Package: rstanarm (via r-universe)

October 29, 2026

Type Package

Title Bayesian Applied Regression Modeling via Stan

Version 2.32.2

Date 2025-09-29

Encoding UTF-8

Description Estimates previously compiled regression models using the 'rstan' package, which provides the R interface to the Stan C++ library for Bayesian estimation. Users specify models via the customary R syntax with a formula and data.frame plus some additional arguments for priors.

License GPL (>= 3)

Depends R (>= 3.4.0), Rcpp (>= 0.12.0), methods

Imports bayesplot (>= 1.7.0), ggplot2 (>= 2.2.1), lme4 (>= 1.1-8), loo (>= 2.1.0), Matrix (>= 1.2-13), nlme (>= 3.1-124), posterior, rstan (>= 2.32.0), rstantools (>= 2.1.0), shinystan (>= 2.3.0), stats, survival (>= 2.40.1), RcppParallel (>= 5.0.1), utils, reformulas

Suggests biglm, betareg, data.table (>= 1.10.0), digest, gridExtra, HSAUR3, knitr (>= 1.15.1), MASS, mgcv (>= 1.8-13), rmarkdown, roxygen2, StanHeaders (>= 2.21.0), testthat (>= 1.0.2), gamm4, shiny, V8

LinkingTo StanHeaders (>= 2.32.0), rstan (>= 2.32.0), BH (>= 1.72.0-2), Rcpp (>= 0.12.0), RcppEigen (>= 0.3.3.3.0), RcppParallel (>= 5.0.1)

SystemRequirements GNU make, pandoc (>= 1.12.3), pandoc-citeproc

VignetteBuilder knitr

LazyData true

UseLTO true

NeedsCompilation yes

URL https://mc-stan.org/rstanarm/, https://discourse.mc-stan.org

BugReports https://github.com/stan-dev/rstanarm/issues

RoxygenNote 7.3.3

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Config/pak/sysreqs make

Repository https://cran.r-universe.dev

Date/Publication 2025-09-30 08:00:02 UTC

RemoteUrl https://github.com/cran/rstanarm

RemoteRef HEAD

RemoteSha 1b96334c4eccab99caf36304315035d9ea6f9c38

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`rstanarm-package` *Applied Regression Modeling via RStan*

Description

The **rstanarm** package is an appendage to the **rstan** package that enables many of the most common applied regression models to be estimated using Markov Chain Monte Carlo, variational approximations to the posterior distribution, or optimization. The **rstanarm** package allows these models to be specified using the customary R modeling syntax (e.g., like that of `glm` with a `formula` and a `data.frame`).

The sections below provide an overview of the modeling functions and estimation algorithms used by **rstanarm**.

Details

The set of models supported by **rstanarm** is large (and will continue to grow), but also limited enough so that it is possible to integrate them tightly with the `pp_check` function for graphical posterior predictive checks with **bayesplot** and the `posterior_predict` function to easily estimate the effect of specific manipulations of predictor variables or to predict the outcome in a training set.

The objects returned by the **rstanarm** modeling functions are called `stanreg` objects. In addition to all of the typical `methods` defined for fitted model objects, stanreg objects can be passed to the `loo` function in the **loo** package for model comparison or to the `launch_shinystan` function in the **shinystan** package in order to visualize the posterior distribution using the ShinyStan graphical user interface. See the **rstanarm** vignettes for more details about the entire process.

Prior distributions

See priors help page and the vignette *Prior Distributions for rstanarm Models* for an overview of the various choices the user can make for prior distributions. The package vignettes for the modeling functions also provide examples of using many of the available priors as well as more detailed descriptions of some of the novel priors used by **rstanarm**.

Modeling functions

The model estimating functions are described in greater detail in their individual help pages and vignettes. Here we provide a very brief overview:

`stan_lm`**,** `stan_aov`**,** `stan_biglm` Similar to `lm` or `aov` but with novel regularizing priors on the model parameters that are driven by prior beliefs about R^2, the proportion of variance in the outcome attributable to the predictors in a linear model.

`stan_glm`**,** `stan_glm.nb` Similar to `glm` but with various possible prior distributions for the coefficients and, if applicable, a prior distribution for any auxiliary parameter in a Generalized Linear Model (GLM) that is characterized by a `family` object (e.g. the shape parameter in Gamma models). It is also possible to estimate a negative binomial model in a similar way to the `glm.nb` function in the **MASS** package.

`stan_glmer`**,** `stan_glmer.nb`**,** `stan_lmer` Similar to the `glmer`, `glmer.nb` and `lmer` functions in the **lme4** package in that GLMs are augmented to have group-specific terms that deviate from the common coefficients according to a mean-zero multivariate normal distribution with a highly-structured but unknown covariance matrix (for which **rstanarm** introduces an innovative prior distribution). MCMC provides more appropriate estimates of uncertainty for models that consist of a mix of common and group-specific parameters.

`stan_nlmer` Similar to `nlmer` in the **lme4** package for nonlinear "mixed-effects" models, but the group-specific coefficients have flexible priors on their unknown covariance matrices.

`stan_gamm4` Similar to `gamm4` in the **gamm4** package, which augments a GLM (possibly with group-specific terms) with nonlinear smooth functions of the predictors to form a Generalized Additive Mixed Model (GAMM). Rather than calling `glmer` like `gamm4` does, `stan_gamm4` essentially calls `stan_glmer`, which avoids the optimization issues that often crop up with GAMMs and provides better estimates for the uncertainty of the parameter estimates.

`stan_polr` Similar to `polr` in the **MASS** package in that it models an ordinal response, but the Bayesian model also implies a prior distribution on the unknown cutpoints. Can also be used

to model binary outcomes, possibly while estimating an unknown exponent governing the probability of success.

`stan_betareg` Similar to `betareg` in that it models an outcome that is a rate (proportion) but, rather than performing maximum likelihood estimation, full Bayesian estimation is performed by default, with customizable prior distributions for all parameters.

`stan_clogit` Similar to `clogit` in that it models an binary outcome where the number of successes and failures is fixed within each stratum by the research design. There are some minor syntactical differences relative to `clogit` that allow `stan_clogit` to accept group-specific terms as in `stan_glmer`.

`stan_mvmer` A multivariate form of `stan_glmer`, whereby the user can specify one or more submodels each consisting of a GLM with group-specific terms. If more than one submodel is specified (i.e. there is more than one outcome variable) then a dependence is induced by assuming that the group-specific terms for each grouping factor are correlated across submodels.

`stan_jm` Estimates shared parameter joint models for longitudinal and time-to-event (i.e. survival) data. The joint model can be univariate (i.e. one longitudinal outcome) or multivariate (i.e. more than one longitudinal outcome). A variety of parameterisations are available for linking the longitudinal and event processes (i.e. a variety of association structures).

Estimation algorithms

The modeling functions in the **rstanarm** package take an `algorithm` argument that can be one of the following:

Sampling (`algorithm="sampling"`) Uses Markov Chain Monte Carlo (MCMC) — in particular, Hamiltonian Monte Carlo (HMC) with a tuned but diagonal mass matrix — to draw from the posterior distribution of the parameters. See `sampling` (**rstan**) for more details. This is the slowest but most reliable of the available estimation algorithms and it is **the default and recommended algorithm for statistical inference.**

Mean-field (`algorithm="meanfield"`) Uses mean-field variational inference to draw from an approximation to the posterior distribution. In particular, this algorithm finds the set of independent normal distributions in the unconstrained space that — when transformed into the constrained space — most closely approximate the posterior distribution. Then it draws repeatedly from these independent normal distributions and transforms them into the constrained space. The entire process is much faster than HMC and yields independent draws but **is not recommended for final statistical inference**. It can be useful to narrow the set of candidate models in large problems, particularly when specifying `QR=TRUE` in `stan_glm`, `stan_glmer`, and `stan_gamm4`, but is **only an approximation to the posterior distribution**.

Full-rank (`algorithm="fullrank"`) Uses full-rank variational inference to draw from an approximation to the posterior distribution by finding the multivariate normal distribution in the unconstrained space that — when transformed into the constrained space — most closely approximates the posterior distribution. Then it draws repeatedly from this multivariate normal distribution and transforms the draws into the constrained space. This process is slower than meanfield variational inference but is faster than HMC. Although still an approximation to the posterior distribution and thus **not recommended for final statistical inference**, the approximation is more realistic than that of mean-field variational inference because the parameters are not assumed to be independent in the unconstrained space. Nevertheless, fullrank variational inference is a more difficult optimization problem and the algorithm is more prone to non-convergence or convergence to a local optimum.

Optimizing (`algorithm="optimizing"`) Finds the posterior mode using a C++ implementation of the LBGFS algorithm. See `optimizing` for more details. If there is no prior information, then this is equivalent to maximum likelihood, in which case there is no great reason to use the functions in the **rstanarm** package over the emulated functions in other packages. However, if priors are specified, then the estimates are penalized maximum likelihood estimates, which may have some redeeming value. Currently, optimization is only supported for `stan_glm`.

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Gabry, J. , Simpson, D. , Vehtari, A. , Betancourt, M. and Gelman, A. (2019), Visualization in Bayesian workflow. *J. R. Stat. Soc. A*, 182: 389-402. doi:10.1111/rssa.12378, arXiv preprint, code on GitHub)

Muth, C., Oravecz, Z., and Gabry, J. (2018) User-friendly Bayesian regression modeling: A tutorial with rstanarm and shinystan. *The Quantitative Methods for Psychology*. 14(2), 99–119. https://www.tqmp.org/RegularArticles/vol14-2/p099/p099.pdf

See Also

- https://mc-stan.org/ for more information on the Stan C++ package used by **rstanarm** for model fitting.
- https://github.com/stan-dev/rstanarm/issues/ to submit a bug report or feature request.
- https://discourse.mc-stan.org to ask a question about **rstanarm** on the Stan-users forum.

---

adapt_delta adapt_delta*: Target average acceptance probability*

Description

Details about the adapt_delta argument to **rstanarm**'s modeling functions.

Details

For the No-U-Turn Sampler (NUTS), the variant of Hamiltonian Monte Carlo used used by **rstanarm**, adapt_delta is the target average proposal acceptance probability during Stan's adaptation period. adapt_delta is ignored by **rstanarm** if the algorithm argument is not set to "sampling".

The default value of adapt_delta is 0.95, except when the prior for the regression coefficients is R2, hs, or hs_plus, in which case the default is 0.99.

These defaults are higher (more conservative) than the default of adapt_delta=0.8 used in the **rstan** package, which may result in slower sampling speeds but will be more robust to posterior distributions with high curvature.

In general you should not need to change adapt_delta unless you see a warning message about divergent transitions, in which case you can increase adapt_delta from the default to a value *closer* to 1 (e.g. from 0.95 to 0.99, or from 0.99 to 0.999, etc). The step size used by the numerical integrator is a function of adapt_delta in that increasing adapt_delta will result in a smaller step size and fewer divergences. Increasing adapt_delta will typically result in a slower sampler, but it will always lead to a more robust sampler.

References

Stan Development Team. *Stan Modeling Language Users Guide and Reference Manual.* https://mc-stan.org/users/documentation/.

Brief Guide to Stan's Warnings: https://mc-stan.org/misc/warnings.html#divergent-transitions-after-warmup

---

`as.matrix.stanreg` *Extract the posterior sample*

Description

For models fit using MCMC (`algorithm="sampling"`), the posterior sample —the post-warmup draws from the posterior distribution— can be extracted from a fitted model object as a matrix, data frame, or array. The `as.matrix` and `as.data.frame` methods merge all chains together, whereas the `as.array` method keeps the chains separate. For models fit using optimization (`"optimizing"`) or variational inference (`"meanfield"` or `"fullrank"`), there is no posterior sample but rather a matrix (or data frame) of 1000 draws from either the asymptotic multivariate Gaussian sampling distribution of the parameters or the variational approximation to the posterior distribution.

Usage

```
## S3 method for class 'stanreg'
as.matrix(x, ..., pars = NULL, regex_pars = NULL)

## S3 method for class 'stanreg'
as.array(x, ..., pars = NULL, regex_pars = NULL)

## S3 method for class 'stanreg'
as.data.frame(x, ..., pars = NULL, regex_pars = NULL)
```

Arguments

`x`	A fitted model object returned by one of the **rstanarm** modeling functions. See `stanreg-objects`.
`...`	Ignored.
`pars`	An optional character vector of parameter names.
`regex_pars`	An optional character vector of regular expressions to use for parameter selection. `regex_pars` can be used in place of `pars` or in addition to `pars`. Currently, all functions that accept a `regex_pars` argument ignore it for models fit using optimization.

Value

A matrix, data.frame, or array, the dimensions of which depend on `pars` and `regex_pars`, as well as the model and estimation algorithm (see the Description section above).

See Also

stanreg-draws-formats, stanreg-methods

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {

if (!exists("example_model")) example(example_model)
# Extract posterior sample after MCMC
draws <- as.matrix(example_model)
print(dim(draws))

# For example, we can see that the median of the draws for the intercept
# is the same as the point estimate rstanarm uses
print(median(draws[, "(Intercept)"]))
print(example_model$coefficients["(Intercept)"])

# The as.array method keeps the chains separate
draws_array <- as.array(example_model)
print(dim(draws_array)) # iterations x chains x parameters

# Extract draws from asymptotic Gaussian sampling distribution
# after optimization
fit <- stan_glm(mpg ~ wt, data = mtcars, algorithm = "optimizing")
draws <- as.data.frame(fit)
print(colnames(draws))
print(nrow(draws)) # 1000 draws are taken

# Extract draws from variational approximation to the posterior distribution
fit2 <- update(fit, algorithm = "meanfield")
draws <- as.data.frame(fit2, pars = "wt")
print(colnames(draws))
print(nrow(draws)) # 1000 draws are taken

}
```

---

available-algorithms *Estimation algorithms available for* **rstanarm** *models*

Description

Estimation algorithms available for **rstanarm** models

Estimation algorithms

The modeling functions in the **rstanarm** package take an `algorithm` argument that can be one of the following:

Sampling (`algorithm="sampling"`) Uses Markov Chain Monte Carlo (MCMC) — in particular, Hamiltonian Monte Carlo (HMC) with a tuned but diagonal mass matrix — to draw from the posterior distribution of the parameters. See `sampling` (**rstan**) for more details. This is the slowest but most reliable of the available estimation algorithms and it is **the default and recommended algorithm for statistical inference.**

Mean-field (`algorithm="meanfield"`) Uses mean-field variational inference to draw from an approximation to the posterior distribution. In particular, this algorithm finds the set of independent normal distributions in the unconstrained space that — when transformed into the constrained space — most closely approximate the posterior distribution. Then it draws repeatedly from these independent normal distributions and transforms them into the constrained space. The entire process is much faster than HMC and yields independent draws but **is not recommended for final statistical inference**. It can be useful to narrow the set of candidate models in large problems, particularly when specifying `QR=TRUE` in `stan_glm`, `stan_glmer`, and `stan_gamm4`, but is **only an approximation to the posterior distribution**.

Full-rank (`algorithm="fullrank"`) Uses full-rank variational inference to draw from an approximation to the posterior distribution by finding the multivariate normal distribution in the unconstrained space that — when transformed into the constrained space — most closely approximates the posterior distribution. Then it draws repeatedly from this multivariate normal distribution and transforms the draws into the constrained space. This process is slower than meanfield variational inference but is faster than HMC. Although still an approximation to the posterior distribution and thus **not recommended for final statistical inference**, the approximation is more realistic than that of mean-field variational inference because the parameters are not assumed to be independent in the unconstrained space. Nevertheless, fullrank variational inference is a more difficult optimization problem and the algorithm is more prone to non-convergence or convergence to a local optimum.

Optimizing (`algorithm="optimizing"`) Finds the posterior mode using a C++ implementation of the LBGFS algorithm. See `optimizing` for more details. If there is no prior information, then this is equivalent to maximum likelihood, in which case there is no great reason to use the functions in the **rstanarm** package over the emulated functions in other packages. However, if priors are specified, then the estimates are penalized maximum likelihood estimates, which may have some redeeming value. Currently, optimization is only supported for `stan_glm`.

See Also

https://mc-stan.org/rstanarm/

`available-models` *Modeling functions available in* **rstanarm**

Description

Modeling functions available in **rstanarm**

Modeling functions

The model estimating functions are described in greater detail in their individual help pages and vignettes. Here we provide a very brief overview:

`stan_lm`, `stan_aov`, `stan_biglm` Similar to `lm` or `aov` but with novel regularizing priors on the model parameters that are driven by prior beliefs about R^2, the proportion of variance in the outcome attributable to the predictors in a linear model.

`stan_glm`, `stan_glm.nb` Similar to `glm` but with various possible prior distributions for the coefficients and, if applicable, a prior distribution for any auxiliary parameter in a Generalized Linear Model (GLM) that is characterized by a `family` object (e.g. the shape parameter in Gamma models). It is also possible to estimate a negative binomial model in a similar way to the `glm.nb` function in the **MASS** package.

`stan_glmer`, `stan_glmer.nb`, `stan_lmer` Similar to the `glmer`, `glmer.nb` and `lmer` functions in the **lme4** package in that GLMs are augmented to have group-specific terms that deviate from the common coefficients according to a mean-zero multivariate normal distribution with a highly-structured but unknown covariance matrix (for which **rstanarm** introduces an innovative prior distribution). MCMC provides more appropriate estimates of uncertainty for models that consist of a mix of common and group-specific parameters.

`stan_nlmer` Similar to `nlmer` in the **lme4** package for nonlinear "mixed-effects" models, but the group-specific coefficients have flexible priors on their unknown covariance matrices.

`stan_gamm4` Similar to `gamm4` in the **gamm4** package, which augments a GLM (possibly with group-specific terms) with nonlinear smooth functions of the predictors to form a Generalized Additive Mixed Model (GAMM). Rather than calling `glmer` like `gamm4` does, `stan_gamm4` essentially calls `stan_glmer`, which avoids the optimization issues that often crop up with GAMMs and provides better estimates for the uncertainty of the parameter estimates.

`stan_polr` Similar to `polr` in the **MASS** package in that it models an ordinal response, but the Bayesian model also implies a prior distribution on the unknown cutpoints. Can also be used to model binary outcomes, possibly while estimating an unknown exponent governing the probability of success.

`stan_betareg` Similar to `betareg` in that it models an outcome that is a rate (proportion) but, rather than performing maximum likelihood estimation, full Bayesian estimation is performed by default, with customizable prior distributions for all parameters.

`stan_clogit` Similar to `clogit` in that it models an binary outcome where the number of successes and failures is fixed within each stratum by the research design. There are some minor syntactical differences relative to `clogit` that allow `stan_clogit` to accept group-specific terms as in `stan_glmer`.

`stan_mvmer` A multivariate form of `stan_glmer`, whereby the user can specify one or more submodels each consisting of a GLM with group-specific terms. If more than one submodel is specified (i.e. there is more than one outcome variable) then a dependence is induced by assuming that the group-specific terms for each grouping factor are correlated across submodels.

`stan_jm` Estimates shared parameter joint models for longitudinal and time-to-event (i.e. survival) data. The joint model can be univariate (i.e. one longitudinal outcome) or multivariate (i.e. more than one longitudinal outcome). A variety of parameterisations are available for linking the longitudinal and event processes (i.e. a variety of association structures).

See Also

https://mc-stan.org/rstanarm/

---

bayes_R2.stanreg *Compute a Bayesian version of R-squared or LOO-adjusted R-squared for regression models.*

Description

Compute a Bayesian version of R-squared or LOO-adjusted R-squared for regression models.

Usage

```
## S3 method for class 'stanreg'
bayes_R2(object, ..., re.form = NULL)

## S3 method for class 'stanreg'
loo_R2(object, ...)
```

Arguments

object	A fitted model object returned by one of the **rstanarm** modeling functions. See stanreg-objects.
...	Currently ignored.
re.form	For models with group-level terms, re.form is passed to posterior_epred if specified.

Value

A vector of R-squared values with length equal to the posterior sample size (the posterior distribution of R-squared).

References

Andrew Gelman, Ben Goodrich, Jonah Gabry, and Aki Vehtari (2019). R-squared for Bayesian regression models. *The American Statistician*, to appear. doi:10.1080/00031305.2018.1549100 (Article, Notebook)

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
fit <- stan_glm(
  mpg ~ wt + cyl,
  data = mtcars,
  QR = TRUE,
  chains = 2,
  refresh = 0
```

```
)
rsq <- bayes_R2(fit)
print(median(rsq))
hist(rsq)

loo_rsq <- loo_R2(fit)
print(median(loo_rsq))

# multilevel binomial model
if (!exists("example_model")) example(example_model)
print(example_model)
median(bayes_R2(example_model))
median(bayes_R2(example_model, re.form = NA)) # exclude group-level
}
```

`example_jm` *Example joint longitudinal and time-to-event model*

Description

A model for use in the **rstanarm** examples related to `stan_jm`.

Format

Calling `example("example_jm")` will run the model in the Examples section, below, and the resulting stanmvreg object will then be available in the global environment. The `chains` and `iter` arguments are specified to make this example be small in size. In practice, we recommend that they be left unspecified in order to use the default values or increased if there are convergence problems. The `cores` argument is optional and on a multicore system, the user may well want to set that equal to the number of chains being executed.

Examples

```
# set.seed(123)
if (.Platform$OS.type != "windows" || .Platform$r_arch !="i386")
example_jm <-
   stan_jm(formulaLong = logBili ~ year + (1 | id),
           dataLong = pbcLong[1:101,],
           formulaEvent = survival::Surv(futimeYears, death) ~ sex + trt,
           dataEvent = pbcSurv[1:15,],
           time_var = "year",
           # this next line is only to keep the example small in size!
           chains = 1, seed = 12345, iter = 100, refresh = 0)
```

example_model *Example model*

Description

A model for use in **rstanarm** examples.

Format

Calling `example("example_model")` will run the model in the Examples section, below, and the resulting stanreg object will then be available in the global environment. The `chains` and `iter` arguments are specified to make this example be small in size. In practice, we recommend that they be left unspecified in order to use the default values (4 and 2000 respectively) or increased if there are convergence problems. The `cores` argument is optional and on a multicore system, the user may well want to set that equal to the number of chains being executed.

See Also

`cbpp` for a description of the data.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
example_model <-
  stan_glmer(cbind(incidence, size - incidence) ~ size + period + (1|herd),
             data = lme4::cbpp, family = binomial, QR = TRUE,
             # this next line is only to keep the example small in size!
             chains = 2, cores = 1, seed = 12345, iter = 1000, refresh = 0)
example_model
}
```

kfold.stanreg *K-fold cross-validation*

Description

The `kfold` method performs exact K-fold cross-validation. First the data are randomly partitioned into K subsets of equal size (or as close to equal as possible), or the user can specify the `folds` argument to determine the partitioning. 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).

Usage

```
## S3 method for class 'stanreg'
kfold(
  x,
  K = 10,
  ...,
  folds = NULL,
  save_fits = FALSE,
  cores = getOption("mc.cores", 1)
)
```

Arguments

x	A fitted model object returned by one of the rstanarm modeling functions. See stanreg-objects.
K	For kfold, the number of subsets (folds) 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 folds. If the folds argument is specified then K will automatically be set to length(unique(folds)), otherwise the specified value of K is passed to loo::kfold_split_random to randomly partition the data into K subsets of equal (or as close to equal as possible) size.
...	Currently ignored.
folds	For kfold, an optional integer vector with one element per observation in the data used to fit the model. 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).
save_fits	For kfold, if TRUE, a component 'fits' is added to the returned object to store the cross-validated stanreg objects and the indices of the omitted observations for each fold. Defaults to FALSE.
cores	The number of cores to use for parallelization. Instead fitting separate Markov chains for the same model on different cores, by default kfold will distribute the K models to be fit across the cores (using parLapply on Windows and mclapply otherwise). The Markov chains for each model will be run sequentially. This will often be the most efficient option, especially if many cores are available, but in some cases it may be preferable to fit the K models sequentially and instead use the cores for the Markov chains. This can be accomplished by setting options(mc.cores) to be the desired number of cores to use for the Markov chains *and* also manually specifying cores=1 when calling the kfold function. See the end of the **Examples** section for a demonstration.

Value

An object with classes 'kfold' and 'loo' that has a similar structure as the objects returned by the loo and waic methods and is compatible with the loo_compare function for comparing models.

References

Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*. 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4. arXiv preprint: https://arxiv.org/abs/1507.04544

Yao, Y., Vehtari, A., Simpson, D., and Gelman, A. (2018) Using stacking to average Bayesian predictive distributions. *Bayesian Analysis*, advance publication, doi:10.1214/17BA1091.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {

fit1 <- stan_glm(mpg ~ wt, data = mtcars, refresh = 0)
fit2 <- stan_glm(mpg ~ wt + cyl, data = mtcars, refresh = 0)
fit3 <- stan_glm(mpg ~ disp * as.factor(cyl), data = mtcars, refresh = 0)

# 10-fold cross-validation
# (if possible also specify the 'cores' argument to use multiple cores)
(kfold1 <- kfold(fit1, K = 10))
kfold2 <- kfold(fit2, K = 10)
kfold3 <- kfold(fit3, K = 10)
loo_compare(kfold1, kfold2, kfold3)

# stratifying by a grouping variable
# (note: might get some divergences warnings with this model but
# this is just intended as a quick example of how to code this)
fit4 <- stan_lmer(mpg ~ disp + (1|cyl), data = mtcars, refresh = 0)
table(mtcars$cyl)
folds_cyl <- loo::kfold_split_stratified(K = 3, x = mtcars$cyl)
table(cyl = mtcars$cyl, fold = folds_cyl)
kfold4 <- kfold(fit4, folds = folds_cyl, cores = 2)
print(kfold4)

}
# Example code demonstrating the different ways to specify the number
# of cores and how the cores are used
#
# options(mc.cores = NULL)
#
# # spread the K models over N_CORES cores (method 1)
# kfold(fit, K, cores = N_CORES)
#
# # spread the K models over N_CORES cores (method 2)
# options(mc.cores = N_CORES)
# kfold(fit, K)
#
# # fit K models sequentially using N_CORES cores for the Markov chains each time
# options(mc.cores = N_CORES)
# kfold(fit, K, cores = 1)
```

launch_shinystan.stanreg *Using the ShinyStan GUI with rstanarm models*

Description

The ShinyStan interface provides visual and numerical summaries of model parameters and convergence diagnostics.

Usage

```
## S3 method for class 'stanreg'
launch_shinystan(
  object,
  ppd = TRUE,
  seed = 1234,
  model_name = NULL,
  note = NULL,
  rstudio = getOption("shinystan.rstudio"),
  ...
)
```

Arguments

object	A fitted model object returned by one of the **rstanarm** modeling functions. See stanreg-objects.
ppd	Should **rstanarm** draw from the posterior predictive distribution before launching ShinyStan? The default is TRUE, although for very large objects it can be convenient to set it to FALSE as drawing from the posterior predictive distribution can be time consuming. If ppd is TRUE then graphical posterior predictive checks are available when ShinyStan is launched.
seed	Passed to pp_check if ppd is TRUE.
model_name, note	Optional arguments passed to as.shinystan.
rstudio	Only relevant for 'RStudio' users. The default (FALSE) is to launch the app in the user's default web browser rather than the pop-up Viewer provided by 'RStudio'. Users can change the default to TRUE by setting the global option options(shinystan.rstudio = TRUE).
...	Optional arguments passed to runApp.

Details

The launch_shinystan function will accept a stanreg object as input. Currently, almost any model fit using one of **rstanarm**'s model-fitting functions can be used with ShinyStan. The only exception is that ShinyStan does not currently support **rstanarm** models fit using algorithm='optimizing'. See the **shinystan** package documentation for more information.

Faster launch times

For some **rstanarm** models ShinyStan may take a very long time to launch. If this is the case with one of your models you may be able to speed up `launch_shinystan` in one of several ways:

Prevent ShinyStan from preparing graphical posterior predictive checks: When used with a `stanreg` object (**rstanarm** model object) ShinyStan will draw from the posterior predictive distribution and prepare graphical posterior predictive checks before launching. That way when you go to the PPcheck page the plots are immediately available. This can be time consuming for models fit to very large datasets and you can prevent this behavior by creating a shinystan object before calling `launch_shinystan`. To do this use `as.shinystan` with optional argument ppd set to `FALSE` (see the Examples section below). When you then launch ShinyStan and go to the PPcheck page the plots will no longer be automatically generated and you will be presented with the standard interface requiring you to first specify the appropriate y and $yrep$, which can be done for many but not all **rstanarm** models.

Use a shinystan object: Even if you don't want to prevent ShinyStan from preparing graphical posterior predictive checks, first creating a shinystan object using `as.shinystan` can reduce *future* launch times. That is, `launch_shinystan(sso)` will be faster than `launch_shinystan(fit)`, where `sso` is a shinystan object and `fit` is a stanreg object. It still may take some time for `as.shinystan` to create `sso` initially, but each time you subsequently call `launch_shinystan(sso)` it will reuse `sso` instead of internally creating a shinystan object every time. See the Examples section below.

References

Gabry, J. , Simpson, D. , Vehtari, A. , Betancourt, M. and Gelman, A. (2019), Visualization in Bayesian workflow. *J. R. Stat. Soc. A*, 182: 389-402. doi:10.1111/rssa.12378, arXiv preprint, code on GitHub)

Muth, C., Oravecz, Z., and Gabry, J. (2018) User-friendly Bayesian regression modeling: A tutorial with rstanarm and shinystan. *The Quantitative Methods for Psychology*. 14(2), 99–119. https://www.tqmp.org/RegularArticles/vol14-2/p099/p099.pdf

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
## Not run:
if (!exists("example_model")) example(example_model)

# Launch the ShinyStan app without saving the resulting shinystan object
if (interactive()) launch_shinystan(example_model)

# Launch the ShinyStan app (saving resulting shinystan object as sso)
if (interactive()) sso <- launch_shinystan(example_model)

# First create shinystan object then call launch_shinystan
sso <- shinystan::as.shinystan(example_model)
if (interactive()) launch_shinystan(sso)

# Prevent ShinyStan from preparing graphical posterior predictive checks that
# can be time consuming. example_model is small enough that it won't matter
# much here but in general this can help speed up launch_shinystan
```

```
sso <- shinystan::as.shinystan(example_model, ppd = FALSE)
if (interactive()) launch_shinystan(sso)

## End(Not run)
}
```

`log_lik.stanreg` *Pointwise log-likelihood matrix*

Description

For models fit using MCMC only, the `log_lik` method returns the S by N pointwise log-likelihood matrix, where S is the size of the posterior sample and N is the number of data points, or in the case of the `stanmvreg` method (when called on `stan_jm` model objects) an S by $Npat$ matrix where $Npat$ is the number of individuals.

Usage

```
## S3 method for class 'stanreg'
log_lik(object, newdata = NULL, offset = NULL, ...)

## S3 method for class 'stanmvreg'
log_lik(object, m = 1, newdata = NULL, ...)

## S3 method for class 'stanjm'
log_lik(object, newdataLong = NULL, newdataEvent = NULL, ...)
```

Arguments

`object`	A fitted model object returned by one of the **rstanarm** modeling functions. See `stanreg-objects`.
`newdata`	An optional data frame of new data (e.g. holdout data) to use when evaluating the log-likelihood. See the description of `newdata` for `posterior_predict`.
`offset`	A vector of offsets. Only required if `newdata` is specified and an `offset` was specified when fitting the model.
`...`	Currently ignored.
`m`	Integer specifying the number or name of the submodel
`newdataLong, newdataEvent`	Optional data frames containing new data (e.g. holdout data) to use when evaluating the log-likelihood for a model estimated using `stan_jm`. If the fitted model was a multivariate joint model (i.e. more than one longitudinal outcome), then `newdataLong` is allowed to be a list of data frames. If supplying new data, then `newdataEvent` should also include variables corresponding to the event time and event indicator as these are required for evaluating the log likelihood for the event submodel. For more details, see the description of `newdataLong` and `newdataEvent` for `posterior_survfit`.

Value

For the `stanreg` and `stanmvreg` methods an S by N matrix, where S is the size of the posterior sample and N is the number of data points. For the `stanjm` method an S by $Npat$ matrix where $Npat$ is the number of individuals.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {

 roaches$roach100 <- roaches$roach1 / 100
 fit <- stan_glm(
    y ~ roach100 + treatment + senior,
    offset = log(exposure2),
    data = roaches,
    family = poisson(link = "log"),
    prior = normal(0, 2.5),
    prior_intercept = normal(0, 10),
    iter = 500, # just to speed up example,
    refresh = 0
 )
 ll <- log_lik(fit)
 dim(ll)
 all.equal(ncol(ll), nobs(fit))

 # using newdata argument
 nd <- roaches[1:2, ]
 nd$treatment[1:2] <- c(0, 1)
 ll2 <- log_lik(fit, newdata = nd, offset = c(0, 0))
 head(ll2)
 dim(ll2)
 all.equal(ncol(ll2), nrow(nd))

}
```

---

logit *Logit and inverse logit*

Description

Logit and inverse logit

Usage

```
logit(x)

invlogit(x)
```

Arguments

x	Numeric vector.

Value

A numeric vector the same length as x.

---

loo.stanreg *Information criteria and cross-validation*

Description

For models fit using MCMC, compute approximate leave-one-out cross-validation (LOO, LOOIC) or, less preferably, the Widely Applicable Information Criterion (WAIC) using the **loo** package. (For K-fold cross-validation see kfold.stanreg.) Functions for model comparison, and model weighting/averaging are also provided.

Note: these functions are not guaranteed to work properly unless the data argument was specified when the model was fit. Also, as of **loo** version 2.0.0 the default number of cores is now only 1, but we recommend using as many (or close to as many) cores as possible by setting the cores argument or using options(mc.cores = VALUE) to set it for an entire session.

Usage

```
## S3 method for class 'stanreg'
loo(
  x,
  ...,
  cores = getOption("mc.cores", 1),
  save_psis = FALSE,
  k_threshold = NULL,
  r_eff = FALSE
)

## S3 method for class 'stanreg'
waic(x, ...)

## S3 method for class 'stanreg'
loo_compare(x, ..., criterion = c("loo", "kfold", "waic"), detail = FALSE)

## S3 method for class 'stanreg_list'
loo_compare(x, ..., criterion = c("loo", "kfold", "waic"), detail = FALSE)

## S3 method for class 'stanreg_list'
loo_model_weights(x, ..., cores = getOption("mc.cores", 1), k_threshold = NULL)

compare_models(..., loos = list(), detail = FALSE)
```

Arguments

x	For loo and waic, a fitted model object returned by one of the rstanarm modeling functions. See stanreg-objects. For the loo_model_weights method, x should be a "stanreg_list" object, which is a list of fitted model objects created by stanreg_list. loo_compare also allows x to be a single stanreg object, with the remaining objects passed via ..., or a single stanreg_list object.
...	For loo_compare.stanreg, ... can contain objects returned by the loo, kfold, or waic method (see the **Examples** section, below). For loo_model_weights, ... should contain arguments (e.g. method) to pass to the default loo_model_weights method from the **loo** package.
cores, save_psis	Passed to loo.
k_threshold	Threshold for flagging estimates of the Pareto shape parameters k estimated by loo. See the *How to proceed when* loo *gives warnings* section, below, for details.
r_eff	TRUE or FALSE indicating whether to compute the r_eff argument to pass to the **loo** package. If TRUE, **rstanarm** will call relative_eff to compute the r_eff argument to pass to the **loo** package. If FALSE (the default), we avoid computing r_eff, which can be very slow. r_eff measures the amount of autocorrelation in MCMC draws, and is used to compute more accurate ESS and MCSE estimates for pointwise and total ELPDs. When r_eff=FALSE, the reported ESS and MCSE estimates may be over-optimistic if the posterior draws are far from independent.
criterion	For loo_compare.stanreg and loo_compare.stanreg_list, should the comparison be based on LOO-CV (criterion="loo"), K-fold-CV (criterion="kfold"), or WAIC (criterion="waic"). The default is LOO-CV. See the **Comparing models** and **Examples** sections below.
detail	For loo_compare.stanreg and loo_compare.stanreg_list, if TRUE then extra information about each model (currently just the model formulas) will be printed with the output.
loos	a list of objects produced by the loo function

Value

The structure of the objects returned by loo and waic methods are documented in detail in the **Value** section in loo and waic (from the **loo** package).

loo_compare returns a matrix with class 'compare.loo'. See the **Comparing models** section below for more details.

Approximate LOO CV

The loo method for stanreg objects provides an interface to the **loo** package for approximate leave-one-out cross-validation (LOO). The LOO Information Criterion (LOOIC) has the same purpose as the Akaike Information Criterion (AIC) that is used by frequentists. Both are intended to estimate the expected log predictive density (ELPD) for a new dataset. However, the AIC ignores priors and

assumes that the posterior distribution is multivariate normal, whereas the functions from the **loo** package do not make this distributional assumption and integrate over uncertainty in the parameters. This only assumes that any one observation can be omitted without having a major effect on the posterior distribution, which can be judged using the diagnostic plot provided by the `plot.loo` method and the warnings provided by the `print.loo` method (see the *How to Use the rstanarm Package* vignette for an example of this process).

How to proceed when `loo` gives warnings (k_threshold): The `k_threshold` argument to the `loo` method for **rstanarm** models is provided as a possible remedy when the diagnostics reveal problems stemming from the posterior's sensitivity to particular observations. 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). The `k_threshold` argument can be used to set the k value above which an observation is flagged. If `k_threshold` is not `NULL` and there are J observations with k estimates above `k_threshold` then when `loo` is called it 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 object created by `loo`. Another option to consider is K-fold cross-validation, which is documented on a separate page (see `kfold`).

Note: in the warning messages issued by `loo` about large Pareto k estimates we recommend setting `k_threshold` to at least 0.7. There is a theoretical reason, explained in Vehtari, Gelman, and Gabry (2017), for setting the threshold to the stricter value of 0.5, but in practice they find that errors in the LOO approximation start to increase non-negligibly when $k > 0.7$.

Comparing models

"loo" (or "waic" or "kfold") objects can be passed to the `loo_compare` function in the **loo** package to perform model comparison. **rstanarm** also provides a `loo_compare.stanreg` method that can be used if the "loo" (or "waic" or "kfold") object has been added to the fitted model object (see the **Examples** section below for how to do this). This second method allows **rstanarm** to perform some extra checks that can't be done by the **loo** package itself (e.g., verifying that all models to be compared were fit using the same outcome variable).

`loo_compare` will return a matrix with one row per model and columns containing the ELPD difference and the standard error of the difference. In the first row of the matrix will be the model with the largest ELPD (smallest LOOIC) and will contain zeros (there is no difference between this model and itself). For each of the remaining models the ELPD difference and SE are reported relative to the model with the best ELPD (the first row). See the **Details** section at the `loo_compare` page in the **loo** package for more information.

Model weights

The `loo_model_weights` method can be used to compute model weights for a `"stanreg_list"` object, which is a list of fitted model objects made with `stanreg_list`. The end of the **Examples** section has a demonstration. For details see the `loo_model_weights` documentation in the **loo** package.

References

Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*. 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4. arXiv preprint: https://arxiv.org/abs/1507.04544

Yao, Y., Vehtari, A., Simpson, D., and Gelman, A. (2018) Using stacking to average Bayesian predictive distributions. *Bayesian Analysis*, advance publication, doi:10.1214/17BA1091.

Gabry, J. , Simpson, D. , Vehtari, A. , Betancourt, M. and Gelman, A. (2019), Visualization in Bayesian workflow. *J. R. Stat. Soc. A*, 182: 389-402. doi:10.1111/rssa.12378, arXiv preprint, code on GitHub)

See Also

- The **loo** package vignettes and various **rstanarm** vignettes for more examples using `loo` and related functions with **rstanarm** models.
- `pareto-k-diagnostic` in the **loo** package for more on Pareto k diagnostics.
- `log_lik.stanreg` to directly access the pointwise log-likelihood matrix.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {

fit1 <- stan_glm(mpg ~ wt, data = mtcars, refresh = 0)
fit2 <- stan_glm(mpg ~ wt + cyl, data = mtcars, refresh = 0)

# (for bigger models use as many cores as possible)
loo1 <- loo(fit1, cores = 1)
print(loo1)
loo2 <- loo(fit2, cores = 1)
print(loo2)

# when comparing models the loo objects can be passed to loo_compare
# as individual arguments or as a list of loo objects
loo_compare(loo1, loo2)
loo_compare(list(loo1, loo2))

# if the fitted model objects contain a loo object in the component "loo"
# then the model objects can be passed directly or as a stanreg_list
fit1$loo <- loo1
fit2$loo <- loo2
loo_compare(fit1, fit2)

# if the fitted model objects contain a loo object _and_ a waic or kfold
# object, then the criterion argument determines which of them the comparison
# is based on
fit1$waic <- waic(fit1)
fit2$waic <- waic(fit2)
loo_compare(fit1, fit2, criterion = "waic")

# the models can also be combined into a stanreg_list object, and more
# informative model names can be provided to use when printing
```

```
model_list <- stanreg_list(fit1, fit2, model_names = c("Fewer predictors", "More predictors"))
loo_compare(model_list)

fit3 <- stan_glm(mpg ~ disp * as.factor(cyl), data = mtcars, refresh = 0)
loo3 <- loo(fit3, cores = 2, k_threshold = 0.7)
loo_compare(loo1, loo2, loo3)

# setting detail=TRUE will also print model formulas if used with
# loo_compare.stanreg or loo_compare.stanreg_list
fit3$loo <- loo3
model_list <- stanreg_list(fit1, fit2, fit3)
loo_compare(model_list, detail=TRUE)

# Computing model weights
#
# if the objects in model_list already have 'loo' components then those
# will be used. otherwise loo will be computed for each model internally
# (in which case the 'cores' argument may also be used and is passed to loo())
loo_model_weights(model_list)  # defaults to method="stacking"
loo_model_weights(model_list,  method = "pseudobma")
loo_model_weights(model_list,  method = "pseudobma", BB = FALSE)

# you can also pass precomputed loo objects directly to loo_model_weights
loo_list <- list(A = loo1, B = loo2, C = loo3) # names optional (affects printing)
loo_model_weights(loo_list)

}
```

`loo_predict.stanreg` *Compute weighted expectations using LOO*

Description

These functions are wrappers around the `E_loo` function (**loo** package) that provide compatibility for **rstanarm** models.

Usage

```
## S3 method for class 'stanreg'
loo_predict(
  object,
  type = c("mean", "var", "quantile"),
  probs = 0.5,
  ...,
  psis_object = NULL
)

## S3 method for class 'stanreg'
loo_linpred(
```

```
  object,
  type = c("mean", "var", "quantile"),
  probs = 0.5,
  transform = FALSE,
  ...,
  psis_object = NULL
)

## S3 method for class 'stanreg'
loo_predictive_interval(object, prob = 0.9, ..., psis_object = NULL)
```

Arguments

object	A fitted model object returned by one of the **rstanarm** modeling functions. See stanreg-objects.
type	The type of expectation to compute. The options are "mean", "variance", "sd", and "quantile".
probs	For computing quantiles, a vector of probabilities.
...	Currently unused.
psis_object	An object returned by psis. If missing then psis will be run internally, which may be time consuming for models fit to very large datasets.
transform	Passed to 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

A list with elements value and pareto_k.

For loo_predict and loo_linpred the value component is a vector with one element per observation.

For loo_predictive_interval the value component is a matrix with one row per observation and two columns (like predictive_interval). 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.

See E_loo and pareto-k-diagnostic for details on the pareto_k diagnostic.

References

Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*. 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4. arXiv preprint: https://arxiv.org/abs/1507.04544

Yao, Y., Vehtari, A., Simpson, D., and Gelman, A. (2018) Using stacking to average Bayesian predictive distributions. *Bayesian Analysis*, advance publication, doi:10.1214/17BA1091.

Gabry, J. , Simpson, D. , Vehtari, A. , Betancourt, M. and Gelman, A. (2019), Visualization in Bayesian workflow. *J. R. Stat. Soc. A*, 182: 389-402. doi:10.1111/rssa.12378, arXiv preprint, code on GitHub)

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
## Not run:
if (!exists("example_model")) example(example_model)

# optionally, log-weights can be pre-computed and reused
psis_result <- loo::psis(log_ratios = -log_lik(example_model))

loo_probs <- loo_linpred(example_model, type = "mean", transform = TRUE, psis_object = psis_result)
str(loo_probs)

loo_pred_var <- loo_predict(example_model, type = "var", psis_object = psis_result)
str(loo_pred_var)

loo_pred_ints <- loo_predictive_interval(example_model, prob = 0.8, psis_object = psis_result)
str(loo_pred_ints)

## End(Not run)
}
```

---

neg_binomial_2 *Family function for negative binomial GLMs*

Description

Specifies the information required to fit a Negative Binomial GLM in a similar way to `negative.binomial`. However, here the overdispersion parameter `theta` is not specified by the user and always estimated (really the *reciprocal* of the dispersion parameter is estimated). A call to this function can be passed to the `family` argument of `stan_glm` or `stan_glmer` to estimate a Negative Binomial model. Alternatively, the `stan_glm.nb` and `stan_glmer.nb` wrapper functions may be used, which call `neg_binomial_2` internally.

Usage

```
neg_binomial_2(link = "log")
```

Arguments

`link`	The same as for `poisson`, typically a character vector of length one among `"log"`, `"identity"`, and `"sqrt"`.

Value

An object of class `family` very similar to that of `poisson` but with a different family name.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386")
stan_glm(Days ~ Sex/(Age + Eth*Lrn), data = MASS::quine, seed = 123,
         family = neg_binomial_2, QR = TRUE, algorithm = "optimizing")

# or, equivalently, call stan_glm.nb() without specifying the family
```

`nobs.stanmvreg` *Methods for stanreg objects*

Description

The methods documented on this page are actually some of the least important methods defined for stanreg objects. The most important methods are documented separately, each with its own page. Links to those pages are provided in the **See Also** section, below.

Usage

```
## S3 method for class 'stanmvreg'
nobs(object, ...)

## S3 method for class 'stanreg'
coef(object, ...)

## S3 method for class 'stanreg'
confint(object, parm, level = 0.95, ...)

## S3 method for class 'stanreg'
fitted(object, ...)

## S3 method for class 'stanreg'
nobs(object, ...)

## S3 method for class 'stanreg'
residuals(object, ...)

## S3 method for class 'stanreg'
se(object, ...)

## S3 method for class 'stanreg'
update(object, formula., ..., evaluate = TRUE)

## S3 method for class 'stanreg'
vcov(object, correlation = FALSE, ...)

## S3 method for class 'stanreg'
```

```
fixef(object, ...)

## S3 method for class 'stanreg'
ngrps(object, ...)

## S3 method for class 'stanreg'
nsamples(object, ...)

## S3 method for class 'stanreg'
ranef(object, ...)

## S3 method for class 'stanreg'
sigma(object, ...)

## S3 method for class 'stanreg'
VarCorr(x, sigma = 1, ...)
```

Arguments

`object`, `x`	A fitted model object returned by one of the **rstanarm** modeling functions. See `stanreg-objects`.
`...`	Ignored, except by the `update` method. See `update`.
`parm`	For `confint`, an optional character vector of parameter names.
`level`	For `confint`, a scalar between 0 and 1 indicating the confidence level to use.
`formula.`, `evaluate`	See `update`.
`correlation`	For `vcov`, if `FALSE` (the default) the covariance matrix is returned. If `TRUE`, the correlation matrix is returned instead.
`sigma`	Ignored (included for compatibility with `VarCorr`).

Details

The methods documented on this page are similar to the methods defined for objects of class 'lm', 'glm', 'glmer', etc. However there are a few key differences:

`residuals` Residuals are *always* of type `"response"` (not `"deviance"` residuals or any other type). However, in the case of `stan_polr` with more than two response categories, the residuals are the difference between the latent utility and its linear predictor.

`coef` Medians are used for point estimates. See the *Point estimates* section in `print.stanreg` for more details.

`se` The `se` function returns standard errors based on `mad`. See the *Uncertainty estimates* section in `print.stanreg` for more details.

`confint` For models fit using optimization, confidence intervals are returned via a call to `confint.default`. If `algorithm` is `"sampling"`, `"meanfield"`, or `"fullrank"`, the `confint` will throw an error because the `posterior_interval` function should be used to compute Bayesian uncertainty intervals.

`nsamples` The number of draws from the posterior distribution obtained

See Also

- The print, summary, and prior_summary methods for stanreg objects for information on the fitted model.
- launch_shinystan to use the ShinyStan GUI to explore a fitted **rstanarm** model.
- The plot method to plot estimates and diagnostics.
- The pp_check method for graphical posterior predictive checking.
- The posterior_predict and predictive_error methods for predictions and predictive errors.
- The posterior_interval and predictive_interval methods for uncertainty intervals for model parameters and predictions.
- The loo, kfold, and log_lik methods for leave-one-out or K-fold cross-validation, model comparison, and computing the log-likelihood of (possibly new) data.
- The as.matrix, as.data.frame, and as.array methods to access posterior draws.

---

pairs.stanreg *Pairs method for stanreg objects*

Description

Interface to **bayesplot**'s mcmc_pairs function for use with **rstanarm** models. Be careful not to specify too many parameters to include or the plot will be both hard to read and slow to render.

Usage

```
## S3 method for class 'stanreg'
pairs(
  x,
  pars = NULL,
  regex_pars = NULL,
  condition = pairs_condition(nuts = "accept_stat__"),
  ...
)
```

Arguments

x	A fitted model object returned by one of the **rstanarm** modeling functions. See stanreg-objects.
pars	An optional character vector of parameter names. All parameters are included by default, but for models with more than just a few parameters it may be far too many to visualize on a small computer screen and also may require substantial computing time.
regex_pars	An optional character vector of regular expressions to use for parameter selection. regex_pars can be used in place of pars or in addition to pars. Currently, all functions that accept a regex_pars argument ignore it for models fit using optimization.

condition — Same as the condition argument to mcmc_pairs except the *default is different* for **rstanarm** models. By default, the mcmc_pairs function in the **bayesplot** package plots some of the Markov chains (half, in the case of an even number of chains) in the panels above the diagonal and the other half in the panels below the diagonal. However since we know that **rstanarm** models were fit using Stan (which **bayesplot** doesn't assume) we can make the default more useful by splitting the draws according to the accept_stat__ diagnostic. The plots below the diagonal will contain realizations that are below the median accept_stat__ and the plots above the diagonal will contain realizations that are above the median accept_stat__. To change this behavior see the documentation of the condition argument at mcmc_pairs.

... — Optional arguments passed to mcmc_pairs. The np, lp, and max_treedepth arguments to mcmc_pairs are handled automatically by **rstanarm** and do not need to be specified by the user in .... The arguments that can be specified in ... include transformations, diag_fun, off_diag_fun, diag_args, off_diag_args, and np_style. These arguments are documented thoroughly on the help page for mcmc_pairs.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {

if (!exists("example_model")) example(example_model)

bayesplot::color_scheme_set("purple")

# see 'condition' argument above for details on the plots below and
# above the diagonal. default is to split by accept_stat__.
pairs(example_model, pars = c("(Intercept)", "log-posterior"))

# for demonstration purposes, intentionally fit a model that
# will (almost certainly) have some divergences
fit <- stan_glm(
  mpg ~ ., data = mtcars,
  iter = 1000,
  # this combo of prior and adapt_delta should lead to some divergences
  prior = hs(),
  adapt_delta = 0.9,
  refresh = 0
)

pairs(fit, pars = c("wt", "sigma", "log-posterior"))

# requires hexbin package
# pairs(
# fit,
#   pars = c("wt", "sigma", "log-posterior"),
#   transformations = list(sigma = "log"), # show log(sigma) instead of sigma
#  off_diag_fun = "hex" # use hexagonal heatmaps instead of scatterplots
# )
```

```
bayesplot::color_scheme_set("brightblue")
pairs(
  fit,
  pars = c("(Intercept)", "wt", "sigma", "log-posterior"),
  transformations = list(sigma = "log"),
 off_diag_args = list(size = 3/4, alpha = 1/3), # size and transparency of scatterplot points
 np_style = pairs_style_np(div_color = "black", div_shape = 2) # color and shape of the divergences
)

# Using the condition argument to show divergences above the diagonal
pairs(
  fit,
  pars = c("(Intercept)", "wt", "log-posterior"),
  condition = pairs_condition(nuts = "divergent__")
)


}
```

`plot.predict.stanjm` *Plot the estimated subject-specific or marginal longitudinal trajectory*

Description

This generic `plot` method for `predict.stanjm` objects will plot the estimated subject-specific or marginal longitudinal trajectory using the data frame returned by a call to `posterior_traj`. To ensure that enough data points are available to plot the longitudinal trajectory, it is assumed that the call to `posterior_traj` would have used the default `interpolate = TRUE`, and perhaps also `extrapolate = TRUE` (the latter being optional, depending on whether or not the user wants to see extrapolation of the longitudinal trajectory beyond the last observation time).

Usage

```
## S3 method for class 'predict.stanjm'
plot(
  x,
  ids = NULL,
  limits = c("ci", "pi", "none"),
  xlab = NULL,
  ylab = NULL,
  vline = FALSE,
  plot_observed = FALSE,
  facet_scales = "free_x",
  ci_geom_args = NULL,
  grp_overlay = FALSE,
  ...
)
```

Arguments

x	A data frame and object of class predict.stanjm returned by a call to the function posterior_traj. The object contains point estimates and uncertainty interval limits for the fitted values of the longitudinal response.
ids	An optional vector providing a subset of subject IDs for whom the predicted curves should be plotted.
limits	A quoted character string specifying the type of limits to include in the plot. Can be one of: "ci" for the Bayesian posterior uncertainty interval for the estimated mean longitudinal response (often known as a credible interval); "pi" for the prediction interval for the estimated (raw) longitudinal response; or "none" for no interval limits.
xlab, ylab	An optional axis label passed to labs.
vline	A logical. If TRUE then a vertical dashed line is added to the plot indicating the event or censoring time for the individual. Can only be used if each plot within the figure is for a single individual.
plot_observed	A logical. If TRUE then the observed longitudinal measurements are overlaid on the plot.
facet_scales	A character string passed to the scales argument of facet_wrap when plotting the longitudinal trajectory for more than one individual.
ci_geom_args	Optional arguments passed to geom_ribbon and used to control features of the plotted interval limits. They should be supplied as a named list.
grp_overlay	Only relevant if the model had lower level units clustered within an individual. If TRUE, then the fitted trajectories for the lower level units will be overlaid in the same plot region (that is, all lower level units for a single individual will be shown within a single facet). If FALSE, then the fitted trajectories for each lower level unit will be shown in a separate facet.
...	Optional arguments passed to geom_smooth and used to control features of the plotted longitudinal trajectory.

Value

A ggplot object, also of class plot.predict.stanjm. This object can be further customised using the **ggplot2** package. It can also be passed to the function plot_stack_jm.

See Also

posterior_traj, plot_stack_jm, posterior_survfit, plot.survfit.stanjm

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {

  # Run example model if not already loaded
  if (!exists("example_jm")) example(example_jm)

  # For a subset of individuals in the estimation dataset we will
```

```
  # obtain subject-specific predictions for the longitudinal submodel
  # at evenly spaced times between 0 and their event or censoring time.
  pt1 <- posterior_traj(example_jm, ids = c(7,13,15), interpolate = TRUE)
  plot(pt1)                  # credible interval for mean response
  plot(pt1, limits = "pi")   # prediction interval for raw response
  plot(pt1, limits = "none") # no uncertainty interval

  # We can also extrapolate the longitudinal trajectories.
  pt2 <- posterior_traj(example_jm, ids = c(7,13,15), interpolate = TRUE,
                        extrapolate = TRUE)
  plot(pt2)
  plot(pt2, vline = TRUE)    # add line indicating event or censoring time
  plot(pt2, vline = TRUE, plot_observed = TRUE)  # overlay observed longitudinal data

  # We can change or add attributes to the plot
  plot1 <- plot(pt2, ids = c(7,13,15), xlab = "Follow up time",
                    vline = TRUE, plot_observed = TRUE,
                    facet_scales = "fixed", color = "blue", linetype = 2,
                    ci_geom_args = list(fill = "red"))
  plot1

  # Since the returned plot is also a ggplot object, we can
  # modify some of its attributes after it has been returned
  plot1 +
    ggplot2::theme(strip.background = ggplot2::element_blank()) +
    ggplot2::labs(title = "Some plotted longitudinal trajectories")

}
```

`plot.stanreg` *Plot method for stanreg objects*

Description

The `plot` method for stanreg-objects provides a convenient interface to the MCMC module in the **bayesplot** package for plotting MCMC draws and diagnostics. It is also straightforward to use the functions from the **bayesplot** package directly rather than via the `plot` method. Examples of both methods of plotting are given below.

Usage

```
## S3 method for class 'stanreg'
plot(x, plotfun = "intervals", pars = NULL, regex_pars = NULL, ...)
```

Arguments

`x`	A fitted model object returned by one of the **rstanarm** modeling functions. See `stanreg-objects`.

plotfun	A character string naming the **bayesplot** MCMC function to use. The default is to call mcmc_intervals. plotfun can be specified either as the full name of a **bayesplot** plotting function (e.g. "mcmc_hist") or can be abbreviated to the part of the name following the "mcmc_" prefix (e.g. "hist"). To get the names of all available MCMC functions see available_mcmc.
pars	An optional character vector of parameter names.
regex_pars	An optional character vector of regular expressions to use for parameter selection. regex_pars can be used in place of pars or in addition to pars. Currently, all functions that accept a regex_pars argument ignore it for models fit using optimization.
...	Additional arguments to pass to plotfun for customizing the plot. These are described on the help pages for the individual plotting functions. For example, the arguments accepted for the default plotfun="intervals" can be found at mcmc_intervals.

Value

Either a ggplot object that can be further customized using the **ggplot2** package, or an object created from multiple ggplot objects (e.g. a gtable object created by arrangeGrob).

References

Gabry, J. , Simpson, D. , Vehtari, A. , Betancourt, M. and Gelman, A. (2019), Visualization in Bayesian workflow. *J. R. Stat. Soc. A*, 182: 389-402. doi:10.1111/rssa.12378, arXiv preprint, code on GitHub)

See Also

- The vignettes in the **bayesplot** package for many examples.
- MCMC-overview (**bayesplot**) for links to the documentation for all the available plotting functions.
- color_scheme_set (**bayesplot**) to change the color scheme used for plotting.
- pp_check for graphical posterior predictive checks.
- plot_nonlinear for models with nonlinear smooth functions fit using stan_gamm4.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {

# Use rstanarm example model
if (!exists("example_model")) example(example_model)
fit <- example_model

####################################
### Intervals and point estimates ###
####################################
plot(fit) # same as plot(fit, "intervals"), plot(fit, "mcmc_intervals")
```

```
p <- plot(fit, pars = "size", regex_pars = "period",
          prob = 0.5, prob_outer = 0.9)
p + ggplot2::ggtitle("Posterior medians \n with 50% and 90% intervals")

# Shaded areas under densities
bayesplot::color_scheme_set("brightblue")
plot(fit, "areas", regex_pars = "period",
     prob = 0.5, prob_outer = 0.9)

# Make the same plot by extracting posterior draws and calling
# bayesplot::mcmc_areas directly
x <- as.array(fit, regex_pars = "period")
bayesplot::mcmc_areas(x, prob = 0.5, prob_outer = 0.9)

# Ridgelines version of the areas plot
bayesplot::mcmc_areas_ridges(x, regex_pars = "period", prob = 0.9)


#################################
### Histograms & density plots ###
#################################
plot_title <- ggplot2::ggtitle("Posterior Distributions")
plot(fit, "hist", regex_pars = "period") + plot_title
plot(fit, "dens_overlay", pars = "(Intercept)",
     regex_pars = "period") + plot_title

###################
### Scatterplots ###
###################
bayesplot::color_scheme_set("teal")
plot(fit, "scatter", pars = paste0("period", 2:3))
plot(fit, "scatter", pars = c("(Intercept)", "size"),
     size = 3, alpha = 0.5) +
     ggplot2::stat_ellipse(level = 0.9)


################################################
### Rhat, effective sample size, autocorrelation ###
################################################
bayesplot::color_scheme_set("red")

# rhat
plot(fit, "rhat")
plot(fit, "rhat_hist")

# ratio of effective sample size to total posterior sample size
plot(fit, "neff")
plot(fit, "neff_hist")

# autocorrelation by chain
plot(fit, "acf", pars = "(Intercept)", regex_pars = "period")
plot(fit, "acf_bar", pars = "(Intercept)", regex_pars = "period")
```

```
##################
### Traceplots ###
##################
# NOTE: rstanarm doesn't store the warmup draws (to save space because they
# are not so essential for diagnosing the particular models implemented in
# rstanarm) so the iterations in the traceplot are post-warmup iterations

bayesplot::color_scheme_set("pink")
(trace <- plot(fit, "trace", pars = "(Intercept)"))

# change traceplot colors to ggplot defaults or custom values
trace + ggplot2::scale_color_discrete()
trace + ggplot2::scale_color_manual(values = c("maroon", "skyblue2"))

# changing facet layout
plot(fit, "trace", pars = c("(Intercept)", "period2"),
     facet_args = list(nrow = 2))
# same plot by calling bayesplot::mcmc_trace directly
x <- as.array(fit, pars = c("(Intercept)", "period2"))
bayesplot::mcmc_trace(x, facet_args = list(nrow = 2))


#############
### More ###
#############

# regex_pars examples
plot(fit, regex_pars = "herd:1\\]")
plot(fit, regex_pars = "herd:[279]")
plot(fit, regex_pars = "herd:[279]|period2")
plot(fit, regex_pars = c("herd:[279]", "period2"))


# For graphical posterior predictive checks see
# help("pp_check.stanreg")
}
```

`plot.survfit.stanjm` *Plot the estimated subject-specific or marginal survival function*

Description

This generic `plot` method for `survfit.stanjm` objects will plot the estimated subject-specific or marginal survival function using the data frame returned by a call to `posterior_survfit`. The call to `posterior_survfit` should ideally have included an "extrapolation" of the survival function, obtained by setting the `extrapolate` argument to `TRUE`.

The `plot_stack_jm` function takes arguments containing the plots of the estimated subject-specific longitudinal trajectory (or trajectories if a multivariate joint model was estimated) and the plot of the estimated subject-specific survival function and combines them into a single figure. This is most easily understood by running the **Examples** below.

Usage

```
## S3 method for class 'survfit.stanjm'
plot(
  x,
  ids = NULL,
  limits = c("ci", "none"),
  xlab = NULL,
  ylab = NULL,
  facet_scales = "free",
  ci_geom_args = NULL,
  ...
)

plot_stack_jm(yplot, survplot)
```

Arguments

x	A data frame and object of class survfit.stanjm returned by a call to the function posterior_survfit. The object contains point estimates and uncertainty interval limits for estimated values of the survival function.
ids	An optional vector providing a subset of subject IDs for whom the predicted curves should be plotted.
limits	A quoted character string specifying the type of limits to include in the plot. Can be one of: "ci" for the Bayesian posterior uncertainty interval for the estimated survival probability (often known as a credible interval); or "none" for no interval limits.
xlab, ylab	An optional axis label passed to labs.
facet_scales	A character string passed to the scales argument of facet_wrap when plotting the longitudinal trajectory for more than one individual.
ci_geom_args	Optional arguments passed to geom_ribbon and used to control features of the plotted interval limits. They should be supplied as a named list.
...	Optional arguments passed to geom_line and used to control features of the plotted survival function.
yplot	An object of class plot.predict.stanjm, returned by a call to the generic plot method for objects of class predict.stanjm. If there is more than one longitudinal outcome, then a list of such objects can be provided.
survplot	An object of class plot.survfit.stanjm, returned by a call to the generic plot method for objects of class survfit.stanjm.

Value

The plot method returns a ggplot object, also of class plot.survfit.stanjm. This object can be further customised using the **ggplot2** package. It can also be passed to the function plot_stack_jm.

plot_stack_jm returns an object of class bayesplot_grid that includes plots of the estimated subject-specific longitudinal trajectories stacked on top of the associated subject-specific survival curve.

See Also

posterior_survfit, plot_stack_jm, posterior_traj, plot.predict.stanjm

plot.predict.stanjm, plot.survfit.stanjm, posterior_predict, posterior_survfit

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {

  # Run example model if not already loaded
  if (!exists("example_jm")) example(example_jm)

  # Obtain subject-specific conditional survival probabilities
  # for all individuals in the estimation dataset.
  ps1 <- posterior_survfit(example_jm, extrapolate = TRUE)

  # We then plot the conditional survival probabilities for
  # a subset of individuals
  plot(ps1, ids = c(7,13,15))
  # We can change or add attributes to the plot
  plot(ps1, ids = c(7,13,15), limits = "none")
  plot(ps1, ids = c(7,13,15), xlab = "Follow up time")
  plot(ps1, ids = c(7,13,15), ci_geom_args = list(fill = "red"),
       color = "blue", linetype = 2)
  plot(ps1, ids = c(7,13,15), facet_scales = "fixed")

  # Since the returned plot is also a ggplot object, we can
  # modify some of its attributes after it has been returned
  plot1 <- plot(ps1, ids = c(7,13,15))
  plot1 +
    ggplot2::theme(strip.background = ggplot2::element_blank()) +
    ggplot2::coord_cartesian(xlim = c(0, 15)) +
    ggplot2::labs(title = "Some plotted survival functions")

  # We can also combine the plot(s) of the estimated
  # subject-specific survival functions, with plot(s)
  # of the estimated longitudinal trajectories for the
  # same individuals
  ps1 <- posterior_survfit(example_jm, ids = c(7,13,15))
  pt1 <- posterior_traj(example_jm, , ids = c(7,13,15))
  plot_surv <- plot(ps1)
  plot_traj <- plot(pt1, vline = TRUE, plot_observed = TRUE)
  plot_stack_jm(plot_traj, plot_surv)

  # Lastly, let us plot the standardised survival function
  # based on all individuals in our estimation dataset
  ps2 <- posterior_survfit(example_jm, standardise = TRUE, times = 0,
                           control = list(epoints = 20))
  plot(ps2)

}
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
```

```
  if (!exists("example_jm")) example(example_jm)
  ps1 <- posterior_survfit(example_jm, ids = c(7,13,15))
  pt1 <- posterior_traj(example_jm, ids = c(7,13,15), extrapolate = TRUE)
  plot_surv <- plot(ps1)
  plot_traj <- plot(pt1, vline = TRUE, plot_observed = TRUE)
  plot_stack_jm(plot_traj, plot_surv)

}
```

`posterior_interval.stanreg` *Posterior uncertainty intervals*

Description

For models fit using MCMC (`algorithm="sampling"`) or one of the variational approximations (`"meanfield"` or `"fullrank"`), the `posterior_interval` function computes Bayesian posterior uncertainty intervals. These intervals are often referred to as *credible* intervals, but we use the term *uncertainty* intervals to highlight the fact that wider intervals correspond to greater uncertainty.

Usage

```
## S3 method for class 'stanreg'
posterior_interval(
  object,
  prob = 0.9,
  type = "central",
  pars = NULL,
  regex_pars = NULL,
  ...
)
```

Arguments

`object`	A fitted model object returned by one of the **rstanarm** modeling functions. See `stanreg-objects`.
`prob`	A number $p \in (0, 1)$ indicating the desired probability mass to include in the intervals. The default is to report 90% intervals (`prob=0.9`) rather than the traditionally used 95% (see Details).
`type`	The type of interval to compute. Currently the only option is `"central"` (see Details). A central $100p\%$ interval is defined by the $\alpha/2$ and $1 - \alpha/2$ quantiles, where $\alpha = 1 - p$.
`pars`	An optional character vector of parameter names.
`regex_pars`	An optional character vector of regular expressions to use for parameter selection. `regex_pars` can be used in place of `pars` or in addition to `pars`. Currently, all functions that accept a `regex_pars` argument ignore it for models fit using optimization.
`...`	Currently ignored.

Details

Interpretation: Unlike for a frenquentist confidence interval, it is valid to say that, conditional on the data and model, we believe that with probability p the value of a parameter is in its $100p\%$ posterior interval. This intuitive interpretation of Bayesian intervals is often erroneously applied to frequentist confidence intervals. See Morey et al. (2015) for more details on this issue and the advantages of using Bayesian posterior uncertainty intervals (also known as credible intervals).

Default 90% intervals: We default to reporting 90% intervals rather than 95% intervals for several reasons:

- Computational stability: 90% intervals are more stable than 95% intervals (for which each end relies on only 2.5% of the posterior draws).
- Relation to Type-S errors (Gelman and Carlin, 2014): 95% of the mass in a 90% central interval is above the lower value (and 95% is below the upper value). For a parameter θ, it is therefore easy to see if the posterior probability that $\theta > 0$ (or $\theta < 0$) is larger or smaller than 95%.

Of course, if 95% intervals are desired they can be computed by specifying `prob=0.95`.

Types of intervals: Currently `posterior_interval` only computes central intervals because other types of intervals are rarely useful for the models that **rstanarm** can estimate. Additional possibilities may be provided in future releases as more models become available.

Value

A matrix with two columns and as many rows as model parameters (or the subset of parameters specified by `pars` and/or `regex_pars`). For a given value of `prob`, p, the columns correspond to the lower and upper $100p\%$ interval limits and have the names $100\alpha/2\%$ and $100(1-\alpha/2)\%$, where $\alpha = 1 - p$. For example, if `prob=0.9` is specified (a 90% interval), then the column names will be `"5%"` and `"95%"`, respectively.

References

Gelman, A. and Carlin, J. (2014). Beyond power calculations: assessing Type S (sign) and Type M (magnitude) errors. *Perspectives on Psychological Science*. 9(6), 641–51.

Morey, R. D., Hoekstra, R., Rouder, J., Lee, M. D., and Wagenmakers, E. (2016). The fallacy of placing confidence in confidence intervals. *Psychonomic Bulletin & Review*. 23(1), 103–123.

See Also

`confint.stanreg`, which, for models fit using optimization, can be used to compute traditional confidence intervals.

`predictive_interval` for predictive intervals.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
if (!exists("example_model")) example(example_model)
posterior_interval(example_model)
posterior_interval(example_model, regex_pars = "herd")
```

```
posterior_interval(example_model, pars = "period2", prob = 0.5)
}
```

---

posterior_linpred.stanreg *Posterior distribution of the (possibly transformed) linear predictor*

Description

Extract the posterior draws of the linear predictor, possibly transformed by the inverse-link function. This function is occasionally useful, but it should be used sparingly: inference and model checking should generally be carried out using the posterior predictive distribution (i.e., using posterior_predict).

Usage

```
## S3 method for class 'stanreg'
posterior_linpred(
  object,
  transform = FALSE,
  newdata = NULL,
  draws = NULL,
  re.form = NULL,
  offset = NULL,
  XZ = FALSE,
  ...
)

## S3 method for class 'stanreg'
posterior_epred(
  object,
  newdata = NULL,
  draws = NULL,
  re.form = NULL,
  offset = NULL,
  XZ = FALSE,
  ...
)
```

Arguments

object	A fitted model object returned by one of the **rstanarm** modeling functions. See stanreg-objects.
transform	Should the linear predictor be transformed using the inverse-link function? The default is FALSE. This argument is still allowed but not recommended because the posterior_epred function now provides the equivalent of posterior_linpred(..., transform=TRUE). See **Examples**.

newdata, draws, re.form, offset
: Same as for posterior_predict.

XZ
: If TRUE then instead of computing the linear predictor the design matrix X (or cbind(X,Z) for models with group-specific terms) constructed from newdata is returned. The default is FALSE.

...
: Currently ignored.

Details

The posterior_linpred function returns the posterior distribution of the linear predictor, while the posterior_epred function returns the posterior distribution of the conditional expectation. In the special case of a Gaussian likelihood with an identity link function, these two concepts are the same. The posterior_epred function is a less noisy way to obtain expectations over the output of posterior_predict.

Value

The default is to return a draws by nrow(newdata) matrix of simulations from the posterior distribution of the (possibly transformed) linear predictor. The exception is if the argument XZ is set to TRUE (see the XZ argument description above).

Note

For models estimated with stan_clogit, the number of successes per stratum is ostensibly fixed by the research design. Thus, when calling posterior_linpred with new data and transform = TRUE, the data.frame passed to the newdata argument must contain an outcome variable and a stratifying factor, both with the same name as in the original data.frame. Then, the probabilities will condition on this outcome in the new data.

See Also

posterior_predict to draw from the posterior predictive distribution of the outcome, which is typically preferable.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
if (!exists("example_model")) example(example_model)
print(family(example_model))

# linear predictor on log-odds scale
linpred <- posterior_linpred(example_model)
colMeans(linpred)

# probabilities
# same as posterior_linpred(example_model, transform = TRUE)
probs <- posterior_epred(example_model)
colMeans(probs)

# not conditioning on any group-level parameters
```

```
probs2 <- posterior_epred(example_model, re.form = NA)
apply(probs2, 2, median)
}
```

`posterior_predict.stanreg` *Draw from posterior predictive distribution*

Description

The posterior predictive distribution is the distribution of the outcome implied by the model after using the observed data to update our beliefs about the unknown parameters in the model. Simulating data from the posterior predictive distribution using the observed predictors is useful for checking the fit of the model. Drawing from the posterior predictive distribution at interesting values of the predictors also lets us visualize how a manipulation of a predictor affects (a function of) the outcome(s). With new observations of predictor variables we can use the posterior predictive distribution to generate predicted outcomes.

Usage

```
## S3 method for class 'stanreg'
posterior_predict(
  object,
  newdata = NULL,
  draws = NULL,
  re.form = NULL,
  fun = NULL,
  seed = NULL,
  offset = NULL,
  ...
)

## S3 method for class 'stanmvreg'
posterior_predict(
  object,
  m = 1,
  newdata = NULL,
  draws = NULL,
  re.form = NULL,
  fun = NULL,
  seed = NULL,
  offset = NULL,
  ...
)
```

Arguments

object	A fitted model object returned by one of the **rstanarm** modeling functions. See stanreg-objects.
newdata	Optionally, a data frame in which to look for variables with which to predict. If omitted, the model matrix is used. If newdata is provided and any variables were transformed (e.g. rescaled) in the data used to fit the model, then these variables must also be transformed in newdata. This only applies if variables were transformed before passing the data to one of the modeling functions and *not* if transformations were specified inside the model formula. Also see the Note section below for a note about using the newdata argument with with binomial models.
draws	An integer indicating the number of draws to return. The default and maximum number of draws is the size of the posterior sample.
re.form	If object contains group-level parameters, a formula indicating which group-level parameters to condition on when making predictions. re.form is specified in the same form as for predict.merMod. The default, NULL, indicates that all estimated group-level parameters are conditioned on. To refrain from conditioning on any group-level parameters, specify NA or ~0. The newdata argument may include new *levels* of the grouping factors that were specified when the model was estimated, in which case the resulting posterior predictions marginalize over the relevant variables.
fun	An optional function to apply to the results. fun is found by a call to match.fun and so can be specified as a function object, a string naming a function, etc.
seed	An optional seed to use.
offset	A vector of offsets. Only required if newdata is specified and an offset argument was specified when fitting the model.
...	For stanmvreg objects, argument m can be specified indicating the submodel for which you wish to obtain predictions.
m	Integer specifying the number or name of the submodel

Value

A draws by nrow(newdata) matrix of simulations from the posterior predictive distribution. Each row of the matrix is a vector of predictions generated using a single draw of the model parameters from the posterior distribution.

Note

For binomial models with a number of trials greater than one (i.e., not Bernoulli models), if newdata is specified then it must include all variables needed for computing the number of binomial trials to use for the predictions. For example if the left-hand side of the model formula is cbind(successes, failures) then both successes and failures must be in newdata. The particular values of successes and failures in newdata do not matter so long as their sum is the desired number of trials. If the left-hand side of the model formula were cbind(successes, trials - successes) then both trials and successes would need to be in newdata, probably with successes set to 0

and `trials` specifying the number of trials. See the Examples section below and the *How to Use the rstanarm Package* for examples.

For models estimated with `stan_clogit`, the number of successes per stratum is ostensibly fixed by the research design. Thus, when doing posterior prediction with new data, the `data.frame` passed to the `newdata` argument must contain an outcome variable and a stratifying factor, both with the same name as in the original `data.frame`. Then, the posterior predictions will condition on this outcome in the new data.

See Also

`pp_check` for graphical posterior predictive checks. Examples of posterior predictive checking can also be found in the **rstanarm** vignettes and demos.

`predictive_error` and `predictive_interval`.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
if (!exists("example_model")) example(example_model)
yrep <- posterior_predict(example_model)
table(yrep)


# Using newdata
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
dat <- data.frame(counts, treatment, outcome)
fit3 <- stan_glm(
  counts ~ outcome + treatment,
  data = dat,
  family = poisson(link="log"),
  prior = normal(0, 1, autoscale = FALSE),
  prior_intercept = normal(0, 5, autoscale = FALSE),
  refresh = 0
)
nd <- data.frame(treatment = factor(rep(1,3)), outcome = factor(1:3))
ytilde <- posterior_predict(fit3, nd, draws = 500)
print(dim(ytilde))  # 500 by 3 matrix (draws by nrow(nd))

ytilde <- data.frame(
  count = c(ytilde),
  outcome = rep(nd$outcome, each = 500)
)
ggplot2::ggplot(ytilde, ggplot2::aes(x=outcome, y=count)) +
  ggplot2::geom_boxplot() +
  ggplot2::ylab("predicted count")


# Using newdata with a binomial model.
# example_model is binomial so we need to set
# the number of trials to use for prediction.
```

```
# This could be a different number for each
# row of newdata or the same for all rows.
# Here we'll use the same value for all.
nd <- lme4::cbpp
print(formula(example_model))  # cbind(incidence, size - incidence) ~ ...
nd$size <- max(nd$size) + 1L   # number of trials
nd$incidence <- 0  # set to 0 so size - incidence = number of trials
ytilde <- posterior_predict(example_model, newdata = nd)


# Using fun argument to transform predictions
mtcars2 <- mtcars
mtcars2$log_mpg <- log(mtcars2$mpg)
fit <- stan_glm(log_mpg ~ wt, data = mtcars2, refresh = 0)
ytilde <- posterior_predict(fit, fun = exp)

}
```

`posterior_survfit` *Estimate subject-specific or standardised survival probabilities*

Description

This function allows us to generate estimated survival probabilities based on draws from the posterior predictive distribution. By default the survival probabilities are conditional on an individual's group-specific coefficients (i.e. their individual-level random effects). If prediction data is provided via the `newdataLong` and `newdataEvent` arguments, then the default behaviour is to sample new group-specific coefficients for the individuals in the new data using a Monte Carlo scheme that conditions on their longitudinal outcome data provided in `newdataLong` (sometimes referred to as "dynamic predictions", see Rizopoulos (2011)). This default behaviour can be stopped by specifying `dynamic = FALSE`, in which case the predicted survival probabilities will be marginalised over the distribution of the group-specific coefficients. This has the benefit that the user does not need to provide longitudinal outcome measurements for the new individuals, however, it does mean that the predictions will incorporate all the uncertainty associated with between-individual variation, since the predictions aren't conditional on any observed data for the individual. In addition, by default, the predicted subject-specific survival probabilities are conditional on observed values of the fixed effect covariates (ie, the predictions will be obtained using either the design matrices used in the original `stan_jm` model call, or using the covariate values provided in the `newdataLong` and `newdataEvent` arguments). However, if you wish to average over the observed distribution of the fixed effect covariates then this is possible – such predictions are sometimes referred to as standardised survival probabilties – see the `standardise` argument below.

Usage

```
posterior_survfit(
  object,
  newdataLong = NULL,
  newdataEvent = NULL,
```

```
  extrapolate = TRUE,
  control = list(),
  condition = NULL,
  last_time = NULL,
  prob = 0.95,
  ids,
  times = NULL,
  standardise = FALSE,
  dynamic = TRUE,
  scale = 1.5,
  draws = NULL,
  seed = NULL,
  ...
)
```

Arguments

`object` A fitted model object returned by the `stan_jm` modelling function. See `stanreg-objects`.

`newdataLong, newdataEvent`
Optionally, a data frame (or in the case of `newdataLong` this can be a list of data frames) in which to look for variables with which to predict. If omitted, the model matrices are used. If new data is provided, then it should also contain the longitudinal outcome data on which to condition when drawing the new group-specific coefficients for individuals in the new data. Note that there is only allowed to be one row of data for each individual in `newdataEvent`, that is, time-varying covariates are not allowed in the prediction data for the event submodel. Also, `newdataEvent` can optionally include a variable with information about the last known survival time for the new individuals – see the description for the `last_time` argument below – however also note that when generating the survival probabilities it is of course assumed that all individuals in `newdataEvent` have not yet experienced the event (that is, any variable in `newdataEvent` that corresponds to the event indicator will be ignored).

`extrapolate` A logical specifying whether to extrapolate the estimated survival probabilities beyond the times specified in the `times` argument. If `TRUE` then the extrapolation can be further controlled using the `control` argument.

`control` A named list with parameters controlling extrapolation of the estimated survival function when `extrapolate = TRUE`. The list can contain one or more of the following named elements:

`epoints` a positive integer specifying the number of discrete time points at which to calculate the forecasted survival probabilities. The default is 10.

`edist` a positive scalar specifying the amount of time across which to forecast the estimated survival function, represented in units of the time variable `time_var` (from fitting the model). The default is to extrapolate between the times specified in the `times` argument and the maximum event or censoring time in the original data. If `edist` leads to times that are beyond the maximum event or censoring time in the original data then the estimated

survival probabilities will be truncated at that point, since the estimate for the baseline hazard is not available beyond that time.

`condition` A logical specifying whether the estimated subject-specific survival probabilities at time `t` should be conditioned on survival up to a fixed time point `u`. The default is for `condition` to be set to `TRUE`, unless standardised survival probabilities have been requested (by specifying `standardise = TRUE`), in which case `condition` must (and will) be set to `FALSE`. When conditional survival probabilities are requested, the fixed time point `u` will be either: (i) the value specified via the `last_time` argument; or if the `last_time` argument is `NULL` then the latest observation time for each individual (taken to be the value in the `times` argument if `newdataEvent` is specified, or the observed event or censoring time if `newdataEvent` is `NULL`.

`last_time` A scalar, character string, or `NULL`. This argument specifies the last known survival time for each individual when conditional predictions are being obtained. If `newdataEvent` is provided and conditional survival predictions are being obtained, then the `last_time` argument can be one of the following: (i) a scalar, this will use the same last time for each individual in `newdataEvent`; (ii) a character string, naming a column in `newdataEvent` in which to look for the last time for each individual; (iii) `NULL`, in which case the default is to use the time of the latest longitudinal observation in `newdataLong`. If `newdataEvent` is `NULL` then the `last_time` argument cannot be specified directly; instead it will be set equal to the event or censoring time for each individual in the dataset that was used to estimate the model. If standardised survival probabilities are requested (i.e. `standardise = TRUE`) then conditional survival probabilities are not allowed and therefore the `last_time` argument is ignored.

`prob` A scalar between 0 and 1 specifying the width to use for the uncertainty interval (sometimes called credible interval) for the predictions. For example `prob = 0.95` (the default) means that the 2.5th and 97.5th percentiles will be provided.

`ids` An optional vector specifying a subset of IDs for whom the predictions should be obtained. The default is to predict for all individuals who were used in estimating the model or, if `newdataLong` and `newdataEvent` are specified, then all individuals contained in the new data.

`times` A scalar, a character string, or `NULL`. Specifies the times at which the estimated survival probabilities should be calculated. It can be either: (i) `NULL`, in which case it will default to the last known survival time for each individual, as determined by the `last_time` argument; (ii) a scalar, specifying a time to estimate the survival probability for each of the individuals; or (iii) if `newdataEvent` is provided, it can be the name of a variable in `newdataEvent` that indicates the time at which the survival probabilities should be calculated for each individual.

`standardise` A logical specifying whether the estimated subject-specific survival probabilities should be averaged across all individuals for whom the subject-specific predictions are being obtained. This can be used to average over the covariate and random effects distributions of the individuals used in estimating the model, or the individuals included in the `newdata` arguments. This approach of averaging across the observed distribution of the covariates is sometimes referred to as a "standardised" survival curve. If `standardise = TRUE`, then the `times` argument

must be specified and it must be constant across individuals, that is, the survival probabilities must be calculated at the same time for all individuals.

`dynamic` A logical that is only relevant if new data is provided via the `newdataLong` and `newdataEvent` arguments. If `dynamic = TRUE`, then new group-specific parameters are drawn for the individuals in the new data, conditional on their longitudinal biomarker data contained in `newdataLong`. These group-specific parameters are then used to generate individual-specific survival probabilities for these individuals. These are often referred to as "dynamic predictions" in the joint modelling context, because the predictions can be updated each time additional longitudinal biomarker data is collected on the individual. On the other hand, if `dynamic = FALSE` then the survival probabilities will just be marginalised over the distribution of the group-specific coefficients; this will mean that the predictions will incorporate all uncertainty due to between-individual variation so there will likely be very wide credible intervals on the predicted survival probabilities.

`scale` A scalar, specifying how much to multiply the asymptotic variance-covariance matrix for the random effects by, which is then used as the "width" (ie. variance-covariance matrix) of the multivariate Student-t proposal distribution in the Metropolis-Hastings algorithm. This is only relevant when `newdataEvent` is supplied and `dynamic = TRUE`, in which case new random effects are simulated for the individuals in the new data using the Metropolis-Hastings algorithm.

`draws` An integer indicating the number of MCMC draws to return. The default is to set the number of draws equal to 200, or equal to the size of the posterior sample if that is less than 200.

`seed` An optional `seed` to use.

`...` Currently unused.

Value

A data frame of class `survfit.stanjm`. The data frame includes columns for each of the following: (i) the median of the posterior predictions of the estimated survival probabilities (`survpred`); (ii) each of the lower and upper limits of the corresponding uncertainty interval for the estimated survival probabilities (`ci_lb` and `ci_ub`); (iii) a subject identifier (`id_var`), unless standardised survival probabilities were estimated; (iv) the time that the estimated survival probability is calculated for (`time_var`). The returned object also includes a number of additional attributes.

Note

Note that if any variables were transformed (e.g. rescaled) in the data used to fit the model, then these variables must also be transformed in `newdataLong` and `newdataEvent`. This only applies if variables were transformed before passing the data to one of the modeling functions and *not* if transformations were specified inside the model formula.

References

Rizopoulos, D. (2011). Dynamic predictions and prospective accuracy in joint models for longitudinal and time-to-event data. *Biometrics* **67**, 819.

See Also

plot.survfit.stanjm for plotting the estimated survival probabilities, ps_check for for graphical checks of the estimated survival function, and posterior_traj for estimating the marginal or subject-specific longitudinal trajectories, and plot_stack_jm for combining plots of the estimated subject-specific longitudinal trajectory and survival function.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {

  # Run example model if not already loaded
  if (!exists("example_jm")) example(example_jm)

  # Obtain subject-specific survival probabilities for a few
  # selected individuals in the estimation dataset who were
  # known to survive up until their censoring time. By default
  # the posterior_survfit function will estimate the conditional
  # survival probabilities, that is, conditional on having survived
  # until the event or censoring time, and then by default will
  # extrapolate the survival predictions forward from there.
  ps1 <- posterior_survfit(example_jm, ids = c(7,13,15))
  # We can plot the estimated survival probabilities using the
  # associated plot function
  plot(ps1)

  # If we wanted to estimate the survival probabilities for the
  # same three individuals as the previous example, but this time
  # we won't condition on them having survived up until their
  # censoring time. Instead, we will estimate their probability
  # of having survived between 0 and 5 years given their covariates
  # and their estimated random effects.
  # The easiest way to achieve the time scale we want (ie, 0 to 5 years)
  # is to specify that we want the survival time estimated at time 0
  # and then extrapolated forward 5 years. We also specify that we
  # do not want to condition on their last known survival time.
  ps2 <- posterior_survfit(example_jm, ids = c(7,13,15), times = 0,
    extrapolate = TRUE, condition = FALSE, control = list(edist = 5))

  # Instead we may want to estimate subject-specific survival probabilities
  # for a set of new individuals. To demonstrate this, we will simply take
  # the first two individuals in the estimation dataset, but pass their data
  # via the newdata arguments so that posterior_survfit will assume we are
  # predicting survival for new individuals and draw new random effects
  # under a Monte Carlo scheme (see Rizopoulos (2011)).
  ndL <- pbcLong[pbcLong$id %in% c(1,2),]
  ndE <- pbcSurv[pbcSurv$id %in% c(1,2),]
  ps3 <- posterior_survfit(example_jm,
    newdataLong = ndL, newdataEvent = ndE,
    last_time = "futimeYears", seed = 12345)
  head(ps3)
  # We can then compare the estimated random effects for these
  # individuals based on the fitted model and the Monte Carlo scheme
```

```
  ranef(example_jm)$Long1$id[1:2,,drop=FALSE] # from fitted model
  colMeans(attr(ps3, "b_new"))                # from Monte Carlo scheme

  # Lastly, if we wanted to obtain "standardised" survival probabilities,
  # (by averaging over the observed distribution of the fixed effect
  # covariates, as well as averaging over the estimated random effects
  # for individuals in our estimation sample or new data) then we can
  # specify 'standardise = TRUE'. We can then plot the resulting
  # standardised survival curve.
  ps4 <- posterior_survfit(example_jm, standardise = TRUE,
                           times = 0, extrapolate = TRUE)
  plot(ps4)

}
```

`posterior_traj` *Estimate the subject-specific or marginal longitudinal trajectory*

Description

This function allows us to generate an estimated longitudinal trajectory (either subject-specific, or by marginalising over the distribution of the group-specific parameters) based on draws from the posterior predictive distribution.

Usage

```
posterior_traj(
  object,
  m = 1,
  newdata = NULL,
  newdataLong = NULL,
  newdataEvent = NULL,
  interpolate = TRUE,
  extrapolate = FALSE,
  control = list(),
  last_time = NULL,
  prob = 0.95,
  ids,
  dynamic = TRUE,
  scale = 1.5,
  draws = NULL,
  seed = NULL,
  return_matrix = FALSE,
  ...
)
```

Arguments

object	A fitted model object returned by the stan_jm modelling function. See stanreg-objects.
m	Integer specifying the number or name of the submodel
newdata	**Deprecated**: please use newdataLong instead. Optionally, a data frame in which to look for variables with which to predict. If omitted, the model matrix is used. If newdata is provided and any variables were transformed (e.g. rescaled) in the data used to fit the model, then these variables must also be transformed in newdata. This only applies if variables were transformed before passing the data to one of the modeling functions and *not* if transformations were specified inside the model formula.
newdataLong, newdataEvent	Optionally, a data frame (or in the case of newdataLong this can be a list of data frames) in which to look for variables with which to predict. If omitted, the model matrices are used. If new data is provided, then two options are available. Either one can provide observed covariate and outcome data, collected up to some time *t*, and use this data to draw new individual-specific coefficients (i.e. individual-level random effects). This is the default behaviour when new data is provided, determined by the argument dynamic = TRUE, and requiring both newdataLong and newdataEvent to be specified. Alternatively, one can specify dynamic = FALSE, and then predict using just covariate data, by marginalising over the distribution of the group-specific coefficients; in this case, only newdataLong needs to be specified and it only needs to be a single data frame with the covariate data for the predictions for the one longitudinal submodel.
interpolate	A logical specifying whether to interpolate the estimated longitudinal trajectory in between the observation times. This can be used to achieve a smooth estimate of the longitudinal trajectory across the entire follow up time. If TRUE then the interpolation can be further controlled using the control argument.
extrapolate	A logical specifying whether to extrapolate the estimated longitudinal trajectory beyond the time of the last known observation time. If TRUE then the extrapolation can be further controlled using the control argument.
control	A named list with parameters controlling the interpolation or extrapolation of the estimated longitudinal trajectory when either interpolate = TRUE or extrapolate = TRUE. The list can contain one or more of the following named elements:

ipoints a positive integer specifying the number of discrete time points at which to calculate the estimated longitudinal response for interpolate = TRUE. These time points are evenly spaced starting at 0 and ending at the last known observation time for each individual. The last observation time for each individual is taken to be either: the event or censoring time if no new data is provided; the time specified in the "last_time" column if provided in the new data (see **Details** section below); or the time of the last longitudinal measurement if new data is provided but no "last_time" column is included. The default is 15.

epoints a positive integer specifying the number of discrete time points at which to calculate the estimated longitudinal response for extrapolate

= TRUE. These time points are evenly spaced between the last known observation time for each individual and the extrapolation distance specifed using either edist or eprop. The default is 15.

eprop a positive scalar between 0 and 1 specifying the amount of time across which to extrapolate the longitudinal trajectory, represented as a proportion of the total observed follow up time for each individual. For example specifying eprop = 0.2 means that for an individual for whom the latest of their measurement, event or censoring times was 10 years, their estimated longitudinal trajectory will be extrapolated out to 12 years (i.e. 10 + (0.2 * 10)). The default value is 0.2.

edist a positive scalar specifying the amount of time across which to extrapolate the longitudinal trajectory for each individual, represented in units of the time variable time_var (from fitting the model). This cannot be specified if eprop is specified.

last_time A scalar, character string, or NULL. This argument specifies the last known survival time for each individual when conditional predictions are being obtained. If newdataEvent is provided and conditional survival predictions are being obtained, then the last_time argument can be one of the following: (i) a scalar, this will use the same last time for each individual in newdataEvent; (ii) a character string, naming a column in newdataEvent in which to look for the last time for each individual; (iii) NULL, in which case the default is to use the time of the latest longitudinal observation in newdataLong. If newdataEvent is NULL then the last_time argument cannot be specified directly; instead it will be set equal to the event or censoring time for each individual in the dataset that was used to estimate the model. If standardised survival probabilities are requested (i.e. standardise = TRUE) then conditional survival probabilities are not allowed and therefore the last_time argument is ignored.

prob A scalar between 0 and 1 specifying the width to use for the uncertainty interval (sometimes called credible interval) for the predicted mean response and the prediction interval for the predicted (raw) response. For example prob = 0.95 (the default) means that the 2.5th and 97.5th percentiles will be provided. Only relevant when return_matrix is FALSE.

ids An optional vector specifying a subset of subject IDs for whom the predictions should be obtained. The default is to predict for all individuals who were used in estimating the model or, if newdata is specified, then all individuals contained in newdata.

dynamic A logical that is only relevant if new data is provided via the newdata argument. If dynamic = TRUE, then new group-specific parameters are drawn for the individuals in the new data, conditional on their longitudinal biomarker data contained in newdata. These group-specific parameters are then used to generate individual-specific survival probabilities for these individuals. These are often referred to as "dynamic predictions" in the joint modelling context, because the predictions can be updated each time additional longitudinal biomarker data is collected on the individual. On the other hand, if dynamic = FALSE then the survival probabilities will just be marginalised over the distribution of the group-specific coefficients; this will mean that the predictions will incorporate all uncertainty due to between-individual variation so there will likely be very wide credible intervals on the predicted survival probabilities.

scale	A scalar, specifying how much to multiply the asymptotic variance-covariance matrix for the random effects by, which is then used as the "width" (ie. variance-covariance matrix) of the multivariate Student-t proposal distribution in the Metropolis-Hastings algorithm. This is only relevant when newdataEvent is supplied and dynamic = TRUE, in which case new random effects are simulated for the individuals in the new data using the Metropolis-Hastings algorithm.
draws	An integer indicating the number of MCMC draws to return. The default is to set the number of draws equal to 200, or equal to the size of the posterior sample if that is less than 200.
seed	An optional seed to use.
return_matrix	A logical. If TRUE then a draws by nrow(newdata) matrix is returned which contains all the actual simulations or draws from the posterior predictive distribution. Otherwise if return_matrix is set to FALSE (the default) then a data frame is returned, as described in the **Value** section below.
...	Other arguments passed to posterior_predict, for example draws, re.form, seed, etc.

Details

The posterior_traj function acts as a wrapper to the posterior_predict function, but allows predictions to be easily generated at time points that are interpolated and/or extrapolated between time zero (baseline) and the last known survival time for the individual, thereby providing predictions that correspond to a smooth estimate of the longitudinal trajectory (useful for the plotting via the associated plot.predict.stanjm method). In addition it returns a data frame by default, whereas the posterior_predict function returns a matrix; see the **Value** section below for details. Also, posterior_traj allows predictions to only be generated for a subset of individuals, via the ids argument.

Value

When return_matrix = FALSE, a data frame of class predict.stanjm. The data frame includes a column for the median of the posterior predictions of the mean longitudinal response (yfit), a column for each of the lower and upper limits of the uncertainty interval corresponding to the posterior predictions of the mean longitudinal response (ci_lb and ci_ub), and a column for each of the lower and upper limits of the prediction interval corresponding to the posterior predictions of the (raw) longitudinal response. The data frame also includes columns for the subject ID variable, and each of the predictor variables. The returned object also includes a number of attributes.

When return_matrix = TRUE, the returned object is the same as that described for posterior_predict.

See Also

plot.predict.stanjm, posterior_predict, posterior_survfit

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {

  # Run example model if not already loaded
```

```
if (!exists("example_jm")) example(example_jm)

# Obtain subject-specific predictions for all individuals
# in the estimation dataset
pt1 <- posterior_traj(example_jm, interpolate = FALSE, extrapolate = FALSE)
head(pt1)

# Obtain subject-specific predictions only for a few selected individuals
pt2 <- posterior_traj(example_jm, ids = c(1,3,8))

# If we wanted to obtain subject-specific predictions in order to plot the
# longitudinal trajectories, then we might want to ensure a full trajectory
# is obtained by interpolating and extrapolating time. We can then use the
# generic plot function to plot the subject-specific predicted trajectories
# for the first three individuals. Interpolation and extrapolation is
# carried out by default.
pt3 <- posterior_traj(example_jm)
head(pt3) # predictions at additional time points compared with pt1
plot(pt3, ids = 1:3)

# If we wanted to extrapolate further in time, but decrease the number of
# discrete time points at which we obtain predictions for each individual,
# then we could specify a named list in the 'control' argument
pt4 <- posterior_traj(example_jm, control = list(ipoints = 10, epoints = 10, eprop = 0.5))

# If we have prediction data for a new individual, and we want to
# estimate the longitudinal trajectory for that individual conditional
# on this new data (perhaps extrapolating forward from our last
# longitudinal measurement) then we can do that. It requires drawing
# new individual-specific parameters, based on the full likelihood,
# so we must supply new data for both the longitudinal and event
# submodels. These are sometimes known as dynamic predictions.
ndL <- pbcLong[pbcLong$id == 8, , drop = FALSE]
ndE <- pbcSurv[pbcSurv$id == 8, , drop = FALSE]
ndL$id <- "new_subject" # new id can't match one used in training data
ndE$id <- "new_subject"
pt5 <- posterior_traj(example_jm,
                      newdataLong = ndL,
                      newdataEvent = ndE)

# By default it is assumed that the last known survival time for
# the individual is the time of their last biomarker measurement,
# but if we know they survived to some later time then we can
# condition on that information using the last_time argument
pt6 <- posterior_traj(example_jm,
                      newdataLong = ndL,
                      newdataEvent = ndE,
                      last_time = "futimeYears")

# Alternatively we may want to estimate the marginal longitudinal
# trajectory for a given set of covariates. To do this, we can pass
# the desired covariate values in a new data frame (however the only
# covariate in our fitted model was the time variable, year). To make sure
```

```
  # that we marginalise over the random effects, we need to specify an ID value
  # which does not correspond to any of the individuals who were used in the
  # model estimation and specify the argument dynamic=FALSE.
  # The marginal prediction is obtained by generating subject-specific
  # predictions using a series of random draws from the random
  # effects distribution, and then integrating (ie, averaging) over these.
  # Our marginal prediction will therefore capture the between-individual
  # variation associated with the random effects.

  nd <- data.frame(id = rep("new1", 11), year = (0:10 / 2))
  pt7 <- posterior_traj(example_jm, newdataLong = nd, dynamic = FALSE)
  head(pt7)  # note the greater width of the uncertainty interval compared
             # with the subject-specific predictions in pt1, pt2, etc

  # Alternatively, we could have estimated the "marginal" trajectory by
  # ignoring the random effects (ie, assuming the random effects were set
  # to zero). This will generate a predicted longitudinal trajectory only
  # based on the fixed effect component of the model. In essence, for a
  # linear mixed effects model (ie, a model that uses an identity link
  # function), we should obtain a similar point estimate ("yfit") to the
  # estimates obtained in pt5 (since the mean of the estimated random effects
  # distribution will be approximately 0). However, it is important to note that
  # the uncertainty interval will be much more narrow, since it completely
  # ignores the between-individual variability captured by the random effects.
  # Further, if the model uses a non-identity link function, then the point
  # estimate ("yfit") obtained only using the fixed effect component of the
  # model will actually provide a biased estimate of the marginal prediction.
  # Nonetheless, to demonstrate how we can obtain the predictions only using
  # the fixed effect component of the model, we simply specify 're.form = NA'.
  # (We will use the same covariate values as used in the prediction for
  # example for pt5).

  pt8 <- posterior_traj(example_jm, newdataLong = nd, dynamic = FALSE,
                        re.form = NA)
  head(pt8)  # note the much narrower ci, compared with pt5

}
```

`posterior_vs_prior` *Juxtapose prior and posterior*

Description

Plot medians and central intervals comparing parameter draws from the prior and posterior distributions. If the plotted priors look different than the priors you think you specified it is likely either because of internal rescaling or the use of the `QR` argument (see the documentation for the `prior_summary` method for details on these special cases).

Usage

```
posterior_vs_prior(object, ...)

## S3 method for class 'stanreg'
posterior_vs_prior(
  object,
  pars = NULL,
  regex_pars = NULL,
  prob = 0.9,
  color_by = c("parameter", "vs", "none"),
  group_by_parameter = FALSE,
  facet_args = list(),
  ...
)
```

Arguments

`object`	A fitted model object returned by one of the **rstanarm** modeling functions. See `stanreg-objects`.
`...`	The S3 generic uses `...` to pass arguments to any defined methods. For the method for stanreg objects, `...` is for arguments (other than `color`) passed to `geom_pointrange` in the **ggplot2** package to control the appearance of the plotted intervals.
`pars`	An optional character vector specifying a subset of parameters to display. Parameters can be specified by name or several shortcuts can be used. Using `pars="beta"` will restrict the displayed parameters to only the regression coefficients (without the intercept). `"alpha"` can also be used as a shortcut for `"(Intercept)"`. If the model has varying intercepts and/or slopes they can be selected using `pars = "varying"`. In addition, for `stanmvreg` objects there are some additional shortcuts available. Using `pars = "long"` will display the parameter estimates for the longitudinal submodels only (excluding group-specific pparameters, but including auxiliary parameters). Using `pars = "event"` will display the parameter estimates for the event submodel only, including any association parameters. Using `pars = "assoc"` will display only the association parameters. Using `pars = "fixef"` will display all fixed effects, but not the random effects or the auxiliary parameters. `pars` and `regex_pars` are set to `NULL` then all fixed effect regression coefficients are selected, as well as any auxiliary parameters and the log posterior. If `pars` is `NULL` all parameters are selected for a `stanreg` object, while for a `stanmvreg` object all fixed effect regression coefficients are selected as well as any auxiliary parameters and the log posterior. See **Examples**.
`regex_pars`	An optional character vector of regular expressions to use for parameter selection. `regex_pars` can be used in place of `pars` or in addition to `pars`. Currently, all functions that accept a `regex_pars` argument ignore it for models fit using optimization.

prob — A number $p \in (0, 1)$ indicating the desired posterior probability mass to include in the (central posterior) interval estimates displayed in the plot. The default is 0.9.

color_by — How should the estimates be colored? Use "parameter" to color by parameter name, "vs" to color the prior one color and the posterior another, and "none" to use no color. Except when color_by="none", a variable is mapped to the color aesthetic and it is therefore also possible to change the default colors by adding one of the various discrete color scales available in ggplot2 (scale_color_manual, scale_colour_brewer, etc.). See Examples.

group_by_parameter — Should estimates be grouped together by parameter (TRUE) or by posterior and prior (FALSE, the default)?

facet_args — A named list of arguments passed to facet_wrap (other than the facets argument), e.g., nrow or ncol to change the layout, scales to allow axis scales to vary across facets, etc. See Examples.

Value

A ggplot object that can be further customized using the **ggplot2** package.

References

Gabry, J. , Simpson, D. , Vehtari, A. , Betancourt, M. and Gelman, A. (2019), Visualization in Bayesian workflow. *J. R. Stat. Soc. A*, 182: 389-402. doi:10.1111/rssa.12378, arXiv preprint, code on GitHub)

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
## Not run:
if (!exists("example_model")) example(example_model)
# display non-varying (i.e. not group-level) coefficients
posterior_vs_prior(example_model, pars = "beta")

# show group-level (varying) parameters and group by parameter
posterior_vs_prior(example_model, pars = "varying",
                   group_by_parameter = TRUE, color_by = "vs")

# group by parameter and allow axis scales to vary across facets
posterior_vs_prior(example_model, regex_pars = "period",
                   group_by_parameter = TRUE, color_by = "none",
                   facet_args = list(scales = "free"))

# assign to object and customize with functions from ggplot2
(gg <- posterior_vs_prior(example_model, pars = c("beta", "varying"), prob = 0.8))

gg +
 ggplot2::geom_hline(yintercept = 0, size = 0.3, linetype = 3) +
 ggplot2::coord_flip() +
 ggplot2::ggtitle("Comparing the prior and posterior")
```

```
# compare very wide and very narrow priors using roaches example
# (see help(roaches, "rstanarm") for info on the dataset)
roaches$roach100 <- roaches$roach1 / 100
wide_prior <- normal(0, 10)
narrow_prior <- normal(0, 0.1)
fit_pois_wide_prior <- stan_glm(y ~ treatment + roach100 + senior,
                                offset = log(exposure2),
                                family = "poisson", data = roaches,
                                prior = wide_prior)
posterior_vs_prior(fit_pois_wide_prior, pars = "beta", prob = 0.5,
                   group_by_parameter = TRUE, color_by = "vs",
                   facet_args = list(scales = "free"))

fit_pois_narrow_prior <- update(fit_pois_wide_prior, prior = narrow_prior)
posterior_vs_prior(fit_pois_narrow_prior, pars = "beta", prob = 0.5,
                   group_by_parameter = TRUE, color_by = "vs",
                   facet_args = list(scales = "free"))


# look at cutpoints for ordinal model
fit_polr <- stan_polr(tobgp ~ agegp, data = esoph, method = "probit",
                      prior = R2(0.2, "mean"), init_r = 0.1)
(gg_polr <- posterior_vs_prior(fit_polr, regex_pars = "\\|", color_by = "vs",
                               group_by_parameter = TRUE))
# flip the x and y axes
gg_polr + ggplot2::coord_flip()

## End(Not run)
}
```

`pp_check.stanreg` *Graphical posterior predictive checks*

Description

Interface to the PPC (posterior predictive checking) module in the **bayesplot** package, providing various plots comparing the observed outcome variable y to simulated datasets y^{rep} from the posterior predictive distribution. The pp_check method for stanreg-objects prepares the arguments required for the specified **bayesplot** PPC plotting function and then calls that function. It is also straightforward to use the functions from the **bayesplot** package directly rather than via the pp_check method. Examples of both are given below.

Usage

```
## S3 method for class 'stanreg'
pp_check(object, plotfun = "dens_overlay", nreps = NULL, seed = NULL, ...)
```

Arguments

object	A fitted model object returned by one of the **rstanarm** modeling functions. See stanreg-objects.
plotfun	A character string naming the **bayesplot** PPC function to use. The default is to call ppc_dens_overlay. plotfun can be specified either as the full name of a **bayesplot** plotting function (e.g. "ppc_hist") or can be abbreviated to the part of the name following the "ppc_" prefix (e.g. "hist"). To get the names of all available PPC functions see available_ppc.
nreps	The number of y^{rep} datasets to generate from the posterior predictive distribution and show in the plots. The default depends on plotfun. For functions that plot each yrep dataset separately (e.g. ppc_hist), nreps defaults to a small value to make the plots readable. For functions that overlay many yrep datasets (e.g., ppc_dens_overlay) a larger number is used by default, and for other functions (e.g. ppc_stat) the default is to set nreps equal to the posterior sample size.
seed	An optional seed to pass to posterior_predict.
...	Additonal arguments passed to the **bayesplot** function called. For many plotting functions ... is optional, however for functions that require a group or x argument, these arguments should be specified in .... If specifying group and/or x, they can be provided as either strings naming variables (in which case they are searched for in the model frame) or as vectors containing the actual values of the variables. See the **Examples** section, below.

Value

pp_check returns a ggplot object that can be further customized using the **ggplot2** package.

Note

For binomial data, plots of y and y^{rep} show the proportion of 'successes' rather than the raw count. Also for binomial models see ppc_error_binned for binned residual plots.

References

Gelman, A., Carlin, J. B., Stern, H. S., Dunson, D. B., Vehtari, A., and Rubin, D. B. (2013). *Bayesian Data Analysis.* Chapman & Hall/CRC Press, London, third edition. (Ch. 6)

Gabry, J. , Simpson, D. , Vehtari, A. , Betancourt, M. and Gelman, A. (2019), Visualization in Bayesian workflow. *J. R. Stat. Soc. A*, 182: 389-402. doi:10.1111/rssa.12378, arXiv preprint, code on GitHub)

See Also

- The vignettes in the **bayesplot** package for many examples. Examples of posterior predictive checks can also be found in the **rstanarm** vignettes and demos.
- PPC-overview (**bayesplot**) for links to the documentation for all the available plotting functions.
- posterior_predict for drawing from the posterior predictive distribution.
- color_scheme_set to change the color scheme of the plots.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
fit <- stan_glmer(
  mpg ~ wt + am + (1|cyl),
  data = mtcars,
  iter = 400, # iter and chains small just to keep example quick
  chains = 2,
  refresh = 0
)

# Compare distribution of y to distributions of multiple yrep datasets
pp_check(fit)
pp_check(fit, plotfun = "boxplot", nreps = 10, notch = FALSE)
pp_check(fit, plotfun = "hist", nreps = 3)


# Same plot (up to RNG noise) using bayesplot package directly
bayesplot::ppc_hist(y = mtcars$mpg, yrep = posterior_predict(fit, draws = 3))

# Check histograms of test statistics by level of grouping variable 'cyl'
pp_check(fit, plotfun = "stat_grouped", stat = "median", group = "cyl")

# Defining a custom test statistic
q25 <- function(y) quantile(y, probs = 0.25)
pp_check(fit, plotfun = "stat_grouped", stat = "q25", group = "cyl")

# Scatterplot of two test statistics
pp_check(fit, plotfun = "stat_2d", stat = c("mean", "sd"))

# Scatterplot of y vs. average yrep
pp_check(fit, plotfun = "scatter_avg") # y vs. average yrep
# Same plot (up to RNG noise) using bayesplot package directly
bayesplot::ppc_scatter_avg(y = mtcars$mpg, yrep = posterior_predict(fit))

# Scatterplots of y vs. several individual yrep datasets
pp_check(fit, plotfun = "scatter", nreps = 3)

# Same plot (up to RNG noise) using bayesplot package directly
bayesplot::ppc_scatter(y = mtcars$mpg, yrep = posterior_predict(fit, draws = 3))

# yrep intervals with y points overlaid
# by default 1:length(y) used on x-axis but can also specify an x variable
pp_check(fit, plotfun = "intervals")
pp_check(fit, plotfun = "intervals", x = "wt") + ggplot2::xlab("wt")

# Same plot (up to RNG noise) using bayesplot package directly
bayesplot::ppc_intervals(y = mtcars$mpg, yrep = posterior_predict(fit),
                         x = mtcars$wt) + ggplot2::xlab("wt")

# predictive errors
pp_check(fit, plotfun = "error_hist", nreps = 6)
pp_check(fit, plotfun = "error_scatter_avg_vs_x", x = "wt") +
```

```
  ggplot2::xlab("wt")

# Example of a PPC for ordinal models (stan_polr)
fit2 <- stan_polr(tobgp ~ agegp, data = esoph, method = "probit",
                  prior = R2(0.2, "mean"), init_r = 0.1,
                  refresh = 0)
pp_check(fit2, plotfun = "bars", nreps = 500, prob = 0.5)
pp_check(fit2, plotfun = "bars_grouped", group = esoph$agegp,
         nreps = 500, prob = 0.5)

}
```

`pp_validate` *Model validation via simulation*

Description

The `pp_validate` function is based on the methods described in Cook, Gelman, and Rubin (2006) for validating software developed to fit particular Bayesian models. Here we take the perspective that models themselves are software and thus it is useful to apply this validation approach to individual models.

Usage

```
pp_validate(object, nreps = 20, seed = 12345, ...)
```

Arguments

`object`	A fitted model object returned by one of the **rstanarm** modeling functions. See `stanreg-objects`.
`nreps`	The number of replications to be performed. `nreps` must be sufficiently large so that the statistics described below in Details are meaningful. Depending on the model and the size of the data, running `pp_validate` may be slow. See also the Note section below for advice on avoiding numerical issues.
`seed`	A seed passed to Stan to use when refitting the model.
`...`	Currently ignored.

Details

We repeat `nreps` times the process of simulating parameters and data from the model and refitting the model to this simulated data. For each of the `nreps` replications we do the following:

1. Refit the model but *without* conditioning on the data (setting `prior_PD=TRUE`), obtaining draws θ^{true} from the *prior* distribution of the model parameters.
2. Given θ^{true}, simulate data y^* from the *prior* predictive distribution (calling `posterior_predict` on the fitted model object obtained in step 1).
3. Fit the model to the simulated outcome y^*, obtaining parameters θ^{post}.

For any individual parameter, the quantile of the "true" parameter value with respect to its posterior distribution *should* be uniformly distributed. The validation procedure entails looking for deviations from uniformity by computing statistics for a test that the quantiles are uniformly distributed. The absolute values of the computed test statistics are plotted for batches of parameters (e.g., non-varying coefficients are grouped into a batch called "beta", parameters that vary by group level are in batches named for the grouping variable, etc.). See Cook, Gelman, and Rubin (2006) for more details on the validation procedure.

Value

A ggplot object that can be further customized using the **ggplot2** package.

Note

In order to make it through `nreps` replications without running into numerical difficulties you may have to restrict the range for randomly generating initial values for parameters when you fit the *original* model. With any of **rstanarm**'s modeling functions this can be done by specifying the optional argument `init_r` as some number less than the default of 2.

References

Cook, S., Gelman, A., and Rubin, D. (2006). Validation of software for Bayesian models using posterior quantiles. *Journal of Computational and Graphical Statistics*. 15(3), 675–692.

See Also

`pp_check` for graphical posterior predictive checks and `posterior_predict` to draw from the posterior predictive distribution.

`color_scheme_set` to change the color scheme of the plot.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
## Not run:
if (!exists("example_model")) example(example_model)
try(pp_validate(example_model)) # fails with default seed / priors

## End(Not run)
}
```

---

predict.stanreg *Predict method for stanreg objects*

Description

This method is primarily intended to be used only for models fit using optimization. For models fit using MCMC or one of the variational approximations, see `posterior_predict`.

Usage

```
## S3 method for class 'stanreg'
predict(
  object,
  ...,
  newdata = NULL,
  type = c("link", "response"),
  se.fit = FALSE
)
```

Arguments

object	A fitted model object returned by one of the **rstanarm** modeling functions. See stanreg-objects.
...	Ignored.
newdata	Optionally, a data frame in which to look for variables with which to predict. If omitted, the model matrix is used.
type	The type of prediction. The default 'link' is on the scale of the linear predictors; the alternative 'response' is on the scale of the response variable.
se.fit	A logical scalar indicating if standard errors should be returned. The default is FALSE.

Value

A vector if se.fit is FALSE and a list if se.fit is TRUE.

See Also

posterior_predict

---

predictive_error.stanreg

In-sample or out-of-sample predictive errors

Description

This is a convenience function for computing $y - y^{rep}$ (in-sample, for observed y) or $y - \tilde{y}$ (out-of-sample, for new or held-out y). The method for stanreg objects calls posterior_predict internally, whereas the method for matrices accepts the matrix returned by posterior_predict as input and can be used to avoid multiple calls to posterior_predict.

Usage

```
## S3 method for class 'stanreg'
predictive_error(
  object,
  newdata = NULL,
  draws = NULL,
  re.form = NULL,
  seed = NULL,
  offset = NULL,
  ...
)

## S3 method for class 'matrix'
predictive_error(object, y, ...)

## S3 method for class 'ppd'
predictive_error(object, y, ...)
```

Arguments

`object`	Either a fitted model object returned by one of the **rstanarm** modeling functions (a stanreg object) or, for the matrix method, a matrix of draws from the posterior predictive distribution returned by `posterior_predict`.
`newdata, draws, seed, offset, re.form`	Optional arguments passed to `posterior_predict`. For binomial models, please see the **Note** section below if `newdata` will be specified.
`...`	Currently ignored.
`y`	For the matrix method only, a vector of y values the same length as the number of columns in the matrix used as `object`. The method for stanreg objects takes `y` directly from the fitted model object.

Value

A `draws` by `nrow(newdata)` matrix. If `newdata` is not specified then it will be `draws` by `nobs(object)`.

Note

The **Note** section in `posterior_predict` about `newdata` for binomial models also applies for `predictive_error`, with one important difference. For `posterior_predict` if the left-hand side of the model formula is `cbind(successes, failures)` then the particular values of `successes` and `failures` in `newdata` don't matter, only that they add to the desired number of trials. **This is not the case for** `predictive_error`. For `predictive_error` the particular value of `successes` matters because it is used as y when computing the error.

See Also

`posterior_predict` to draw from the posterior predictive distribution without computing predictive errors.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
if (!exists("example_model")) example(example_model)
err1 <- predictive_error(example_model, draws = 50)
hist(err1)

# Using newdata with a binomial model
formula(example_model)
nd <- data.frame(
 size = c(10, 20),
 incidence = c(5, 10),
 period = factor(c(1,2)),
 herd = c(1, 15)
)
err2 <- predictive_error(example_model, newdata = nd, draws = 10, seed = 1234)

# stanreg vs matrix methods
fit <- stan_glm(mpg ~ wt, data = mtcars, iter = 300)
preds <- posterior_predict(fit, seed = 123)
all.equal(
  predictive_error(fit, seed = 123),
  predictive_error(preds, y = fit$y)
)
}
```

---

predictive_interval.stanreg

Predictive intervals

Description

For models fit using MCMC (`algorithm="sampling"`) or one of the variational approximations (`"meanfield"` or `"fullrank"`), the `predictive_interval` function computes Bayesian predictive intervals. The method for stanreg objects calls `posterior_predict` internally, whereas the method for matrices accepts the matrix returned by `posterior_predict` as input and can be used to avoid multiple calls to `posterior_predict`.

Usage

```
## S3 method for class 'stanreg'
predictive_interval(
  object,
  prob = 0.9,
  newdata = NULL,
  draws = NULL,
  re.form = NULL,
  fun = NULL,
  seed = NULL,
```

```
  offset = NULL,
  ...
)

## S3 method for class 'matrix'
predictive_interval(object, prob = 0.9, ...)

## S3 method for class 'ppd'
predictive_interval(object, prob = 0.9, ...)
```

Arguments

`object`	Either a fitted model object returned by one of the **rstanarm** modeling functions (a stanreg object) or, for the matrix method, a matrix of draws from the posterior predictive distribution returned by `posterior_predict`.
`prob`	A number $p \in (0, 1)$ indicating the desired probability mass to include in the intervals. The default is to report 90% intervals (`prob=0.9`) rather than the traditionally used 95% (see Details).
`newdata, draws, fun, offset, re.form, seed`	Passed to `posterior_predict`.
`...`	Currently ignored.

Value

A matrix with two columns and as many rows as are in `newdata`. If `newdata` is not provided then the matrix will have as many rows as the data used to fit the model. For a given value of `prob`, p, the columns correspond to the lower and upper $100p\%$ central interval limits and have the names $100\alpha/2\%$ and $100(1 - \alpha/2)\%$, where $\alpha = 1 - p$. For example, if `prob=0.9` is specified (a 90% interval), then the column names will be `"5%"` and `"95%"`, respectively.

See Also

`predictive_error`, `posterior_predict`, `posterior_interval`

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
fit <- stan_glm(mpg ~ wt, data = mtcars, iter = 300)
predictive_interval(fit)
predictive_interval(fit, newdata = data.frame(wt = range(mtcars$wt)),
                    prob = 0.5)

# stanreg vs matrix methods
preds <- posterior_predict(fit, seed = 123)
all.equal(
  predictive_interval(fit, seed = 123),
  predictive_interval(preds)
)
}
```

print.stanreg *Print method for stanreg objects*

Description

The print method for stanreg objects displays a compact summary of the fitted model. See the **Details** section below for descriptions of the different components of the printed output. For additional summary statistics and diagnostics use the summary method.

Usage

```
## S3 method for class 'stanreg'
print(x, digits = 1, detail = TRUE, ...)

## S3 method for class 'stanmvreg'
print(x, digits = 3, ...)
```

Arguments

x	A fitted model object returned by one of the **rstanarm** modeling functions. See stanreg-objects.
digits	Number of digits to use for formatting numbers.
detail	Logical, defaulting to TRUE. If FALSE a more minimal summary is printed consisting only of the parameter estimates.
...	Ignored.

Details

Point estimates: Regardless of the estimation algorithm, point estimates are medians computed from simulations. For models fit using MCMC ("sampling") the posterior sample is used. For optimization ("optimizing"), the simulations are generated from the asymptotic Gaussian sampling distribution of the parameters. For the "meanfield" and "fullrank" variational approximations, draws from the variational approximation to the posterior are used. In all cases, the point estimates reported are the same as the values returned by coef.

Uncertainty estimates (MAD_SD): The standard deviations reported (labeled MAD_SD in the print output) are computed from the same set of draws described above and are proportional to the median absolute deviation (mad) from the median. Compared to the raw posterior standard deviation, the MAD_SD will be more robust for long-tailed distributions. These are the same as the values returned by se.

Additional output:

- For GLMs with group-specific terms (see stan_glmer) the printed output also shows point estimates of the standard deviations of the group effects (and correlations if there are both intercept and slopes that vary by group).

- For analysis of variance models (see stan_aov) models, an ANOVA-like table is also displayed.
- For joint longitudinal and time-to-event (see stan_jm) models the estimates are presented separately for each of the distinct submodels.

Value

Returns x, invisibly.

See Also

summary.stanreg, stanreg-methods

---

prior_summary.stanreg *Summarize the priors used for an rstanarm model*

Description

The prior_summary method provides a summary of the prior distributions used for the parameters in a given model. In some cases the user-specified prior does not correspond exactly to the prior used internally by **rstanarm** (see the sections below). Especially in these cases, but also in general, it can be much more useful to visualize the priors. Visualizing the priors can be done using the posterior_vs_prior function, or alternatively by fitting the model with the prior_PD argument set to TRUE (to draw from the prior predictive distribution instead of conditioning on the outcome) and then plotting the parameters.

Usage

```
## S3 method for class 'stanreg'
prior_summary(object, digits = 2, ...)
```

Arguments

object	A fitted model object returned by one of the **rstanarm** modeling functions. See stanreg-objects.
digits	Number of digits to use for rounding.
...	Currently ignored by the method for stanreg objects.

Value

A list of class "prior_summary.stanreg", which has its own print method.

Intercept (after predictors centered)

For **rstanarm** modeling functions that accept a `prior_intercept` argument, the specified prior for the intercept term applies to the intercept after **rstanarm** internally centers the predictors so they each have mean zero. The estimate of the intercept returned to the user correspond to the intercept with the predictors as specified by the user (unmodified by **rstanarm**), but when *specifying* the prior the intercept can be thought of as the expected outcome when the predictors are set to their means. The only exception to this is for models fit with the `sparse` argument set to `TRUE` (which is only possible with a subset of the modeling functions and never the default).

Adjusted scales

For some models you may see "`adjusted scale`" in the printed output and adjusted scales included in the object returned by `prior_summary`. These adjusted scale values are the prior scales actually used by **rstanarm** and are computed by adjusting the prior scales specified by the user to account for the scales of the predictors (as described in the documentation for the `autoscale` argument). To disable internal prior scale adjustments set the `autoscale` argument to `FALSE` when setting a prior using one of the distributions that accepts an `autoscale` argument. For example, `normal(0, 5, autoscale=FALSE)` instead of just `normal(0, 5)`.

Coefficients in Q-space

For the models fit with an **rstanarm** modeling function that supports the `QR` argument (see e.g, `stan_glm`), if `QR` is set to `TRUE` then the prior distributions for the regression coefficients specified using the `prior` argument are not relative to the original predictor variables X but rather to the variables in the matrix Q obtained from the QR decomposition of X.

In particular, if `prior = normal(location,scale)`, then this prior on the coefficients in Q-space can be easily translated into a joint multivariate normal (MVN) prior on the coefficients on the original predictors in X. Letting θ denote the coefficients on Q and β the coefficients on X then if $\theta \sim N(\mu, \sigma)$ the corresponding prior on β is $\beta \sim MVN(R\mu, R'R\sigma^2)$, where μ and σ are vectors of the appropriate length. Technically, **rstanarm** uses a scaled QR decomposition to ensure that the columns of the predictor matrix used to fit the model all have unit scale, when the `autoscale` argument to the function passed to the `prior` argument is `TRUE` (the default), in which case the matrices actually used are $Q^* = Q\sqrt{n-1}$ and $R^* = \frac{1}{\sqrt{n-1}}R$. If `autoscale = FALSE` we instead scale such that the lower-right element of R^* is 1, which is useful if you want to specify a prior on the coefficient of the last predictor in its original units (see the documentation for the `QR` argument).

If you are interested in the prior on β implied by the prior on θ, we strongly recommend visualizing it as described above in the **Description** section, which is simpler than working it out analytically.

See Also

The priors help page and the *Prior Distributions* vignette.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
if (!exists("example_model")) example(example_model)
prior_summary(example_model)
```

```
priors <- prior_summary(example_model)
names(priors)
priors$prior$scale
priors$prior$adjusted_scale

# for a glm with adjusted scales (see Details, above), compare
# the default (rstanarm adjusting the scales) to setting
# autoscale=FALSE for prior on coefficients
fit <- stan_glm(mpg ~ wt + am, data = mtcars,
                prior = normal(0, c(2.5, 4)),
                prior_intercept = normal(0, 5),
                iter = 10, chains = 1) # only for demonstration
prior_summary(fit)

fit2 <- update(fit, prior = normal(0, c(2.5, 4), autoscale=FALSE),
               prior_intercept = normal(0, 5, autoscale=FALSE))
prior_summary(fit2)
}
```

`priors` *Prior distributions and options*

Description

The functions described on this page are used to specify the prior-related arguments of the various modeling functions in the **rstanarm** package (to view the priors used for an existing model see `prior_summary`).

The default priors used in the various **rstanarm** modeling functions are intended to be *weakly informative* in that they provide moderate regularization and help stabilize computation. For many applications the defaults will perform well, but prudent use of more informative priors is encouraged. Uniform prior distributions are possible (e.g. by setting `stan_glm`'s `prior` argument to `NULL`) but, unless the data is very strong, they are not recommended and are *not* non-informative, giving the same probability mass to implausible values as plausible ones.

More information on priors is available in the vignette *Prior Distributions for rstanarm Models* as well as the vignettes for the various modeling functions. For details on the priors used for multilevel models in particular see the vignette *Estimating Generalized (Non-)Linear Models with Group-Specific Terms with rstanarm* and also the **Covariance matrices** section lower down on this page.

Usage

```
normal(location = 0, scale = NULL, autoscale = FALSE)

student_t(df = 1, location = 0, scale = NULL, autoscale = FALSE)

cauchy(location = 0, scale = NULL, autoscale = FALSE)

hs(df = 1, global_df = 1, global_scale = 0.01, slab_df = 4, slab_scale = 2.5)
```

```
hs_plus(
  df1 = 1,
  df2 = 1,
  global_df = 1,
  global_scale = 0.01,
  slab_df = 4,
  slab_scale = 2.5
)

laplace(location = 0, scale = NULL, autoscale = FALSE)

lasso(df = 1, location = 0, scale = NULL, autoscale = FALSE)

product_normal(df = 2, location = 0, scale = 1)

exponential(rate = 1, autoscale = FALSE)

decov(regularization = 1, concentration = 1, shape = 1, scale = 1)

lkj(regularization = 1, scale = 10, df = 1, autoscale = TRUE)

dirichlet(concentration = 1)

R2(location = NULL, what = c("mode", "mean", "median", "log"))

default_prior_intercept(family)

default_prior_coef(family)
```

Arguments

location	Prior location. In most cases, this is the prior mean, but for cauchy (which is equivalent to student_t with df=1), the mean does not exist and location is the prior median. The default value is 0, except for R2 which has no default value for location. For R2, location pertains to the prior location of the R^2 under a Beta distribution, but the interpretation of the location parameter depends on the specified value of the what argument (see the *R2 family* section in **Details**).
scale	Prior scale. The default depends on the family (see **Details**).
autoscale	If TRUE then the scales of the priors on the intercept and regression coefficients may be additionally modified internally by **rstanarm** in the following cases. First, for Gaussian models only, the prior scales for the intercept, coefficients, and the auxiliary parameter sigma (error standard deviation) are multiplied by sd(y). Additionally — not only for Gaussian models — if the QR argument to the model fitting function (e.g. stan_glm) is FALSE then we also divide the prior scale(s) by sd(x). Prior autoscaling is also discussed in the vignette *Prior Distributions for rstanarm Models*
df, df1, df2	Prior degrees of freedom. The default is 1 for student_t, in which case it is

equivalent to cauchy. For the hierarchical shrinkage priors (hs and hs_plus) the degrees of freedom parameter(s) default to 1. For the product_normal prior, the degrees of freedom parameter must be an integer (vector) that is at least 2 (the default).

global_df, global_scale, slab_df, slab_scale
: Optional arguments for the hierarchical shrinkage priors. See the *Hierarchical shrinkage family* section below.

rate
: Prior rate for the exponential distribution. Defaults to 1. For the exponential distribution, the rate parameter is the *reciprocal* of the mean.

regularization
: Exponent for an LKJ prior on the correlation matrix in the decov or lkj prior. The default is 1, implying a joint uniform prior.

concentration
: Concentration parameter for a symmetric Dirichlet distribution. The default is 1, implying a joint uniform prior.

shape
: Shape parameter for a gamma prior on the scale parameter in the decov prior. If shape and scale are both 1 (the default) then the gamma prior simplifies to the unit-exponential distribution.

what
: A character string among 'mode' (the default), 'mean', 'median', or 'log' indicating how the location parameter is interpreted in the LKJ case. If 'log', then location is interpreted as the expected logarithm of the R^2 under a Beta distribution. Otherwise, location is interpreted as the what of the R^2 under a Beta distribution. If the number of predictors is less than or equal to two, the mode of this Beta distribution does not exist and an error will prompt the user to specify another choice for what.

family
: Not currently used.

Details

The details depend on the family of the prior being used:

Student t family: Family members:

- normal(location, scale)
- student_t(df, location, scale)
- cauchy(location, scale)

Each of these functions also takes an argument autoscale.

For the prior distribution for the intercept, location, scale, and df should be scalars. For the prior for the other coefficients they can either be vectors of length equal to the number of coefficients (not including the intercept), or they can be scalars, in which case they will be recycled to the appropriate length. As the degrees of freedom approaches infinity, the Student t distribution approaches the normal distribution and if the degrees of freedom are one, then the Student t distribution is the Cauchy distribution.

If scale is not specified it will default to 2.5, unless the probit link function is used, in which case these defaults are scaled by a factor of dnorm(0)/dlogis(0), which is roughly 1.6.

If the autoscale argument is TRUE, then the scales will be further adjusted as described above in the documentation of the autoscale argument in the **Arguments** section.

Hierarchical shrinkage family: Family members:

- `hs(df, global_df, global_scale, slab_df, slab_scale)`
- `hs_plus(df1, df2, global_df, global_scale, slab_df, slab_scale)`

The hierarchical shrinkage priors are normal with a mean of zero and a standard deviation that is also a random variable. The traditional hierarchical shrinkage prior utilizes a standard deviation that is distributed half Cauchy with a median of zero and a scale parameter that is also half Cauchy. This is called the "horseshoe prior". The hierarchical shrinkage (`hs`) prior in the **rstanarm** package instead utilizes a regularized horseshoe prior, as described by Piironen and Vehtari (2017), which recommends setting the `global_scale` argument equal to the ratio of the expected number of non-zero coefficients to the expected number of zero coefficients, divided by the square root of the number of observations.

The hierarhical shrinkpage plus (`hs_plus`) prior is similar except that the standard deviation that is distributed as the product of two independent half Cauchy parameters that are each scaled in a similar way to the `hs` prior.

The hierarchical shrinkage priors have very tall modes and very fat tails. Consequently, they tend to produce posterior distributions that are very concentrated near zero, unless the predictor has a strong influence on the outcome, in which case the prior has little influence. Hierarchical shrinkage priors often require you to increase the `adapt_delta` tuning parameter in order to diminish the number of divergent transitions. For more details on tuning parameters and divergent transitions see the Troubleshooting section of the *How to Use the rstanarm Package* vignette.

Laplace family: Family members:

- `laplace(location, scale)`
- `lasso(df, location, scale)`

Each of these functions also takes an argument `autoscale`.

The Laplace distribution is also known as the double-exponential distribution. It is a symmetric distribution with a sharp peak at its mean / median / mode and fairly long tails. This distribution can be motivated as a scale mixture of normal distributions and the remarks above about the normal distribution apply here as well.

The lasso approach to supervised learning can be expressed as finding the posterior mode when the likelihood is Gaussian and the priors on the coefficients have independent Laplace distributions. It is commonplace in supervised learning to choose the tuning parameter by cross-validation, whereas a more Bayesian approach would be to place a prior on "it", or rather its reciprocal in our case (i.e. *smaller* values correspond to more shrinkage toward the prior location vector). We use a chi-square prior with degrees of freedom equal to that specified in the call to `lasso` or, by default, 1. The expectation of a chi-square random variable is equal to this degrees of freedom and the mode is equal to the degrees of freedom minus 2, if this difference is positive.

It is also common in supervised learning to standardize the predictors before training the model. We do not recommend doing so. Instead, it is better to specify `autoscale = TRUE`, which will adjust the scales of the priors according to the dispersion in the variables. See the documentation of the `autoscale` argument above and also the `prior_summary` page for more information.

Product-normal family: Family members:

- `product_normal(df, location, scale)`

The product-normal distribution is the product of at least two independent normal variates each with mean zero, shifted by the `location` parameter. It can be shown that the density of a product-normal variate is symmetric and infinite at `location`, so this prior resembles a "spike-and-slab"

prior for sufficiently large values of the scale parameter. For better or for worse, this prior may be appropriate when it is strongly believed (by someone) that a regression coefficient "is" equal to the location, parameter even though no true Bayesian would specify such a prior.

Each element of df must be an integer of at least 2 because these "degrees of freedom" are interpreted as the number of normal variates being multiplied and then shifted by location to yield the regression coefficient. Higher degrees of freedom produce a sharper spike at location.

Each element of scale must be a non-negative real number that is interpreted as the standard deviation of the normal variates being multiplied and then shifted by location to yield the regression coefficient. In other words, the elements of scale may differ, but the k-th standard deviation is presumed to hold for all the normal deviates that are multiplied together and shifted by the k-th element of location to yield the k-th regression coefficient. The elements of scale are not the prior standard deviations of the regression coefficients. The prior variance of the regression coefficients is equal to the scale raised to the power of 2 times the corresponding element of df. Thus, larger values of scale put more prior volume on values of the regression coefficient that are far from zero.

Dirichlet family: Family members:

- dirichlet(concentration)

The Dirichlet distribution is a multivariate generalization of the beta distribution. It is perhaps the easiest prior distribution to specify because the concentration parameters can be interpreted as prior counts (although they need not be integers) of a multinomial random variable.

The Dirichlet distribution is used in stan_polr for an implicit prior on the cutpoints in an ordinal regression model. More specifically, the Dirichlet prior pertains to the prior probability of observing each category of the ordinal outcome when the predictors are at their sample means. Given these prior probabilities, it is straightforward to add them to form cumulative probabilities and then use an inverse CDF transformation of the cumulative probabilities to define the cutpoints.

If a scalar is passed to the concentration argument of the dirichlet function, then it is replicated to the appropriate length and the Dirichlet distribution is symmetric. If concentration is a vector and all elements are 1, then the Dirichlet distribution is jointly uniform. If all concentration parameters are equal but greater than 1 then the prior mode is that the categories are equiprobable, and the larger the value of the identical concentration parameters, the more sharply peaked the distribution is at the mode. The elements in concentration can also be given different values to represent that not all outcome categories are a priori equiprobable.

Covariance matrices: Family members:

- decov(regularization, concentration, shape, scale)
- lkj(regularization, scale, df)

(Also see vignette for stan_glmer, *Estimating Generalized (Non-)Linear Models with Group-Specific Terms with rstanarm*)

Covariance matrices are decomposed into correlation matrices and variances. The variances are in turn decomposed into the product of a simplex vector and the trace of the matrix. Finally, the trace is the product of the order of the matrix and the square of a scale parameter. This prior on a covariance matrix is represented by the decov function.

The prior for a correlation matrix is called LKJ whose density is proportional to the determinant of the correlation matrix raised to the power of a positive regularization parameter minus one. If regularization = 1 (the default), then this prior is jointly uniform over all correlation matrices

of that size. If `regularization > 1`, then the identity matrix is the mode and in the unlikely case that `regularization < 1`, the identity matrix is the trough.

The trace of a covariance matrix is equal to the sum of the variances. We set the trace equal to the product of the order of the covariance matrix and the *square* of a positive scale parameter. The particular variances are set equal to the product of a simplex vector — which is non-negative and sums to 1 — and the scalar trace. In other words, each element of the simplex vector represents the proportion of the trace attributable to the corresponding variable.

A symmetric Dirichlet prior is used for the simplex vector, which has a single (positive) `concentration` parameter, which defaults to 1 and implies that the prior is jointly uniform over the space of simplex vectors of that size. If `concentration > 1`, then the prior mode corresponds to all variables having the same (proportion of total) variance, which can be used to ensure the the posterior variances are not zero. As the `concentration` parameter approaches infinity, this mode becomes more pronounced. In the unlikely case that `concentration < 1`, the variances are more polarized.

If all the variables were multiplied by a number, the trace of their covariance matrix would increase by that number squared. Thus, it is reasonable to use a scale-invariant prior distribution for the positive scale parameter, and in this case we utilize a Gamma distribution, whose `shape` and `scale` are both 1 by default, implying a unit-exponential distribution. Set the `shape` hyperparameter to some value greater than 1 to ensure that the posterior trace is not zero.

If `regularization`, `concentration`, `shape` and / or `scale` are positive scalars, then they are recycled to the appropriate length. Otherwise, each can be a positive vector of the appropriate length, but the appropriate length depends on the number of covariance matrices in the model and their sizes. A one-by-one covariance matrix is just a variance and thus does not have `regularization` or `concentration` parameters, but does have `shape` and `scale` parameters for the prior standard deviation of that variable.

Note that for `stan_mvmer` and `stan_jm` models an additional prior distribution is provided through the `lkj` function. This prior is in fact currently used as the default for those modelling functions (although `decov` is still available as an option if the user wishes to specify it through the `prior_covariance` argument). The `lkj` prior uses the same decomposition of the covariance matrices into correlation matrices and variances, however, the variances are not further decomposed into a simplex vector and the trace; instead the standard deviations (square root of the variances) for each of the group specific parameters are given a half Student t distribution with the scale and df parameters specified through the `scale` and `df` arguments to the `lkj` function. The scale parameter default is 10 which is then autoscaled, whilst the df parameter default is 1 (therefore equivalent to a half Cauchy prior distribution for the standard deviation of each group specific parameter). This prior generally leads to similar results as the `decov` prior, but it is also likely to be **less** diffuse compared with the `decov` prior; therefore it sometimes seems to lead to faster estimation times, hence why it has been chosen as the default prior for `stan_mvmer` and `stan_jm` where estimation times can be long.

R2 family: Family members:

- `R2(location, what)`

The `stan_lm`, `stan_aov`, and `stan_polr` functions allow the user to utilize a function called `R2` to convey prior information about all the parameters. This prior hinges on prior beliefs about the location of R^2, the proportion of variance in the outcome attributable to the predictors, which has a `Beta` prior with first shape hyperparameter equal to half the number of predictors and second shape hyperparameter free. By specifying `what` to be the prior mode (the default), mean, median, or expected log of R^2, the second shape parameter for this Beta distribution is determined internally.

If `what = 'log'`, location should be a negative scalar; otherwise it should be a scalar on the $(0, 1)$ interval.

For example, if $R^2 = 0.5$, then the mode, mean, and median of the `Beta` distribution are all the same and thus the second shape parameter is also equal to half the number of predictors. The second shape parameter of the `Beta` distribution is actually the same as the shape parameter in the LKJ prior for a correlation matrix described in the previous subsection. Thus, the smaller is R^2, the larger is the shape parameter, the smaller are the prior correlations among the outcome and predictor variables, and the more concentrated near zero is the prior density for the regression coefficients. Hence, the prior on the coefficients is regularizing and should yield a posterior distribution with good out-of-sample predictions *if* the prior location of R^2 is specified in a reasonable fashion.

Value

A named list to be used internally by the **rstanarm** model fitting functions.

References

Gelman, A., Carlin, J. B., Stern, H. S., Dunson, D. B., Vehtari, A., and Rubin, D. B. (2013). *Bayesian Data Analysis.* Chapman & Hall/CRC Press, London, third edition. https://stat.columbia.edu/~gelman/book/

Gelman, A., Jakulin, A., Pittau, M. G., and Su, Y. (2008). A weakly informative default prior distribution for logistic and other regression models. *Annals of Applied Statistics*. 2(4), 1360–1383.

Piironen, J., and Vehtari, A. (2017). Sparsity information and regularization in the horseshoe and other shrinkage priors. https://arxiv.org/abs/1707.01694

Stan Development Team. *Stan Modeling Language Users Guide and Reference Manual.* https://mc-stan.org/users/documentation/.

See Also

The various vignettes for the **rstanarm** package also discuss and demonstrate the use of some of the supported prior distributions.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
fmla <- mpg ~ wt + qsec + drat + am

# Draw from prior predictive distribution (by setting prior_PD = TRUE)
prior_pred_fit <- stan_glm(fmla, data = mtcars, prior_PD = TRUE,
                           chains = 1, seed = 12345, iter = 250, # for speed only
                           prior = student_t(df = 4, 0, 2.5),
                           prior_intercept = cauchy(0,10),
                           prior_aux = exponential(1/2))
plot(prior_pred_fit, "hist")


# Can assign priors to names
N05 <- normal(0, 5)
```

```
fit <- stan_glm(fmla, data = mtcars, prior = N05, prior_intercept = N05)


# Visually compare normal, student_t, cauchy, laplace, and product_normal
compare_priors <- function(scale = 1, df_t = 2, xlim = c(-10, 10)) {
  dt_loc_scale <- function(x, df, location, scale) {
    1/scale * dt((x - location)/scale, df)
  }
  dlaplace <- function(x, location, scale) {
    0.5 / scale * exp(-abs(x - location) / scale)
  }
  dproduct_normal <- function(x, scale) {
    besselK(abs(x) / scale ^ 2, nu = 0) / (scale ^ 2 * pi)
  }
  stat_dist <- function(dist, ...) {
    ggplot2::stat_function(ggplot2::aes_(color = dist), ...)
  }
  ggplot2::ggplot(data.frame(x = xlim), ggplot2::aes(x)) +
    stat_dist("normal", size = .75, fun = dnorm,
              args = list(mean = 0, sd = scale)) +
    stat_dist("student_t", size = .75, fun = dt_loc_scale,
              args = list(df = df_t, location = 0, scale = scale)) +
    stat_dist("cauchy", size = .75, linetype = 2, fun = dcauchy,
              args = list(location = 0, scale = scale)) +
    stat_dist("laplace", size = .75, linetype = 2, fun = dlaplace,
              args = list(location = 0, scale = scale)) +
    stat_dist("product_normal", size = .75, linetype = 2, fun = dproduct_normal,
              args = list(scale = 1))
}
# Cauchy has fattest tails, followed by student_t, laplace, and normal
compare_priors()

# The student_t with df = 1 is the same as the cauchy
compare_priors(df_t = 1)

# Even a scale of 5 is somewhat large. It gives plausibility to rather
# extreme values
compare_priors(scale = 5, xlim = c(-20,20))

# If you use a prior like normal(0, 1000) to be "non-informative" you are
# actually saying that a coefficient value of e.g. -500 is quite plausible
compare_priors(scale = 1000, xlim = c(-1000,1000))
}
```

---

ps_check *Graphical checks of the estimated survival function*

Description

This function plots the estimated marginal survival function based on draws from the posterior predictive distribution of the fitted joint model, and then overlays the Kaplan-Meier curve based on

the observed data.

Usage

```
ps_check(
  object,
  check = "survival",
  limits = c("ci", "none"),
  draws = NULL,
  seed = NULL,
  xlab = NULL,
  ylab = NULL,
  ci_geom_args = NULL,
  ...
)
```

Arguments

object	A fitted model object returned by the stan_jm modelling function. See stanreg-objects.
check	The type of plot to show. Currently only "survival" is allowed, which compares the estimated marginal survival function under the joint model to the estimated Kaplan-Meier curve based on the observed data.
limits	A quoted character string specifying the type of limits to include in the plot. Can be one of: "ci" for the Bayesian posterior uncertainty interval (often known as a credible interval); or "none" for no interval limits.
draws	An integer indicating the number of MCMC draws to use to to estimate the survival function. The default and maximum number of draws is the size of the posterior sample.
seed	An optional seed to use.
xlab, ylab	An optional axis label passed to labs.
ci_geom_args	Optional arguments passed to geom_ribbon and used to control features of the plotted interval limits. They should be supplied as a named list.
...	Optional arguments passed to geom_line and used to control features of the plotted trajectory.

Value

A ggplot object that can be further customized using the **ggplot2** package.

See Also

posterior_survfit for the estimated marginal or subject-specific survival function based on draws of the model parameters from the posterior distribution, posterior_predict for drawing from the posterior predictive distribution for the longitudinal submodel, and pp_check for graphical checks of the longitudinal submodel.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {

if (!exists("example_jm")) example(example_jm)
# Compare estimated survival function to Kaplan-Meier curve
ps <- ps_check(example_jm)
ps +
 ggplot2::scale_color_manual(values = c("red", "black")) + # change colors
 ggplot2::scale_size_manual(values = c(0.5, 3)) + # change line sizes
 ggplot2::scale_fill_manual(values = c(NA, NA)) # remove fill

}
```

QR-argument *The* QR *argument*

Description

Details about the QR argument to **rstanarm**'s modeling functions.

Details

The QR argument is a logical scalar defaulting to FALSE, but if TRUE applies a scaled qr decomposition to the design matrix, $X = Q^*R^*$. If autoscale = TRUE (the default) in the call to the function passed to the prior argument, then $Q^* = Q\sqrt{n-1}$ and $R^* = \frac{1}{\sqrt{n-1}}R$. When autoscale = FALSE, R is scaled such that the lower-right element of R^* is 1.

The coefficients relative to Q^* are obtained and then premultiplied by the inverse of R^* to obtain coefficients relative to the original predictors, X. Thus, when autoscale = FALSE, the coefficient on the last column of X is the same as the coefficient on the last column of Q^*.

These transformations do not change the likelihood of the data but are recommended for computational reasons when there are multiple predictors. Importantly, while the columns of X are almost generally correlated, the columns of Q^* are uncorrelated by design, which often makes sampling from the posterior easier. However, because when QR is TRUE the prior argument applies to the coefficients relative to Q^* (and those are not very interpretable), setting QR=TRUE is only recommended if you do not have an informative prior for the regression coefficients or if the only informative prior is on the last regression coefficient (in which case you should set autoscale = FALSE when specifying such priors).

For more details see the Stan case study *The QR Decomposition For Regression Models* at https://mc-stan.org/users/documentation/case-studies/qr_regression.html.

References

Stan Development Team. *Stan Modeling Language Users Guide and Reference Manual.* https://mc-stan.org/users/documentation/.

`rstanarm-datasets` *Datasets for rstanarm examples*

Description

Small datasets for use in **rstanarm** examples and vignettes.

Format

`bball1970` Data on hits and at-bats from the 1970 Major League Baseball season for 18 players.

Source: Efron and Morris (1975).

18 obs. of 5 variables

- `Player` Player's last name
- `Hits` Number of hits in the first 45 at-bats of the season
- `AB` Number of at-bats (45 for all players)
- `RemainingAB` Number of remaining at-bats (different for most players)
- `RemainingHits` Number of remaining hits

`bball2006` Hits and at-bats for the entire 2006 American League season of Major League Baseball.

Source: Carpenter (2009)

302 obs. of 2 variables

- `y` Number of hits
- `K` Number of at-bats

`kidiq` Data from a survey of adult American women and their children (a subsample from the National Longitudinal Survey of Youth).

Source: Gelman and Hill (2007)

434 obs. of 4 variables

- `kid_score` Child's IQ score
- `mom_hs` Indicator for whether the mother has a high school degree
- `mom_iq` Mother's IQ score
- `mom_age` Mother's age

`mortality` Surgical mortality rates in 12 hospitals performing cardiac surgery in babies.

Source: Spiegelhalter et al. (1996).

12 obs. of 2 variables

- `y` Number of deaths
- `K` Number of surgeries

`pbcLong,pbcSurv` Longitudinal biomarker and time-to-event survival data for 40 patients with primary biliary cirrhosis who participated in a randomised placebo controlled trial of D-penicillamine conducted at the Mayo Clinic between 1974 and 1984.

Source: Therneau and Grambsch (2000)

304 obs. of 8 variables (`pbcLong`) and 40 obs. of 7 variables (`pbcSurv`)

- `age` in years

- albumin serum albumin (g/dl)
- logBili logarithm of serum bilirubin
- death indicator of death at endpoint
- futimeYears time (in years) between baseline and the earliest of death, transplantion or censoring
- id numeric ID unique to each individual
- platelet platelet count
- sex gender (m = male, f = female)
- status status at endpoint (0 = censored, 1 = transplant, 2 = dead)
- trt binary treatment code (0 = placebo, 1 = D-penicillamine)
- year time (in years) of the longitudinal measurements, taken as time since baseline)

radon Data on radon levels in houses in the state of Minnesota.

Source: Gelman and Hill (2007)

919 obs. of 4 variables

- log_radon Radon measurement from the house (log scale)
- log_uranium Uranium level in the county (log scale)
- floor Indicator for radon measurement made on the first floor of the house (0 = basement, 1 = first floor)
- county County name (factor)

roaches Data on the efficacy of a pest management system at reducing the number of roaches in urban apartments.

Source: Gelman and Hill (2007)

262 obs. of 6 variables

- y Number of roaches caught
- roach1 Pretreatment number of roaches
- treatment Treatment indicator
- senior Indicator for only elderly residents in building
- exposure2 Number of days for which the roach traps were used

tumors Tarone (1982) provides a data set of tumor incidence in historical control groups of rats; specifically endometrial stromal polyps in female lab rats of type F344.

Source: Gelman and Hill (2007)

71 obs. of 2 variables

- y Number of rats with tumors
- K Number of rats

wells A survey of 3200 residents in a small area of Bangladesh suffering from arsenic contamination of groundwater. Respondents with elevated arsenic levels in their wells had been encouraged to switch their water source to a safe public or private well in the nearby area and the survey was conducted several years later to learn which of the affected residents had switched wells.

Souce: Gelman and Hill (2007)

3020 obs. of 5 variables

- switch Indicator for well-switching

- `arsenic` Arsenic level in respondent's well
- `dist` Distance (meters) from the respondent's house to the nearest well with safe drinking water.
- `assoc` Indicator for member(s) of household participate in community organizations
- `educ` Years of education (head of household)

References

Carpenter, B. (2009) Bayesian estimators for the beta-binomial model of batting ability. https://web.archive.org/web/20220618114439/https://lingpipe-blog.com/2009/09/23/

Efron, B. and Morris, C. (1975) Data analysis using Stein's estimator and its generalizations. *Journal of the American Statistical Association* **70**(350), 311–319.

Gelman, A. and Hill, J. (2007). *Data Analysis Using Regression and Multilevel/Hierarchical Models.* Cambridge University Press, Cambridge, UK. https://stat.columbia.edu/~gelman/arm/

Spiegelhalter, D., Thomas, A., Best, N., & Gilks, W. (1996) BUGS 0.5 Examples. MRC Biostatistics Unit, Institute of Public health, Cambridge, UK.

Tarone, R. E. (1982) The use of historical control information in testing for a trend in proportions. *Biometrics* **38**(1):215–220.

Therneau, T. and Grambsch, P. (2000) *Modeling Survival Data: Extending the Cox Model*. Springer-Verlag, New York, US.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
# Using 'kidiq' dataset
fit <- stan_lm(kid_score ~ mom_hs * mom_iq, data = kidiq,
               prior = R2(location = 0.30, what = "mean"),
               # the next line is only to make the example go fast enough
               chains = 1, iter = 500, seed = 12345)
pp_check(fit, nreps = 20)

bayesplot::color_scheme_set("brightblue")
pp_check(fit, plotfun = "stat_grouped", stat = "median",
         group = factor(kidiq$mom_hs, labels = c("No HS", "HS")))

}
```

`rstanarm-deprecated` *Deprecated functions*

Description

These functions are deprecated and will be removed in a future release. The **Arguments** section below provides details on how the functionality obtained via each of the arguments has been replaced.

Usage

```
prior_options(
  prior_scale_for_dispersion = 5,
  min_prior_scale = 1e-12,
  scaled = TRUE
)
```

Arguments

`prior_scale_for_dispersion`, `min_prior_scale`, `scaled`

Arguments to deprecated `prior_options` function. The functionality provided by the now deprecated `prior_options` function has been replaced as follows:

`prior_scale_for_dispersion` Instead of using the `prior_scale_for_dispersion` argument to `prior_options`, priors for these parameters can now be specified directly when calling `stan_glm` (or `stan_glmer`, etc.) using the new `prior_aux` argument.

`scaled` Instead of setting `prior_options(scaled=FALSE)`, internal rescaling is now toggled using the new `autoscale` arguments to `normal`, `student_t`, and `cauchy` (the other prior distributions do not support 'autoscale').

`min_prior_scale` No replacement. `min_prior_scale` (the minimum possible scale parameter value that be used for priors) is now fixed to `1e-12`.

---

stan_aov *Bayesian regularized linear models via Stan*

Description

Bayesian inference for linear modeling with regularizing priors on the model parameters that are driven by prior beliefs about R^2, the proportion of variance in the outcome attributable to the predictors. See `priors` for an explanation of this critical point. `stan_glm` with `family="gaussian"` also estimates a linear model with normally-distributed errors and allows for various other priors on the coefficients.

Usage

```
stan_aov(
  formula,
  data,
  projections = FALSE,
  contrasts = NULL,
  ...,
  prior = R2(stop("'location' must be specified")),
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank"),
  adapt_delta = NULL
)
```

```
stan_lm(
  formula,
  data,
  subset,
  weights,
  na.action,
  model = TRUE,
  x = FALSE,
  y = FALSE,
  singular.ok = TRUE,
  contrasts = NULL,
  offset,
  ...,
  prior = R2(stop("'location' must be specified")),
  prior_intercept = NULL,
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank"),
  adapt_delta = NULL
)

stan_lm.wfit(
  x,
  y,
  w,
  offset = NULL,
  singular.ok = TRUE,
  ...,
  prior = R2(stop("'location' must be specified")),
  prior_intercept = NULL,
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank"),
  adapt_delta = NULL
)

stan_lm.fit(
  x,
  y,
  offset = NULL,
  singular.ok = TRUE,
  ...,
  prior = R2(stop("'location' must be specified")),
  prior_intercept = NULL,
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank"),
  adapt_delta = NULL
)
```

Arguments

formula, data, subset
: Same as lm, but *we strongly advise against omitting the* data *argument*. Unless data is specified (and is a data frame) many post-estimation functions (including update, loo, kfold) are not guaranteed to work properly.

projections
: For stan_aov, a logical scalar (defaulting to FALSE) indicating whether proj should be called on the fit.

...
: Further arguments passed to the function in the **rstan** package (sampling, vb, or optimizing), corresponding to the estimation method named by algorithm. For example, if algorithm is "sampling" it is possible to specify iter, chains, cores, and other MCMC controls.

  Another useful argument that can be passed to **rstan** via ... is refresh, which specifies how often to print updates when sampling (i.e., show the progress every refresh iterations). refresh=0 turns off the iteration updates.

prior
: Must be a call to R2 with its location argument specified or NULL, which would indicate a standard uniform prior for the R^2.

prior_PD
: A logical scalar (defaulting to FALSE) indicating whether to draw from the prior predictive distribution instead of conditioning on the outcome.

algorithm
: A string (possibly abbreviated) indicating the estimation approach to use. Can be "sampling" for MCMC (the default), "optimizing" for optimization, "meanfield" for variational inference with independent normal distributions, or "fullrank" for variational inference with a multivariate normal distribution. See rstanarm-package for more details on the estimation algorithms. NOTE: not all fitting functions support all four algorithms.

adapt_delta
: Only relevant if algorithm="sampling". See the adapt_delta help page for details.

na.action, singular.ok, contrasts
: Same as lm, but rarely specified.

model, offset, weights
: Same as lm, but rarely specified.

x, y
: In stan_lm, stan_aov, logical scalars indicating whether to return the design matrix and response vector. In stan_lm.fit or stan_lm.wfit, a design matrix and response vector.

prior_intercept
: Either NULL (the default) or a call to normal. If a normal prior is specified without a scale, then the standard deviation is taken to be the marginal standard deviation of the outcome divided by the square root of the sample size, which is legitimate because the marginal standard deviation of the outcome is a primitive parameter being estimated.

  Note: If using a dense representation of the design matrix —i.e., if the sparse argument is left at its default value of FALSE— then the prior distribution for the intercept is set so it applies to the value *when all predictors are centered*. If you prefer to specify a prior on the intercept without the predictors being auto-centered, then you have to omit the intercept from the formula and include a column of ones as a predictor, in which case some element of prior specifies the

prior on it, rather than prior_intercept. Regardless of how prior_intercept is specified, the reported *estimates* of the intercept always correspond to a parameterization without centered predictors (i.e., same as in glm).

w Same as in lm.wfit but rarely specified.

Details

The stan_lm function is similar in syntax to the lm function but rather than choosing the parameters to minimize the sum of squared residuals, samples from the posterior distribution are drawn using MCMC (if algorithm is "sampling"). The stan_lm function has a formula-based interface and would usually be called by users but the stan_lm.fit and stan_lm.wfit functions might be called by other functions that parse the data themselves and are analogous to lm.fit and lm.wfit respectively.

In addition to estimating sigma — the standard deviation of the normally-distributed errors — this model estimates a positive parameter called log-fit_ratio. If it is positive, the marginal posterior variance of the outcome will exceed the sample variance of the outcome by a multiplicative factor equal to the square of fit_ratio. Conversely if log-fit_ratio is negative, then the model underfits. Given the regularizing nature of the priors, a slight underfit is good.

Finally, the posterior predictive distribution is generated with the predictors fixed at their sample means. This quantity is useful for checking convergence because it is reasonably normally distributed and a function of all the parameters in the model.

The stan_aov function is similar to aov, but does a Bayesian analysis of variance that is basically equivalent to stan_lm with dummy variables. stan_aov has a somewhat customized print method that prints an ANOVA-like table in addition to the output printed for stan_lm models.

Value

A stanreg object is returned for stan_lm, stan_aov.

A stanfit object (or a slightly modified stanfit object) is returned if stan_lm.fit or stan_lm.wfit is called directly.

References

Lewandowski, D., Kurowicka D., and Joe, H. (2009). Generating random correlation matrices based on vines and extended onion method. *Journal of Multivariate Analysis*. **100**(9), 1989–2001.

See Also

The vignettes for stan_lm and stan_aov, which have more thorough descriptions and examples. https://mc-stan.org/rstanarm/articles/

Also see stan_glm, which — if family = gaussian(link="identity") — also estimates a linear model with normally-distributed errors but specifies different priors.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {

op <- options(contrasts = c("contr.helmert", "contr.poly"))
```

```
fit_aov <- stan_aov(yield ~ block + N*P*K, data = npk,
         prior = R2(0.5), seed = 12345)
options(op)
print(fit_aov)

}
if (.Platform$OS.type != "windows" || .Platform$r_arch !="i386") {
(fit <- stan_lm(mpg ~ wt + qsec + am, data = mtcars, prior = R2(0.75),
                # the next line is only to make the example go fast enough
                chains = 1, iter = 300, seed = 12345, refresh = 0))
plot(fit, "hist", pars = c("wt", "am", "qsec", "sigma"),
     transformations = list(sigma = "log"))
}
```

---

stan_betareg *Bayesian beta regression models via Stan*

Description

Beta regression modeling with optional prior distributions for the coefficients, intercept, and auxiliary parameter phi (if applicable).

Usage

```
stan_betareg(
  formula,
  data,
  subset,
  na.action,
  weights,
  offset,
  link = c("logit", "probit", "cloglog", "cauchit", "log", "loglog"),
  link.phi = NULL,
  model = TRUE,
  y = TRUE,
  x = FALSE,
  ...,
  prior = normal(autoscale = TRUE),
  prior_intercept = normal(autoscale = TRUE),
  prior_z = normal(autoscale = TRUE),
  prior_intercept_z = normal(autoscale = TRUE),
  prior_phi = exponential(autoscale = TRUE),
  prior_PD = FALSE,
  algorithm = c("sampling", "optimizing", "meanfield", "fullrank"),
  adapt_delta = NULL,
  QR = FALSE
)
```

```
stan_betareg.fit(
  x,
  y,
  z = NULL,
  weights = rep(1, NROW(x)),
  offset = rep(0, NROW(x)),
  link = c("logit", "probit", "cloglog", "cauchit", "log", "loglog"),
  link.phi = NULL,
  ...,
  prior = normal(autoscale = TRUE),
  prior_intercept = normal(autoscale = TRUE),
  prior_z = normal(autoscale = TRUE),
  prior_intercept_z = normal(autoscale = TRUE),
  prior_phi = exponential(autoscale = TRUE),
  prior_PD = FALSE,
  algorithm = c("sampling", "optimizing", "meanfield", "fullrank"),
  adapt_delta = NULL,
  QR = FALSE
)
```

Arguments

`formula`, `data`, `subset`
: Same as `betareg`, but *we strongly advise against omitting the* `data` *argument*. Unless `data` is specified (and is a data frame) many post-estimation functions (including `update`, `loo`, `kfold`) are not guaranteed to work properly.

`na.action`
: Same as `betareg`, but rarely specified.

`link`
: Character specification of the link function used in the model for mu (specified through `x`). Currently, "logit", "probit", "cloglog", "cauchit", "log", and "loglog" are supported.

`link.phi`
: If applicable, character specification of the link function used in the model for `phi` (specified through `z`). Currently, "identity", "log" (default), and "sqrt" are supported. Since the "sqrt" link function is known to be unstable, it is advisable to specify a different link function (or to model `phi` as a scalar parameter instead of via a linear predictor by excluding `z` from the `formula` and excluding `link.phi`).

`model`, `offset`, `weights`
: Same as `betareg`.

`x`, `y`
: In `stan_betareg`, logical scalars indicating whether to return the design matrix and response vector. In `stan_betareg.fit`, a design matrix and response vector.

`...`
: Further arguments passed to the function in the **rstan** package (`sampling`, `vb`, or `optimizing`), corresponding to the estimation method named by `algorithm`. For example, if `algorithm` is `"sampling"` it is possible to specify `iter`, `chains`, `cores`, and other MCMC controls.

  Another useful argument that can be passed to **rstan** via `...` is `refresh`, which specifies how often to print updates when sampling (i.e., show the progress every `refresh` iterations). `refresh=0` turns off the iteration updates.

prior

The prior distribution for the (non-hierarchical) regression coefficients.

The default priors are described in the vignette *Prior Distributions for rstanarm Models*. If not using the default, prior should be a call to one of the various functions provided by **rstanarm** for specifying priors. The subset of these functions that can be used for the prior on the coefficients can be grouped into several "families":

Family	**Functions**
Student t family	normal, student_t, cauchy
Hierarchical shrinkage family	hs, hs_plus
Laplace family	laplace, lasso
Product normal family	product_normal

See the priors help page for details on the families and how to specify the arguments for all of the functions in the table above. To omit a prior —i.e., to use a flat (improper) uniform prior— prior can be set to NULL, although this is rarely a good idea.

Note: Unless QR=TRUE, if prior is from the Student t family or Laplace family, and if the autoscale argument to the function used to specify the prior (e.g. normal) is left at its default and recommended value of TRUE, then the default or user-specified prior scale(s) may be adjusted internally based on the scales of the predictors. See the priors help page and the *Prior Distributions* vignette for details on the rescaling and the prior_summary function for a summary of the priors used for a particular model.

prior_intercept

The prior distribution for the intercept (after centering all predictors, see note below).

The default prior is described in the vignette *Prior Distributions for rstanarm Models*. If not using the default, prior_intercept can be a call to normal, student_t or cauchy. See the priors help page for details on these functions. To omit a prior on the intercept —i.e., to use a flat (improper) uniform prior— prior_intercept can be set to NULL.

Note: If using a dense representation of the design matrix —i.e., if the sparse argument is left at its default value of FALSE— then the prior distribution for the intercept is set so it applies to the value *when all predictors are centered* (you don't need to manually center them). This is explained further in [Prior Distributions for rstanarm Models](https://mc-stan.org/rstanarm/articles/priors.html) If you prefer to specify a prior on the intercept without the predictors being auto-centered, then you have to omit the intercept from the formula and include a column of ones as a predictor, in which case some element of prior specifies the prior on it, rather than prior_intercept. Regardless of how prior_intercept is specified, the reported *estimates* of the intercept always correspond to a parameterization without centered predictors (i.e., same as in glm).

prior_z

Prior distribution for the coefficients in the model for phi (if applicable). Same options as for prior.

`prior_intercept_z`
: Prior distribution for the intercept in the model for `phi` (if applicable). Same options as for `prior_intercept`.

`prior_phi`
: The prior distribution for `phi` if it is *not* modeled as a function of predictors. If `z` variables are specified then `prior_phi` is ignored and `prior_intercept_z` and `prior_z` are used to specify the priors on the intercept and coefficients in the model for `phi`. When applicable, `prior_phi` can be a call to `exponential` to use an exponential distribution, or one of `normal`, `student_t` or `cauchy` to use half-normal, half-t, or half-Cauchy prior. See `priors` for details on these functions. To omit a prior —i.e., to use a flat (improper) uniform prior— set `prior_phi` to `NULL`.

`prior_PD`
: A logical scalar (defaulting to `FALSE`) indicating whether to draw from the prior predictive distribution instead of conditioning on the outcome.

`algorithm`
: A string (possibly abbreviated) indicating the estimation approach to use. Can be `"sampling"` for MCMC (the default), `"optimizing"` for optimization, `"meanfield"` for variational inference with independent normal distributions, or `"fullrank"` for variational inference with a multivariate normal distribution. See `rstanarm-package` for more details on the estimation algorithms. NOTE: not all fitting functions support all four algorithms.

`adapt_delta`
: Only relevant if `algorithm="sampling"`. See the adapt_delta help page for details.

`QR`
: A logical scalar defaulting to `FALSE`, but if `TRUE` applies a scaled `qr` decomposition to the design matrix. The transformation does not change the likelihood of the data but is recommended for computational reasons when there are multiple predictors. See the QR-argument documentation page for details on how **rstanarm** does the transformation and important information about how to interpret the prior distributions of the model parameters when using `QR=TRUE`.

`z`
: For `stan_betareg.fit`, a regressor matrix for `phi`. Defaults to an intercept only.

Details

The `stan_betareg` function is similar in syntax to `betareg` but rather than performing maximum likelihood estimation, full Bayesian estimation is performed (if `algorithm` is `"sampling"`) via MCMC. The Bayesian model adds priors (independent by default) on the coefficients of the beta regression model. The `stan_betareg` function calls the workhorse `stan_betareg.fit` function, but it is also possible to call the latter directly.

Value

A stanreg object is returned for `stan_betareg`.

A stanfit object (or a slightly modified stanfit object) is returned if `stan_betareg.fit` is called directly.

References

Ferrari, SLP and Cribari-Neto, F (2004). Beta regression for modeling rates and proportions. *Journal of Applied Statistics*. 31(7), 799–815.

See Also

stanreg-methods and betareg.

The vignette for stan_betareg. https://mc-stan.org/rstanarm/articles/

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
### Simulated data
N <- 200
x <- rnorm(N, 2, 1)
z <- rnorm(N, 2, 1)
mu <- binomial(link = "logit")$linkinv(1 + 0.2*x)
phi <- exp(1.5 + 0.4*z)
y <- rbeta(N, mu * phi, (1 - mu) * phi)
hist(y, col = "dark grey", border = FALSE, xlim = c(0,1))
fake_dat <- data.frame(y, x, z)

fit <- stan_betareg(
  y ~ x | z, data = fake_dat,
  link = "logit",
  link.phi = "log",
  algorithm = "optimizing" # just for speed of example
 )
print(fit, digits = 2)
}
```

---

stan_biglm *Bayesian regularized linear but big models via Stan*

Description

This is the same model as with stan_lm but it utilizes the output from biglm in the **biglm** package in order to proceed when the data is too large to fit in memory.

Usage

```
stan_biglm(
  biglm,
  xbar,
  ybar,
  s_y,
  ...,
  prior = R2(stop("'location' must be specified")),
  prior_intercept = NULL,
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank"),
  adapt_delta = NULL
)
```

```
stan_biglm.fit(
  b,
  R,
  SSR,
  N,
  xbar,
  ybar,
  s_y,
  has_intercept = TRUE,
  ...,
  prior = R2(stop("'location' must be specified")),
  prior_intercept = NULL,
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank", "optimizing"),
  adapt_delta = NULL,
  importance_resampling = TRUE,
  keep_every = 1
)
```

Arguments

biglm	The list output by biglm in the **biglm** package.
xbar	A numeric vector of column means in the implicit design matrix excluding the intercept for the observations included in the model.
ybar	A numeric scalar indicating the mean of the outcome for the observations included in the model.
s_y	A numeric scalar indicating the unbiased sample standard deviation of the outcome for the observations included in the model.
...	Further arguments passed to the function in the **rstan** package (sampling, vb, or optimizing), corresponding to the estimation method named by algorithm. For example, if algorithm is "sampling" it is possible to specify iter, chains, cores, and other MCMC controls. Another useful argument that can be passed to **rstan** via ... is refresh, which specifies how often to print updates when sampling (i.e., show the progress every refresh iterations). refresh=0 turns off the iteration updates.
prior	Must be a call to R2 with its location argument specified or NULL, which would indicate a standard uniform prior for the R^2.
prior_intercept	Either NULL (the default) or a call to normal. If a normal prior is specified without a scale, then the standard deviation is taken to be the marginal standard deviation of the outcome divided by the square root of the sample size, which is legitimate because the marginal standard deviation of the outcome is a primitive parameter being estimated. **Note:** If using a dense representation of the design matrix —i.e., if the sparse argument is left at its default value of FALSE— then the prior distribution for the intercept is set so it applies to the value *when all predictors are centered*. If

you prefer to specify a prior on the intercept without the predictors being auto-centered, then you have to omit the intercept from the formula and include a column of ones as a predictor, in which case some element of prior specifies the prior on it, rather than prior_intercept. Regardless of how prior_intercept is specified, the reported *estimates* of the intercept always correspond to a parameterization without centered predictors (i.e., same as in glm).

prior_PD — A logical scalar (defaulting to FALSE) indicating whether to draw from the prior predictive distribution instead of conditioning on the outcome.

algorithm — A string (possibly abbreviated) indicating the estimation approach to use. Can be "sampling" for MCMC (the default), "optimizing" for optimization, "meanfield" for variational inference with independent normal distributions, or "fullrank" for variational inference with a multivariate normal distribution. See rstanarm-package for more details on the estimation algorithms. NOTE: not all fitting functions support all four algorithms.

adapt_delta — Only relevant if algorithm="sampling". See the adapt_delta help page for details.

b — A numeric vector of OLS coefficients, excluding the intercept

R — A square upper-triangular matrix from the QR decomposition of the design matrix, excluding the intercept

SSR — A numeric scalar indicating the sum-of-squared residuals for OLS

N — A integer scalar indicating the number of included observations

has_intercept — A logical scalar indicating whether to add an intercept to the model when estimating it.

importance_resampling — Logical scalar indicating whether to use importance resampling when approximating the posterior distribution with a multivariate normal around the posterior mode, which only applies when algorithm is "optimizing" but defaults to TRUE in that case

keep_every — Positive integer, which defaults to 1, but can be higher in order to thin the importance sampling realizations and also only apples when algorithm is "optimizing" but defaults to TRUE in that case

Details

The stan_biglm function is intended to be used in the same circumstances as the biglm function in the **biglm** package but with an informative prior on the R^2 of the regression. Like biglm, the memory required to estimate the model depends largely on the number of predictors rather than the number of observations. However, stan_biglm and stan_biglm.fit have additional required arguments that are not necessary in biglm, namely xbar, ybar, and s_y. If any observations have any missing values on any of the predictors or the outcome, such observations do not contribute to these statistics.

Value

The output of both stan_biglm and stan_biglm.fit is an object of stanfit-class rather than stanreg-objects, which is more limited and less convenient but necessitated by the fact that

stan_biglm does not bring the full design matrix into memory. Without the full design matrix,some of the elements of a stanreg-objects object cannot be calculated, such as residuals. Thus, the functions in the **rstanarm** package that input stanreg-objects, such as posterior_predict cannot be used.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
# create inputs
ols <- lm(mpg ~ wt + qsec + am, data = mtcars, # all row are complete so ...
          na.action = na.exclude)              # not necessary in this case
b <- coef(ols)[-1]
R <- qr.R(ols$qr)[-1,-1]
SSR <- crossprod(ols$residuals)[1]
not_NA <- !is.na(fitted(ols))
N <- sum(not_NA)
xbar <- colMeans(mtcars[not_NA,c("wt", "qsec", "am")])
y <- mtcars$mpg[not_NA]
ybar <- mean(y)
s_y <- sd(y)
post <- stan_biglm.fit(b, R, SSR, N, xbar, ybar, s_y, prior = R2(.75),
                       # the next line is only to make the example go fast
                       chains = 1, iter = 500, seed = 12345)
cbind(lm = b, stan_lm = rstan::get_posterior_mean(post)[13:15,]) # shrunk
}
```

---

stan_clogit *Conditional logistic (clogit) regression models via Stan*

Description

A model for case-control studies with optional prior distributions for the coefficients, intercept, and auxiliary parameters.

Usage

```
stan_clogit(
  formula,
  data,
  subset,
  na.action = NULL,
  contrasts = NULL,
  ...,
  strata,
  prior = normal(autoscale = TRUE),
  prior_covariance = decov(),
  prior_PD = FALSE,
  algorithm = c("sampling", "optimizing", "meanfield", "fullrank"),
  adapt_delta = NULL,
```

```
  QR = FALSE,
  sparse = FALSE
)
```

Arguments

`formula`, `data`, `subset`, `na.action`, `contrasts`

Same as for `glmer`, except that any global intercept included in the formula will be dropped. *We strongly advise against omitting the* `data` *argument*. Unless `data` is specified (and is a data frame) many post-estimation functions (including `update`, `loo`, `kfold`) are not guaranteed to work properly.

`...`

Further arguments passed to the function in the **rstan** package (`sampling`, `vb`, or `optimizing`), corresponding to the estimation method named by `algorithm`. For example, if `algorithm` is `"sampling"` it is possible to specify `iter`, `chains`, `cores`, and other MCMC controls.

Another useful argument that can be passed to **rstan** via `...` is `refresh`, which specifies how often to print updates when sampling (i.e., show the progress every `refresh` iterations). `refresh=0` turns off the iteration updates.

`strata`

A factor indicating the groups in the data where the number of successes (possibly one) is fixed by the research design. It may be useful to use `interaction` or `strata` to create this factor. However, the `strata` argument must not rely on any object besides the `data` `data.frame`.

`prior`

The prior distribution for the (non-hierarchical) regression coefficients.

The default priors are described in the vignette *Prior Distributions for rstanarm Models*. If not using the default, `prior` should be a call to one of the various functions provided by **rstanarm** for specifying priors. The subset of these functions that can be used for the prior on the coefficients can be grouped into several "families":

Family	**Functions**
Student t family	`normal`, `student_t`, `cauchy`
Hierarchical shrinkage family	`hs`, `hs_plus`
Laplace family	`laplace`, `lasso`
Product normal family	`product_normal`

See the priors help page for details on the families and how to specify the arguments for all of the functions in the table above. To omit a prior —i.e., to use a flat (improper) uniform prior— `prior` can be set to `NULL`, although this is rarely a good idea.

Note: Unless `QR=TRUE`, if `prior` is from the Student t family or Laplace family, and if the `autoscale` argument to the function used to specify the prior (e.g. `normal`) is left at its default and recommended value of `TRUE`, then the default or user-specified prior scale(s) may be adjusted internally based on the scales of the predictors. See the priors help page and the *Prior Distributions* vignette for details on the rescaling and the `prior_summary` function for a summary of the priors used for a particular model.

prior_covariance
: Cannot be NULL when lme4-style group-specific terms are included in the formula. See decov for more information about the default arguments. Ignored when there are no group-specific terms.

prior_PD
: A logical scalar (defaulting to FALSE) indicating whether to draw from the prior predictive distribution instead of conditioning on the outcome.

algorithm
: A string (possibly abbreviated) indicating the estimation approach to use. Can be "sampling" for MCMC (the default), "optimizing" for optimization, "meanfield" for variational inference with independent normal distributions, or "fullrank" for variational inference with a multivariate normal distribution. See rstanarm-package for more details on the estimation algorithms. NOTE: not all fitting functions support all four algorithms.

adapt_delta
: Only relevant if algorithm="sampling". See the adapt_delta help page for details.

QR
: A logical scalar defaulting to FALSE, but if TRUE applies a scaled qr decomposition to the design matrix. The transformation does not change the likelihood of the data but is recommended for computational reasons when there are multiple predictors. See the QR-argument documentation page for details on how **rstanarm** does the transformation and important information about how to interpret the prior distributions of the model parameters when using QR=TRUE.

sparse
: A logical scalar (defaulting to FALSE) indicating whether to use a sparse representation of the design (X) matrix. If TRUE, the the design matrix is not centered (since that would destroy the sparsity) and likewise it is not possible to specify both QR = TRUE and sparse = TRUE. Depending on how many zeros there are in the design matrix, setting sparse = TRUE may make the code run faster and can consume much less RAM.

Details

The stan_clogit function is mostly similar in syntax to clogit but rather than performing maximum likelihood estimation of generalized linear models, full Bayesian estimation is performed (if algorithm is "sampling") via MCMC. The Bayesian model adds priors (independent by default) on the coefficients of the GLM.

The data.frame passed to the data argument must be sorted by the variable passed to the strata argument.

The formula may have group-specific terms like in stan_glmer but should not allow the intercept to vary by the stratifying variable, since there is no information in the data with which to estimate such deviations in the intercept.

Value

A stanreg object is returned for stan_clogit.

See Also

stanreg-methods and clogit.

The vignette for Bernoulli and binomial models, which has more details on using stan_clogit. https://mc-stan.org/rstanarm/articles/

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
dat <- infert[order(infert$stratum), ] # order by strata
post <- stan_clogit(case ~ spontaneous + induced + (1 | education),
                    strata = stratum,
                    data = dat,
                    subset = parity <= 2,
                    QR = TRUE,
                    chains = 2, iter = 500) # for speed only

nd <- dat[dat$parity > 2, c("case", "spontaneous", "induced", "education", "stratum")]
# next line would fail without case and stratum variables
pr <- posterior_epred(post, newdata = nd) # get predicted probabilities

# not a random variable b/c probabilities add to 1 within strata
all.equal(rep(sum(nd$case), nrow(pr)), rowSums(pr))
}
```

---

stan_gamm4 *Bayesian generalized linear additive models with optional group-specific terms via Stan*

Description

Bayesian inference for GAMMs with flexible priors.

Usage

```
stan_gamm4(
  formula,
  random = NULL,
  family = gaussian(),
  data,
  weights = NULL,
  subset = NULL,
  na.action,
  knots = NULL,
  drop.unused.levels = TRUE,
  ...,
  prior = default_prior_coef(family),
  prior_intercept = default_prior_intercept(family),
  prior_smooth = exponential(autoscale = FALSE),
  prior_aux = exponential(autoscale = TRUE),
  prior_covariance = decov(),
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank"),
  adapt_delta = NULL,
  QR = FALSE,
```

```
  sparse = FALSE
)

plot_nonlinear(
  x,
  smooths,
  ...,
  prob = 0.9,
  facet_args = list(),
  alpha = 1,
  size = 0.75
)
```

Arguments

`formula`, `random`, `family`, `data`, `knots`, `drop.unused.levels`

Same as for `gamm4`. *We strongly advise against omitting the* `data` *argument*. Unless `data` is specified (and is a data frame) many post-estimation functions (including `update`, `loo`, `kfold`) are not guaranteed to work properly.

`subset`, `weights`, `na.action`

Same as `glm`, but rarely specified.

`...`

Further arguments passed to `sampling` (e.g. `iter`, `chains`, `cores`, etc.) or to `vb` (if `algorithm` is `"meanfield"` or `"fullrank"`).

`prior`

The prior distribution for the (non-hierarchical) regression coefficients.

The default priors are described in the vignette *Prior Distributions for rstanarm Models*. If not using the default, `prior` should be a call to one of the various functions provided by **rstanarm** for specifying priors. The subset of these functions that can be used for the prior on the coefficients can be grouped into several "families":

Family	**Functions**
Student t family	`normal`, `student_t`, `cauchy`
Hierarchical shrinkage family	`hs`, `hs_plus`
Laplace family	`laplace`, `lasso`
Product normal family	`product_normal`

See the priors help page for details on the families and how to specify the arguments for all of the functions in the table above. To omit a prior —i.e., to use a flat (improper) uniform prior— `prior` can be set to `NULL`, although this is rarely a good idea.

Note: Unless `QR=TRUE`, if `prior` is from the Student t family or Laplace family, and if the `autoscale` argument to the function used to specify the prior (e.g. `normal`) is left at its default and recommended value of `TRUE`, then the default or user-specified prior scale(s) may be adjusted internally based on the scales of the predictors. See the priors help page and the *Prior Distributions* vignette for details on the rescaling and the `prior_summary` function for a summary of the priors used for a particular model.

prior_intercept

The prior distribution for the intercept (after centering all predictors, see note below).

The default prior is described in the vignette *Prior Distributions for rstanarm Models*. If not using the default, prior_intercept can be a call to normal, student_t or cauchy. See the priors help page for details on these functions. To omit a prior on the intercept —i.e., to use a flat (improper) uniform prior— prior_intercept can be set to NULL.

Note: If using a dense representation of the design matrix —i.e., if the sparse argument is left at its default value of FALSE— then the prior distribution for the intercept is set so it applies to the value *when all predictors are centered* (you don't need to manually center them). This is explained further in [Prior Distributions for rstanarm Models](https://mc-stan.org/rstanarm/articles/priors.html) If you prefer to specify a prior on the intercept without the predictors being auto-centered, then you have to omit the intercept from the formula and include a column of ones as a predictor, in which case some element of prior specifies the prior on it, rather than prior_intercept. Regardless of how prior_intercept is specified, the reported *estimates* of the intercept always correspond to a parameterization without centered predictors (i.e., same as in glm).

prior_smooth The prior distribution for the hyperparameters in GAMs, with lower values yielding less flexible smooth functions.

prior_smooth can be a call to exponential to use an exponential distribution, or normal, student_t or cauchy, which results in a half-normal, half-t, or half-Cauchy prior. See priors for details on these functions. To omit a prior —i.e., to use a flat (improper) uniform prior— set prior_smooth to NULL. The number of hyperparameters depends on the model specification but a scalar prior will be recylced as necessary to the appropriate length.

prior_aux The prior distribution for the "auxiliary" parameter (if applicable). The "auxiliary" parameter refers to a different parameter depending on the family. For Gaussian models prior_aux controls "sigma", the error standard deviation. For negative binomial models prior_aux controls "reciprocal_dispersion", which is similar to the "size" parameter of rnbinom: smaller values of "reciprocal_dispersion" correspond to greater dispersion. For gamma models prior_aux sets the prior on to the "shape" parameter (see e.g., rgamma), and for inverse-Gaussian models it is the so-called "lambda" parameter (which is essentially the reciprocal of a scale parameter). Binomial and Poisson models do not have auxiliary parameters.

The default prior is described in the vignette *Prior Distributions for rstanarm Models*. If not using the default, prior_aux can be a call to exponential to use an exponential distribution, or normal, student_t or cauchy, which results in a half-normal, half-t, or half-Cauchy prior. See priors for details on these functions. To omit a prior —i.e., to use a flat (improper) uniform prior— set prior_aux to NULL.

prior_covariance

Cannot be NULL; see decov for more information about the default arguments.

prior_PD A logical scalar (defaulting to FALSE) indicating whether to draw from the prior predictive distribution instead of conditioning on the outcome.

algorithm	A string (possibly abbreviated) indicating the estimation approach to use. Can be "sampling" for MCMC (the default), "optimizing" for optimization, "meanfield" for variational inference with independent normal distributions, or "fullrank" for variational inference with a multivariate normal distribution. See rstanarm-package for more details on the estimation algorithms. NOTE: not all fitting functions support all four algorithms.
adapt_delta	Only relevant if algorithm="sampling". See the adapt_delta help page for details.
QR	A logical scalar defaulting to FALSE, but if TRUE applies a scaled qr decomposition to the design matrix. The transformation does not change the likelihood of the data but is recommended for computational reasons when there are multiple predictors. See the QR-argument documentation page for details on how **rstanarm** does the transformation and important information about how to interpret the prior distributions of the model parameters when using QR=TRUE.
sparse	A logical scalar (defaulting to FALSE) indicating whether to use a sparse representation of the design (X) matrix. If TRUE, the the design matrix is not centered (since that would destroy the sparsity) and likewise it is not possible to specify both QR = TRUE and sparse = TRUE. Depending on how many zeros there are in the design matrix, setting sparse = TRUE may make the code run faster and can consume much less RAM.
x	An object produced by stan_gamm4.
smooths	An optional character vector specifying a subset of the smooth functions specified in the call to stan_gamm4. The default is include all smooth terms.
prob	For univarite smooths, a scalar between 0 and 1 governing the width of the uncertainty interval.
facet_args	An optional named list of arguments passed to facet_wrap (other than the facets argument).
alpha, size	For univariate smooths, passed to geom_ribbon. For bivariate smooths, size/2 is passed to geom_contour.

Details

The stan_gamm4 function is similar in syntax to gamm4 in the **gamm4** package. But rather than performing (restricted) maximum likelihood estimation with the **lme4** package, the stan_gamm4 function utilizes MCMC to perform Bayesian estimation. The Bayesian model adds priors on the common regression coefficients (in the same way as stan_glm), priors on the standard deviations of the smooth terms, and a prior on the decomposition of the covariance matrices of any group-specific parameters (as in stan_glmer). Estimating these models via MCMC avoids the optimization issues that often crop up with GAMMs and provides better estimates for the uncertainty in the parameter estimates.

See gamm4 for more information about the model specicification and priors for more information about the priors on the main coefficients. The formula should include at least one smooth term, which can be specified in any way that is supported by the jagam function in the **mgcv** package. The prior_smooth argument should be used to specify a prior on the unknown standard deviations that govern how smooth the smooth function is. The prior_covariance argument can be used to specify the prior on the components of the covariance matrix for any (optional) group-specific terms.

The gamm4 function in the **gamm4** package uses group-specific terms to implement the departure from linearity in the smooth terms, but that is not the case for stan_gamm4 where the group-specific terms are exactly the same as in stan_glmer.

The plot_nonlinear function creates a ggplot object with one facet for each smooth function specified in the call to stan_gamm4 in the case where all smooths are univariate. A subset of the smooth functions can be specified using the smooths argument, which is necessary to plot a bivariate smooth or to exclude the bivariate smooth and plot the univariate ones. In the bivariate case, a plot is produced using geom_contour. In the univariate case, the resulting plot is conceptually similar to plot.gam except the outer lines here demark the edges of posterior uncertainty intervals (credible intervals) rather than confidence intervals and the inner line is the posterior median of the function rather than the function implied by a point estimate. To change the colors used in the plot see color_scheme_set.

Value

A stanreg object is returned for stan_gamm4.

plot_nonlinear returns a ggplot object.

References

Crainiceanu, C., Ruppert D., and Wand, M. (2005). Bayesian analysis for penalized spline regression using WinBUGS. *Journal of Statistical Software*. **14**(14), 1–22. https://www.jstatsoft.org/article/view/v014i14

See Also

stanreg-methods and gamm4.

The vignette for stan_glmer, which also discusses stan_gamm4. https://mc-stan.org/rstanarm/articles/

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
# from example(gamm4, package = "gamm4"), prefixing gamm4() call with stan_

dat <- mgcv::gamSim(1, n = 400, scale = 2) ## simulate 4 term additive truth
## Now add 20 level random effect `fac'...
dat$fac <- fac <- as.factor(sample(1:20, 400, replace = TRUE))
dat$y <- dat$y + model.matrix(~ fac - 1) %*% rnorm(20) * .5

br <- stan_gamm4(y ~ s(x0) + x1 + s(x2), data = dat, random = ~ (1 | fac),
                 chains = 1, iter = 500) # for example speed
print(br)
plot_nonlinear(br)
plot_nonlinear(br, smooths = "s(x0)", alpha = 2/3)

}
```

stan_glm *Bayesian generalized linear models via Stan*

Description

Generalized linear modeling with optional prior distributions for the coefficients, intercept, and auxiliary parameters.

Usage

```
stan_glm(
  formula,
  family = gaussian(),
  data,
  weights,
  subset,
  na.action = NULL,
  offset = NULL,
  model = TRUE,
  x = FALSE,
  y = TRUE,
  contrasts = NULL,
  ...,
  prior = default_prior_coef(family),
  prior_intercept = default_prior_intercept(family),
  prior_aux = exponential(autoscale = TRUE),
  prior_PD = FALSE,
  algorithm = c("sampling", "optimizing", "meanfield", "fullrank"),
  mean_PPD = algorithm != "optimizing" && !prior_PD,
  adapt_delta = NULL,
  QR = FALSE,
  sparse = FALSE
)

stan_glm.nb(
  formula,
  data,
  weights,
  subset,
  na.action = NULL,
  offset = NULL,
  model = TRUE,
  x = FALSE,
  y = TRUE,
  contrasts = NULL,
  link = "log",
  ...,
```

```
  prior = default_prior_coef(family),
  prior_intercept = default_prior_intercept(family),
  prior_aux = exponential(autoscale = TRUE),
  prior_PD = FALSE,
  algorithm = c("sampling", "optimizing", "meanfield", "fullrank"),
  mean_PPD = algorithm != "optimizing",
  adapt_delta = NULL,
  QR = FALSE
)

stan_glm.fit(
  x,
  y,
  weights = rep(1, NROW(y)),
  offset = rep(0, NROW(y)),
  family = gaussian(),
  ...,
  prior = default_prior_coef(family),
  prior_intercept = default_prior_intercept(family),
  prior_aux = exponential(autoscale = TRUE),
  prior_smooth = exponential(autoscale = FALSE),
  prior_ops = NULL,
  group = list(),
  prior_PD = FALSE,
  algorithm = c("sampling", "optimizing", "meanfield", "fullrank"),
  mean_PPD = algorithm != "optimizing" && !prior_PD,
  adapt_delta = NULL,
  QR = FALSE,
  sparse = FALSE,
  importance_resampling = algorithm != "sampling",
  keep_every = algorithm != "sampling"
)
```

Arguments

`formula`, `data`, `subset`
: Same as `glm`, but *we strongly advise against omitting the* `data` *argument*. Unless `data` is specified (and is a data frame) many post-estimation functions (including `update`, `loo`, `kfold`) are not guaranteed to work properly.

`family`
: Same as `glm`, except negative binomial GLMs are also possible using the `neg_binomial_2` family object.

`na.action`, `contrasts`
: Same as `glm`, but rarely specified.

`model`, `offset`, `weights`
: Same as `glm`.

`x`
: In `stan_glm`, logical scalar indicating whether to return the design matrix. In `stan_glm.fit`, usually a design matrix but can also be a list of design matrices

with the same number of rows, in which case the first element of the list is interpreted as the primary design matrix and the remaining list elements collectively constitute a basis for a smooth nonlinear function of the predictors indicated by the `formula` argument to `stan_gamm4`.

`y` In `stan_glm`, logical scalar indicating whether to return the response vector. In `stan_glm.fit`, a response vector.

`...` Further arguments passed to the function in the **rstan** package (`sampling`, `vb`, or `optimizing`), corresponding to the estimation method named by `algorithm`. For example, if `algorithm` is `"sampling"` it is possible to specify `iter`, `chains`, `cores`, and other MCMC controls.

Another useful argument that can be passed to **rstan** via `...` is `refresh`, which specifies how often to print updates when sampling (i.e., show the progress every `refresh` iterations). `refresh=0` turns off the iteration updates.

`prior` The prior distribution for the (non-hierarchical) regression coefficients.

The default priors are described in the vignette *Prior Distributions for rstanarm Models*. If not using the default, `prior` should be a call to one of the various functions provided by **rstanarm** for specifying priors. The subset of these functions that can be used for the prior on the coefficients can be grouped into several "families":

Family	**Functions**
Student t family	`normal`, `student_t`, `cauchy`
Hierarchical shrinkage family	`hs`, `hs_plus`
Laplace family	`laplace`, `lasso`
Product normal family	`product_normal`

See the priors help page for details on the families and how to specify the arguments for all of the functions in the table above. To omit a prior —i.e., to use a flat (improper) uniform prior— `prior` can be set to `NULL`, although this is rarely a good idea.

Note: Unless `QR=TRUE`, if `prior` is from the Student t family or Laplace family, and if the `autoscale` argument to the function used to specify the prior (e.g. `normal`) is left at its default and recommended value of `TRUE`, then the default or user-specified prior scale(s) may be adjusted internally based on the scales of the predictors. See the priors help page and the *Prior Distributions* vignette for details on the rescaling and the `prior_summary` function for a summary of the priors used for a particular model.

`prior_intercept`

The prior distribution for the intercept (after centering all predictors, see note below).

The default prior is described in the vignette *Prior Distributions for rstanarm Models*. If not using the default, `prior_intercept` can be a call to `normal`, `student_t` or `cauchy`. See the priors help page for details on these functions. To omit a prior on the intercept —i.e., to use a flat (improper) uniform prior— `prior_intercept` can be set to `NULL`.

Note: If using a dense representation of the design matrix —i.e., if the `sparse` argument is left at its default value of `FALSE`— then the prior distribution for the intercept is set so it applies to the value *when all predictors are centered* (you don't need to manually center them). This is explained further in [Prior Distributions for rstanarm Models](https://mc-stan.org/rstanarm/articles/priors.html) If you prefer to specify a prior on the intercept without the predictors being auto-centered, then you have to omit the intercept from the `formula` and include a column of ones as a predictor, in which case some element of `prior` specifies the prior on it, rather than `prior_intercept`. Regardless of how `prior_intercept` is specified, the reported *estimates* of the intercept always correspond to a parameterization without centered predictors (i.e., same as in `glm`).

`prior_aux` The prior distribution for the "auxiliary" parameter (if applicable). The "auxiliary" parameter refers to a different parameter depending on the `family`. For Gaussian models `prior_aux` controls `"sigma"`, the error standard deviation. For negative binomial models `prior_aux` controls `"reciprocal_dispersion"`, which is similar to the `"size"` parameter of `rnbinom`: smaller values of `"reciprocal_dispersion"` correspond to greater dispersion. For gamma models `prior_aux` sets the prior on to the `"shape"` parameter (see e.g., `rgamma`), and for inverse-Gaussian models it is the so-called `"lambda"` parameter (which is essentially the reciprocal of a scale parameter). Binomial and Poisson models do not have auxiliary parameters.

The default prior is described in the vignette *Prior Distributions for rstanarm Models*. If not using the default, `prior_aux` can be a call to `exponential` to use an exponential distribution, or `normal`, `student_t` or `cauchy`, which results in a half-normal, half-t, or half-Cauchy prior. See `priors` for details on these functions. To omit a prior —i.e., to use a flat (improper) uniform prior— set `prior_aux` to `NULL`.

`prior_PD` A logical scalar (defaulting to `FALSE`) indicating whether to draw from the prior predictive distribution instead of conditioning on the outcome.

`algorithm` A string (possibly abbreviated) indicating the estimation approach to use. Can be `"sampling"` for MCMC (the default), `"optimizing"` for optimization, `"meanfield"` for variational inference with independent normal distributions, or `"fullrank"` for variational inference with a multivariate normal distribution. See `rstanarm-package` for more details on the estimation algorithms. NOTE: not all fitting functions support all four algorithms.

`mean_PPD` A logical value indicating whether the sample mean of the posterior predictive distribution of the outcome should be calculated in the `generated quantities` block. If `TRUE` then `mean_PPD` is computed and displayed as a diagnostic in the printed output. The default is `TRUE` except if `algorithm=="optimizing"`. A useful heuristic is to check if `mean_PPD` is plausible when compared to `mean(y)`. If it is plausible then this does *not* mean that the model is good in general (only that it can reproduce the sample mean), but if `mean_PPD` is implausible then there may be something wrong, e.g., severe model misspecification, problems with the data and/or priors, computational issues, etc.

`adapt_delta` Only relevant if `algorithm="sampling"`. See the adapt_delta help page for details.

QR — A logical scalar defaulting to FALSE, but if TRUE applies a scaled qr decomposition to the design matrix. The transformation does not change the likelihood of the data but is recommended for computational reasons when there are multiple predictors. See the QR-argument documentation page for details on how **rstanarm** does the transformation and important information about how to interpret the prior distributions of the model parameters when using QR=TRUE.

sparse — A logical scalar (defaulting to FALSE) indicating whether to use a sparse representation of the design (X) matrix. If TRUE, the the design matrix is not centered (since that would destroy the sparsity) and likewise it is not possible to specify both QR = TRUE and sparse = TRUE. Depending on how many zeros there are in the design matrix, setting sparse = TRUE may make the code run faster and can consume much less RAM.

link — For stan_glm.nb only, the link function to use. See neg_binomial_2.

prior_smooth — The prior distribution for the hyperparameters in GAMs, with lower values yielding less flexible smooth functions.

prior_smooth can be a call to exponential to use an exponential distribution, or normal, student_t or cauchy, which results in a half-normal, half-t, or half-Cauchy prior. See priors for details on these functions. To omit a prior —i.e., to use a flat (improper) uniform prior— set prior_smooth to NULL. The number of hyperparameters depends on the model specification but a scalar prior will be recylced as necessary to the appropriate length.

prior_ops — Deprecated. See rstanarm-deprecated for details.

group — A list, possibly of length zero (the default), but otherwise having the structure of that produced by mkReTrms to indicate the group-specific part of the model. In addition, this list must have elements for the regularization, concentration shape, and scale components of a decov prior for the covariance matrices among the group-specific coefficients.

importance_resampling — Logical scalar indicating whether to use importance resampling when approximating the posterior distribution with a multivariate normal around the posterior mode, which only applies when algorithm is "optimizing" but defaults to TRUE in that case

keep_every — Positive integer, which defaults to 1, but can be higher in order to "thin" the importance sampling realizations. Applies only when importance_resampling=TRUE.

Details

The stan_glm function is similar in syntax to glm but rather than performing maximum likelihood estimation of generalized linear models, full Bayesian estimation is performed (if algorithm is "sampling") via MCMC. The Bayesian model adds priors (independent by default) on the coefficients of the GLM. The stan_glm function calls the workhorse stan_glm.fit function, but it is also possible to call the latter directly.

The stan_glm.nb function, which takes the extra argument link, is a wrapper for stan_glm with family = neg_binomial_2(link).

Value

A stanreg object is returned for `stan_glm`, `stan_glm.nb`.

A stanfit object (or a slightly modified stanfit object) is returned if `stan_glm.fit` is called directly.

References

Gelman, A. and Hill, J. (2007). *Data Analysis Using Regression and Multilevel/Hierarchical Models.* Cambridge University Press, Cambridge, UK. (Ch. 3-6)

Muth, C., Oravecz, Z., and Gabry, J. (2018) User-friendly Bayesian regression modeling: A tutorial with rstanarm and shinystan. *The Quantitative Methods for Psychology*. 14(2), 99–119. https://www.tqmp.org/RegularArticles/vol14-2/p099/p099.pdf

See Also

`stanreg-methods` and `glm`.

The various vignettes for `stan_glm` at https://mc-stan.org/rstanarm/articles/.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
### Linear regression
mtcars$mpg10 <- mtcars$mpg / 10
fit <- stan_glm(
  mpg10 ~ wt + cyl + am,
  data = mtcars,
  QR = TRUE,
  # for speed of example only (default is "sampling")
  algorithm = "fullrank",
  refresh = 0
 )

plot(fit, prob = 0.5)
plot(fit, prob = 0.5, pars = "beta")
plot(fit, "hist", pars = "sigma")

### Logistic regression
head(wells)
wells$dist100 <- wells$dist / 100
fit2 <- stan_glm(
  switch ~ dist100 + arsenic,
  data = wells,
  family = binomial(link = "logit"),
  prior_intercept = normal(0, 10),
  QR = TRUE,
  refresh = 0,
  # for speed of example only
  chains = 2, iter = 200
)
print(fit2)
prior_summary(fit2)
```

```
# ?bayesplot::mcmc_areas
plot(fit2, plotfun = "areas", prob = 0.9,
     pars = c("(Intercept)", "arsenic"))

# ?bayesplot::ppc_error_binned
pp_check(fit2, plotfun = "error_binned")


### Poisson regression (example from help("glm"))
count_data <- data.frame(
 counts = c(18,17,15,20,10,20,25,13,12),
 outcome = gl(3,1,9),
 treatment = gl(3,3)
)
fit3 <- stan_glm(
  counts ~ outcome + treatment,
  data = count_data,
  family = poisson(link="log"),
  prior = normal(0, 2),
  refresh = 0,
  # for speed of example only
  chains = 2, iter = 250
)
print(fit3)

bayesplot::color_scheme_set("viridis")
plot(fit3)
plot(fit3, regex_pars = c("outcome", "treatment"))
plot(fit3, plotfun = "combo", regex_pars = "treatment") # ?bayesplot::mcmc_combo
posterior_vs_prior(fit3, regex_pars = c("outcome", "treatment"))

### Gamma regression (example from help("glm"))
clotting <- data.frame(log_u = log(c(5,10,15,20,30,40,60,80,100)),
                       lot1 = c(118,58,42,35,27,25,21,19,18),
                       lot2 = c(69,35,26,21,18,16,13,12,12))
fit4 <- stan_glm(
  lot1 ~ log_u,
  data = clotting,
  family = Gamma(link="log"),
  iter = 500, # for speed of example only
  refresh = 0
 )
print(fit4, digits = 2)

fit5 <- update(fit4, formula = lot2 ~ log_u)

# ?bayesplot::ppc_dens_overlay
bayesplot::bayesplot_grid(
  pp_check(fit4, seed = 123),
  pp_check(fit5, seed = 123),
  titles = c("lot1", "lot2")
)
```

```
### Negative binomial regression
fit6 <- stan_glm.nb(
  Days ~ Sex/(Age + Eth*Lrn),
  data = MASS::quine,
  link = "log",
  prior_aux = exponential(1.5, autoscale=TRUE),
  chains = 2, iter = 200, # for speed of example only
  refresh = 0
)

prior_summary(fit6)
bayesplot::color_scheme_set("brightblue")
plot(fit6)
pp_check(fit6, plotfun = "hist", nreps = 5) # ?bayesplot::ppc_hist

# 80% interval of estimated reciprocal_dispersion parameter
posterior_interval(fit6, pars = "reciprocal_dispersion", prob = 0.8)
plot(fit6, "areas", pars = "reciprocal_dispersion", prob = 0.8)

}
```

---

stan_glmer *Bayesian generalized linear models with group-specific terms via Stan*

Description

Bayesian inference for GLMs with group-specific coefficients that have unknown covariance matrices with flexible priors.

Usage

```
stan_glmer(
  formula,
  data = NULL,
  family = gaussian,
  subset,
  weights,
  na.action = getOption("na.action", "na.omit"),
  offset,
  contrasts = NULL,
  ...,
  prior = default_prior_coef(family),
  prior_intercept = default_prior_intercept(family),
  prior_aux = exponential(autoscale = TRUE),
  prior_covariance = decov(),
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank"),
```

```
  adapt_delta = NULL,
  QR = FALSE,
  sparse = FALSE
)

stan_lmer(
  formula,
  data = NULL,
  subset,
  weights,
  na.action = getOption("na.action", "na.omit"),
  offset,
  contrasts = NULL,
  ...,
  prior = default_prior_coef(family),
  prior_intercept = default_prior_intercept(family),
  prior_aux = exponential(autoscale = TRUE),
  prior_covariance = decov(),
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank"),
  adapt_delta = NULL,
  QR = FALSE
)

stan_glmer.nb(
  formula,
  data = NULL,
  subset,
  weights,
  na.action = getOption("na.action", "na.omit"),
  offset,
  contrasts = NULL,
  link = "log",
  ...,
  prior = default_prior_coef(family),
  prior_intercept = default_prior_intercept(family),
  prior_aux = exponential(autoscale = TRUE),
  prior_covariance = decov(),
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank"),
  adapt_delta = NULL,
  QR = FALSE
)
```

Arguments

formula, data	Same as for glmer. *We strongly advise against omitting the* data *argument.* Unless data is specified (and is a data frame) many post-estimation functions (including update, loo, kfold) are not guaranteed to work properly.

`family` Same as for `glmer` except it is also possible to use `family=mgcv::betar` to estimate a Beta regression with `stan_glmer`.

`subset, weights, offset`
Same as `glm`.

`na.action, contrasts`
Same as `glm`, but rarely specified.

`...` For `stan_glmer`, further arguments passed to `sampling` (e.g. `iter`, `chains`, `cores`, etc.) or to `vb` (if `algorithm` is `"meanfield"` or `"fullrank"`). For `stan_lmer` and `stan_glmer.nb`, `...` should also contain all relevant arguments to pass to `stan_glmer` (except `family`).

`prior` The prior distribution for the (non-hierarchical) regression coefficients.

The default priors are described in the vignette *Prior Distributions for rstanarm Models*. If not using the default, `prior` should be a call to one of the various functions provided by **rstanarm** for specifying priors. The subset of these functions that can be used for the prior on the coefficients can be grouped into several "families":

Family	**Functions**
Student t family	`normal`, `student_t`, `cauchy`
Hierarchical shrinkage family	`hs`, `hs_plus`
Laplace family	`laplace`, `lasso`
Product normal family	`product_normal`

See the priors help page for details on the families and how to specify the arguments for all of the functions in the table above. To omit a prior —i.e., to use a flat (improper) uniform prior— `prior` can be set to `NULL`, although this is rarely a good idea.

Note: Unless `QR=TRUE`, if `prior` is from the Student t family or Laplace family, and if the `autoscale` argument to the function used to specify the prior (e.g. `normal`) is left at its default and recommended value of `TRUE`, then the default or user-specified prior scale(s) may be adjusted internally based on the scales of the predictors. See the priors help page and the *Prior Distributions* vignette for details on the rescaling and the `prior_summary` function for a summary of the priors used for a particular model.

`prior_intercept`
The prior distribution for the intercept (after centering all predictors, see note below).

The default prior is described in the vignette *Prior Distributions for rstanarm Models*. If not using the default, `prior_intercept` can be a call to `normal`, `student_t` or `cauchy`. See the priors help page for details on these functions. To omit a prior on the intercept —i.e., to use a flat (improper) uniform prior— `prior_intercept` can be set to `NULL`.

Note: If using a dense representation of the design matrix —i.e., if the `sparse` argument is left at its default value of `FALSE`— then the prior distribution for the intercept is set so it applies to the value *when all predictors are centered* (you

don't need to manually center them). This is explained further in [Prior Distributions for rstanarm Models](https://mc-stan.org/rstanarm/articles/priors.html) If you prefer to specify a prior on the intercept without the predictors being auto-centered, then you have to omit the intercept from the formula and include a column of ones as a predictor, in which case some element of prior specifies the prior on it, rather than prior_intercept. Regardless of how prior_intercept is specified, the reported *estimates* of the intercept always correspond to a parameterization without centered predictors (i.e., same as in glm).

prior_aux — The prior distribution for the "auxiliary" parameter (if applicable). The "auxiliary" parameter refers to a different parameter depending on the family. For Gaussian models prior_aux controls "sigma", the error standard deviation. For negative binomial models prior_aux controls "reciprocal_dispersion", which is similar to the "size" parameter of rnbinom: smaller values of "reciprocal_dispersion" correspond to greater dispersion. For gamma models prior_aux sets the prior on to the "shape" parameter (see e.g., rgamma), and for inverse-Gaussian models it is the so-called "lambda" parameter (which is essentially the reciprocal of a scale parameter). Binomial and Poisson models do not have auxiliary parameters.

The default prior is described in the vignette *Prior Distributions for rstanarm Models*. If not using the default, prior_aux can be a call to exponential to use an exponential distribution, or normal, student_t or cauchy, which results in a half-normal, half-t, or half-Cauchy prior. See priors for details on these functions. To omit a prior —i.e., to use a flat (improper) uniform prior— set prior_aux to NULL.

prior_covariance — Cannot be NULL; see decov for more information about the default arguments.

prior_PD — A logical scalar (defaulting to FALSE) indicating whether to draw from the prior predictive distribution instead of conditioning on the outcome.

algorithm — A string (possibly abbreviated) indicating the estimation approach to use. Can be "sampling" for MCMC (the default), "optimizing" for optimization, "meanfield" for variational inference with independent normal distributions, or "fullrank" for variational inference with a multivariate normal distribution. See rstanarm-package for more details on the estimation algorithms. NOTE: not all fitting functions support all four algorithms.

adapt_delta — Only relevant if algorithm="sampling". See the adapt_delta help page for details.

QR — A logical scalar defaulting to FALSE, but if TRUE applies a scaled qr decomposition to the design matrix. The transformation does not change the likelihood of the data but is recommended for computational reasons when there are multiple predictors. See the QR-argument documentation page for details on how **rstanarm** does the transformation and important information about how to interpret the prior distributions of the model parameters when using QR=TRUE.

sparse — A logical scalar (defaulting to FALSE) indicating whether to use a sparse representation of the design (X) matrix. If TRUE, the the design matrix is not centered (since that would destroy the sparsity) and likewise it is not possible to specify

both QR = TRUE and sparse = TRUE. Depending on how many zeros there are in the design matrix, setting sparse = TRUE may make the code run faster and can consume much less RAM.

link — For stan_glmer.nb only, the link function to use. See neg_binomial_2.

Details

The stan_glmer function is similar in syntax to glmer but rather than performing (restricted) maximum likelihood estimation of generalized linear models, Bayesian estimation is performed via MCMC. The Bayesian model adds priors on the regression coefficients (in the same way as stan_glm) and priors on the terms of a decomposition of the covariance matrices of the group-specific parameters. See priors for more information about the priors.

The stan_lmer function is equivalent to stan_glmer with family = gaussian(link = "identity").

The stan_glmer.nb function, which takes the extra argument link, is a wrapper for stan_glmer with family = neg_binomial_2(link).

Value

A stanreg object is returned for stan_glmer, stan_lmer, stan_glmer.nb.

A list with classes stanreg, glm, lm, and lmerMod. The conventions for the parameter names are the same as in the lme4 package with the addition that the standard deviation of the errors is called sigma and the variance-covariance matrix of the group-specific deviations from the common parameters is called Sigma, even if this variance-covariance matrix only has one row and one column (in which case it is just the group-level variance).

References

Gelman, A. and Hill, J. (2007). *Data Analysis Using Regression and Multilevel/Hierarchical Models*. Cambridge University Press, Cambridge, UK. (Ch. 11-15)

Muth, C., Oravecz, Z., and Gabry, J. (2018) User-friendly Bayesian regression modeling: A tutorial with rstanarm and shinystan. *The Quantitative Methods for Psychology*. 14(2), 99–119. https://www.tqmp.org/RegularArticles/vol14-2/p099/p099.pdf

See Also

stanreg-methods and glmer.

The vignette for stan_glmer and the *Hierarchical Partial Pooling* vignette. https://mc-stan.org/rstanarm/articles/

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
# see help(example_model) for details on the model below
if (!exists("example_model")) example(example_model)
print(example_model, digits = 1)
}
```

stan_jm *Bayesian joint longitudinal and time-to-event models via Stan*

Description

Fits a shared parameter joint model for longitudinal and time-to-event (e.g. survival) data under a Bayesian framework using Stan.

Usage

```
stan_jm(
  formulaLong,
  dataLong,
  formulaEvent,
  dataEvent,
  time_var,
  id_var,
  family = gaussian,
  assoc = "etavalue",
  lag_assoc = 0,
  grp_assoc,
  scale_assoc = NULL,
  epsilon = 1e-05,
  basehaz = c("bs", "weibull", "piecewise"),
  basehaz_ops,
  qnodes = 15,
  init = "prefit",
  weights,
  priorLong = normal(autoscale = TRUE),
  priorLong_intercept = normal(autoscale = TRUE),
  priorLong_aux = cauchy(0, 5, autoscale = TRUE),
  priorEvent = normal(autoscale = TRUE),
  priorEvent_intercept = normal(autoscale = TRUE),
  priorEvent_aux = cauchy(autoscale = TRUE),
  priorEvent_assoc = normal(autoscale = TRUE),
  prior_covariance = lkj(autoscale = TRUE),
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank"),
  adapt_delta = NULL,
  max_treedepth = 10L,
  QR = FALSE,
  sparse = FALSE,
  ...
)
```

Arguments

formulaLong	A two-sided linear formula object describing both the fixed-effects and random-effects parts of the longitudinal submodel, similar in vein to formula specification in the **lme4** package (see glmer or the **lme4** vignette for details). Note however that the double bar (||) notation is not allowed when specifying the random-effects parts of the formula, and neither are nested grouping factors (e.g. (1 | g1/g2)) or (1 | g1:g2), where g1, g2 are grouping factors. Offset terms can also be included in the model formula. For a multivariate joint model (i.e. more than one longitudinal marker) this should be a list of such formula objects, with each element of the list providing the formula for one of the longitudinal submodels.
dataLong	A data frame containing the variables specified in formulaLong. If fitting a multivariate joint model, then this can be either a single data frame which contains the data for all longitudinal submodels, or it can be a list of data frames where each element of the list provides the data for one of the longitudinal submodels.
formulaEvent	A two-sided formula object describing the event submodel. The left hand side of the formula should be a Surv() object. See Surv.
dataEvent	A data frame containing the variables specified in formulaEvent.
time_var	A character string specifying the name of the variable in dataLong which represents time.
id_var	A character string specifying the name of the variable in dataLong which distinguishes between individuals. This can be left unspecified if there is only one grouping factor (which is assumed to be the individual). If there is more than one grouping factor (i.e. clustering beyond the level of the individual) then the id_var argument must be specified.
family	The family (and possibly also the link function) for the longitudinal submodel(s). See glmer for details. If fitting a multivariate joint model, then this can optionally be a list of families, in which case each element of the list specifies the family for one of the longitudinal submodels.
assoc	A character string or character vector specifying the joint model association structure. Possible association structures that can be used include: "etavalue" (the default); "etaslope"; "etaauc"; "muvalue"; "muslope"; "muauc"; "shared_b"; "shared_coef"; or "null". These are described in the **Details** section below. For a multivariate joint model, different association structures can optionally be used for each longitudinal submodel by specifying a list of character vectors, with each element of the list specifying the desired association structure for one of the longitudinal submodels. Specifying assoc = NULL will fit a joint model with no association structure (equivalent to fitting separate longitudinal and time-to-event models). It is also possible to include interaction terms between the association term ("etavalue", "etaslope", "muvalue", "muslope") and observed data/covariates. It is also possible, when fitting a multivariate joint model, to include interaction terms between the association terms ("etavalue" or "muvalue") corresponding to the different longitudinal outcomes. See the **Details** section as well as the **Examples** below.
lag_assoc	A non-negative scalar specifying the time lag that should be used for the association structure. That is, the hazard of the event at time t will be assumed to

be associated with the value/slope/auc of the longitudinal marker at time *t*-*u*, where *u* is the time lag. If fitting a multivariate joint model, then a different time lag can be used for each longitudinal marker by providing a numeric vector of lags, otherwise if a scalar is provided then the specified time lag will be used for all longitudinal markers. Note however that only one time lag can be specified for linking each longitudinal marker to the event, and that that time lag will be used for all association structure types (e.g. `"etavalue"`, `"etaslope"`, `"etaauc"`, `"muvalue"`, etc) that are specified for that longitudinal marker in the `assoc` argument.

`grp_assoc` Character string specifying the method for combining information across lower level units clustered within an individual when forming the association structure. This is only relevant when a grouping factor is specified in `formulaLong` that corresponds to clustering within individuals. This can be specified as either `"sum"`, `mean`, `"min"` or `"max"`. For example, specifying `grp_assoc = "sum"` indicates that the association structure should be based on a summation across the lower level units clustered within an individual, or specifying `grp_assoc = "mean"` indicates that the association structure should be based on the mean (i.e. average) taken across the lower level units clustered within an individual. So, for example, specifying `assoc = "muvalue"` and `grp_assoc = "sum"` would mean that the log hazard at time *t* for individual *i* would be linearly related to the sum of the expected values at time *t* for each of the lower level units (which may be for example tumor lesions) clustered within that individual.

`scale_assoc` A non-zero numeric value specifying an optional scaling parameter for the association structure. This multiplicatively scales the value/slope/auc of the longitudinal marker by `scale_assoc` within the event submodel. When fitting a multivariate joint model, a scaling parameter must be specified for each longitudinal submodel using a vector of numeric values. Note that only one scaling parameter can be specified for each longitudinal submodel, and it will be used for all association structure types (e.g. `"etavalue"`, `"etaslope"`, `"etaauc"`, `"muvalue"`, etc) that are specified for that longitudinal marker in the `assoc` argument.

`epsilon` The half-width of the central difference used to numerically calculate the derivate when the `"etaslope"` association structure is used.

`basehaz` A character string indicating which baseline hazard to use for the event submodel. Options are a B-splines approximation estimated for the log baseline hazard (`"bs"`, the default), a Weibull baseline hazard (`"weibull"`), or a piecewise constant baseline hazard (`"piecewise"`). (Note however that there is currently limited post-estimation functionality available for models estimated using a piecewise constant baseline hazard).

`basehaz_ops` A named list specifying options related to the baseline hazard. Currently this can include:

- `df` A positive integer specifying the degrees of freedom for the B-splines if `basehaz = "bs"`, or the number of intervals used for the piecewise constant baseline hazard if `basehaz = "piecewise"`. The default is 6.
- `knots` An optional numeric vector specifying the internal knot locations for the B-splines if `basehaz = "bs"`, or the internal cut-points for defining inter-

vals of the piecewise constant baseline hazard if basehaz = "piecewise". Knots cannot be specified if df is specified. If not specified, then the default is to use df - 4 knots if basehaz = "bs", or df - 1 knots if basehaz = "piecewise", which are placed at equally spaced percentiles of the distribution of observed event times.

qnodes The number of nodes to use for the Gauss-Kronrod quadrature that is used to evaluate the cumulative hazard in the likelihood function. Options are 15 (the default), 11 or 7.

init The method for generating the initial values for the MCMC. The default is "prefit", which uses those obtained from fitting separate longitudinal and time-to-event models prior to fitting the joint model. The separate longitudinal model is a (possibly multivariate) generalised linear mixed model estimated using variational bayes. This is achieved via the stan_mvmer function with algorithm = "meanfield". The separate Cox model is estimated using coxph. This is achieved using the and time-to-event models prior to fitting the joint model. The separate models are estimated using the glmer and coxph functions. This should provide reasonable initial values which should aid the MCMC sampler. Parameters that cannot be obtained from fitting separate longitudinal and time-to-event models are initialised using the "random" method for stan. However it is recommended that any final analysis should ideally be performed with several MCMC chains each initiated from a different set of initial values; this can be obtained by setting init = "random". In addition, other possibilities for specifying init are the same as those described for stan.

weights Experimental and should be used with caution. The user can optionally supply a 2-column data frame containing a set of 'prior weights' to be used in the estimation process. The data frame should contain two columns: the first containing the IDs for each individual, and the second containing the corresponding weights. The data frame should only have one row for each individual; that is, weights should be constant within individuals.

priorLong, priorEvent, priorEvent_assoc

The prior distributions for the regression coefficients in the longitudinal submodel(s), event submodel, and the association parameter(s). Can be a call to one of the various functions provided by **rstanarm** for specifying priors. The subset of these functions that can be used for the prior on the coefficients can be grouped into several "families":

Family	**Functions**
Student t family	normal, student_t, cauchy
Hierarchical shrinkage family	hs, hs_plus
Laplace family	laplace, lasso

See the priors help page for details on the families and how to specify the arguments for all of the functions in the table above. To omit a prior —i.e., to use a flat (improper) uniform prior— prior can be set to NULL, although this is rarely a good idea.

Note: Unless QR=TRUE, if prior is from the Student t family or Laplace family, and if the autoscale argument to the function used to specify the prior

(e.g. normal) is left at its default and recommended value of TRUE, then the default or user-specified prior scale(s) may be adjusted internally based on the scales of the predictors. See the priors help page for details on the rescaling and the prior_summary function for a summary of the priors used for a particular model.

priorLong_intercept, priorEvent_intercept

The prior distributions for the intercepts in the longitudinal submodel(s) and event submodel. Can be a call to normal, student_t or cauchy. See the priors help page for details on these functions. To omit a prior on the intercept —i.e., to use a flat (improper) uniform prior— prior_intercept can be set to NULL.

Note: The prior distribution for the intercept is set so it applies to the value when all predictors are centered. Moreover, note that a prior is only placed on the intercept for the event submodel when a Weibull baseline hazard has been specified. For the B-splines and piecewise constant baseline hazards there is not intercept parameter that is given a prior distribution; an intercept parameter will be shown in the output for the fitted model, but this just corresponds to the necessary post-estimation adjustment in the linear predictor due to the centering of the predictiors in the event submodel.

priorLong_aux The prior distribution for the "auxiliary" parameters in the longitudinal submodels (if applicable). The "auxiliary" parameter refers to a different parameter depending on the family. For Gaussian models priorLong_aux controls "sigma", the error standard deviation. For negative binomial models priorLong_aux controls "reciprocal_dispersion", which is similar to the "size" parameter of rnbinom: smaller values of "reciprocal_dispersion" correspond to greater dispersion. For gamma models priorLong_aux sets the prior on to the "shape" parameter (see e.g., rgamma), and for inverse-Gaussian models it is the so-called "lambda" parameter (which is essentially the reciprocal of a scale parameter). Binomial and Poisson models do not have auxiliary parameters.

priorLong_aux can be a call to exponential to use an exponential distribution, or normal, student_t or cauchy, which results in a half-normal, half-t, or half-Cauchy prior. See priors for details on these functions. To omit a prior —i.e., to use a flat (improper) uniform prior— set priorLong_aux to NULL.

If fitting a multivariate joint model, you have the option to specify a list of prior distributions, however the elements of the list that correspond to any longitudinal submodel which does not have an auxiliary parameter will be ignored.

priorEvent_aux The prior distribution for the "auxiliary" parameters in the event submodel. The "auxiliary" parameters refers to different parameters depending on the baseline hazard. For basehaz = "weibull" the auxiliary parameter is the Weibull shape parameter. For basehaz = "bs" the auxiliary parameters are the coefficients for the B-spline approximation to the log baseline hazard. For basehaz = "piecewise" the auxiliary parameters are the piecewise estimates of the log baseline hazard.

prior_covariance

Cannot be NULL; see priors for more information about the prior distributions on covariance matrices. Note however that the default prior for covariance matrices in stan_jm is slightly different to that in stan_glmer (the details of which are described on the priors page).

prior_PD — A logical scalar (defaulting to FALSE) indicating whether to draw from the prior predictive distribution instead of conditioning on the outcome.

algorithm — A string (possibly abbreviated) indicating the estimation approach to use. Can be "sampling" for MCMC (the default), "optimizing" for optimization, "meanfield" for variational inference with independent normal distributions, or "fullrank" for variational inference with a multivariate normal distribution. See rstanarm-package for more details on the estimation algorithms. NOTE: not all fitting functions support all four algorithms.

adapt_delta — Only relevant if algorithm="sampling". See the adapt_delta help page for details.

max_treedepth — A positive integer specifying the maximum treedepth for the non-U-turn sampler. See the control argument in stan.

QR — A logical scalar defaulting to FALSE, but if TRUE applies a scaled qr decomposition to the design matrix. The transformation does not change the likelihood of the data but is recommended for computational reasons when there are multiple predictors. See the QR-argument documentation page for details on how **rstanarm** does the transformation and important information about how to interpret the prior distributions of the model parameters when using QR=TRUE.

sparse — A logical scalar (defaulting to FALSE) indicating whether to use a sparse representation of the design (X) matrix. If TRUE, the the design matrix is not centered (since that would destroy the sparsity) and likewise it is not possible to specify both QR = TRUE and sparse = TRUE. Depending on how many zeros there are in the design matrix, setting sparse = TRUE may make the code run faster and can consume much less RAM.

... — Further arguments passed to the function in the **rstan** package (sampling, vb, or optimizing), corresponding to the estimation method named by algorithm. For example, if algorithm is "sampling" it is possible to specify iter, chains, cores, and other MCMC controls.

Another useful argument that can be passed to **rstan** via ... is refresh, which specifies how often to print updates when sampling (i.e., show the progress every refresh iterations). refresh=0 turns off the iteration updates.

Details

The stan_jm function can be used to fit a joint model (also known as a shared parameter model) for longitudinal and time-to-event data under a Bayesian framework. The underlying estimation is carried out using the Bayesian C++ package Stan (https://mc-stan.org/).

The joint model may be univariate (with only one longitudinal submodel) or multivariate (with more than one longitudinal submodel). For the longitudinal submodel a (possibly multivariate) generalised linear mixed model is assumed with any of the family choices allowed by glmer. If a multivariate joint model is specified (by providing a list of formulas in the formulaLong argument), then the multivariate longitudinal submodel consists of a multivariate generalized linear model (GLM) with group-specific terms that are assumed to be correlated across the different GLM submodels. That is, within a grouping factor (for example, patient ID) the group-specific terms are assumed to be correlated across the different GLM submodels. It is possible to specify a different

outcome type (for example a different family and/or link function) for each of the GLM submodels, by providing a list of family objects in the family argument. Multi-level clustered data are allowed, and that additional clustering can occur at a level higher than the individual-level (e.g. patients clustered within clinics), or at a level lower than the individual-level (e.g. tumor lesions clustered within patients). If the clustering occurs at a level lower than the individual, then the user needs to indicate how the lower level clusters should be handled when forming the association structure between the longitudinal and event submodels (see the grp_assoc argument described above).

For the event submodel a parametric proportional hazards model is assumed. The baseline hazard can be estimated using either a cubic B-splines approximation (basehaz = "bs", the default), a Weibull distribution (basehaz = "weibull"), or a piecewise constant baseline hazard (basehaz = "piecewise"). If the B-spline or piecewise constant baseline hazards are used, then the degrees of freedom or the internal knot locations can be (optionally) specified. If the degrees of freedom are specified (through the df argument) then the knot locations are automatically generated based on the distribution of the observed event times (not including censoring times). Otherwise internal knot locations can be specified directly through the knots argument. If neither df or knots is specified, then the default is to set df equal to 6. It is not possible to specify both df and knots.

Time-varying covariates are allowed in both the longitudinal and event submodels. These should be specified in the data in the same way as they normally would when fitting a separate longitudinal model using lmer or a separate time-to-event model using coxph. These time-varying covariates should be exogenous in nature, otherwise they would perhaps be better specified as an additional outcome (i.e. by including them as an additional longitudinal outcome in the joint model).

Bayesian estimation of the joint model is performed via MCMC. The Bayesian model includes independent priors on the regression coefficients for both the longitudinal and event submodels, including the association parameter(s) (in much the same way as the regression parameters in stan_glm) and priors on the terms of a decomposition of the covariance matrices of the group-specific parameters. See priors for more information about the priors distributions that are available.

Gauss-Kronrod quadrature is used to numerically evaluate the integral over the cumulative hazard in the likelihood function for the event submodel. The accuracy of the numerical approximation can be controlled using the number of quadrature nodes, specified through the qnodes argument. Using a higher number of quadrature nodes will result in a more accurate approximation.

Association structures: The association structure for the joint model can be based on any of the following parameterisations:

- current value of the linear predictor in the longitudinal submodel ("etavalue")
- first derivative (slope) of the linear predictor in the longitudinal submodel ("etaslope")
- the area under the curve of the linear predictor in the longitudinal submodel ("etaauc")
- current expected value of the longitudinal submodel ("muvalue")
- the area under the curve of the expected value from the longitudinal submodel ("muauc")
- shared individual-level random effects ("shared_b")
- shared individual-level random effects which also incorporate the corresponding fixed effect as well as any corresponding random effects for clustering levels higher than the individual) ("shared_coef")

- interactions between association terms and observed data/covariates ("etavalue_data", "etaslope_data", "muvalue_data", "muslope_data"). These are described further below.
- interactions between association terms corresponding to different longitudinal outcomes in a multivariate joint model ("etavalue_etavalue(#)", "etavalue_muvalue(#)", "muvalue_etavalue(#)", "muvalue_muvalue(#)"). These are described further below.
- no association structure (equivalent to fitting separate longitudinal and event models) ("null" or NULL)

More than one association structure can be specified, however, not all possible combinations are allowed. Note that for the lagged association structures baseline values (time = 0) are used for the instances where the time lag results in a time prior to baseline. When using the "etaauc" or "muauc" association structures, the area under the curve is evaluated using Gauss-Kronrod quadrature with 15 quadrature nodes. By default, "shared_b" and "shared_coef" contribute all random effects to the association structure; however, a subset of the random effects can be chosen by specifying their indices between parentheses as a suffix, for example, "shared_b(1)" or "shared_b(1:3)" or "shared_b(1,2,4)", and so on.

In addition, several association terms ("etavalue", "etaslope", "muvalue", "muslope") can be interacted with observed data/covariates. To do this, use the association term's main handle plus a suffix of "_data" then followed by the model matrix formula in parentheses. For example if we had a variable in our dataset for gender named sex then we might want to obtain different estimates for the association between the current slope of the marker and the risk of the event for each gender. To do this we would specify assoc = c("etaslope", "etaslope_data(~ sex)").

It is also possible, when fitting a multivariate joint model, to include interaction terms between the association terms themselves (this only applies for interacting "etavalue" or "muvalue"). For example, if we had a joint model with two longitudinal markers, we could specify assoc = list(c("etavalue", "etavalue_etavalue(2)"), "etavalue"). The first element of list says we want to use the value of the linear predictor for the first marker, as well as it's interaction with the value of the linear predictor for the second marker. The second element of the list says we want to also include the expected value of the second marker (i.e. as a "main effect"). Therefore, the linear predictor for the event submodel would include the "main effects" for each marker as well as their interaction.

There are additional examples in the **Examples** section below.

Value

A stanjm object is returned.

See Also

stanreg-objects, stanmvreg-methods, print.stanmvreg, summary.stanmvreg, posterior_traj, posterior_survfit, posterior_predict, posterior_interval, pp_check, ps_check, stan_mvmer.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch !="i386") {
```

```
#####
# Univariate joint model, with association structure based on the
# current value of the linear predictor
f1 <- stan_jm(formulaLong = logBili ~ year + (1 | id),
              dataLong = pbcLong,
              formulaEvent = Surv(futimeYears, death) ~ sex + trt,
              dataEvent = pbcSurv,
              time_var = "year",
              # this next line is only to keep the example small in size!
              chains = 1, cores = 1, seed = 12345, iter = 1000)
print(f1)
summary(f1)

#####
# Univariate joint model, with association structure based on the
# current value and slope of the linear predictor
f2 <- stan_jm(formulaLong = logBili ~ year + (year | id),
              dataLong = pbcLong,
              formulaEvent = Surv(futimeYears, death) ~ sex + trt,
              dataEvent = pbcSurv,
              assoc = c("etavalue", "etaslope"),
              time_var = "year",
              chains = 1, cores = 1, seed = 12345, iter = 1000)
print(f2)

#####
# Univariate joint model, with association structure based on the
# lagged value of the linear predictor, where the lag is 2 time
# units (i.e. 2 years in this example)
f3 <- stan_jm(formulaLong = logBili ~ year + (1 | id),
              dataLong = pbcLong,
              formulaEvent = Surv(futimeYears, death) ~ sex + trt,
              dataEvent = pbcSurv,
              time_var = "year",
              assoc = "etavalue", lag_assoc = 2,
              chains = 1, cores = 1, seed = 12345, iter = 1000)
print(f3)

#####
# Univariate joint model, where the association structure includes
# interactions with observed data. Here we specify that we want to use
# an association structure based on the current value of the linear
# predictor from the longitudinal submodel (i.e. "etavalue"), but we
# also want to interact this with the treatment covariate (trt) from
# pbcLong data frame, so that we can estimate a different association
# parameter (i.e. estimated effect of log serum bilirubin on the log
# hazard of death) for each treatment group
f4 <- stan_jm(formulaLong = logBili ~ year + (1 | id),
              dataLong = pbcLong,
              formulaEvent = Surv(futimeYears, death) ~ sex + trt,
              dataEvent = pbcSurv,
              time_var = "year",
              assoc = c("etavalue", "etavalue_data(~ trt)"),
```

```
              chains = 1, cores = 1, seed = 12345, iter = 1000)
print(f4)

######
# Multivariate joint model, with association structure based
# on the current value and slope of the linear predictor in the
# first longitudinal submodel and the area under the marker
# trajectory for the second longitudinal submodel
mv1 <- stan_jm(
        formulaLong = list(
          logBili ~ year + (1 | id),
          albumin ~ sex + year + (year | id)),
        dataLong = pbcLong,
        formulaEvent = Surv(futimeYears, death) ~ sex + trt,
        dataEvent = pbcSurv,
        assoc = list(c("etavalue", "etaslope"), "etaauc"),
        time_var = "year",
        chains = 1, cores = 1, seed = 12345, iter = 100)
print(mv1)

#####
# Multivariate joint model, where the association structure is formed by
# including the expected value of each longitudinal marker (logBili and
# albumin) in the linear predictor of the event submodel, as well as their
# interaction effect (i.e. the interaction between the two "etavalue" terms).
# Note that whether such an association structure based on a marker by
# marker interaction term makes sense will depend on the context of your
# application -- here we just show it for demostration purposes).
mv2 <- stan_jm(
        formulaLong = list(
          logBili ~ year + (1 | id),
          albumin ~ sex + year + (year | id)),
        dataLong = pbcLong,
        formulaEvent = Surv(futimeYears, death) ~ sex + trt,
        dataEvent = pbcSurv,
        assoc = list(c("etavalue", "etavalue_etavalue(2)"), "etavalue"),
        time_var = "year",
        chains = 1, cores = 1, seed = 12345, iter = 100)

#####
# Multivariate joint model, with one bernoulli marker and one
# Gaussian marker. We will artificially create the bernoulli
# marker by dichotomising log serum bilirubin
pbcLong$ybern <- as.integer(pbcLong$logBili >= mean(pbcLong$logBili))
mv3 <- stan_jm(
        formulaLong = list(
          ybern ~ year + (1 | id),
          albumin ~ sex + year + (year | id)),
        dataLong = pbcLong,
        formulaEvent = Surv(futimeYears, death) ~ sex + trt,
        dataEvent = pbcSurv,
        family = list(binomial, gaussian),
        time_var = "year",
```

```
          chains = 1, cores = 1, seed = 12345, iter = 1000)
}
```

`stan_mvmer` *Bayesian multivariate generalized linear models with correlated group-specific terms via Stan*

Description

Bayesian inference for multivariate GLMs with group-specific coefficients that are assumed to be correlated across the GLM submodels.

Usage

```
stan_mvmer(
  formula,
  data,
  family = gaussian,
  weights,
  prior = normal(autoscale = TRUE),
  prior_intercept = normal(autoscale = TRUE),
  prior_aux = cauchy(0, 5, autoscale = TRUE),
  prior_covariance = lkj(autoscale = TRUE),
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank"),
  adapt_delta = NULL,
  max_treedepth = 10L,
  init = "random",
  QR = FALSE,
  sparse = FALSE,
  ...
)
```

Arguments

`formula` A two-sided linear formula object describing both the fixed-effects and random-effects parts of the longitudinal submodel similar in vein to formula specification in the **lme4** package (see `glmer` or the **lme4** vignette for details). Note however that the double bar (`||`) notation is not allowed when specifying the random-effects parts of the formula, and neither are nested grouping factors (e.g. `(1 | g1/g2))` or `(1 | g1:g2)`, where `g1`, `g2` are grouping factors. For a multivariate GLM this should be a list of such formula objects, with each element of the list providing the formula for one of the GLM submodels.

`data` A data frame containing the variables specified in `formula`. For a multivariate GLM, this can be either a single data frame which contains the data for all GLM submodels, or it can be a list of data frames where each element of the list provides the data for one of the GLM submodels.

`family` The family (and possibly also the link function) for the GLM submodel(s). See `glmer` for details. If fitting a multivariate GLM, then this can optionally be a list of families, in which case each element of the list specifies the family for one of the GLM submodels. In other words, a different family can be specified for each GLM submodel.

`weights` Same as in `glm`, except that when fitting a multivariate GLM and a list of data frames is provided in `data` then a corresponding list of weights must be provided. If weights are provided for one of the GLM submodels, then they must be provided for all GLM submodels.

`prior`, `prior_intercept`, `prior_aux`
Same as in `stan_glmer` except that for a multivariate GLM a list of priors can be provided for any of `prior`, `prior_intercept` or `prior_aux` arguments. That is, different priors can optionally be specified for each of the GLM submodels. If a list is not provided, then the same prior distributions are used for each GLM submodel. Note that the `"product_normal"` prior is not allowed for `stan_mvmer`.

`prior_covariance`
Cannot be `NULL`; see `priors` for more information about the prior distributions on covariance matrices. Note however that the default prior for covariance matrices in `stan_mvmer` is slightly different to that in `stan_glmer` (the details of which are described on the `priors` page).

`prior_PD` A logical scalar (defaulting to `FALSE`) indicating whether to draw from the prior predictive distribution instead of conditioning on the outcome.

`algorithm` A string (possibly abbreviated) indicating the estimation approach to use. Can be `"sampling"` for MCMC (the default), `"optimizing"` for optimization, `"meanfield"` for variational inference with independent normal distributions, or `"fullrank"` for variational inference with a multivariate normal distribution. See `rstanarm-package` for more details on the estimation algorithms. NOTE: not all fitting functions support all four algorithms.

`adapt_delta` Only relevant if `algorithm="sampling"`. See the adapt_delta help page for details.

`max_treedepth` A positive integer specifying the maximum treedepth for the non-U-turn sampler. See the `control` argument in `stan`.

`init` The method for generating initial values. See `stan`.

`QR` A logical scalar defaulting to `FALSE`, but if `TRUE` applies a scaled `qr` decomposition to the design matrix. The transformation does not change the likelihood of the data but is recommended for computational reasons when there are multiple predictors. See the QR-argument documentation page for details on how **rstanarm** does the transformation and important information about how to interpret the prior distributions of the model parameters when using `QR=TRUE`.

`sparse` A logical scalar (defaulting to `FALSE`) indicating whether to use a sparse representation of the design (X) matrix. If `TRUE`, the the design matrix is not centered

(since that would destroy the sparsity) and likewise it is not possible to specify both QR = TRUE and sparse = TRUE. Depending on how many zeros there are in the design matrix, setting sparse = TRUE may make the code run faster and can consume much less RAM.

... Further arguments passed to the function in the **rstan** package (sampling, vb, or optimizing), corresponding to the estimation method named by algorithm. For example, if algorithm is "sampling" it is possible to specify iter, chains, cores, and other MCMC controls.

Another useful argument that can be passed to **rstan** via ... is refresh, which specifies how often to print updates when sampling (i.e., show the progress every refresh iterations). refresh=0 turns off the iteration updates.

Details

The stan_mvmer function can be used to fit a multivariate generalized linear model (GLM) with group-specific terms. The model consists of distinct GLM submodels, each which contains group-specific terms; within a grouping factor (for example, patient ID) the grouping-specific terms are assumed to be correlated across the different GLM submodels. It is possible to specify a different outcome type (for example a different family and/or link function) for each of the GLM submodels.

Bayesian estimation of the model is performed via MCMC, in the same way as for stan_glmer. Also, similar to stan_glmer, an unstructured covariance matrix is used for the group-specific terms within a given grouping factor, with priors on the terms of a decomposition of the covariance matrix.See priors for more information about the priors distributions that are available for the covariance matrices, the regression coefficients and the intercept and auxiliary parameters.

Value

A stanmvreg object is returned.

See Also

stan_glmer, stan_jm, stanreg-objects, stanmvreg-methods, print.stanmvreg, summary.stanmvreg, posterior_predict, posterior_interval.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch !="i386") {

#####
# A multivariate GLM with two submodels. For the grouping factor 'id', the
# group-specific intercept from the first submodel (logBili) is assumed to
# be correlated with the group-specific intercept and linear slope in the
# second submodel (albumin)
f1 <- stan_mvmer(
        formula = list(
          logBili ~ year + (1 | id),
          albumin ~ sex + year + (year | id)),
        data = pbcLong,
        # this next line is only to keep the example small in size!
```

```
        chains = 1, cores = 1, seed = 12345, iter = 1000)
summary(f1)

#####
# A multivariate GLM with one bernoulli outcome and one
# gaussian outcome. We will artificially create the bernoulli
# outcome by dichotomising log serum bilirubin
pbcLong$ybern <- as.integer(pbcLong$logBili >= mean(pbcLong$logBili))
f2 <- stan_mvmer(
        formula = list(
          ybern ~ year + (1 | id),
          albumin ~ sex + year + (year | id)),
        data = pbcLong,
        family = list(binomial, gaussian),
        chains = 1, cores = 1, seed = 12345, iter = 1000)

}
```

---

stan_nlmer *Bayesian nonlinear models with group-specific terms via Stan*

Description

Bayesian inference for NLMMs with group-specific coefficients that have unknown covariance matrices with flexible priors.

Usage

```
stan_nlmer(
  formula,
  data = NULL,
  subset,
  weights,
  na.action,
  offset,
  contrasts = NULL,
  ...,
  prior = normal(autoscale = TRUE),
  prior_aux = exponential(autoscale = TRUE),
  prior_covariance = decov(),
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank"),
  adapt_delta = NULL,
  QR = FALSE,
  sparse = FALSE
)
```

Arguments

`formula, data` Same as for `nlmer`. *We strongly advise against omitting the* `data` *argument.* Unless `data` is specified (and is a data frame) many post-estimation functions (including `update`, `loo`, `kfold`) are not guaranteed to work properly.

`subset, weights, offset`
Same as `glm`.

`na.action, contrasts`
Same as `glm`, but rarely specified.

`...` Further arguments passed to the function in the **rstan** package (`sampling`, `vb`, or `optimizing`), corresponding to the estimation method named by `algorithm`. For example, if `algorithm` is `"sampling"` it is possible to specify `iter`, `chains`, `cores`, and other MCMC controls.

Another useful argument that can be passed to **rstan** via `...` is `refresh`, which specifies how often to print updates when sampling (i.e., show the progress every `refresh` iterations). `refresh=0` turns off the iteration updates.

`prior` The prior distribution for the (non-hierarchical) regression coefficients.

The default priors are described in the vignette *Prior Distributions for rstanarm Models*. If not using the default, `prior` should be a call to one of the various functions provided by **rstanarm** for specifying priors. The subset of these functions that can be used for the prior on the coefficients can be grouped into several "families":

Family	**Functions**
Student t family	`normal`, `student_t`, `cauchy`
Hierarchical shrinkage family	`hs`, `hs_plus`
Laplace family	`laplace`, `lasso`
Product normal family	`product_normal`

See the priors help page for details on the families and how to specify the arguments for all of the functions in the table above. To omit a prior —i.e., to use a flat (improper) uniform prior— `prior` can be set to `NULL`, although this is rarely a good idea.

Note: Unless `QR=TRUE`, if `prior` is from the Student t family or Laplace family, and if the `autoscale` argument to the function used to specify the prior (e.g. `normal`) is left at its default and recommended value of `TRUE`, then the default or user-specified prior scale(s) may be adjusted internally based on the scales of the predictors. See the priors help page and the *Prior Distributions* vignette for details on the rescaling and the `prior_summary` function for a summary of the priors used for a particular model.

`prior_aux` The prior distribution for the "auxiliary" parameter (if applicable). The "auxiliary" parameter refers to a different parameter depending on the `family`. For Gaussian models `prior_aux` controls `"sigma"`, the error standard deviation. For negative binomial models `prior_aux` controls `"reciprocal_dispersion"`, which is similar to the `"size"` parameter of `rnbinom`: smaller values of `"reciprocal_dispersion"` correspond to greater dispersion. For gamma models `prior_aux` sets the prior

on to the "shape" parameter (see e.g., rgamma), and for inverse-Gaussian models it is the so-called "lambda" parameter (which is essentially the reciprocal of a scale parameter). Binomial and Poisson models do not have auxiliary parameters.

The default prior is described in the vignette *Prior Distributions for rstanarm Models*. If not using the default, prior_aux can be a call to exponential to use an exponential distribution, or normal, student_t or cauchy, which results in a half-normal, half-t, or half-Cauchy prior. See priors for details on these functions. To omit a prior —i.e., to use a flat (improper) uniform prior— set prior_aux to NULL.

prior_covariance

Cannot be NULL; see decov for more information about the default arguments.

prior_PD

A logical scalar (defaulting to FALSE) indicating whether to draw from the prior predictive distribution instead of conditioning on the outcome.

algorithm

A string (possibly abbreviated) indicating the estimation approach to use. Can be "sampling" for MCMC (the default), "optimizing" for optimization, "meanfield" for variational inference with independent normal distributions, or "fullrank" for variational inference with a multivariate normal distribution. See rstanarm-package for more details on the estimation algorithms. NOTE: not all fitting functions support all four algorithms.

adapt_delta

Only relevant if algorithm="sampling". See the adapt_delta help page for details.

QR

A logical scalar defaulting to FALSE, but if TRUE applies a scaled qr decomposition to the design matrix. The transformation does not change the likelihood of the data but is recommended for computational reasons when there are multiple predictors. See the QR-argument documentation page for details on how **rstanarm** does the transformation and important information about how to interpret the prior distributions of the model parameters when using QR=TRUE.

sparse

A logical scalar (defaulting to FALSE) indicating whether to use a sparse representation of the design (X) matrix. If TRUE, the the design matrix is not centered (since that would destroy the sparsity) and likewise it is not possible to specify both QR = TRUE and sparse = TRUE. Depending on how many zeros there are in the design matrix, setting sparse = TRUE may make the code run faster and can consume much less RAM.

Details

The stan_nlmer function is similar in syntax to nlmer but rather than performing (approximate) maximum marginal likelihood estimation, Bayesian estimation is by default performed via MCMC. The Bayesian model adds independent priors on the "coefficients" — which are really intercepts — in the same way as stan_nlmer and priors on the terms of a decomposition of the covariance matrices of the group-specific parameters. See priors for more information about the priors.

The supported transformation functions are limited to the named "self-starting" functions in the **stats** library: SSasymp, SSasympOff, SSasympOrig, SSbiexp, SSfol, SSfpl, SSgompertz, SSlogis, SSmicmen, and SSweibull.

Value

A stanreg object is returned for stan_nlmer.

See Also

stanreg-methods and nlmer.

The vignette for stan_glmer, which also discusses stan_nlmer models. https://mc-stan.org/rstanarm/articles/

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch !="i386") {

data("Orange", package = "datasets")
Orange$circumference <- Orange$circumference / 100
Orange$age <- Orange$age / 100
fit <- stan_nlmer(
  circumference ~ SSlogis(age, Asym, xmid, scal) ~ Asym|Tree,
  data = Orange,
  # for speed only
  chains = 1,
  iter = 1000
 )
print(fit)
posterior_interval(fit)
plot(fit, regex_pars = "b\\[")

}
```

---

stan_polr *Bayesian ordinal regression models via Stan*

Description

Bayesian inference for ordinal (or binary) regression models under a proportional odds assumption.

Usage

```
stan_polr(
  formula,
  data,
  weights,
  ...,
  subset,
  na.action = getOption("na.action", "na.omit"),
  contrasts = NULL,
  model = TRUE,
  method = c("logistic", "probit", "loglog", "cloglog", "cauchit"),
```

```
  prior = R2(stop("'location' must be specified")),
  prior_counts = dirichlet(1),
  shape = NULL,
  rate = NULL,
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank"),
  adapt_delta = NULL,
  do_residuals = NULL
)

stan_polr.fit(
  x,
  y,
  wt = NULL,
  offset = NULL,
  method = c("logistic", "probit", "loglog", "cloglog", "cauchit"),
  ...,
  prior = R2(stop("'location' must be specified")),
  prior_counts = dirichlet(1),
  shape = NULL,
  rate = NULL,
  prior_PD = FALSE,
  algorithm = c("sampling", "meanfield", "fullrank"),
  adapt_delta = NULL,
  do_residuals = algorithm == "sampling"
)
```

Arguments

`formula`, `data`, `subset`
: Same as `polr`, but *we strongly advise against omitting the* `data` *argument*. Unless `data` is specified (and is a data frame) many post-estimation functions (including `update`, `loo`, `kfold`) are not guaranteed to work properly.

`weights`, `na.action`, `contrasts`, `model`
: Same as `polr`, but rarely specified.

`...`
: Further arguments passed to the function in the **rstan** package (`sampling`, `vb`, or `optimizing`), corresponding to the estimation method named by `algorithm`. For example, if `algorithm` is `"sampling"` it is possible to specify `iter`, `chains`, `cores`, and other MCMC controls.

  Another useful argument that can be passed to **rstan** via `...` is `refresh`, which specifies how often to print updates when sampling (i.e., show the progress every `refresh` iterations). `refresh=0` turns off the iteration updates.

`method`
: One of 'logistic', 'probit', 'loglog', 'cloglog' or 'cauchit', but can be abbreviated. See `polr` for more details.

`prior`
: Prior for coefficients. Should be a call to `R2` to specify the prior location of the R^2 but can be `NULL` to indicate a standard uniform prior. See `priors`.

`prior_counts`
: A call to `dirichlet` to specify the prior counts of the outcome when the predictors are at their sample means.

shape	Either NULL or a positive scalar that is interpreted as the shape parameter for a GammaDistribution on the exponent applied to the probability of success when there are only two outcome categories. If NULL, which is the default, then the exponent is taken to be fixed at 1.
rate	Either NULL or a positive scalar that is interpreted as the rate parameter for a GammaDistribution on the exponent applied to the probability of success when there are only two outcome categories. If NULL, which is the default, then the exponent is taken to be fixed at 1.
prior_PD	A logical scalar (defaulting to FALSE) indicating whether to draw from the prior predictive distribution instead of conditioning on the outcome.
algorithm	A string (possibly abbreviated) indicating the estimation approach to use. Can be "sampling" for MCMC (the default), "optimizing" for optimization, "meanfield" for variational inference with independent normal distributions, or "fullrank" for variational inference with a multivariate normal distribution. See rstanarm-package for more details on the estimation algorithms. NOTE: not all fitting functions support all four algorithms.
adapt_delta	Only relevant if algorithm="sampling". See the adapt_delta help page for details.
do_residuals	A logical scalar indicating whether or not to automatically calculate fit residuals after sampling completes. Defaults to TRUE if and only if algorithm="sampling". Setting do_residuals=FALSE is only useful in the somewhat rare case that stan_polr appears to finish sampling but hangs instead of returning the fitted model object.
x	A design matrix.
y	A response variable, which must be a (preferably ordered) factor.
wt	A numeric vector (possibly NULL) of observation weights.
offset	A numeric vector (possibly NULL) of offsets.

Details

The stan_polr function is similar in syntax to polr but rather than performing maximum likelihood estimation of a proportional odds model, Bayesian estimation is performed (if algorithm = "sampling") via MCMC. The stan_polr function calls the workhorse stan_polr.fit function, but it is possible to call the latter directly.

As for stan_lm, it is necessary to specify the prior location of R^2. In this case, the R^2 pertains to the proportion of variance in the latent variable (which is discretized by the cutpoints) attributable to the predictors in the model.

Prior beliefs about the cutpoints are governed by prior beliefs about the outcome when the predictors are at their sample means. Both of these are explained in the help page on priors and in the **rstanarm** vignettes.

Unlike polr, stan_polr also allows the "ordinal" outcome to contain only two levels, in which case the likelihood is the same by default as for stan_glm with family = binomial but the prior on the coefficients is different. However, stan_polr allows the user to specify the shape and rate hyperparameters, in which case the probability of success is defined as the logistic CDF of the linear predictor, raised to the power of alpha where alpha has a gamma prior with the specified shape

and rate. This likelihood is called "scobit" by Nagler (1994) because if alpha is not equal to 1, then the relationship between the linear predictor and the probability of success is skewed. If shape or rate is NULL, then alpha is assumed to be fixed to 1.

Otherwise, it is usually advisible to set shape and rate to the same number so that the expected value of alpha is 1 while leaving open the possibility that alpha may depart from 1 a little bit. It is often necessary to have a lot of data in order to estimate alpha with much precision and always necessary to inspect the Pareto shape parameters calculated by loo to see if the results are particularly sensitive to individual observations.

Users should think carefully about how the outcome is coded when using a scobit-type model. When alpha is not 1, the asymmetry implies that the probability of success is most sensitive to the predictors when the probability of success is less than 0.63. Reversing the coding of the successes and failures allows the predictors to have the greatest impact when the probability of failure is less than 0.63. Also, the gamma prior on alpha is positively skewed, but you can reverse the coding of the successes and failures to circumvent this property.

Value

A stanreg object is returned for stan_polr.

A stanfit object (or a slightly modified stanfit object) is returned if stan_polr.fit is called directly.

References

Nagler, J., (1994). Scobit: An Alternative Estimator to Logit and Probit. *American Journal of Political Science*. 230 – 255.

See Also

stanreg-methods and polr.

The vignette for stan_polr. https://mc-stan.org/rstanarm/articles/

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch !="i386") {
 fit <- stan_polr(tobgp ~ agegp, data = esoph, method = "probit",
          prior = R2(0.2, "mean"), init_r = 0.1, seed = 12345,
          algorithm = "fullrank") # for speed only
 print(fit)
 plot(fit)
}
```

stanmvreg-methods *Methods for stanmvreg objects*

Description

S3 methods for stanmvreg objects. There are also several methods (listed in **See Also**, below) with their own individual help pages. The main difference between these methods and the stanreg methods is that the methods described here generally include an additional argument `m` which allows the user to specify which submodel they wish to return the result for. If the argument `m` is set to `NULL` then the result will generally be a named list with each element of the list containing the result for one of the submodels.

Usage

```
## S3 method for class 'stanmvreg'
coef(object, m = NULL, ...)

## S3 method for class 'stanmvreg'
fitted(object, m = NULL, ...)

## S3 method for class 'stanmvreg'
residuals(object, m = NULL, ...)

## S3 method for class 'stanmvreg'
se(object, m = NULL, ...)

## S3 method for class 'stanmvreg'
formula(x, fixed.only = FALSE, random.only = FALSE, m = NULL, ...)

## S3 method for class 'stanmvreg'
update(object, formula., ..., evaluate = TRUE)

## S3 method for class 'stanjm'
update(object, formulaLong., formulaEvent., ..., evaluate = TRUE)

## S3 method for class 'stanmvreg'
fixef(object, m = NULL, remove_stub = TRUE, ...)

## S3 method for class 'stanmvreg'
ngrps(object, ...)

## S3 method for class 'stanmvreg'
ranef(object, m = NULL, ...)

## S3 method for class 'stanmvreg'
sigma(object, m = NULL, ...)
```

Arguments

object, x	A fitted model object returned by one of the multivariate **rstanarm** modelling functions. See stanreg-objects.
m	Integer specifying the number or name of the submodel
...	Ignored, except by the update method. See update.
fixed.only	A logical specifying whether to only retain the fixed effect part of the longitudinal submodel formulas
random.only	A logical specifying whether to only retain the random effect part of the longitudinal submodel formulas
formula.	An updated formula for the model. For a multivariate model formula. should be a list of formulas, as described for the formula argument in stan_mvmer.
evaluate	See update.
formulaLong., formulaEvent.	An updated formula for the longitudinal or event submodel, when object was estimated using stan_jm. For a multivariate joint model formulaLong. should be a list of formulas, as described for the formulaLong argument in stan_jm.
remove_stub	Logical specifying whether to remove the string identifying the submodel (e.g. y1|, y2|, Long1|, Long2|, Event|) from each of the parameter names.

Details

Most of these methods are similar to the methods defined for objects of class 'lm', 'glm', 'glmer', etc. However there are a few exceptions:

coef Medians are used for point estimates. See the *Point estimates* section in print.stanmvreg for more details. coef returns a list equal to the length of the number of submodels. The first elements of the list are the coefficients from each of the fitted longitudinal submodels and are the same layout as those returned by coef method of the **lme4** package, that is, the sum of the random and fixed effects coefficients for each explanatory variable for each level of each grouping factor. The final element of the returned list is a vector of fixed effect coefficients from the event submodel.

se The se function returns standard errors based on mad. See the *Uncertainty estimates* section in print.stanmvreg for more details.

confint Not supplied, since the posterior_interval function should be used instead to compute Bayesian uncertainty intervals.

residuals Residuals are *always* of type "response" (not "deviance" residuals or any other type).

See Also

- The print, summary, and prior_summary methods for stanmvreg objects for information on the fitted model.
- The plot method to plot estimates and diagnostics.
- The pp_check method for graphical posterior predictive checking of the longitudinal or glmer submodels.

- The ps_check method for graphical posterior predictive checking of the event submodel.
- The posterior_traj for predictions for the longitudinal submodel (for models estimated using stan_jm), as well as it's associated plot method.
- The posterior_survfit for predictions for the event submodel, including so-called "dynamic" predictions (for models estimated using stan_jm), as well as it's associated plot method.
- The posterior_predict for predictions for the glmer submodel (for models estimated using stan_mvmer).
- The posterior_interval for uncertainty intervals for model parameters.
- The loo, and log_lik methods for leave-one-out model comparison, and computing the log-likelihood of (possibly new) data.
- The as.matrix, as.data.frame, and as.array methods to access posterior draws.

Other S3 methods for stanmvreg objects, which have separate documentation, including print.stanmvreg, and summary.stanmvreg.

Also posterior_interval for an alternative to confint, and posterior_predict, posterior_traj and posterior_survfit for predictions based on the fitted joint model.

---

stanreg-draws-formats *Create a* draws *object from a* stanreg *object*

Description

Convert a stanreg object to a format supported by the **posterior** package.

Usage

```
## S3 method for class 'stanreg'
as_draws(x, ...)

## S3 method for class 'stanreg'
as_draws_matrix(x, ...)

## S3 method for class 'stanreg'
as_draws_array(x, ...)

## S3 method for class 'stanreg'
as_draws_df(x, ...)

## S3 method for class 'stanreg'
as_draws_list(x, ...)

## S3 method for class 'stanreg'
as_draws_rvars(x, ...)
```

Arguments

x	A stanreg object returned by one of the **rstanarm** modeling functions.
...	Arguments (e.g., pars, regex_pars) passed internally to as.matrix.stanreg or as.array.stanreg.

Details

To subset iterations, chains, or draws, use subset_draws after making the draws object. To subset variables use ... to pass the pars and/or regex_pars arguments to as.matrix.stanreg or as.array.stanreg (these are called internally by as_draws.stanreg), or use subset_draws after making the draws object.

Value

A draws object from the **posterior** package. See the **posterior** package documentation and vignettes for details on working with these objects.

Examples

```
fit <- stan_glm(mpg ~ wt + as.factor(cyl), data = mtcars)
as_draws_matrix(fit) # matrix format combines all chains
as_draws_df(fit, regex_pars = "cyl")
posterior::summarize_draws(as_draws_array(fit))
```

---

stanreg-objects *Fitted model objects*

Description

The **rstanarm** model-fitting functions return an object of class 'stanreg', which is a list containing at a minimum the components listed below. Each stanreg object will also have additional classes (e.g. 'aov', 'betareg', 'glm', 'polr', etc.) and several additional components depending on the model and estimation algorithm.

Some additional details apply to models estimated using the stan_mvmer or stan_jm modelling functions. The stan_mvmer modelling function returns an object of class 'stanmvreg', which inherits the 'stanreg' class, but has a number of additional elements described in the subsection below. The stan_jm modelling function returns an object of class 'stanjm', which inherits both the 'stanmvreg' and 'stanreg' classes, but has a number of additional elements described in the subsection below. Both the 'stanjm' and 'stanmvreg' classes have several of their own methods for situations in which the default 'stanreg' methods are not suitable; see the **See Also** section below.

Elements for `stanreg` objects

`coefficients` Point estimates, as described in `print.stanreg`.

`ses` Standard errors based on `mad`, as described in `print.stanreg`.

`residuals` Residuals of type `'response'`.

`fitted.values` Fitted mean values. For GLMs the linear predictors are transformed by the inverse link function.

`linear.predictors` Linear fit on the link scale. For linear models this is the same as `fitted.values`.

`covmat` Variance-covariance matrix for the coefficients based on draws from the posterior distribution, the variational approximation, or the asymptotic sampling distribution, depending on the estimation algorithm.

`model,x,y` If requested, the the model frame, model matrix and response variable used, respectively.

`family` The `family` object used.

`call` The matched call.

`formula` The model `formula`.

`data,offset,weights` The `data`, `offset`, and `weights` arguments.

`algorithm` The estimation method used.

`prior.info` A list with information about the prior distributions used.

`stanfit,stan_summary` The object of `stanfit-class` returned by RStan and a matrix of various summary statistics from the stanfit object.

`rstan_version` The version of the **rstan** package that was used to fit the model.

Elements for `stanmvreg` objects

The `stanmvreg` objects contain the majority of the elements described above for `stanreg` objects, but in most cases these will be a list with each elements of the list correponding to one of the submodels (for example, the `family` element of a `stanmvreg` object will be a list with each element of the list containing the `family` object for one submodel). In addition, `stanmvreg` objects contain the following additional elements:

The names of the grouping factors and group specific parameters, collapsed across the longitudinal or glmer submodels.

`flevels` The unique factor levels for each grouping factor, collapsed across the longitudinal or glmer submodels.

`n_markers` The number of longitudinal or glmer submodels.

`n_yobs` The number of observations for each longitudinal or glmer submodel.

`n_grps` The number of levels for each grouping factor (for models estimated using `stan_jm`, this will be equal to `n_subjects` if the individual is the only grouping factor).

`runtime` The time taken to fit the model (in minutes).

Additional elements for `stanjm` objects

The `stanjm` objects contain the elements described above for `stanmvreg` objects, but also contain the following additional elements:

The names of the variables distinguishing between individuals, and representing time in the longitudinal submodel.

`id_var,time_var`

`n_subjects` The number of individuals.

`n_events` The number of non-censored events.

`eventtime,status` The event (or censoring) time and status indicator for each individual.

`basehaz` A list containing information about the baseline hazard.

`assoc` An array containing information about the association structure.

`epsilon` The width of the one-sided difference used to numerically evaluate the slope of the longitudinal trajectory; only relevant if a slope-based association structure was specified (e.g. etaslope, muslope, etc).

`qnodes` The number of Gauss-Kronrod quadrature nodes used to evaluate the cumulative hazard in the joint likelihood function.

Note

The `stan_biglm` function is an exception. It returns a stanfit object rather than a stanreg object.

See Also

`stanreg-methods`, `stanmvreg-methods`

---

stanreg_list *Create lists of fitted model objects, combine them, or append new models to existing lists of models.*

Description

Create lists of fitted model objects, combine them, or append new models to existing lists of models.

Usage

```
stanreg_list(..., model_names = NULL)

stanmvreg_list(..., model_names = NULL)

stanjm_list(..., model_names = NULL)

## S3 method for class 'stanreg_list'
print(x, ...)
```

Arguments

...	Objects to combine into a "stanreg_list", "stanmvreg_list", or "stanjm_list". Can be fitted model objects, existing "stan*_list" objects to combine, or one existing "stan*_list" object followed by fitted model objects to append to the list.
model_names	Optionally, a character vector of model names. If not specified then the names are inferred from the name of the objects passed in via .... These model names are used, for example, when printing the results of the loo_compare.stanreg_list and loo_model_weights.stanreg_list methods.
x	The object to print.

Value

A list of class "stanreg_list", "stanmvreg_list", or "stanjm_list", containing the fitted model objects and some metadata stored as attributes.

See Also

loo_model_weights for usage of stanreg_list.

---

summary.stanreg *Summary method for stanreg objects*

Description

Summaries of parameter estimates and MCMC convergence diagnostics (Monte Carlo error, effective sample size, Rhat).

Usage

```
## S3 method for class 'stanreg'
summary(
  object,
  pars = NULL,
  regex_pars = NULL,
  probs = c(0.1, 0.5, 0.9),
  ...,
  digits = 1
)

## S3 method for class 'summary.stanreg'
print(x, digits = max(1, attr(x, "print.digits")), ...)

## S3 method for class 'summary.stanreg'
as.data.frame(x, ...)
```

```
## S3 method for class 'stanmvreg'
summary(object, pars = NULL, regex_pars = NULL, probs = NULL, ..., digits = 3)

## S3 method for class 'summary.stanmvreg'
print(x, digits = max(1, attr(x, "print.digits")), ...)
```

Arguments

object	A fitted model object returned by one of the **rstanarm** modeling functions. See stanreg-objects.
pars	An optional character vector specifying a subset of parameters to display. Parameters can be specified by name or several shortcuts can be used. Using pars="beta" will restrict the displayed parameters to only the regression coefficients (without the intercept). "alpha" can also be used as a shortcut for "(Intercept)". If the model has varying intercepts and/or slopes they can be selected using pars = "varying". In addition, for stanmvreg objects there are some additional shortcuts available. Using pars = "long" will display the parameter estimates for the longitudinal submodels only (excluding group-specific pparameters, but including auxiliary parameters). Using pars = "event" will display the parameter estimates for the event submodel only, including any association parameters. Using pars = "assoc" will display only the association parameters. Using pars = "fixef" will display all fixed effects, but not the random effects or the auxiliary parameters. pars and regex_pars are set to NULL then all fixed effect regression coefficients are selected, as well as any auxiliary parameters and the log posterior. If pars is NULL all parameters are selected for a stanreg object, while for a stanmvreg object all fixed effect regression coefficients are selected as well as any auxiliary parameters and the log posterior. See **Examples**.
regex_pars	An optional character vector of regular expressions to use for parameter selection. regex_pars can be used in place of pars or in addition to pars. Currently, all functions that accept a regex_pars argument ignore it for models fit using optimization.
probs	For models fit using MCMC or one of the variational algorithms, an optional numeric vector of probabilities passed to quantile.
...	Currently ignored.
digits	Number of digits to use for formatting numbers when printing. When calling summary, the value of digits is stored as the "print.digits" attribute of the returned object.
x	An object of class "summary.stanreg".

Details

mean_PPD diagnostic: Summary statistics are also reported for mean_PPD, the sample average posterior predictive distribution of the outcome. This is useful as a quick diagnostic. A useful heuristic is to check if mean_PPD is plausible when compared to mean(y). If it is plausible then this does *not* mean that the model is good in general (only that it can reproduce the sample

mean), however if mean_PPD is implausible then it is a sign that something is wrong (severe model misspecification, problems with the data, computational issues, etc.).

Value

The summary method returns an object of class "summary.stanreg" (or "summary.stanmvreg", inheriting "summary.stanreg"), which is a matrix of summary statistics and diagnostics, with attributes storing information for use by the print method. The print method for summary.stanreg or summary.stanmvreg objects is called for its side effect and just returns its input. The as.data.frame method for summary.stanreg objects converts the matrix to a data.frame, preserving row and column names but dropping the print-related attributes.

See Also

prior_summary to extract or print a summary of the priors used for a particular model.

Examples

```
if (.Platform$OS.type != "windows" || .Platform$r_arch != "i386") {
if (!exists("example_model")) example(example_model)
summary(example_model, probs = c(0.1, 0.9))

# These produce the same output for this example,
# but the second method can be used for any model
summary(example_model, pars = c("(Intercept)", "size",
                                paste0("period", 2:4)))
summary(example_model, pars = c("alpha", "beta"))

# Only show parameters varying by group
summary(example_model, pars = "varying")
as.data.frame(summary(example_model, pars = "varying"))
}
```

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