default for technical reasons. See `brmsformula` how to obtain prior draws for the intercept. If `sample_prior` is set to "only", draws are drawn solely from the priors ignoring the likelihood, which allows among others to generate draws from the prior predictive distribution. In this case, all parameters must have proper priors.

**stanvars**
An optional `stanvars` object generated by function `stanvar` to define additional variables for use in Stan's program blocks.
threads
Number of threads to use in within-chain parallelization. For more control over
the threading process, threads may also be a brmstthreads object created by
threading. Within-chain parallelization is experimental! We recommend its
use only if you are experienced with Stan’s reduce_sum function and have a
slow running model that cannot be sped up by any other means. Can be set glob-
ally for the current R session via the “brms.threads” option (see options).

knots
Optional list containing user specified knot values to be used for basis construc-
tion of smoothing terms. See gamm for more details.

drop_unused_levels
Should unused factors levels in the data be dropped? Defaults to TRUE.

... Other arguments for internal use.

Value
A named list of objects containing the required data to fit a brms model with Stan.

Author(s)
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Examples
sdata1 <- make_standata(rating ~ treat + period + carry + (1|subject),
data = inhaler, family = "cumulative")
str(sdata1)
sdata2 <- make_standata(count ~ zAge + zBase * Trt + (1|patient),
data = epilepsy, family = "poisson")
str(sdata2)

mcmc_plot.brmsfit MCMC Plots Implemented in bayesplot

Description
Convenient way to call MCMC plotting functions implemented in the bayesplot package.

Usage
## S3 method for class 'brmsfit'
mcmc_plot(
  object,
pars = NA,
type = "intervals",
variable = NULL,
regex = FALSE,
mcmc_plot.brmsfit

```r
fixed = FALSE,
...
)

mcmc_plot(object, ...)
```

**Arguments**

- **object**: An R object typically of class `brmsfit`
- **pars**: Deprecated alias of `variable`. Names of the parameters to plot, as given by a character vector or a regular expression.
- **type**: The type of the plot. Supported types are (as names) `hist`, `dens`, `hist_by_chain`, `dens_overlay`, `violin`, `intervals`, `areas`, `acf`, `acf_bar`, `trace`, `trace_highlight`, `scatter`, `rhat`, `rhat_hist`, `neff`, `neff_hist`, `nuts_acceptance`, `nuts_divergence`, `nuts_stepsize`, `nuts_treedepth`, and `nuts_energy`. For an overview on the various plot types see `MCMC-overview`.
- **variable**: Names of the variables (parameters) to plot, as given by a character vector or a regular expression (if `regex = TRUE`). By default, a hopefully not too large selection of variables is plotted.
- **regex**: Logical; Indicates whether `variable` should be treated as regular expressions. Defaults to `FALSE`.
- **fixed** (Deprecated) Indicates whether parameter names should be matched exactly (TRUE) or treated as regular expressions (FALSE). Default is FALSE and only works with argument `pars`.
- **...**: Additional arguments passed to the plotting functions. See `MCMC-overview` for more details.

**Details**

Also consider using the `shinystan` package available via method `launch_shinystan` in `brms` for flexible and interactive visual analysis.

**Value**

A `ggplot` object that can be further customized using the `ggplot2` package.

**Examples**

```r
## Not run:
model <- brm(count ~ zAge + zBase * Trt + (1|patient),
             data = epilepsy, family = "poisson")

# plot posterior intervals
mcmc_plot(model)

# only show population-level effects in the plots
mcmc_plot(model, variable = "^b_", regex = TRUE)
```


# show histograms of the posterior distributions
mcmc_plot(model, type = "hist")

# plot some diagnostics of the sampler
mcmc_plot(model, type = "neff")
mcmc_plot(model, type = "rhat")

# plot some diagnostics specific to the NUTS sampler
mcmc_plot(model, type = "nuts_acceptance")
mcmc_plot(model, type = "nuts_divergence")

## End(Not run)

---

### me

**Predictors with Measurement Error in brms Models**

#### Description

(Soft deprecated) Specify predictors with measurement error. The function does not evaluate its arguments – it exists purely to help set up a model.

#### Usage

```r
me(x, sdx, gr = NULL)
```

#### Arguments

- **x**: The variable measured with error.
- **sdx**: Known measurement error of `x` treated as standard deviation.
- **gr**: Optional grouping factor to specify which values of `x` correspond to the same value of the latent variable. If `NULL` (the default) each observation will have its own value of the latent variable.

#### Details

For detailed documentation see `help(brmsformula)`. `me` terms are soft deprecated in favor of the more general and consistent `mi` terms. By default, latent noise-free variables are assumed to be correlated. To change that, add `set_mecor(FALSE)` to your model formula object (see examples).

#### See Also

`brmsformula`, `brmsformula-helpers`
### mi

**Predictors with Missing Values in brms Models**

#### Description

Specify predictor term with missing values in brms. The function does not evaluate its arguments – it exists purely to help set up a model. For documentation on how to specify missing values in response variables, see `resp_mi`.

#### Usage

```r
mi(x, idx = NA)
```

#### Arguments

- `x`  
The variable containing missing values.
- `idx`  
An optional variable containing indices of observations in `x` that are to be used in the model. This is mostly relevant in partially subsetted models (via `resp_subset`) but may also have other applications that I haven’t thought of.

#### Details

For detailed documentation see `help(brmsformula)`.

#### See Also

`brmsformula`
## Examples

```r
## Not run:
data("nhanes", package = "mice")
N <- nrow(nhanes)

# simple model with missing data
bform1 <- bf(bmi | mi() ~ age * mi(chl)) +
  bf(chl | mi() ~ age) +
  set_rescor(FALSE)

fit1 <- brm(bform1, data = nhanes)
summary(fit1)
plot(conditional_effects(fit1, resp = "bmi"), ask = FALSE)
loo(fit1, newdata = na.omit(fit1$data))

# simulate some measurement noise
nhanes$se <- rexp(N, 2)

# measurement noise can be handled within 'mi' terms
# with or without the presence of missing values
bform2 <- bf(bmi | mi() ~ age * mi(chl)) +
  bf(chl | mi(se) ~ age) +
  set_rescor(FALSE)

fit2 <- brm(bform2, data = nhanes)
summary(fit2)
plot(conditional_effects(fit2, resp = "bmi"), ask = FALSE)

# 'mi' terms can also be used when some responses are subsetted
nhanes$sub <- TRUE
nhanes$sub[1:2] <- FALSE
nhanes$id <- 1:N
nhanes$idx <- sample(3:N, N, TRUE)

# this requires the addition term 'index' being specified
# in the subsetted part of the model
bform3 <- bf(bmi | mi() ~ age * mi(chl, idx)) +
  bf(chl | mi(se) + subset(sub) + index(id) ~ age) +
  set_rescor(FALSE)

fit3 <- brm(bform3, data = nhanes)
summary(fit3)
plot(conditional_effects(fit3, resp = "bmi"), ask = FALSE)

## End(Not run)
```
mixture

Finite Mixture Families in \textit{brms}

Description

Set up a finite mixture family for use in \textit{brms}.

Usage

\texttt{mixture(..., flist = NULL, nmix = 1, order = NULL)}

Arguments

\texttt{...} \quad One or more objects providing a description of the response distributions to be combined in the mixture model. These can be family functions, calls to family functions or character strings naming the families. For details of supported families see \texttt{brmsfamily}.

\texttt{flist} \quad Optional list of objects, which are treated in the same way as objects passed via the \texttt{...} argument.

\texttt{nmix} \quad Optional numeric vector specifying the number of times each family is repeated. If specified, it must have the same length as the number of families passed via \texttt{...} and \texttt{flist}.

\texttt{order} \quad Ordering constraint to identify mixture components. If 'mu' or TRUE, population-level intercepts of the mean parameters are ordered in non-ordinal models and fixed to the same value in ordinal models (see details). If 'none' or FALSE, no ordering constraint is applied. If NULL (the default), order is set to 'mu' if all families are the same and 'none' otherwise. Other ordering constraints may be implemented in the future.

Details

Most families supported by \textit{brms} can be used to form mixtures. The response variable has to be valid for all components of the mixture family. Currently, the number of mixture components has to be specified by the user. It is not yet possible to estimate the number of mixture components from the data.

Ordering intercepts in mixtures of ordinal families is not possible as each family has itself a set of vector of intercepts (i.e. ordinal thresholds). Instead, \textit{brms} will fix the vector of intercepts across components in ordinal mixtures, if desired, so that users can try to identify the mixture model via selective inclusion of predictors.

For most mixture models, you may want to specify priors on the population-level intercepts via \texttt{set_prior} to improve convergence. In addition, it is sometimes necessary to set \texttt{init = 0} in the call to \textit{brm} to allow chains to initialize properly.

For more details on the specification of mixture models, see \texttt{brmsformula}.
Value

An object of class mixfamily.

Examples

```r
## Not run:
## simulate some data
set.seed(1234)
dat <- data.frame(
  y = c(rnorm(200), rnorm(100, 6)),
  x = rnorm(300),
  z = sample(0:1, 300, TRUE)
)

## fit a simple normal mixture model
mix <- mixture(gaussian, gaussian)
prior <- c(
  prior(normal(0, 7), Intercept, dpar = mu1),
  prior(normal(5, 7), Intercept, dpar = mu2)
)
fit1 <- brm(bf(y ~ x + z), dat, family = mix,
  prior = prior, chains = 2)
summary(fit1)
pp_check(fit1)

## use different predictors for the components
fit2 <- brm(bf(y ~ 1, mu1 ~ x, mu2 ~ z), dat, family = mix,
  prior = prior, chains = 2)
summary(fit2)

## fix the mixing proportions
fit3 <- brm(bf(y ~ x + z, theta1 = 1, theta2 = 2),
  dat, family = mix, prior = prior,
  init = 0, chains = 2)
summary(fit3)
pp_check(fit3)

## predict the mixing proportions
fit4 <- brm(bf(y ~ x + z, theta2 ~ x),
  dat, family = mix, prior = prior,
  init = 0, chains = 2)
summary(fit4)
pp_check(fit4)

## compare model fit
LOO(fit1, fit2, fit3, fit4)

## End(Not run)
```
Set up multi-membership grouping terms in \textbf{brms}

\textbf{Description}

Function to set up a multi-membership grouping term in \textbf{brms}. The function does not evaluate its arguments – it exists purely to help set up a model with grouping terms.

\textbf{Usage}

\begin{verbatim}
mm( 
  ..., 
  weights = NULL, 
  scale = TRUE, 
  by = NULL, 
  cor = TRUE, 
  id = NA, 
  cov = NULL, 
  dist = "gaussian"
)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{...}: One or more terms containing grouping factors.
  \item \texttt{weights}: A matrix specifying the weights of each member. It should have as many columns as grouping terms specified in \texttt{...}. If \texttt{NULL} (the default), equally weights are used.
  \item \texttt{scale}: Logical; if \texttt{TRUE} (the default), weights are standardized in order to sum to one per row. If negative weights are specified, \texttt{scale} needs to be set to \texttt{FALSE}.
  \item \texttt{by}: An optional factor matrix, specifying sub-populations of the groups. It should have as many columns as grouping terms specified in \texttt{...}. For each level of the by variable, a separate variance-covariance matrix will be fitted. Levels of the grouping factor must be nested in levels of the by variable matrix.
  \item \texttt{cor}: Logical. If \texttt{TRUE} (the default), group-level terms will be modelled as correlated.
  \item \texttt{id}: Optional character string. All group-level terms across the model with the same \texttt{id} will be modeled as correlated (if \texttt{cor} is \texttt{TRUE}). See \texttt{brmsformula} for more details.
  \item \texttt{cov}: An optional matrix which is proportional to the within-group covariance matrix of the group-level effects. All levels of the grouping factor should appear as row-names of the corresponding matrix. This argument can be used, among others, to model pedigrees and phylogenetic effects. See \texttt{vignette("brms\_phylogenetics")} for more details. By default, levels of the same grouping factor are modeled as independent of each other.
  \item \texttt{dist}: Name of the distribution of the group-level effects. Currently \texttt{"gaussian"} is the only option.
\end{itemize}
See Also

brmsformula, mmc

Examples

```r
## Not run:
# simulate some data
dat <- data.frame(
  y = rnorm(100), x1 = rnorm(100), x2 = rnorm(100),
  g1 = sample(1:10, 100, TRUE), g2 = sample(1:10, 100, TRUE))

# multi-membership model with two members per group and equal weights
fit1 <- brm(y ~ x1 + (1|mm(g1, g2)), data = dat)
summary(fit1)

# weight the first member two times for than the second member
dat$w1 <- rep(2, 100)
dat$w2 <- rep(1, 100)
fit2 <- brm(y ~ x1 + (1|mm(g1, g2, weights = cbind(w1, w2))), data = dat)
summary(fit2)

# multi-membership model with level specific covariate values
dat$xc <- (dat$x1 + dat$x2) / 2
fit3 <- brm(y ~ xc + (1 + mmc(x1, x2) | mm(g1, g2)), data = dat)
summary(fit3)

## End(Not run)
```

---

**mmc**

*Multi-Membership Covariates*

### Description

Specify covariates that vary over different levels of multi-membership grouping factors thus requiring special treatment. This function is almost solely useful, when called in combination with `mm`. Outside of multi-membership terms it will behave very much like `cbind`. 

### Usage

```r
mmc(...)
```

### Arguments

- `...`: One or more terms containing covariates corresponding to the grouping levels specified in `mm`. 
Value

A matrix with covariates as columns.

See Also

mm

Examples

```r
## Not run:
# simulate some data
dat <- data.frame(
  y = rnorm(100), x1 = rnorm(100), x2 = rnorm(100),
  g1 = sample(1:10, 100, TRUE), g2 = sample(1:10, 100, TRUE)
)

# multi-membership model with level specific covariate values
dat$xc <- (dat$x1 + dat$x2) / 2
fit <- brm(y ~ xc + (1 + mmc(x1, x2) | mm(g1, g2)), data = dat)
summary(fit)
## End(Not run)
```

---

### Monotonic Predictors in brms Models

**Description**

Specify a monotonic predictor term in *brms*. The function does not evaluate its arguments – it exists purely to help set up a model.

**Usage**

```r
mo(x, id = NA)
```

**Arguments**

- `x` An integer variable or an ordered factor to be modeled as monotonic.
- `id` Optional character string. All monotonic terms with the same id within one formula will be modeled as having the same simplex (shape) parameter vector. If all monotonic terms of the same predictor have the same id, the resulting predictions will be conditionally monotonic for all values of interacting covariates (Bürkner & Charpentier, 2020).

**Details**

See Bürkner and Charpentier (2020) for the underlying theory. For detailed documentation of the formula syntax used for monotonic terms, see `help(brmsformula)` as well as `vignette("brms_monotonic").`
References


See Also

brmsformula

Examples

```r
## Not run:
# generate some data
income_options <- c("below_20", "20_to_40", "40_to_100", "greater_100")
income <- factor(sample(income_options, 100, TRUE),
  levels = income_options, ordered = TRUE)
mean_ls <- c(30, 60, 70, 75)
ls <- mean_ls[income] + rnorm(100, sd = 7)
dat <- data.frame(income, ls)

# fit a simple monotonic model
fit1 <- brm(ls ~ mo(income), data = dat)
summary(fit1)
plot(fit1, N = 6)
plot(conditional_effects(fit1), points = TRUE)

# model interaction with other variables
dat$x <- sample(c("a", "b", "c"), 100, TRUE)
fit2 <- brm(ls ~ mo(income)*x, data = dat)
summary(fit2)
plot(conditional_effects(fit2), points = TRUE)

# ensure conditional monotonicity
fit3 <- brm(ls ~ mo(income, id = "i")*x, data = dat)
summary(fit3)
plot(conditional_effects(fit3), points = TRUE)

## End(Not run)
```

Description

Compute model weights in various ways, for instance, via stacking of posterior predictive distributions, Akaike weights, or marginal likelihoods.
Usage

## S3 method for class 'brmsfit'
model_weights(x, ..., weights = "stacking", model_names = NULL)

model_weights(x, ...)

Arguments

x
A `brmsfit` object.

...  
More `brmsfit` objects or further arguments passed to the underlying post-processing functions. In particular, see `prepare_predictions` for further supported arguments.

weights  
Name of the criterion to compute weights from. Should be one of "loo", "waic", "kfold", "stacking" (current default), or "bma", "pseudobma". For the former three options, Akaike weights will be computed based on the information criterion values returned by the respective methods. For "stacking" and "pseudobma", method `loo_model_weights` will be used to obtain weights. For "bma", method `post_prob` will be used to compute Bayesian model averaging weights based on log marginal likelihood values (make sure to specify reasonable priors in this case). For some methods, weights may also be a numeric vector of pre-specified weights.

model_names  
If NULL (the default) will use model names derived from deparsing the call. Otherwise will use the passed values as model names.

Value

A numeric vector of weights for the models.

Examples

## Not run:
# model with 'treat' as predictor
fit1 <- brm(rating ~ treat + period + carry, data = inhaler)
summary(fit1)

# model without 'treat' as predictor
fit2 <- brm(rating ~ period + carry, data = inhaler)
summary(fit2)

# obtain Akaike weights based on the WAIC
model_weights(fit1, fit2, weights = "waic")

## End(Not run)
MultiNormal

The Multivariate Normal Distribution

Description
Density function and random generation for the multivariate normal distribution with mean vector \( \mu \) and covariance matrix \( \Sigma \).

Usage
\[
d\text{multi}_\text{normal}(x, \mu, \Sigma, \text{log} = \text{FALSE}, \text{check} = \text{FALSE})
\]
\[
r\text{multi}_\text{normal}(n, \mu, \Sigma, \text{check} = \text{FALSE})
\]

Arguments
- \( x \), vector or matrix of quantiles. If \( x \) is a matrix, each row is taken to be a quantile.
- \( \mu \), mean vector with length equal to the number of dimensions.
- \( \Sigma \), covariance matrix.
- \( \text{log} \), logical; If \text{TRUE}, values are returned on the log scale.
- \( \text{check} \), logical; Indicates whether several input checks should be performed. Defaults to \text{FALSE} to improve efficiency.
- \( n \), number of draws to sample from the distribution.

Details
See the Stan user’s manual https://mc-stan.org/documentation/ for details on the parameterization.

MultiStudentT

The Multivariate Student-t Distribution

Description
Density function and random generation for the multivariate Student-t distribution with location vector \( \mu \), covariance matrix \( \Sigma \), and degrees of freedom \( df \).

Usage
\[
d\text{multi}_\text{student}_\text{t}(x, df, \mu, \Sigma, \text{log} = \text{FALSE}, \text{check} = \text{FALSE})
\]
\[
r\text{multi}_\text{student}_\text{t}(n, df, \mu, \Sigma, \text{check} = \text{FALSE})
\]
mvbind

Arguments

  x  Vector or matrix of quantiles. If x is a matrix, each row is taken to be a quantile.
  df Vector of degrees of freedom.
  mu Location vector with length equal to the number of dimensions.
  Sigma Covariance matrix.
  log Logical; If TRUE, values are returned on the log scale.
  check Logical; Indicates whether several input checks should be performed. Defaults
to FALSE to improve efficiency.
  n Number of draws to sample from the distribution.

Details

See the Stan user’s manual https://mc-stan.org/documentation/ for details on the parameter-
ization

mvbind Bind response variables in multivariate models

Description

Can be used to specify a multivariate brms model within a single formula. Outside of brmsformula,
it just behaves like cbind.

Usage

  mvbind(...) 

Arguments

  ... Same as in cbind

See Also

  brmsformula, mvbrmsformula

Examples

  bf(mvbind(y1, y2) ~ x)
Set up a multivariate model formula for use in the `brms` package allowing to define (potentially non-linear) additive multilevel models for all parameters of the assumed response distributions.

### Usage

```r
mvbrmsformula(..., flist = NULL, rescor = NULL)
```

### Arguments

- `...`: Objects of class `formula` or `brmsformula`, each specifying a univariate model. See `brmsformula` for details on how to specify univariate models.

- `flist`: Optional list of formulas, which are treated in the same way as formulas passed via the `...` argument.

- `rescor`: Logical; Indicates if residual correlation between the response variables should be modeled. Currently, this is only possible in multivariate gaussian and student models. If `NULL` (the default), `rescor` is internally set to `TRUE` when possible.

### Details

See vignette("brms_multivariate") for a case study.

### Value

An object of class `mvbrmsformula`, which is essentially a list containing all model formulas as well as some additional information for multivariate models.

### See Also

`brmsformula`, `brmsformula-helpers`

### Examples

```r
bf1 <- bf(y1 ~ x + (1|g))
bf2 <- bf(y2 ~ s(z))
mvbf(bf1, bf2)
```
ngrps.brmsfit 

**Number of Grouping Factor Levels**

**Description**

Extract the number of levels of one or more grouping factors.

**Usage**

```r
## S3 method for class 'brmsfit'
ngrps(object, ...)
```

**Arguments**

- `object`: An R object.
- `...`: Currently ignored.

**Value**

A named list containing the number of levels per grouping factor.

---

nsamples.brmsfit 

**(Deprecated) Number of Posterior Samples**

**Description**

Extract the number of posterior samples (draws) stored in a fitted Bayesian model. Method `nsamples` is deprecated. Please use `ndraws` instead.

**Usage**

```r
## S3 method for class 'brmsfit'
nsamples(object, subset = NULL, incl_warmup = FALSE, ...)
```

**Arguments**

- `object`: An object of class `brmsfit`.
- `subset`: An optional integer vector defining a subset of samples to be considered.
- `incl_warmup`: A flag indicating whether to also count warmup / burn-in samples.
- `...`: Currently ignored.
GPU support in Stan via OpenCL

Description

Use OpenCL for GPU support in Stan via the brms interface. Only some Stan functions can be run on a GPU at this point and so a lot of brms models won’t benefit from OpenCL for now.

Usage

opencl(ids = NULL)

Arguments

ids (integer vector of length 2) The platform and device IDs of the OpenCL device to use for fitting. If you don’t know the IDs of your OpenCL device, c(0, 0) is most likely what you need.

Details


Value

A brmsopencl object which can be passed to the opencl argument of brm and related functions.

Examples

## Not run:
# this model just serves as an illustration
# OpenCL may not actually speed things up here
fit <- brm(count ~ zAge + zBase * Trt + (1|patient),
           data = epilepsy, family = poisson(),
           chains = 2, cores = 2, opencl = opencl(c(0, 0)),
           backend = "cmdstanr"
summary(fit)

## End(Not run)
Create a matrix of output plots from a `brmsfit` object

**Description**

A `pairs` method that is customized for MCMC output.

**Usage**

```r
## S3 method for class 'brmsfit'  
pairs(x, pars = NA, variable = NULL, regex = FALSE, fixed = FALSE, ...)  
```

**Arguments**

- `x`: An object of class `brmsfit`  
- `pars`: Deprecated alias of `variable`. Names of the parameters to plot, as given by a character vector or a regular expression.  
- `variable`: Names of the variables (parameters) to plot, as given by a character vector or a regular expression (if `regex = TRUE`). By default, a hopefully not too large selection of variables is plotted.  
- `regex`: Logical; Indicates whether `variable` should be treated as regular expressions. Defaults to `FALSE`.  
- `fixed`: (Deprecated) Indicates whether parameter names should be matched exactly (TRUE) or treated as regular expressions (FALSE). Default is FALSE and only works with argument `pars`.  
- `...`: Further arguments to be passed to `mcmc_pairs`.  

**Details**

For a detailed description see `mcmc_pairs`.

**Examples**

```r
## Not run:  
fit <- brm(count ~ zAge + zBase * Trt  
  + (1|patient) + (1|visit),  
  data = epilepsy, family = "poisson")  
pairs(fit, variable = variables(fit)[1:3])  
pairs(fit, variable = "sd_", regex = TRUE)  
## End(Not run)
```
Extract Parameter Names

Description
Extract all parameter names of a given model.

Usage
parnames(x, ...)

Arguments
x
An R object

... Further arguments passed to or from other methods.

Value
A character vector containing the parameter names of the model.

Trace and Density Plots for MCMC Draws

Description
Trace and Density Plots for MCMC Draws

Usage

## S3 method for class 'brmsfit'
plot(
x,
pars = NA,
combo = c("dens", "trace"),
N = 5,
variable = NULL,
regex = FALSE,
fixed = FALSE,
theme = NULL,
plot = TRUE,
ask = TRUE,
newpage = TRUE,
...
)

plot.brmsfit

Arguments

- **x**: An object of class `brmsfit`.
- **pars**: Deprecated alias of `variable`. Names of the parameters to plot, as given by a character vector or a regular expression.
- **combo**: A character vector with at least two elements. Each element of `combo` corresponds to a column in the resulting graphic and should be the name of one of the available `MCMC` functions (omitting the `mcmc_` prefix).
- **N**: The number of parameters plotted per page.
- **variable**: Names of the variables (parameters) to plot, as given by a character vector or a regular expression (if `regex = TRUE`). By default, a hopefully not too large selection of variables is plotted.
- **regex**: Logical; Indicates whether `variable` should be treated as regular expressions. Defaults to `FALSE`.
- **fixed**: (Deprecated) Indicates whether parameter names should be matched exactly (`TRUE`) or treated as regular expressions (`FALSE`). Default is `FALSE` and only works with argument `pars`.
- **theme**: A `theme` object modifying the appearance of the plots. For some basic themes see `ggtheme` and `theme_default`.
- **plot**: Logical; indicates if plots should be plotted directly in the active graphic device. Defaults to `TRUE`.
- **ask**: Logical; indicates if the user is prompted before a new page is plotted. Only used if `plot` is `TRUE`.
- **newpage**: Logical; indicates if the first set of plots should be plotted to a new page. Only used if `plot` is `TRUE`.
- **...**: Further arguments passed to `mcmc_combo`.

Value

An invisible list of `gtable` objects.

Examples

```r
## Not run:
fit <- brm(count ~ zAge + zBase * Trt + (1|patient) + (1|visit),
  data = epilepsy, family = "poisson")
plot(fit)
## plot population-level effects only
plot(fit, variable = "b_", regex = TRUE)

## End(Not run)
```

Posterior draws of parameters averaged across models

Description

Extract posterior draws of parameters averaged across models. Weighting can be done in various ways, for instance using Akaike weights based on information criteria or marginal likelihoods.

Usage

```r
## S3 method for class 'brmsfit'
posterior_average(
  x,
  ..., 
  variable = NULL,
  pars = NULL,
  weights = "stacking",
  ndraws = NULL,
  nsamples = NULL,
  missing = NULL,
  model_names = NULL,
  control = list(),
  seed = NULL
)
```

Arguments

- `x` A `brmsfit` object.
- `...` More `brmsfit` objects or further arguments passed to the underlying post-processing functions. In particular, see `prepare_predictions` for further supported arguments.
- `variable` Names of variables (parameters) for which to average across models. Only those variables can be averaged that appear in every model. Defaults to all overlapping variables.
- `pars` Deprecated alias of `variable`.
- `weights` Name of the criterion to compute weights from. Should be one of "loo", "waic", "kfold", "stacking" (current default), or "bma", "pseudobma". For the former three options, Akaike weights will be computed based on the information criterion values returned by the respective methods. For "stacking" and "pseudobma", method `loo_model_weights` will be used to obtain weights. For "bma", method `post_prob` will be used to compute Bayesian model averaging weights based on log marginal likelihood values (make sure to specify reasonable priors in this case). For some methods, `weights` may also be a numeric vector of pre-specified weights.
ndraws Total number of posterior draws to use.
nsamples Deprecated alias of ndraws.
missing An optional numeric value or a named list of numeric values to use if a model does not contain a variable for which posterior draws should be averaged. Defaults to NULL, in which case only those variables can be averaged that are present in all of the models.
model_names If NULL (the default) will use model names derived from deparsing the call. Otherwise will use the passed values as model names.
control Optional list of further arguments passed to the function specified in weights.
seed A single numeric value passed to set.seed to make results reproducible.

Details
Weights are computed with the model_weights method.

Value
A data.frame of posterior draws.

See Also
model_weights, pp_average

Examples
## Not run:
# model with 'treat' as predictor
fit1 <- brm(rating ~ treat + period + carry, data = inhaler)
summary(fit1)

# model without 'treat' as predictor
fit2 <- brm(rating ~ period + carry, data = inhaler)
summary(fit2)

# compute model-averaged posteriors of overlapping parameters
posterior_average(fit1, fit2, weights = "waic")

## End(Not run)
Description

Compute posterior draws of the expected value of the posterior predictive distribution. Can be performed for the data used to fit the model (posterior predictive checks) or for new data. By definition, these predictions have smaller variance than the posterior predictions performed by the `posterior_predict.brmsfit` method. This is because only the uncertainty in the expected value of the posterior predictive distribution is incorporated in the draws computed by `posterior_epred` while the residual error is ignored there. However, the estimated means of both methods averaged across draws should be very similar.

Usage

```r
## S3 method for class 'brmsfit'
posterior_epred(
  object,
  newdata = NULL,
  re_formula = NULL,
  re.form = NULL,
  resp = NULL,
  dpar = NULL,
  nlpar = NULL,
  ndraws = NULL,
  draw_ids = NULL,
  sort = FALSE,
  ...
)
```

Arguments

- **object**: An object of class `brmsfit`.
- **newdata**: An optional data.frame for which to evaluate predictions. If `NULL` (default), the original data of the model is used. `NA` values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.
- **re_formula**: formula containing group-level effects to be considered in the prediction. If `NULL` (default), include all group-level effects; if `NA`, include no group-level effects.
- **re.form**: Alias of `re_formula`.
- **resp**: Optional names of response variables. If specified, predictions are performed only for the specified response variables.
- **dpar**: Optional name of a predicted distributional parameter. If specified, expected predictions of this parameters are returned.
- **nlpar**: Optional name of a predicted non-linear parameter. If specified, expected predictions of this parameters are returned.
- **ndraws**: Positive integer indicating how many posterior draws should be used. If `NULL` (the default) all draws are used. Ignored if `draw_ids` is not `NULL`. 
posterior_interval.brmsfit

Description

Compute posterior uncertainty intervals for brmsfit objects.
Usage

## S3 method for class 'brmsfit'
posterior_interval(object, pars = NA, variable = NULL, prob = 0.95, ...)

Arguments

object  
An object of class brmsfit.

pars  
Deprecated alias of variable. For reasons of backwards compatibility, pars is interpreted as a vector of regular expressions by default unless fixed = TRUE is specified.

variable  
A character vector providing the variables to extract. By default, all variables are extracted.

prob  
A value between 0 and 1 indicating the desired probability to be covered by the uncertainty intervals. The default is 0.95.

...  
More arguments passed to as.matrix.brmsfit.

Value

A matrix with lower and upper interval bounds as columns and as many rows as selected variables.

Examples

## Not run:
fit <- brm(count ~ zAge + zBase * Trt, 
data = epilepsy, family = negbinomial())
posterior_interval(fit)

## End(Not run)

posterior_linpred.brmsfit

Posterior Draws of the Linear Predictor

Description

Compute posterior draws of the linear predictor, that is draws before applying any link functions or other transformations. Can be performed for the data used to fit the model (posterior predictive checks) or for new data.
Usage

```r
## S3 method for class 'brmsfit'
posterior_linpred(
  object,
  transform = FALSE,
  newdata = NULL,
  re_formula = NULL,
  re.form = NULL,
  resp = NULL,
  dpar = NULL,
  nlpar = NULL,
  incl_thres = NULL,
  ndraws = NULL,
  draw_ids = NULL,
  sort = FALSE,
  ...
)
```

Arguments

- **object**: An object of class `brmsfit`.
- **transform**: Logical; if `FALSE` (the default), draws of the linear predictor are returned. If `TRUE`, draws of the transformed linear predictor, that is, after applying the inverse link function are returned.
- **newdata**: An optional data.frame for which to evaluate predictions. If `NULL` (default), the original data of the model is used. NA values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.
- **re_formula**: formula containing group-level effects to be considered in the prediction. If `NULL` (default), include all group-level effects; if `NA`, include no group-level effects.
- **re.form**: Alias of `re_formula`.
- **resp**: Optional names of response variables. If specified, predictions are performed only for the specified response variables.
- **dpar**: Name of a predicted distributional parameter for which draws are to be returned. By default, draws of the main distributional parameter(s) "mu" are returned.
- **nlpar**: Optional name of a predicted non-linear parameter. If specified, expected predictions of this parameters are returned.
- **incl_thres**: Logical; only relevant for ordinal models when `transform` is `FALSE`, and ignored otherwise. Shall the thresholds and category-specific effects be included in the linear predictor? For backwards compatibility, the default is to not include them.
- **ndraws**: Positive integer indicating how many posterior draws should be used. If `NULL` (the default) all draws are used. Ignored if `draw_ids` is not `NULL`.
- **draw_ids**: An integer vector specifying the posterior draws to be used. If `NULL` (the default), all draws are used.
sort Logical. Only relevant for time series models. Indicating whether to return predicted values in the original order (FALSE; default) or in the order of the time series (TRUE).

Further arguments passed to prepare_predictions that control several aspects of data validation and prediction.

See Also

posterior_epred.brmsfit

Examples

```r
## Not run:
## fit a model
fit <- brm(rating ~ treat + period + carry + (1|subject),
    data = inhaler)

## extract linear predictor values
pl <- posterior_linpred(fit)
str(pl)

## End(Not run)
```

posterior_predict.brmsfit

*Draws from the Posterior Predictive Distribution*

Description

Compute posterior draws of the posterior predictive distribution. Can be performed for the data used to fit the model (posterior predictive checks) or for new data. By definition, these draws have higher variance than draws of the expected value of the posterior predictive distribution computed by posterior_epred.brmsfit. This is because the residual error is incorporated in posterior_predict. However, the estimated means of both methods averaged across draws should be very similar.

Usage

```r
## S3 method for class 'brmsfit'
posterior_predict(
    object, 
    newdata = NULL, 
    re_formula = NULL, 
    re.form = NULL, 
    transform = NULL, 
    resp = NULL, 
    negative_rt = FALSE, 
    ndraws = NULL,
```
Arguments

- **object**: An object of class `brmsfit`.
- **newdata**: An optional data.frame for which to evaluate predictions. If `NULL` (default), the original data of the model is used. NA values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.
- **re_formula**: formula containing group-level effects to be considered in the prediction. If `NULL` (default), include all group-level effects; if `NA`, include no group-level effects.
- **re.form**: Alias of `re_formula`.
- **transform**: (Deprecated) A function or a character string naming a function to be applied on the predicted responses before summary statistics are computed.
- **resp**: Optional names of response variables. If specified, predictions are performed only for the specified response variables.
- **negative.rt**: Only relevant for Wiener diffusion models. A flag indicating whether response times of responses on the lower boundary should be returned as negative values. This allows to distinguish responses on the upper and lower boundary. Defaults to `FALSE`.
- **ndraws**: Positive integer indicating how many posterior draws should be used. If `NULL` (the default) all draws are used. Ignored if `draw_ids` is not `NULL`.
- **draw_ids**: An integer vector specifying the posterior draws to be used. If `NULL` (the default), all draws are used.
- **sort**: Logical. Only relevant for time series models. Indicating whether to return predicted values in the original order (FALSE; default) or in the order of the time series (TRUE).
- **ntrys**: Parameter used in rejection sampling for truncated discrete models only (defaults to 5). See Details for more information.
- **cores**: Number of cores (defaults to 1). On non-Windows systems, this argument can be set globally via the `mc.cores` option.
- **...**: Further arguments passed to `prepare_predictions` that control several aspects of data validation and prediction.

Details

NA values within factors in `newdata`, are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.
In multilevel models, it is possible to allow new levels of grouping factors to be used in the predictions. This can be controlled via argument `allow_new_levels`. New levels can be sampled in multiple ways, which can be controlled via argument `sample_new_levels`. Both of these arguments are documented in `prepare_predictions` along with several other useful arguments to control specific aspects of the predictions.

For truncated discrete models only: In the absence of any general algorithm to sample from truncated discrete distributions, rejection sampling is applied in this special case. This means that values are sampled until a value lies within the defined truncation boundaries. In practice, this procedure may be rather slow (especially in R). Thus, we try to do approximate rejection sampling by sampling each value `ntrys` times and then select a valid value. If all values are invalid, the closest boundary is used, instead. If there are more than a few of these pathological cases, a warning will occur suggesting to increase argument `ntrys`.

### Value

An array of draws. In univariate models, the output is as an $S \times N$ matrix, where $S$ is the number of posterior draws and $N$ is the number of observations. In multivariate models, an additional dimension is added to the output which indexes along the different response variables.

### Examples

```r
## Not run:
# fit a model
fit <- brm(time | cens(censored) ~ age + sex + (1 + age || patient),
          data = kidney, family = "exponential", init = "0")

# predicted responses
pp <- posterior_predict(fit)
str(pp)

# predicted responses excluding the group-level effect of age
pp <- posterior_predict(fit, re_formula = ~ (1 | patient))
str(pp)

# predicted responses of patient 1 for new data
newdata <- data.frame(
   sex = factor(c("male", "female")),
   age = c(20, 50),
   patient = c(1, 1)
)
pp <- posterior_predict(fit, newdata = newdata)
str(pp)

# End(Not run)
```
posterior_samples.brmsfit

(Deprecated) Extract Posterior Samples

Description

Extract posterior samples of specified parameters. The posterior_samples method is deprecated. We recommend using the more modern and consistent as_draws_* extractor functions of the posterior package instead.

Usage

## S3 method for class 'brmsfit'
posterior_samples(
x,  
pars = NA,
fixed = FALSE,
add_chain = FALSE,
subset = NULL,
as.matrix = FALSE,
as.array = FALSE,
...
)

posterior_samples(x, pars = NA, ...)

Arguments

x An R object typically of class brmsfit
pars Names of parameters for which posterior samples should be returned, as given by a character vector or regular expressions. By default, all posterior samples of all parameters are extracted.
fixed Indicates whether parameter names should be matched exactly (TRUE) or treated as regular expressions (FALSE). Default is FALSE.
add_chain A flag indicating if the returned data.frame should contain two additional columns. The chain column indicates the chain in which each sample was generated, the iter column indicates the iteration number within each chain.
subset A numeric vector indicating the rows (i.e., posterior samples) to be returned. If NULL (the default), all posterior samples are returned.
as.matrix Should the output be a matrix instead of a data.frame? Defaults to FALSE.
as.array Should the output be an array instead of a data.frame? Defaults to FALSE.
...
Arguments passed to individual methods (if applicable).

Value

A data.frame (matrix or array) containing the posterior samples.
See Also

as_draws, as.data.frame

Examples

## Not run:
fit <- brm(rating ~ treat + period + carry + (1|subject),
    data = inhaler, family = "cumulative")

# extract posterior samples of population-level effects
samples1 <- posterior_samples(fit, pars = "^b")
head(samples1)

# extract posterior samples of group-level standard deviations
samples2 <- posterior_samples(fit, pars = "^sd_")
head(samples2)

## End(Not run)
Arguments

object

An object of class \texttt{brmsfit}.

smooth

Name of a single smooth term for which predictions should be computed.

newdata

An optional \texttt{data.frame} for which to evaluate predictions. If NULL (default), the original data of the model is used. Only those variables appearing in the chosen smooth term are required.

resp

Optional names of response variables. If specified, predictions are performed only for the specified response variables.

dpar

Optional name of a predicted distributional parameter. If specified, expected predictions of this parameters are returned.

nlpar

Optional name of a predicted non-linear parameter. If specified, expected predictions of this parameters are returned.

ndraws

Positive integer indicating how many posterior draws should be used. If NULL (the default) all draws are used. Ignored if \texttt{draw_ids} is not NULL.

draw_ids

An integer vector specifying the posterior draws to be used. If NULL (the default), all draws are used.

...

Currently ignored.

Value

An \( S \times N \) matrix, where \( S \) is the number of posterior draws and \( N \) is the number of observations.

Examples

```r
## Not run:
set.seed(0)
dat <- mgcv::gamSim(1, n = 200, scale = 2)
fit <- brm(y ~ s(x0) + s(x1) + s(x2) + s(x3), data = dat)
summary(fit)
newdata <- data.frame(x2 = seq(0, 1, 10))
str(posterior_smooths(fit, smooth = "s(x2)", newdata = newdata))
## End(Not run)
```

posterior_summary

\textit{Summarize Posterior draws}

Description

Summarizes posterior draws based on point estimates (mean or median), estimation errors (SD or MAD) and quantiles. This function mainly exists to retain backwards compatibility. It will eventually be replaced by functions of the \texttt{posterior} package (see examples below).
Usage

posterior_summary(x, ...)

## Default S3 method:
posterior_summary(x, probs = c(0.025, 0.975), robust = FALSE, ...)

## S3 method for class 'brmsfit'
posterior_summary(
  x,
  pars = NA,
  variable = NULL,
  probs = c(0.025, 0.975),
  robust = FALSE,
  ...
)

Arguments

x  An R object.
...
probs  The percentiles to be computed by the quantile function.
robust  If FALSE (the default) the mean is used as the measure of central tendency and the standard deviation as the measure of variability. If TRUE, the median and the median absolute deviation (MAD) are applied instead.
pars  Deprecated alias of variable. For reasons of backwards compatibility, pars is interpreted as a vector of regular expressions by default unless fixed = TRUE is specified.
variable  A character vector providing the variables to extract. By default, all variables are extracted.

Value

A matrix where rows indicate variables and columns indicate the summary estimates.

See Also

summarize_draws

Examples

## Not run:
fit <- brm(time ~ age * sex, data = kidney)
posterior_summary(fit)

# recommended workflow using posterior
library(posterior)
draws <- as_draws_array(fit)
summarise_draws(draws, default_summary_measures())
posterior_table

Table Creation for Posterior Draws

Description
Create a table for unique values of posterior draws. This is usually only useful when summarizing predictions of ordinal models.

Usage
posterior_table(x, levels = NULL)

Arguments
- **x**: A matrix of posterior draws where rows indicate draws and columns indicate parameters.
- **levels**: Optional values of possible posterior values. Defaults to all unique values in x.

Value
A matrix where rows indicate parameters and columns indicate the unique values of posterior draws.

Examples
```r
## Not run:
fit <- brm(rating ~ period + carry + treat,
           data = inhaler, family = cumulative())
pr <- predict(fit, summary = FALSE)
posterior_table(pr)
## End(Not run)
```
Posterior Model Probabilities from Marginal Likelihoods

Description

Compute posterior model probabilities from marginal likelihoods. The `brmsfit` method is just a thin wrapper around the corresponding method for bridge objects.

Usage

```r
## S3 method for class 'brmsfit'
post_prob(x, ..., prior_prob = NULL, model_names = NULL)
```

Arguments

- `x`: A `brmsfit` object.
- `...`: More `brmsfit` objects or further arguments passed to the underlying post-processing functions. In particular, see `prepare_predictions` for further supported arguments.
- `prior_prob`: Numeric vector with prior model probabilities. If omitted, a uniform prior is used (i.e., all models are equally likely a priori). The default `NULL` corresponds to equal prior model weights.
- `model_names`: If `NULL` (the default) will use model names derived from deparsing the call. Otherwise will use the passed values as model names.

Details

Computing the marginal likelihood requires samples of all variables defined in Stan's `parameters` block to be saved. Otherwise `post_prob` cannot be computed. Thus, please set `save_all_pars = TRUE` in the call to `brm`, if you are planning to apply `post_prob` to your models.

The computation of model probabilities based on bridge sampling requires a lot more posterior samples than usual. A good conservative rule of thump is perhaps 10-fold more samples (read: the default of 4000 samples may not be enough in many cases). If not enough posterior samples are provided, the bridge sampling algorithm tends to be unstable leading to considerably different results each time it is run. We thus recommend running `post_prob` multiple times to check the stability of the results.

More details are provided under `bridgesampling::post_prob`.

See Also

`bridge_sampler`, `bayes_factor`
Examples

```r
## Not run:
# model with the treatment effect
fit1 <- brm(
  count ~ zAge + zBase + Trt,
  data = epilepsy, family = negbinomial(),
  prior = prior(normal(0, 1), class = b),
  save_all_pars = TRUE
)
summary(fit1)

# model without the treatment effect
fit2 <- brm(
  count ~ zAge + zBase,
  data = epilepsy, family = negbinomial(),
  prior = prior(normal(0, 1), class = b),
  save_all_pars = TRUE
)
summary(fit2)

# compute the posterior model probabilities
post_prob(fit1, fit2)

# specify prior model probabilities
post_prob(fit1, fit2, prior_prob = c(0.8, 0.2))

## End(Not run)
```

**pp_average.brmsfit**  
Posterior predictive draws averaged across models

**Description**

Compute posterior predictive draws averaged across models. Weighting can be done in various ways, for instance using Akaike weights based on information criteria or marginal likelihoods.

**Usage**

```r
## S3 method for class 'brmsfit'
pp_average(
  x,
  ..., 
  weights = "stacking",
  method = "posterior_predict",
  ndraws = NULL,
  nsamples = NULL,
  summary = TRUE,
  probs = c(0.025, 0.975),
```
Arguments

x
A `brmsfit` object.

... More `brmsfit` objects or further arguments passed to the underlying post-processing functions. In particular, see `prepare_predictions` for further supported arguments.

weights Name of the criterion to compute weights from. Should be one of "loo", "waic", "kfold", "stacking" (current default), or "bma", "pseudobma". For the former three options, Akaike weights will be computed based on the information criterion values returned by the respective methods. For "stacking" and "pseudobma", method `loo_model_weights` will be used to obtain weights. For "bma", method `post_prob` will be used to compute Bayesian model averaging weights based on log marginal likelihood values (make sure to specify reasonable priors in this case). For some methods, weights may also be a numeric vector of pre-specified weights.

method Method used to obtain predictions to average over. Should be one of "posterior_predict" (default), "posterior_epred", "posterior_linpred" or "predictive_error".

ndraws Total number of posterior draws to use.

nsamples Deprecated alias of ndraws.

summary Should summary statistics (i.e. means, sds, and 95% intervals) be returned instead of the raw values? Default is TRUE.

probs The percentiles to be computed by the quantile function. Only used if summary is TRUE.

robust If FALSE (the default) the mean is used as the measure of central tendency and the standard deviation as the measure of variability. If TRUE, the median and the median absolute deviation (MAD) are applied instead. Only used if summary is TRUE.

model_names If NULL (the default) will use model names derived from deparsing the call. Otherwise will use the passed values as model names.

control Optional list of further arguments passed to the function specified in weights.

seed A single numeric value passed to `set.seed` to make results reproducible.

Details

Weights are computed with the `model_weights` method.

Value

Same as the output of the method specified in argument method.
See Also

`model_weights`, `posterior_average`

Examples

```r
## Not run:
# model with 'treat' as predictor
fit1 <- brm(rating ~ treat + period + carry, data = inhaler)
summary(fit1)

# model without 'treat' as predictor
fit2 <- brm(rating ~ period + carry, data = inhaler)
summary(fit2)

# compute model-averaged predicted values
(df <- unique(inhaler[, c("treat", "period", "carry")]))
pp_average(fit1, fit2, newdata = df)

# compute model-averaged fitted values
pp_average(fit1, fit2, method = "fitted", newdata = df)
## End(Not run)
```

---

**pp_check.brmsfit**

**Posterior Predictive Checks for brmsfit Objects**

**Description**

Perform posterior predictive checks with the help of the `bayesplot` package.

**Usage**

```r
## S3 method for class 'brmsfit'
pp_check(
  object,
  type,
  ndraws = NULL,
  prefix = c("ppc", "ppd"),
  group = NULL,
  x = NULL,
  newdata = NULL,
  resp = NULL,
  draw_ids = NULL,
  nsamples = NULL,
  subset = NULL,
  ...
)
```
pp_check.brmsfit

Arguments

object An object of class brmsfit.
type Type of the ppc plot as given by a character string. See PPC for an overview of currently supported types. You may also use an invalid type (e.g. type = "xyz") to get a list of supported types in the resulting error message.
ndraws Positive integer indicating how many posterior draws should be used. If NULL all draws are used. If not specified, the number of posterior draws is chosen automatically. Ignored if draw_ids is not NULL.
prefix The prefix of the bayesplot function to be applied. Either "ppc" (posterior predictive check; the default) or "ppd" (posterior predictive distribution), the latter being the same as the former except that the observed data is not shown for "ppd".
group Optional name of a factor variable in the model by which to stratify the ppc plot. This argument is required for ppc_*_grouped types and ignored otherwise.
x Optional name of a variable in the model. Only used for ppc types having an x argument and ignored otherwise.
newdata An optional data.frame for which to evaluate predictions. If NULL (default), the original data of the model is used. NA values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.
resp Optional names of response variables. If specified, predictions are performed only for the specified response variables.
draw_ids An integer vector specifying the posterior draws to be used. If NULL (the default), all draws are used.
nsamples Deprecated alias of ndraws.
subset Deprecated alias of draw_ids.
... Further arguments passed to predict.brmsfit as well as to the PPC function specified in type.

Details

For a detailed explanation of each of the ppc functions, see the PPC documentation of the bayesplot package.

Value

A ggplot object that can be further customized using the ggplot2 package.

Examples

```r
# Not run:
fit <- brm(count ~ zAge + zBase * Trt + (1|patient) + (1|obs),
       data = epilepsy, family = poisson())

pp_check(fit) # shows dens_overlay plot by default
```
pp_check(fit, type = "error_hist", ndraws = 11)
pp_check(fit, type = "scatter_avg", ndraws = 100)
pp_check(fit, type = "stat_2d")
pp_check(fit, type = "rootogram")
pp_check(fit, type = "loo_pit")

## get an overview of all valid types
pp_check(fit, type = "xyz")

## get a plot without the observed data
pp_check(fit, prefix = "ppd")

## End(Not run)

---

pp_mixture.brmsfit  
Posterior Probabilities of Mixture Component Memberships

**Description**

Compute the posterior probabilities of mixture component memberships for each observation including uncertainty estimates.

**Usage**

```r
## S3 method for class 'brmsfit'
pp_mixture(
x,  
newdata = NULL,
re_formula = NULL,
resp = NULL,
ndraws = NULL,
draw_ids = NULL,
log = FALSE,
summary = TRUE,
robust = FALSE,
probs = c(0.025, 0.975),
...
)

pp_mixture(x, ...)
```

**Arguments**

- **x**  
  An R object usually of class `brmsfit`.

- **newdata**  
  An optional data.frame for which to evaluate predictions. If NULL (default), the original data of the model is used. NA values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.
re_formula formula containing group-level effects to be considered in the prediction. If
NULL (default), include all group-level effects; if NA, include no group-level ef-
cfects.

resp Optional names of response variables. If specified, predictions are performed
only for the specified response variables.

ndraws Positive integer indicating how many posterior draws should be used. If NULL
(the default) all draws are used. Ignored if draw_ids is not NULL.

draw_ids An integer vector specifying the posterior draws to be used. If NULL (the default),
all draws are used.

log Logical; Indicates whether to return probabilities on the log-scale.

summary Should summary statistics be returned instead of the raw values? Default is
TRUE.

robust If FALSE (the default) the mean is used as the measure of central tendency and
the standard deviation as the measure of variability. If TRUE, the median and the
median absolute deviation (MAD) are applied instead. Only used if summary is
TRUE.

probs The percentiles to be computed by the quantile function. Only used if summary
is TRUE.

... Further arguments passed to prepare_predictions that control several aspects
of data validation and prediction.

Details

The returned probabilities can be written as $P(K_n = k|Y_n)$, that is the posterior probability that
observation $n$ originates from component $k$. They are computed using Bayes' Theorem

$$P(K_n = k|Y_n) = P(Y_n|K_n = k)P(K_n = k)/P(Y_n),$$

where $P(Y_n|K_n = k)$ is the (posterior) likelihood of observation $n$ for component $k$, $P(K_n = k)$
is the (posterior) mixing probability of component $k$ (i.e. parameter theta<k>), and

$$P(Y_n) = \sum_{k=1}^{K} P(Y_n|K_n = k)P(K_n = k)$$

is a normalizing constant.

Value

If summary = TRUE, an N x E x K array, where N is the number of observations, K is the number
of mixture components, and E is equal to length(probs) + 2. If summary = FALSE, an S x N x K
array, where S is the number of posterior draws.

Examples

```r
## Not run:
## simulate some data
set.seed(1234)
dat <- data.frame(
  y = c(rnorm(100), rnorm(50, 2)),
)```
x = rnorm(150)
)
## fit a simple normal mixture model
mix <- mixture(gaussian, nmix = 2)
prior <- c(  
prior(normal(0, 5), Intercept, nlpar = mu1),  
prior(normal(0, 5), Intercept, nlpar = mu2),  
prior(dirichlet(2, 2), theta)
)
fit1 <- brm(bf(y ~ x), dat, family = mix,
  prior = prior, chains = 2, init = 0)
summary(fit1)
## compute the membership probabilities
ppm <- pp_mixture(fit1)
str(ppm)
## extract point estimates for each observation
head(ppm[, 1, ])
## classify every observation according to
## the most likely component
apply(ppm[, 1, ], 1, which.max)
## End(Not run)

---

**predict.brmsfit**

*Draws from the Posterior Predictive Distribution*

**Description**

This method is an alias of `posterior_predict.brmsfit` with additional arguments for obtaining summaries of the computed draws.

**Usage**

```r
## S3 method for class 'brmsfit'
predict(  
oobject,  
nnewdata = NULL,  
re_formula = NULL,  
transform = NULL,  
resp = NULL,  
negative_rt = FALSE,  
nndraws = NULL,  
ndraw_ids = NULL,  
nsort = FALSE,  
ntrys = 5,
```
```r
cores = NULL,
summary = TRUE,
robust = FALSE,
probs = c(0.025, 0.975),
...
)
```

**Arguments**

- `object` An object of class `brmsfit`.
- `newdata` An optional data.frame for which to evaluate predictions. If `NULL` (default), the original data of the model is used. `NA` values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.
- `re_formula` formula containing group-level effects to be considered in the prediction. If `NULL` (default), include all group-level effects; if `NA`, include no group-level effects.
- `transform` (Deprecated) A function or a character string naming a function to be applied on the predicted responses before summary statistics are computed.
- `resp` Optional names of response variables. If specified, predictions are performed only for the specified response variables.
- `negative_rt` Only relevant for Wiener diffusion models. A flag indicating whether response times of responses on the lower boundary should be returned as negative values. This allows to distinguish responses on the upper and lower boundary. Defaults to `FALSE`.
- `ndraws` Positive integer indicating how many posterior draws should be used. If `NULL` (the default) all draws are used. Ignored if `draw_ids` is not `NULL`.
- `draw_ids` An integer vector specifying the posterior draws to be used. If `NULL` (the default), all draws are used.
- `sort` Logical. Only relevant for time series models. Indicating whether to return predicted values in the original order (`FALSE`; default) or in the order of the time series (`TRUE`).
- `ntrys` Parameter used in rejection sampling for truncated discrete models only (defaults to 5). See Details for more information.
- `cores` Number of cores (defaults to 1). On non-Windows systems, this argument can be set globally via the `mc.cores` option.
- `summary` Should summary statistics be returned instead of the raw values? Default is `TRUE`.
- `robust` If `FALSE` (the default) the mean is used as the measure of central tendency and the standard deviation as the measure of variability. If `TRUE`, the median and the median absolute deviation (MAD) are applied instead. Only used if `summary` is `TRUE`.
- `probs` The percentiles to be computed by the `quantile` function. Only used if `summary` is `TRUE`.
- `...` Further arguments passed to `prepare_predictions` that control several aspects of data validation and prediction.
predictive_error.brmsfit

Value

An array of predicted response values. If summary = FALSE the output resembles those of posterior_predict.brmsfit. If summary = TRUE the output depends on the family: For categorical and ordinal families, the output is an N x C matrix, where N is the number of observations, C is the number of categories, and the values are predicted category probabilities. For all other families, the output is a N x E matrix where E = 2 + length(probs) is the number of summary statistics: The Estimate column contains point estimates (either mean or median depending on argument robust), while the Est.Error column contains uncertainty estimates (either standard deviation or median absolute deviation depending on argument robust). The remaining columns starting with Q contain quantile estimates as specified via argument probs.

See Also

posterior_predict.brmsfit

Examples

```r
## Not run:
## fit a model
fit <- brm(time | cens(censored) ~ age + sex + (1 + age || patient),
          data = kidney, family = "exponential", init = "0")

## predicted responses
pp <- predict(fit)
head(pp)

## predicted responses excluding the group-level effect of age
pp <- predict(fit, re_formula = ~ (1 | patient))
head(pp)

## predicted responses of patient 1 for new data
newdata <- data.frame(
  sex = factor(c("male", "female")),
  age = c(20, 50),
  patient = c(1, 1)
)
predict(fit, newdata = newdata)

## End(Not run)
```

predictive_error.brmsfit

Posterior Draws of Predictive Errors

Description

Compute posterior draws of predictive errors, that is, observed minus predicted responses. Can be performed for the data used to fit the model (posterior predictive checks) or for new data.
## predictive_error.brmsfit

### Usage

```r
## S3 method for class 'brmsfit'
predictive_error(
  object,
  newdata = NULL,
  re_formula = NULL,
  re.form = NULL,
  resp = NULL,
  ndraws = NULL,
  draw_ids = NULL,
  sort = FALSE,
  ...
)
```

### Arguments

- `object`: An object of class `brmsfit`.
- `newdata`: An optional data.frame for which to evaluate predictions. If `NULL` (default), the original data of the model is used. NA values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.
- `re_formula`: formula containing group-level effects to be considered in the prediction. If `NULL` (default), include all group-level effects; if `NA`, include no group-level effects.
- `re.form`: Alias of `re_formula`.
- `resp`: Optional names of response variables. If specified, predictions are performed only for the specified response variables.
- `ndraws`: Positive integer indicating how many posterior draws should be used. If `NULL` (the default) all draws are used. Ignored if `draw_ids` is not `NULL`.
- `draw_ids`: An integer vector specifying the posterior draws to be used. If `NULL` (the default), all draws are used.
- `sort`: Logical. Only relevant for time series models. Indicating whether to return predicted values in the original order (`FALSE`; default) or in the order of the time series (`TRUE`).
- `...`: Further arguments passed to `prepare_predictions` that control several aspects of data validation and prediction.

### Value

An S x N array of predictive error draws, where S is the number of posterior draws and N is the number of observations.

### Examples

```r
## Not run:
## fit a model
```
fit <- brm(rating ~ treat + period + carry + (1|subject),
  data = inhaler, cores = 2)

## extract predictive errors
pe <- predictive_error(fit)
str(pe)

## End(Not run)

predictive_interval.brmsfit

*Predictive Intervals*

**Description**

Compute intervals from the posterior predictive distribution.

**Usage**

```r
## S3 method for class 'brmsfit'
predictive_interval(object, prob = 0.9, ...)
```

**Arguments**

- `object` An R object of class `brmsfit`.
- `prob` A number `p (0 < p < 1)` indicating the desired probability mass to include in the intervals. Defaults to `0.9`.
- `...` Further arguments passed to `posterior_predict`.

**Value**

A matrix with 2 columns for the lower and upper bounds of the intervals, respectively, and as many rows as observations being predicted.

**Examples**

```r
## Not run:
fit <- brm(count ~ zBase, data = epilepsy, family = poisson())
predictive_interval(fit)

## End(Not run)```
**Description**

This method helps in preparing *brms* models for certain post-processing tasks most notably various forms of predictions. Unless you are a package developer, you will rarely need to call `prepare_predictions` directly.

**Usage**

```r
## S3 method for class 'brmsfit'
prepare_predictions(
  x,
  newdata = NULL,
  re_formula = NULL,
  allow_new_levels = FALSE,
  sample_new_levels = "uncertainty",
  incl_autocor = TRUE,
  oos = NULL,
  resp = NULL,
  ndraws = NULL,
  draw_ids = NULL,
  nsamples = NULL,
  subset = NULL,
  nug = NULL,
  smooths_only = FALSE,
  offset = TRUE,
  newdata2 = NULL,
  new_objects = NULL,
  point_estimate = NULL,
  ndraws_point_estimate = 1,
  ...
)
```

**Arguments**

- **x**: An *R* object typically of class `brmsfit`.
- **newdata**: An optional data.frame for which to evaluate predictions. If `NULL` (default), the original data of the model is used. `NA` values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.
re_formula  formula containing group-level effects to be considered in the prediction. If NULL (default), include all group-level effects; if NA, include no group-level effects.

allow_new_levels  A flag indicating if new levels of group-level effects are allowed (defaults to FALSE). Only relevant if newdata is provided.

sample_new_levels  Indicates how to sample new levels for grouping factors specified in re_formula. This argument is only relevant if newdata is provided and allow_new_levels is set to TRUE. If "uncertainty" (default), each posterior sample for a new level is drawn from the posterior draws of a randomly chosen existing level. Each posterior sample for a new level may be drawn from a different existing level such that the resulting set of new posterior draws represents the variation across existing levels. If "gaussian", sample new levels from the (multivariate) normal distribution implied by the group-level standard deviations and correlations. This options may be useful for conducting Bayesian power analysis or predicting new levels in situations where relatively few levels where observed in the old_data. If "old_levels", directly sample new levels from the existing levels, where a new level is assigned all of the posterior draws of the same (randomly chosen) existing level.

incl_autocor  A flag indicating if correlation structures originally specified via autocor should be included in the predictions. Defaults to TRUE.

oos  Optional indices of observations for which to compute out-of-sample rather than in-sample predictions. Only required in models that make use of response values to make predictions, that is, currently only ARMA models.

resp  Optional names of response variables. If specified, predictions are performed only for the specified response variables.

ndraws  Positive integer indicating how many posterior draws should be used. If NULL (the default) all draws are used. Ignored if draw_ids is not NULL.

draw_ids  An integer vector specifying the posterior draws to be used. If NULL (the default), all draws are used.

nsamples  Deprecated alias of ndraws.

subset  Deprecated alias of draw_ids.

nug  Small positive number for Gaussian process terms only. For numerical reasons, the covariance matrix of a Gaussian process might not be positive definite. Adding a very small number to the matrix’s diagonal often solves this problem. If NULL (the default), nug is chosen internally.

smooths_only  Logical; If TRUE only predictions related to the

offset  Logical; Indicates if offsets should be included in the predictions. Defaults to TRUE.

newdata2  A named list of objects containing new data, which cannot be passed via argument newdata. Required for some objects used in autocorrelation structures, or stanvars.

new_objects  Deprecated alias of newdata2.
**point_estimate**  Shall the returned object contain only point estimates of the parameters instead of their posterior draws? Defaults to NULL in which case no point estimate is computed. Alternatively, may be set to "mean" or "median". This argument is primarily implemented to ensure compatibility with the `loo_subsample` method.

**ndraws_point_estimate**  Only used if `point_estimate` is not NULL. How often shall the point estimate’s value be repeated? Defaults to 1.

...  Further arguments passed to `validate_newdata`.

**Value**

An object of class 'brmsprep' or 'mvbrmsprep', depending on whether a univariate or multivariate model is passed.

---

**print.brmsfit**  _Print a summary for a fitted model represented by a brmsfit object_

**Description**

Print a summary for a fitted model represented by a brmsfit object

**Usage**

```r
## S3 method for class 'brmsfit'
print(x, digits = 2, ...)
```

**Arguments**

- `x`  An object of class brmsfit
- `digits`  The number of significant digits for printing out the summary; defaults to 2. The effective sample size is always rounded to integers.
- `...`  Additional arguments that would be passed to method summary of brmsfit.

**See Also**

`summary.brmsfit`
print.brmsprior  

Print method for brmsprior objects

Description
Print method for brmsprior objects

Usage

## S3 method for class 'brmsprior'
print(x, show_df = NULL, ...)

Arguments

x  An object of class brmsprior.
show_df  Logical; Print priors as a single data.frame (TRUE) or as a sequence of sampling statements (FALSE)?
...  Currently ignored.

prior Draws  

Extract Prior Draws

Description
Extract prior draws of specified parameters

Usage

## S3 method for class 'brmsfit'
prior_draws(x, variable = NULL, pars = NULL, ...)
prior_draws(x, ...)
prior_samples(x, ...)

Arguments

x  An R object typically of class brmsfit.
variable  A character vector providing the variables to extract. By default, all variables are extracted.
pars  Deprecated alias of variable. For reasons of backwards compatibility, pars is interpreted as a vector of regular expressions by default unless fixed = TRUE is specified.
...  Arguments passed to individual methods (if applicable).
Details

To make use of this function, the model must contain draws of prior distributions. This can be ensured by setting `sample_prior = TRUE` in function `brm`. Priors of certain parameters cannot be saved for technical reasons. For instance, this is the case for the population-level intercept, which is only computed after fitting the model by default. If you want to treat the intercept as part of all the other regression coefficients, so that sampling from its prior becomes possible, use `... ~ 0 + Intercept + ...` in the formulas.

Value

A `data.frame` containing the prior draws.

Examples

```r
## Not run:
fit <- brm(rating ~ treat + period + carry + (1|subject),
           data = inhaler, family = "cumulative",
           prior = set_prior("normal(0,2)", class = "b"),
           sample_prior = TRUE)

# extract all prior draws
draws1 <- prior_draws(fit)
head(draws1)

# extract prior draws for the coefficient of 'treat'
draws2 <- prior_draws(fit, "b_treat")
head(draws2)

## End(Not run)
```

prior_summary.brmsfit  

Extract Priors of a Bayesian Model Fitted with `brms`

Description

Extract Priors of a Bayesian Model Fitted with `brms`

Usage

```r
## S3 method for class 'brmsfit'
prior_summary(object, all = TRUE, ...)
```

Arguments

- `object`  
  An object of class `brmsfit`.
- `all`  
  Logical; Show all parameters in the model which may have priors (TRUE) or only those with proper priors (FALSE)?
- `...`  
  Further arguments passed to or from other methods.
Value

For `brmsfit` objects, an object of class `brmsprior`.

Examples

```r
## Not run:
fit <- brm(count ~ zAge + zBase * Trt + (1|patient) + (1|obs),
          data = epilepsy, family = poisson(),
          prior = c(prior(student_t(5,0,10), class = b),
                    prior(cauchy(0,2), class = sd)))

prior_summary(fit)
prior_summary(fit, all = FALSE)
print(prior_summary(fit, all = FALSE), show_df = FALSE)

## End(Not run)
```

---

### R2D2

#### R2-D2 Priors in `brms`

**Description**

Function used to set up R2D2 priors for population-level effects in `brms`. The function does not evaluate its arguments – it exists purely to help set up the model.

#### Usage

```r
R2D2(mean_R2 = 0.5, prec_R2 = 2, cons_D2 = 1, autoscale = TRUE)
```

#### Arguments

- `mean_R2`: mean of the Beta prior on the coefficient of determination $R^2$.
- `prec_R2`: precision of the Beta prior on the coefficient of determination $R^2$.
- `cons_D2`: concentration vector of the Dirichlet prior on the variance decomposition parameters.
- `autoscale`: Logical; indicating whether the R2D2 prior should be scaled using the residual standard deviation `sigma` if possible and sensible (defaults to `TRUE`). Autoscaling is not applied for distributional parameters or when the model does not contain the parameter `sigma`.

#### References

ranef.brmsfit

Extract Group-Level Estimates

Description

Extract the group-level ('random') effects of each level from a brmsfit object.

Usage

```r
## S3 method for class 'brmsfit'
ranef(
  object,
  summary = TRUE,
  robust = FALSE,
  probs = c(0.025, 0.975),
  pars = NULL,
  groups = NULL,
  ...
)
```

Arguments

- **object**: An object of class brmsfit.
- **summary**: Should summary statistics be returned instead of the raw values? Default is TRUE.
- **robust**: If FALSE (the default) the mean is used as the measure of central tendency and the standard deviation as the measure of variability. If TRUE, the median and the median absolute deviation (MAD) are applied instead. Only used if summary is TRUE.
- **probs**: The percentiles to be computed by the quantile function. Only used if summary is TRUE.
- **pars**: Optional names of coefficients to extract. By default, all coefficients are extracted.
- **groups**: Optional names of grouping variables for which to extract effects.
- **...**: Currently ignored.

Examples

```r
set_prior(R2D2(mean_R2 = 0.8, prec_R2 = 10))
```

See Also

- `set_prior`
recompile_model

Value

A list of 3D arrays (one per grouping factor). If summary is TRUE, the 1st dimension contains the factor levels, the 2nd dimension contains the summary statistics (see posterior_summary), and the 3rd dimension contains the group-level effects. If summary is FALSE, the 1st dimension contains the posterior draws, the 2nd dimension contains the factor levels, and the 3rd dimension contains the group-level effects.

Examples

```r
## Not run:
fit <- brm(count ~ zAge + zBase * Trt + (1+Trt|visit),
            data = epilepsy, family = gaussian(), chains = 2)
ranef(fit)
## End(Not run)
```

recompile_model  Recompile Stan models in brmsfit objects

Description

Recompile the Stan model inside a brmsfit object, if necessary. This does not change the model, it simply recreates the executable so that sampling is possible again.

Usage

```r
recompile_model(x, recompile = NULL)
```

Arguments

- **x**: An object of class brmsfit.
- **recompile**: Logical, indicating whether the Stan model should be recompiled. If NULL (the default), recompile_model tries to figure out internally, if recompilation is necessary. Setting it to FALSE will cause recompile_model to always return the brmsfit object unchanged.

Value

A (possibly updated) brmsfit object.
Description

Compute exact cross-validation for problematic observations for which approximate leave-one-out cross-validation may return incorrect results. Models for problematic observations can be run in parallel using the `future` package.

Usage

```r
## S3 method for class 'brmsfit'
reloo(
x, 
loo, 
k_threshold = 0.7, 
newdata = NULL, 
resp = NULL, 
check = TRUE, 
recompile = NULL, 
future_args = list(), 
...
)
```

```r
## S3 method for class 'loo'
reloo(x, fit, ...)
```

Arguments

- `x`: An R object of class `brmsfit` or `loo` depending on the method.
- `loo`: An R object of class `loo`.
- `k_threshold`: The threshold at which Pareto $k$ estimates are treated as problematic. Defaults to 0.7. See `pareto_k_ids` for more details.
- `newdata`: An optional data.frame for which to evaluate predictions. If `NULL` (default), the original data of the model is used. NA values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.
- `resp`: Optional names of response variables. If specified, predictions are performed only for the specified response variables.
- `check`: Logical; If `TRUE` (the default), some checks are performed if the `loo` object was generated from the `brmsfit` object passed to argument `fit`.
- `recompile`: Logical, indicating whether the Stan model should be recompiled. This may be necessary if you are running `reloo` on another machine than the one used to fit the model.
rename_pars

**future_args**  
A list of further arguments passed to `future` for additional control over parallel execution if activated.

...  
Further arguments passed to `update.brmsfit` and `log_lik.brmsfit`.

**fit**  
An R object of class `brmsfit`.

## Details

Warnings about Pareto $k$ estimates indicate observations for which the approximation to LOO is problematic (this is described in detail in Vehtari, Gelman, and Gabry (2017) and the `loo` package documentation). If there are $J$ observations with $k$ estimates above $k_{\text{threshold}}$, then `reloo` will refit the original model $J$ times, each time leaving out one of the $J$ problematic observations. The pointwise contributions of these observations to the total ELPD are then computed directly and substituted for the previous estimates from these $J$ observations that are stored in the original `loo` object.

## Value

An object of the class `loo`.

## See Also

`loo`, `kfold`

## Examples

```r
## Not run:
fit1 <- brm(count ~ zAge + zBase * Trt + (1|patient),
            data = epilepsy, family = poisson())
# throws warning about some pareto k estimates being too high
(loo1 <- loo(fit1))
(reloo1 <- reloo(fit1, loo = loo1, chains = 1))
## End(Not run)
```

---

**rename_pars**  

**Rename Parameters**

## Description

Rename parameters within the `stanfit` object after model fitting to ensure reasonable parameter names. This function is usually called automatically by `brm` and users will rarely be required to call it themselves.

## Usage

`rename_pars(x)`
Arguments

x

A brmsfit object.

Value

A brmfit object with adjusted parameter names.

Examples

```r
## Not run:
# fit a model manually via rstan
scode <- make_stancode(count ~ Trt, data = epilepsy)
sdata <- make_standata(count ~ Trt, data = epilepsy)
stanfit <- rstan::stan(model_code = scode, data = sdata)

# feed the Stan model back into brms
fit <- brm(count ~ Trt, data = epilepsy, empty = TRUE)
fit$fit <- stanfit
fit <- rename_pars(fit)
summary(fit)
## End(Not run)
```

residuals.brmsfit

Posterior Draws of Residuals/Predictive Errors

Description

This method is an alias of `predictive_error.brmsfit` with additional arguments for obtaining summaries of the computed draws.

Usage

```r
## S3 method for class 'brmsfit'
residuals(
  object,
  newdata = NULL,
  re_formula = NULL,
  method = "posterior_epred",
  type = c("ordinary", "pearson"),
  resp = NULL,
  ndraws = NULL,
  draw_ids = NULL,
  sort = FALSE,
  summary = TRUE,
  robust = FALSE,
  probs = c(0.025, 0.975),
)```
Arguments

object: An object of class `brmsfit`.

ewdata: An optional data.frame for which to evaluate predictions. If NULL (default), the original data of the model is used. NA values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.

re_formula: formula containing group-level effects to be considered in the prediction. If NULL (default), include all group-level effects; if NA, include no group-level effects.

method: Method used to obtain predictions. Either "posterior_epred" (the default) or "posterior_predict". Using "posterior_predict" is recommended but "posterior_epred" is the current default for reasons of backwards compatibility.

type: The type of the residuals, either "ordinary" or "pearson". More information is provided under 'Details'.

resp: Optional names of response variables. If specified, predictions are performed only for the specified response variables.

ndraws: Positive integer indicating how many posterior draws should be used. If NULL (the default) all draws are used. Ignored if draw_ids is not NULL.

draw_ids: An integer vector specifying the posterior draws to be used. If NULL (the default), all draws are used.

sort: Logical. Only relevant for time series models. Indicating whether to return predicted values in the original order (FALSE; default) or in the order of the time series (TRUE).

summary: Should summary statistics be returned instead of the raw values? Default is TRUE.

robust: If FALSE (the default) the mean is used as the measure of central tendency and the standard deviation as the measure of variability. If TRUE, the median and the median absolute deviation (MAD) are applied instead. Only used if summary is TRUE.

probs: The percentiles to be computed by the quantile function. Only used if summary is TRUE.

...: Further arguments passed to `prepare_predictions` that control several aspects of data validation and prediction.

Details

Residuals of type 'ordinary' are of the form \( R = Y - Y_{rep} \), where \( Y \) is the observed and \( Y_{rep} \) is the predicted response. Residuals of type 'pearson' are of the form \( R = (Y - Y_{rep}) / SD(Y_{rep}) \), where \( SD(Y_{rep}) \) is an estimate of the standard deviation of \( Y_{rep} \).
Value

An array of predictive error/residual draws. If `summary = FALSE` the output resembles those of `predictive_error.brmsfit`. If `summary = TRUE` the output is an \(N \times E\) matrix, where \(N\) is the number of observations and \(E\) denotes the summary statistics computed from the draws.

Examples

```r
## Not run:
## fit a model
fit <- brm(rating ~ treat + period + carry + (1|subject),
data = inhaler, cores = 2)

## extract residuals/predictive errors
res <- residuals(fit)
head(res)

## End(Not run)
```

---

**restructure**

**Restructure Old brmsfit Objects**

Description

Restructure old `brmsfit` objects to work with the latest `brms` version. This function is called internally when applying post-processing methods. However, in order to avoid unnecessary run time caused by the restructuring, I recommend explicitly calling `restructure` once per model after updating `brms`.

Usage

```r
restructure(x, ...)
```

Arguments

- `x` An object of class `brmsfit`.
- `...` Currently ignored.

Value

A `brmsfit` object compatible with the latest version of `brms`.
**rows2labels**  
*Convert Rows to Labels*

**Description**  
Convert information in rows to labels for each row.

**Usage**  
```
rows2labels(x, digits = 2, sep = " & ", incl_vars = TRUE, ...)
```

**Arguments**  
- **x**  
  A `data.frame` for which to extract labels.
- **digits**  
  Minimal number of decimal places shown in the labels of numeric variables.
- **sep**  
  A single character string defining the separator between variables used in the labels.
- **incl_vars**  
  Indicates if variable names should be part of the labels. Defaults to `TRUE`.
- **...**  
  Currently unused.

**Value**  
A character vector of the same length as the number of rows of `x`.

**See Also**  
- `make_conditions`, `conditional_effects`

**s**  
*Defining smooths in brms formulas*

**Description**  
Functions used in definition of smooth terms within a model formulas. The function does not evaluate a (spline) smooth - it exists purely to help set up a model using spline based smooths.

**Usage**  
```
s(...)  
t2(...)  
```

**Arguments**  
- **...**  
  Arguments passed to `mgcv::s` or `mgcv::t2`. 

Details

The function defined here are just simple wrappers of the respective functions of the `mgcv` package. When using them, please cite the appropriate references obtained via `citation("mgcv")`.

`brms` uses the "random effects" parameterization of smoothing splines as explained in `mgcv::gamm`. A nice tutorial on this topic can be found in Pedersen et al. (2019). The answers provided in this Stan discourse post may also be helpful.

References


See Also

`brmsformula, mgcv::s, mgcv::t2`

Examples

```r
## Not run:
# simulate some data
dat <- mgcv::gamSim(1, n = 200, scale = 2)

# fit univariate smooths for all predictors
fit1 <- brm(y ~ s(x0) + s(x1) + s(x2) + s(x3),
            data = dat, chains = 2)
summary(fit1)
plot(conditional_smooths(fit1), ask = FALSE)

# fit a more complicated smooth model
fit2 <- brm(y ~ t2(x0, x1) + s(x2, by = x3),
            data = dat, chains = 2)
summary(fit2)
plot(conditional_smooths(fit2), ask = FALSE)

## End(Not run)
```

---

**sar**

Spatial simultaneous autoregressive (SAR) structures

Description

Set up an spatial simultaneous autoregressive (SAR) term in `brms`. The function does not evaluate its arguments – it exists purely to help set up a model with SAR terms.

Usage

`sar(M, type = "lag")`
Arguments

**M**  
An object specifying the spatial weighting matrix. Can be either the spatial weight matrix itself or an object of class `listw` or `nb`, from which the spatial weighting matrix can be computed.

**type**  
Type of the SAR structure. Either "lag" (for SAR of the response values) or "error" (for SAR of the residuals). More information is provided in the 'Details' section.

Details

The `lagsar` structure implements SAR of the response values:

\[ y = \rho Wy + \eta + e \]

The `errorsar` structure implements SAR of the residuals:

\[ y = \eta + u, u = \rho Wu + e \]

In the above equations, \( \eta \) is the predictor term and \( e \) are independent normally or t-distributed residuals. Currently, only families `gaussian` and `student` support SAR structures.

Value

An object of class 'sar_term', which is a list of arguments to be interpreted by the formula parsing functions of `brms`.

See Also

`autocor-terms`

Examples

```r
## Not run:
data(oldcol, package = "spdep")
fit1 <- brm(CRIME ~ INC + HOVAL + sar(COL.nb, type = "lag"),
            data = COL.OLD, data2 = list(COL.nb = COL.nb),
            chains = 2, cores = 2)
summary(fit1)
plot(fit1)

fit2 <- brm(CRIME ~ INC + HOVAL + sar(COL.nb, type = "error"),
            data = COL.OLD, data2 = list(COL.nb = COL.nb),
            chains = 2, cores = 2)
summary(fit2)
plot(fit2)
## End(Not run)
```
save_pars

Control Saving of Parameter Draws

Description

Control which (draws of) parameters should be saved in a \texttt{brms} model. The output of this function is ment for usage in the \texttt{save_pars} argument of \texttt{brm}.

Usage

\begin{verbatim}
save_pars(group = TRUE, latent = FALSE, all = FALSE, manual = NULL)
\end{verbatim}

Arguments

- \texttt{group} A flag to indicate if group-level coefficients for each level of the grouping factors should be saved (default is \texttt{TRUE}). Set to \texttt{FALSE} to save memory. Alternatively, group may also be a character vector naming the grouping factors for which to save draws of coefficients.

- \texttt{latent} A flag to indicate if draws of latent variables obtained by using \texttt{me} and \texttt{mi} terms should be saved (default is \texttt{FALSE}). Saving these draws allows to better use methods such as \texttt{posterior_predict} with the latent variables but leads to very large \texttt{R} objects even for models of moderate size and complexity. Alternatively, \texttt{latent} may also be a character vector naming the latent variables for which to save draws.

- \texttt{all} A flag to indicate if draws of all variables defined in Stan’s \texttt{parameters} block should be saved (default is \texttt{FALSE}). Saving these draws is required in order to apply the certain methods such as \texttt{bridge_sampler} and \texttt{bayes_factor}.

- \texttt{manual} A character vector naming Stan variable names which should be saved. These names should match the variable names inside the Stan code before renaming. This feature is meant for power users only and will rarely be useful outside of very special cases.

Value

A list of class "save_pars".

Examples

\begin{verbatim}
## Not run:
# don't store group-level coefficients
fit <- brm(count ~ zAge + zBase * Trt + (1|patient),
            data = epilepsy, family = poisson(),
            save_pars = save_pars(group = FALSE))
variables(fit)
## End(Not run)
\end{verbatim}
Prior Definitions for **brms** Models

Description

Define priors for specific parameters or classes of parameters.

Usage

```r
set_prior(
  prior,
  class = "b",
  coef = "",
  group = "",
  resp = "",
  dpar = "",
  nlpar = "",
  lb = NA,
  ub = NA,
  check = TRUE
)
```

```r
prior(prior, ...)
prior_(prior, ...)
prior_string(prior, ...)
empty_prior()
```

Arguments

- `prior`: A character string defining a distribution in Stan language
- `class`: The parameter class. Defaults to "b" (i.e. population-level effects). See 'Details' for other valid parameter classes.
- `coef`: Name of the coefficient within the parameter class.
- `group`: Grouping factor for group-level parameters.
- `resp`: Name of the response variable. Only used in multivariate models.
- `dpar`: Name of a distributional parameter. Only used in distributional models.
- `nlpar`: Name of a non-linear parameter. Only used in non-linear models.
- `lb`: Lower bound for parameter restriction. Currently only allowed for classes "b". Defaults to NULL, that is no restriction.
- `ub`: Upper bound for parameter restriction. Currently only allowed for classes "b". Defaults to NULL, that is no restriction.
check Logical; Indicates whether priors should be checked for validity (as far as possible). Defaults to TRUE. If FALSE, prior is passed to the Stan code as is, and all other arguments are ignored.

Arguments passed to set_prior.

Details

set_prior is used to define prior distributions for parameters in brms models. The functions prior, prior_, and prior_string are aliases of set_prior each allowing for a different kind of argument specification. prior allows specifying arguments as expression without quotation marks using non-standard evaluation. prior_ allows specifying arguments as one-sided formulas or wrapped in quote. prior_string allows specifying arguments as strings just as set_prior itself.

Below, we explain its usage and list some common prior distributions for parameters. A complete overview on possible prior distributions is given in the Stan Reference Manual available at https://mc-stan.org/.

To combine multiple priors, use c(...) or the + operator (see 'Examples'). brms does not check if the priors are written in correct Stan language. Instead, Stan will check their syntactical correctness when the model is parsed to C++ and returns an error if they are not. This, however, does not imply that priors are always meaningful if they are accepted by Stan. Although brms tries to find common problems (e.g., setting bounded priors on unbounded parameters), there is no guarantee that the defined priors are reasonable for the model. Below, we list the types of parameters in brms models, for which the user can specify prior distributions.

1. Population-level ('fixed') effects

Every Population-level effect has its own regression parameter represents the name of the corresponding population-level effect. Suppose, for instance, that \( y \) is predicted by \( x_1 \) and \( x_2 \) (i.e., \( y \sim x_1 + x_2 \) in formula syntax). Then, \( x_1 \) and \( x_2 \) have regression parameters \( b_{x_1} \) and \( b_{x_2} \) respectively. The default prior for population-level effects (including monotonic and category specific effects) is an improper flat prior over the reals. Other common options are normal priors or student-t priors. If we want to have a normal prior with mean 0 and standard deviation 5 for \( x_1 \), and a unit student-t prior with 10 degrees of freedom for \( x_2 \), we can specify this via set_prior("normal(0,5)", class = "b", coef = "x1") and set_prior("student_t(10, 0, 1)", class = "b", coef = "x2"). To put the same prior on all population-level effects at once, we may write as a shortcut set_prior("<prior>", class = "b"). This also leads to faster sampling, because priors can be vectorized in this case. Both ways of defining priors can be combined using for instance set_prior("normal(0, 2)", class = "b") and set_prior("normal(0, 10)", class = "b", coef = "x1") at the same time. This will set a normal(0, 10) prior on the effect of \( x_1 \) and a normal(0, 2) prior on all other population-level effects. However, this will break vectorization and may slow down the sampling procedure a bit.

In case of the default intercept parameterization (discussed in the 'Details' section of brmsformula), general priors on class "b" will not affect the intercept. Instead, the intercept has its own parameter class named "Intercept" and priors can thus be specified via set_prior("<prior>", class = "Intercept"). Setting a prior on the intercept will not break vectorization of the other population-level effects. Note that technically, this prior is set on an intercept that results when internally centering all population-level predictors around zero to improve sampling efficiency. On this centered intercept, specifying a prior is actually much easier and intuitive than on the original intercept, since the former represents the expected response value when all predictors are at their means. To
treat the intercept as an ordinary population-level effect and avoid the centering parameterization, use \( 0 + \text{Intercept} \) on the right-hand side of the model formula.

A special shrinkage prior to be applied on population-level effects is the (regularized) horseshoe prior and related priors. See `horseshoe` for details. Another shrinkage prior is the so-called lasso prior. See `lasso` for details.

In non-linear models, population-level effects are defined separately for each non-linear parameter. Accordingly, it is necessary to specify the non-linear parameter in `set_prior` so that priors we can be assigned correctly. If, for instance, \( \alpha \) is the parameter and \( x \) the predictor for which we want to define the prior, we can write `set_prior("<prior>", coef = "x", nlpar = "alpha")`. As a shortcut we can use `set_prior("<prior>", nlpar = "alpha")` to set the same prior on all population-level effects of \( \alpha \) at once.

If desired, population-level effects can be restricted to fall only within a certain interval using the `lb` and `ub` arguments of `set_prior`. This is often required when defining priors that are not defined everywhere on the real line, such as uniform or gamma priors. When defining a `uniform(2,4)` prior, you should write `set_prior("uniform(2,4)", lb = 2, ub = 4)`. When using a prior that is defined on the positive reals only (such as a gamma prior) set `lb = 0`. In most situations, it is not useful to restrict population-level parameters through bounded priors (non-linear models are an important exception), but if you really want to this is the way to go.

2. Standard deviations of group-level ('random') effects

Each group-level effect of each grouping factor has a standard deviation named `sd_<group>_<coef>`. Consider, for instance, the formula \( y \sim x_1 + x_2 + (1 + x_1 | g) \). We see that the intercept as well as \( x_1 \) are group-level effects nested in the grouping factor \( g \). The corresponding standard deviation parameters are named as `sd_g_Intercept` and `sd_g_x1` respectively. These parameters are restricted to be non-negative and, by default, have a half student-t prior with 3 degrees of freedom and a scale parameter that depends on the standard deviation of the response after applying the link function. Minimally, the scale parameter is 2.5. This prior is used (a) to be only weakly informative in order to influence results as few as possible, while (b) providing at least some regularization to considerably improve convergence and sampling efficiency. To define a prior distribution only for standard deviations of a specific grouping factor, use `set_prior("<prior>", class = "sd", group = "<group>")`. To define a prior distribution only for a specific standard deviation of a specific grouping factor, you may write `set_prior("<prior>", class = "sd", group = "<group>", coef = "<coef>")`. Recommendations on useful prior distributions for standard deviations are given in Gelman (2006), but note that he is no longer recommending uniform priors, anymore.

When defining priors on group-level parameters in non-linear models, please make sure to specify the corresponding non-linear parameter through the `nlpar` argument in the same way as for population-level effects.

3. Correlations of group-level ('random') effects

If there is more than one group-level effect per grouping factor, the correlations between those effects have to be estimated. The prior `lkj_corr_cholesky(\eta)` or in short `lkj(\eta)` with \( \eta > 0 \) is essentially the only prior for (Cholesky factors) of correlation matrices. If \( \eta = 1 \) (the default) all correlations matrices are equally likely a priori. If \( \eta > 1 \), extreme correlations become less likely, whereas \( 0 < \eta < 1 \) results in higher probabilities for extreme correlations. Correlation matrix parameters in `brms` models are named as `cor_<group>`, (e.g., `cor_g` if \( g \) is the grouping factor). To set the same prior on every correlation matrix, use for instance `set_prior("lkj(2)", class =`
Internally, the priors are transformed to be put on the Cholesky factors of the correlation matrices to improve efficiency and numerical stability. The corresponding parameter class of the Cholesky factors is \( L \), but it is not recommended to specify priors for this parameter class directly.

4. Splines

Splines are implemented in \texttt{brms} using the 'random effects’ formulation as explained in \texttt{gamm}). Thus, each spline has its corresponding standard deviations modeling the variability within this term. In \texttt{brms}, this parameter class is called \texttt{sds} and priors can be specified via \texttt{set_prior("<prior>", class = "sds", coef = "<term label>"}). The default prior is the same as for standard deviations of group-level effects.

5. Gaussian processes

Gaussian processes as currently implemented in \texttt{brms} have two parameters, the standard deviation parameter \( \text{sdgp} \), and characteristic length-scale parameter \( \text{lscale} \) (see \texttt{gp} for more details). The default prior of \( \text{sdgp} \) is the same as for standard deviations of group-level effects. The default prior of \( \text{lscale} \) is an informative inverse-gamma prior specifically tuned to the covariates of the Gaussian process (for more details see \url{https://betanalpha.github.io/assets/case_studies/gp_part3/part3.html}). This tuned prior may be overly informative in some cases, so please consider other priors as well to make sure inference is robust to the prior specification. If tuning fails, a half-normal prior is used instead.

6. Autocorrelation parameters

The autocorrelation parameters currently implemented are named \texttt{ar} (autoregression), \texttt{ma} (moving average), \texttt{sderr} (standard deviation of latent residuals in latent ARMA models), \texttt{cosy} (compound symmetry correlation), \texttt{car} (spatial conditional autoregression), as well as \texttt{lagsar} and \texttt{errorsar} (spatial simultaneous autoregression).

Priors can be defined by \texttt{set_prior("<prior>", class = "ar") for \texttt{ar} and similar for other autocorrelation parameters. By default, \texttt{ar} and \texttt{ma} are bounded between \(-1\) and \(1\); \texttt{cosy}, \texttt{car}, \texttt{lagsar}, and \texttt{errorsar} are bounded between \(0\) and \(1\). The default priors are flat over the respective definition areas.

7. Parameters of measurement error terms

Latent variables induced via measurement error \texttt{me} terms require both mean and standard deviation parameters, whose prior classes are named "\texttt{meanme}" and "\texttt{sdme}", respectively. If multiple latent variables are induced this way, their correlation matrix will be modeled as well and corresponding priors can be specified via the "\texttt{corme}" class. All of the above parameters have flat priors over their respective definition spaces by default.

8. Distance parameters of monotonic effects

As explained in the details section of \texttt{brm}, monotonic effects make use of a special parameter vector to estimate the 'normalized distances' between consecutive predictor categories. This is realized in \texttt{Stan} using the \texttt{simplex} parameter type. This class is named "\texttt{simo}" (short for simplex monotonic) in \texttt{brms}. The only valid prior for simplex parameters is the dirichlet prior, which accepts a vector of length \( K - 1 \) (\( K \) = number of predictor categories) as input defining the 'concentration' of the distribution. Explaining the dirichlet prior is beyond the scope of this documentation, but we want to describe how to define this prior syntactically correct. If a predictor \( x \) with \( K \) categories is modeled as monotonic, we can define a prior on its corresponding simplex via \texttt{prior(dirichlet(<vector>), class = simo, coef = mox1)}. The \( 1 \) in the end of \texttt{coef} indicates that this is the first simplex in this term. If interactions between multiple monotonic variables are modeled, multiple simplexes per term are required. For \texttt{<vector>}, we can put in any \texttt{R} expression.
defining a vector of length \( K - 1 \). The default is a uniform prior (i.e. \(<vector> = \text{rep}(1, K-1)\)) over all simplexes of the respective dimension.

9. Parameters for specific families

Some families need additional parameters to be estimated. Families gaussian, student, skew_normal, lognormal, and gen_extreme_value need the parameter sigma to account for the residual standard deviation. By default, sigma has a half student-t prior that scales in the same way as the group-level standard deviations. Further, family student needs the parameter nu representing the degrees of freedom of students-t distribution. By default, nu has prior \(\text{gamma}(2, 0.1)\) and a fixed lower bound of 1. Families gamma, weibull, inverse.gaussian, and negbinomial need a shape parameter that has a \(\text{gamma}(0.01, 0.01)\) prior by default. For families cumulative, cratio, sratio, and acat, and only if threshold = "equidistant", the parameter delta is used to model the distance between two adjacent thresholds. By default, delta has an improper flat prior over the reals. The von_mises family needs the parameter kappa, representing the concentration parameter. By default, kappa has prior \(\text{gamma}(2, 0.01)\).

Every family specific parameter has its own prior class, so that set_prior("<prior>", class = "<parameter>") is the right way to go. All of these priors are chosen to be weakly informative, having only minimal influence on the estimations, while improving convergence and sampling efficiency.

Fixing parameters to constants is possible by using the constant function, for example, \(\text{constant}(1)\) to fix a parameter to 1. Broadcasting to vectors and matrices is done automatically.

Often, it may not be immediately clear, which parameters are present in the model. To get a full list of parameters and parameter classes for which priors can be specified (depending on the model) use function get_prior.

Value

An object of class brmsprior to be used in the prior argument of \text{brm}.

Functions

- \text{prior}(): Alias of set_prior allowing to specify arguments as expressions without quotation marks.
- \text{prior_}(): Alias of set_prior allowing to specify arguments as as one-sided formulas or wrapped in quote.
- \text{prior_string}(): Alias of set_prior allowing to specify arguments as strings.
- \text{empty_prior}(): Create an empty brmsprior object.

References


See Also

\text{get_prior}
Examples

```r
## use alias functions
(prior1 <- prior(cauchy(0, 1), class = sd))
(prior2 <- prior(-cauchy(0, 1), class = -sd))
(prior3 <- prior_string("cauchy(0, 1)", class = "sd")
identical(prior1, prior2)
identical(prior1, prior3)

# check which parameters can have priors
get_prior(rating ~ treat + period + carry + (1|subject),
          data = inhaler, family = cumulative())

# define some priors
bprior <- c(prior_string("normal(0,10)", class = "b"),
            prior(normal(1,2), class = b, coef = treat),
            prior_(~cauchy(0,2), class = ~sd,
                    group = ~subject, coef = ~Intercept))

# verify that the priors indeed found their way into Stan's model code
make_stancode(rating ~ treat + period + carry + (1|subject),
              data = inhaler, family = cumulative(),
              prior = bprior)

# use the horseshoe prior to model sparsity in regression coefficients
make_stancode(count ~ zAge + zBase * Trt,
               data = epilepsy, family = poisson(),
               prior = set_prior("horseshoe(3)"))

# fix certain priors to constants
bprior <- prior(constant(1), class = "b") +
         prior(constant(2), class = "b", coef = "zBase") +
         prior(constant(0.5), class = "sd")
make_stancode(count ~ zAge + zBase + (1 | patient),
              data = epilepsy, prior = bprior)

# pass priors to Stan without checking
prior <- prior_string("target += normal_lpdf(b[1] | 0, 1)", check = FALSE)
make_stancode(count ~ Trt, data = epilepsy, prior = prior)
```

---

**Shifted Lognormal**

The Shifted Log Normal Distribution

**Description**

Density, distribution function, quantile function and random generation for the shifted log normal distribution with mean meanlog, standard deviation sdlog, and shift parameter shift.
Usage

dshifted_lnorm(x, meanlog = 0, sdlog = 1, shift = 0, log = FALSE)

pshifted_lnorm(
  q,
  meanlog = 0,
  sdlog = 1,
  shift = 0,
  lower.tail = TRUE,
  log.p = FALSE
)

qshifted_lnorm(
  p,
  meanlog = 0,
  sdlog = 1,
  shift = 0,
  lower.tail = TRUE,
  log.p = FALSE
)

rshifted_lnorm(n, meanlog = 0, sdlog = 1, shift = 0)

Arguments

x, q Vector of quantiles.
meanlog Vector of means.
sdlog Vector of standard deviations.
shift Vector of shifts.
log Logical; If TRUE, values are returned on the log scale.
lower.tail Logical; If TRUE (default), return \( P(X \leq x) \). Else, return \( P(X > x) \).
log.p Logical; If TRUE, values are returned on the log scale.
p Vector of probabilities.
n Number of draws to sample from the distribution.

Details

See vignette("brms_families") for details on the parameterization.
SkewNormal

The Skew-Normal Distribution

Description
Density, distribution function, and random generation for the skew-normal distribution with mean mu, standard deviation sigma, and skewness alpha.

Usage

dskew_normal(x, mu = 0, sigma = 1, alpha = 0, xi = NULL, omega = NULL, log = FALSE)

pskew_normal(q, mu = 0, sigma = 1, alpha = 0, xi = NULL, omega = NULL, lower.tail = TRUE, log.p = FALSE)

qskew_normal(p, mu = 0, sigma = 1, alpha = 0, xi = NULL, omega = NULL, lower.tail = TRUE, log.p = FALSE, tol = 1e-08)

rskew_normal(n, mu = 0, sigma = 1, alpha = 0, xi = NULL, omega = NULL)

Arguments

x, q Vector of quantiles.
mu

Vector of mean values.

sigma

Vector of standard deviation values.

alpha

Vector of skewness values.

xi

Optional vector of location values. If NULL (the default), will be computed internally.

omega

Optional vector of scale values. If NULL (the default), will be computed internally.

log

Logical; If TRUE, values are returned on the log scale.

lower.tail

Logical; If TRUE (default), return P(X <= x). Else, return P(X > x).

log.p

Logical; If TRUE, values are returned on the log scale.

p

Vector of probabilities.

tol

Tolerance of the approximation used in the computation of quantiles.

n

Number of draws to sample from the distribution.

Details

See vignette("brms_families") for details on the parameterization.

---

stancode.brmsfit  

*Extract Stan model code*

---

**Description**

Extract Stan code that was used to specify the model.

**Usage**

```r
## S3 method for class 'brmsfit' 
stancode(
  object,
  version = TRUE,
  regenerate = NULL,
  threads = NULL,
  backend = NULL,
  ...
)

stancode(object, ...)
```
**Arguments**

- **object**: An object of class `brmsfit`.
- **version**: Logical; indicates if the first line containing the `brms` version number should be included. Defaults to `TRUE`.
- **regenerate**: Logical; indicates if the Stan code should be regenerated with the current `brms` version. By default, `regenerate` will be `FALSE` unless required to be `TRUE` by other arguments.
- **threads**: Controls whether the Stan code should be threaded. See `threading` for details.
- **backend**: Controls the Stan backend. See `brm` for details.
- **...**: Further arguments passed to `make_stancode` if the Stan code is regenerated.

**Value**

Stan model code for further processing.

---

**Description**

Extract all data that was used by Stan to fit the model.

**Usage**

```r
# S3 method for class 'brmsfit'
standata(
  object,
  newdata = NULL,
  re_formula = NULL,
  newdata2 = NULL,
  new_objects = NULL,
  incl_autocor = TRUE,
  ...
)

standata(object, ...)
```

**Arguments**

- **object**: An object of class `brmsfit`.
- **newdata**: An optional data.frame for which to evaluate predictions. If `NULL` (default), the original data of the model is used. `NA` values within factors are interpreted as if all dummy variables of this factor are zero. This allows, for instance, to make predictions of the grand mean when using sum coding.
**re_formula**  
formula containing group-level effects to be considered in the prediction. If NULL (default), include all group-level effects; if NA, include no group-level effects.

**newdata2**  
A named list of objects containing new data, which cannot be passed via argument newdata. Required for some objects used in autocorrelation structures, or `stanvars`.

**new_objects**  
Deprecated alias of `newdata2`.

**incl_autocor**  
A flag indicating if correlation structures originally specified via `autocor` should be included in the predictions. Defaults to TRUE.

...  
More arguments passed to `make_standata` and `validate_newdata`.

**Value**

A named list containing the data originally passed to Stan.

---

**stanvar**  
*User-defined variables passed to Stan*

**Description**

Prepare user-defined variables to be passed to one of Stan’s program blocks. This is primarily useful for defining more complex priors, for refitting models without recompilation despite changing priors, or for defining custom Stan functions.

**Usage**

```r
stanvar(
  x = NULL,
  name = NULL,
  scode = NULL,
  block = "data",
  position = "start",
  pll_args = NULL
)
```

**Arguments**

- **x**  
  An R object containing data to be passed to Stan. Only required if `block = 'data'` and ignored otherwise.

- **name**  
  Optional character string providing the desired variable name of the object in `x`. If NULL (the default) the variable name is directly inferred from `x`.

- **scode**  
  Line of Stan code to define the variable in Stan language. If `block = 'data'`, the Stan code is inferred based on the class of `x` by default.
block Name of one of Stan’s program blocks in which the variable should be defined. Can be 'data', 'tdata' (transformed data), 'parameters', 'tparameters' (transformed parameters), 'model', 'likelihood' (part of the model block where the likelihood is given), 'genquant' (generated quantities) or 'functions'.

position Name of the position within the block where the Stan code should be placed. Currently allowed are 'start' (the default) and 'end' of the block.

pll_args Optional Stan code to be put into the header of partial_log_lik functions. This ensures that the variables specified in scode can be used in the likelihood even when within-chain parallelization is activated via threading.

Value

An object of class stanvars.

Examples

```r
bprior <- prior(normal(mean_intercept, 10), class = "Intercept")
stanvars <- stanvar(5, name = "mean_intercept")
make_stancode(count ~ Trt, epilepsy, prior = bprior,
  stanvars = stanvars)

# define a multi-normal prior with known covariance matrix
bprior <- prior(multi_normal(M, V), class = "b")
stanvars <- stanvar(rep(0, 2), "M", scode = " vector[K] M;") +
  stanvar(diag(2), "V", scode = " matrix[K, K] V;")
make_stancode(count ~ Trt + zBase, epilepsy,
  prior = bprior, stanvars = stanvars)

# define a hierachical prior on the regression coefficients
bprior <- set_prior("normal(0, tau)", class = "b") +
  set_prior("target += normal_lpdf(tau | 0, 10)", check = FALSE)
stanvars <- stanvar(scode = "real<lower=0> tau;",
  block = "parameters")
make_stancode(count ~ Trt + zBase, epilepsy,
  prior = bprior, stanvars = stanvars)

# ensure that 'tau' is passed to the likelihood of a threaded model
# not necessary for this example but may be necessary in other cases
stanvars <- stanvar(scode = "real<lower=0> tau;",
  block = "parameters", pll_args = "real tau")
make_stancode(count ~ Trt + zBase, epilepsy,
  stanvars = stanvars, threads = threading(2))
```

StudentT The Student-t Distribution
Description
Density, distribution function, quantile function and random generation for the Student-t distribution with location mu, scale sigma, and degrees of freedom df.

Usage

dstudent_t(x, df, mu = 0, sigma = 1, log = FALSE)
pstudent_t(q, df, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)
qstudent_t(p, df, mu = 0, sigma = 1, lower.tail = TRUE, log.p = FALSE)
rstudent_t(n, df, mu = 0, sigma = 1)

Arguments
x Vector of quantiles.
df Vector of degrees of freedom.
mu Vector of location values.
sigma Vector of scale values.
log Logical; If TRUE, values are returned on the log scale.
q Vector of quantiles.
lower.tail Logical; If TRUE (default), return P(X <= x). Else, return P(X > x).
log.p Logical; If TRUE, values are returned on the log scale.
p Vector of probabilities.
n Number of draws to sample from the distribution.

Details
See vignette("brms_families") for details on the parameterization.

See Also

TDist

summary.brmsfit Create a summary of a fitted model represented by a brmsfit object

Description
Create a summary of a fitted model represented by a brmsfit object
Usage

```r
## S3 method for class 'brmsfit'
summary(
  object,
  priors = FALSE,
  prob = 0.95,
  robust = FALSE,
  mc_se = FALSE,
  ...
)
```

Arguments

- `object`: An object of class `brmsfit`.
- `priors`: Logical; indicating if priors should be included in the summary. Default is `FALSE`.
- `prob`: A value between 0 and 1 indicating the desired probability to be covered by the uncertainty intervals. The default is 0.95.
- `robust`: If `FALSE` (the default) the mean is used as the measure of central tendency and the standard deviation as the measure of variability. If `TRUE`, the median and the median absolute deviation (MAD) are applied instead.
- `mc_se`: Logical; indicating if the uncertainty in `Estimate` caused by the MCMC sampling should be shown in the summary. Defaults to `FALSE`.
- `...`: Other potential arguments

Details

The convergence diagnostics `Rhat`, `Bulk_ESS`, and `Tail_ESS` are described in detail in Vehtari et al. (2020).

References


Description

A black theme for ggplot graphics inspired by a blog post of Jon Lefcheck (https://jonlefcheck.net/2013/03/11/black-theme-for-ggplot2-2/).
Usage

theme_black(base_size = 12, base_family = "")

Arguments

base_size base font size
base_family base font family

Details

When using theme_black in plots powered by the bayesplot package such as pp_check or stanplot, I recommend using the "viridisC" color scheme (see examples).

Value

A theme object used in ggplot2 graphics.

Examples

```r
## Not run:
# change default ggplot theme
ggplot2::theme_set(theme_black())

# change default bayesplot color scheme
bayesplot::color_scheme_set("viridisC")

# fit a simple model
fit <- brm(count ~ zAge + zBase * Trt + (1|patient),
            data = epilepsy, family = poisson(), chains = 2)
summary(fit)

# create various plots
plot(marginal_effects(fit), ask = FALSE)
pp_check(fit)
mcmc_plot(fit, type = "hex", variable = c("b_Intercept", "b_Trt1"))

## End(Not run)
```

theme_default

**Default bayesplot Theme for ggplot2 Graphics**

Description

This theme is imported from the bayesplot package. See theme_default for a complete documentation.
threading

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>base_size</td>
<td>base font size</td>
</tr>
<tr>
<td>base_family</td>
<td>base font family</td>
</tr>
</tbody>
</table>

Value

A theme object used in ggplot2 graphics.

Threading in Stan

Description

Use threads for within-chain parallelization in Stan via the brms interface. Within-chain parallelization is experimental! We recommend its use only if you are experienced with Stan’s reduce_sum function and have a slow running model that cannot be sped up by any other means.

Usage

threading(threads = NULL, grainsize = NULL, static = FALSE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>threads</td>
<td>Number of threads to use in within-chain parallelization.</td>
</tr>
<tr>
<td>grainsize</td>
<td>Number of observations evaluated together in one chunk on one of the CPUs used for threading. If NULL (the default), grainsize is currently chosen as max(100, N / (2 * threads)), where N is the number of observations in the data. This default is experimental and may change in the future without prior notice.</td>
</tr>
<tr>
<td>static</td>
<td>Logical. Apply the static (non-adaptive) version of reduce_sum? Defaults to FALSE. Setting it to TRUE is required to achieve exact reproducibility of the model results (if the random seed is set as well).</td>
</tr>
</tbody>
</table>

Details

The adaptive scheduling procedure used by reduce_sum will prevent the results to be exactly reproducible even if you set the random seed. If you need exact reproducibility, you have to set argument static = TRUE which may reduce efficiency a bit.

To ensure that chunks (whose size is defined by grainsize) require roughly the same amount of computing time, we recommend storing observations in random order in the data. At least, please avoid sorting observations after the response values. This is because the latter often cause variations in the computing time of the pointwise log-likelihood, which makes up a big part of the parallelized code.

Value

A brmsthreads object which can be passed to the threads argument of brm and related functions.
Examples

## Not run:
# this model just serves as an illustration
# threading may not actually speed things up here
fit <- brm(count ~ zAge + zBase * Trt + (1|patient),
            data = epilepsy, family = negbinomial(),
            chains = 1, threads = threading(2, grainsize = 100),
            backend = "cmdstanr")
summary(fit)

## End(Not run)

---

unstr  

Set up UNSTR correlation structures

Description

Set up an unstructured (UNSTR) correlation term in `brms`. The function does not evaluate its arguments – it exists purely to help set up a model with UNSTR terms.

Usage

`unstr(time, gr)`

Arguments

- `time`: An optional time variable specifying the time ordering of the observations. By default, the existing order of the observations in the data is used.
- `gr`: An optional grouping variable. If specified, the correlation structure is assumed to apply only to observations within the same grouping level.

Value

An object of class 'unstr_term', which is a list of arguments to be interpreted by the formula parsing functions of `brms`.

See Also

- `autocor-terms`

Examples

## Not run:
# add an unstructured correlation matrix for visits within the same patient
fit <- brm(count ~ Trt + unstr(visit, patient), data = epilepsy)
summary(fit)

## End(Not run)
**update.brmsfit**

Update brms models

**Description**

This method allows to update an existing brmsfit object.

**Usage**

```r
## S3 method for class 'brmsfit'
update(object, formula., newdata = NULL, recompile = NULL, ...)
```

**Arguments**

- `object`: An object of class `brmsfit`
- `formula.`: Changes to the formula; for details see `update.formula` and `brmsformula`.
- `newdata`: Optional `data.frame` to update the model with new data. Data-dependent default priors will not be updated automatically.
- `recompile`: Logical, indicating whether the Stan model should be recompiled. If `NULL` (the default), `update` tries to figure out internally, if recompilation is necessary. Setting it to `FALSE` will cause all Stan code changing arguments to be ignored.
- `...`: Other arguments passed to `brm`.

**Details**

When updating a `brmsfit` created with the `cmdstanr` backend in a different R session, a recompilation will be triggered because by default, `cmdstanr` writes the model executable to a temporary directory. To avoid that, set option "cmdstanr_write_stan_file_dir" to a nontemporary path of your choice before creating the original `brmsfit` (see section 'Examples' below).

**Examples**

```r
## Not run:
fit1 <- brm(time | cens(censored) ~ age * sex + disease + (1|patient),
            data = kidney, family = gaussian("log"))
summary(fit1)

## remove effects of 'disease'
fit2 <- update(fit1, formula. = ~ . - disease)
summary(fit2)

## remove the group specific term of 'patient' and
## change the data (just take a subset in this example)
fit3 <- update(fit1, formula. = ~ . - (1|patient),
              newdata = kidney[1:38, ])
summary(fit3)
```
## use another family and add population-level priors
fit4 <- update(fit1, family = weibull(), init = "0",
       prior = set_prior("normal(0,5)")
)  
summary(fit4)

## to avoid a recompilation when updating a 'cmdstanr'-backend fit in a fresh
## R session, set option 'cmdstanr_write_stan_file_dir' before creating the
## initial 'brmsfit'
## CAUTION: the following code creates some files in the current working
## directory: two 'model_<hash>.stan' files, one 'model_<hash>.exe'
## executable, and one 'fit_cmdstanr_<some_number>.rds' file
set.seed(7)
fname <- paste0("fit_cmdstanr_", sample.int(.Machine$integer.max, 1))
options(cmdstanr_write_stan_file_dir = getwd())
fit_cmdstanr <- brm(rate ~ conc + state,
        data = Puromycin,
        backend = "cmdstanr",
        file = fname)

# now restart the R session and run the following (after attaching 'brms')
set.seed(7)
fname <- paste0("fit_cmdstanr_", sample.int(.Machine$integer.max, 1))
fit_cmdstanr <- brm(rate ~ conc + state,
        data = Puromycin,
        backend = "cmdstanr",
        file = fname)

upd_cmdstanr <- update(fit_cmdstanr,
        formula. = rate ~ conc)

## End(Not run)

---

**update.brmsfit_multiple**

*Update brms models based on multiple data sets*

### Description

This method allows to update an existing `brmsfit_multiple` object.

### Usage

```r
## S3 method for class 'brmsfit_multiple'
update(object, formula., newdata = NULL, ...)
```

### Arguments

- **object**
  An object of class `brmsfit_multiple`.
- **formula.**
  Changes to the formula; for details see `update.formula` and `brmsformula`. 
newdata List of data.frames to update the model with new data. Currently required even if the original data should be used.

... Other arguments passed to `update.brmsfit` and `brm_multiple`.

Examples

```r
## Not run:
library(mice)
imp <- mice(nhanes2)

# initially fit the model
fit_imp1 <- brm_multiple(bmi ~ age + hyp + chl, data = imp, chains = 1)
summary(fit_imp1)

# update the model using fewer predictors
fit_imp2 <- update(fit_imp1, formula. = . ~ hyp + chl, newdata = imp)
summary(fit_imp2)

## End(Not run)
```

---

**update_adterms**

**Update Formula Addition Terms**

**Description**

Update additions terms used in formulas of `brms`. See `addition-terms` for details.

**Usage**

```r
update_adterms(formula, adform, action = c("update", "replace"))
```

**Arguments**

- `formula` Two-sided formula to be updated.
- `adform` One-sided formula containing addition terms to update formula with.
- `action` Indicates what should happen to the existing addition terms in `formula`. If "update" (the default), old addition terms that have no corresponding term in `adform` will be kept. If "replace", all old addition terms will be removed.

**Value**

An object of class `formula`. 
validate_newdata

Validate New Data

Description

Validate new data passed to post-processing methods of `brms`. Unless you are a package developer, you will rarely need to call `validate_newdata` directly.

Usage

```r
validate_newdata(
  newdata,
  object,
  re_formula = NULL,
  allow_new_levels = FALSE,
  newdata2 = NULL,
  resp = NULL,
  check_response = TRUE,
  incl_autocor = TRUE,
  group_vars = NULL,
  req_vars = NULL,
  ...
)
```

Arguments

- `newdata` A `data.frame` containing new data to be validated.
- `object` A `brmsfit` object.
- `re_formula` formula containing group-level effects to be considered in the prediction. If `NULL` (default), include all group-level effects; if `NA`, include no group-level effects.
- `allow_new_levels` A flag indicating if new levels of group-level effects are allowed (defaults to `FALSE`). Only relevant if `newdata` is provided.
- `newdata2` A named list of objects containing new data, which cannot be passed via argument `newdata`. Required for some objects used in autocorrelation structures, or `stanvars`. 

Examples

```r
form <- y | trials(size) ~ x
update_adterms(form, ~ trials(10))
update_adterms(form, ~ weights(w))
update_adterms(form, ~ weights(w), action = "replace")
update_adterms(y ~ x, ~ trials(10))
```
validate_prior

resp

Optional names of response variables. If specified, predictions are performed only for the specified response variables.

check_response

Logical; Indicates if response variables should be checked as well. Defaults to TRUE.

incl_autocor

A flag indicating if correlation structures originally specified via autocor should be included in the predictions. Defaults to TRUE.

group_vars

Optional names of grouping variables to be validated. Defaults to all grouping variables in the model.

req_vars

Optional names of variables required in newdata. If NULL (the default), all variables in the original data are required (unless ignored for some other reason).

Value

A validated 'data.frame' based on newdata.

validate_prior  Validate Prior for brms Models

Description

Validate priors supplied by the user. Return a complete set of priors for the given model, including default priors.

Usage

validate_prior(
prior,
formula,
data,
family = gaussian(),
sample_prior = "no",
data2 = NULL,
knots = NULL,
drop_unused_levels = TRUE,
...
)

Arguments

prior One or more brmsprior objects created by set_prior or related functions and combined using the c method or the + operator. See also get_prior for more help.

formula An object of class formula, brmsformula, or mvbrmsformula (or one that can be coerced to that classes): A symbolic description of the model to be fitted. The details of model specification are explained in brmsformula.
data An object of class data.frame (or one that can be coerced to that class) containing data of all variables used in the model.

family A description of the response distribution and link function to be used in the model. This can be a family function, a call to a family function or a character string naming the family. Every family function has a `link` argument allowing to specify the link function to be applied on the response variable. If not specified, default links are used. For details of supported families see `brmsfamily`. By default, a linear gaussian model is applied. In multivariate models, family might also be a list of families.

data2 A named list of objects containing data, which cannot be passed via argument `data`. Required for some objects used in autocorrelation structures to specify dependency structures as well as for within-group covariance matrices.

knots Optional list containing user specified knot values to be used for basis construction of smoothing terms. See `gamm` for more details.

drop_unused_levels Should unused factors levels in the data be dropped? Defaults to `TRUE`.

... Other arguments for internal usage only.

Value

An object of class `brmsprior`.

See Also

`get_prior`, `set_prior`.

Examples

```r
prior1 <- prior(normal(0,10), class = b) +
prior(cauchy(0,2), class = sd)
validate_prior(prior1, count ~ zAge + zBase * Trt + (1|patient),
  data = epilepsy, family = poisson())
```
VarCorr.brmsfit

Extract Variance and Correlation Components

Description

This function calculates the estimated standard deviations, correlations and covariances of the
group-level terms in a multilevel model of class brmsfit. For linear models, the residual standard
deviations, correlations and covariances are also returned.

Usage

```r
## S3 method for class 'brmsfit'
VarCorr(
  x,
  sigma = 1,
  summary = TRUE,
  robust = FALSE,
  probs = c(0.025, 0.975),
  ...
)
```

Arguments

- `x`: An object of class brmsfit.
- `sigma`: Ignored (included for compatibility with VarCorr).
- `summary`: Should summary statistics be returned instead of the raw values? Default is TRUE.
- `robust`: If FALSE (the default) the mean is used as the measure of central tendency and the standard deviation as the measure of variability. If TRUE, the median and the median absolute deviation (MAD) are applied instead. Only used if summary is TRUE.
- `probs`: The percentiles to be computed by the quantile function. Only used if summary is TRUE.
- `...`: Currently ignored.

Value

A list of lists (one per grouping factor), each with three elements: a matrix containing the standard
deviations, an array containing the correlation matrix, and an array containing the covariance matrix
with variances on the diagonal.

Examples

```r
## Not run:
fit <- brm(count ~ zAge + zBase * Trt + (1+Trt|visit),
            data = epilepsy, family = gaussian(), chains = 2)
```
vcor.brmsfit

Covariance and Correlation Matrix of Population-Level Effects

Description

Get a point estimate of the covariance or correlation matrix of population-level parameters

Usage

## S3 method for class 'brmsfit'
vcor(object, correlation = FALSE, pars = NULL, ...)

Arguments

- object: An object of class brmsfit.
- correlation: Logical; if FALSE (the default), compute the covariance matrix, if TRUE, compute the correlation matrix.
- pars: Optional names of coefficients to extract. By default, all coefficients are extracted.
- ...: Currently ignored.

Details

Estimates are obtained by calculating the maximum likelihood covariances (correlations) of the posterior draws.

Value

covariance or correlation matrix of population-level parameters

Examples

## Not run:
fit <- brm(count ~ zAge + zBase * Trt + (1|Trt|visit),
           data = epilepsy, family = gaussian(), chains = 2)
vcov(fit)
## End(Not run)
VonMises

The von Mises Distribution

Description
Density, distribution function, and random generation for the von Mises distribution with location \( \mu \), and precision \( \kappa \).

Usage
\[
\text{dvon_mises}(x, \mu, \kappa, \text{log} = \text{FALSE})
\]
\[
\text{pvon_mises}(q, \mu, \kappa, \text{lower.tail} = \text{TRUE}, \text{log.p} = \text{FALSE}, \text{acc} = 1e-20)
\]
\[
\text{rvon_mises}(n, \mu, \kappa)
\]

Arguments
- \( x, q \): Vector of quantiles.
- \( \mu \): Vector of location values.
- \( \kappa \): Vector of precision values.
- \( \text{log} \): Logical; If TRUE, values are returned on the log scale.
- \( \text{lower.tail} \): Logical; If TRUE (default), return \( P(X \leq x) \). Else, return \( P(X > x) \).
- \( \text{log.p} \): Logical; If TRUE, values are returned on the log scale.
- \( \text{acc} \): Accuracy of numerical approximations.
- \( n \): Number of draws to sample from the distribution.

Details
See vignette("brms_families") for details on the parameterization.

waic.brmsfit

Widely Applicable Information Criterion (WAIC)

Description
Compute the widely applicable information criterion (WAIC) based on the posterior likelihood using the \texttt{loo} package. For more details see \texttt{waic}.
Usage

```r
## S3 method for class 'brmsfit'
waic(
  x,
  ..., 
  compare = TRUE,
  resp = NULL,
  pointwise = FALSE,
  model_names = NULL
)
```

Arguments

- `x`: A `brmsfit` object.
- `...`: More `brmsfit` objects or further arguments passed to the underlying post-processing functions. In particular, see `prepare_predictions` for further supported arguments.
- `compare`: A flag indicating if the information criteria of the models should be compared to each other via `loo_compare`.
- `resp`: Optional names of response variables. If specified, predictions are performed only for the specified response variables.
- `pointwise`: A flag indicating whether to compute the full log-likelihood matrix at once or separately for each observation. The latter approach is usually considerably slower but requires much less working memory. Accordingly, if one runs into memory issues, `pointwise = TRUE` is the way to go.
- `model_names`: If `NULL` (the default) will use model names derived from deparsing the call. Otherwise will use the passed values as model names.

Details

See `loo_compare` for details on model comparisons. For `brmsfit` objects, WAIC is an alias of `waic`. Use method `add_criterion` to store information criteria in the fitted model object for later usage.

Value

If just one object is provided, an object of class `loo`. If multiple objects are provided, an object of class `loolist`.

References


## Examples

```r
## Not run:
# model with population-level effects only
fit1 <- brm(rating ~ treat + period + carry,
        data = inhaler)
(waic1 <- waic(fit1))

# model with an additional varying intercept for subjects
fit2 <- brm(rating ~ treat + period + carry + (1|subject),
        data = inhaler)
(waic2 <- waic(fit2))

# compare both models
loo_compare(waic1, waic2)

## End(Not run)
```

---

**Wiener**  
*The Wiener Diffusion Model Distribution*

### Description

Density function and random generation for the Wiener diffusion model distribution with boundary separation alpha, non-decision time tau, bias beta and drift rate delta.

### Usage

```r
dwiener(  
    x,  
    alpha,  
    tau,  
    beta,  
    delta,  
    resp = 1,  
    log = FALSE,  
    backend = getOption("wiener_backend", "Rwiener")
)
```

```r
rwiener(  
    n,  
    alpha,  
    tau,  
    beta,  
    delta,  
    types = c("q", "resp"),  
    backend = getOption("wiener_backend", "Rwiener")
)
```
Arguments

- **x**: Vector of quantiles.
- **alpha**: Boundary separation parameter.
- **tau**: Non-decision time parameter.
- **beta**: Bias parameter.
- **delta**: Drift rate parameter.
- **resp**: Response: "upper" or "lower". If no character vector, it is coerced to logical where TRUE indicates "upper" and FALSE indicates "lower".
- **log**: Logical; If TRUE, values are returned on the log scale.
- **backend**: Name of the package to use as backend for the computations. Either "Rwiener" (the default) or "rtdists". Can be set globally for the current R session via the "wiener_backend" option (see options).
- **n**: Number of draws to sample from the distribution.
- **types**: Which types of responses to return? By default, return both the response times "q" and the dichotomous responses "resp". If either "q" or "resp", return only one of the two types.

Details

These are wrappers around functions of the RWiener or rtdists package (depending on the chosen backend). See vignette("brms_families") for details on the parameterization.

See Also

- wienerdist, Diffusion

ZeroInflated

Zero-Inflated Distributions

Description

Density and distribution functions for zero-inflated distributions.

Usage

- dzero_inflated_poisson(x, lambda, zi, log = FALSE)
- pzero_inflated_poisson(q, lambda, zi, lower.tail = TRUE, log.p = FALSE)
- dzero_inflated_negbinomial(x, mu, shape, zi, log = FALSE)
- pzero_inflated_negbinomial(q, mu, shape, zi, lower.tail = TRUE, log.p = FALSE)
- dzero_inflated_binomial(x, size, prob, zi, log = FALSE)
pzero_inflated_binomial(q, size, prob, zi, lower.tail = TRUE, log.p = FALSE)

dzero_inflated_beta_binomial(x, size, mu, phi, zi, log = FALSE)

pzero_inflated_beta_binomial(  
  q,  
  size,  
  mu,  
  phi,  
  zi,  
  lower.tail = TRUE,  
  log.p = FALSE  
)

dzero_inflated_beta(x, shape1, shape2, zi, log = FALSE)

pzero_inflated_beta(q, shape1, shape2, zi, lower.tail = TRUE, log.p = FALSE)

**Arguments**

- **x**: Vector of quantiles.
- **zi**: zero-inflation probability
- **log**: Logical; If TRUE, values are returned on the log scale.
- **q**: Vector of quantiles.
- **lower.tail**: Logical; If TRUE (default), return P(X <= x). Else, return P(X > x).
- **log.p**: Logical; If TRUE, values are returned on the log scale.
- **mu, lambda**: location parameter
- **shape, shape1, shape2**: shape parameter
- **size**: number of trials
- **prob**: probability of success on each trial
- **phi**: precision parameter

**Details**

The density of a zero-inflated distribution can be specified as follows. If \( x = 0 \) set \( f(x) = \theta + (1 - \theta) \times g(0) \). Else set \( f(x) = (1 - \theta) \times g(x) \), where \( g(x) \) is the density of the non-zero-inflated part.
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