

Package: lmebayesCore (via r-universe)

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Type Package

Title Core C++ Sampling Engine for lmebayes

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Description Core C++ engine for lmebayes: envelope-based iid samplers, two-block Gibbs mixed-model engines, and optional OpenCL acceleration. Full-featured developer backend for lmebayes and extensions. End users should use lmebayes for lmer/glmer-style mixed-model workflows.

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URL <https://github.com/knygren/lmebayesCore>

BugReports <https://github.com/knygren/lmebayesCore/issues>

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RdMacros Rdpack

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lmebayesCore-package *lmebayesCore: Core C++ Sampling Engine for lmebayes*

Description

Core C++ engine for envelope-based iid samplers, two-block Gibbs mixed-model engines, and optional OpenCL acceleration. Full-featured developer backend for **lmebayes** and related extensions. End users should install **lmebayes** for lmer/glmer-style mixed-model workflows.

Details

Low-level entry points include envelope construction ([EnvelopeBuild](#), [EnvelopeOrchestrator](#)), registered simulation pipelines ([rNormalGLM_std](#), [rIndepNormalGammaReg_std](#)), matrix-input samplers ([rglmb](#), [rlmb](#)), the two-block Gibbs mixed-model engines ([rlmerb](#), [rglmerb](#)), and OpenCL kernel loaders. Formula interfaces lmerb and glmerb live in **lmebayes**; **lmebayesCore** supplies the sampling engine.

OpenCL startup checks

In interactive sessions, attaching the package with `library(lmebayesCore)` may emit a short `packageStartupMessage` when `glmbayesCore_has_opengl()` is `FALSE` but a GPU or OpenCL stack appears available on the host. Set `options(glmbayes.quiet_opengl_startup = TRUE)` to suppress attach notes (recommended for CI and R CMD check).

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- The R Core Team (R Mathlib sources, R stats modeling code, and derived/adapted routines) [contributor, copyright holder]
- The R Foundation (Portions of R Mathlib and R source code) [copyright holder]
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- Robert Gentleman (Portions of R Mathlib) [contributor, copyright holder]
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- Morten Welinder (Portions of R Mathlib) [contributor, copyright holder]
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References

There are no references for Rd macro `\insertAllCites` on this help page.

See Also

lmebayes for the end-user modelling package.

AMI

Amitriptyline overdose data

Description

Data with information on 17 overdoses of the drug amitriptyline

Usage

`data(AMI)`

Format

This data frame contains the following columns:

TOT total TCAD plasma level

AMI amount of amitriptyline present in the TCAD plasma level

GEN gender (male = 0, female = 1)

AMT amount of drug taken at time of overdose

PR PR wave measurement

DIAP diastolic blood pressure

QRS QRS wave measurement

Details

Each row is one overdose episode. Variables include total tricyclic antidepressant level, amitriptyline component, gender, reported amount ingested, and ECG-related measures (PR interval, QRS duration, diastolic blood pressure). The dataset is used in package examples for binomial and related regression; see (Dobson 1990) for analogous generalized linear modelling of clinical outcomes.

References

Dobson A~J (1990). *An Introduction to Generalized Linear Models*. Chapman and Hall, London.

Examples

```
##### Start of AMI dataset example #####

data(AMI)
summary(AMI)

#####
## End of AMI dataset example
#####
```

BikeSharing

Bike Sharing Dataset (Processed)

Description

A processed version of the UCI Bike Sharing Dataset (hourly data). The data include derived variables for part of day, quarter, and Fourier terms for cyclic effects of hour and month.

Usage

BikeSharing

Format

A data frame with 17,379 observations and 25 variables (original plus derived):

instant Record index.

dteday Date.

season Season (1: spring, 2: summer, 3: fall, 4: winter).

yr Year (0: 2011, 1: 2012).

mnth Month (1–12).

hr Hour (0–23).

holiday Whether the day is a holiday (0/1).

weekday Day of week (0–6).

workingday Working day (0/1).

weathersit Weather situation (1–4).

temp Normalized temperature.

atemp Normalized feeling temperature.

hum Normalized humidity.

windspeed Normalized wind speed.

casual Count of casual users.

registered Count of registered users.

cnt Total count (casual + registered).

hr_num Hour as numeric (same as hr).

month_num Month as integer.

part_of_day Factor: Night (0–5h), Morning (6–11h), Afternoon (12–17h), Evening (18–23h).

quarter Factor: Q1–Q4.

hr_sin Sine term for 24-hour cycle.

hr_cos Cosine term for 24-hour cycle.

mon_sin Sine term for 12-month cycle.

mon_cos Cosine term for 12-month cycle.

Source

UCI Machine Learning Repository: Bike Sharing Dataset. <https://archive.ics.uci.edu/dataset/275/bike+sharing+dataset>

Examples

```
##### Start of BikeSharing dataset example #####
```

```
data("BikeSharing")
head(BikeSharing)
dim(BikeSharing)
```

```
#####
## End of BikeSharing dataset example
#####
```

block_simfuncs	<i>Conditionally independent block simulation (Gibbs / product likelihood)</i>
----------------	--

Description

Draw from blockwise full conditionals when the posterior factorizes across observation blocks. `block_rNormalReg` uses `.block_rNormalReg_cpp()` (Gaussian; each block calls `rNormalReg`). `block_rNormalGLM` uses `.block_rNormalGLM_cpp()` (GLM envelope; C++ partition and prior payload; each block calls `rNormalGLM`). Typical use is **block Gibbs** ($n = 1$ per outer step); $n > 1$ gives iid draws from the product conditional.

Usage

```
block_rNormalGLM(
  n,
  y,
  x,
  block,
  prior_list = NULL,
  prior_lists = NULL,
  offset = NULL,
  weights = 1,
  family = gaussian(),
  Gridtype = 2L,
  n_envopt = NULL,
  use_parallel = TRUE,
  use_opengl = FALSE,
  verbose = FALSE,
  progbar = FALSE
)
```

```
block_rNormalReg(
  n,
  y,
  x,
  block,
  prior_list = NULL,
  prior_lists = NULL,
  offset = NULL,
  weights = 1,
  Gridtype = 2L
)
```

```
block_rNormalReg_update(
  mu_all,
  P = NULL,
```

```

    dispersion = NULL,
    y,
    x,
    block,
    prior_list = NULL,
    prior_lists = NULL,
    offset = NULL,
    weights = 1,
    Gridtype = 2L,
    coef_cols = NULL
)

block_rNormalGLM_update(
  mu_all,
  sigma_theta_sq = NULL,
  y,
  x,
  block,
  family = poisson(),
  prior_list = NULL,
  prior_lists = NULL,
  offset = NULL,
  weights = 1,
  Gridtype = 2L,
  n_envopt = 1L,
  use_parallel = TRUE,
  use_opengl = FALSE,
  verbose = FALSE,
  progbar = FALSE,
  theta_coef_col = 1L
)

normalize_block(block, 12)

```

Arguments

n	Number of iid draws per block (n = 1 typical for Gibbs).
y	Response vector of length nrow(x).
x	Design matrix nrow(x) by ncol(x); same ncol in every block.
block	Block partition: factor or integer vector of length 12, 12_blocks counts summing to 12, or a list of disjoint row-index vectors covering 1:12.
prior_list	Single prior specification recycled to all blocks, or with mu as 11 by k matrix or blocks sublist.
prior_lists	Optional list of length k (or 1) of per-block prior_list objects.
offset	Optional numeric vector (length 1 or length(y)); partitioned across blocks like y.
weights	Optional weights; same recycling and blocking as offset.

family	GLM family (not gaussian()).
Gridtype	Passed to each block's sampler (Armadillo Gridtype).
n_envopt	Passed to each block; defaults to 1 when NULL.
use_parallel, use_opengl, verbose, progbar	Passed to each block's GLM sampler.
mu_all	Numeric matrix $l1 \times k$ or vector of length $l1$ (recycled to all blocks): prior means per block (e.g. $X_{\text{hyper}}\gamma$). Required unless prior_lists or prior_list is supplied.
P	Prior precision matrix $l1 \times l1$ (inverse of Σ_{ranef}). Shared across all blocks when building per-block priors from mu_all.
dispersion	Residual variance σ^2 . Shared across all blocks when building per-block priors from mu_all.
coef_cols	Column indices of coefficients to return as b_draws (default NULL returns all columns).
sigma_theta_sq	Shared prior variance for scalar blocks when building prior_lists from mu_all.
theta_coef_col	Column index of coefficients to return as theta (default 1 for scalar intercept blocks).
l2	Number of observations (rows) after model.frame.

Details

Output layout: coefficients and coef.mode are matrices with **rows = blocks** and **columns = predictors**.

See inst/DESIGN_RGLM_BLOCKS.md.

Per-block prior mean: pass prior_list\$mu as an $l1 \times k$ matrix (one column per block). Standard for Block~1 of the lmebayes Gibbs sampler, where $\mu_j = X_{\text{hyper}}\gamma$ depends on the current fixed-effects draw.

Dispersion: must be supplied via prior_list\$dispersion (residual variance σ^2).

Value

A list with class "block_rNormalGLM" including:

coefficients Matrix $k \times p$; row b is the draw for block b .

coef.mode Matrix $k \times p$; posterior mode per block.

block_info Block partition metadata.

block_results List of length k with each block's sampler output.

A list with class "block_rNormalReg" including coefficients, coef.mode, dispersion, and block_info.

A list with b_draws, coefficients, coef.mode, and block_rNormalReg (full block sampler output).

A list with theta, coefficients, coef.mode, and block_rNormalGLM (full block sampler output).

List with k , ids, l2_blocks, starts, and rows (per-block row indices).

Functions

- `block_rNormalReg()`: Gaussian blockwise full conditionals via `.block_rNormalReg_cpp()` (C++ partition, prior payload, and `rNormalReg()` per block). This is the Gaussian counterpart of `block_rNormalGLM`.
- `block_rNormalReg_update()`: One Gibbs block update via `block_rNormalReg`: draw a single blockwise Gaussian posterior sample ($n = 1$) and return coefficient draws for two-block Gibbs samplers where each group is its own block (e.g. school-level random effects b_j). When `prior_lists` and `prior_list` are both omitted, per-block `dNormal` priors are built from `mu_all`, `P`, and `dispersion`.
- `block_rNormalGLM_update()`: One Gibbs block update via `block_rNormalGLM`: draw a single blockwise GLM posterior sample ($n = 1$) and return latent-level draws (e.g. updated θ) for two-block Gibbs samplers where each observation or group is its own block. When `prior_lists` and `prior_list` are both omitted, per-block `dNormal` priors are built from `mu_all` and `sigma_theta_sq`.
- `normalize_block()`: Normalize a row-block partition for BY-style fits and block Gibbs samplers.

See Also

[rNormal_reg](#), [simfunction](#), [normalize_block](#), [inst/DESIGN_RGLM_BLOCKS.md](#)

Examples

```
## Conditionally independent block GLM draw (Poisson, 3 outcome groups)

set.seed(42)

## Dobson (1990) p. 93 RCT
counts <- c(18, 17, 15, 20, 10, 20, 25, 13, 12)
outcome <- gl(3, 1, 9)
treatment <- gl(3, 3)
d.AD <- data.frame(outcome, treatment, counts)

ps <- Prior_Setup(counts ~ treatment, family = poisson(), data = d.AD)
y <- ps$y
x <- ps$x
block <- outcome

out <- block_rNormalGLM(
  n = 1L,
  y = y,
  x = x,
  block = block,
  prior_list = list(mu = ps$mu, Sigma = ps$Sigma),
  family = poisson(),
  use_parallel = FALSE
)

out$coefficients
out$coef.mode
```

```

## Conditionally independent block Gaussian draw (3 school groups)

set.seed(42)

## Simulate a simple two-level data set: 3 schools, ~10 students each
n_schools <- 3L
n_per      <- 10L
school     <- rep(seq_len(n_schools), each = n_per)
x          <- cbind(1, rnorm(n_schools * n_per)) # intercept + covariate
b_true     <- matrix(c(5, 0.5, 3, -0.2, 7, 0.3), nrow = n_schools, byrow = TRUE)
sigma2     <- 1.5 # residual variance

y <- rowSums(x * b_true[school, ]) + rnorm(nrow(x), sd = sqrt(sigma2))

## Flat prior (large Sigma) shared across all schools; dispersion = sigma2
l1      <- ncol(x)
prior_list <- list(
  mu      = rep(0, l1),
  Sigma   = diag(100, l1),
  dispersion = sigma2,
  ddef    = FALSE
)

out <- block_rNormalReg(
  n      = 1L,
  y      = y,
  x      = x,
  block  = school,
  prior_list = prior_list
)

out$coefficients ## k x l1 matrix: one row of b_j draws per school
out$coef.mode
## One block_rNormalReg_update step: draw b_j given current fixed effects

set.seed(7)

## Simulate data: 3 schools, 10 students each
n_schools <- 3L
n_per      <- 10L
school     <- rep(seq_len(n_schools), each = n_per)
Z          <- cbind(1, rnorm(n_schools * n_per)) # within-school design
b_true     <- matrix(c(5, 0.5, 3, -0.2, 7, 0.3), nrow = n_schools, byrow = TRUE)
sigma2     <- 1.5

y <- rowSums(Z * b_true[school, ]) + rnorm(nrow(Z), sd = sqrt(sigma2))

## Precision matrix for the random-effect prior (shared across schools)
l1 <- ncol(Z)
P_b <- diag(0.01, l1) # vague prior

## Current "fixed-effects" prior mean (one vector recycled to all blocks)
mu_current <- rep(0, l1)

```

```

out <- block_rNormalReg_update(
  mu_all      = mu_current,  ## recycled to all k blocks (prior_list path)
  P           = P_b,
  dispersion  = sigma2,
  y           = y,
  x           = Z,
  block      = school
)

out$b_draws      ## k x l1 matrix of updated random effects
out$coefficients ## same content (all columns)
## One Gibbs block update: scalar intercept per observation (Poisson)

set.seed(42)

n <- 5L
y <- rpois(n, 2)
x <- matrix(1, n, 1)
mu <- rep(0, n)

upd <- block_rNormalGLM_update(
  mu_all = mu,
  sigma_theta_sq = 1,
  y = y,
  x = x,
  block = seq_len(n),
  family = poisson(),
  use_parallel = FALSE
)

upd$theta
upd$coefficients
## Block partition helpers (factor, l2_blocks counts, or row-index list)

l2 <- 10L

## One level per row (length l2)
normalize_block(factor(rep(c("A", "B"), each = 5L)), l2)

## Contiguous counts summing to l2
normalize_block(c(4L, 6L), l2)

## Explicit row-index list
normalize_block(list(A = 1:4, B = 5:10), l2)

```

Description

A copy of [Boston](#) where all predictors (every column except medv) have been mean-centered (subtract column means, no scaling).

Usage

```
data("Boston_centered")
```

Format

A data frame with 506 observations and 14 variables (same names as [Boston](#)). See `?MASS::Boston` for variable descriptions.

Source

Derived from `MASS::Boston`. Original data described in Harrison and Rubinfeld (1978); see `?Boston` in **MASS**.

build_mu_all	<i>Build per-group random-effect prior means for Block 1 sampling</i>
--------------	---

Description

Forms the `mu_all` matrix passed to [block_rNormalReg_update](#): for each grouping level j and each random-effect column k of the level-1 design Z ,

$$\mu_{\text{all}}[k, j] = X_{\text{hyper}, k}[j,]^T \gamma_k,$$

where γ_k is the current hyper-parameter vector for RE k (Block 2 state).

Usage

```
build_mu_all(design, fixef, group_levels = NULL, use_cpp = TRUE)
```

Arguments

design	List with components <code>X_hyper</code> , <code>re_coef_names</code> , and <code>groups</code> (typically supplied by a downstream mixed-effects model setup step).
fixef	Named list of hyper-parameter vectors, one entry per RE column of Z . Names must match <code>design\$re_coef_names</code> . Each <code>fixef[[k]]</code> is a numeric vector of length <code>ncol(X_hyper[[k]])</code> with names matching <code>colnames(X_hyper[[k]])</code> .
group_levels	Character vector of grouping levels defining the <i>column order</i> of <code>mu_all</code> . Defaults to <code>levels(design\$groups)</code> , which is the canonical ordering used in two-block mixed models and consistent with <code>lmer</code> and block_rNormalReg (which preserves the input factor's level order).
use_cpp	Logical; if TRUE (default), compute <code>mu_all</code> in C++ via <code>.two_block_build_mu_all_cpp</code> ; if FALSE, use the R reference implementation <code>build_mu_all_r()</code> .

Value

A list with:

`mu_all` Numeric matrix $p_re \times J$ (p_re = number of RE columns, J = number of groups). Row names are `design$re_coef_names`; column names are `group_levels` in the order supplied.

`re_coef_names` Copy of `design$re_coef_names`.

`group_levels` Grouping levels used for columns.

See Also

[lmerb_posterior_mean](#), [two_block_rNormal_reg](#), [block_rNormalReg_update](#)

carinsca

Canadian Automobile Insurance Claims for 1957-1958

Description

The data give the Canadian automobile insurance experience for policy years 1956 and 1957 as of June 30, 1959. The data includes virtually every insurance company operating in Canada and was collated by the Statistical Agency (Canadian Underwriters' Association - Statistical Department) acting under instructions from the Superintendent of Insurance. The data given here is for private passenger automobile liability for non-farmers for all of Canada excluding Saskatchewan.

Usage

```
data(carinsca)
```

Format

A data frame with 20 observations on the following 6 variables:

`Merit` Merit Rating:

- 3 - licensed and accident free 3 or more years
- 2 - licensed and accident free 2 years
- 1 - licensed and accident free 1 year
- 0 - all others

`Class` 1 - pleasure, no male operator under 25

- 2 - pleasure, non-principal male operator under 25
- 3 - business use
- 4 - unmarried owner or principal operator under 25
- 5 - married owner or principal operator under 25

`Insured` Earned car years

`Premium` Earned premium in 1000's

(adjusted to what the premium would have been had all cars been written at 01 rates)

`Claims` Number of claims

`Cost` Total cost of the claim in 1000's of dollars

Details

One could apply Poisson regression to the number of claims and gamma regression to the cost per claim.

Source

Bailey, R. A., and Simon, LeRoy J. (1960). Two studies in automobile insurance ratemaking. *ASTIN Bulletin*, 192-217.

References

Data downloaded from <http://www.statsci.org/data/general/carinsca.html>. That site also contains classical Poisson and Gamma regression examples.

Examples

```
##### Start of carinsca dataset example #####

data(carinsca)
str(carinsca)
head(carinsca)

#####
## End of carinsca dataset example
#####
```

Cleveland

Cleveland Heart Disease Dataset

Description

A cleaned version of the Cleveland heart disease dataset from the UCI Machine Learning Repository. This version contains only complete cases and includes a derived binary outcome variable `hd` indicating the presence ("Yes") or absence ("No") of heart disease.

Usage

```
data("Cleveland")
```

Format

A data frame with 297 observations and 15 variables:

age Age in years (numeric).
sex Sex (0 = female, 1 = male).
cp Chest pain type (numeric code 1–4).
trestbps Resting blood pressure (mm Hg).

chol Serum cholesterol (mg/dl).
fbs Fasting blood sugar > 120 mg/dl (1 = true, 0 = false).
restecg Resting electrocardiographic results (numeric code).
thalach Maximum heart rate achieved.
exang Exercise-induced angina (1 = yes, 0 = no).
oldpeak ST depression induced by exercise relative to rest.
slope Slope of the peak exercise ST segment.
ca Number of major vessels colored by fluoroscopy (0–3).
thal Thalassemia status (numeric code).
num Original UCI disease score (0–4).
hd Binary heart disease indicator: "No" (num = 0) or "Yes" (num > 0).

Source

UCI Machine Learning Repository: Heart Disease Data Set. <https://archive.ics.uci.edu/dataset/45/heart+disease>

compute_gaussian_prior

Compute Calibrated Gaussian Normal–Gamma Prior Components

Description

Internal Gaussian calibration routine used by [Prior_Setup](#). Given weighted Gaussian regression inputs and a dispersion–independent coefficient–scale prior covariance Σ_0 , this function computes all Normal–Gamma quantities required by the Gaussian prior families: dispersion, shape, shape_ING, rate, rate_gamma, and the calibrated coefficient–scale covariance Sigma. The input Sigma_0 is returned unchanged.

Usage

```
compute_gaussian_prior(
  X,
  Y,
  weights,
  offset,
  dispersion = NULL,
  n_effective,
  bhat,
  mu,
  Sigma_0,
  Sigma = NULL,
  n_prior,
  k = 1
)
```

Arguments

X	Numeric model matrix with $\text{nrow}(X) == \text{length}(Y)$.
Y	Numeric response vector.
weights	Numeric vector of case weights.
offset	Numeric offset vector.
dispersion	Optional scalar dispersion. If supplied, overrides the calibrated value.
n_effective	Effective sample size (typically $\text{sum}(\text{weights})$).
bhat	Numeric coefficient vector, usually the weighted least-squares estimate.
mu	Numeric prior mean vector.
Sigma_0	Dispersion-independent prior covariance matrix $[p \times p]$.
Sigma	Optional coefficient-scale covariance matrix. If supplied, overrides the calibrated Sigma.
n_prior	Effective prior sample size.
k	Non-negative scalar with $k + p \geq 2$. Controls tail behavior of the variance prior; does not affect posterior means.

Details

The computation follows a structured pipeline:

1. Validate dimensions and numeric inputs.
2. Compute the weighted residual sum of squares at `bhat`.
3. Form the weighted Gram matrix $X^\top W X$, invert it, and construct the marginal quadratic term S_{marg} .
4. Map `n_prior` and `k` to the Normal-Gamma shape and rate.
5. Calibrate the implied dispersion and coefficient covariance.
6. Return all calibrated prior components.

The function assumes the Chapter 11 convention that Σ_0 is *dispersion-free*: it encodes prior structure on the precision-weighted coefficient scale. The returned `Sigma` is the corresponding coefficient-scale covariance after calibration.

A common choice is the Zellner-type form

$$\Sigma_0 = \frac{1 - \text{pwt}}{\text{pwt}} (X^\top W X)^{-1},$$

where `pwt` is a scalar prior weight. More generally, `Sigma_0` may be any positive-definite matrix.

The function computes:

- The marginal quadratic term

$$S_{\text{marg}} = R S S_w + (\hat{\beta} - \mu)^\top (\Sigma_0 + (X^\top W X)^{-1})^{-1} (\hat{\beta} - \mu).$$

- Prior Gamma shape: $a_0 = (n_{\text{prior}} + k)/2$.

- Posterior Gamma shape: $a_n = (n_{\text{prior}} + n_w + k)/2$, where $n_w = n_{\text{effective}}$.
- Calibrated dispersion:

$$E[\sigma^2 \mid y] = \frac{S_{\text{marg}}}{n_w - p},$$

the usual weighted residual-df estimator.

- Prior Gamma rate:

$$b_0 = \frac{1}{2} S_{\text{marg}} \frac{n_{\text{prior}} + k + p - 2}{n_w - p},$$

ensuring $E[\sigma^2 \mid y] = S_{\text{marg}}/(n_w - p)$.

- Calibrated coefficient covariance:

$$\Sigma = \frac{n_w}{n_{\text{prior}}} E[\sigma^2 \mid y] (X^\top W X)^{-1}.$$

Limiting behavior.

- As $n_{\text{prior}} \rightarrow \infty$, the prior becomes increasingly concentrated and dominates the likelihood.
- As $n_{\text{prior}} \rightarrow 0^+$ with $n_w > p$, $S_{\text{marg}} \rightarrow RSS_w$ and $E[\sigma^2 \mid y] \rightarrow RSS_w/(n_w - p)$, matching the classical weighted Gaussian estimator.
- Strict positivity of the prior rate requires $n_{\text{prior}} + k + p > 2$.
- The prior mean μ is never altered; this function calibrates only scale parameters.

Value

A list with components:

- dispersion — calibrated Gaussian dispersion.
- shape — Gamma shape for residual precision.
- shape_ING — shape for the independent Normal–Gamma prior.
- rate — Gamma rate for residual precision.
- rate_gamma — Gamma rate for the fixed- β path ([dGamma](#)).
- Sigma — calibrated coefficient–scale covariance.
- Sigma_0 — the input dispersion–free covariance.

References

There are no references for Rd macro `\insertAllCites` on this help page.

dGamma_list

Build a named list of dGamma measurement-dispersion priors

Description

Generic for constructing a named list of [dGamma](#) prior objects from a prior-specification object. For mixed models, one dGamma() per group level supplies Block~1 observation-level σ_j^2 priors for `lmerb(..., dispersion_ranef = ...)`.

Usage

```
dGamma_list(object, ...)
```

Arguments

`object` A prior-specification object.
`...` Additional arguments passed to methods (e.g. `max_disp_perc`, `disp_upper_anchor`).

Value

A named list whose elements are objects of class "pfamily".

See Also

[dGamma](#), [Prior_Setup_lmebayes](#), [pfamily_list](#)

dGamma_list.lmebayes_prior_setup

Build per-group dGamma priors from a Prior_Setup_lmebayes object

Description

Converts the per-group Block~1 measurement-dispersion calibration stored in a [Prior_Setup_lmebayes](#) object into a named list of [dGamma](#) pfamily objects, one per group level.

Usage

```
## S3 method for class 'lmebayes_prior_setup'
dGamma_list(
  object,
  max_disp_perc = NULL,
  disp_center = c("sigma2_hat", "dispersion2"),
  disp_upper_anchor = c("blup", "symmetric"),
  warn_asymmetric = NULL,
  print_asymmetric = NULL,
```

```

asymmetric_R_lo = NULL,
asymmetric_R_hi = NULL,
n_rss_iter = 10L,
...
)

```

Arguments

object	An object of class "lmebayes_prior_setup" as returned by Prior_Setup_lmebayes (Gaussian models only).
max_disp_perc	Scalar in (0.5, 1); defaults to object\$max_disp_perc.
disp_center	Character: "sigma2_hat" (default) mean-matches the truncation window at each group's calibrated point estimate (disp_upper_anchor controls upper-tail widening); "dispersion2" mean-matches symmetrically at an envelope-centering dispersion estimate that integrates over random-effect uncertainty instead (Part III of inst/DGAMMA_LIST_MARGINAL_AND_BOUNDS.md; ignores disp_upper_anchor).
disp_upper_anchor	Character: "blup" (default) scales the upper-bound rate by RSS_{blup}/RSS_{ols} per group; "symmetric" uses the same rate as the lower bound. Ignored when disp_center = "dispersion2".
warn_asymmetric	If TRUE (default), warn when any group's truncation window is flagged as asymmetric. Defaults to option glmbayesCore.dgamma_window_warn when NULL.
print_asymmetric	If TRUE, print a table of flagged groups after the warning. Defaults to option glmbayesCore.dgamma_window_print when NULL.
asymmetric_R_lo	Flag when $R_{lo} = lo_pct_BLUP/lo_pct_OLS$ is below this threshold (default 0.25, or option glmbayesCore.dgamma_window_R_lo).
asymmetric_R_hi	Flag when $R_{hi} = hi_pct_OLS/hi_pct_BLUP$ exceeds this threshold (default 4, or option glmbayesCore.dgamma_window_R_hi).
n_rss_iter	Positive integer; number of fixed-point iterations for the disp_center = "dispersion2" envelope-centering estimate (default 10L). Ignored when disp_center = "sigma2_hat".
...	Currently ignored.

Details

Prior density (shape_ING, rate from S_{marg} A12 3.3.4) comes from object\$ing_prior_measurement_group (calibrated in Prior_Setup_lmebayes()) via [compute_gaussian_prior](#) with shared population sd_tau). Truncation bounds use an approximate posterior at $n_{\text{combined},j} = n_{\text{prior},j} + n_j$, mean-matched at one of two per-group centers (disp_center):

"sigma2_hat" (**default**) disp_lower is OLS-anchored at sigma2_hat_j; disp_upper widens by the BLUP/OLS residual RSS inflation ratio when disp_upper_anchor = "blup" (default).

"dispersion2" Both bounds are mean-matched, symmetrically, at a dispersion estimate that integrates over the random effect's own posterior uncertainty (an EnvelopeCentering()-style trace correction; disp_upper_anchor is ignored). Tends to produce narrower, better-centered upper tails than "sigma2_hat" for groups with large BLUP/OLS inflation.

See inst/DGAMMA_LIST_MARGINAL_AND_BOUNDS.md (Parts II and III) for the full derivation of both constructions and their empirical validation.

The returned list carries attribute "window_diagnostics": a data frame with cross-percentiles of the asymmetric truncation window and flag asymmetric_window when $R_{lo} = lo_pct_BLUP/lo_pct_OLS < asymmetric_R_lo$ (default 0.25) or $R_{hi} = hi_pct_OLS/hi_pct_BLUP > asymmetric_R_hi$ (default 4). A **warning** is emitted for flagged groups when warn_asymmetric = TRUE.

Value

A named list of "pfamily" objects keyed by group levels, suitable for lmerb(..., dispersion_ranef = dGamma_list(ps)), with attributes "window_diagnostics" (data frame, one row per group), "dispersion_fit" (object\$dispersion_fit, the glmmTMB reference fit used for calibration – lmerb()/glmerb() reuse it as their own dispersion_fit instead of re-fitting glmmTMB when dispersion_ranef carries this attribute), and "calibration_source" (object\$calibration_source).

See Also

[Prior_Setup_lmebayes](#), [dGamma_list](#), [dGamma](#)

Examples

```
if (requireNamespace("bayesrules", quietly = TRUE)) {
  data(big_word_club, package = "bayesrules")
  dat <- big_word_club
  dat$school_id <- factor(dat$school_id)
  dat <- subset(dat, !is.na(score_ppvt))

  ps <- Prior_Setup_lmebayes(
    score_ppvt ~ private_school + (1 | school_id),
    data = dat,
    pwt_measurement = 0.01,
    dispformula = ~school_id
  )
  disp_pf <- dGamma_list(ps)
  print(disp_pf[[1L]])
}
```

Description

Compile-time OpenCL probing for **glmbytes**, plus `diagnose_glmbytes()` — a readable report that combines **opencitools** host/runtime checks with this package’s OpenCL build status (`glmbytesCore_has_opencit`).

Workstation probes (GPU vendor detection, drivers, ICD/PATH, and related helpers) live in **opencitools**; call `opencitools::` . . . or see `?opencitools`.

Usage

```
diagnose_glmbytes()
```

```
glmbytesCore_has_opencit()
```

Details

GPU acceleration speeds up envelope construction and grid evaluation when you pass `use_opencit = TRUE` in `rglmb`, `rlmb`, and related functions. CPU-only builds remain fully usable for standard modelling.

Start with `diagnose_glmbytes()` for a single readable report; use `glmbytesCore_has_opencit()` for a quick boolean when scripting. Full install notes: `vignette("Chapter-16", package = "glmbytes")` ((Nygren 2025)).

Diagnostics exported from glmbytes

- `diagnose_glmbytes()` — full report including compile-time OpenCL status for this package.
- `glmbytesCore_has_opencit()` — TRUE if this build was compiled with OpenCL support.
- `opencitools::has_opencit()` — compile-time flag for **opencitools** (distinct).

Host / runtime checks (opencitools)

- `detect_environment_and_gpus()`
- `detect_compute_runtimes()`
- `verify_opencit_runtime()`
- `check_runtime_env()`
- `get_opencit_core_count()`
- `load_kernel_source()`, `load_kernel_library()` (pass `package = "lmebytesCore"` for kernels under `inst/cl/`)
- `add_to_path_windows()` and related PATH helpers

References

Nygren K (2025). “Chapter 16: Large models — GPU acceleration using OpenCL.” Vignette in the `glmbytes` R package. R vignette name: `Chapter-16`.

See Also

`diagnose_glmbytes`, `glmbytesCore_has_opencit`, **opencitools**, `rglmb`, `rlmb`.

Description

GPU-Accelerated Envelope Construction for Posterior Simulation

Usage

```
EnvelopeBuild(bStar,A,y,x,mu,P,alpha,wt,family = "binomial",link = "logit",
Gridtype = 2L,n = 1L,n_envopt=NULL,sortgrid = FALSE,use_openc1 = FALSE,verbose = FALSE)
```

```
EnvelopeSetGrid(GridIndex, cbars, Lint)
```

```
EnvelopeSetLogP(logP, NegLL, cbars, G3)
```

Arguments

bStar	Point at which envelope should be centered (typically posterior mode).
A	Diagonal precision matrix for the log-likelihood in standard form.
y	A vector of observations of length m.
x	A design matrix of dimension m * p.
mu	A vector giving the prior means of the variables.
P	Prior precision matrix of the variables (positive-definite).
alpha	Offset vector.
wt	A vector of weights.
family	Family for the envelope: binomial, quasibinomial, poisson, quasipoisson, or Gamma.
link	Link function ("logit", "probit", "cloglog" for binomial; "log" for Poisson/Gamma).
Gridtype	Method to determine the number of subgradient densities in the grid.
n	Number of draws from the posterior (used for grid sizing).
n_envopt	Effective sample size passed to EnvelopeOpt for grid construction. Defaults to match n. Larger values encourage tighter envelopes.
sortgrid	Logical; if TRUE, sort the envelope descending by component probability.
use_openc1	Logical; if TRUE, use OpenCL for gradient evaluations.
verbose	Logical; if TRUE, print progress messages.
GridIndex	A matrix indicating, for each grid component, whether the component lies in the left tail, center, or right tail of the density. Rows correspond to grid components; columns correspond to standardized variables.
cbars	A matrix containing the subgradient of the (adjusted) negative log-likelihood at each grid component.

Lint	A matrix storing the lower and upper bounds for each grid component, depending on whether sampling is from the left, center, or right.
logP	A matrix (typically two columns) with information for each grid component. The first column usually holds the output from <code>EnvelopeSetGrid()</code> , corresponding to the restricted normal density.
NegLL	A vector of negative log-likelihood evaluations at each grid component.
G3	A matrix of tangency points used in the grid.

Details

Constructs an enveloping function for posterior simulation using a grid of tangency points. The envelope is used in accept-reject sampling to guarantee iid draws from the posterior distribution. The implementation follows (Nygren and Nygren 2006), with extensions for GPU acceleration (via OpenCL), dynamic grid optimization, and parallelized evaluation.

The envelope is typically built around the posterior mode θ^* for a model in standard form (which in this context means a model with a diagonal posterior precision matrix and prior identity precision matrix - `glmb_Standardize_Model`). It uses dimension-specific width parameters ω_i derived from the precision matrix. Tangency points are selected per dimension, and the full grid is formed via Cartesian expansion. Negative log-likelihood and gradient values are computed at each grid point, either on CPU or GPU depending on the `use_openc1` flag. These values are used to construct a piecewise envelope function that dominates the posterior density.

Value

`EnvelopeBuild()` A list of envelope components used for accept-reject sampling:

- `GridIndex` Integer matrix encoding sampling type (tail, center, line) per dimension and region.
- `thetabars` Matrix of tangency points $\bar{\theta}_j$ for each grid region.
- `cbars` Matrix of subgradients $c(\bar{\theta}_j)$ of the negative log-likelihood at tangency.
- `loglt` Matrix of log left-tail probabilities per dimension and region.
- `logrt` Matrix of log right-tail probabilities per dimension and region.
- `logU` Matrix of selected per-dimension log-density contributions (tail/center) for each region.
- `logP` Matrix of total log-probabilities per region (first column); used to derive mixture weights.
- `PLSD` Vector of normalized mixture weights over grid regions used to draw region indices.
- `LLconst` Vector of acceptance-test constants per region used in the inequality for rejection sampling.

`EnvelopeSetGrid()` A list of matrices computed for grid-based log-density evaluation:

- `Down` Lower bounds for truncated-normal evaluation per dimension and region.
- `Up` Upper bounds for truncated-normal evaluation per dimension and region.
- `lglt` Log left-tail probabilities (from $(-\infty, Up]$) per dimension and region.
- `lgrr` Log right-tail probabilities (from $[Down, \infty)$) per dimension and region.
- `lgcr` Log central-interval probabilities (from $[Down, Up]$) per dimension and region.
- `logU` Selected log-probability per grid cell based on `GridIndex` (tail or center).
- `logP` Matrix with row-wise sums of `logU` (first column) used to form mixture weights.

EnvelopeSetLogP() A list with updated mixture-weight and acceptance constants:

logP Input logP with its second column populated by the log of unnormalized visit probabilities per region (mixture denominators).

LLconst Vector of acceptance constants $-\log f(y | \bar{\theta}_j) - c(\bar{\theta}_j)^T \bar{\theta}_j$ used in the accept-reject test.

Models in standard form

The standard-form restriction and its closed-form truncated-normal integrals follow (Nygren and Nygren 2006). See (Nygren 2025) for the full theoretical details (standard form restriction, closed-form truncated-normal integrals, and the resulting log-scale tractability).

In the implementation, these standard-form quantities determine the grid-based tangency shifts and the precomputed region constants (e.g., the log-CDF pieces) that drive the mixture weights used by the envelope sampler.

Construction of restricted subgradient densities

For the full restricted density construction and the resulting envelope constants, see (Nygren 2025).

In the implementation, these theory objects become the precomputed region log-constants (via closed-form CDF pieces) that are used to normalize the envelope mixture weights for the accept-reject sampler.

Mixture construction and tractable probabilities

The mixture construction and its tractable region probabilities are derived in (Nygren 2025). In the implementation, these theory objects become the precomputed region log-constants and the mixture weights (PLSD) used by the envelope-based accept-reject sampler.

Log-scale properties of the envelope function

The log-scale form of the envelope factor and the subgradient inequality that imply envelope dominance are given in (Nygren 2025). In the implementation, these properties allow pointwise evaluation in the log-domain and provide the theoretical basis for the rejection test inside the sampler.

Use of the envelope during sampling

The standardized sampler called through `.rNormalGLM_std_cpp()` uses the envelope to generate posterior samples via rejection sampling. Although not exported, this routine is called internally by `.rNormalGLM_cpp()`, which in turn is invoked by the user-facing function `rNormal_reg()`. Together, these routines implement envelope-based sampling for generalized linear models with log-concave likelihood functions and multivariate normal priors.

The envelope provides a mixture of restricted likelihood-subgradient densities, each defined over a region A_i , with associated mixture weights $\tilde{p}_i$ stored in PLSD. The sampling proceeds as follows:

1. A region index $J(i)$ is drawn from the discrete distribution defined by PLSD.
2. A candidate θ_i is drawn from the restricted density $q_{A_{J(i)}}^{\bar{\theta}_{J(i)}}$, using the normal CDF bounds `loglt` and `logrt`, and subgradient vector `cbars`. Simulation for each dimension uses the internal C++ function `ctrnorm_cpp()`, which explicitly uses these inputs.

3. The log-likelihood $\log f(y \mid \theta_i)$ is computed and stored in `testll[0]` using the appropriate likelihood function `f2`.

The acceptance test is performed using the inequality

$$\log(U_2) \leq \text{LLconst}[J(i)] + \text{cbars}[J(i),]^T \theta_i + \log f(y \mid \theta_i),$$

which is equivalent to

$$\log(U_2) \leq \log f(y \mid \theta_i) - (\log f(y \mid \bar{\theta}_{J(i)}) - c(\bar{\theta}_{J(i)})^T (\theta_i - \bar{\theta}_{J(i)})),$$

where:

- `LLconst[J(i)]` stores the precomputed quantity $-\log f(y \mid \bar{\theta}_{J(i)}) - c(\bar{\theta}_{J(i)})^T \bar{\theta}_{J(i)}$, computed during envelope construction via `EnvelopeSet_LogP_C2()`.
- `cbars[J(i), ]` is the precomputed subgradient vector $c(\bar{\theta}_{J(i)})$, extracted via `cbars(J(i), _)`. It defines the exponential tilt direction used to evaluate the envelope.
- `testll[0]` is the log-likelihood at the candidate draw θ_i , evaluated using the model specified by family and link.
- $-\log(U_2)$ is the threshold from a uniform draw $U_2 \sim \text{Unif}(0, 1)$.

The right-hand side of this inequality is always non-positive, and equals zero when $\theta_i = \bar{\theta}_{J(i)}$. This reflects the fact that the envelope is tangent to the log-likelihood at each $\bar{\theta}_j$, and lies above it elsewhere.

This procedure guarantees that accepted samples are drawn from the posterior $\pi(\theta \mid y)$. The envelope ensures bounded rejection probability, and the mixture structure allows efficient sampling across regions. The output `out` contains accepted draws, and `draws` records the number of attempts per sample.

The components returned by `EnvelopeBuild()` are used in specific steps of the sampling procedure as follows:

- `PLSD` is used to randomly select a region index $J(i)$ from the envelope mixture.
- `loglt` and `logrt` define the truncated normal bounds for each dimension, used together with `cbars` to generate candidate values θ_i .
- `cbars` provides the subgradient vectors $c(\bar{\theta}_j)$ used both for candidate generation and for computing the acceptance test.
- `LLconst` stores precomputed constants used in the acceptance inequality, avoiding recomputation of posterior terms at tangency points.
- `logU` stores the per-dimension log-density contributions for each region, computed during envelope setup. These values are summed to produce `logP`, which determines the mixture weights `PLSD`.
- `logP` contains the total log-probabilities for each grid component, which are normalized to form the mixture weights `PLSD`.
- `thetabars` stores the tangency points $\bar{\theta}_j$ used to define subgradients and region-specific densities.
- `GridIndex` encodes the sampling type (tail, center, line) used for each dimension and region, guiding how each coordinate is simulated.

Algorithmic steps (linked to theory)

The implementation of EnvelopeBuild follows the envelope construction in (Nygren and Nygren 2006) for models in standard form (see Section 3–3.3 there). Each computational step corresponds to a theoretical guarantee:

1. **Compute width parameters ω_i from the diagonal precision matrix.** In particular, let θ^* denote the unique posterior mode. For each dimension i , define

$$\omega_i := \frac{\sqrt{2} - \exp(-1.20491 - 0.7321 \sqrt{0.5 - \partial^2 \log f(\theta^* | y) / \partial \theta_i^2})}{\sqrt{1 - \partial^2 \log f(\theta^* | y) / \partial \theta_i^2}}.$$

As seen from the above, the widths ω_i are derived from the local curvature of the log-likelihood at the posterior mode. This ensures that the three-interval construction per dimension below yields an envelope whose efficiency does not deteriorate with sample size.

2. **Use the width parameters to construct intervals around the posterior mode θ^* .** Specifically, we set

$$\ell_{i,1} = \theta_i^* - 0.5 \omega_i, \quad \ell_{i,2} = \theta_i^* + 0.5 \omega_i,$$

and construct three intervals per dimension:

$$A_{i,1} = (-\infty, \ell_{i,1}), \quad A_{i,2} = [\ell_{i,1}, \ell_{i,2}], \quad A_{i,3} = (\ell_{i,2}, \infty).$$

For each dimension i , let $J_i = \{1, 2, 3\}$ and define $J = \prod_{i=1}^p J_i$, which has 3^p elements. Each $j \in J$ is a vector $(j_1, \dots, j_p)$, and we define

$$A_j^* = \prod_{i=1}^p A_{i,j_i}.$$

The collection $A^* = \{A_j^* : j \in J\}$ forms a partition of Θ .

1. **For each member of the partition, select tangency points $\theta^* \pm \omega_i$.**

For each $j \in J$, define index sets

$$C_{j1} = \{i : j_i = 1\}, \quad C_{j2} = \{i : j_i = 2\}, \quad C_{j3} = \{i : j_i = 3\}.$$

The tangency points $\bar{\theta}_j$ are then defined componentwise by

$$\bar{\theta}_{j,i} = \begin{cases} \theta_i^* - \omega_i, & i \in C_{j1}, \\ \theta_i^*, & i \in C_{j2}, \\ \theta_i^* + \omega_i, & i \in C_{j3}. \end{cases}$$

The tangency points are hence chosen so that the envelope touches the log-likelihood at representative points in each interval, guaranteeing dominance and tightness.

1. **Build the full grid of tangency points (Cartesian product across dimensions).**

The Cartesian product of per-dimension partitions yields the 3^p restricted densities described in the paper, ensuring coverage of the full parameter space.

2. **Evaluate negative log-likelihood and gradients at each grid point to construct the likelihood subgradient densities and to facilitate accept rejection sampling**

The subgradients $c(\bar{\theta})$ enter the likelihood-subgradient density construction ((Nygren and Nygren 2006); see also (Nygren 2025)), and both subgradients and negative log-likelihoods (through $h_{\bar{\theta}}(\cdot)$) are used in the accept-reject procedure. CPU and GPU routines compute these values efficiently.

- On CPU: via `f2_f3_non_opengl`.
- On GPU: via `f2_f3_opengl`, which computes these in parallel across faces

3. **Call `EnvelopeSet_Grid_C2_pointwise` to evaluate restricted multivariate normal log-densities.** Each restricted density corresponds to a subset of the partition, normalized as in Remark 5 of (Nygren and Nygren 2006).

4. **Call `EnvelopeSet_LogP_C2` to compute component log-probabilities and constants.** The constants $\tilde{a}$ and mixture weights $\tilde{p}_i$ are computed explicitly as in Remark 6 of the paper, ensuring that the mixture envelope is properly normalized.

5. **Normalize probabilities (PLSD) and optionally sort grid components.** Normalization implements Claim 2 of the paper so the mixture forms a valid dominating density for the posterior. Sorting is an implementation detail to improve sampling efficiency.

Theory reference (JASA paper and vignette)

Definitions, claims, theorems, remarks, and examples through Remark 16 (including standard form, the 3^p partition, and sampling remarks) are in (Nygren and Nygren 2006). An expanded narrative is in `vignette("Chapter-A08", package = "glmbyes")`.

Subgradient density formulation

Each grid component corresponds to a tilted multivariate normal density, normalized using the moment-generating function (MGF). In the single-point case, centered at the posterior mode θ^* , the density is:

$$f(\theta) = \frac{1}{(2\pi)^{p/2} |A|^{-1/2} \cdot \text{MGF}_A(c)} \exp \left(-\frac{1}{2} (\theta - \mu)^T A (\theta - \mu) + c^T (\theta - \theta^*) \right)$$

where:

- A is the precision matrix,
- μ is the prior mean vector,
- c is the gradient of the log-likelihood at θ^* ,
- $\text{MGF}_A(c)$ is the moment-generating function:

$$\text{MGF}_A(c) = \exp \left(\frac{1}{2} c^T A^{-1} c \right)$$

This closed-form density dominates the posterior locally and is used when `Gridtype = 1`. For richer envelopes, multiple such components are constructed at tangency points θ_j , each with its own gradient c_j , and combined into a mixture:

$$f_{\text{env}}(\theta) = \sum_{j=1}^K p_j f_j(\theta)$$

where the weights p_j are computed using log-CDF differences and constants:

$$\log p_j = \log \Phi(U_j) - \log \Phi(L_j) - \text{NegLL}_j + \text{LLconst}_j$$

Gridtype logic

The Gridtype argument controls how many tangency points are used per dimension:

- 1: Threshold rule. If $1 + a_i \leq 2/\sqrt{\pi}$, use a single-point envelope at the mode; otherwise use three points.
- 2: Dynamic optimization via EnvelopeOpt, which balances grid build cost and expected acceptance rate. Grid size is scaled by n and the number of OpenCL cores when GPU is enabled.
- 3: Always use three points per dimension.
- 4: Always use a single point (mode only).

Supported families and links

The following families and link functions are supported:

- Binomial: logit, probit, cloglog
- Quasibinomial: logit, probit
- Poisson: log
- Quasipoisson: log
- Gamma: log
- Gaussian: identity

GPU acceleration (`use_opengl = TRUE`) is available for all of the above except Gaussian, which is always evaluated on CPU.

GPU acceleration

When `use_opengl = TRUE`, likelihood and gradient evaluations are offloaded to the GPU using OpenCL. This can substantially reduce runtime for high-dimensional models or large grids. Results are mathematically equivalent to the CPU version, but small numerical differences may occur due to floating-point arithmetic. If reproducibility across hardware is critical, prefer the CPU path.

If OpenCL support was not detected at compile time, the flag is ignored and the CPU implementation is used. Diagnostic messages are printed when `verbose = TRUE`.

Verbose output

When `verbose = TRUE`, the function prints:

- Grid type, number of draws, OpenCL usage, and detected core count.
- Grid size after expansion.
- Time-stamped messages when entering the grid loop, starting likelihood evaluations, starting gradient evaluations, and invoking GPU kernels.
- Messages when setting grid values, computing log-probabilities, and sorting.

Any constants needed by the sampling are added to a list and returned.

References

Nygren K (2025). “Chapter A08: Overview of Envelope Related Functions.” Vignette in the glm-bayes R package. R vignette name: Chapter-A08.

Nygren K~N, Nygren L~M (2006). “Likelihood Subgradient Densities.” *Journal of the American Statistical Association*, **101**(475), 1144–1156. doi:10.1198/016214506000000357.

See Also

[EnvelopeSize](#), [EnvelopeEval](#), [EnvelopeSort](#), [glmb_Standardize_Model](#); [rNormal_reg](#), [rglmb](#), [rlmb](#). Theory and vignettes: (Nygren and Nygren 2006); (Nygren 2025, 2025).

Examples

```
data(menarche, package="MASS")
Age2=menarche$Age-13

summary(menarche)
plot(Menarche/Total ~ Age, data=menarche)

x<-matrix(as.numeric(1.0),nrow=length(Age2),ncol=2)
x[,2]=Age2

y=menarche$Menarche/menarche$Total
wt=menarche$Total

mu<-matrix(as.numeric(0.0),nrow=2,ncol=1)
mu[2,1]=(log(0.9/0.1)-log(0.5/0.5))/3

V1<-1*diag(as.numeric(2.0))

# 2 standard deviations for prior estimate at age 13 between 0.1 and 0.9
## Specifies uncertainty around the point estimates

V1[1,1]<-((log(0.9/0.1)-log(0.5/0.5))/2)^2
V1[2,2]=(3*mu[2,1]/2)^2 # Allows slope to be up to 1 times as large as point estimate

famfunc<-glmbfamfunc(binomial(logit))

f1<-famfunc$f1
f2<-famfunc$f2
f3<-famfunc$f3
f5<-famfunc$f5
f6<-famfunc$f6

dispersion2<-as.numeric(1.0)
start <- mu
offset2=rep(as.numeric(0.0),length(y))
P=solve(V1)
n=1000
```

```
##### Adjust weight for dispersion

wt2=wt/dispersion2

##### Shift mean vector to offset so that adjusted model has 0 mean

alpha=x%*%as.vector(mu)+offset2
mu2=0*as.vector(mu)
P2=P
x2=x

##### Optimization step to find posterior mode and associated Precision

parin=start-mu

opt_out=optim(parin,f2,f3,y=as.vector(y),x=as.matrix(x),mu=as.vector(mu2),
              P=as.matrix(P),alpha=as.vector(alpha),wt=as.vector(wt2),
              method="BFGS",hessian=TRUE
)

bstar=opt_out$par ## Posterior mode for adjusted model
bstar
bstar+as.vector(mu) # mode for actual model
A1=opt_out$hessian # Approximate Precision at mode

## Standardize Model

Standard_Mod=glmb_Standardize_Model(y=as.vector(y), x=as.matrix(x),P=as.matrix(P),
                                     bstar=as.matrix(bstar,ncol=1), A1=as.matrix(A1))

bstar2=Standard_Mod$bstar2
A=Standard_Mod$A
x2=Standard_Mod$x2
mu2=Standard_Mod$mu2
P2=Standard_Mod$P2
L2Inv=Standard_Mod$L2Inv
L3Inv=Standard_Mod$L3Inv

Env2=EnvelopeBuild(as.vector(bstar2), as.matrix(A),y, as.matrix(x2),
as.matrix(mu2,ncol=1),as.matrix(P2),as.vector(alpha),as.vector(wt2),
family="binomial",link="logit",Gridtype=as.integer(3), n=as.integer(n),
sortgrid=TRUE)

## These now seem to match

Env2
```

Description

EnvelopeCentering() computes an initial dispersion and the expected posterior weighted RSS (closed form under the Normal posterior for coefficients) for use in envelope construction when the dispersion is unknown. The dispersion-anchoring loop updates dispersion from the Gamma posterior using that expected RSS each iteration. This step is typically called inside rIndepNormalGammaReg() before [EnvelopeOrchestrator](#), but may be used directly for diagnostics or custom workflows.

Usage

```
EnvelopeCentering(
  y,
  x,
  mu,
  P,
  offset,
  wt,
  shape,
  rate,
  Gridtype = 2L,
  verbose = FALSE
)
```

Arguments

y	Numeric response vector of length m.
x	Numeric design matrix of dimension m * p.
mu	Numeric vector of prior means (length p).
P	Numeric matrix of prior precision (p * p).
offset	Numeric vector of length m. Use rep(0, m) for none.
wt	Numeric vector of prior weights.
shape	Numeric. Shape parameter of the Gamma prior for the dispersion.
rate	Numeric. Rate parameter of the Gamma prior for the dispersion.
Gridtype	Integer. Grid construction method (default 2).
verbose	Logical. Reserved for API compatibility; currently unused in C++.

Details

The function first obtains an initial dispersion via `lm.wfit` residual variance, then iteratively: (1) computes the expected weighted RSS under the Normal posterior (closed form), (2) updates the dispersion via the Gamma posterior using the expected RSS. The result is used as `dispersion2` and `RSS_Post2` in downstream envelope construction (e.g., [EnvelopeOrchestrator](#)).

This anchors the joint Normal–Gamma accept–reject construction in (Nygren and Nygren 2006); see vignettes Chapter–A07, Chapter–A11, and (Nygren 2025, 2025).

Value

A list with components:

dispersion Numeric. Anchored dispersion value.

RSS_post Numeric. Expected posterior weighted RSS (closed form; last iteration).

References

Nygren K (2025). “Chapter A08: Overview of Envelope Related Functions.” Vignette in the glm-bayes R package. R vignette name: Chapter-A08.

Nygren K (2025). “Independent Normal–Gamma Regression Sampler.” Vignette in the glmbayes R package. R vignette name: independent-norm-gamma.

Nygren K~N, Nygren L~M (2006). “Likelihood Subgradient Densities.” *Journal of the American Statistical Association*, **101**(475), 1144–1156. doi:10.1198/016214506000000357.

See Also

[EnvelopeOrchestrator](#) for envelope construction; [EnvelopeBuild](#), [EnvelopeDispersionBuild](#); [rindepNormalGamma_reg](#) for the full simulation routine; [rlmb](#) for the user-facing linear-model interface.

Examples

```
##### Start of EnvelopeCentering example #####

# This example demonstrates EnvelopeCentering in isolation. It computes an
# initial dispersion and posterior RSS for use in envelope construction when
# the dispersion is unknown (Gaussian regression with Normal-Gamma prior).
# This is Step A of the full pipeline in Ex_EnvelopeDispersionBuild and
# Ex_rIndepNormalGammaReg_std.

ctl <- c(4.17, 5.58, 5.18, 6.11, 4.50, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)

ps <- Prior_Setup(weight ~ group, gaussian())

x <- as.matrix(ps$x)
y <- as.vector(ps$y)
mu <- ps$mu
Sigma <- ps$Sigma
shape <- ps$shape
rate <- ps$rate

n_obs <- length(y)
wt <- rep(1, n_obs)
offset2 <- rep(0, n_obs)
```

```

# Reconstruct coefficient precision P (matches rindepNormalGamma_reg)
Rchol <- chol(Sigma)
Pinv <- chol2inv(Rchol)
P <- 0.5 * (Pinv + t(Pinv))

Gridtype_core <- as.integer(2)

#####
# EnvelopeCentering: initial dispersion + dispersion anchoring loop
#####
centering <- EnvelopeCentering(
  y = y,
  x = x,
  mu = as.vector(mu),
  P = P,
  offset = offset2,
  wt = wt,
  shape = shape,
  rate = rate,
  Gridtype = Gridtype_core,
  verbose = FALSE
)

centering$dispersion
centering$RSS_post

#####
# End of EnvelopeCentering example
#####

```

EnvelopeDispersionBuild

Builds Dispersion-Aware Envelope for Simulation

Description

Constructs a dispersion-aware envelope for simulation in Gaussian models with uncertain variance. This function extrapolates the coefficient envelope across a high-probability interval for the dispersion parameter σ^2 , and builds a global upper bound for the log-posterior remainder. It also computes mixture weights for envelope faces and adjusts the Gamma proposal for precision.

The envelope is constructed using the slopes of the face constants with respect to dispersion, evaluated at an anchor point. The resulting structure supports exact i.i.d. sampling via accept-reject correction.

The procedure follows these steps:

1. **Posterior precision (Gamma) parameters.** Using the prior and posterior-predictive RSS, set

$$\text{shape2} = \text{Shape} + n_{\text{obs}}/2, \quad \text{rate3} = \text{Rate} + \text{RSS}_{\text{post}}/2$$

These parameterize the posterior precision $v = 1/\sigma^2 \sim \text{Gamma}(\text{shape2}, \text{rate3})$.

2. **Central credible interval for dispersion (low, upp).** Choose a central mass level `max_disp_perc` (e.g., 0.99) for precision, then invert the corresponding Gamma quantiles to dispersion:

$$\text{low} = 1/Q_{\Gamma}(\text{max_disp_perc}; \text{shape2}, \text{rate3}), \quad \text{upp} = 1/Q_{\Gamma}(1-\text{max_disp_perc}; \text{shape2}, \text{rate3})$$

The interval $[\text{low}, \text{upp}]$ is the domain over which all envelopes must dominate.

3. **Face slopes at an anchor (dispstar).**

$$\text{dispstar} = \text{rate3}/(\text{shape2} - 1)$$

(posterior mean of σ^2). Compute New_LL_Slope_j for each face j .

4. **Linear extrapolation of face constants.**

$$\theta_j^{\text{low}} = \theta_j^{\text{base}} + (\text{low} - \text{dispstar}) \cdot \text{New_LL_Slope}_j$$

$$\theta_j^{\text{upp}} = \theta_j^{\text{base}} + (\text{upp} - \text{dispstar}) \cdot \text{New_LL_Slope}_j$$

5. **Global upper line and endpoint maxima.**

$$\text{max_low} = \max_j \theta_j^{\text{low}}, \quad \text{max_upp} = \max_j \theta_j^{\text{upp}}$$

$$\text{new_slope} = (\text{max_upp} - \text{max_low})/(\text{upp} - \text{low}), \quad \text{new_int} = \text{max_low} - \text{new_slope} \cdot \text{low}$$

6. **Face slack and mixture weights.**

$$\text{lg_prob_factor}_j = \max(\theta_j^{\text{upp}} - \text{max_upp}, \theta_j^{\text{low}} - \text{max_low})$$

Combine with $\text{New_logP2}_j = \log P_j + \frac{1}{2} \|\bar{c}_j\|^2$ to form mixture weights $\text{PLSD}_j \propto \exp(\text{New_logP2}_j + \text{lg_prob_factor}_j)$.

7. **Gamma tilt and dispersion-axis envelope.**

$$\text{dispstar} = (\text{upp} - \text{low})/\log(\text{upp}/\text{low})$$

$$\text{lm_log2} = \text{new_slope} \cdot \text{dispstar}, \quad \text{lm_log1} = \text{new_int} + \text{new_slope} \cdot \text{dispstar} - \text{new_slope} \cdot \log(\text{dispstar})$$

Tilt the Gamma proposal via $\text{shape3} = \text{shape2} - \text{lm_log2}$.

Usage

```
EnvelopeDispersionBuild(
  Env, Shape, Rate, P, y, x, alpha, n_obs, RSS_post, RSS_ML,
  mu, wt, max_disp_perc = 0.99,
  disp_lower = NULL, disp_upper = NULL,
  verbose = FALSE, use_parallel = TRUE
)
```

Arguments

Env	Envelope object from EnvelopeBuild , containing tangency points and gradients
Shape	Prior shape parameter for precision $v = 1 / \sigma^2$
Rate	Prior rate parameter for precision
P	Prior precision matrix for coefficients
y	Numeric response vector of length m
x	a design matrix of dimension $m \times p$
alpha	Numeric offset vector of length m
n_obs	Number of observations
RSS_post	Expected posterior weighted residual sum of squares (i.e., $\mathbb{E}[\text{RSS}(\beta) \mid y, \phi]$ under the Normal posterior for β at fixed dispersion $\phi = d$). This value is used for dispersion anchoring / Gamma updates.
RSS_ML	Residual sum of squares associated with MLE estimate
mu	Prior mean parameter
wt	weight vector
max_disp_perc	Truncation level for dispersion (default 0.99)
disp_lower	lower bound truncation for dispersion
disp_upper	upper bound truncation for dispersion
verbose	Option to have verbose output
use_parallel	Logical. Whether to use parallel processing.

Details

This function is designed to complement [EnvelopeBuild](#) for Gaussian models with Normal-Gamma priors. It enables exact sampling of both coefficients and dispersion by constructing a joint envelope that respects posterior curvature in both dimensions.

The dispersion anchor point is chosen as the log-scale center of the credible interval, and the Gamma proposal is tilted to match the envelope slope at this point. Theory and narrative: (Nygren and Nygren 2006); vignettes Chapter-A07, Chapter-A11; (Nygren 2025, 2025).

Value

EnvelopeDispersionBuild() A list containing:

Env_out	Envelope object with updated mixture weights (PLSD)
gamma_list	Posterior Gamma tilt parameters
shape3	Adjusted shape parameter after slope correction
rate2	Posterior rate parameter, defined as $\text{Rate} + \text{rss_min_global}/2$
disp_upper	Upper bound of the dispersion interval σ^2
disp_lower	Lower bound of the dispersion interval σ^2
UB_list	Upper-bound diagnostics
RSS_ML	Residual sum of squares at the maximum-likelihood estimate
RSS_Min	Minimum residual sum of squares across envelope faces

max_New_LL_UB Maximum extrapolated face constant at the upper dispersion bound
 max_LL_log_disp Log-posterior upper bound evaluated at disp_upper
 lm_log1 Intercept term of the global upper line approximation
 lm_log2 Slope term of the global upper line approximation
 lg_prob_factor Per-face slack factors used in mixture weighting
 lmc1 Linear extrapolation constant (intercept)
 lmc2 Linear extrapolation constant (slope)
 UB2min Minimum UB2 value across faces, used for diagnostics
 diagnostics Internal diagnostic values
 dispstar Anchor dispersion value (posterior mean or geometric mean)
 New_LL_Slope Vector of slopes of face constants at dispstar
 shape2 Posterior shape parameter before tilt correction
 rate3 Posterior rate parameter before tilt correction
 shape3 Adjusted shape parameter (same as in gamma_list)
 max_low Maximum extrapolated face constant at the lower dispersion bound
 max_upp Maximum extrapolated face constant at the upper dispersion bound
 new_slope Slope of the global upper line across dispersion bounds
 new_int Intercept of the global upper line across dispersion bounds
 prob_factor Normalized mixture weights across faces
 UB2min Minimum UB2 diagnostic value (duplicated for consistency)
 EnvBuildLinBound() Numeric vector of slopes of face constants with respect to dispersion, evaluated at the anchor dispstar
 thetabar_const() Numeric vector of base face constants computed from tangency points and gradient vectors under prior precision P
 Inv_f3_with_disp() Numeric matrix of inverse function evaluations at a given dispersion and face subset, returned by the C++ routine _glmbyes_Inv_f3_with_disp
 UB2() Numeric scalar representing the UB2 upper-bound criterion for a given dispersion and face, defined as $(1/dispersion) * (RSS - rss_min_global)$
 rss_face_at_disp() Numeric scalar giving the residual sum of squares for a specified face at a given dispersion, computed from cached matrices and the inverse function evaluation

Use in accept/reject procedure

The accept/reject sampler relies on a decomposition of the log-posterior into a test statistic and several bounding terms. Each component is constructed so that its sign is controlled, ensuring the validity of the accept/reject step.

test1 (log-likelihood bound) Placeholder: explain how test1 is formed and why it is non-positive.

UB1 (if applicable) Placeholder: describe UB1's role and why it is non-negative.

UB2 (residual sum of squares bound) Placeholder: explain how UB2 is constructed from RSS differences and why it is non-negative.

UB3A (face-wise quadratic/linear envelope surplus) Placeholder: explain how lg_prob_factor, lmc1, and lmc2 are derived and why UB3A ≥ 0 .

UB3B (dispersion-axis envelope surplus) Placeholder: explain how `lm_log1`, `lm_log2`, and `max_New_LL_UB` are used and why `UB3B >= 0`.

Together, these components define

$$test = test1 - UB2 - UB3A - UB3B,$$

with $test1 \leq 0$ and each UB term ≥ 0 , ensuring the accept/reject procedure is valid and unbiased.

References

Nygren K (2025). “Chapter A08: Overview of Envelope Related Functions.” Vignette in the `glm-bayes` R package. R vignette name: Chapter-A08.

Nygren K (2025). “Independent Normal–Gamma Regression Sampler.” Vignette in the `glmbayes` R package. R vignette name: independent-norm-gamma.

Nygren K~N, Nygren L~M (2006). “Likelihood Subgradient Densities.” *Journal of the American Statistical Association*, **101**(475), 1144–1156. doi:10.1198/016214506000000357.

See Also

[EnvelopeBuild](#), [EnvelopeOrchestrator](#), [EnvelopeCentering](#) (for obtaining `RSS_post` and anchored dispersion), [rindepNormalGamma_reg](#), [rlmb](#); [rglmb](#), [glmbfamfunc](#).

Examples

```
##### Start of EnvelopeDispersionBuild example #####

# This example mirrors the current C++ algorithm path for Gaussian regression
# with an independent Normal-Gamma prior:
#   rIndepNormalGammaReg:
#   - Step A: EnvelopeCentering (initial dispersion + dispersion anchoring loop)
#   - Step B: optimize posterior mode for coefficients (optim + f2/f3)
#   - Step C: standardize the model (glmb_Standardize_Model)
#   - Step D: build coefficient envelope (EnvelopeBuild)
#   - Step E: build dispersion-aware envelope (EnvelopeDispersionBuild)
#   - Step F: sort envelope components (EnvelopeSort)
# It stops after envelope construction (no standardized-envelope sampling).

ctl <- c(4.17, 5.58, 5.18, 6.11, 4.50, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)

ps <- Prior_Setup(weight ~ group, gaussian())

x <- as.matrix(ps$x)
y <- as.vector(ps$y)
mu <- ps$mu
Sigma <- ps$Sigma
shape <- ps$shape
```

```

rate <- ps$rate

n_obs <- length(y)
wt <- rep(1, n_obs)
offset2 <- rep(0, n_obs)

# Reconstruct coefficient precision P (matches rindepNormalGamma_reg)
Rchol <- chol(Sigma)
Pinv <- chol2inv(Rchol)
P <- 0.5 * (Pinv + t(Pinv))

famfunc <- glmbfamfunc(gaussian())
f2 <- famfunc$f2
f3 <- famfunc$f3

Gridtype_core <- as.integer(2)

#####
# Step A: EnvelopeCentering (initial dispersion + dispersion anchoring loop)
#####
centering <- EnvelopeCentering(
  y = y,
  x = x,
  mu = as.vector(mu),
  P = P,
  offset = offset2,
  wt = wt,
  shape = shape,
  rate = rate,
  Gridtype = Gridtype_core,
  verbose = FALSE
)

dispersion2 <- centering$dispersion
RSS_Post2 <- centering$RSS_post

n_w <- sum(wt)

#####
# Step B: Coefficient posterior mode optimization (optim + f2/f3)
#####
dispstar <- dispersion2

wt2_opt <- wt / dispstar
alpha <- as.vector(x %*% as.vector(mu) + offset2)

mu2 <- rep(0, length(as.vector(mu))) # mu2 = 0 * mu (as in C++)
parin <- rep(0, length(as.vector(mu))) # parin = 0 vector (mu - mu)

opt_out <- optim(
  par = parin,
  fn = f2,

```

```

    gr = f3,
    y = as.vector(y),
    x = as.matrix(x),
    mu = as.vector(mu2),
    P = as.matrix(P),
    alpha = as.vector(alpha),
    wt = as.vector(wt2_opt),
    method = "BFGS",
    hessian = TRUE
  )

bstar <- opt_out$par
A1 <- opt_out$hessian

#####
# Step C: Standardize model (glmb_Standardize_Model)
#####
Standard_Mod <- glmb_Standardize_Model(
  y = as.vector(y),
  x = as.matrix(x),
  P = as.matrix(P),
  bstar = as.matrix(bstar, ncol = 1),
  A1 = as.matrix(A1)
)

bstar2 <- Standard_Mod$bstar2
A <- Standard_Mod$A
x2_std <- Standard_Mod$x2
mu2_std <- Standard_Mod$mu2
P2_std <- Standard_Mod$P2

#####
# Step D: EnvelopeBuild (coefficient envelope at Gridtype = 3)
#####
max_disp_perc <- 0.99
n_env <- as.integer(200) # used by EnvelopeBuild for diagnostics/overhead
Gridtype_env <- as.integer(3) # EnvelopeOrchestrator overrides to 3

shape2_env <- shape + n_w / 2.0
rate3_env <- rate + RSS_Post2 / 2.0
d1_star <- rate3_env / (shape2_env - 1.0)

wt2_env <- wt / d1_star

Env2 <- EnvelopeBuild(
  bStar = as.vector(bstar2),
  A = as.matrix(A),
  y = as.vector(y),
  x = as.matrix(x2_std),
  mu = as.matrix(mu2_std, ncol = 1),
  P = as.matrix(P2_std),
  alpha = as.vector(alpha),
  wt = as.vector(wt2_env),

```

```

    family = "gaussian",
    link = "identity",
    Gridtype = Gridtype_env,
    n = n_env,
    n_envopt = as.integer(1),
    sortgrid = FALSE,
    use_openc1 = FALSE,
    verbose = FALSE
)

#####
# Step E: EnvelopeDispersionBuild (dispersion-aware envelope)
#####
disp_env_out <- EnvelopeDispersionBuild(
  Env = Env2,
  Shape = shape,
  Rate = rate,
  P = as.matrix(P2_std),
  y = as.vector(y),
  x = as.matrix(x2_std),
  alpha = as.vector(alpha),
  n_obs = as.integer(n_obs),
  RSS_post = RSS_Post2,
  RSS_ML = NA_real_,
  mu = as.matrix(mu2_std, ncol = 1),
  wt = as.vector(wt),
  max_disp_perc = max_disp_perc,
  disp_lower = NULL,
  disp_upper = NULL,
  verbose = FALSE,
  use_parallel = TRUE
)

#####
# Step F: EnvelopeSort (mirror EnvelopeOrchestrator: disp_grid_type = 2)
#####
Env3_raw <- disp_env_out$Env_out
UB_list_new <- disp_env_out$UB_list
gamma_list_new <- disp_env_out$gamma_list

cbars <- Env3_raw$cbars
l1 <- ncol(cbars)
l2 <- nrow(cbars)

logP_vec <- Env3_raw$logP
logP_mat <- matrix(logP_vec, nrow = length(logP_vec), ncol = 1)

Env3 <- EnvelopeSort(
  l1 = l1,
  l2 = l2,
  GIndex = Env3_raw$GridIndex,
  G3 = Env3_raw$thetabars,
  cbars = cbars,

```

```

logU = Env3_raw$logU,
logrt = Env3_raw$logrt,
loglt = Env3_raw$loglt,
logP = logP_mat,
LLconst = Env3_raw$LLconst,
PLSD = Env3_raw$PLSD,
a1 = Env3_raw$a1,
E_draws = Env3_raw$E_draws,
lg_prob_factor = UB_list_new$lg_prob_factor,
UB2min = UB_list_new$UB2min
)

UB_list_final <- UB_list_new
UB_list_final$lg_prob_factor <- Env3$lg_prob_factor
UB_list_final$UB2min <- Env3$UB2min

env_final <- list(
  Env = Env3,
  gamma_list = gamma_list_new,
  UB_list = UB_list_final,
  diagnostics = disp_env_out$diagnostics,
  low = gamma_list_new$disp_lower,
  upp = gamma_list_new$disp_upper
)

print(env_final$low)
print(env_final$upp)
print(env_final$gamma_list[c("shape3", "rate2")])

env_final

#####
# End: envelope construction only
#####

```

EnvelopeEval

Evaluate Negative Log-Likelihood and Gradients

Description

EnvelopeEval() evaluates the negative log-likelihood and gradients at a grid of parameter values, optionally using OpenCL acceleration.

Usage

```

EnvelopeEval(G4, y, x, mu, P, alpha, wt,
             family, link,
             use_opengl = FALSE, verbose = FALSE)

```

Arguments

G4	Numeric matrix of parameter values (parameters * grid points).
y	Numeric response vector.
x	Numeric design matrix.
mu	Numeric matrix of offsets or prior means.
P	Numeric matrix representing the portion of the prior precision shifted into the likelihood.
alpha	Numeric offset vector of length m
wt	Numeric vector of weights.
family	Character string; model family (e.g. "gaussian").
link	Character string; link function (e.g. "identity").
use_opengl	Logical; if TRUE, attempt OpenGL acceleration.
verbose	Logical; if TRUE, print diagnostic output.

Details

The lower-level helpers `f2_f3_non_opengl` and `f2_f3_opengl` are internal C++ kernels used by the CPU and OpenGL backends. The internal routine `run_opengl_pilot` benchmarks OpenGL performance on a pilot subset of the grid to estimate runtime before full evaluation.

These functions implement the grid evaluation logic used in envelope construction for rejection sampling. They make use of the theory described in (Nygren and Nygren 2006) and the general implementation outlined in (Nygren 2025).

The evaluation workflow has several layers: **1. High-level dispatch** (`EnvelopeEval`)

- `EnvelopeEval()` is the user-facing entry point. It accepts a grid of parameter values (G4) and the data (y, x, mu, P, alpha, wt).
- If the grid is large (≥ 14 columns), it first calls `run_opengl_pilot` to benchmark OpenGL performance and optionally report estimated runtime.
- It then dispatches to either the CPU or GPU backend:
 - If `use_opengl = TRUE` and the family is not "gaussian", it calls `f2_f3_opengl` (an internal C++ kernel).
 - Otherwise, it calls `f2_f3_non_opengl` (the CPU kernel).

2. CPU backend (`f2_f3_non_opengl`)

- This function evaluates the negative log-likelihood and gradients using standard CPU routines.
- It inspects the family and link arguments and routes to the correct pair of kernels (`f2_*` for the likelihood, `f3_*` for the gradient).
- For example:
 - "binomial" with "logit" calls `f2_binomial_logit()` and `f3_binomial_logit()`.
 - "poisson" calls `f2_poisson()` and `f3_poisson()`.
 - "gaussian" calls `f2_gaussian()` and `f3_gaussian()`.

- These kernels ultimately rely on the same C math routines that R itself uses (from the `nmath/rmath` libraries), ensuring numerical consistency with base R functions like `dnorm`, `dpois`, etc.

3. GPU backend (`f2_f3_openc1`)

- This function mirrors the CPU backend but executes the likelihood and gradient calculations on an OpenCL device (GPU or CPU).
- It flattens the input matrices/vectors and allocates output buffers.
- It then constructs a full OpenCL program by concatenating:
 - a generic OpenCL support header (`OPENCL.CL`),
 - OpenCL ports of R's `rmath`, `nmath`, and `dpq` libraries,
 - and the family/link-specific kernel source (e.g. `f2_f3_binomial_logit.cl`).
- The resulting program is compiled and passed to a kernel runner (`f2_f3_kernel_runner`) which executes the likelihood and gradient calculations in parallel on the device.
- This ensures that the GPU backend produces results consistent with the CPU backend, but can scale to much larger grids efficiently.

4. Pilot timing (`run_openc1_pilot`)

- This helper runs a small subset of the grid through the OpenCL backend to estimate runtime.
- It is used by `EnvelopeEval()` to inform users (when `verbose = TRUE`) whether OpenCL acceleration is likely to be beneficial.

5. Returned values

- All backends return a list with:
 - `NegLL`: numeric vector of negative log-likelihood values.
 - `cbars`: numeric matrix of gradients (`parameters * grid points`).

6. Role of likelihood and gradients in sampling

- The outputs of `EnvelopeEval()` - the negative log-likelihood values (`NegLL`) and the gradient matrix (`cbars`) - are not endpoints in themselves. They form the *envelope* used in the rejection sampler implemented by internal functions such as `.rNormalGLM_std_cpp()`.
- This routine is called by `.rNormalGLM_cpp()`, which underlies the user-facing function `rNormal_reg()`. Together they implement envelope-based posterior sampling for GLMs with log-concave likelihoods and multivariate normal priors.

7. Simulation execution (accept/reject procedure)

The acceptance test is performed using

$$\log(U_2) \leq \log f(y \mid \theta_i) - \left(\log f(y \mid \bar{\theta}_{J(i)}) - c(\bar{\theta}_{J(i)})^T (\theta_i - \bar{\theta}_{J(i)}) \right) \leq 0$$

Connections between code and notation:

- The arguments `G4` (in `EnvelopeEval`) and `b` (in `f2_f3_*`) both represent the grid of tangency points $\bar{\theta}_j$.
- The output `NegLL` corresponds to $-\log f(y \mid \bar{\theta}_{J(i)})$, i.e. the negative log-likelihood evaluated at each tangency point.

- The output `cbars` corresponds to the subgradient vectors $c(\bar{\theta}_{J(i)})$, which define the tangent hyperplanes used in the envelope construction.

Precomputation for efficiency:

- Both `NegLL` and `cbars` are computed once during envelope construction, prior to the simulation stage.
- This means the sampler does not need to recompute likelihoods or gradients at every candidate draw - it simply reuses the stored values (`NegLL`, `cbars`, and `LLconst`) in the acceptance inequality.

This design ensures that the envelope is tangent to the log-likelihood at each $\bar{\theta}_j$, lies above it elsewhere, and that the accept-reject procedure can run efficiently while still producing samples from the true posterior $\pi(\theta \mid y)$.

Value

EnvelopeEval List with components `NegLL` (numeric vector of negative log-likelihood values) and `cbars` (numeric matrix of gradients).

f2_f3_non_opencl List with components `qf` (negative log-likelihood) and `grad` (gradients) from the CPU kernel.

f2_f3_opencl List with components `qf` and `grad` from the OpenCL kernel.

run_opencl_pilot Numeric scalar giving estimated runtime (seconds) for OpenCL evaluation on a pilot subset of the grid.

References

Nygren K (2025). “Chapter A05: Simulation Methods – Likelihood Subgradient Densities.” Vignette in the `glmbayes` R package. R vignette name: Chapter-A05.

Nygren K~N, Nygren L~M (2006). “Likelihood Subgradient Densities.” *Journal of the American Statistical Association*, **101**(475), 1144–1156. doi:10.1198/016214506000000357.

See Also

[EnvelopeBuild](#), [EnvelopeSize](#), [EnvelopeSort](#); [rNormal_reg](#), [rglmb](#). Vignettes: (Nygren 2025, 2025).

Examples

```
##### Start of EnvelopeEval example #####

# This example demonstrates EnvelopeEval in isolation. EnvelopeEval evaluates
# the negative log-likelihood and gradients at a grid of parameter values.
# It is called internally by EnvelopeBuild. Here we build the same inputs
# (grid G4, standardized model) using EnvelopeSize and expand.grid, then
# call EnvelopeEval directly. The setup mirrors Ex_EnvelopeBuild through
# the standardization step.

data(menarche, package = "MASS")
```

```

Age2 <- menarche$Age - 13

x <- matrix(as.numeric(1.0), nrow = length(Age2), ncol = 2)
x[, 2] <- Age2

y <- menarche$Menarche / menarche$Total
wt <- menarche$Total

mu <- matrix(as.numeric(0.0), nrow = 2, ncol = 1)
mu[2, 1] <- (log(0.9 / 0.1) - log(0.5 / 0.5)) / 3

V1 <- 1 * diag(as.numeric(2.0))
V1[1, 1] <- ((log(0.9 / 0.1) - log(0.5 / 0.5)) / 2)^2
V1[2, 2] <- (3 * mu[2, 1] / 2)^2

famfunc <- glmbfamfunc(binomial(logit))
f2 <- famfunc$f2
f3 <- famfunc$f3

dispersion2 <- as.numeric(1.0)
start <- mu
offset2 <- rep(as.numeric(0.0), length(y))
P <- solve(V1)
n <- 1000

wt2 <- wt / dispersion2
alpha <- x %*% as.vector(mu) + offset2
mu2 <- 0 * as.vector(mu)
P2 <- P
x2 <- x

parin <- start - mu
opt_out <- optim(parin, f2, f3,
  y = as.vector(y), x = as.matrix(x), mu = as.vector(mu2),
  P = as.matrix(P), alpha = as.vector(alpha), wt = as.vector(wt2),
  method = "BFGS", hessian = TRUE
)

bstar <- opt_out$par
A1 <- opt_out$hessian

Standard_Mod <- glmb_Standardize_Model(
  y = as.vector(y), x = as.matrix(x), P = as.matrix(P),
  bstar = as.matrix(bstar, ncol = 1), A1 = as.matrix(A1)
)

bstar2 <- Standard_Mod$bstar2
A <- Standard_Mod$A
x2 <- Standard_Mod$x2
mu2 <- Standard_Mod$mu2
P2 <- Standard_Mod$P2

#####

```

```

# Build grid G4 via EnvelopeSize and expand.grid (as EnvelopeBuild does)
#####
a <- diag(A)
omega <- (sqrt(2) - exp(-1.20491 - 0.7321 * sqrt(0.5 + a))) / sqrt(1 + a)
b2 <- as.vector(bstar2)
G1 <- rbind(b2 - omega, b2, b2 + omega)

size_info <- EnvelopeSize(a, G1, Gridtype = 3L, n = n)
G2 <- size_info$G2

G3 <- as.matrix(do.call(expand.grid, G2))
G4 <- t(G3)

#####
# EnvelopeEval: negative log-likelihood and gradients at grid points
#####
eval_out <- EnvelopeEval(
  G4 = G4,
  y = y,
  x = as.matrix(x2),
  mu = as.matrix(mu2, ncol = 1),
  P = as.matrix(P2),
  alpha = as.vector(alpha),
  wt = as.vector(wt2),
  family = "binomial",
  link = "logit",
  use_openc1 = FALSE,
  verbose = FALSE
)

eval_out$NegLL
eval_out$cbars

#####
# End of EnvelopeEval example
#####

```

EnvelopeOrchestrator *Envelope Construction Orchestrator for Bayesian Gaussian Regression*

Description

EnvelopeOrchestrator() provides a unified interface for constructing the fixed-dispersion and dispersion-aware envelopes used in likelihood-subgradient simulation for Bayesian Gaussian regression with Normal–Gamma priors.

This function coordinates:

- fixed-dispersion envelope construction via [EnvelopeBuild](#),
- dispersion-refined envelope construction via [EnvelopeDispersionBuild](#),

- envelope sorting and reindexing via [EnvelopeSort](#), and
- UB-list alignment (reordered lg_prob_factor and UB2min).

It is typically used inside *.cpp routines such as `rIndepNormalGammaReg()`, but may also be called directly for diagnostics, envelope visualization, or custom simulation workflows.

Usage

```
EnvelopeOrchestrator(
  bstar2,
  A,
  y,
  x2,
  mu2,
  P2,
  alpha,
  wt,
  n,
  Gridtype,
  n_envopt,
  shape,
  rate,
  RSS_Post2,
  RSS_ML,
  max_disp_perc,
  disp_lower,
  disp_upper,
  use_parallel = TRUE,
  use_openc1 = FALSE,
  verbose = FALSE
)
```

Arguments

<code>bstar2</code>	Numeric vector. Posterior mode of the standardized regression coefficients (from the standardized model).
<code>A</code>	Numeric matrix. Posterior precision matrix (Hessian) at the mode.
<code>y</code>	Numeric response vector of length m .
<code>x2</code>	Numeric matrix of standardized predictors ($m \times p$).
<code>mu2</code>	Numeric vector. Standardized prior mean (typically a zero vector).
<code>P2</code>	Numeric matrix. Standardized prior precision component moved into the log-likelihood.
<code>alpha</code>	Numeric vector. Offset-adjusted mean component.
<code>wt</code>	Numeric vector of prior weights.
<code>n</code>	Integer. Number of envelope grid points or simulation draws.
<code>Gridtype</code>	Integer specifying the envelope grid construction method for API compatibility. The C++ orchestrator overrides this to 3L (full 3^p grid): unknown dispersion does not use smaller grids.

n_envopt	Optional integer. Effective sample size passed to EnvelopeOpt during grid construction. Larger values encourage tighter envelopes.
shape	Numeric. Shape parameter of the Gamma prior for the dispersion.
rate	Numeric. Rate parameter of the Gamma prior for the dispersion.
RSS_Post2	Numeric. Expected posterior weighted RSS used to anchor the dispersion axis (typically centering_out\$RSS_post from EnvelopeCentering inside rindepNormalGamma_reg ; see vignette Chapter-A11).
RSS_ML	Numeric. Maximum-likelihood residual sum of squares.
max_disp_perc	Numeric in $(0, 1)$. Tail probability used to determine dispersion bounds when not explicitly supplied.
disp_lower	Optional numeric. Lower bound for the dispersion (σ^2). If supplied, overrides quantile-based bounds.
disp_upper	Optional numeric. Upper bound for the dispersion (σ^2). Must be strictly greater than disp_lower.
use_parallel	Logical. Whether to allow parallel computation inside EnvelopeDispersion-Build .
use_opengl	Logical. Whether to allow OpenCL acceleration inside EnvelopeBuild .
verbose	Logical. Whether to print detailed progress and timing messages.

Details

EnvelopeOrchestrator() is the **envelope-construction stage** for Bayesian **Gaussian regression with an independent Normal-Gamma prior** on (β, ϕ) (dispersion ϕ ; precision $\tau = 1/\phi$ in much of the theory). It is implemented in ‘src/EnvelopeOrchestrator.cpp’ and composes direct C++ calls to EnvelopeBuild and EnvelopeDispersionBuild with an R call to [EnvelopeSort](#).

What this function does not do. It does **not** run the iterative dispersion centering loop ([EnvelopeCentering](#)), **not** optimize the posterior mode or Hessian, **not** standardize the model ([glmb_Standardize_Model](#)), and **not** draw posterior samples. Those steps are performed by [rindepNormalGamma_reg](#) (see vignette Chapter-A11) before and after the orchestrator. Inputs such as bstar2, A, x2, mu2, and P2 must therefore already be in **standard form** for the coefficient subproblem, exactly as passed from that workflow.

What the return value is for. The returned Env, gamma_list, and UB_list are consumed by the internal standardized samplers rIndepNormalGammaReg_std and rIndepNormalGammaReg_std_parallel in ‘src/rIndepNormalGammaReg.cpp’, which implement the joint accept-reject procedure over (β, ϕ) . Theory for the dispersion envelope and bounding arguments is in vignette Chapter-A07; the end-to-end implementation map is in Chapter-A11. The coefficient-only likelihood-subgradient envelope ((Nygren and Nygren 2006)) is documented under [EnvelopeBuild](#) and vignette Chapter-A08.

The function does **not** perform simulation. Simulation is carried out afterward via `.rIndepNormalGammaReg_std_cpp()` or `.rIndepNormalGammaReg_std_parallel_cpp()`, depending on use_parallel.

Value

A list with components:

Env The fully constructed and sorted envelope, including the PLSD component inserted by the dispersion-aware refinement step.

`gamma_list` Updated Gamma-prior parameters for the dispersion (shape, rate, and dispersion bounds).
`UB_list` Updated UB-list including reordered `lg_prob_factor` and `UB2min`.
`diagnostics` Diagnostic quantities returned by `EnvelopeDispersionBuild`, useful for debugging or envelope visualization.
`low` Lower dispersion bound used.
`upp` Upper dispersion bound used.

Use of the envelope during sampling

After `EnvelopeOrchestrator()` returns, `rinddepNormalGamma_reg` delegates iid simulation to `rIndepNormalGammaReg_std` (serial) or `rIndepNormalGammaReg_std_parallel` (parallel). These routines are **not exported**; they are the direct analogues of the fixed-dispersion path `rNormalGLM_std_cpp()` for GLMs, but for the **joint** posterior $\pi(\beta, \phi \mid y)$ under the independent Normal–Gamma prior.

Dominating proposal (conceptual). The envelope list `Env` still describes a **mixture of restricted multivariate Normal** proposal pieces for the **standardized** regression coefficients, with mixture weights $\tilde{p}_j$ stored in `PLSD`. After `EnvelopeDispersionBuild`, those weights and the per-face constants are adjusted so that, together with a **truncated inverse-Gamma** (dispersion) proposal derived from `gamma_list`, the joint proposal dominates the target posterior on the truncated dispersion interval `[low, upp]`. `vignette("Chapter-A07", package = "glmbayes")` derives the dispersion-related bounds; `vignette("Chapter-A11", package = "glmbayes")` records how `UB_list` entries enter the code.

One accept–reject iteration (standardized coordinates) proceeds as follows:

1. **Draw a mixture component (face) J .** An index J is drawn from the discrete distribution with probabilities `PLSD`.
2. **Propose coefficients β^* .** Conditional on J , each coordinate is drawn from the **restricted Normal** used in the fixed-dispersion construction: cumulative-normal tail probabilities `loglt[J, ]`, `logrt[J, ]`, and subgradient shift `-cbars[J, ]` (internal `rnorm_ct` truncated Normal sampling, same structural role as `ctrnorm_cpp()` in the GLM path).
3. **Propose dispersion ϕ .** A draw is taken from the truncated inverse-Gamma / Gamma piece defined by `shape3`, `rate2`, `disp_lower`, and `disp_upper` in `gamma_list` (`rinvgamma_ct_safe`).
4. **Re-weight the likelihood for ϕ .** Observation weights in the Gaussian log-likelihood are scaled by $1/\phi$ (`wt2 = wt / dispersion` in the C++ sources).
5. **Dispersion-adjusted tangency.** Because the tangency point for the linear upper bound depends on dispersion, the code recomputes a **face-specific** $\bar{\theta}_J(\phi)$ via `Inv_f3_with_disp` (using a one-time cache from `Inv_f3_precompute_disp` built from `cbars` and the data). The negative log-likelihood at that point feeds the **UB1** tangent term.
6. **Log-likelihood at the proposal.** Compute $-\log f(y \mid \beta^*, \phi)$ with the same ϕ and scaled weights (output `LL_Test` in the serial implementation).

Acceptance inequality (structure). Write $\ell(\beta, \phi)$ for the Gaussian log-likelihood (weighted, with offset). The serial sampler forms **UB1** from the tangent to $-\ell$ at $\bar{\theta}_J(\phi)$ along subgradient $c_J = \text{cbars}[J,]$:

$$\text{UB1} = -\ell(\bar{\theta}_J(\phi), \phi) - c_J^\top (\beta^* - \bar{\theta}_J(\phi)).$$

Additional terms bound RSS variation along ϕ (**UB2**, using `RSS_Min` and `UB2min` from `UB_list`) and dispersion-axis majorization (**UB3A**, **UB3B**) built from `lg_prob_factor`, `lmc1`, `lmc2`, `lm_log1`,

lm_log2, max_New_LL_UB, and max_LL_log_disp. With $L_{\text{test}} = -\ell(\beta^*, \phi)$, define $T_1 = L_{\text{test}} - \text{UB1}$ and $T = T_1 - (\text{UB2} + \text{UB3A} + \text{UB3B})$. The code draws $U_2 \sim \text{Unif}(0, 1)$ and **accepts** (β^*, ϕ) when

$$T - \log(U_2) \geq 0.$$

Serial and parallel workers use the same logical decomposition up to implementation detail. Under the construction in [EnvelopeDispersionBuild](#), the terms are arranged so that $T_1 \leq 0$ and UB2, UB3A, UB3B are nonnegative up to controlled numerical slack. Iteration counts are stored in `iters_out`.

Mapping orchestrator outputs to the sampler.

- `Env$PLSD`: mixture probabilities over envelope faces for Step 1.
- `Env$loglt`, `Env$logrt`, `Env$cbars`: restricted Normal proposal for β^* in Step 2.
- `Env$GridIndex`, `Env$thetabars`, `Env$logU`, `Env$logP`: same role as in [EnvelopeBuild](#) for the coefficient mixture; dispersion refinement may update PLSD before sorting.
- `gamma_list`: truncated dispersion proposal parameters (`shape3`, `rate2`, `bounds`) for Step 3.
- `UB_list`: global and per-face constants (`RSS_Min`, `UB2min`, `lg_prob_factor`, linear `lmc/lm_log` pieces) for UB2, UB3A, UB3B.
- `low`, `upp`: dispersion interval endpoints (duplicated from `gamma_list` for convenience).

Unlike the fixed-dispersion GLM sampler, this path does **not** apply the stored `LLconst` vector directly in the acceptance test; the tangent piece is recomputed as UB1 once ϕ and $\theta_J(\phi)$ are known.

Algorithmic steps

The orchestrator implements the **independent Normal–Gamma** envelope pipeline: first a **coefficient** envelope at a **dispersion anchor** ((Nygren and Nygren 2006); vignette Chapter-A08), then **dispersion-aware** refinement (Chapter-A07), then sorting. Steps 3–8 repeat the internal logic of [EnvelopeBuild](#) (same formulas on that help page); here the likelihood is **Gaussian** with **identity** link, weights are w_i/d_* with d_* from the anchor below, and the first pass uses `sortgrid = FALSE` so sorting runs **after** dispersion refinement.

1. **Force full grid for unknown dispersion.** The argument `Gridtype` is overridden to 3L so the coefficient grid always uses the full 3^p partition (implementation policy in `'src/EnvelopeOrchestrator.cpp'`).
2. **Anchor dispersion and rescale weights for EnvelopeBuild.** Let $n_w = \sum_i w_i$. With prior hyperparameters `shape` (a_0) and `rate` (b_0) and centered RSS `RSS_Post2`, define $s = a_0 + n_w/2$ and $r = b_0 + \text{RSS}_{\text{post}}/2$ where `RSS_post` denotes `RSS_Post2` (the C++ code names the scalars `shape2` and `rate3`). The dispersion anchor is $d_* = r/(s-1)$, and observation weights w_i passed into the embedded `EnvelopeBuild` call are scaled by $1/d_*$. This ties the coefficient envelope to the Gamma posterior for the precision conditional on the centered RSS (Chapters A07, A11).
3. **Compute width parameters ω_i from the diagonal precision matrix.** Let θ^* be the standardized posterior mode. For each dimension i ,

$$\omega_i := \frac{\sqrt{2} - \exp(-1.20491 - 0.7321 \sqrt{0.5 - \partial^2 \log f(\theta^* | y) / \partial \theta_i^2})}{\sqrt{1 - \partial^2 \log f(\theta^* | y) / \partial \theta_i^2}}.$$

Here f is the weighted Gaussian log-posterior for β at the anchored dispersion.

4. **Construct intervals and the 3^p partition** around θ^* . Set

$$\ell_{i,1} = \theta_i^* - 0.5\omega_i, \quad \ell_{i,2} = \theta_i^* + 0.5\omega_i,$$

and

$$A_{i,1} = (-\infty, \ell_{i,1}), \quad A_{i,2} = [\ell_{i,1}, \ell_{i,2}], \quad A_{i,3} = (\ell_{i,2}, \infty).$$

With $J = \prod_{i=1}^p \{1, 2, 3\}$ and $j = (j_1, \dots, j_p)$, $A_j^* = \prod_{i=1}^p A_{i,j_i}$ partitions standardized coefficient space.

5. **Select tangency points $\bar{\theta}_j$ per cell** (left / mode / right of each interval). For index sets C_{j1}, C_{j2}, C_{j3} by coordinate,

$$\bar{\theta}_{j,i} = \begin{cases} \theta_i^* - \omega_i, & i \in C_{j1}, \\ \theta_i^*, & i \in C_{j2}, \\ \theta_i^* + \omega_i, & i \in C_{j3}. \end{cases}$$

6. **Evaluate negative log-likelihood and gradient at each grid point.** Subgradients $c(\bar{\theta}_j)$ and negative log-likelihoods define the likelihood-subgradient envelope pieces ((Nygren and Nygren 2006); Chapter-A08). CPU: f2_f3_non_openc1; GPU (optional): f2_f3_openc1.
7. **Call** `EnvelopeSet_Grid_C2_pointwise` **and** `EnvelopeSet_LogP_C2 (C++ pipeline)` to obtain restricted Normal log-densities, mixture log-probabilities, and constants as in Remarks 5–6 of the JASA paper (same as [EnvelopeBuild](#)).
8. **Normalize to PLSD without sorting.** The embedded `EnvelopeBuild` call sets `sortgrid = FALSE` so an intermediate sort is not wasted before [EnvelopeDispersionBuild](#) revises mixture weights for the joint (β, ϕ) target and [EnvelopeSort](#) runs once at the end.
9. **Call** `EnvelopeDispersionBuild (C++)`. Pass the coefficient envelope list, prior shape, rate, standardized P2, data y , x_2 , α , μ_2 , wt , RSS_Post2 , RSS_ML , dispersion controls (`max_disp_perc`, optional bounds), and `use_parallel`. This constructs the dispersion truncation interval, updates Gamma proposal parameters (`gamma_list`), computes `UB_list`, and returns `Env_out` with adjusted PLSD. See Chapter-A07 and Chapter-A11, Section 3.3.
10. **Call** [EnvelopeSort \(R\)](#). Reorder envelope components and align `lg_prob_factor` and `UB2min` with the sorted indexing. If sorting cannot allocate safely, the implementation falls back to unsorted `Env_out` with `UB` fields patched (`'src/EnvelopeOrchestrator.cpp'`).
11. **Return** `Env`, `gamma_list`, `UB_list`, `diagnostics`, `low`, and `upp` for the standardized samplers.

References

Nygren K~N, Nygren L~M (2006). “Likelihood Subgradient Densities.” *Journal of the American Statistical Association*, **101**(475), 1144–1156. doi:10.1198/016214506000000357.

See Also

- [EnvelopeBuild](#) – fixed-dispersion envelope construction
- [EnvelopeDispersionBuild](#) – dispersion-aware envelope refinement
- [EnvelopeSort](#) – envelope sorting and reindexing
- [EnvelopeCentering](#) – `RSS_Post2` and dispersion anchor

- `glmb_Standardize_Model` – standardized inputs for the orchestrator
- `rindepNormalGamma_reg` – full Normal–Gamma workflow (R + C++)
- `rlmb`, `rglmb`, `simfuncs` – higher-level sampling entry points
- Vignettes Chapter–A07, Chapter–A08, Chapter–A11; cited as (Nygren and Nygren 2006; Nygren 2025, 2025)

Examples

```
##### Start of EnvelopeOrchestrator example #####

# This example demonstrates calling EnvelopeOrchestrator directly for Gaussian
# regression with an independent Normal-Gamma prior. It mirrors the algorithm
# path used inside rindepNormalGammaReg:
# - Step A: Initial dispersion via weighted lm.wfit residual variance
# - Step B: EnvelopeCentering loop (closed-form expected RSS, update
#         dispersion2 via Gamma posterior) to anchor the envelope
# - Step C: Coefficient posterior mode optimization (optim + f2/f3)
# - Step D: Standardize the model (glmb_Standardize_Model)
# - Step E: EnvelopeOrchestrator (EnvelopeBuild + EnvelopeDispersionBuild
#         + EnvelopeSort in one call)
# It stops after envelope construction (no sampling).

ctl <- c(4.17, 5.58, 5.18, 6.11, 4.50, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)

ps <- Prior_Setup(weight ~ group, gaussian())

x <- as.matrix(ps$x)
y <- as.vector(ps$y)
mu <- ps$mu
Sigma <- ps$Sigma
shape <- ps$shape
rate <- ps$rate

n_obs <- length(y)
wt <- rep(1, n_obs)
offset2 <- rep(0, n_obs)

# Reconstruct coefficient precision P (matches rindepNormalGamma_reg)
Rchol <- chol(Sigma)
Pinv <- chol2inv(Rchol)
P <- 0.5 * (Pinv + t(Pinv))

famfunc <- glmbfamfunc(gaussian())
f2 <- famfunc$f2
f3 <- famfunc$f3

Gridtype_core <- as.integer(2)

#####
```

```

# Step A/B: EnvelopeCentering (starting at weighted lm.wfit dispersion and
# iteratively refining it via closed-form expected RSS)
#####
centering <- EnvelopeCentering(
  y = as.vector(y),
  x = as.matrix(x),
  mu = as.vector(mu),
  P = as.matrix(P),
  offset = as.vector(offset2),
  wt = as.vector(wt),
  shape = shape,
  rate = rate,
  Gridtype = Gridtype_core,
  verbose = FALSE
)

dispersion2 <- centering$dispersion
RSS_Post2 <- centering$RSS_post

#####
# Step C: Coefficient posterior mode optimization (optim + f2/f3)
#####
dispstar <- dispersion2
wt2_opt <- wt / dispstar
alpha <- as.vector(x %*% as.vector(mu) + offset2)

mu2_opt <- rep(0, length(as.vector(mu)))
parin <- rep(0, length(as.vector(mu)))

opt_out <- optim(
  par = parin,
  fn = f2,
  gr = f3,
  y = as.vector(y),
  x = as.matrix(x),
  mu = as.vector(mu2_opt),
  P = as.matrix(P),
  alpha = as.vector(alpha),
  wt = as.vector(wt2_opt),
  method = "BFGS",
  hessian = TRUE
)

bstar <- opt_out$par
A1 <- opt_out$hessian

#####
# Step D: Standardize model (glmb_Standardize_Model)
#####
Standard_Mod <- glmb_Standardize_Model(
  y = as.vector(y),
  x = as.matrix(x),
  P = as.matrix(P),

```

```

    bstar = as.matrix(bstar, ncol = 1),
    A1 = as.matrix(A1)
  )

bstar2 <- Standard_Mod$bstar2
A <- Standard_Mod$A
x2_std <- Standard_Mod$x2
mu2_std <- Standard_Mod$mu2
P2_std <- Standard_Mod$P2

#####
# Step E: EnvelopeOrchestrator (EnvelopeBuild + EnvelopeDispersionBuild
#           + EnvelopeSort in one call)
#####
max_disp_perc <- 0.99
n_env <- as.integer(200)
Gridtype_env <- as.integer(3) # EnvelopeOrchestrator overrides to 3 for unknown dispersion

env_out <- EnvelopeOrchestrator(
  bstar2 = as.vector(bstar2),
  A = as.matrix(A),
  y = as.vector(y),
  x2 = as.matrix(x2_std),
  mu2 = as.matrix(mu2_std, ncol = 1),
  P2 = as.matrix(P2_std),
  alpha = as.vector(alpha),
  wt = as.vector(wt),
  n = n_env,
  Gridtype = Gridtype_env,
  n_envopt = as.integer(1),
  shape = shape,
  rate = rate,
  RSS_Post2 = RSS_Post2,
  RSS_ML = NA_real_,
  max_disp_perc = max_disp_perc,
  disp_lower = NULL,
  disp_upper = NULL,
  use_parallel = TRUE,
  use_opencl = FALSE,
  verbose = FALSE
)

# Output structure matches that from the step-by-step Ex_EnvelopeDispersionBuild
print(env_out$low)
print(env_out$upp)
print(env_out$gamma_list[c("shape3", "rate2")])

env_out

#####
# End: envelope construction only
#####

```

EnvelopeSize	<i>Envelope Sizing and Optimization</i>
--------------	---

Description

EnvelopeSize() is the high-level entry point that constructs per-dimension grids and expected draw counts, while EnvelopeOpt() performs the adaptive optimization used when Gridtype = 2.

Usage

```
EnvelopeSize(a, G1, Gridtype = 2L, n = 1000L, n_envopt = -1,
             use_openc1 = FALSE, verbose = FALSE)
```

```
EnvelopeOpt(a1, n, core_cnt=1L)
```

Arguments

a	Numeric vector of diagonal precisions for the log-likelihood (posterior precision is $1 + a_i$).
G1	Numeric matrix of candidate grid points (3 * 11).
Gridtype	Integer code controlling grid sizing logic: • 1 = static threshold test • 2 = adaptive optimization via EnvelopeOpt() • 3 = always three-point grid • 4 = always single-point grid
n	Integer; number of posterior draws to generate (used for grid sizing).
n_envopt	Integer; effective sample size passed to EnvelopeOpt. Defaults to -1, which means "use n".
use_openc1	Logical; if TRUE, attempt GPU acceleration.
verbose	Logical; if TRUE, print progress messages.
a1	Numeric vector of diagonal elements of the data precision matrix (used by EnvelopeOpt).
core_cnt	Integer; number of OpenCL cores or parallel workers available (default 1). When >1, envelope build cost is scaled down to reflect parallel construction.

Details

These functions implement the grid sizing logic used in envelope construction for rejection sampling. They make use of the theory described in (Nygren and Nygren 2006) and the general implementation outlined in (Nygren 2025).

EnvelopeSize() returns the constructed grid (G2), index vectors (GIndex1), expected draw count (E_draws), and the per-dimension grid index.

EnvelopeOpt() implements the adaptive optimization used in Gridtype = 2, ranking dimensions by posterior variance and promoting them to three-point tangents when the tradeoff is favorable.

Value

EnvelopeSize() A list with components G2, GIndex1, E_draws, and gridindex.

EnvelopeOpt() An integer vector of length $l1$ with entries 1 (single-point) or 3 (three-point).

Gridtype Logic and Candidates per Draw

The envelope sizing logic follows the analysis of (Nygren and Nygren 2006).

Gridtype 1: Static Threshold For each dimension i , if $\sqrt{1 + a_i} \leq 2/\sqrt{\pi} \approx 1.128379$, then a single tangent at the posterior mode suffices. Expected candidates per draw in that dimension: $\sqrt{1 + a_i}$. Otherwise, a symmetric three-point envelope is used at $(\theta_i^* - \omega_i, \theta_i^*, \theta_i^* + \omega_i)$, with expected candidates per draw bounded above by $2/\sqrt{\pi}$.

Gridtype 2: Adaptive Optimization Each dimension is assigned either a single-point or three-point envelope by minimizing

$$T_{\text{total}}(g_i) = T_{\text{build}}(g_i) + T_{\text{sample}}(n, acc_i(g_i)).$$

The optimizer balances build cost (grows with number of tangents) against sampling cost (decreases as acceptance improves). Expected candidates per draw: $\prod_j \text{scaleest}_{i,j}$, where each factor is either $\sqrt{1 + a_j}$ (single-point) or $2/\sqrt{\pi}$ (three-point), depending on the optimization outcome.

Gridtype 3: Always Three-Point Every dimension uses a symmetric three-point envelope. Expected candidates per draw:

$$\left(\frac{2}{\sqrt{\pi}}\right)^k$$

for k dimensions, as shown in Theorem 3 of (Nygren and Nygren 2006).

Gridtype 4: Always Single-Point Every dimension uses a single tangent at the posterior mode. Expected candidates per draw:

$$\prod_{i=1}^k \sqrt{1 + a_i}$$

(Example 1 in (Nygren and Nygren 2006)).

References

Nygren K (2025). “Chapter A05: Simulation Methods – Likelihood Subgradient Densities.” Vignette in the glmbayes R package. R vignette name: Chapter-A05.

Nygren K~N, Nygren L~M (2006). “Likelihood Subgradient Densities.” *Journal of the American Statistical Association*, **101**(475), 1144–1156. doi:10.1198/016214506000000357.

See Also

EnvelopeBuild, EnvelopeEval, EnvelopeSort; rNormal_reg, rglmb for user-facing sampling that uses these grids. Vignettes: (Nygren 2025, 2025).

Examples

```

data(menarche,package="MASS")

summary(menarche)
plot(Menarche/Total ~ Age, data=menarche)

Age2=menarche$Age-13

x<-matrix(as.numeric(1.0),nrow=length(Age2),ncol=2)
x[,2]=Age2

y=menarche$Menarche/menarche$Total
wt=menarche$Total

mu<-matrix(as.numeric(0.0),nrow=2,ncol=1)
mu[2,1]=(log(0.9/0.1)-log(0.5/0.5))/3

V1<-1*diag(as.numeric(2.0))

# 2 standard deviations for prior estimate at age 13 between 0.1 and 0.9
## Specifies uncertainty around the point estimates

V1[1,1]<-((log(0.9/0.1)-log(0.5/0.5))/2)^2
V1[2,2]=(3*mu[2,1]/2)^2 # Allows slope to be up to 1 times as large as point estimate

famfunc<-glm famfunc(binomial(logit))

f1<-famfunc$f1
f2<-famfunc$f2
f3<-famfunc$f3
f5<-famfunc$f5
f6<-famfunc$f6

dispersion2<-as.numeric(1.0)
start <- mu
offset2=rep(as.numeric(0.0),length(y))
P=solve(V1)
n=1000

##### Adjust weight for dispersion

wt2=wt/dispersion2

##### Shift mean vector to offset so that adjusted model has 0 mean

alpha=x%*as.vector(mu)+offset2
mu2=0*as.vector(mu)
P2=P
x2=x

```

```
##### Optimization step to find posterior mode and associated Precision

parin=start-mu

opt_out=optim(parin,f2,f3,y=as.vector(y),x=as.matrix(x),mu=as.vector(mu2),
              P=as.matrix(P),alpha=as.vector(alpha),wt=as.vector(wt2),
              method="BFGS",hessian=TRUE
)

bstar=opt_out$par ## Posterior mode for adjusted model
bstar
bstar+as.vector(mu) # mode for actual model
A1=opt_out$hessian # Approximate Precision at mode

## Standardize Model

Standard_Mod=glmb_Standardize_Model(y=as.vector(y), x=as.matrix(x),
P=as.matrix(P),bstar=as.matrix(bstar,ncol=1), A1=as.matrix(A1))

bstar2=Standard_Mod$bstar2
A=Standard_Mod$A
x2=Standard_Mod$x2
mu2=Standard_Mod$mu2
P2=Standard_Mod$P2
L2Inv=Standard_Mod$L2Inv
L3Inv=Standard_Mod$L3Inv

## Derive a and G1 (as EnvelopeBuild does internally)
a <- diag(A)
omega <- (sqrt(2) - exp(-1.20491 - 0.7321*sqrt(0.5 + a))) / sqrt(1 + a)
b2 <- as.vector(bstar2)
G1 <- rbind(b2 - omega, b2, b2 + omega)

## EnvelopeOpt: standalone call (used by EnvelopeSize when Gridtype=2)
grid_opt <- EnvelopeOpt(a, n)
grid_opt

## EnvelopeSize for each Gridtype
size_1 <- EnvelopeSize(a, G1, Gridtype=1L, n=n) # static threshold
size_2 <- EnvelopeSize(a, G1, Gridtype=2L, n=n) # uses EnvelopeOpt
size_3 <- EnvelopeSize(a, G1, Gridtype=3L, n=n) # always 3-point
size_4 <- EnvelopeSize(a, G1, Gridtype=4L, n=n) # always single-point

## EnvelopeBuild for each Gridtype
Env_1 <- EnvelopeBuild(as.vector(bstar2), as.matrix(A), y, as.matrix(x2),
                      as.matrix(mu2,ncol=1), as.matrix(P2), as.vector(alpha), as.vector(wt2),
                      family="binomial", link="logit", Gridtype=1L, n=as.integer(n), sortgrid=FALSE)
Env_2 <- EnvelopeBuild(as.vector(bstar2), as.matrix(A), y, as.matrix(x2),
                      as.matrix(mu2,ncol=1), as.matrix(P2), as.vector(alpha), as.vector(wt2),
                      family="binomial", link="logit", Gridtype=2L, n=as.integer(n), sortgrid=FALSE)
Env_3 <- EnvelopeBuild(as.vector(bstar2), as.matrix(A), y, as.matrix(x2),
                      as.matrix(mu2,ncol=1), as.matrix(P2), as.vector(alpha), as.vector(wt2),
```

```

family="binomial", link="logit", Gridtype=3L, n=as.integer(n), sortgrid=FALSE)
Env_4 <- EnvelopeBuild(as.vector(bstar2), as.matrix(A), y, as.matrix(x2),
  as.matrix(mu2,ncol=1), as.matrix(P2), as.vector(alpha), as.vector(wt2),
  family="binomial", link="logit", Gridtype=4L, n=as.integer(n), sortgrid=FALSE)

Env_3

```

EnvelopeSort

Sorts Envelope function for simulation

Description

Sorts Enveloping function for simulation. how frequently each component of the resulting grid should be sampled during simulation.

Usage

```

EnvelopeSort(
  l1,
  l2,
  GIndex,
  G3,
  cbars,
  logU,
  logrt,
  loglt,
  logP,
  LLconst,
  PLSD,
  a1,
  E_draws,
  lg_prob_factor = NULL,
  UB2min = NULL
)

```

Arguments

l1	dimension for model (number of independent variables in X matrix)
l2	dimension for Envelope (number of components)
GIndex	matrix containing information on how each dimension should be sampled (1 means left tail of a restricted normal, 2 center, 3 right tail, and 4 the entire line)
G3	A matrix containing the points of tangencies associated with each component of the grid
cbars	A matrix containing the gradients for the negative log-likelihood at each tangency

logU	A matrix containing the log of the cumulative probability associated with each dimension
logrt	A matrix containing the log of the probability associated with the right tail (i.e. that to the right of the lower bound)
loglt	A matrix containing the log of the probability associated with the left tail (i.e., that to the left of the upper bound)
logP	A matrix containing log-probabilities related to the components of the grid
LLconst	A vector containing constant for each component of the grid used during the accept-reject procedure
PLSD	A vector containing the probability of each component in the Grid
a1	A vector containing the diagonal of the standardized precision matrix
E_draws	Bound on Expected number of candidates per accepted draw
lg_prob_factor	vector of lg_prob_factors used for the Envelope connected to the independent normal gamma prior
UB2min	Vector containing min for UB2 for each component (relevant for EnvelopeDispersionBuild)

Details

This function sorts the envelope in descending order based on the probability associated with each component in the Grid. Sorting helps speed up simulation once the envelope is constructed. If memory allocation fails (e.g. for very large grids), the function returns the unsorted envelope with `sort_ok = FALSE`; the sampler remains valid but may have poorer acceptance.

Used after [EnvelopeBuild](#) and (for Normal–Gamma models) [EnvelopeDispersionBuild](#); see (Nygren and Nygren 2006; Nygren 2025).

Value

The function returns a list consisting of the following components (the first six of which are matrices with number of rows equal to the number of components in the Grid and columns equal to the number of parameters):

GridIndex	A matrix containing information on how each dimension should be sampled (1 means left tail of a restricted normal, 2 center, 3 right tail, and 4 the entire line)
thetabars	A matrix containing the points of tangencies associated with each component of the grid
cbars	A matrix containing the gradients for the negative log-likelihood at each tangency
logU	A matrix containing the log of the cumulative probability associated with each dimension
logrt	A matrix containing the log of the probability associated with the right tail (i.e. that to the right of the lower bound)
loglt	A matrix containing the log of the probability associated with the left tail (i.e., that to the left of the upper bound)

LLconst	A vector containing constant for each component of the grid used during the accept-reject procedure
logP	A matrix containing log-probabilities related to the components of the grid
PLSD	A vector containing the probability of each component in the Grid
E_draws	A containing a computed theoretical bound on the expected number of draws
sort_ok	Logical; TRUE if sort succeeded, FALSE if memory allocation failed and unsorted envelope was returned (sampler remains valid)

References

Nygren K (2025). “Chapter A08: Overview of Envelope Related Functions.” Vignette in the glm-bayes R package. R vignette name: Chapter-A08.

Nygren K~N, Nygren L~M (2006). “Likelihood Subgradient Densities.” *Journal of the American Statistical Association*, **101**(475), 1144–1156. doi:10.1198/016214506000000357.

See Also

[EnvelopeBuild](#), [EnvelopeOrchestrator](#), [EnvelopeDispersionBuild](#), [rNormal_reg](#), [rglmb](#).

Examples

```
data(menarche, package="MASS")
Age2=menarche$Age-13

summary(menarche)
plot(Menarche/Total ~ Age, data=menarche)

x<-matrix(as.numeric(1.0),nrow=length(Age2),ncol=2)
x[,2]=Age2

y=menarche$Menarche/menarche$Total
wt=menarche$Total

mu<-matrix(as.numeric(0.0),nrow=2,ncol=1)
mu[2,1]=(log(0.9/0.1)-log(0.5/0.5))/3

V1<-1*diag(as.numeric(2.0))

# 2 standard deviations for prior estimate at age 13 between 0.1 and 0.9
## Specifies uncertainty around the point estimates

V1[1,1]<-((log(0.9/0.1)-log(0.5/0.5))/2)^2
V1[2,2]=(3*mu[2,1]/2)^2 # Allows slope to be up to 1 times as large as point estimate

famfunc<-glmbfamfunc(binomial(logit))

f1<-famfunc$f1
f2<-famfunc$f2
```

```

f3<-famfunc$f3
f5<-famfunc$f5
f6<-famfunc$f6

dispersion2<-as.numeric(1.0)
start <- mu
offset2=rep(as.numeric(0.0),length(y))
P=solve(V1)
n=1000

## Appears that the type for some of these arguments are important/problematic

### This example constructs and sorts an envelope without calling the
### lower-level sampler directly.

##### Adjust weight for dispersion

wt2=wt/dispersion2

##### Shift mean vector to offset so that adjusted model has 0 mean

alpha=x%*%as.vector(mu)+offset2
mu2=0*as.vector(mu)
P2=P
x2=x

##### Optimization step to find posterior mode and associated Precision

parin=start-mu

opt_out=optim(parin,f2,f3,y=as.vector(y),x=as.matrix(x),mu=as.vector(mu2),
              P=as.matrix(P),alpha=as.vector(alpha),wt=as.vector(wt2),
              method="BFGS",hessian=TRUE
)

bstar=opt_out$par ## Posterior mode for adjusted model
bstar
bstar+as.vector(mu) # mode for actual model
A1=opt_out$hessian # Approximate Precision at mode

## Standardize Model

Standard_Mod=glmb_Standardize_Model(y=as.vector(y), x=as.matrix(x),
P=as.matrix(P),bstar=as.matrix(bstar,ncol=1), A1=as.matrix(A1))

bstar2=Standard_Mod$bstar2
A=Standard_Mod$A
x2=Standard_Mod$x2
mu2=Standard_Mod$mu2
P2=Standard_Mod$P2
L2Inv=Standard_Mod$L2Inv

```

```

L3Inv=Standard_Mod$L3Inv

Env2=EnvelopeBuild(as.vector(bstar2), as.matrix(A),y, as.matrix(x2),
as.matrix(mu2,ncol=1),as.matrix(P2),as.vector(alpha),as.vector(wt2),
family="binomial",link="logit",Gridtype=as.integer(3),
n=as.integer(n),sortgrid=FALSE)

## Extract l1, l2 from envelope (as done in C++) and call EnvelopeSort
l1 <- ncol(Env2$cbars)
l2 <- nrow(Env2$cbars)
logP_mat <- matrix(Env2$logP, ncol = 1)

Env_sorted <- EnvelopeSort(l1, l2,
  GIndex = Env2$GridIndex,
  G3      = Env2$thetabars,
  cbars   = Env2$cbars,
  logU    = Env2$logU,
  logrt   = Env2$logrt,
  loglt   = Env2$loglt,
  logP    = logP_mat,
  LLconst = Env2$LLconst,
  PLSD    = Env2$PLSD,
  a1      = Env2$a1,
  E_draws = Env2$E_draws
)

Env_sorted

```

formula.summary.rglmb *Model Formulae for summary.rglmb Objects*

Description

Extract a formula for a `summary.rglmb` object by refitting a reference `glm` with the stored response and design matrix.

Usage

```
## S3 method for class 'summary.rglmb'
formula(x, ...)
```

Arguments

`x` an object of class `summary.rglmb`, typically from `summary.rglmb`.

`...` further arguments passed to or from other methods.

Value

A model formula.

See Also

[rglmb](#), [summary.rglmb](#), [rlmb](#), [formula](#).

Gamma_ct	<i>The Central Gamma Distribution</i>
----------	---------------------------------------

Description

Distribution function and random generation for the center (between a lower and an upper bound) of the Gamma distribution with shape and rate parameters. These functions provide numerically stable evaluation and sampling when the truncation interval is narrow or when the Gamma density is highly skewed.

Usage

```
rgamma_ct(n, shape, rate, lower_prec = NULL, upper_prec = NULL)
```

Arguments

n	Number of draws to generate. If <code>length(n) > 1</code> , the length is taken to be the number required.
shape	Shape parameter of the Gamma distribution.
rate	Rate parameter of the Gamma distribution.
lower_prec	Lower truncation point on the precision scale. If <code>NULL</code> , no lower truncation is applied.
upper_prec	Upper truncation point on the precision scale. If <code>NULL</code> , no upper truncation is applied.

Details

The function `pgamma_ct` computes the probability mass between a lower bound `a` and an upper bound `b` under a Gamma density with the specified shape and rate parameters. This is particularly useful when the interval `b - a` is small, where the naive computation `pgamma(b) - pgamma(a)` may underflow to zero even when the true probability is positive.

The function `ctrgamma` provides a numerically robust sampler for the Gamma distribution under one-sided or two-sided truncation. It handles:

- no truncation (reducing to `rgamma`)
- lower truncation only
- upper truncation only
- two-sided truncation with `lower_prec < upper_prec`

- exact degeneracy when the truncation interval collapses
- numerical degeneracy when the Gamma CDF collapses in floating point

All computations are performed on the log scale using stable log–CDF and log–sum–exp transformations. This avoids the catastrophic cancellation that occurs when the Gamma CDF values at the truncation points are extremely close.

These functions are primarily intended for use in hierarchical Bayesian models where precision parameters are updated under tight truncation constraints, and where numerical stability is essential for reliable sampling performance. They are used in envelope-based dispersion sampling (Nygren and Nygren 2006).

Value

For `pgamma_ct`, a vector of probabilities corresponding to the mass of the Gamma distribution between `a` and `b`. For `rgamma_ct` or `ctrgamma`, a vector of length `nn` containing random draws from the Gamma distribution restricted to the interval `[a, b]` (or `[lower_prec, upper_prec]` on the precision scale).

References

Nygren K~N, Nygren L~M (2006). “Likelihood Subgradient Densities.” *Journal of the American Statistical Association*, **101**(475), 1144–1156. doi:[10.1198/016214506000000357](https://doi.org/10.1198/016214506000000357).

See Also

[Normal_ct](#), [InvGamma_ct](#), [EnvelopeDispersionBuild](#)

Examples

```
##### Start of Gamma_ct example #####

## Basic usage: rgamma_ct samples from Gamma truncated to [lower_prec, upper_prec]
shape <- 2
rate <- 1
lower <- 0.999
upper <- 1.001

## Naive pgamma(b) - pgamma(a) can underflow when a and b are very close
pgamma(upper, shape, rate) - pgamma(lower, shape, rate)

## rgamma_ct samples correctly from the narrow interval
set.seed(42)
x <- rgamma_ct(100, shape, rate, lower_prec = lower, upper_prec = upper)
range(x)
mean(x)

## Example where difference between two pgamma calls fails (catastrophic cancellation)
## but rgamma_ct still samples correctly from the narrow interval
a <- 1.0
b <- 1.0 + 1e-14
pgamma(b, 2, 1) - pgamma(a, 2, 1)
```

```
## Stable computation via log-space (as used inside rgamma_ct)
log_F_a <- pgamma(a, 2, 1, log.p = TRUE)
log_F_b <- pgamma(b, 2, 1, log.p = TRUE)
exp(log_F_b + log(-expm1(log_F_a - log_F_b)))

## rgamma_ct samples from [a, b] even when the interval is extremely narrow
set.seed(123)
rgamma_ct(5, 2, 1, lower_prec = a, upper_prec = b)

#####
## End of Gamma_ct example
#####
```

glmb_Standardize_Model

Standardize A Non-Gaussian Model

Description

Standardizes a Non-Gaussian Model prior to Envelope Creation

Usage

```
glmb_Standardize_Model(y, x, P, bstar, A1)
```

Arguments

y	a vector of observations of length m
x	a design matrix of dimension m*p
P	a positive-definite symmetric matrix specifying the prior precision matrix of the variables.
bstar	a matrix containing the posterior mode from an optimization step
A1	a matrix containing the posterior precision matrix at the posterior mode

Details

This functions starts with basic information about the model in the argument list and then uses the following steps to further standardize the model (the model is already assumed to have a 0 prior mean vector when this step is applied).

1. An eigenvalue composition is applied to the posterior precision matrix, and the model is (as an interim step) standardized to have a posterior precision matrix equal to the identity matrix. Please note that this means that the prior precision matrix after this step is "smaller" than the identity matrix.

2. A diagonal matrix epsilon is pulled out from the standardized prior precision matrix so that the remaining part of the prior precision matrix still is positive definite. That part is then treated as part of the likelihood for the rest of the standardization and simulation and only the part connected to epsilon is treated as part of the prior. Note that the exact epsilon chosen seems not to matter. Hence there are many possible ways of doing this standardization and future versions of this package may tweak the current approach if it helps improve numerical accuracy or acceptance rates.
3. The model is next standardized (using a second eigenvalue decomposition) so that the prior (i.e., the portion connected to epsilon) is the identity matrix. The standardized model then simultaneously has the feature that the prior precision matrix is the identity matrix and that the data precision A (at the posterior mode) is a diagonal matrix. Hence the variables in the standardized model are approximately independent at the posterior mode.

The steps here are based on the procedure described in (Nygren and Nygren 2006).

Value

A list with the following components

bstar2	Standardized Posterior Mode
A	Standardized Data Precision Matrix
x2	Standardized Design Matrix
mu2	Standardized Prior Mean vector
P2	Standardized Precision Matrix Added to log-likelihood
L2Inv	A matrix used when undoing the first step in standardization described below
L3Inv	A matrix used when undoing the second step in standardization described below

References

Nygren K~N, Nygren L~M (2006). "Likelihood Subgradient Densities." *Journal of the American Statistical Association*, **101**(475), 1144–1156. doi:[10.1198/016214506000000357](https://doi.org/10.1198/016214506000000357).

Examples

```
data(menarche, package="MASS")
Age2=menarche$Age-13

summary(menarche)
plot(Menarche/Total ~ Age, data=menarche)

x<-matrix(as.numeric(1.0),nrow=length(Age2),ncol=2)
x[,2]=Age2

y=menarche$Menarche/menarche$Total
wt=menarche$Total

mu<-matrix(as.numeric(0.0),nrow=2,ncol=1)
mu[2,1]=(log(0.9/0.1)-log(0.5/0.5))/3
```

```

V1<-1*diag(as.numeric(2.0))

# 2 standard deviations for prior estimate at age 13 between 0.1 and 0.9
## Specifies uncertainty around the point estimates

V1[1,1]<-((log(0.9/0.1)-log(0.5/0.5))/2)^2
V1[2,2]=(3*mu[2,1]/2)^2 # Allows slope to be up to 1 times as large as point estimate

famfunc<-glmbfamfunc(binomial(logit))

f1<-famfunc$f1
f2<-famfunc$f2
f3<-famfunc$f3
f5<-famfunc$f5
f6<-famfunc$f6

dispersion2<-as.numeric(1.0)
start <- mu
offset2=rep(as.numeric(0.0),length(y))
P=solve(V1)
n=1000

## Appears that the type for some of these arguments are important/problematic

##### Adjust weight for dispersion

wt2=wt/dispersion2

##### Shift mean vector to offset so that adjusted model has 0 mean

alpha=x*%as.vector(mu)+offset2
mu2=0*as.vector(mu)
P2=P
x2=x

##### Optimization step to find posterior mode and associated Precision

parin=start-mu

opt_out=optim(parin,f2,f3,y=as.vector(y),x=as.matrix(x),mu=as.vector(mu2),
              P=as.matrix(P),alpha=as.vector(alpha),wt=as.vector(wt2),
              method="BFGS",hessian=TRUE
)

bstar=opt_out$par ## Posterior mode for adjusted model
bstar
bstar+as.vector(mu) # mode for actual model
A1=opt_out$hessian # Approximate Precision at mode

```

```
## Standardize Model

Standard_Mod=glmb_Standardize_Model(y=as.vector(y), x=as.matrix(x),P=as.matrix(P),
                                     bstar=as.matrix(bstar,ncol=1), A1=as.matrix(A1))

bstar2=Standard_Mod$bstar2
A=Standard_Mod$A
x2=Standard_Mod$x2
mu2=Standard_Mod$mu2
P2=Standard_Mod$P2
L2Inv=Standard_Mod$L2Inv
L3Inv=Standard_Mod$L3Inv
```

glmbfamfunc

Return family functions used during simulation and post processing

Description

This function takes as input a [family](#) object and returns a set of functions that are used during simulation and summarization of models using the [rglmb](#) and [rlmb](#) functions.

Usage

```
glmbfamfunc(family, lik_shape = 1)

## S3 method for class 'glmbfamfunc'
print(x, ...)
```

Arguments

family	an object of class family
lik_shape	Known shape parameter of the Gamma likelihood; used only for the Gamma(link = "identity") branch where the regression coefficient is the Gamma <i>rate</i> . Ignored for all other family/link combinations. Defaults to 1 (i.e.\ exponential likelihood).
x	an object of class "glmbfamfunc" for which a printed output is desired.
...	additional optional arguments

Details

glmbfamfunc is the canonical R closure bundle for likelihood, posterior, gradient, and deviance quantities across all supported family/link combinations.

Registration requirement. A branch must exist inside glmbfamfunc for every family/link combination that is used in the package. If a combination is missing, the closures f1–f4 will never be assigned and any downstream code that accesses them will fail with *"object 'f1' not found"*. New family/link combinations must therefore be explicitly added here before they can produce valid DIC or log-likelihood output.

Currently implemented family/link combinations:

Family	Link
gaussian	identity
poisson, quasipoisson	log
poisson, quasipoisson	identity
binomial, quasibinomial	logit
binomial, quasibinomial	probit
binomial, quasibinomial	cloglog
binomial, quasibinomial	identity
Gamma	log
Gamma	identity

Any family/link not in this table will fall through all branches silently and produce the error above at the point of first use. For `Gamma(link = "identity")`, pass the known Gamma likelihood shape `lik_shape` (default 1) so that `f1–f4` and `f7` use the correct parameterization (coefficient = Gamma rate β).

Relationship to C++ simulation paths. Many simulation procedures in the package have been fully or partially migrated to `*.cpp` routines, which receive their own objective functions directly. For those paths `glmbfamfunc` may not be called at all during sampling. However, R-side post-processing (e.g. [summary.rglmb](#)) may still use `famfunc\%f1` and `famfunc\%f4`, so a registered branch is still required for those outputs even when the sampler itself has moved to C++.

Value

A list (class "glmbfamfunc") whose first four components are **always** present for every supported family and link. The names `f1–f4` are stable: they mean the same roles across families (only the internal formulas change).

`f1` Negative log-likelihood as a function of coefficients `b` (arguments typically `b`, `y`, `x`, optional `alpha`, `wt`).

`f2` Negative log-posterior (likelihood plus Normal prior quadratic form in `b` with precision `P` and mean `mu`).

`f3` Gradient of `f2` with respect to `b` (same argument pattern as `f2`).

`f4` Deviance-related quantity (twice negative log-likelihood contrast vs. saturated model, with a dispersion argument for quasi-families); used in DIC-style summaries.

`f7` Family-specific matrix: weighted sum of outer products of predictor rows, i.e. a curvature / expected negative Hessian of the log-likelihood w.r.t. `b` at the supplied `b` (used e.g. for multivariate prior–posterior diagnostics in **glmbayes**).

Slots `f5` and `f6` are **not** returned: they were reserved for alternate or C++-aligned likelihood/posterior routines and remain commented out in the implementation (only `f1`, `f2`, `f3`, `f4`, and `f7` are assigned in the returned list).

Examples

```
famfunc <- glmbfamfunc(binomial(logit))

print(famfunc)

## f1--f4 and f7 are always present for supported families; f5 and f6 are not returned.
f1 <- famfunc$f1
f2 <- famfunc$f2
f3 <- famfunc$f3
f4 <- famfunc$f4
f7 <- famfunc$f7
stopifnot(is.function(f1), is.function(f2), is.function(f3),
          is.function(f4), is.function(f7))
```

InvGamma_ct

The Central Inverse-Gamma Distribution

Description

Distribution function, quantile function, and random generation for the inverse-Gamma distribution on the dispersion scale. These functions provide numerically stable evaluation and sampling when the dispersion parameter is restricted to lie between a lower and an upper bound.

Usage

```
pinvgamma_ct(dispersion, shape, rate)

qinvgamma_ct(p, shape, rate, disp_upper, disp_lower)

rinvgamma_ct(n, shape, rate, disp_upper, disp_lower)
```

Arguments

dispersion	Value(s) at which the inverse-Gamma distribution function is evaluated.
shape	Shape parameter of the inverse-Gamma distribution.
rate	Rate parameter of the inverse-Gamma distribution.
p	Probability value(s) for the quantile function.
disp_upper	Upper bound of the dispersion parameter.
disp_lower	Lower bound of the dispersion parameter.
n	Number of random draws to generate. If $\text{length}(n) > 1$, the length is taken to be the number required.

Details

The inverse-Gamma distribution is defined by the transformation $D = 1/X$, where X follows a Gamma distribution with the same shape and rate parameters. The functions `pinvgamma_ct` and `qinvgamma_ct` therefore compute probabilities and quantiles by mapping the dispersion value D to the corresponding Gamma scale and applying the Gamma CDF or quantile function.

The function `rinvgamma_ct` generates random draws from a truncated inverse-Gamma distribution by sampling a uniform probability and inverting the truncated CDF on the Gamma scale. This approach avoids numerical instability when the truncation interval is narrow or when the dispersion parameter is close to zero.

These functions are primarily intended for hierarchical Bayesian models in which dispersion parameters are updated under tight truncation constraints. They provide a stable alternative to direct manipulation of the Gamma distribution when working on the dispersion scale is more natural or more numerically robust. They are used in envelope-based dispersion sampling (Nygren and Nygren 2006).

Value

For `pinvgamma_ct`, a vector of distribution function values evaluated at dispersion. For `qinvgamma_ct`, a vector of quantiles corresponding to the probabilities p . For `rinvgamma_ct`, a vector of length n containing random draws from the inverse-Gamma distribution restricted to the interval $[\text{disp_lower}, \text{disp_upper}]$.

References

Nygren K~N, Nygren L~M (2006). “Likelihood Subgradient Densities.” *Journal of the American Statistical Association*, **101**(475), 1144–1156. doi:10.1198/016214506000000357.

See Also

[Gamma_ct](#), [Normal_ct](#), [EnvelopeDispersionBuild](#)

Examples

```
##### Start of InvGamma_ct example #####

## pinvgamma_ct: CDF on the dispersion scale
shape <- 2
rate <- 1
pinvgamma_ct(1.5, shape, rate)

## Equivalent via pgamma on the precision scale
1 - pgamma(1 / 1.5, shape, rate)

## Example where interval mass pinvgamma_ct(disp_upper) - pinvgamma_ct(disp_lower)
## fails due to catastrophic cancellation when bounds are very close
disp_lower <- 0.999
disp_upper <- 0.999 + 1e-14
pinvgamma_ct(disp_upper, shape, rate) - pinvgamma_ct(disp_lower, shape, rate)

## On the precision scale this is pgamma(1/disp_lower) - pgamma(1/disp_upper);
```

```
## the same cancellation affects the Gamma CDF when precision bounds are close

## rinvgamma_ct samples from truncated inverse-Gamma on the dispersion scale
disp_lower <- 0.99
disp_upper <- 1.01
set.seed(42)
y <- rinvgamma_ct(100, shape = 2, rate = 1,
                  disp_upper = disp_upper, disp_lower = disp_lower)
range(y)
mean(y)

#####
## End of InvGamma_ct example
#####
```

lmebayes_posterior_icm

Joint posterior mean or mode of the two-block mixed model (ICM)

Description

Joint Block~1/Block~2 posterior location for the two-block posterior targeted by [two_block_rNormal_reg](#) and [rGLMM_reg](#). `lmerb_posterior_mean()` solves for the *exact* joint Gaussian mean in closed form (no iteration). `glmerb_posterior_mode()` uses iterated conditional modes (ICM): Block~2 hyperparameters γ and Block~1 random effects b are updated alternately until `fixef` stabilizes.

Usage

```
lmerb_posterior_mean(design, measurement_prior_list, tol = 1e-10, maxit = 200L)

glmerb_posterior_mode(
  design,
  family = gaussian(),
  measurement_prior_list,
  tol = 1e-10,
  maxit = 200L
)
```

Arguments

<code>design</code>	Design list with <code>y</code> , <code>Z</code> , <code>groups</code> , <code>X_hyper</code> , and <code>re_coef_names</code> .
<code>measurement_prior_list</code>	List with <code>Sigma_ranef</code> and <code>prior_list</code> . <code>dispersion_ranef</code> (σ^2) is required for <code>lmerb_posterior_mean()</code> and for <code>glmerb_posterior_mode()</code> when <code>family = gaussian()</code> ; omit for non-Gaussian GLMM families. Each <code>prior_list[[k]]</code> must contain <code>mu_fixef</code> , <code>Sigma_fixef</code> , and <code>dispersion_fixef</code> .

tol	Convergence tolerance for <code>glmerb_posterior_mode()</code> 's ICM loop, on the change in <code>fixef</code> between successive iterations, measured as a Mahalanobis distance in each RE component's own posterior-precision metric ($\sqrt{(\gamma_k^{new} - \gamma_k)^\top P_{\gamma_k}^{post} (\gamma_k^{new} - \gamma_k)}$, maximized over components k), not a raw coordinate-wise ℓ_∞ change. This makes convergence invariant to rescaling or whitening any <code>X_hyper[[k]]</code> column. Default <code>1e-10</code> . Accepted but unused by <code>lmerb_posterior_mean()</code> , which solves exactly (see Details) and always returns <code>converged = TRUE</code> , <code>iterations = 1L</code> , <code>delta = 0</code> ; kept for interface parity with <code>glmerb_posterior_mode()</code> .
maxit	Maximum number of ICM iterations for <code>glmerb_posterior_mode()</code> . Default <code>200L</code> . Accepted but unused by <code>lmerb_posterior_mean()</code> (see <code>tol</code>).
family	A <code>family</code> object. Defaults to <code>gaussian()</code> .

Details

Shared Block~2 update. For each RE component k :

$$E[\gamma_k | b_k] = (X_k^\top X_k / \tau_k^2 + P_{\gamma_k})^{-1} (X_k^\top b_k / \tau_k^2 + P_{\gamma_k} \mu_{\gamma_k})$$

where b_k is the k -th column of the current Block~1 matrix, $X_k = \text{design}\$X_hyper[[k]]$, $\tau_k^2 = \text{dispersion_fixef}$, and $P_{\gamma_k} = \Sigma_{\gamma_k}^{-1}$ from `prior_list`.

Block~1 update differs by function; see `lmerb_posterior_mean` (exact closed-form Gaussian solve) vs `glmerb_posterior_mode` (ICM using the `rglmb` mode for general GLMM families).

When the response is Gaussian and variance components are fixed, the joint posterior is multivariate normal, so `glmerb_posterior_mode()` with `family = gaussian()` targets the same mean as `lmerb_posterior_mean()` (via ICM rather than the closed form).

Value

A list with components `fixef`, `b_mean`, `converged`, `iterations`, and `delta` (the Mahalanobis-distance stopping statistic described under `tol`; always `0` for `lmerb_posterior_mean()`).

Functions

- `lmerb_posterior_mean()`: Joint posterior *mean* of the two-block Gaussian model (= joint mode when variance components are fixed), computed *exactly* in closed form – no ICM iteration. Block~1's conditional mean per group j ,

$$E[b_j | \gamma] = (Z_j^\top Z_j / \sigma^2 + P_b)^{-1} (Z_j^\top y_j / \sigma^2 + P_b \mu_j(\gamma)),$$

is affine in γ (via $\mu_j(\gamma)$ from `build_mu_all`), and b_j couples only to the shared γ – never to another group's $b_{j'}$. Substituting this affine relationship into the Block~2 update (see Details) eliminates all b_j algebraically, leaving one linear system in γ alone (dimension = total hyperparameter count, independent of the number of groups J); solving it once gives the exact joint mean, and one back-substitution pass gives `b_mean`. Forming this system costs $O(J)$ (one $p_{re} \times p_{re}$ solve per group plus a small accumulation), never a $J \times J$ or $J p_{re}$ -dimensional matrix, so it scales to large numbers of groups.

- `glmerb_posterior_mode()`: Joint posterior *mode* of the two-block GLMM. Block~1 uses `rglmb` with $n = 1L$ and a `dNormal` prior per group; the mode is read from `coef.mode`. For `family = gaussian()`, this matches the closed-form update in `lmerb_posterior_mean`.

See Also

[build_mu_all](#), [two_block_rNormal_reg](#), [rglmb](#)

model_setup

Bayesian mixed model setup (single-factor lmer/glmer gate)

Description

Wrapper around [lmer](#) or [glmer](#) for models with exactly one grouping factor. Design matrices come from formula (including cross-level RE moderation terms). Random-effect and residual variance components (vcov_re, residual_var) come from the same reference lmer/glmer fit on formula, so printed summaries match `summary(lmer(...))` on that formula.

Usage

```
model_setup(
  formula,
  data = NULL,
  vcov_formula = NULL,
  family = gaussian(),
  REML = TRUE,
  control = NULL,
  start = NULL,
  verbose = 0L,
  subset,
  weights,
  na.action,
  offset,
  contrasts = NULL,
  devFunOnly = FALSE,
  fit_mer = TRUE,
  ...
)

## S3 method for class 'model_setup'
print(x, ...)
```

Arguments

formula	Mixed-model formula for design extraction and the reference lmer/glmer fit (fixed effects, hyper calibration, and variance components).
data	Optional data frame.
vcov_formula	Ignored (deprecated). Variance components are taken from the full formula fit so lmer reference output is consistent.
family	A family object. Defaults to <code>gaussian()</code> , in which case lmer is used. Non-Gaussian families use glmer .

REML	Logical; passed to <code>lmer</code> when <code>family = gaussian()</code> .
control	<code>lmerControl</code> when <code>family = gaussian()</code> , otherwise <code>glmerControl</code> ; passed through to the reference fit when <code>fit_mer = TRUE</code> .
start	Optional starting values for the inner optimization.
verbose	Passed to <code>lmer</code> .
subset, weights, na.action, offset, contrasts	Passed to <code>lmer</code> .
devFunOnly	If TRUE, return the deviance function only (Gaussian <code>lmer</code> fits only).
fit_mer	If TRUE (default), fit reference <code>lmer</code> / <code>glmer</code> models and extract variance components. If FALSE, return design matrices and rank diagnostics only (used by <code>glmerb()</code> in <code>lmebayes</code>).
...	Ignored.
x	A <code>model_setup</code> object.

Details

Uncorrelated random effects (||). The sampler treats `Sigma_ranef` as diagonal (no off-diagonal covariance). Multi-coefficient random terms must use `||`, e.g. `(1 + x || group)` rather than `(1 + x | group)`. A single random intercept may use `(1 | group)`; `(1 || group)` is not supported by `lme4`.

Fixed-effect constraints. `model_setup` accepts the same formula language as `lmer`, subject to one structural rule: every fixed effect that does *not* correspond to a random-slope term must be a *group-constant* (level-2) covariate—a predictor whose value is the same for every observation within a given group. School-level attributes such as `private_school` or `title1` satisfy this constraint. Student-level covariates that vary *within* groups may appear as fixed main effects only when they *also* appear as random slopes (they then represent the population mean slope γ_{10} , e.g., `distracted_ppvt`). Cross-level interactions of the form `level2_var:random_slope` (e.g., `free_reduced_lunch:distracted_a1`) are additionally permitted; they moderate the prior mean of the corresponding random slope across groups (see `extract_re_hyper_matrices`). Fixed terms that are none of these three types—level-2 covariate, population mean slope, or cross-level moderation interaction—are rejected with an informative error.

Two-step identifiability assessment. After fitting `lmer`, `model_setup` performs a two-step rank check that assesses whether the model is empirically identified at both the within-group and across-group levels:

1. *Level 1 (within-group):* For each group j , the within-group random-effects design submatrix $\mathbf{Z}_j$ is checked for full column rank (`re_rank`). A rank-deficient group has too few distinct observations to estimate all random slopes independently; its BLUPs are identified through the prior rather than the data alone. Such groups are flagged in `re_rank` but are retained in the `lmer` fit; `Prior_Setup_lmebayes` excludes them when calibrating priors.
2. *Level 2 (across-group):* Restricting to the full-rank groups from Step 1, each hyper-design matrix $\mathbf{X}_{\text{hyper}}[[k]]$ is checked for full column rank (`hyper_rank`). Rank deficiency at this level means the level-2 hyperparameters μ_k —the prior means for random-effect coefficient k across groups—are not identified by the data, even as the number of full-rank groups grows.

The scalar `rank_ok` is TRUE only when every $\mathbf{X}_{\text{hyper}}[[k]]$ is full-rank after Step 2. This is a necessary condition for `Prior_Setup_lmebayes` to derive default priors automatically; models with `rank_ok = FALSE` require user-supplied hyperpriors.

The example uses `big_word_club` from the Suggested package **bayesrules** (see `?bayesrules::big_word_club`) and the same formula as the full `lmerb()` demo in `lmebayes` (`demo("Ex_12_lmerb_BigWordClub", package = "lmebayes")`).

Value

Object of class "model_setup": `y`, `Z`, `groups`, `X_hyper`, `formula`, `family`, `vcov_formula` (deprecated alias of `formula`), `lmer_fit` / `glmer_fit`, `lmer_vcov_fit` / `glmer_vcov_fit` (same object as the full-formula fit), `varcorr`, `vcov_re`, `residual_var`, and `re_rank` (named logical vector: TRUE if `Z_j` is full column rank for that group).

See Also

[extract_re_hyper_matrices](#), [lmerb_default_vcov_formula](#), [extract_lmer_variance_components](#)

Examples

```
## model_setup() on bayesrules::big_word_club
##
## Same model as the full lmerb demo, demo/Ex_12_lmerb_BigWordClub.R (see
## also Prior_Setup_lmebayes / lmerb development scripts in data-raw/).
##
## Level 1 (students):
##   y ~ b0[j] + b_ppvt[j]*distracted_ppvt + b_a1[j]*distracted_a1
##
## Level 2 (schools):
##   b0[j]      ~ private_school + title1 + free_reduced_lunch + u0[j]
##   b_ppvt[j]  ~ 1 + u_ppvt[j]
##   b_a1[j]    ~ 1 + free_reduced_lunch + u_a1[j]
##              (cross-level: free_reduced_lunch:distracted_a1 in formula)
##
## Each random slope has a matching fixed main effect (required for
## Prior_Setup_lmebayes() default calibration).

data(big_word_club, package = "bayesrules")

dat <- big_word_club
dat$school_id <- factor(dat$school_id)
dat <- subset(
  dat,
  !is.na(score_ppvt) &
  !is.na(invalid_ppvt) & invalid_ppvt == 0L &
  complete.cases(dat[, c(
    "score_ppvt", "distracted_a1", "distracted_ppvt",
    "private_school", "title1", "free_reduced_lunch", "school_id"
  )])
)

form_lmer <- score_ppvt ~
  private_school + title1 + free_reduced_lunch +
  distracted_a1 + distracted_ppvt +
```

```

    free_reduced_lunch:distracted_a1 +
    (1 + distracted_ppvt + distracted_a1 || school_id)

ctrl_bobyqa <- lme4::lmerControl(optimizer = "bobyqa", optCtrl = list(maxfun = 2e5))

## -----
## 1. lmer fit: raw output
## -----
cat("--- lmer fit ---\n")
fit <- lme4::lmer(form_lmer, data = dat, control = ctrl_bobyqa)
print(summary(fit))

cat("\n--- fixef(fit): population-level (gamma) estimates ---\n")
print(lme4::fixef(fit))

cat("\n--- coef(fit): per-group coefficients (fixef + ranef) ---\n")
print(coef(fit))

## -----
## 2. model_setup: structured view of the same model
## -----
design <- model_setup(form_lmer, data = dat, control = ctrl_bobyqa)
print(design)

## -----
## 3. Random effects b[j]: first 10 schools
## -----
cat("--- Random effects b[j]: first 10", design$group_name, "---\n")
re_df <- as.data.frame(lme4::ranef(design$lmer_fit)[[design$group_name]])
print(utils::head(re_df, 10))

## -----
## 4. Gamma estimates organised to match the Random Effects Model above
##
##   Mapping (intercept RE): X_hyper columns map directly to fixef() names.
##   Mapping (slope RE, hyper ~ 1): (Intercept) column -> fixef[slope_name].
## -----
cat("\n--- Random effects model (gamma estimates) ---\n")

fe      <- lme4::fixef(design$lmer_fit)
coef_df <- coef(design$lmer_fit)[[design$group_name]]
coef_means <- colMeans(coef_df)
coef_vars <- apply(coef_df, 2L, var)
coef_sds  <- sqrt(coef_vars)
w        <- max(nchar(design$re_coef_names))

for (nm in design$re_coef_names) {
  Xj    <- design$X_hyper[[nm]]
  other <- setdiff(colnames(Xj), "(Intercept)")
  hyper_rhs <- if (length(other) == 0L) "1" else paste(c("1", other), collapse = " + ")

  gamma <- setNames(
    vapply(colnames(Xj), function(col) {

```

```

    if (nm == "(Intercept)") {
      if (col %in% names(fe)) unname(fe[col]) else 0
    } else if (col == "(Intercept)") {
      if (nm %in% names(fe)) unname(fe[nm]) else unname(coef_means[nm])
    } else {
      cand <- c(paste0(col, ":", nm), paste0(nm, ":", col))
      hit <- cand[cand %in% names(fe)]
      if (length(hit)) unname(fe[hit[1L]]) else 0
    }
  }, numeric(1L)),
  colnames(Xj)
)

cat(sprintf(" %-*s ~ %s\n", w, nm, hyper_rhs))
print(gamma)
cat("\n")
}

## -----
## 5. Empirical SD/variance of per-school coefficients vs lmer VarCorr
## -----
cat("--- Between-school SD of random coefficients vs lmer VarCorr ---\n")
vc <- as.data.frame(lme4::VarCorr(design$lmer_fit))
cat(sprintf(" %-16s empirical_sd=%7.4f empirical_var=%8.4f lmer_sd=%7.4f lmer_var=%8.4f\n",
  "(Intercept)",
  coef_sds["(Intercept)"], coef_vars["(Intercept)"],
  vc$sdcor[vc$var1 == "(Intercept)" & is.na(vc$var2)][1L],
  vc$vcov[vc$var1 == "(Intercept)" & is.na(vc$var2)][1L]))
for (nm in setdiff(design$re_coef_names, "(Intercept)")) {
  if (!nm %in% colnames(coef_df)) next
  lmer_row <- vc[vc$var1 == nm & is.na(vc$var2), ]
  cat(sprintf(" %-16s empirical_sd=%7.4f empirical_var=%8.4f lmer_sd=%7.4f lmer_var=%8.4f\n",
    nm,
    coef_sds[nm], coef_vars[nm],
    if (nrow(lmer_row)) lmer_row$sdcor[1L] else NA_real_,
    if (nrow(lmer_row)) lmer_row$vcov[1L] else NA_real_))
}

## -----
## 6. lmer refitted on full-rank schools only (same subset as Prior_Setup)
## -----
cat("\n--- lmer refit: full-rank schools only ---\n")
full_rank_schools <- names(design$re_rank)[design$re_rank]
cat(sprintf(" Using %d of %d schools (dropping rank-deficient: %s)\n\n",
  length(full_rank_schools),
  nlevels(design$groups),
  paste(names(design$re_rank)[!design$re_rank], collapse = ", ")))

dat_fr <- subset(dat, school_id %in% full_rank_schools)
dat_fr$school_id <- droplevels(dat_fr$school_id)
fit_fr <- lme4::lmer(form_lmer, data = dat_fr, control = ctrl_bobyqa)
print(summary(fit_fr))

```

```

cat("\n--- VarCorr comparison: all schools vs full-rank schools only ---\n")
vc_fr <- as.data.frame(lme4::VarCorr(fit_fr))
cat(sprintf(" %-16s all_schools_sd=%7.4f full_rank_sd=%7.4f\n",
            "(Intercept)",
            vc$sddcor[vc$var1 == "(Intercept)" & is.na(vc$var2)][1L],
            vc_fr$sddcor[vc_fr$var1 == "(Intercept)" & is.na(vc_fr$var2)][1L]))
for (nm in setdiff(design$re_coef_names, "(Intercept)")) {
  row_all <- vc[vc$var1 == nm & is.na(vc$var2), ]
  row_fr <- vc_fr[vc_fr$var1 == nm & is.na(vc_fr$var2), ]
  cat(sprintf(" %-16s all_schools_sd=%7.4f full_rank_sd=%7.4f\n",
              nm,
              if (nrow(row_all)) row_all$sddcor[1L] else NA_real_,
              if (nrow(row_fr)) row_fr$sddcor[1L] else NA_real_))
}

## =====
## 7. Optional stress test (NOT the lmerb example model): esl_observed RE
## =====
cat("\n\n=== Section 7 (optional): esl_observed added as random slope ===\n\n")

dat_esl <- subset(
  dat,
  complete.cases(dat[, c("esl_observed")]))
)
form_esl <- score_ppvt ~
  private_school + title1 + free_reduced_lunch +
  distracted_a1 + distracted_ppvt +
  free_reduced_lunch:distracted_a1 + esl_observed +
  (1 + distracted_ppvt + distracted_a1 + esl_observed || school_id)

design_esl <- model_setup(form_esl, data = dat_esl, control = ctrl_bobyqa)
print(design_esl)

```

multi_prior_setup	<i>Prior setup for multiple Gaussian responses</i>
-------------------	--

Description

Prior setup for multiple Gaussian responses

Usage

```

multi_prior_setup(
  formula,
  family = gaussian(),
  data = NULL,
  weights = NULL,
  subset = NULL,
  na.action = na.fail,
  offset = NULL,

```

```

contrasts = NULL,
pwt = NULL,
pwt_default_low = 0.01,
pwt_default_high = 0.05,
n_prior = NULL,
sd = NULL,
dispersion = NULL,
intercept_source = c("null_model", "full_model"),
effects_source = c("null_effects", "full_model"),
mu = NULL,
k = 1,
...
)

```

Arguments

formula	an object of class " formula " (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
family	a description of the error distribution and link function to be used in the model.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>glm</code> is called.
weights	an optional vector of 'prior weights' to be used in the fitting process. Should be <code>NULL</code> or a numeric vector.
subset	an optional vector specifying a subset of observations to be used in the fitting process. (See additional details about how this argument interacts with data-dependent bases in the 'Details' below.)
na.action	how NAs are treated. The default is first, any na.action attribute of data, second a <code>na.action</code> setting of options , and third <code>na.fail</code> if that is unset. The factory-fresh default is <code>na.omit</code> . Another possible value is <code>NULL</code> .
offset	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. This should be <code>NULL</code> or a numeric vector of length equal to the number of cases. One or more offset terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See model.offset .
contrasts	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
pwt	Weight on the prior relative to the likelihood function at the maximum likelihood estimate. If supplied, this value is used directly (scalar or one value per coefficient). If <code>n_prior</code> is provided and <code>pwt</code> is still a scalar and <code>sd</code> was not supplied, <code>pwt</code> is set to <code>n_prior / (n_prior + n_effective)</code> . If <code>length(pwt) > 1</code> (including from <code>sd</code>) or <code>sd</code> was supplied, <code>n_prior</code> does not overwrite <code>pwt</code> ; it is used only as a scalar for <code>Gamma / S_marg</code> steps. If <code>sd</code> is provided, <code>pwt</code> is computed from the prior standard deviations. If none of these are supplied, <code>pwt</code> defaults to <code>pwt_default_low</code> for models with fewer than 14 coefficients, and <code>pwt_default_high</code> otherwise.

pwt_default_low	Default prior weight used when pwt is not supplied and the model dimension is below 14. Defaults to 0.01.
pwt_default_high	Default prior weight used when pwt is not supplied and the model dimension is 14 or greater. Defaults to 0.05.
n_prior	Optional scalar effective prior sample size (on the <code>n_effective</code> scale). If provided with scalar pwt and without sd, pwt is recomputed from n_prior. With vector pwt or with sd, pwt is left unchanged and n_prior is used for the Gamma prior on precision and related Gaussian calibration only. If missing and pwt is scalar, $n_prior = (pwt / (1 - pwt)) * n_effective$.
sd	Optional vector argument with the prior standard deviations for the coefficients
dispersion	Optional scalar dispersion override (default NULL). For now, this is documented as an optional argument used to scale the Sigma (variance-covariance) matrix; see Details for additional context.
intercept_source	Specifies the method through which the prior mean for the intercept term is set. Options are based on the null intercept only model (<code>null_model</code>) or <code>full_models</code> . The default is the null model which is safer if variables are not centered.
effects_source	Specifies the method through which the prior means for the effects terms are set. Options are <code>null_effects</code> (prior means set to zero) or <code>full_model</code> (effect means set to match maximum likelihood estimates).
mu	Optional vector argument with the prior means for the coefficients
k	Scalar (default 1), non-negative ($k \geq 0$), with $k + p \geq 2$ where p is the number of coefficients (columns of the model matrix). k controls the tail behavior and effective degrees of freedom of the variance prior. It does not change the posterior mean of σ^2 or the covariance of β , but larger k makes the prior and posterior for σ^2 more concentrated and less heavy-tailed. Not yet used in calibration; passed through to <code>compute_gaussian_prior</code> for future use.
...	For glm: arguments to be used to form the default <code>control</code> argument if it is not supplied directly. For weights: further arguments passed to or from other methods.

Value

A named list of class "multi_PriorSetup". Each element is a [Prior_Setup](#) result for one column of the response (names from `colnames(y)` or `Y1, Y2, ...`).

See Also

Other prior: [Prior_Check\(\)](#), [Prior_Setup\(\)](#)

multi_rlmb

*Multi-response Bayesian regression and simulation***Description**

These functions run the corresponding single-response sampler once per column of a matrix y , sharing the same design matrix x (as `lm` with `cbind` responses). Each returns a named list of class "mrglmb"; element j is the fit for column j of y . Use `summary.mrglmb` for column-wise summaries.

Usage

```
multi_rlmb(
  n = 1,
  y,
  x,
  pfamily_list,
  offset = NULL,
  weights = NULL,
  Gridtype = 2,
  n_envopt = NULL,
  use_parallel = TRUE,
  use_openc1 = FALSE,
  verbose = FALSE,
  progbar = FALSE
)

multi_rNormalGamma_reg(
  n,
  y,
  x,
  prior_list,
  offset = NULL,
  weights = 1,
  family = gaussian(),
  Gridtype = 2,
  n_envopt = NULL,
  use_parallel = TRUE,
  use_openc1 = FALSE,
  verbose = FALSE,
  progbar = TRUE
)

multi_rindepNormalGamma_reg(
  n,
  y,
  x,
  prior_list,
```

```

    offset = NULL,
    weights = 1,
    family = gaussian(),
    Gridtype = 2,
    n_envopt = NULL,
    use_parallel = TRUE,
    use_opengl = FALSE,
    verbose = FALSE,
    progbar = TRUE
  )

```

Arguments

<code>n</code>	number of draws to generate. If <code>length(n) > 1</code> , the length is taken to be the number required.
<code>y</code>	a vector of observations of length <code>m</code> .
<code>x</code>	for <code>rlmb</code> a design matrix of dimension <code>m * p</code> and for <code>print.rlmb</code> the object to be printed.
<code>pfamily_list</code>	List of length <code>ncol(y)</code> of <code>pfamily</code> objects.
<code>offset</code>	an optional numeric vector of known offset to be included in the linear predictor.
<code>weights</code>	an optional numeric vector of prior weights for the observations.
<code>Gridtype</code>	an optional argument specifying tangent points for envelope construction.
<code>n_envopt</code>	Effective sample size passed to <code>EnvelopeOpt</code> for grid construction.
<code>use_parallel</code>	Logical. Whether to use parallel processing during simulation.
<code>use_opengl</code>	Logical. Whether to use OpenCL acceleration during Envelope construction.
<code>verbose</code>	Logical. Whether to print progress messages.
<code>progbar</code>	Logical. Whether to display a progress base during simulation.
<code>prior_list</code>	List of length <code>ncol(y)</code> of per-column prior lists.
<code>family</code>	A description of the error distribution and link function (see family).

Details

`multi_rlmb` Same arguments as `rlmb` except `pfamily` is replaced by `pfamily_list` (length `ncol(y)` of `pfamily` objects). Each element is class `"rlmb"` (and `"rglmb"`).

`multi_rNormalGamma_reg` Same arguments as `rNormalGamma_reg` except `prior_list` is a list of per-column prior lists (`mu`, `Sigma` or `P`, `shape`, `rate`).

`multi_rindepNormalGamma_reg` Same arguments as `rindepNormalGamma_reg` except `prior_list` is a list of per-column prior lists (`mu`, `Sigma`, `shape`, `rate`, optional dispersion bounds).

`multi_prior_setup` Same arguments as `Prior_Setup`, but the formula left-hand side may be several responses (`cbind(...)`). Returns a named list of `"PriorSetup"` objects (one per response column).

Value

A named list of class "mrglmb". Metadata (call, y, x, ll, p, coef_names, pred_names) are attributes; per-column priors are in `attr(..., "prior_lists")` or `attr(..., "pfamily_lists")` for `multi_rlmb`.

Functions

- `multi_rlmb()`: Gaussian `rlmb` simulation with multiple responses.
- `multi_rNormalGamma_reg()`: Normal–Gamma regression with multiple responses.
- `multi_rindepNormalGamma_reg()`: Independent Normal–Gamma regression with multiple responses.

See Also

`summary.mrglmb`, `multi_rNormal_reg`, `rlmb`, `rNormal_reg`, `rNormalGamma_reg`, `rindepNormalGamma_reg`
 glmbayes Modeling Functions `rglmb()`, `rlmb()`
 glmbayes Simulation Functions `multi_rNormal_reg()`, `rGLMM_Re_Draw()`, `rGLMM_reg()`, `rGLMM_sweep()`,
`rLMM_reg`, `rindepNormalGamma_reg_with_envelope()`, `simfuncs`, `two_block_optimize_pilot_cost()`,
`two_block_rNormal_reg()`, `two_block_rate()`, `two_block_tv_bound()`
 glmbayes Simulation Functions `multi_rNormal_reg()`, `rGLMM_Re_Draw()`, `rGLMM_reg()`, `rGLMM_sweep()`,
`rLMM_reg`, `rindepNormalGamma_reg_with_envelope()`, `simfuncs`, `two_block_optimize_pilot_cost()`,
`two_block_rNormal_reg()`, `two_block_rate()`, `two_block_tv_bound()`

Examples

```
## Multi-response samplers (iris): shared y and x via multi_prior_setup
## y: four numeric columns; x: intercept + Species (p = 3)

set.seed(42)

n_draw <- 150L
common <- list(
  n = n_draw,
  family = gaussian(),
  use_parallel = FALSE,
  progbar = FALSE
)

ps_multi <- multi_prior_setup(
  cbind(Sepal.Length, Sepal.Width, Petal.Length, Petal.Width) ~ Species,
  data = iris,
  family = gaussian()
)

x <- ps_multi[[1L]]$x
y <- do.call(cbind, lapply(ps_multi, function(ps) ps$y))
colnames(y) <- names(ps_multi)

## --- multi_rlmb (pfamily_list) -----
```

```

pfamily_list <- lapply(ps_multi, function(ps) {
  dNormal_Gamma(
    mu = ps$mu, Sigma_0 = ps$Sigma_0, shape = ps$shape, rate = ps$rate
  )
})
out_rlmb <- multi_rlmb(
  n = n_draw, y = y, x = x, pfamily_list = pfamily_list,
  use_parallel = FALSE, progbar = FALSE
)
summary(out_rlmb)

## --- multi_rNormal_reg (shared-x path) -----
prior_list_normal <- lapply(ps_multi, function(ps) {
  list(mu = as.numeric(ps$mu), Sigma = ps$Sigma, dispersion = ps$dispersion)
})
out_normal <- do.call(
  multi_rNormal_reg, c(common, list(y = y, x = x, prior_list = prior_list_normal))
)
summary(out_normal)

## --- multi_rNormalGamma_reg -----
prior_list_ng <- lapply(ps_multi, function(ps) {
  list(
    mu = as.numeric(ps$mu), Sigma = ps$Sigma_0,
    shape = ps$shape, rate = ps$rate
  )
})
out_ng <- do.call(
  multi_rNormalGamma_reg, c(common, list(y = y, x = x, prior_list = prior_list_ng))
)
summary(out_ng)

## --- multi_rindepNormalGamma_reg -----
prior_list_ing <- lapply(ps_multi, function(ps) {
  list(
    mu = as.numeric(ps$mu), Sigma = ps$Sigma,
    shape = ps$shape_ING, rate = ps$rate
  )
})
out_ing <- do.call(
  multi_rindepNormalGamma_reg,
  c(common, list(y = y, x = x, prior_list = prior_list_ing))
)
summary(out_ing)

```

Description

Runs `rNormal_reg` once per column of `y`. Argument `x` may be a single shared design matrix or a **list of matrices** with one entry per response column. The list path allows each column of `y` to have a different number of predictors, which is required for Block 2 of `two_block_rNormal_reg`.

Usage

```
multi_rNormal_reg(
  n,
  y,
  x,
  prior_list,
  offset = NULL,
  weights = 1,
  family = gaussian(),
  Gridtype = 2,
  n_envopt = NULL,
  use_parallel = TRUE,
  use_opengl = FALSE,
  verbose = FALSE,
  progbar = TRUE
)
```

Arguments

<code>n</code>	Number of draws per column of <code>y</code> .
<code>y</code>	Numeric matrix with one column per random-effect component.
<code>x</code>	Shared design matrix, or list of per-column design matrices.
<code>prior_list</code>	List of per-column prior lists (<code>mu</code> , <code>Sigma</code> or <code>P</code> , optional dispersion).
<code>offset</code>	Optional numeric vector of length <code>m</code> specifying known components of the linear predictor.
<code>weights</code>	Optional numeric vector of prior weights.
<code>family</code>	A description of the error distribution and link function (see family).
<code>Gridtype</code>	Optional integer specifying the method used to construct the envelope function.
<code>n_envopt</code>	Effective sample size passed to <code>EnvelopeOpt</code> for grid construction. Defaults to match <code>n</code> . Larger values encourage tighter envelopes.
<code>use_parallel</code>	Logical. Whether to use parallel processing.
<code>use_opengl</code>	Logical. Whether to use OpenCL acceleration.
<code>verbose</code>	Logical. Whether to print progress messages.
<code>progbar</code>	Logical. Whether to display a progress base during simulation.

Value

For shared `x`, an object of class `"mrg1mb"`. For list `x`, a plain named list of `rNormal_reg` results.

See Also

```
rNormal_reg, two_block_rNormal_reg  
  
glmbayes Simulation Functions multi_rlmb(), rGLMM_Re_Draw(), rGLMM_reg(), rGLMM_sweep(),  
rLMM_reg, rindepNormalGamma_reg_with_envelope(), simfuncs, two_block_optimize_pilot_cost(),  
two_block_rNormal_reg(), two_block_rate(), two_block_tv_bound()
```

Normal_ct	<i>The Central Normal Distribution</i>
-----------	--

Description

Distribution function and random generation for the center (between a lower and an upper bound) of the normal distribution with mean equal to mu and standard deviation equal to sigma.

Usage

```
pnorm_ct(a = -Inf, b = Inf, mu = 0, sigma = 1, log.p = TRUE, Diff = FALSE)  
  
rnorm_ct(n, lgrt, lglt, mu = 0, sigma = 1)
```

Arguments

a	Lower bound for the interval. Numeric vector; must be finite when used in rnorm_ct.
b	Upper bound for the interval. Numeric vector; must be finite when used in rnorm_ct.
mu	mean parameter of the underlying normal distribution.
sigma	standard deviation of the underlying normal distribution.
log.p	Logical argument. If TRUE, the log probability is provided
Diff	Logical argument. If TRUE the second parameter is the difference between the lower and upper bound
n	number of draws to generate. If length(n) > 1, the length is taken to be the number required
lgrt	log of the distribution function between the lower bound and infinity. Numeric vectors of length n; used internally to avoid cancellation when b - a is small.
lglt	log of the distribution function between negative infinity and the upper bound. Numeric vectors of length n; used internally to avoid cancellation when b - a is small.

Details

The distribution function `pnorm_ct` finds the probability of the center of a normal density (the probability of the area between a lower bound `a` and an upper bound `b`) while the random number generator `rnorm_ct` samples from a restricted normal density where `lgrr` is the log of the distribution between the lower bound and infinity and `lgrr` is the log of the distribution function between negative infinity and the upper bound. The sum of the exponentiated values for the two ($\exp(\lgrr) + \exp(\lgrr)$) must sum to more than 1.

These functions are mainly used to handle cases where the differences between the upper and lower bounds $b - a$ are small. In such cases, using $\text{pnorm}(b) - \text{pnorm}(a)$ may result in 0 being returned even when the difference is supposed to be positive. They are used in envelope-based accept-reject sampling for Bayesian GLMs (Nygren and Nygren 2006).

Value

For `pnorm_ct`, vector of length equal to length of `a` and for `rnorm_ct`, a vector with length determined by `n` containing draws from the center of the normal distribution.

References

Nygren K~N, Nygren L~M (2006). “Likelihood Subgradient Densities.” *Journal of the American Statistical Association*, **101**(475), 1144–1156. doi:10.1198/016214506000000357.

See Also

[Gamma_ct](#), [EnvelopeBuild](#)

Examples

```
pnorm_ct(0.2,0.4)
exp(pnorm_ct(0.2,0.4))
pnorm_ct(0.2,0.4,log.p=FALSE)
log(pnorm_ct(0.2,0.4,log.p=FALSE))
## Example where difference between two pnorm calls fail
## but call to pnorm_ct works
pnorm(0.5)-pnorm(0.4999999999999999)
pnorm_ct(0.4999999999999999,0.5,log.p=FALSE)
```

pfamily

Prior Family Objects for Bayesian Models

Description

Prior family objects provide a convenient way to specify the details of the priors used by matrix-input samplers such as [rglmb](#) and [rlmb](#). See the documentation for [rglmb](#) and [rlmb](#) for the details of how such model fitting takes place.

Under a $\text{Beta}(\text{shape1}, \text{shape2})$ prior on the binomial probability θ and a $\text{Binomial}(n_i, \theta)$ likelihood with identity link ($\theta = \beta$ directly), the posterior is:

$$\theta \mid y \sim \text{Beta}(\text{shape1} + \sum n_i y_i, \text{shape2} + \sum n_i (1 - y_i)).$$

Usage

```

pfamily(object, ...)

dNormal(mu, Sigma, dispersion = NULL)

dGamma(
  shape,
  rate,
  beta,
  Inv_Dispersion = TRUE,
  lik_shape = 1,
  max_disp_perc = 0.99,
  disp_lower = NULL,
  disp_upper = NULL
)

dBeta(shape1, shape2, beta)

## S3 method for class 'pfamily'
print(x, ...)

dNormal_Gamma(mu, Sigma_0, shape, rate)

dIndependent_Normal_Gamma(
  mu,
  Sigma,
  shape,
  rate,
  max_disp_perc = 0.99,
  disp_lower = NULL,
  disp_upper = NULL
)

```

Arguments

object	the function pfamily accesses the pfamily objects which are stored within objects created by modelling functions (e.g., rglmb).
mu	a prior mean vector for the the modeling coefficients used in several pfamilies
Sigma	a prior variance-covariance matrix for dNormal() and dIndependent_Normal_Gamma().
dispersion	the dispersion to be assumed when it is not given a prior. Should be provided when the Normal prior is for the gaussian(), Gamma(), quasibinomial, or quasipoisson families. The binomial() and poisson() families do not have dispersion coefficients. Omitted or NULL uses the internal default 1 and sets ddef in prior_list (see Details).
shape	The prior shape parameter for the gamma piece (inverse dispersion / precision). When taking defaults from Prior_Setup , use ps\$shape with dNormal_Gamma()

	and <code>dGamma()</code> , and <code>ps\$shape_ING</code> with <code>dIndependent_Normal_Gamma()</code> on the Gaussian calibrated path (see Details).
<code>rate</code>	The prior rate parameter paired with <code>shape</code> . With Gaussian <code>Prior_Setup</code> , <code>dNormal_Gamma()</code> and <code>dIndependent_Normal_Gamma()</code> use <code>ps\$rate</code> ; for <code>dGamma()</code> with fixed <code>beta</code> , prefer <code>ps\$rate_gamma</code> when that field is non-NULL (see Details).
<code>beta</code>	Initial coefficient matrix (1×1); typically set to the prior mean $\text{shape1}/(\text{shape1}+\text{shape2})$.
<code>Inv_Dispersion</code>	Logical (default TRUE). Controls which of the two Gamma prior roles <code>dGamma()</code> plays: • TRUE (default): prior on inverse dispersion (precision / shape parameter $k = 1/\phi$). This is the classical path used for dispersion estimation in Gaussian and Gamma(log) regression (<code>simfun = rGamma_reg</code>). • FALSE: conjugate prior on the Gamma or Poisson rate β directly (intercept-only, identity link). The posterior is a closed-form Gamma draw (<code>simfun = rGamma_Conjugate_reg</code>).
<code>lik_shape</code>	Known shape parameter $k > 0$ of the Gamma likelihood. Only used when <code>Inv_Dispersion = FALSE</code> and <code>family = Gamma(link = "identity")</code> . The intercept coefficient is then the Gamma rate β , and the conjugate posterior is $\beta \mid y \sim \text{Gamma}(\alpha_0 + nk, \beta_0 + \sum y_i)$. Defaults to 1 (exponential distribution). Ignored for Poisson families and whenever <code>Inv_Dispersion = TRUE</code> .
<code>max_disp_perc</code>	Specifies the percentile used to truncate the posterior dispersion distribution when constructing the envelope for accept-reject sampling. This determines the lower and upper bounds for the dispersion (σ^2) used in the simulation. A value of 0.99 corresponds to using the central 98 percent of the posterior dispersion mass (i.e., excluding the outer 1 percent in each tail). Smaller values yield tighter bounds and may improve acceptance rates, while larger values allow broader dispersion support but may increase envelope complexity.
<code>disp_lower</code>	lower bound truncation for dispersion
<code>disp_upper</code>	upper bound truncation for dispersion
<code>shape1</code>	First shape parameter $\alpha > 0$ of the Beta prior (prior successes + 1).
<code>shape2</code>	Second shape parameter $\beta > 0$ of the Beta prior (prior failures + 1).
<code>x</code>	an object, a pfamily function that is to be printed
<code>Sigma_0</code>	prior variance-covariance on the precision-weighted coefficient scale for <code>dNormal_Gamma()</code> only (Gaussian). Stored in <code>prior_list\$Sigma</code> for compatibility with downstream samplers.
<code>...</code>	additional argument(s) for methods.

Details

`pfamily` is a generic with methods for fitted objects such as `rglmb` and `rlmb`. The `dNormal()` prior is supported for all response families. The `gaussian()` family additionally supports `dNormal_Gamma()`, `dIndependent_Normal_Gamma()`, and `dGamma()` (precision prior). Intercept-only models with an identity link support two closed-form conjugate priors: `dBeta()` for `binomial(link = "identity")` and `dGamma(Inv_Dispersion = FALSE)` for `poisson(link = "identity")` and `Gamma(link = "identity")`.

A `pfamily` object represents a structured prior specification for use in Bayesian generalized linear modeling. Each constructor function (e.g., `dNormal()`, `dGamma()`, `dNormal_Gamma()`, `dBeta()`)

returns an object of class "pfamily" containing the prior parameters, supported likelihood families, compatible link functions, and a simulation function for posterior sampling.

These priors are designed to integrate seamlessly with modeling functions such as `rglmb()` and `rlmb()` in the **glmbayes** package, which consume the pfamily object to define the prior distribution over model parameters. The `pfamily()` generic retrieves the embedded prior from a fitted model object, while `print.pfamily()` displays its structure.

`prior_list` and `simfun`. The named list `prior_list` holds the hyperparameters for the chosen prior family. When a model function draws from the posterior, it passes `prior_list` into the element `simfun` (e.g., `rNormal_reg`, `rGamma_reg`) so the low-level sampler receives one consistent list structure regardless of which constructor built the pfamily.

Prior_Setup and default hyperparameters. `Prior_Setup()` fits an auxiliary GLM and returns default `mu`, `Sigma / Sigma_0`, `dispersion`, `Gamma` shape and rate, and related fields aligned with the data and prior-weight (`pwt`) choices. Those values can be supplied as arguments to the pfamily constructors when you want package-default priors on the same scale as the model matrix. Recommended use of shape and rate is not identical across constructors: for `dIndependent_Normal_Gamma()`, pass `shape = ps$shape_ING` from `Prior_Setup` (not the scalar `ps$shape` used by `dNormal_Gamma()`). For `dGamma()` with fixed coefficients (`beta`), pass `rate = ps$rate_gamma` when that field is present (otherwise `ps$rate`); see `Prior_Setup` and `compute_gaussian_prior`.

Prior Families:

- `dNormal()`: Specifies a multivariate normal prior over regression coefficients. It is conjugate for Gaussian likelihoods with an identity link function, and serves as the primary implemented prior for all other supported likelihood families in the current framework. This structure facilitates efficient posterior sampling and analytical tractability. The returned `prior_list` includes `ddef`: `TRUE` when dispersion was omitted or `NULL` (so the default 1 was used), `FALSE` when dispersion was supplied explicitly (including 1).
For models with log-concave likelihood functions—such as Poisson, Binomial, and Gamma families—posterior sampling under a `dNormal` prior is performed using a (Nygren and Nygren 2006) likelihood subgradient approach. This method constructs tight enveloping functions around the posterior using subgradients of the log-likelihood, enabling efficient accept-reject sampling even in high dimensions.
When the posterior distribution is approximately normal (typically the case for large sample sizes), the area under the enveloping function is bounded above by a constant factor—approximately $2/\sqrt{\pi} \approx 1.128$ in the univariate case, and $(2/\sqrt{\pi})^k$ in k -dimensional models. These bounds ensure that the rejection rate remains manageable and that the sampler remains computationally efficient.
The concept of conjugate priors was first formalized by (Raiffa and Schlaifer 1961), and further developed for regression models using g-prior structures by (Zellner 1986).
- `dGamma()`: A Gamma prior with two distinct roles controlled by `Inv_Dispersion`:
 - `Inv_Dispersion = TRUE` (default): prior on the inverse dispersion (precision $1/\phi$ or shape k). Used for dispersion estimation in Gaussian and Gamma(log) models, typically in a Gibbs step with `beta` held fixed (Gelman et al. 2013; Dobson 1990; McCullagh and Nelder 1989). With Gaussian `Prior_Setup` output, prefer `rate_gamma` for rate (see Details above).
 - `Inv_Dispersion = FALSE`: conjugate Gamma prior on the rate parameter β directly. Supports intercept-only models with an identity link: Poisson (Gamma–Poisson conjugacy) and Gamma (Gamma–Gamma conjugacy). Posterior draws are closed-form IID

samples via `rGamma_Conjugate_reg`. The `lik_shape` argument specifies the known Gamma likelihood shape (default 1, i.e. exponential). `Prior_Setup` returns calibrated `conj_poisson` hyperparameters for this path.

- `dBeta()`: A Beta prior on the binomial probability θ for intercept-only binomial(`link = "identity"`) models. The posterior is a closed-form Beta draw (Beta–Binomial conjugacy) produced by `rBeta_reg`. Arguments `shape1` and `shape2` are the prior pseudo-success and pseudo-failure counts. `Prior_Setup` returns calibrated `conj_beta` hyperparameters for this path.
- `dNormal_Gamma()`: Combines a multivariate normal prior on coefficients with a gamma prior on precision, forming a conjugate structure for Gaussian models with unknown variance. The second argument is `Sigma_0` (precision-weighted scale); it is aliased internally to `Sigma` in `prior_list`. This formulation parallels classical Normal-Gamma models and is compatible with hierarchical extensions (Gelman et al. 2013; Raiffa and Schlaifer 1961).
- `dIndependent_Normal_Gamma()`: Similar to `dNormal_Gamma()`, but assumes independence between the coefficient and precision priors. This structure is useful for models where prior independence is desired or analytically convenient. With `Prior_Setup` on a Gaussian model, pass `shape_ING` as the `shape` argument (see Details above).

Each `pfamily` object includes:

- `pfamily`, `prior_list`, `okfamilies`, `plinks`, and `simfun` (see Value).

`mu / Sigma`: the surrogate Normal mean is $\text{shape1}/(\text{shape1}+\text{shape2})$ and the surrogate variance is the Beta variance $\text{shape1}*\text{shape2}/((\text{shape1}+\text{shape2})^2*(\text{shape1}+\text{shape2}+1))$.

Value

An object of class "pfamily" (with a concise print method). A list with elements:

<code>pfamily</code>	Character string: the constructor name (" <code>dNormal</code> ", " <code>dGamma</code> ", " <code>dNormal_Gamma</code> ", " <code>dIndependent_Normal_Gamma</code> ", or " <code>dBeta</code> ").
<code>prior_list</code>	Named list of prior hyperparameters. It is passed into <code>simfun</code> when sampling so the relevant low-level routine receives the prior in a fixed list form. Contents depend on the constructor: <code>dNormal</code> : <code>mu</code> , <code>Sigma</code> , <code>dispersion</code> , and logical <code>ddef</code> (TRUE if dispersion was omitted or NULL, so the default 1 was used; FALSE if set explicitly). <code>dGamma</code> : <code>shape</code> , <code>rate</code> , <code>beta</code> , <code>Inv_Dispersion</code> , <code>max_disp_perc</code> , <code>disp_lower</code> , <code>disp_upper</code> . When <code>Inv_Dispersion = FALSE</code> , also includes surrogate <code>mu</code> and <code>Sigma</code> (computed from the Gamma prior moments) and <code>lik_shape</code> . <code>dNormal_Gamma</code> : <code>mu</code> , <code>Sigma</code> (the <code>Sigma_0</code> precision-weighted input), <code>shape</code> , <code>rate</code> . <code>dIndependent_Normal_Gamma</code> : <code>mu</code> , <code>Sigma</code> (coefficient-scale covariance), <code>shape</code> , <code>rate</code> , <code>max_disp_perc</code> , <code>disp_lower</code> , <code>disp_upper</code> . <code>dBeta</code> : <code>shape1</code> , <code>shape2</code> , <code>beta</code> , and surrogate <code>mu</code> and <code>Sigma</code> computed from the Beta prior moments ($\text{mu} = \text{shape1}/(\text{shape1}+\text{shape2})$, $\text{Sigma} = \text{shape1}*\text{shape2}/((\text{shape1}+\text{shape2})^2*(\text{shape1}+\text{shape2}+1))$).
<code>okfamilies</code>	Character vector of implemented family names for which this <code>pfamily</code> may be used.
<code>plinks</code>	Function of one family argument returning allowed link names for that family.

`simfun` Function used to generate posterior draws (e.g., `rNormal_reg`, `rGamma_reg`, `rGamma_Conjugate_reg`, `rNormalGamma_reg`, `rindNormalGamma_reg`); for standard use these produce i.i.d.\ posterior samples for the implemented settings.

Author(s)

The design of the pfamily set of functions was developed by Kjell Nygren and was inspired by the family used by `rglmb` to specify the likelihood function. That design in turn was inspired by S functions of the same names from the statistical modeling literature.

References

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See Also

`rglmb`, `rlmb` for modeling functions that consume pfamily objects.

`rNormal_reg`, `rNormalGamma_reg`, `rGamma_reg`, `rGamma_Conjugate_reg`, `rindNormalGamma_reg` for lower-level sampling functions used by pfamily constructors.

`Prior_Setup`, `Prior_Check` for initializing and validating prior specifications.

`EnvelopeBuild` for envelope construction methods used in likelihood subgradient sampling (Nygren and Nygren 2006).

See also (Hastie and Pregibon 1992) for the original S modeling framework that inspired the design of pfamily.

Examples

```
## Dobson (1990) Page 93: Randomized Controlled Trial :
counts    <- c(18, 17, 15, 20, 10, 20, 25, 13, 12)
outcome   <- gl(3, 1, 9)
treatment <- gl(3, 3)
print(d.AD <- data.frame(treatment, outcome, counts))

## Set up Prior for Poisson Model
```

```

ps <- Prior_Setup(counts ~ outcome + treatment, family = poisson())
ps

## Normal prior for rglmb
rglmb.D93 <- rglmb(
  n = 1000,
  y = ps$y,
  x = as.matrix(ps$x),
  pfamily = dNormal(mu = ps$mu, Sigma = ps$Sigma),
  family = poisson(),
  weights = rep(1, nrow(ps$x))
)

pfamily(rglmb.D93)

## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.
ctl <- c(4.17, 5.58, 5.18, 6.11, 4.50, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)

## Set up prior for gaussian model
ps2 <- Prior_Setup(weight ~ group, family = gaussian())
ps2

y <- ps2$y
x <- as.matrix(ps2$x)
wt <- rep(1, length(y))

## Conjugate Normal Prior (fixed dispersion)
rlmb.D9 <- rlmb(
  n = 1000,
  y = y,
  x = x,
  pfamily = dNormal(mu = ps2$mu, ps2$Sigma, dispersion = ps2$dispersion),
  weights = wt
)
pfamily(rlmb.D9)

## Conjugate Normal_Gamma Prior
rlmb.D9_v2 <- rlmb(
  n = 1000,
  y = y,
  x = x,
  pfamily = dNormal_Gamma(
    ps2$mu,
    Sigma_0 = ps2$Sigma_0,
    shape = ps2$shape,
    rate = ps2$rate
  ),
  weights = wt
)

```

```

pfamily(rlmb.D9_v2)

## Independent_Normal_Gamma_Prior
rlmb.D9_v3 <- rlmb(
  n = 1000,
  y = y,
  x = x,
  pfamily = dIndependent_Normal_Gamma(
    ps2$mu,
    ps2$Sigma,
    shape = ps2$shape_ING,
    rate = ps2$rate
  ),
  weights = wt
)
pfamily(rlmb.D9_v3)

```

pfamily_list

Build a named list of pfamily objects

Description

Generic for constructing a named list of [pfamily](#) prior objects from a prior-specification object. Packages that define prior setup containers (e.g. [Prior_Setup_lmebayes](#)) provide methods that map each component of the container to a pfamily constructor such as [dNormal](#) or [dIndependent_Normal_Gamma](#).

Usage

```
pfamily_list(object, ...)
```

Arguments

object	A prior-specification object.
...	Additional arguments passed to methods (e.g. ptypes).

Value

A named list whose elements are objects of class "pfamily".

See Also

[pfamily](#), [dNormal](#), [dIndependent_Normal_Gamma](#), [Prior_Setup_lmebayes](#)

pfamily_list.lmebayes_prior_setup

Build pfamily objects from a Prior_Setup_lmebayes object

Description

Converts the per-component Block~2 hyperprior parameters stored in a [Prior_Setup_lmebayes](#) object into a named list of [pfamily](#) objects, one per random-effect coefficient (e.g. "(Intercept)", slope names).

Usage

```
## S3 method for class 'lmebayes_prior_setup'
pfamily_list(object, ptypes = "dNormal", ...)
```

Arguments

object	An object of class "lmebayes_prior_setup" as returned by Prior_Setup_lmebayes .
ptypes	Character: either a single string applied to every random-effect component, or a character vector / list with one string per component. Allowed values are "dNormal" and "dIndependent_Normal_Gamma". A vector may be named with the random-effect coefficient names (any order); unnamed vectors are matched positionally against names(object\$prior_list).
...	Currently ignored.

Details

For each random-effect coefficient k , the prior parameters come from `object$prior_list[[k]]`:

- "dNormal": `dNormal(mu = mu_fixef, Sigma = Sigma_fixef, dispersion = dispersion_fixef)`. The Block~2 dispersion (the random-effect variance τ_k^2) is treated as known.
- "dIndependent_Normal_Gamma": the same `mu` and `Sigma`, plus a Gamma prior on the Block~2 precision $1/\tau_k^2$ calibrated with the same convention as [Prior_Setup](#). The per-component effective prior sample size n_0 is taken from `object$n_prior_dispersion[[k]]` (set by [Prior_Setup_lmebayes](#) via `pwt_dispersion / n_prior_dispersion`, derived from `pwt` by default). Then

$$shape = (n_0 + 1 + p_k)/2, \quad rate = \tau_k^2 (n_0 + p_k - 1)/2,$$

where p_k is the number of Block~2 coefficients for component k (the `shape_ING` convention with the `lmebayesCore` default rate b_0). Because $rate = \tau_k^2(shape - 1)$, the implied inverse-Gamma prior on the dispersion has mean exactly τ_k^2 for every n_0 and p_k , while small `pwt_dispersion` keeps it deliberately diffuse.

The dispersion prior must not outweigh the data: $\backslash eqn\{n_0 \leq J\}$ (equivalently `\code{pwt_dispersion} \backslash eqn\{\leq 0.5\}`) is required, mirroring the sampler-side guard in

plot_sweep_history_diag

Plot Block~2 sweep-history diagnostics (cross-chain mean or SD)

Description

Plots cross-chain Block~2 hyperparameter summaries stored on an object of class "two_block_sweep_history" (typically fit\$sweep_history\$pilot or fit\$sweep_history\$main from [rmlmerb](#), [rglmerb](#), or formula drivers such as `lmerb()` / `glmerb()` in **lmebayes**; see [print.two_block_sweep_history](#)).

Usage

```
plot_sweep_history_diag(
  hist,
  coef_focus,
  what = c("sd", "mean"),
  engine = c("base", "ggplot"),
  stage_label = hist$stage
)
```

Arguments

hist	Object of class "two_block_sweep_history" (see print.two_block_sweep_history).
coef_focus	List of length-2 character vectors <code>c(re_component, covariate)</code> , matching rows of <code>hist\$table</code> . Example: <code>list(c("(Intercept)", "(Intercept)"), c("violent_i", "(Intercept)"))</code> .
what	One or both of "sd" and "mean" (cross-chain summary after each inner sweep). Default both (sd first).
engine	"base" for one panel per coefficient (default), or "ggplot" for a single faceted figure (requires ggplot2).
stage_label	Character label for titles; defaults to <code>hist\$stage</code> .

Value

hist invisibly.

See Also

[rmlmerb](#), [rglmerb](#), [print.two_block_sweep_history](#)

Prior_Check

Checks for Prior-data conflicts

Description

Checks if the credible intervals for the prior overlap with the implied confidence intervals from the classical model (obtained via [glm](#)). The approach relates to prior-data conflict checks (Evans and Moshonov 2006).

Usage

```
Prior_Check(
  formula,
  family,
  pfamily,
  level = 0.95,
  data = NULL,
  weights,
  subset,
  na.action,
  start = NULL,
  etastart,
  mustart,
  offset,
  control = list(...),
  model = TRUE,
  method = "glm.fit",
  x = FALSE,
  y = TRUE,
  contrasts = NULL,
  ...
)
```

Arguments

formula	an object of class " formula " (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
family	a description of the error distribution and link function to be used in the model. For <code>glm</code> this can be a character string naming a family function, a family function or the result of a call to a family function. For <code>glm.fit</code> only the third option is supported. (See family for details of family functions.)
pfamily	a pfamily object specifying the prior distribution to check against the data.
level	the confidence level at which the Prior-data conflict should be checked.

data	an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>glm</code> is called.
weights	an optional vector of ‘prior weights’ to be used in the fitting process. Should be NULL or a numeric vector.
subset	an optional vector specifying a subset of observations to be used in the fitting process. (See additional details about how this argument interacts with data-dependent bases in the ‘Details’ below.)
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the <code>na.action</code> setting of <code>options</code> , and is <code>na.fail</code> if that is unset. The ‘factory-fresh’ default is <code>na.omit</code> . Another possible value is NULL, no action. Value <code>na.exclude</code> can be useful.
start	starting values for the parameters in the linear predictor.
etastart	starting values for the linear predictor.
mustart	starting values for the vector of means.
offset	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more <code>offset</code> terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See <code>model.offset</code> .
control	a list of parameters for controlling the fitting process. For <code>glm.fit</code> this is passed to <code>glm.control</code> .
model	a logical value indicating whether <i>model frame</i> should be included as a component of the returned value.
method	the method to be used in fitting the model. The default method “<code>glm.fit</code>” uses iteratively reweighted least squares (IWLS); the alternative “<code>model.frame</code>” returns the model frame and does no fitting. User-supplied fitting functions can be supplied either as a function or a character string naming a function, with a function which takes the same arguments as <code>glm.fit</code>. If specified as a character string it is looked up from within the stats namespace.
x, y	For <code>glm</code>: logical values indicating whether the response vector and model matrix used in the fitting process should be returned as components of the returned value. For <code>glm.fit</code>: <code>x</code> is a design matrix of dimension $n * p$, and <code>y</code> is a vector of observations of length <code>n</code>.
contrasts	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
...	For <code>glm</code>: arguments to be used to form the default <code>control</code> argument if it is not supplied directly. For weights: further arguments passed to or from other methods.

Value

A vector where each item provided the ratio of the absolute value for the difference between the prior and maximum likelihood estimate divided by the length of the sum of half of the two intervals (where normality is assumed)

References

Evans M, Moshonov H (2006). “Checking for prior-data conflict.” *Bayesian Analysis*, **1**(4), 893–914. doi:[10.1214/06BA129](https://doi.org/10.1214/06BA129).

See Also

[Prior_Setup](#), [rglmb](#); see (Nygren 2025) for prior tailoring; (Nygren 2025) for full derivations.
Other prior: [Prior_Setup\(\)](#), [multi_prior_setup\(\)](#)

Examples

```
## Dobson (1990) Page 93: Randomized Controlled Trial :
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
print(d.AD <- data.frame(treatment, outcome, counts))
## Step 1: Set up Prior
ps=Prior_Setup(counts ~ outcome + treatment)
mu=ps$mu
V=ps$Sigma
# Step2A: Check the Prior
Prior_Check(counts ~ outcome + treatment,family = poisson(),
             pfamily=dNormal(mu=mu,Sigma=V))
# Step2B: Update and Re-Check the Prior
mu[1,1]=log(mean(counts))
Prior_Check(counts ~ outcome + treatment,family = poisson(),
             pfamily=dNormal(mu=mu,Sigma=V))
```

Prior_Setup

Setup Prior Objects

Description

Helper function to facilitate the Setup of Prior Distributions for glm models.

Usage

```
Prior_Setup(
  formula,
  family = gaussian(),
  data = NULL,
  weights = NULL,
```

```

subset = NULL,
na.action = na.fail,
offset = NULL,
contrasts = NULL,
pwt = NULL,
pwt_default_low = 0.01,
pwt_default_high = 0.05,
n_prior = NULL,
sd = NULL,
dispersion = NULL,
intercept_source = c("null_model", "full_model"),
effects_source = c("null_effects", "full_model"),
mu = NULL,
k = 1,
...
)

## S3 method for class 'PriorSetup'
print(x, ...)

```

Arguments

formula	an object of class " formula " (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under 'Details'.
family	a description of the error distribution and link function to be used in the model.
data	an optional data frame, list or environment (or object coercible by as.data.frame to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>glm</code> is called.
weights	an optional vector of 'prior weights' to be used in the fitting process. Should be <code>NULL</code> or a numeric vector.
subset	an optional vector specifying a subset of observations to be used in the fitting process. (See additional details about how this argument interacts with data-dependent bases in the 'Details' below.)
na.action	how NAs are treated. The default is first, any na.action attribute of data, second a <code>na.action</code> setting of options , and third <code>na.fail</code> if that is unset. The factory-fresh default is <code>na.omit</code> . Another possible value is <code>NULL</code> .
offset	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. This should be <code>NULL</code> or a numeric vector of length equal to the number of cases. One or more offset terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See model.offset .
contrasts	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
pwt	Weight on the prior relative to the likelihood function at the maximum likelihood estimate. If supplied, this value is used directly (scalar or one value per

	coefficient). If <code>n_prior</code> is provided and <code>pwt</code> is still a scalar and <code>sd</code> was not supplied, <code>pwt</code> is set to <code>n_prior / (n_prior + n_effective)</code> . If <code>length(pwt) > 1</code> (including from <code>sd</code>) or <code>sd</code> was supplied, <code>n_prior</code> does not overwrite <code>pwt</code> ; it is used only as a scalar for Gamma / S_marg steps. If <code>sd</code> is provided, <code>pwt</code> is computed from the prior standard deviations. If none of these are supplied, <code>pwt</code> defaults to <code>pwt_default_low</code> for models with fewer than 14 coefficients, and <code>pwt_default_high</code> otherwise.
<code>pwt_default_low</code>	Default prior weight used when <code>pwt</code> is not supplied and the model dimension is below 14. Defaults to 0.01.
<code>pwt_default_high</code>	Default prior weight used when <code>pwt</code> is not supplied and the model dimension is 14 or greater. Defaults to 0.05.
<code>n_prior</code>	Optional scalar effective prior sample size (on the <code>n_effective</code> scale). If provided with scalar <code>pwt</code> and without <code>sd</code> , <code>pwt</code> is recomputed from <code>n_prior</code> . With vector <code>pwt</code> or with <code>sd</code> , <code>pwt</code> is left unchanged and <code>n_prior</code> is used for the Gamma prior on precision and related Gaussian calibration only. If missing and <code>pwt</code> is scalar, <code>n_prior = (pwt/(1-pwt))*n_effective</code> .
<code>sd</code>	Optional vector argument with the prior standard deviations for the coefficients
<code>dispersion</code>	Optional scalar dispersion override (default NULL). For now, this is documented as an optional argument used to scale the Sigma (variance-covariance) matrix; see Details for additional context.
<code>intercept_source</code>	Specifies the method through which the prior mean for the intercept term is set. Options are based on the null intercept only model (<code>null_model</code>) or <code>full_models</code> . The default is the null model which is safer if variables are not centered.
<code>effects_source</code>	Specifies the method through which the prior means for the effects terms are set. Options are <code>null_effects</code> (prior means set to zero) or <code>full_model</code> (effect means set to match maximum likelihood estimates).
<code>mu</code>	Optional vector argument with the prior means for the coefficients
<code>k</code>	Scalar (default 1), non-negative ($k \geq 0$), with $k + p \geq 2$ where p is the number of coefficients (columns of the model matrix). k controls the tail behavior and effective degrees of freedom of the variance prior. It does not change the posterior mean of σ^2 or the covariance of β , but larger k makes the prior and posterior for σ^2 more concentrated and less heavy-tailed. Not yet used in calibration; passed through to <code>compute_gaussian_prior</code> for future use.
<code>...</code>	For <code>glm</code> : arguments to be used to form the default <code>control</code> argument if it is not supplied directly. For weights: further arguments passed to or from other methods.
<code>x</code>	An object of class "PriorSetup"

Details

Inputs to the function

The inputs to `Prior_Setup()` fall into three conceptual categories:

1. Model specification

- formula: structure of the GLM (response and predictors).
- family: error distribution and link.
- data, weights, subset, na.action, offset, contrasts, control, ...: as in [glm](#).

2. Prior variance–covariance specification

- pwt: prior weight relative to the likelihood. If scalar, used to construct a Zellner-type g-prior. If vector, applied elementwise.
- n_prior: optional scalar effective prior sample size. Replaces scalar pwt only when pwt is scalar and sd is not used; otherwise supplies precision-prior / calibration only.
- sd: optional vector of prior standard deviations. If provided, used to compute pwt from the diagonal of `vcov(glm_full)`.
- pwt_default_low, pwt_default_high: defaults for pwt when not supplied.

3. Prior mean specification

- intercept_source: method for setting the prior mean of the intercept ("null_model" or "full_model").
- effects_source: method for setting the prior mean of the effects ("null_effects" or "full_model").
- mu: optional user-specified prior mean vector; overrides other centering logic if provided.

Prior covariance and Zellner scaling

Let $V_0 = \text{vcov}(\hat{\beta})$ be the covariance matrix of the full-model GLM coefficients. For non-Gaussian families, the prior covariance is:

$$\Sigma = \begin{cases} \frac{1 - \text{pwt}}{\text{pwt}} V_0, & \text{scalar pwt,} \\ V_0 \circ \left[\sqrt{\frac{1 - \text{pwt}_i}{\text{pwt}_i}} \sqrt{\frac{1 - \text{pwt}_j}{\text{pwt}_j}} \right], & \text{vector pwt,} \end{cases}$$

where $\circ$ denotes elementwise multiplication.

Intercept-only Poisson(link = "identity") conjugate prior on the rate

When the design is a single column (intercept only), `family = poisson()`, `link = "identity"`, scalar pwt, and offsets are zero, the effective conjugate prior observation count n_{prior} already satisfies $n_{\text{prior}} / (n_{\text{prior}} + n_{\text{effective}}) = \text{pwt}$ (otherwise `conj_poisson` remains NULL with a warning). Writing the weighted mean $\bar{y}_w = \sum_i w_i y_i / \sum_i w_i$, the output list component `conj_poisson` stores `shape = n_prior * \bar{y}_w` and `rate = n_prior`, so the prior mean for the rate matches $\bar{y}_w$. Omitting optional `mu` resets the surrogate Normal summaries `mu` and the sole diagonal element of `Sigma` to these Gamma moments (`Sigma_{11} = \bar{y}_w / n_{\text{prior}}`).

For Gaussian families, `Prior_Setup()` also constructs the dispersion-free covariance

$$\Sigma_0 = \Sigma / \text{dispersion},$$

which under scalar pwt and the default calibration reduces to

$$\Sigma_0 = \frac{1 - \text{pwt}}{\text{pwt}} (X^\top W X)^{-1}.$$

Gaussian Normal–Gamma calibration and S_{marg}

For `family = gaussian()`, the function performs the Normal–Gamma calibration described in (Nygren 2025). Let:

- $p = \text{ncol}(x)$,
- $n_{\text{effective}} = \sum_i w_i$,
- $\hat{\beta}$ the weighted least-squares estimator,
- Σ_0 the dispersion-free prior covariance.

The marginal quadratic term is

$$S_{\text{marg}} = \text{RSS}_w + (\hat{\beta} - \mu)^\top (\Sigma_0 + (X^\top W X)^{-1})^{-1} (\hat{\beta} - \mu),$$

where RSS_w is the weighted residual sum of squares at $\hat{\beta}$. Under the default scalar-pwt Zellner mapping $\Sigma_0 = \frac{1-\text{pwt}}{\text{pwt}} (X^\top W X)^{-1}$, this simplifies to

$$S_{\text{marg}} = \text{RSS}_w + \text{pwt} (\hat{\beta} - \mu)^\top (X^\top W X) (\hat{\beta} - \mu),$$

which makes the limiting behavior as $\text{pwt} \rightarrow 0$ transparent.

The calibrated dispersion is

$$\text{dispersion} = \frac{S_{\text{marg}}}{n_{\text{effective}} - p},$$

and the Normal–Gamma hyperparameters are

$$\text{shape} = \frac{n_{\text{prior}} + k}{2}, \quad \text{rate} = \frac{1}{2} S_{\text{marg}} \frac{n_{\text{prior}} + k + p - 2}{n_{\text{effective}} - p}.$$

The independent Normal–Gamma shape is

$$\text{shape}_{\text{ING}} = \text{shape} + \frac{p}{2}.$$

Posterior summaries for the conjugate Normal–Gamma prior

Under the conjugate Normal–Gamma prior (used by `dNormal_Gamma()`), the posterior has:

- Posterior mean

$$E[\beta \mid y] = (1 - \text{pwt}) \hat{\beta} + \text{pwt} \mu.$$

- Posterior expectation of σ^2

$$E[\sigma^2 \mid y] = \frac{S_{\text{marg}}}{n_{\text{effective}} - p}.$$

- Posterior covariance

$$\text{Cov}(\beta \mid y) = E[\sigma^2 \mid y] (\Sigma_0^{-1} + X^\top W X)^{-1}.$$

Weak-prior limits (Theorems 2 and 3)

As $n_{\text{prior}} \rightarrow 0^+$ (equivalently $\text{pwt} \rightarrow 0$), $S_{\text{marg}} \rightarrow \text{RSS}_w$, and the conjugate Normal–Gamma posterior converges to the classical weighted least-squares limit:

$$E[\beta \mid y] \rightarrow \hat{\beta}, \quad E[\sigma^2 \mid y] \rightarrow \frac{\text{RSS}_w}{n_{\text{effective}} - p}, \quad \text{Cov}(\beta \mid y) \rightarrow \frac{\text{RSS}_w}{n_{\text{effective}} - p} (X^\top W X)^{-1}.$$

For the independent Normal–Gamma prior used by `dIndependent_Normal_Gamma()`, neither the posterior mean nor the posterior covariance is available in closed form; the posterior must be obtained by numerical integration or sampling (e.g., `rindepNormalGamma_reg()`). Theorem 3 in (Nygren 2025) shows that the ING posterior has the same weak-prior limit as the conjugate Normal–Gamma posterior:

$$E[\beta \mid y] \rightarrow \hat{\beta}, \quad \text{Cov}(\beta \mid y) \rightarrow \frac{\text{RSS}_w}{n_{\text{effective}} - p} (X^\top W X)^{-1}.$$

Value

A list of class "PriorSetup" with components:

<code>mu</code>	Prior mean vector (length equal to the number of coefficients).
<code>Sigma</code>	Coefficient-scale prior variance–covariance matrix.
<code>Sigma_0</code>	For <code>family = gaussian()</code> only: dispersion-independent prior covariance on the precision-weighted coefficient scale (the <code>Sigma_0</code> passed to <code>compute_gaussian_prior</code>). Under scalar <code>pwt</code> , $\Sigma_0^{-1} = \frac{\text{pwt}}{1-\text{pwt}} X^\top W X$.
<code>dispersion</code>	Calibrated dispersion (Gaussian models only), equal to $S_{\text{marg}}/(n_{\text{effective}} - p)$ under the default calibration.
<code>shape</code>	Derived prior Gamma shape parameter for the Normal–Gamma prior on precision (Gaussian only), $(n_{\text{prior}} + k)/2$.
<code>shape_ING</code>	For <code>gaussian()</code> only when <code>shape</code> is available: dedicated shape parameter for <code>dIndependent_Normal_Gamma()</code> , <code>shape + p/2</code> .
<code>rate</code>	Derived prior Gamma rate parameter (Gaussian only), using the calibrated S_{marg} .
<code>rate_gamma</code>	For <code>gaussian()</code> only, when Gaussian calibration runs: prior Gamma rate for <code>dGamma()</code> / fixed- β use, based on $\text{RSS}_w(\beta_*)$ at the Zellner blend.
<code>coefficients</code>	Named numeric vector of returned coefficient values. For <code>gaussian()</code> with scalar or vector <code>pwt</code> , this is the closed-form posterior-mean blend $(1 - \text{pwt})\hat{\beta} + \text{pwt}\mu$ when inputs are valid; otherwise it falls back to the full-model GLM coefficients.
<code>model</code>	The model frame used to construct the design matrix (if <code>model = TRUE</code>).
<code>x</code>	The model matrix used (if <code>x = TRUE</code>).
<code>y</code>	The response vector used (if <code>y = TRUE</code>).
<code>call</code>	The matched call to <code>Prior_Setup()</code> .
<code>PriorSettings</code>	A list containing prior configuration details, including <code>pwt</code> , <code>n_prior</code> , <code>n_effective</code> , <code>n_likelihood</code> , <code>intercept_source</code> , and <code>effects_source</code> .
<code>conj_poisson</code>	NULL unless <code>family = poisson(link = "identity")</code> with a single-column design (intercept-only), scalar <code>pwt</code> , finite positive scalar <code>n_prior</code> , and negligible offset. Then a named list with conjugate <code>Gamma(shape, rate)</code> hyperparameters on the Poisson rate, with <code>shape = n_prior $\bar{y}_w$</code> , <code>rate = n_prior</code> , and <code>beta</code> centered at the weighted sample mean $\bar{y}_w$; pass to <code>dGamma</code> with <code>Inv_Dispersion = FALSE</code> . See Details.

References

Nygren K (2025). “Chapter A12: Technical Derivations for Priors Returned by Prior_Setup.” Vignette in the glmbayes R package. R vignette name: Chapter-A12.

See Also

[pfamily](#) for prior-family objects and the constructors [dNormal](#), [dNormal_Gamma](#), [dGamma](#), and [dIndependent_Normal_Gamma](#).

[rglmb](#), [rlmb](#) for matrix-input fits with a pfamily built from Prior_Setup() output; [rglmb](#), [rlmb](#) for matrix-based sampling that consumes the same prior structure; [simfuncs](#) for functions that take a prior_list assembled from those components (including [rindepNormalGamma_reg](#) for [dIndependent_Normal_Gamma\(\)](#)). [multi_prior_setup](#) for a matrix/cbind response with Gaussian; use with [rlmb](#) Prior_Setup per column.

(Zellner 1986); (Raiffa and Schlaifer 1961); (Gelman et al. 2013); (McCullagh and Nelder 1989); (Nygren 2025); (Nygren 2025).

Other prior: [Prior_Check\(\)](#), [multi_prior_setup\(\)](#)

Examples

```
## Dobson (1990) Page 93: Randomized Controlled Trial :
counts <- c(18, 17, 15, 20, 10, 20, 25, 13, 12)
outcome <- gl(3, 1, 9)
treatment <- gl(3, 3)
print(d.AD <- data.frame(treatment, outcome, counts))

## Set up Prior for Poisson Model
ps <- Prior_Setup(counts ~ outcome + treatment, family = poisson())
ps

## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.
ctl <- c(4.17, 5.58, 5.18, 6.11, 4.50, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)

## Set up prior for gaussian model
ps2 <- Prior_Setup(weight ~ group, family = gaussian())
ps2

## -----
## Matrix-input bridge: use Prior_Setup outputs with rglmb() and rlmb()
## -----
y <- ps2$y
x <- as.matrix(ps2$x)
wt <- rep(1, length(y))

rglmb.D9 <- rglmb(
  n = 1000,
  y = y,
```

```

    x = x,
    pfamily = dIndependent_Normal_Gamma(
      ps2$mu,
      ps2$Sigma,
      shape = ps2$shape_ING,
      rate = ps2$rate
    ),
    weights = wt,
    family = gaussian()
  )

r1mb.D9 <- r1mb(
  n = 1000,
  y = y,
  x = x,
  pfamily = dIndependent_Normal_Gamma(
    ps2$mu,
    ps2$Sigma,
    shape = ps2$shape_ING,
    rate = ps2$rate
  ),
  weights = wt
)

## -----
## Prior-list templates for lower-level samplers
## -----
prior_list_rNormalGamma <- list(
  mu = ps2$mu,
  Sigma = ps2$Sigma_0,
  shape = ps2$shape,
  rate = ps2$rate
)

prior_list_rindepNormalGamma <- list(
  mu = ps2$mu,
  Sigma = ps2$Sigma,
  dispersion = ps2$dispersion,
  shape = ps2$shape_ING,
  rate = ps2$rate,
  Precision = solve(ps2$Sigma),
  max_disp_perc = 0.99
)

rate_dg <- if (!is.null(ps2$rate_gamma)) ps2$rate_gamma else ps2$rate
prior_list_rGamma <- list(
  beta = ps2$coefficients,
  shape = ps2$shape,
  rate = rate_dg
)

## Note: for a full dGamma run across rGamma_reg/rg1mb/r1mb, see:
## example("summary.rGamma_reg")

```

```
## -----
## dGamma prior illustration: Prior_Setup(shape, rate_gamma or rate) + fixed beta
## -----
out.rGamma_reg <- rGamma_reg(
  n = 1000,
  y = y,
  x = x,
  prior_list = prior_list_rGamma,
  offset = rep(0, length(y)),
  weights = wt,
  family = gaussian()
)

## -----
## Poisson(link = "identity"), intercept-only: `conj_poisson` + dGamma(Inv_Dispersion=FALSE)
## -----
y_p <- c(rep(1L, 3L), rep(0L, 6L))
df_p <- data.frame(y = y_p)
ps_p <- Prior_Setup(
  y ~ 1,
  family = poisson(link = "identity"),
  data = df_p,
  pwt = 0.4
)
if (!is.null(ps_p$conj_poisson)) {
  cp <- ps_p$conj_poisson
  pf_conj <- dGamma(shape = cp$shape, rate = cp$rate, beta = cp$beta, Inv_Dispersion = FALSE)
  ## rgldb(n = 500, y = ps_p$y, x = as.matrix(ps_p$x),
  ##   pfamily = pf_conj, family = poisson(link = "identity"), weights = rep(1, length(ps_p$y)))
}
```

Prior_Setup_lmebayes *Prior setup for the two-block Gibbs lmebayes sampler*

Description

Calibrates priors for the level-2 fixed effects (fixef) of a hierarchical mixed model using the reference lmer/glmer fits on **all** groups (from [model_setup](#)). Per-group design rank (re_rank) is a diagnostic check only and does not subset the data. For family = binomial(), Prior_Setup_lmebayes() also fits a classical glm within each algebraically full-rank group and records design\$re_estimable (whether a finite MLE exists); this does not subset the reference glmer fit. Random-effect variances are treated as fixed at their mixed-model estimates. The returned object two-block Gibbs sampler:

Usage

```
Prior_Setup_lmebayes(
  formula,
  data,
```

```

family = gaussian(),
pwt = 0.01,
pwt_dispersion = NULL,
n_prior_dispersion = NULL,
pwt_measurement = NULL,
n_prior_measurement = NULL,
dispformula = ~1,
max_disp_perc = 0.99,
intercept_source = c("null_model", "full_model"),
effects_source = c("null_effects", "full_model")
)

## S3 method for class 'lmebayes_prior_setup'
print(x, digits = 4L, ...)

```

Arguments

formula	Mixed-model formula passed to <code>model_setup</code> , whose reference lmer/glmer fits (all groups) supply the calibration quantities.
data	Data frame containing all variables in formula.
family	Model <code>family</code> . Default <code>gaussian()</code> . Non-Gaussian families use <code>glmer</code> for calibration; <code>dispersion_ranef</code> is omitted (analogous to <code>Prior_Setup</code> for flat GLMs).
pwt	Prior weight(s) in (0, 1). Either a scalar (applied to every random-effect component and every Block~2 predictor), or a list with one element per random-effect component (named with the RE coefficient names in any order, or unnamed positional). Each list element is a scalar (recycled over that component's Block~2 predictors) or a vector of length p_k (optionally named with the predictor column names of <code>X_hyper[[k]]</code> , reordered to match). The prior covariance for each <code>fixef_k</code> block is scaled relative to <code>vcov(fit_ref)</code> following the <code>Prior_Setup</code> convention: $(1 - \text{pwt})/\text{pwt}$ for a scalar, and elementwise $\sqrt{(1 - \text{pwt}_i)/\text{pwt}_i} \sqrt{(1 - \text{pwt}_j)/\text{pwt}_j}$ for vectors.
pwt_dispersion	Optional <i>relative</i> prior weight(s) in (0, 1) for the Block~2 dispersion (precision) prior, decoupled from pwt. A scalar, or a list / numeric vector with one value per random-effect component (named or positional). Converted internally to an effective prior sample size $n_k = J w_k / (1 - w_k)$ where J is the number of groups. At most one of <code>pwt_dispersion</code> and <code>n_prior_dispersion</code> may be supplied; when neither is, the value is derived from pwt (the mean across a component's predictors), keeping the Block~2 τ_k^2 dispersion prior consistent with the coefficient prior strength. Weak values carry no computational penalty for <code>dIndependent_Normal_Gamma</code> sampling: the τ^2 truncation window comes from limiting-posterior quantiles independent of the prior strength (see <code>ing_prior</code> below).
n_prior_dispersion	Optional <i>absolute</i> effective prior sample size(s) (in group units) for the Block~2 τ_k^2 dispersion prior. A positive scalar, or a list / numeric vector with one value per random-effect component (named or positional). See <code>pwt_dispersion</code> .

pwt_measurement	Optional relative prior weight(s) in (0, 1) for the Block~1 observation σ^2 Gamma prior (Gaussian models only), decoupled from pwt (Block~2 fixef) and from pwt_dispersion (Block~2 τ_k^2). Either a scalar converted to $n_{\text{prior}} = w/(1 - w) \times n$ on the total observation count n (pooled ing_prior_measurement), or a named or positional vector of length J ($J = \text{nlevels}(\text{groups})$) with one weight per group level for per-group dGamma_list() calibration ($n_{\text{prior},j} = w_j/(1 - w_j) \times n_j$). When pwt_measurement is a vector, the pooled ing_prior_measurement continues to use the default $w = 0.01$ on total n (unless n_prior_measurement is supplied explicitly). At most one of pwt_measurement and n_prior_measurement may be supplied; when neither is, scalar pwt_measurement = 0.01 is used for both pooled and per-group paths.
n_prior_measurement	Optional positive scalar: absolute effective prior sample size for the Block~1 σ^2 prior (observation units, not groups). See pwt_measurement.
dispformula	One-sided formula selecting the Block~1 measurement- dispersion structure: ~1 (default, pooled) or ~<group_name> (matching the random-effects grouping factor exactly, requesting per-group dispersion). Gaussian models only compute the per-group ing_prior_measurement_group calibration (a within-group regression fit for every group level, used only by dGamma_list()) when dispformula is the group formula; dispformula = ~1 skips it entirely, so pwt_measurement / n_prior_measurement must then be scalar (pooled). Mirrors the dispformula argument on lmerb()/glmerb() in lmebayes, which gates the analogous choice of sampler route; the two are independent arguments that must be kept consistent by the caller.
max_disp_perc	Scalar in (0.5, 1), default 0.99. Tail probability used to compute the σ^2 (Block~1) and τ_k^2 (Block~2) truncation windows stored in ing_prior_measurement and ing_prior respectively. The window is the central $2 \times \text{max_disp_perc} - 1$ mass interval: $\text{disp_lower} = (1 - \text{max_disp_perc})$ quantile and $\text{disp_upper} = \text{max_disp_perc}$ quantile of the relevant Gamma (precision) distribution, inverted to the dispersion scale. Tighter values (e.g. 0.95) shrink the truncation window and typically improve Block~1 acceptance rates at the cost of slightly less envelope coverage; looser values (e.g. 0.999) widen the window. Passed to dGamma() as max_disp_perc.
intercept_source	Character string controlling the prior mean for the global intercept hyperparameter (Intercept)::(Intercept) only. One of "null_model" (default) or "full_model". When "null_model", the prior mean is taken from a random-intercept-only reference fit $y \sim 1 + (1 \mid \text{group})$ that omits all fixed-effect predictors (analogous to Prior_Setup with intercept_source = "null_model"). When "full_model", the full-model MLE intercept is used.
effects_source	Character string controlling the prior mean for all other Block~2 hyperparameters (including population-mean slopes stored as (Intercept) columns in non-intercept RE components, and any non-intercept columns in X_hyper). One of "null_effects" (default) or "full_model". When "null_effects", prior means are set to zero. When "full_model", full-model MLE values are used.
x	Object of class "lmebayes_prior_setup".

digits	Number of decimal places for numeric output. Default 4.
...	Ignored.

Details

Block 1 (per-group, independent):

$$p(\mathbf{b}_j \mid \mathbf{y}, \text{fixef}, \sigma^2, \Sigma_b) = \mathcal{N}(\boldsymbol{\mu}_{b,j}^*, \Sigma_{b,j}^*)$$

$$\Sigma_{b,j}^{*-1} = \mathbf{Z}_j' \mathbf{Z}_j / \sigma^2 + \text{diag}(1/\tau_k^2)$$

when family = gaussian(). For non-Gaussian families there is no observation-level dispersion; Block~1 uses dNormal with ddef = TRUE (see [dNormal](#)).

Block 2 (per-RE coefficient k , independent):

$$p(\text{fixef}_k \mid \mathbf{b}_k, \tau_k^2) = \mathcal{N}(\boldsymbol{\mu}_{\text{fixef},k}^*, \Sigma_{\text{fixef},k}^*)$$

$$\Sigma_{\text{fixef},k}^{*-1} = \mathbf{X}_k' \mathbf{X}_k / \tau_k^2 + \Sigma_{\text{fixef},k}^{-1}$$

Why default calibration depends on classical estimates. Prior_Setup_lmebayes scales Block~2 covariances from vcov(fit_ref) by $(1 - \text{pwt})/\text{pwt}$ and plugs in RE variances from the full reference fit, where fit_ref is the pooled lmer/glmer fit when dispformula = ~1, or an equivalent glmmTMB fit with the same dispformula when per-group dispersion is requested (see calibration_source and mer_fit above). By default the global intercept prior mean comes from a random-intercept-only null fit; all other prior means are zero (effects_source = "null_effects"). This requires:

1. Converged reference lmer/glmer fit from [model_setup](#) on the full formula (and a random-intercept-only null fit when intercept_source = "null_model"). Fits with lme4 checkConv failures (e.g. \large max|grad|) are rejected.
2. Every X_hyper[[k]] column maps to a fixef(fit_ref) term.
3. Each RE variance τ_k^2 from the reference fit is strictly positive.

Value

Object of class "lmebayes_prior_setup" with fields:

formula Model formula.

family Family object.

pwt Prior weight(s) used: the scalar as supplied, or the canonical named list of per-predictor weight vectors when a list was supplied.

pwt_dispersion Named per-component vector of relative dispersion prior weights (always present; consistent with n_prior_dispersion via $w_k = n_k/(n_k + J)$).

n_prior_dispersion Named per-component vector of effective prior sample sizes for the Block~2 dispersion prior (always present; used by [pfamily_list](#)() to calibrate dIndependent_Normal_Gamma components).

pwt_measurement Gaussian models only: scalar or length- J vector of relative prior weights for Block~1 σ^2 .

- `n_prior_measurement` Gaussian models only: scalar effective prior sample size for pooled Block~1 σ^2 on the observation scale.
- `pwt_measurement_group` Gaussian models only: named length- J vector of resolved per-group measurement prior weights (see `dGamma_list()`).
- `n_prior_measurement_group` Gaussian models only: named length- J vector of per-group $n_{\text{prior},j}$.
- `block_formula` Within-group Block~1 formula: response regressed on the random-coefficient structure only (columns of `design$re_coef_names`); level-2 hyper covariates are excluded. Used by `dGamma_list()`.
- `sd_tau` Named vector `sqrt(vcov_re)` from the reference fit; shared population RE standard deviations for per-group calibration.
- `data` Data frame passed to `Prior_Setup_lmebayes()` (reference for `dGamma_list()` diagnostics).
- `max_disp_perc` The `max_disp_perc` value used for both the σ^2 and τ_k^2 truncation windows.
- `design` Full `model_setup` object (all groups).
- `mer_fit` Reference lmer/glmer fit on all groups (the full-formula fit from `model_setup`), always present regardless of `dispformula` (backs `dispersion_ranef` and `x$lmer/x$glmer` in `lmerb()/glmerb()`).
- `fit_ref` The calibration reference for Block~2 (`fixef/ $\tau_k^2$`) and the per-group Block~1 inputs (`sd_tau`, BLUP coefficients): identical to `mer_fit` when `dispformula = ~1`; otherwise an equivalent `glmmTMB` fit with the same `dispformula` (Gaussian models only). See `calibration_source`.
- `dispersion_fit` NULL when `dispformula = ~1`; otherwise the same `glmmTMB` object as `fit_ref`.
- `sigma2_group` NULL when `dispformula = ~1`; otherwise a named length- J vector of per-group observation-level dispersion read from `fit_ref`'s dispersion linear predictor (`glmmTMB::predict(fit_ref, type = "disp")`, aggregated by group). Diagnostic only – not the value fed to the sampler; compare against `ing_prior_measurement_group`'s `sigma2_hat`.
- `calibration_source` "lme4" or "glmmTMB"; which reference fit produced `fit_ref` (and therefore `prior_list`, `ing_prior`, `sd_tau`, and `ing_prior_measurement_group`).
- `dispersion_ranef` Scalar σ^2 for Gaussian models only; NULL otherwise. Always derived from `mer_fit` (pooled), independent of `dispformula`.
- `Sigma_ranef` Diagonal RE covariance matrix (Block~1).
- `prior_list` Named Block~2 prior list per RE coefficient.
- `ing_prior` Named per-component list of the prospective `dIndependent_Normal_Gamma` calibration: Gamma precision-prior shape = $(n_0 + 1 + p_k)/2$ and rate = $\hat{\tau}_k^2(n_0 + p_k - 1)/2$ (the `lmebayesCore` default calibration with $n_0 = n_prior_dispersion$; since rate = $\hat{\tau}_k^2(\text{shape} - 1)$, the implied inverse-Gamma prior on τ_k^2 has mean exactly $\hat{\tau}_k^2$), and the default τ_k^2 truncation window `disp_lower / disp_upper`: the $(1 - \text{max_disp_perc}) / \text{max_disp_perc}$ quantiles of the *limiting posterior* $\Gamma((J + 1)/2, \hat{\tau}_k^2(J - 1)/2)$ – the weak-prior ($n_0 \rightarrow 0$) limit of the Block~2 posterior Gamma for the precision (`lmebayesCore` Chapter A12, Theorem 2; inverted to a τ^2 interval). This window is identical for all n_0 , covers $\geq 2 \times \text{max_disp_perc} - 1$ of the exact posterior for every prior strength, and keeps the envelope sampler's cost stable as priors weaken; see `inst/ING_TRUNCATION_WINDOW.md`. Used by `pfamily_list()` when `ptypes = "dIndependent_Normal_Gamma"`; ignored for `dNormal` priors.
- `ing_prior_measurement` Gaussian models only: prospective `dGamma()` `dispersion_ranef` calibration for Block~1 ING (observation σ^2 shared across all group levels): mean-matched

shape / rate with $n_{\text{prior}} = \text{pwt_measurement} / (1 - \text{pwt_measurement}) \times n$, $p = p_{\text{re}}$, and $\hat{\sigma}^2 = \text{dispersion_ranef}$ (same ING algebra as `ing_prior` for τ_k^2 ; requires `pwt_measurement` ≤ 0.5), plus `disp_lower` / `disp_upper` as the central $2 \times \text{max_disp_perc} - 1$ prior-mass interval from the same calibrated shape/rate. Pass these fields to `dGamma()`.

`ing_prior_measurement_group` Gaussian models only, and only when `dispformula` requests per-group dispersion: named list (one entry per group level) of per-group `dGamma()` density calibration (`sigma2_hat`, `shape_ING`, `rate_gamma`, `n_prior`, `n_j`, `n_combined`, ...). NULL when `dispformula = ~1`. Used by `dGamma_list()`; truncation bounds are assembled there.

`dispformula` The `dispformula` supplied.

`x` invisibly.

See Also

[model_setup](#), [Prior_Setup](#), [build_mu_all](#)

residuals.rglmb

Deviance Residuals for rglmb and summary.rglmb Objects

Description

Returns a matrix of deviance residuals across posterior draws, using the fitted object's `family$dev.resids` function as in [residuals.glm](#).

Usage

```
## S3 method for class 'rglmb'
residuals(object, ysim = NULL, ...)

## S3 method for class 'summary.rglmb'
residuals(object, ysim = NULL, ...)

## S3 method for class 'rlmb'
residuals(object, ysim = NULL, ...)
```

Arguments

<code>object</code>	an object of class <code>rglmb</code> , <code>rlmb</code> , or <code>summary.rglmb</code> .
<code>ysim</code>	optional simulated responses (matrix with one row per draw).
<code>...</code>	further arguments (currently unused).

Value

A numeric matrix of deviance residuals with one row per draw.

See Also

[rglmb](#), [summary.rglmb](#), [residuals.glm](#).

Description

rglmb is used to generate iid samples for Bayesian Generalized Linear Models. The model is specified by providing a data vector, a design matrix, the family (determining the likelihood function) and the pfamily (determining the prior distribution).

Usage

```
rglmb(
  n = 1,
  y,
  x,
  family = gaussian(),
  pfamily,
  offset = NULL,
  weights = 1,
  Gridtype = 2,
  n_envopt = NULL,
  use_parallel = TRUE,
  use_opengl = FALSE,
  verbose = FALSE
)

## S3 method for class 'rglmb'
print(x, digits = max(3, getOption("digits") - 3), ...)
```

Arguments

n	number of draws to generate. If <code>length(n) > 1</code> , the length is taken to be the number required.
y	a vector of observations of length m.
x	for <code>rglmb</code> a design matrix of dimension $m \times p$ and for <code>print.rglmb</code> the object to be printed.
family	a description of the error distribution and link function to be used in the model.
pfamily	a description of the prior distribution (see pfamily).
offset	this can be used to specify an a priori known component to be included in the linear predictor.
weights	an optional vector of prior weights to be used in the fitting process.
Gridtype	an optional argument specifying the method used to determine tangent points for the envelope.
n_envopt	Effective sample size passed to <code>EnvelopeOpt</code> for grid construction. Defaults to match n. Larger values encourage tighter envelopes.

<code>use_parallel</code>	Logical. Whether to use parallel processing during simulation.
<code>use_opengl</code>	Logical. Whether to use OpenGL acceleration during Envelope construction.
<code>verbose</code>	Logical. Whether to print progress messages.
<code>digits</code>	the number of significant digits to use when printing.
<code>...</code>	further arguments passed to or from other methods.

Details

The function `rglmb` is a minimalistic engine for Bayesian generalized linear model simulation. It is designed to generate independent draws from the posterior distribution of a GLM, given a design matrix. Unlike formula-based interfaces in **glmbayes**, `rglmb` operates directly on numeric inputs and is optimized for speed, transparency, and integration into simulation workflows.

The original R implementation of `glm` was written by Simon Davies (under Ross Ihaka at the University of Auckland) and has since been extensively rewritten by members of the R Core Team; its design was inspired by the S function described in (Hastie and Pregibon 1992), which in turn relies on the formula framework described in (Wilkinson and Rogers 1973).

The design of the `pfamily` family of functions was created by Kjell Nygren and is modeled on how `glm` uses `family` to specify the likelihood. For any implemented combination of family, link, and `pfamily`, `rglmb` generates independent draws from the posterior density-no MCMC chains are required.

A helper, `Prior_Setup`, assists users in choosing prior parameters. It ships with sensible defaults but also allows full customization. In particular, the default for `dNormal` is a reparameterization of Zellner's g-prior (Zellner 1986).

Currently supported response families are `gaussian` (identity link), `poisson` and `quasipoisson` (log link), `gamma` (log link), and `binomial` and `quasibinomial` (logit, probit, cloglog). All families support a `dNormal` prior; the Gaussian family also offers `dNormalGamma` and `dIndependent_Normal_Gamma`.

For the Gaussian family, draws under `dNormal` and `dNormalGamma` come from posterior distributions resulting from conjugate prior distributions (Raiffa and Schlaifer 1961). For all other priors or response families, we use an accept-reject sampler built on the likelihood-subgradient envelope method (Nygren and Nygren 2006). The `Gridtype` argument controls how many tangent points are used in the envelope-trading off envelope tightness against construction cost-and `iters` reports candidate counts before acceptance.

By default, `rglmb` draws `n = 1` sample, uses parallel CPU simulation, and-if `use_opengl = TRUE`-GPU-accelerated envelope building. The function returns a list containing posterior samples, prior specifications, dispersion estimates, and the envelope used during sampling. It does not return a full model object, and does not support formula-based modeling or method dispatch. It is intended for Gibbs sampling implementations or other workflows where full model reconstruction is unnecessary.

Value

`rglmb` returns a object of class `"rglmb"`. The generic accessor functions `coefficients` and `fitted.values` can be used to extract useful features of the value returned by `rglmb`. An object of class `"rglmb"` is a list containing at least the following components:

`coefficients` a matrix of dimension `n` by `length(mu)` with one sample in each row

coef.mode	a vector of length(mu) with the estimated posterior mode coefficients
dispersion	Either a constant provided as part of the call, or a vector of length n with one sample in each row.
Prior	A list with the priors specified for the model in question. Items in the list may vary based on the type of prior
prior.weights	a vector of weights specified or implied by the model
y	a vector with the dependent variable
x	a matrix with the implied design matrix for the model
famfunc	Family functions used during estimation process
iters	an n by 1 matrix giving the number of candidates generated before acceptance for each sample.
Envelope	the envelope that was used during sampling

Objects of class "rglmb" are normally of class `c("rglmb", "glmb", "glm", "lm")`, meaning they inherit from `glmb`, `glm`, and `lm`. This allows methods defined for these upstream classes to be applied to "rglmb" objects when appropriate, while supporting extensions for regularized Bayesian GLMs with structured priors.

Author(s)

The R implementation of `rglmb` has been written by Kjell Nygren and was built to be a Bayesian version of the `glm` function but with a more minimalistic interface than a formula wrapper. It also borrows some of its structure from other random generating function like `rnorm` and hence the `r` prefix.

References

- Hastie T~J, Pregibon D (1992). "Generalized Linear Models." In Chambers J~M, Hastie T~J (eds.), *Statistical Models in S*, chapter 6. Wadsworth & Brooks/Cole, Belmont, CA.
- Nygren K~N, Nygren L~M (2006). "Likelihood Subgradient Densities." *Journal of the American Statistical Association*, **101**(475), 1144–1156. doi:[10.1198/016214506000000357](https://doi.org/10.1198/016214506000000357).
- Raiffa H, Schlaifer R (1961). *Applied Statistical Decision Theory*. Clinton Press, Inc., Boston.
- Wilkinson GN, Rogers CE (1973). "Symbolic Descriptions of Factorial Models for Analysis of Variance." *Applied Statistics*, **22**(3), 392–399. doi:[10.2307/2346786](https://doi.org/10.2307/2346786).
- Zellner A (1986). "On Assessing Prior Distributions and Bayesian Regression Analysis with g-Prior Distributions." In Goel P~K, Zellner A (eds.), *Bayesian Inference and Decision Techniques: Essays in Honor of Bruno de Finetti*, volume 6 of *Studies in Bayesian Econometrics and Statistics*, 233–243. Elsevier.

See Also

`r1mb` for the Gaussian specialization; `lm` and `glm` for classical modeling functions.

[EnvelopeBuild](#), [EnvelopeSize](#), [EnvelopeEval](#) for envelope construction and grid evaluation used in non-conjugate sampling.

[family](#) for documentation of family functions used to specify priors. [pfamily](#) for documentation of pfamily functions used to specify priors.

[Prior_Setup](#), [Prior_Check](#) for functions used to initialize and to check priors,

Further reading: (Nygren and Nygren 2006); (Nygren 2025, 2025); OpenCL/GPU: (Nygren 2025, 2025). [summary.rglmb](#) and [residuals.rglmb](#) provide posterior summaries for matrix-input fits; additional formula-based methods are in **glmbayes**.

glmbayes Modeling Functions [multi_rlmb\(\)](#), [rlmb\(\)](#)

Examples

```
set.seed(333)
## Dobson (1990) Page 93: Randomized Controlled Trial :
counts <- c(18, 17, 15, 20, 10, 20, 25, 13, 12)
outcome <- gl(3, 1, 9)
treatment <- gl(3, 3)
print(d.AD <- data.frame(treatment, outcome, counts))

## Classical Model
glm.D93 <- glm(counts ~ outcome + treatment, family = poisson(link = log))
summary(glm.D93)

## Poisson prior and rglmb (Prior_Setup supplies default g-prior hyperparameters)
ps <- Prior_Setup(counts ~ outcome + treatment, family = poisson(), data = d.AD)
rglmb.D93 <- rglmb(
  n = 1000,
  y = ps$y,
  x = as.matrix(ps$x),
  pfamily = dNormal(mu = ps$mu, Sigma = ps$Sigma),
  family = poisson(),
  weights = rep(1, nrow(ps$x))
)
print(rglmb.D93)

## Menarche model with informative prior. See \code{\link{Prior_Setup}}
## for default g-priors; fitted curves for the menarche data are shown below.
## See \code{vignette("Chapter-05", package = "glmbayes")}
## and \code{vignette("Chapter-06", package = "glmbayes")}.
data(menarche, package = "MASS")

summary(menarche)
design_df <- data.frame(
  Age = menarche$Age,
  Age2 = menarche$Age - 13,
  Proportion = menarche$Menarche / menarche$Total,
  Total = menarche$Total
)
x <- model.matrix(~ Age2, data = design_df)
y <- design_df$Proportion
```

```

wt <- design_df$Total

# Extract coefficient names from design matrix
coef_names <- colnames(x)

# Set up prior mean with names
mu <- matrix(0, nrow = length(coef_names), ncol = 1)
mu[2, 1] <- (log(0.9 / 0.1) - log(0.5 / 0.5)) / 3
rownames(mu) <- coef_names

# Set up prior covariance matrix with named rows and columns
V1 <- 1 * diag(as.numeric(2.0))

# 2 standard deviations for prior estimate at age 13 between 0.1 and 0.9
## Specifies uncertainty around the point estimates
V1[1, 1] <- ((log(0.9 / 0.1) - log(0.5 / 0.5)) / 2)^2
V1[2, 2] <- (3 * mu[2, 1] / 2)^2 # Allows slope to be up to 3 times as large as point estimate
rownames(V1) <- coef_names
colnames(V1) <- coef_names

out <- rglmb(
  n = 1000, y = y, x = x, pfamily = dNormal(mu = mu, Sigma = V1), weights = wt,
  family = binomial(logit)
)
print(out)

## rglmb with dGamma prior (dispersion-only; coefficients fixed)
ctl <- c(4.17, 5.58, 5.18, 6.11, 4.50, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)
ps_dg <- Prior_Setup(weight ~ group, family = gaussian())
rate_dg <- if (!is.null(ps_dg$rate_gamma)) ps_dg$rate_gamma else ps_dg$rate
out_dGamma <- rglmb(
  n = 100, y = ps_dg$y, x = as.matrix(ps_dg$x),
  pfamily = dGamma(shape = ps_dg$shape, rate = rate_dg, beta = ps_dg$coefficients),
  weights = rep(1, length(ps_dg$y)), family = gaussian()
)
print(out_dGamma)

```

Description

Bayesian generalized linear mixed-effects model sampler

Usage

```
rglmerb(
```

```

n,
design,
prior,
family = poisson(),
dispersion_ranef = NULL,
gap_tol = 0.0196,
tv_tol = 0.01,
mode_gap_max = 1,
collect_block1 = TRUE,
verbose = TRUE,
progbar = FALSE
)

```

Arguments

n	Integer. Number of independent chains in the main stage.
design	A model_setup object (from model_setup).
prior	A normalized prior container with Sigma_ranef, prior_list, and pfamily_list.
family	A family object. Default poisson().
dispersion_ranef	Observation-level measurement dispersion σ^2 : required positive scalar for family = gaussian(), or a dGamma() pfamily with Inv_Dispersion = TRUE; must be NULL (default) for poisson() and binomial().
gap_tol	Legacy mode-mean gap for deriving the pilot chain count when tv_tol is NULL. Ignored for Gaussian without ING Block~2 components.
tv_tol	Total variation tolerance for convergence calibration. Inner Gibbs sweeps and pilot chain counts are derived internally.
mode_gap_max	Pilot inner-sweep calibration (non-Gaussian and Gaussian+ING only).
collect_block1	Collect Block~1 coefficients from main chains (non-Gaussian only).
verbose	Print stage headers and diagnostics.
progbar	Progress bars when verbose is FALSE.

Details

Matrix-level sampler for model_setup design objects and normalized prior containers. Routes by response family:

- family = gaussian() delegates to [rLMMNormal_reg_known_vcov](#), [rLMMNormal_reg_estimated_vcov](#), [rLMMIndepNormalGamma_reg_known_vcov](#), or [rLMMIndepNormalGamma_reg_estimated_vcov](#) according to dispersion_ranef and Block~2 pfamily_list.
- Non-Gaussian families delegate via [rGLMM_reg](#) routes (through internal .lmebayes_run_glmm_engine() and REG_ROUTE_TABLE; pilot stage always unless n_pilot = 0L; routes differ in eigenvalue-bound complexity). Inner sweeps use [rGLMM_sweep](#).

For formula-level fitting, glmerb() in the lmebayes package wraps this sampler. Design matrices are built with [model_setup](#) and priors with [Prior_Setup_lmebayes](#).

Value

Object of class `c("rglmerb", "list")` with `Block~2` fields in the `fixef.*` namespace, plus `ranef.mode`, `sigma2` (Gaussian only: scalar or length-`n` vector as for [rmerb](#)), `sigma2.mean`, `Prior`, `design`, and `family`. When a pilot stage runs (ING `Block~2` and/or `dGamma` measurement dispersion), `n_pilot`, `pilot`, and `pilot_chisq` are included; otherwise `n_pilot` is `0L`.

See Also

[rmerb](#), [rLMMNormal_reg_known_vcov](#), [rLMMNormal_reg_estimated_vcov](#), [rLMMindepNormalGamma_reg_known_vcov](#), [rLMMindepNormalGamma_reg_estimated_vcov](#), [rGLMM_reg](#), [Prior_Setup_lmebayes](#)

rGLMM_Re_Draw

*Block~1 random-effect redraw for replicate chains***Description**

Runs one [block_rNormalGLM](#) or [block_rNormalReg](#) envelope draw per chain from prepared `Block~1` `prior_list` objects. This is the `Block~1` draw step inside [rGLMM_sweep](#) after per-chain prep (`fixef` → `mu_all`, τ^2 refresh of `P`).

Usage

```
rGLMM_Re_Draw(
  n,
  prior_lists,
  design,
  family,
  progbar = FALSE,
  progbar_prefix = "",
  progbar_finish_newline = TRUE
)
```

Arguments

<code>n</code>	Integer. Number of independent chains; must equal <code>length(prior_lists)</code> .
<code>prior_lists</code>	List of length <code>n</code> . Each element is a <code>Block~1</code> <code>prior_list</code> with <code>mu</code> (<code>p_re</code> × <code>J</code> matrix, rows = <code>re_names</code> , columns = group levels in block order), <code>P</code> (<code>p_re</code> × <code>p_re</code> precision matrix), dispersion, and optional <code>ddef</code> . Typically built by the prep step that pairs <code>fixef[[k]][i,]</code> with <code>tau2[i, k]</code> for chain <code>i</code> .
<code>design</code>	List with at least <code>y</code> (response), <code>Z</code> (level-1 design, <code>l2</code> × <code>p_re</code>), and groups (block partition of length <code>l2</code>). Same layout as the <code>design</code> argument to rGLMM_sweep .
<code>family</code>	A family object. When <code>gaussian()</code> , uses block_rNormalReg ; otherwise block_rNormalGLM with default offset zero and unit weights.
<code>progbar</code>	Logical. When <code>TRUE</code> and <code>n > 1</code> , show a text progress bar over chains. Default <code>FALSE</code> .

`progbar_prefix` Character prefix for progress-bar lines. Default `""`.
`progbar_finish_newline` Logical. Print a newline after the progress bar finishes. Default `TRUE`.

Details

Each draw uses $n = 1L$ per chain. Outputs are raw block-sampler results; reorder rows of `$coefficients` to `group_levels` and summarize envelope iterations separately (as `rGLMM_sweep` does after this step).

Value

List of length n . Each element is a `block_rNormalGLM` or `block_rNormalReg` object (`$coefficients`, `$coef.mode`, `$block_info`, `$block_results`, ...).

See Also

[rGLMM_sweep](#), [block_rNormalGLM](#), [block_rNormalReg](#)
[glmbayes](#) Simulation Functions [multi_rNormal_reg\(\)](#), [multi_rlmb\(\)](#), [rGLMM_reg\(\)](#), [rGLMM_sweep\(\)](#), [rLMM_reg](#), [rindpNormalGamma_reg_with_envelope\(\)](#), [simfuncs](#), [two_block_optimize_pilot_cost\(\)](#), [two_block_rNormal_reg\(\)](#), [two_block_rate\(\)](#), [two_block_tv_bound\(\)](#)

rGLMM_reg

Matrix-level replicate-chain Gibbs engines for Bayesian GLMMs

Description

Non-Gaussian (and optionally Gaussian) two-block GLMM samplers at matrix level. Each stored draw runs `m_convergence` inner Gibbs sweeps via [rGLMM_sweep](#). Formula-level fitting uses [rglmerb](#) in **lmebayes**; Gaussian models with observation dispersion typically use the [rLMM_reg](#) routes via [rlmerb](#).

Usage

```
rGLMM_reg_known_vcov(
  n,
  y,
  x,
  block,
  x_hyper,
  prior_list,
  pfamily_list,
  icm_tol = 1e-10,
  icm_maxit = 200L,
  offset = NULL,
  weights = 1,
  family = gaussian(),
```

```

    re_coef_names = colnames(x),
    group_levels = levels(block),
    group_name = NULL,
    gap_tol = 0.0196,
    tv_tol = 0.01,
    mode_gap_max = 1,
    Gridtype = 2,
    n_envopt = NULL,
    use_parallel = TRUE,
    use_openc1 = FALSE,
    verbose = FALSE,
    progbar = FALSE,
    stage_verbose = FALSE,
    rate_calibration = NULL,
    collect_block1 = TRUE
  )

rGLMM_reg_estimated_vcov(
  n,
  y,
  x,
  block,
  x_hyper,
  prior_list,
  pfamily_list,
  icm_tol = 1e-10,
  icm_maxit = 200L,
  offset = NULL,
  weights = 1,
  family = gaussian(),
  re_coef_names = colnames(x),
  group_levels = levels(block),
  group_name = NULL,
  gap_tol = 0.0196,
  tv_tol = 0.01,
  mode_gap_max = 1,
  Gridtype = 2,
  n_envopt = NULL,
  use_parallel = TRUE,
  use_openc1 = FALSE,
  verbose = FALSE,
  progbar = FALSE,
  stage_verbose = FALSE,
  rate_calibration = NULL,
  collect_block1 = TRUE
)

rGLMM_reg(

```

```

n,
y,
x,
block,
x_hyper,
prior_list,
pfamily_list,
icm_tol = 1e-10,
icm_maxit = 200L,
offset = NULL,
weights = 1,
family = gaussian(),
re_coef_names = colnames(x),
group_levels = levels(block),
group_name = NULL,
gap_tol = 0.0196,
tv_tol = 0.01,
mode_gap_max = 1,
Gridtype = 2,
n_envopt = NULL,
use_parallel = TRUE,
use_openc1 = FALSE,
verbose = FALSE,
progbar = FALSE,
stage_verbose = FALSE,
rate_calibration = NULL,
collect_block1 = TRUE
)

```

Arguments

<code>n</code>	Number of stored main-stage draws. If <code>length(n) > 1</code> , the length is used.
<code>y</code>	Response vector of length <code>nrow(x)</code> .
<code>x</code>	Level-1 design matrix Z ($l2 \times p_{re}$).
<code>block</code>	Grouping factor or block partition of length <code>l2</code> .
<code>x_hyper</code>	Named list of group-level design matrices ($J \times q_k$), one per column of <code>x</code> .
<code>prior_list</code>	Prior for Block~1: <code>P</code> or <code>Sigma</code> , dispersion (required for <code>gaussian()</code>), optional <code>ddef</code> .
<code>pfamily_list</code>	Named list of <code>pfamily</code> objects for Block~2.
<code>icm_tol, icm_maxit</code>	ICM convergence controls for the internal Block~2 start.
<code>offset, weights, family</code>	Passed to Block~1 (length <code>l2</code> or recycled).
<code>re_coef_names</code>	Character vector naming columns of <code>x</code> .
<code>group_levels</code>	Character vector defining row order of Block~1 draws.
<code>group_name</code>	Name for the grouping column in coefficients.

gap_tol	Legacy mode—mean gap for pilot chain count when tv_tol is NULL.
tv_tol	Total-variation tolerance for Theorem~3 calibration. n_pilot, m_convergence_pilot, and main-stage m_convergence are derived internally.
mode_gap_max	Pilot inner-sweep calibration when a pilot stage runs.
Gridtype, n_envopt, use_parallel, use_opengl	Reserved (not yet forwarded).
verbose	Print stage headers and convergence calibration lines.
progbars	Progress bars during sampling.
stage_verbose	Print pilot chi-squared and post-pilot UB diagnostics.
rate_calibration	Optional rate object for stage_verbose.
collect_block1	Collect Block~1 coefficients from main chains.

Functions

- `rGLMM_reg_known_vcov()`: All Block~2 dNormal (known τ_k^2). Non-Gaussian: pilot always (unless `n_pilot = 0L`); standard fixed-dispersion eigenvalue rate bounds (no ING `disp_lower` path).
- `rGLMM_reg_estimated_vcov()`: ING Block~2 (estimated τ_k^2). Non-Gaussian: pilot always (unless `n_pilot = 0L`); conservative `disp_lower` eigenvalue bounds and pilot-updated τ^2 starts.
- `rGLMM_reg()`: Route by Block~2 `pfamily_list` to known or estimated τ^2 engines.

Two route engines

Both routes run a **pilot stage for non-Gaussian** families (local-Gaussian rate calibration and chain-mean initialisation; skip only with `n_pilot = 0L`). The route split is **not** whether a pilot runs, but how **eigenvalue bounds** are set for Theorem~3 and post-pilot upper-bound calibration:

`rGLMM_reg_known_vcov` All Block~2 dNormal (known τ_k^2): standard fixed-dispersion rate at the mode; post-pilot eigenvalue upper bound from pilot coefficients without ING `disp_lower` conservatism.

`rGLMM_reg_estimated_vcov` At least one ING Block~2 component: conservative `disp_lower` plug-in in `two_block_rate_from_pfamily_list` (upper bound over truncated τ^2); pilot updates τ^2 starts from dispersion draws.

Dispatcher

`rGLMM_reg` validates Block~2 `pfamily_list` and delegates to the appropriate route.

See Also

`rGLMM_sweep`, `rLMM_reg`, `rglmerb`

glmbayes Simulation Functions `multi_rNormal_reg()`, `multi_rlmb()`, `rGLMM_Re_Draw()`, `rGLMM_sweep()`, `rLMM_reg`, `rindepNormalGamma_reg_with_envelope()`, `simfuncs`, `two_block_optimize_pilot_cost()`, `two_block_rNormal_reg()`, `two_block_rate()`, `two_block_tv_bound()`

rGLMM_sweep	<i>Two-block Gibbs sweep for replicate-chain sampling (rGLMM_reg engine)</i>
-------------	--

Description

Executes `n_chains` independent two-block Gibbs chains, each initialised at `start_fixef` and run for `inner_sweeps` sweeps. Loop order is sweep-outer: for each inner sweep, all chains run Block~1, then all chains run Block~2. Each chain stores exactly one draw ($n = 1L$ per chain), so the result is a collection of `n_chains` approximately independent draws from the target posterior (for large enough `inner_sweeps`).

Usage

```
rGLMM_sweep(
  n_chains,
  start_fixef,
  inner_sweeps,
  design,
  block1_prior,
  pfamily_list,
  family,
  re_names,
  group_levels,
  collect_block1 = TRUE,
  progbar = FALSE,
  stage_label = "",
  diag_sweeps = FALSE,
  fixef_mode = NULL,
  b_mode = NULL,
  b_start = NULL,
  ptypes = NULL,
  tau2_start = NULL,
  use_cpp_tau2_row = TRUE,
  use_cpp_b_slice = TRUE,
  use_cpp_iters_ranef_add = TRUE,
  use_cpp_block2 = TRUE
)
```

Arguments

<code>n_chains</code>	Integer. Number of independent chains to run.
<code>start_fixef</code>	Named list of starting hyper-parameter vectors, one named numeric vector per RE component (matches <code>re_names</code>).
<code>inner_sweeps</code>	Integer. Number of inner Gibbs sweeps per chain.

design	List with components y, Z, groups, X_hyper, re_coef_names, and optional group_name.
block1_prior	Block~1 prior list (P or Sigma, dispersion, optional ddef).
pfamily_list	Named list of pfamily objects (one per RE component).
family	A family object for the response model.
re_names	Character vector of RE coefficient names.
group_levels	Character vector of group levels.
collect_block1	Logical. If TRUE, collect and rbind Block~1 (coefficients) draws from every chain. Default TRUE.
progbar	Logical. When TRUE, show text progress bars over chains during each inner sweep. Default FALSE.
stage_label	Character label stored on \$sweep_history (e.g. "pilot" or "main").
diag_sweeps	When TRUE, print one combined Block~2 fixef chain-mean table for the stage when the inner-sweep loop finishes (same layout as print() on \$sweep_history with all sweeps). Sweep history is always collected; use print() on \$sweep_history to display tables later.
fixef_mode	ICM mode reference stored on \$sweep_history.
b_mode	ICM mode reference for random-effect diagnostics.
b_start	Initial random-effect matrix for all chains (J x p_re). Defaults to b_mode when NULL.
ptypes	Per-component pfamily names (optional; derived from pfamily_list when NULL).
tau2_start	Optional named numeric vector of plug-in τ_k^2 values for chain initialisation (one per re_names). When NULL, derived from pfamily_list prior fields (dNormal dispersion or ING rate/shape = $1/E[1/\tau^2]$).
use_cpp_tau2_row	Block~1 step A (batch\$tau2[i,]): when TRUE (default), use .two_block_batch_tau2_chain_row_cpp; FALSE uses pure R row extract (reference oracle during migration).
use_cpp_b_slice	Block~1 step C (batch\$b[, , i] <- out\$b): when TRUE (default), use .two_block_batch_b_assign_cpp; FALSE uses pure R subassignment.
use_cpp_iters_ranef_add	Block~1 step D (batch\$iters_ranef[i] += out\$iters_mean): when TRUE (default), use .two_block_batch_iters_ranef_add_cpp; FALSE uses pure R accumulation.
use_cpp_block2	When TRUE, Block~2 uses two_block_block2_one_chain_cpp (native C++ align + rglmb) instead of the pure-R reference.

Value

A list with components fixef_draws, dispersion_fixef_draws, iters_fixef_draws, iters_ranef_draws, coefficients, mu_all_last, and sweep_history (class "two_block_sweep_history").

See Also

[two_block_rNormal_reg](#), [rGLMM_reg](#)

glmbayes Simulation Functions [multi_rNormal_reg\(\)](#), [multi_rlmb\(\)](#), [rGLMM_Re_Draw\(\)](#), [rGLMM_reg\(\)](#), [rLMM_reg](#), [rindepNormalGamma_reg_with_envelope\(\)](#), [simfuncs](#), [two_block_optimize_pilot_cost\(\)](#), [two_block_rNormal_reg\(\)](#), [two_block_rate\(\)](#), [two_block_tv_bound\(\)](#)

`rindepNormalGamma_reg_with_envelope`

Independent Normal–Gamma regression with envelope artifacts returned

Description

Diagnostic wrapper with the same sampling pipeline as [rindepNormalGamma_reg](#), but also returns the standardized envelope (Envelope), gamma_list, UB_list, and diagnostics used by the joint accept–reject sampler (standardized subproblem; see [EnvelopeOrchestrator](#)). Intended for parity checks and development; production callers should use [rindepNormalGamma_reg](#).

Usage

```
rindepNormalGamma_reg_with_envelope(
  n,
  y,
  x,
  prior_list,
  offset = NULL,
  weights = 1,
  family = gaussian(),
  Gridtype = 2,
  n_envopt = NULL,
  use_parallel = TRUE,
  use_opengl = FALSE,
  verbose = FALSE,
  progbar = TRUE
)
```

Arguments

<code>n</code>	Number of draws to generate. If <code>length(n) > 1</code> , the length is taken to be the number required.
<code>y</code>	A vector of observations of length <code>m</code> .
<code>x</code>	for the simulation functions a design matrix of dimension <code>m * p</code> and for the print functions the object to be printed.
<code>prior_list</code>	A list with prior parameters (e.g., shape, rate, beta) used in the simulation.
<code>offset</code>	Optional numeric vector of length <code>m</code> specifying known components of the linear predictor.

weights	Optional numeric vector of prior weights.
family	A description of the error distribution and link function (see family).
Gridtype	Optional integer specifying the method used to construct the envelope function.
n_envopt	Effective sample size passed to EnvelopeOpt for grid construction. Defaults to match n. Larger values encourage tighter envelopes.
use_parallel	Logical. Whether to use parallel processing.
use_opengl	Logical. Whether to use OpenGL acceleration.
verbose	Logical. Whether to print progress messages.
progbar	Logical. Whether to display a progress base during simulation.

Value

An `rglmb` object like [rindepNormalGamma_reg](#), plus `Envelope`, `gamma_list`, `UB_list`, and diagnostics.

See Also

glmbayes Simulation Functions [multi_rNormal_reg\(\)](#), [multi_rlmb\(\)](#), [rGLMM_Re_Draw\(\)](#), [rGLMM_reg\(\)](#), [rGLMM_sweep\(\)](#), [rLMM_reg](#), [simfuncs](#), [two_block_optimize_pilot_cost\(\)](#), [two_block_rNormal_reg\(\)](#), [two_block_rate\(\)](#), [two_block_tv_bound\(\)](#)

rIndepNormalGammaReg_std

The Bayesian Gaussian Regression with Independent Normal-Gamma Prior in Standard Form

Description

`rIndepNormalGammaReg_std` generates iid samples from a Bayesian Gaussian regression model with an independent Normal-Gamma prior, in standard form. The function should only be called after standardization and envelope construction (e.g., via [EnvelopeOrchestrator](#)).

Usage

```
rIndepNormalGammaReg_std(
  n,
  y,
  x,
  mu,
  P,
  alpha,
  wt,
  f2,
  Envelope,
  gamma_list,
  UB_list,
```

```

    family,
    link,
    progbar = TRUE,
    verbose = FALSE
  )

```

Arguments

n	Number of draws to generate. If <code>length(n) > 1</code> , the length is taken to be the number required.
y	A vector of observations of length m.
x	A design matrix of dimension $m \times p$.
mu	A matrix of prior means (typically standardized to zero) of dimension $p \times 1$.
P	A positive-definite matrix of dimension $p \times p$ specifying the prior precision component shifted into the log-likelihood.
alpha	A numeric vector of length m for the offset-adjusted mean component. See model.offset .
wt	An optional vector of prior weights. Should be NULL or a numeric vector.
f2	Function used to calculate the negative of the log-posterior (kept for signature parity with <code>rNormalGLM_std</code>).
Envelope	An envelope object containing PLSD, <code>loglt</code> , <code>logrt</code> , <code>cbars</code> , and related components from EnvelopeOrchestrator .
gamma_list	A list with <code>shape3</code> , <code>rate2</code> , <code>disp_lower</code> , and <code>disp_upper</code> from the Gamma posterior for the dispersion.
UB_list	A list with <code>lg_prob_factor</code> , <code>UB2min</code> , <code>RSS_Min</code> , and other bounds from EnvelopeOrchestrator .
family	Character vector specifying the family (e.g., "gaussian").
link	Character vector specifying the link (e.g., "identity").
progbar	Logical. Whether to display a progress bar during simulation.
verbose	Logical. Whether to print diagnostic messages.

Details

This function uses the envelope and dispersion bounds from [EnvelopeOrchestrator](#) to sample from the joint posterior of coefficients and dispersion via rejection sampling. It is typically called internally by `rIndepNormalGamma_reg()`, but may be used directly for custom split workflows (e.g., after constructing the envelope separately).

Value

A list with components:

beta_out	A matrix of simulated regression coefficients in standardized space. Each row is one draw.
disp_out	A vector of dispersion draws for each sample.
iters_out	A vector of iteration counts (candidates per acceptance) for each draw.
weight_out	A vector of weights (typically all ones).

See Also

[EnvelopeOrchestrator](#) for envelope construction, [rNormalGLM_std](#) for the non-Gaussian standardized sampler, [rindepNormalGamma_reg](#) for the full simulation routine.

Examples

```
##### Start of rIndepNormalGammaReg_std example #####

# This example demonstrates calling rIndepNormalGammaReg_std directly for Gaussian
# regression with an independent Normal-Gamma prior. It uses Ex_EnvelopeDispersionBuild
# as a starting point (Steps A through F: EnvelopeCentering, mode optimization,
# standardization, EnvelopeBuild, EnvelopeDispersionBuild, EnvelopeSort), then
# adds sampling and back-transformation to unstandardized form (like the C++ code
# and rNormalGLM_std).

ctl <- c(4.17, 5.58, 5.18, 6.11, 4.50, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)

ps <- Prior_Setup(weight ~ group, gaussian())

x <- as.matrix(ps$x)
y <- as.vector(ps$y)
mu <- ps$mu
Sigma <- ps$Sigma
shape <- ps$shape
rate <- ps$rate

n_obs <- length(y)
wt <- rep(1, n_obs)
offset2 <- rep(0, n_obs)

# Reconstruct coefficient precision P (matches rindepNormalGamma_reg)
Rchol <- chol(Sigma)
Pinv <- chol2inv(Rchol)
P <- 0.5 * (Pinv + t(Pinv))

famfunc <- glmbfamfunc(gaussian())
f2 <- famfunc$f2
f3 <- famfunc$f3

Gridtype_core <- as.integer(2)

#####
# Step A: EnvelopeCentering (initial dispersion + dispersion anchoring loop)
#####
centering <- EnvelopeCentering(
  y = y,
  x = x,
  mu = as.vector(mu),
  P = P,
```

```

    offset = offset2,
    wt = wt,
    shape = shape,
    rate = rate,
    Gridtype = Gridtype_core,
    verbose = FALSE
  )

dispersion2 <- centering$dispersion
RSS_Post2 <- centering$RSS_post

n_w <- sum(wt)

#####
# Step B: Coefficient posterior mode optimization (optim + f2/f3)
#####
dispstar <- dispersion2

wt2_opt <- wt / dispstar
alpha <- as.vector(x %*% as.vector(mu) + offset2)

mu2 <- rep(0, length(as.vector(mu))) # mu2 = 0 * mu (as in C++)
parin <- rep(0, length(as.vector(mu))) # parin = 0 vector (mu - mu)

opt_out <- optim(
  par = parin,
  fn = f2,
  gr = f3,
  y = as.vector(y),
  x = as.matrix(x),
  mu = as.vector(mu2),
  P = as.matrix(P),
  alpha = as.vector(alpha),
  wt = as.vector(wt2_opt),
  method = "BFGS",
  hessian = TRUE
)

bstar <- opt_out$par
A1 <- opt_out$hessian

#####
# Step C: Standardize model (glmb_Standardize_Model)
#####
Standard_Mod <- glmb_Standardize_Model(
  y = as.vector(y),
  x = as.matrix(x),
  P = as.matrix(P),
  bstar = as.matrix(bstar, ncol = 1),
  A1 = as.matrix(A1)
)

bstar2 <- Standard_Mod$bstar2

```

```

A <- Standard_Mod$A
x2_std <- Standard_Mod$x2
mu2_std <- Standard_Mod$mu2
P2_std <- Standard_Mod$P2
L2Inv <- Standard_Mod$L2Inv
L3Inv <- Standard_Mod$L3Inv

#####
# Step D: EnvelopeBuild (coefficient envelope at Gridtype = 3)
#####
max_disp_perc <- 0.99
n_env <- as.integer(200) # used by EnvelopeBuild for diagnostics/overhead
Gridtype_env <- as.integer(3) # EnvelopeOrchestrator overrides to 3

shape2_env <- shape + n_w / 2.0
rate3_env <- rate + RSS_Post2 / 2.0
d1_star <- rate3_env / (shape2_env - 1.0)

wt2_env <- wt / d1_star

Env2 <- EnvelopeBuild(
  bStar = as.vector(bstar2),
  A = as.matrix(A),
  y = as.vector(y),
  x = as.matrix(x2_std),
  mu = as.matrix(mu2_std, ncol = 1),
  P = as.matrix(P2_std),
  alpha = as.vector(alpha),
  wt = as.vector(wt2_env),
  family = "gaussian",
  link = "identity",
  Gridtype = Gridtype_env,
  n = n_env,
  n_envopt = as.integer(1),
  sortgrid = FALSE,
  use_openc1 = FALSE,
  verbose = FALSE
)

#####
# Step E: EnvelopeDispersionBuild (dispersion-aware envelope)
#####
disp_env_out <- EnvelopeDispersionBuild(
  Env = Env2,
  Shape = shape,
  Rate = rate,
  P = as.matrix(P2_std),
  y = as.vector(y),
  x = as.matrix(x2_std),
  alpha = as.vector(alpha),
  n_obs = as.integer(n_obs),
  RSS_post = RSS_Post2,
  RSS_ML = NA_real_,

```

```

    mu = as.matrix(mu2_std, ncol = 1),
    wt = as.vector(wt),
    max_disp_perc = max_disp_perc,
    disp_lower = NULL,
    disp_upper = NULL,
    verbose = FALSE,
    use_parallel = TRUE
  )

#####
# Step F: EnvelopeSort (mirror EnvelopeOrchestrator: disp_grid_type = 2)
#####
Env3_raw <- disp_env_out$Env_out
UB_list_new <- disp_env_out$UB_list
gamma_list_new <- disp_env_out$gamma_list

cbars <- Env3_raw$cbars
l1 <- ncol(cbars)
l2 <- nrow(cbars)

logP_vec <- Env3_raw$logP
logP_mat <- matrix(logP_vec, nrow = length(logP_vec), ncol = 1)

Env3 <- EnvelopeSort(
  l1 = l1,
  l2 = l2,
  GIndex = Env3_raw$GridIndex,
  G3 = Env3_raw$thetabars,
  cbars = cbars,
  logU = Env3_raw$logU,
  logrt = Env3_raw$logrt,
  loglt = Env3_raw$loglt,
  logP = logP_mat,
  LLconst = Env3_raw$LLconst,
  PLSD = Env3_raw$PLSD,
  a1 = Env3_raw$a1,
  E_draws = Env3_raw$E_draws,
  lg_prob_factor = UB_list_new$lg_prob_factor,
  UB2min = UB_list_new$UB2min
)

UB_list_final <- UB_list_new
UB_list_final$lg_prob_factor <- Env3$lg_prob_factor
UB_list_final$UB2min <- Env3$UB2min

env_final <- list(
  Env = Env3,
  gamma_list = gamma_list_new,
  UB_list = UB_list_final,
  diagnostics = disp_env_out$diagnostics,
  low = gamma_list_new$disp_lower,
  upp = gamma_list_new$disp_upper
)

```

```
#####
# Step G: Sample via rIndepNormalGammaReg_std (standardized space)
#####
n <- as.integer(100)
sim <- rIndepNormalGammaReg_std(
  n = n,
  y = as.vector(y),
  x = as.matrix(x2_std),
  mu = as.matrix(mu2_std, ncol = 1),
  P = as.matrix(P2_std),
  alpha = as.vector(alpha),
  wt = as.vector(wt),
  f2 = f2,
  Envelope = env_final$Env,
  gamma_list = env_final$gamma_list,
  UB_list = env_final$UB_list,
  family = "gaussian",
  link = "identity",
  progbar = FALSE,
  verbose = FALSE
)

#####
# Step H: Back-transform to unstandardized form (mirror C++ and rNormalGLM_std)
#####
# beta_out is n x p (one draw per row); t(beta_out) is p x n
coef_unstd <- L2Inv %*% L3Inv %*% t(sim$beta_out)
for (i in seq_len(n)) {
  coef_unstd[, i] <- coef_unstd[, i] + as.vector(mu)
}
coefficients <- t(coef_unstd) # n x p, one draw per row
colnames(coefficients) <- colnames(x)

#####
# Summary output
#####
summary(coefficients)
mean(sim$iters_out)
sim$disp_out[1:5]

#####
# End of rIndepNormalGammaReg_std example
#####
```

Description

r1mb is used to generate iid samples from Bayesian Linear Models with multivariate normal priors.

The model is specified by providing a data vector, a design matrix, and a pfamily (determining the prior distribution).

Usage

```
rlmb(
  n = 1,
  y,
  x,
  pfamily,
  offset = rep(0, nobs),
  weights = NULL,
  Gridtype = 2,
  n_envopt = NULL,
  use_parallel = TRUE,
  use_openc1 = FALSE,
  verbose = FALSE,
  progbar = FALSE
)

## S3 method for class 'rlmb'
print(x, digits = max(3, getOption("digits") - 3), ...)
```

Arguments

<code>n</code>	number of draws to generate. If <code>length(n) > 1</code> , the length is taken to be the number required.
<code>y</code>	a vector of observations of length <code>m</code> .
<code>x</code>	for <code>rlmb</code> a design matrix of dimension <code>m * p</code> and for <code>print.rlmb</code> the object to be printed.
<code>pfamily</code>	a description of the prior distribution and associated constants to be used in the model. This should be a pfamily function (see pfamily for details of pfamily functions.)
<code>offset</code>	an optional numeric vector of known offset to be included in the linear predictor.
<code>weights</code>	an optional numeric vector of prior weights for the observations.
<code>Gridtype</code>	an optional argument specifying tangent points for envelope construction.
<code>n_envopt</code>	Effective sample size passed to <code>EnvelopeOpt</code> for grid construction.
<code>use_parallel</code>	Logical. Whether to use parallel processing during simulation.
<code>use_openc1</code>	Logical. Whether to use OpenCL acceleration during Envelope construction.
<code>verbose</code>	Logical. Whether to print progress messages.
<code>progbar</code>	Logical. Whether to display a progress base during simulation.
<code>digits</code>	the number of significant digits to use when printing.
<code>...</code>	further arguments passed to or from other methods.

Details

The function `r1mb` is a minimalistic Bayesian simulation engine for Gaussian linear models. It bypasses classical model fitting and formula parsing, operating directly on numeric inputs such as the design matrix, response vector, and prior specification via the `pfamily` argument. Internally, `r1mb` generates independent draws from the posterior distribution using multivariate normal simulation when conjugate priors are specified.

The modeling framework follows (Wilkinson and Rogers 1973), and the prior structure builds on the S system (Chambers 1992), Zellner's g-prior (Zellner 1986), and the conjugate prior formulation of Raiffa and Schlaifer (Raiffa and Schlaifer 1961).

Prior specification is handled via the `pfamily` argument, which defines the prior mean, covariance, and dispersion. The design of the `pfamily` family of functions was created by Kjell Nygren and is modeled on how `glm` uses `family` to specify the likelihood. A helper function, `Prior_Setup`, assists users in choosing prior parameters. It ships with sensible defaults but also allows full customization. Available priors include the `dNormal`, `dNormalGamma` and `dIndependent_Normal_Gamma` priors. The last of these allows for more flexible prior structures including independent priors on variance components.

Posterior draws are generated using standard simulation procedures for conjugate priors (Raiffa and Schlaifer 1961). For non-conjugate setups, the function uses envelope-based accept-reject sampling via the likelihood-subgradient method (Nygren and Nygren 2006). The `Gridtype` parameter controls how many tangent points are used to construct the envelope-trading off tightness against computational cost- and the `iters` component reports the number of candidate samples generated before acceptance.

The output includes posterior samples, prior specifications, dispersion estimates, and envelope diagnostics. Use `summary.r1mb` (same implementation as `summary.rglm`) for posterior summaries and DIC-style output. Formula-based predict methods are provided by `glmbayes` when that package is installed.

Value

`r1mb` returns a object of class `"r1mb"`. The generic accessor functions `coefficients` and `fitted.values` can be used to extract useful features of the value returned by `r1mb`. An object of class `"r1mb"` is a list containing at least the following components:

<code>coefficients</code>	a matrix of dimension <code>n</code> by <code>length(mu)</code> with one sample in each row
<code>coef.mode</code>	a vector of <code>length(mu)</code> with the estimated posterior mode coefficients
<code>dispersion</code>	Either a constant provided as part of the call, or a vector of length <code>n</code> with one sample in each row.
<code>Prior</code>	A list with the priors specified for the model in question. Items in the list may vary based on the type of prior
<code>prior.weights</code>	a vector of weights specified or implied by the model
<code>y</code>	a vector with the dependent variable
<code>x</code>	a matrix with the implied design matrix for the model
<code>famfunc</code>	Family functions used during estimation process
<code>iters</code>	an <code>n</code> by 1 matrix giving the number of candidates generated before acceptance for each sample.

Envelope the envelope that was used during sampling

Objects of class "rlmb" are normally of class `c("rlmb", "rglmb", "glmb", "glm", "lm")`, meaning they inherit from `rglmb`, `glmb`, `glm`, and `lm`. Well-designed methods for these classes will be applied when appropriate, allowing "rlmb" objects to benefit from existing infrastructure while supporting specialized behavior for restricted linear model priors.

References

Chambers JM (1992). "Linear Models." In Chambers JM, Hastie TJ (eds.), *Statistical Models in S*, chapter 4, 85–124. Wadsworth & Brooks/Cole, Pacific Grove, CA.

Nygren K~N, Nygren L~M (2006). "Likelihood Subgradient Densities." *Journal of the American Statistical Association*, **101**(475), 1144–1156. doi:[10.1198/016214506000000357](https://doi.org/10.1198/016214506000000357).

Raiffa H, Schlaifer R (1961). *Applied Statistical Decision Theory*. Clinton Press, Inc., Boston.

Wilkinson GN, Rogers CE (1973). "Symbolic Descriptions of Factorial Models for Analysis of Variance." *Applied Statistics*, **22**(3), 392–399. doi:[10.2307/2346786](https://doi.org/10.2307/2346786).

Zellner A (1986). "On Assessing Prior Distributions and Bayesian Regression Analysis with g-Prior Distributions." In Goel P~K, Zellner A (eds.), *Bayesian Inference and Decision Techniques: Essays in Honor of Bruno de Finetti*, volume 6 of *Studies in Bayesian Econometrics and Statistics*, 233–243. Elsevier.

See Also

The classical modeling functions `lm` and `glm`.

`rglmb` for the GLM sampler; `EnvelopeBuild`, `EnvelopeOrchestrator` for envelope stages used in non-conjugate Gaussian sampling.

`pfamily` for documentation of `pfamily` functions used to specify priors.

`Prior_Setup`, `Prior_Check` for functions used to initialize and to check priors,

Further reading: (Nygren and Nygren 2006); (Nygren 2025, 2025). User-facing S3 methods for fitted models are provided by `glmbayes`.

`glmbayes` Modeling Functions `multi_rlmb()`, `rglmb()`

Examples

```
## Main Example based on Dobson Plant Weight Data
## Use demo(Ex_07_Schools) for a longer/more complex model

## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.

ctl <- c(4.17, 5.58, 5.18, 6.11, 4.50, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)
```

```

ps <- Prior_Setup(weight ~ group)
x  <- ps$x
mu <- ps$mu
V  <- ps$Sigma
y  <- ps$y
shape  <- ps$shape
rate   <- ps$rate
rate_dg <- if (!is.null(ps$rate_gamma)) ps$rate_gamma else rate

## Two-Block Gibbs sampler for Plant Weight regression model
set.seed(180)

## Note: iteration counts reduced for CRAN checks; increase for production use
n_burnin <- 200
n_samples <- 200

## Initilize dispersion to ML estimate
dispersion2 <- ps$dispersion

## Run burn-in iterations
for (i in 1:n_burnin) {
  ## Update block for regression coefficients
  out1 <- rlmb( n = 1, y = y, x = x,
    pfamily = dNormal(mu = mu, Sigma = V, dispersion = dispersion2) )

  ## Update block for dispersion
  out2 <- rlmb(n = 1, y = y, x = x,
    pfamily = dGamma(shape = shape, rate = rate_dg, beta = out1$coefficients[1, ]))
  dispersion2 <- out2$dispersion
}

## Create Objects to store outputs
beta_out <- matrix(0, nrow = n_samples, ncol = 2)
disp_out <- rep(0, n_samples)

for (i in 1:n_samples) {
  ## Update block for regression coefficients
  out1 <- rlmb( n = 1, y = y, x = x,
    pfamily = dNormal(mu = mu, Sigma = V, dispersion = dispersion2) )

  ## Update block for dispersion
  out2 <- rlmb(n = 1, y = y, x = x,
    pfamily = dGamma(shape = shape, rate = rate_dg, beta = out1$coefficients[1, ]))
  dispersion2 <- out2$dispersion

  ## Store output

  beta_out[i, 1:2] <- out1$coefficients[1, 1:2]
  disp_out[i] <- out2$dispersion
}

mcmc_two_block <- coda::mcmc(cbind( beta1 = beta_out[, 1], beta2 = beta_out[, 2],

```

```

                                dispersion = disp_out  ))

## Review output
cat("\nCODA summary (Two-block Gibbs):\n")
print(summary(mcmc_two_block))
cat("\nEffective sample size (dispersion):\n")
print(coda::effectiveSize(mcmc_two_block)["dispersion"])

## r1merb with dGamma prior (dispersion-only; coefficients fixed)
out_r1merb_dGamma <- r1merb(n = 100, y = y, x = x,
  pfamily = dGamma(shape = shape, rate = rate_dg, beta = ps$coefficients),
  weights = rep(1, length(y)))
print(out_r1merb_dGamma)

```

r1merb

The Bayesian Linear Mixed-Effects Model Distribution

Description

Bayesian linear mixed-effects model sampler (two-block Gibbs engine)

Usage

```

r1merb(
  n,
  design,
  prior,
  dispersion_ranef,
  tv_tol = 0.01,
  progbar = TRUE,
  verbose = TRUE,
  print_icm_table = TRUE,
  gap_tol = 0.0196,
  mode_gap_max = 1,
  diag_sweeps = FALSE
)

```

Arguments

n	Integer. Number of stored draws (each draw is one full pass through <code>m_convergence</code> inner Gibbs sweeps).
design	A <code>model_setup</code> object (from model_setup) supplying <code>y</code> , <code>Z</code> , <code>groups</code> , <code>X_hyper</code> , <code>group_name</code> , and <code>re_coef_names</code> .
prior	Normalized prior container with <code>Sigma_ranef</code> , <code>prior_list</code> , and related <code>Block~2</code> fields (typically from <code>pfamily_list</code> and <code>dispersion_ranef</code> via Prior_Setup_lmebayes or an <code>lmerb()</code> workflow in <code>lmebayes</code>).

dispersion_ranef	Required observation-level dispersion: a positive scalar σ^2 (fixed) or a <code>dGamma()</code> pfamily with <code>Inv_Dispersion = TRUE</code> for a Gamma prior on σ^2 .
tv_tol	Single numeric in $(0, 1)$. Total variation tolerance used for convergence calibration. Default 0.01. Inner Gibbs sweeps per stored draw are derived from Theorem~3.
progbar	Logical. Show a text progress bar during sampling. Default TRUE.
verbose	Logical. Print the reference-vs-ICM table and the convergence calibration line. Default TRUE.
print_icm_table	Logical. When FALSE, skip the reference-vs-ICM table. The convergence calibration line from the Core engine still follows verbose. Default TRUE.
gap_tol	Legacy mode-mean gap tolerance for the pilot stage when any Block~2 component uses <code>dIndependent_Normal_Gamma</code> and <code>tv_tol</code> is NULL. Ignored for all- <code>dNormal</code> models.
mode_gap_max	Pilot inner-sweep calibration for ING Block~2 models (default 1.0). Ignored for all- <code>dNormal</code> models.
diag_sweeps	Diagnostic flag for ING Block~2 models with a pilot stage. When TRUE, auto-print one combined Block~2 chain-mean table per stage when each stage finishes; <code>sweep_history</code> is always stored on the fit. Default FALSE.

Details

Matrix-level sampling engine for Gaussian linear mixed models, parallel to `rlmb` and `rglmerb`. Takes structured design and prior objects, computes the ICM posterior mean internally, and delegates replicate-chain sampling to `rLMMNormal_reg_known_vcov`, `rLMMNormal_reg_estimated_vcov`, `rLMMIndepNormalGamma_reg_known_vcov`, or `rLMMIndepNormalGamma_reg_estimated_vcov` according to `dispersion_ranef` and Block~2 `pfamily_list`.

For formula-level fitting, `lmerb()` in the `lmebayes` package wraps this sampler.

Value

An object of class `c("rlmerb", "list")` with Block~2 fields in the `fixef.*` namespace, Block~1 draws in `coefficients`, `ranef.mode`, `sigma2` (scalar when σ^2 is fixed, length-`n` vector when `dispersion_ranef` is `dGamma()`), `sigma2.mean`, `m_convergence`, `convergence`, `Prior`, and `design`.

See Also

`rglmerb`, `rLMMNormal_reg_known_vcov`, `rLMMNormal_reg_estimated_vcov`, `rLMMIndepNormalGamma_reg_known_vcov`, `rLMMIndepNormalGamma_reg_estimated_vcov`, `Prior_Setup_lmebayes`, `rlmb`

rLMM_reg

*Matrix-level replicate-chain Gibbs engines for Bayesian LMMs***Description**

Gaussian two-block LMM samplers at matrix level (y , Z , x_{hyper} , pfamily_list). Each stored draw runs $m_{\text{convergence}}$ inner Gibbs sweeps (Block~1 random effects, then Block~2 hyperparameters). There is no standalone `rLMM()` function; use the `rGLMM_reg` routes via `rglmerb`; Gaussian LMMs use `rLMM_reg` via `rlmerb`.

Usage

```
rLMMNormal_reg(
  n,
  y,
  x,
  block,
  x_hyper,
  P,
  prior_list,
  pfamily_list,
  icm_tol = 1e-10,
  icm_maxit = 200L,
  tv_tol = 0.01,
  re_coef_names = colnames(x),
  group_levels = levels(block),
  group_name = NULL,
  progbar = TRUE,
  verbose = FALSE
)
```

```
rLMMNormal_reg_known_vcov(
  n,
  y,
  x,
  block,
  x_hyper,
  P,
  prior_list,
  pfamily_list,
  icm_tol = 1e-10,
  icm_maxit = 200L,
  tv_tol = 0.01,
  re_coef_names = colnames(x),
  group_levels = levels(block),
  group_name = NULL,
  progbar = TRUE,
```

```
    verbose = FALSE
  )

  rLMMNormal_reg_estimated_vcov(
    n,
    y,
    x,
    block,
    x_hyper,
    P,
    prior_list,
    pfamily_list,
    icm_tol = 1e-10,
    icm_maxit = 200L,
    tv_tol = 0.01,
    re_coef_names = colnames(x),
    group_levels = levels(block),
    group_name = NULL,
    progbar = TRUE,
    verbose = FALSE,
    gap_tol = 0.0196,
    mode_gap_max = 1,
    diag_sweeps = FALSE,
    stage_verbose = FALSE
  )

  rLMMIndepNormalGamma_reg(
    n,
    y,
    x,
    block,
    x_hyper,
    P,
    prior_list,
    pfamily_list,
    icm_tol = 1e-10,
    icm_maxit = 200L,
    tv_tol = 0.01,
    re_coef_names = colnames(x),
    group_levels = levels(block),
    group_name = NULL,
    progbar = TRUE,
    verbose = FALSE
  )

  rLMMIndepNormalGamma_reg_known_vcov(
    n,
    y,
```

```

    x,
    block,
    x_hyper,
    P,
    prior_list,
    pfamily_list,
    icm_tol = 1e-10,
    icm_maxit = 200L,
    tv_tol = 0.01,
    re_coef_names = colnames(x),
    group_levels = levels(block),
    group_name = NULL,
    progbar = TRUE,
    verbose = FALSE
)

rLMMindNormalGamma_reg_estimated_vcov(
  n,
  y,
  x,
  block,
  x_hyper,
  P,
  prior_list,
  pfamily_list,
  icm_tol = 1e-10,
  icm_maxit = 200L,
  tv_tol = 0.01,
  re_coef_names = colnames(x),
  group_levels = levels(block),
  group_name = NULL,
  progbar = TRUE,
  verbose = FALSE,
  gap_tol = 0.0196,
  mode_gap_max = 1,
  diag_sweeps = FALSE,
  stage_verbose = FALSE
)

```

Arguments

n	Number of stored draws. If $\text{length}(n) > 1$, the length is used.
y	Response vector of length $\text{nrow}(x)$.
x	Level-1 design matrix Z ($12 \times p_{\text{re}}$).
block	Grouping factor or block partition of length 12.
x_hyper	Named list of group-level design matrices ($J \times q_k$), one per column of x .
P	Random-effect prior precision matrix ($p_{\text{re}} \times p_{\text{re}}$).

prior_list	Block~1 prior: list(dispersion = sigma2) for fixed σ^2 routes, dGamma() fields for legacy rLMMindpNormalGamma_reg, or shared ING measurement prior (mu, Sigma, shape, rate, ...) for ING routes (plug-in $\sigma^2 = \text{shape/rate}$ for ICM/TV is derived internally).
pfamily_list	Named list of Block~2 pfamily objects.
icm_tol, icm_maxit	ICM convergence controls for the internal Block~2 start.
tv_tol	Total-variation tolerance in (0, 1) for calibration. Inner Gibbs sweeps per stored draw (m_convergence) are derived from Theorem~3 at the ICM Block~2 start; pilot chain counts likewise.
re_coef_names	Names for columns of x.
group_levels	Character vector defining row order of Block~1 draws.
group_name	Name for the grouping column in coefficients.
progbar	Show a text progress bar during sampling.
verbose	Print convergence calibration / ICM lines.
gap_tol, mode_gap_max, diag_sweeps, stage_verbose	Pilot-stage controls for rLMMNormal_reg_estimated_vcov and ING estimated routes (see route docs).

Functions

- `rLMMNormal_reg()`: Dispatcher for fixed σ^2 : routes to `rLMMNormal_reg_known_vcov` or `rLMMNormal_reg_estimated_vcov` by Block~2 pfamily_list.
- `rLMMNormal_reg_known_vcov()`: Fixed σ^2 ; all Block~2 dNormal (known τ_k^2). Exact Theorem~3 rate calibration.
- `rLMMNormal_reg_estimated_vcov()`: Fixed σ^2 ; ING Block~2 (estimated τ_k^2). Optional pilot stage; conservative disp_lower rate bound.
- `rLMMindpNormalGamma_reg()`: Legacy outer-loop engine: draws σ^2 via `rGamma_reg`, then calls `rLMMNormal_reg` each replicate. Prefer `rLMMindpNormalGamma_reg_known_vcov` or `rLMMindpNormalGamma_reg_estimated_vcov` for the ING Block~1 sweep engine used by `rlmerb`.
- `rLMMindpNormalGamma_reg_known_vcov()`: Random σ^2 (per-group ING Block~1); all Block~2 dNormal. Used by `rlmerb` when dispersion_ranef is dGamma and Block~2 is all dNormal.
- `rLMMindpNormalGamma_reg_estimated_vcov()`: Random σ^2 (per-group ING Block~1); ING Block~2. Pilot/UB calibration via sweep-outer engine. Default path for `rlmerb` with dGamma dispersion_ranef and ING Block~2.

Four route engines

`rLMMNormal_reg_known_vcov` Fixed observation σ^2 ; all Block~2 components dNormal (known τ_k^2).

`rLMMNormal_reg_estimated_vcov` Fixed σ^2 ; at least one ING Block~2 component.

`rLMMindpNormalGamma_reg_known_vcov` Random σ^2 (per-group ING Block~1); all Block~2 dNormal.

`rLMMindpNormalGamma_reg_estimated_vcov` Random σ^2 ; at least one ING Block~2 component.

Dispatchers

[rLMMNormal_reg](#) and [rLMMindepNormalGamma_reg](#) validate inputs and delegate to the appropriate route (or, for the legacy outer-loop [rLMMindepNormalGamma_reg](#), draw σ^2 then call [rLMMNormal_reg](#)).

See Also

[rGLMM_reg](#), [rlmerb](#), [rindepNormalGamma_reg](#)

glmbayes Simulation Functions [multi_rNormal_reg\(\)](#), [multi_rlmb\(\)](#), [rGLMM_Re_Draw\(\)](#), [rGLMM_reg\(\)](#), [rGLMM_sweep\(\)](#), [rindepNormalGamma_reg_with_envelope\(\)](#), [simfuncs](#), [two_block_optimize_pilot_cost\(\)](#), [two_block_rNormal_reg\(\)](#), [two_block_rate\(\)](#), [two_block_tv_bound\(\)](#)

rNormal_reg.wfit

Bayesian Weighted Fitting Engines

Description

These functions provide the Bayesian analogue of `lm.wfit`. They implement the core weighted least squares step used inside Bayesian linear linear models, incorporating prior precision and posterior mode information.

Usage

```
rNormal_reg.wfit(
  x,
  y,
  P,
  mu,
  w,
  offset = NULL,
  method = "qr",
  tol = 1e-07,
  singular.ok = TRUE,
  ...
)

glmb.wfit(
  x,
  y,
  weights = rep.int(1, nobs),
  offset = rep.int(0, nobs),
  family = gaussian(),
  Bbar,
  P,
  betastar,
  method = "qr",
  tol = 1e-07,
```

```

    singular.ok = TRUE,
    ...
  )

```

Arguments

x	design matrix of dimension $n \times p$.
y	vector of observations of length n , or a matrix with n rows.
P	Prior precision matrix of dimension $p \times p$.
mu	Prior mean vector of length p .
w	vector of weights (length n) to be used in the fitting process for the <code>wfit</code> functions. Weighted least squares is used with weights w , i.e., $\sum(w * e^2)$ is minimized.
offset	(numeric of length n). This can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting.
method	currently, only <code>method = "qr"</code> is supported.
tol	tolerance for the <code>qr</code> decomposition. Default is $1e-7$.
singular.ok	logical. If FALSE, a singular model is an error.
...	currently disregarded.
weights	an optional vector of <i>prior weights</i> to be used in the fitting process. Should be NULL or a numeric vector.
family	a description of the error distribution and link function to be used in the model. Should be a family function. (see family for details of family functions.)
Bbar	Prior mean vector of length p .
betastar	Posterior mode vector of length p which has already been estimated.

Details

`rNormal_reg.wfit` performs the Bayesian weighted least squares update for linear models under a Normal prior.

`glmb.wfit` performs the corresponding update for generalized linear models, reconstructing the weighted least squares step using the posterior mode and the GLM family functions.

Value

a [list](#) with components:

a [list](#) with components:

Examples

```

set.seed(333)
## Dobson (1990) Page 93: Randomized Controlled Trial :
counts <- c(18, 17, 15, 20, 10, 20, 25, 13, 12)
outcome <- gl(3, 1, 9)
treatment <- gl(3, 3)

```

```

ps <- Prior_Setup(counts ~ outcome + treatment, family = poisson())
mu <- ps$mu
V0 <- ps$Sigma
out <- rglmb(
  n = 1000,
  y = ps$y,
  x = as.matrix(ps$x),
  pfamily = dNormal(mu = mu, Sigma = V0),
  family = poisson(),
  weights = rep(1, nrow(ps$x))
)

betastar <- out$coef.mode
x <- out$x
y <- out$y
offset2 <- 0 * y
weights2 <- out$prior.weights

fit <- glmb.wfit(x, y, weights2, offset2, family = poisson(), Bbar = mu, P = solve(V0), betastar)
influence.measures(fit)

print(fit)
print(out$coef.mode)

mu1 <- 0 * mu
V1 <- 0.1 * V0
out2 <- rglmb(
  n = 1000,
  y = ps$y,
  x = as.matrix(ps$x),
  pfamily = dNormal(mu = mu1, Sigma = V1),
  family = poisson(),
  weights = rep(1, nrow(ps$x))
)

Bbar2 <- mu1
betastar2 <- out2$coef.mode
fit2 <- glmb.wfit(x, y, weights2, offset2, family = poisson(), Bbar2, P = solve(V1), betastar2)

influence.measures(fit2)

print(fit2)
print(out2$coef.mode)

```

Description

rNormalGLM_std is used to generate iid samplers from Non-Gaussian Generalized Linear Models in standard form. The function should only be called after standardization of a Generalized Linear Model.

Usage

```
rNormalGLM_std(
  n,
  y,
  x,
  mu,
  P,
  alpha,
  wt,
  f2,
  Envelope,
  family,
  link,
  progbar = 1L
)
```

Arguments

n	number of draws to generate. If <code>length(n) > 1</code> , the length is taken to be the number required.
y	a vector of observations of length m.
x	a design matrix of dimension $m \times p$.
mu	a vector of length p giving the prior means of the variables in the design matrix.
P	a positive-definite symmetric matrix of dimension $p \times p$ specifying the prior precision matrix of the variable.
alpha	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more offset terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See model.offset .
wt	an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or a numeric vector.
f2	function used to calculate the negative of the log-posterior function
Envelope	an object of type <code>glmbenvelope</code> .
family	family used for simulation. Used that this is different from the family used in other functions.
link	link function used for simulation.
progbar	dummy for flagging if a progressbar should be produced during the call

Details

This function uses the information contained in the constructed envelope list in order to sample from a model in standard form. The simulation proceeds as follows in order to generate each draw in the required number of samples.

1. A random number between 0 and 1 is generated and is used together with the information in the PLSD vector (from the envelope) in order to identify the part of the grid from which a candidate is to be generated.
2. For the part of the grid selected, the dimensions are looped through and a candidate component for each dimension is generated from a restricted normal using information from the Envelope (in particular, the values for logrt, loglt, and cbars corresponding to that the part of the grid selected and the dimension sampled)
3. The log-likelihood for the standardized model is evaluated for the generated candidate (note that the log-likelihood here includes the portion of the prior that was shifted to the log-likelihood)
4. An additional random number is generated and the log of this random number is compared to a log-acceptance rate that is calculated based on the candidate and the LLconst component from the Envelope component selected in order to determine if the candidate should be accepted or rejected
5. If the candidate was not accepted, the process above is repeated from step 1 until a candidate is accepted

Value

A list consisting of the following:

out	A matrix with simulated draws from a model in standard form. Each row represents one draw from the density
draws	A vector with the number of candidates required before acceptance for each draw

Examples

```
##### Start of rNormalGLM_std examples #####
data(menarche, package="MASS")

summary(menarche)
plot(Menarche/Total ~ Age, data=menarche)

Age2=menarche$Age-13

x<-matrix(as.numeric(1.0),nrow=length(Age2),ncol=2)
x[,2]=Age2

y=menarche$Menarche/menarche$Total
wt=menarche$Total

mu<-matrix(as.numeric(0.0),nrow=2,ncol=1)
mu[2,1]=(log(0.9/0.1)-log(0.5/0.5))/3
```

```

V1<-1*diag(as.numeric(2.0))

# 2 standard deviations for prior estimate at age 13 between 0.1 and 0.9
## Specifies uncertainty around the point estimates

V1[1,1]<-((log(0.9/0.1)-log(0.5/0.5))/2)^2
V1[2,2]=(3*mu[2,1]/2)^2 # Allows slope to be up to 1 times as large as point estimate

famfunc<-glmbfamfunc(binomial(logit))

f1<-famfunc$f1
f2<-famfunc$f2 # Used in optim and glbsim_cpp
f3<-famfunc$f3 # Used in optim
f5<-famfunc$f5
f6<-famfunc$f6

dispersion2<-as.numeric(1.0)
start <- mu
offset2=rep(as.numeric(0.0),length(y))
P=solve(V1)
n=1000

##### Adjust weight for dispersion

wt2=wt/dispersion2

##### Shift mean vector to offset so that adjusted model has 0 mean

alpha=x%*%as.vector(mu)+offset2
mu2=0*as.vector(mu)
P2=P
x2=x

##### Optimization step to find posterior mode and associated Precision

parin=start-mu

opt_out=optim(parin,f2,f3,y=as.vector(y),x=as.matrix(x),mu=as.vector(mu2),
              P=as.matrix(P),alpha=as.vector(alpha),wt=as.vector(wt2),
              method="BFGS",hessian=TRUE
)

bstar=opt_out$par ## Posterior mode for adjusted model
bstar
bstar+as.vector(mu) # mode for actual model
A1=opt_out$hessian # Approximate Precision at mode

## Standardize Model

Standard_Mod=glmb_Standardize_Model(y=as.vector(y), x=as.matrix(x),P=as.matrix(P),

```

```

bstar=as.matrix(bstar,ncol=1), A1=as.matrix(A1))

bstar2=Standard_Mod$bstar2
A=Standard_Mod$A
x2=Standard_Mod$x2
mu2=Standard_Mod$mu2
P2=Standard_Mod$P2
L2Inv=Standard_Mod$L2Inv
L3Inv=Standard_Mod$L3Inv

Env2=EnvelopeBuild(as.vector(bstar2), as.matrix(A),y, as.matrix(x2),
  as.matrix(mu2,ncol=1),as.matrix(P2),as.vector(alpha),as.vector(wt2),
  family="binomial",link="logit",Gridtype=as.integer(3),
  n=as.integer(n),sortgrid=TRUE)

## These now seem to match

Env2

# The low-level sampler is called below with explicit type coercions.

### Note: getting the types correct here is important but potentially difficult for users
### May be better to call an R function wrapper that checks (and converts when possible)
### to correct types

sim=rNormalGLM_std(n=as.integer(n),y=as.vector(y),x=as.matrix(x2),mu=as.matrix(mu2,ncol=1),
  P=as.matrix(P2),alpha=as.vector(alpha),wt=as.vector(wt2),
  f2=f2,Envelope=Env2,family="binomial",link="logit",as.integer(0))

out=L2Inv%%L3Inv%%t(sim$out)

for(i in 1:n){
  out[,i]=out[,i]+mu
}

summary(t(out))
mean(sim$draws)

```

simfuncs

Simulation Functions for Bayesian Generalized Linear Models

Description

Simulation functions provide a unified interface for generating posterior samples from Bayesian GLMs. These functions are typically used within model fitting routines such as `rglmb` and `rlmb`, and are also suitable for use in Block Gibbs sampling and other simulation-based inference techniques.

Usage

```
simfunction(object, ...)
```

```

rNormal_reg(n, y, x, prior_list, offset = NULL, weights = 1,
            family = gaussian(), Gridtype = 2, n_envopt = NULL,
            use_parallel = TRUE, use_openc1 = FALSE, verbose = FALSE, progbar=FALSE)

rNormalGamma_reg(n, y, x, prior_list, offset = NULL, weights = 1, family = gaussian(),
                 Gridtype = 2, n_envopt = NULL,
                 use_parallel = TRUE, use_openc1 = FALSE, verbose = FALSE, progbar=FALSE)

rindepNormalGamma_reg(n, y, x, prior_list, offset = NULL, weights = 1,
                      family = gaussian(), Gridtype = 2, n_envopt = NULL,
                      use_parallel = TRUE, use_openc1 = FALSE, verbose = FALSE,
                      progbar = TRUE)

rGamma_reg(n, y, x, prior_list, offset = NULL, weights = 1, family = gaussian(),
           Gridtype = 2, n_envopt = NULL,
           use_parallel = TRUE, use_openc1 = FALSE, verbose = FALSE, progbar=FALSE)

## S3 method for class 'rGamma_reg'
print(x, digits = max(3, getOption("digits") - 3), ...)

## S3 method for class 'simfunction'
print(x, ...)

rGamma_Conjugate_reg(n, y, x, prior_list, offset = NULL, weights = 1, family = gaussian(),
                    Gridtype = 2, n_envopt = NULL,
                    use_parallel = TRUE, use_openc1 = FALSE, verbose = FALSE, progbar=FALSE)

rBeta_reg(n, y, x, prior_list, offset = NULL, weights = 1,
          family = gaussian(), Gridtype = 2, n_envopt = NULL,
          use_parallel = TRUE, use_openc1 = FALSE,
          verbose = FALSE, progbar = FALSE)

```

Arguments

object	A fitted model object containing a pfamily component. The generic function <code>simfunction()</code> accesses the simulation metadata stored within such objects.
n	Number of draws to generate. If <code>length(n) > 1</code> , the length is taken to be the number required.
y	A vector of observations of length <code>m</code> .
x	for the simulation functions a design matrix of dimension <code>m * p</code> and for the print functions the object to be printed.
prior_list	A list with prior parameters (e.g., shape, rate, beta) used in the simulation.
offset	Optional numeric vector of length <code>m</code> specifying known components of the linear predictor.
weights	Optional numeric vector of prior weights.
family	A description of the error distribution and link function (see family).

<code>Gridtype</code>	Optional integer specifying the method used to construct the envelope function.
<code>n_envopt</code>	Effective sample size passed to <code>EnvelopeOpt</code> for grid construction. Defaults to match <code>n</code> . Larger values encourage tighter envelopes.
<code>use_parallel</code>	Logical. Whether to use parallel processing.
<code>use_opengl</code>	Logical. Whether to use OpenGL acceleration.
<code>verbose</code>	Logical. Whether to print progress messages.
<code>progbar</code>	Logical. Whether to display a progress base during simulation.
<code>digits</code>	Number of significant digits to use for printed output.
<code>...</code>	Additional arguments passed to or from other methods.

Details

The low-level simulation functions `rNormal_reg()`, `rNormalGamma_reg()`, `rindpNormalGamma_reg()`, and `rGamma_reg()` generate iid samples from posterior distributions for specific model components. These model functions are used internally by the functions `rglmb()` and `rlmb()` to generate samples.

The `simfunction()` generic extracts metadata from simulation objects, including the function name, call, and arguments used. This is useful for introspection, reproducibility, and diagnostics.

The lower-level simulation functions generate iid samples from posterior distributions for specific model components. These functions are used internally by `pfamily` constructors and model fitting routines.

Simulation Functions:

- `rNormal_reg()`: Produces iid draws for regression coefficients in models with multivariate normal priors and log-concave likelihood functions. For Gaussian likelihoods, these are conjugate priors and standard simulation procedures for multivariate normal distributions are utilized (Lindley and Smith 1972; Diaconis and Ylvisaker 1979). For all other families/link functions, the likelihood subgradient approach of (Nygren and Nygren 2006) is used to generate iid samples.
- `rNormalGamma_reg()`: Produces iid draws for regression coefficients and the dispersion parameter in models with Normal-Gamma priors and Gaussian likelihoods, where this is a conjugate prior distribution. Standard simulation procedures for gamma and multivariate normal distributions are utilized (Raiffa and Schlaifer 1961; Lindley and Smith 1972).
- `rindpNormalGamma_reg()`: Produces iid draws for regression coefficients and the dispersion parameter in models with independent Normal and truncated Gamma priors. This is a non-conjugate specification but can still be sampled using accept-reject procedures based on an enveloping approach (see vignette (Nygren 2025)).
- `rGamma_reg()`: Simulates dispersion parameters for Gaussian and Gamma families using either standard gamma sampling or accept-reject methods based on likelihood subgradients (Chen 1979; Nygren 2025).

Value

`simfunction()` An object of class "simfunction" containing:

name Character string with the name of the simulation function.

`call` The matched call used to generate the simulation.

`args` A named list of arguments passed to the simulation function.

`rNormal_reg()` A list object with classes `"rglmb"`, `"glmb"`, `"glm"`, and `"lm"`. Elements include:

`coefficients` Matrix ($n \times p$) of simulated regression coefficients, with column names from `x`.

`coef.mode` Posterior mode of the coefficients. Gaussian: from `lm.fit`; non-Gaussian: BFGS mode shifted by prior mean.

`dispersion` Scalar dispersion used. Poisson/Binomial: 1; otherwise the supplied value. Quasi families: mean residual-based dispersion computed in the wrapper.

`Prior` List with `mean` (prior mean vector) and `Precision` (prior precision matrix P).

`prior.weights` Vector of prior weights used in the simulation (unscaled).

`offset` Offset vector passed to the C++ sampler.

`offset2` Offset used internally by the wrapper (copy of input or a zero vector).

`y` Response vector.

`x` Design matrix.

`fit` Fitted/diagnostic object. Gaussian: result of `lm.fit` (class `"lm"`). Non-Gaussian: result of `glmb.wfit(...)`.

`iters` Vector of iteration counts per sample. Gaussian: vector of ones; non-Gaussian: counts from the sampler.

`Envelope` Envelope list used for accept-reject sampling (non-Gaussian); NULL for Gaussian.

`family` Family object describing distribution and link.

`famfunc` Processed family functions used internally (e.g., `f2`, `f3`).

`call` Matched call to `rNormal_reg()`.

`formula` Formula reconstructed from `y` and `x`.

`model` Model frame corresponding to formula.

`data` Data frame combining `y` and `x`.

`rNormalGamma_reg()` A list with class `"rglmb"` containing:

`coefficients` Matrix ($n \times p$) of simulated regression coefficients; row i equals $B_{\text{tilde}} + IR_{ii} \times rnorm(p) \times \sqrt{dispersion[i]}$. Column names are set to `colnames(x)`.

`coef.mode` Posterior mean/mode vector B_{tilde} from `rNormal_reg.wfit()`.

`dispersion` Numeric vector of length n with draws from the inverse-gamma posterior $1/\text{rgamma}(\text{shape} = \text{shape} + \text{nobs}/2, \text{rate} = \text{rate} + 0.5 \times S)$.

`Prior` List with `mean` (as numeric vector μ) and `Precision` (matrix P).

`offset` Offset vector as supplied.

`prior.weights` Vector of prior weights wt .

`y` Response vector.

`x` Design matrix.

`fit` Result from `rNormal_reg.wfit()`, including fields such as B_{tilde} , IR , S , and k .

`famfunc` Processed family functions for Gaussian models (from `glmbfamfunc(gaussian())`).

`iters` Numeric vector (length n) of ones indicating per-draw iteration counts.

`Envelope` NULL; no envelope is constructed in this conjugate setup.

`call` Matched call to `rNormalGamma_reg()`.

`rindepNormalGamma_reg()` A list with class "rglmb" containing:

- `coefficients` Matrix ($n \times p$) of simulated regression coefficients, back-transformed to the original scale; column names set to `colnames(x)`.
- `coef.mode` Vector with the conditional posterior mode used for envelope anchoring (from the Gaussian fit).
- `dispersion` Numeric vector of length n with simulated dispersion draws.
- `Prior` List with prior components: mean (prior mean μ), Sigma (prior covariance), shape and rate (Gamma prior for dispersion), Precision (`solve(Sigma)`).
- `family` The `gaussian()` family object.
- `prior.weights` Vector of prior weights used in the simulation.
- `y` Response vector.
- `x` Design matrix.
- `call` Matched call to `rindepNormalGamma_reg()`.
- `famfunc` Processed family functions for Gaussian models (from `glmbfamfunc`).
- `iters` Vector with per-draw iteration counts returned by the joint sampler.
- `Envelope` NULL; envelope diagnostics are not returned by this function.
- `loglike` NULL; placeholder for log-likelihood values.
- `weight_out` Numeric vector of per-draw weights returned by the C++ routine.
- `sim_bounds` List with low and upp, the dispersion bounds used by the shared envelope.
- `offset2` Offset vector used internally (copy of input or a zero vector).

`rGamma_reg()` An object of class "rGamma_reg" containing:

- `coefficients` A $1 \times p$ matrix of assumed regression coefficients.
- `coef.mode` Currently NULL; reserved for future use.
- `dispersion` A vector of simulated dispersion values.
- `Prior` A list with prior parameters: shape and rate.
- `prior.weights` Vector of prior weights used in the simulation.
- `y` The response vector.

Author(s)

The simulation framework was developed by Kjell Nygren as part of the **glmbayes** package. It builds on the likelihood subgradient approach described in (Nygren and Nygren 2006), and extends classical Bayesian GLM sampling techniques.

References

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Raiffa H, Schlaifer R (1961). *Applied Statistical Decision Theory*. Clinton Press, Inc., Boston.

See Also

`pfamily`, `rglmb`, `rlmb` for modeling functions that consume simulation functions.

`rNormal_reg`, `rNormalGamma_reg`, `rGamma_reg` for individual simulation functions.

`EnvelopeBuild`, `EnvelopeEval`, `EnvelopeSize` for envelope construction and grid evaluation used in likelihood-subgradient sampling.

Theory and implementation narrative: (Nygren and Nygren 2006); (Nygren 2025, 2025).

glmbayes Simulation Functions `multi_rNormal_reg()`, `multi_rlmb()`, `rGLMM_Re_Draw()`, `rGLMM_reg()`, `rGLMM_sweep()`, `rLMM_reg`, `rindNormalGamma_reg_with_envelope()`, `two_block_optimize_pilot_cost()`, `two_block_rNormal_reg()`, `two_block_rate()`, `two_block_tv_bound()`

glmbayes Simulation Functions `multi_rNormal_reg()`, `multi_rlmb()`, `rGLMM_Re_Draw()`, `rGLMM_reg()`, `rGLMM_sweep()`, `rLMM_reg`, `rindNormalGamma_reg_with_envelope()`, `two_block_optimize_pilot_cost()`, `two_block_rNormal_reg()`, `two_block_rate()`, `two_block_tv_bound()`

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glmbayes Simulation Functions `multi_rNormal_reg()`, `multi_rlmb()`, `rGLMM_Re_Draw()`, `rGLMM_reg()`, `rGLMM_sweep()`, `rLMM_reg`, `rindNormalGamma_reg_with_envelope()`, `two_block_optimize_pilot_cost()`, `two_block_rNormal_reg()`, `two_block_rate()`, `two_block_tv_bound()`

glmbayes Simulation Functions `multi_rNormal_reg()`, `multi_rlmb()`, `rGLMM_Re_Draw()`, `rGLMM_reg()`, `rGLMM_sweep()`, `rLMM_reg`, `rindNormalGamma_reg_with_envelope()`, `two_block_optimize_pilot_cost()`, `two_block_rNormal_reg()`, `two_block_rate()`, `two_block_tv_bound()`

glmbayes Simulation Functions `multi_rNormal_reg()`, `multi_rlmb()`, `rGLMM_Re_Draw()`, `rGLMM_reg()`, `rGLMM_sweep()`, `rLMM_reg`, `rindNormalGamma_reg_with_envelope()`, `two_block_optimize_pilot_cost()`, `two_block_rNormal_reg()`, `two_block_rate()`, `two_block_tv_bound()`

Examples

```
##### Start of rNormal_reg examples #####
set.seed(333)

## Dobson (1990) Page 93: Randomized Controlled Trial :
counts <- c(18, 17, 15, 20, 10, 20, 25, 13, 12)
outcome <- gl(3, 1, 9)
treatment <- gl(3, 3)
```

```

print(d.AD <- data.frame(treatment, outcome, counts))

## Poisson Prior and rNormal_reg call (using Prior_Setup for x, y, and prior values)
ps <- Prior_Setup(counts ~ outcome + treatment, family = poisson(), data = d.AD)

out_pois <- rNormal_reg(
  n = 1000,
  y = ps$y,
  x = ps$x,
  prior_list = list(mu = ps$mu, Sigma = ps$Sigma),
  family = poisson(link = "log"),
  weights = rep(1, nrow(ps$x))
)
print(out_pois)

## Menarche Binomial Data Example
data(menarche, package = "MASS")
menarche$Age2 <- menarche$Age - 13

## Logit Prior and rNormal_reg call (use proportion + trial weights)
ps1 <- Prior_Setup(
  Menarche / Total ~ Age2,
  family = binomial(logit),
  data = menarche,
  weights = menarche$Total
)

out_logit <- rNormal_reg(
  n = 1000,
  y = ps1$y,
  x = ps1$x,
  prior_list = list(mu = ps1$mu, Sigma = ps1$Sigma),
  family = binomial(logit),
  weights = menarche$Total
)
print(out_logit)

## Probit Prior and rNormal_reg call
ps2 <- Prior_Setup(
  Menarche / Total ~ Age2,
  family = binomial(probit),
  data = menarche,
  weights = menarche$Total
)

out_probit <- rNormal_reg(
  n = 1000,
  y = ps2$y,
  x = ps2$x,
  prior_list = list(mu = ps2$mu, Sigma = ps2$Sigma),
  family = binomial(probit),
  weights = menarche$Total
)

```

```

)
print(out_probit)

## clog-log Prior and rNormal_reg call
ps3 <- Prior_Setup(
  Menarche / Total ~ Age2,
  family = binomial(cloglog),
  data = menarche,
  weights = menarche$Total
)

out_cloglog <- rNormal_reg(
  n = 1000,
  y = ps3$y,
  x = ps3$x,
  prior_list = list(mu = ps3$mu, Sigma = ps3$Sigma),
  family = binomial(cloglog),
  weights = menarche$Total
)
print(out_cloglog)

## Gamma regression
data(carinsca)
carinsca$Merit <- ordered(carinsca$Merit)
carinsca$Class <- factor(carinsca$Class)
oldopt <- options(contrasts = c("contr.treatment", "contr.treatment"))

psg <- Prior_Setup(
  Cost / Claims ~ Merit + Class,
  family = Gamma(link = "log"),
  data = carinsca,
  weights = carinsca$Claims
)

out_gamma <- rNormal_reg(
  n = 1000,
  y = psg$y,
  x = psg$x,
  prior_list = list(mu = psg$mu, Sigma = psg$Sigma, dispersion = psg$dispersion),
  family = Gamma(link = "log"),
  weights = carinsca$Claims
)
print(out_gamma)
options(oldopt)
##### Start of rNormalGamma_reg examples #####
## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.
ctl <- c(4.17,5.58,5.18,6.11,4.50,4.61,5.17,4.53,5.33,5.14)
trt <- c(4.81,4.17,4.41,3.59,5.87,3.83,6.03,4.89,4.32,4.69)
group <- gl(2, 10, 20, labels = c("Ctl","Trt"))
weight <- c(ctl, trt)

```

```

ps=Prior_Setup(weight ~ group)
mu <- ps$mu
shape <- ps$shape
rate <- ps$rate

y <- ps$y
x <- as.matrix(ps$x)
prior_list <- list(mu = mu, Sigma = ps$Sigma_0, shape = shape, rate = rate)
ngamma.D9 <- rNormalGamma_reg(n = 1000, y = y, x = x,
  prior_list = prior_list)

print(ngamma.D9)
##### Start of rindepNormalGamma_reg examples #####
## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.
ctl <- c(4.17,5.58,5.18,6.11,4.50,4.61,5.17,4.53,5.33,5.14)
trt <- c(4.81,4.17,4.41,3.59,5.87,3.83,6.03,4.89,4.32,4.69)
group <- gl(2, 10, 20, labels = c("Ctl","Trt"))
weight <- c(ctl, trt)
p_setup <- Prior_Setup(weight ~ group, family = gaussian())

mu <- p_setup$mu
Sigma_prior <- p_setup$Sigma
dispersion <- p_setup$dispersion
shape <- p_setup$shape
rate <- p_setup$rate
y <- p_setup$y
x <- p_setup$x

prior_list <- list(
  mu = mu,
  Sigma = Sigma_prior,
  dispersion = dispersion,
  shape = shape,
  rate = rate,
  Precision = solve(Sigma_prior),
  max_disp_perc = 0.99
)

set.seed(360)

sim2 <- rindepNormalGamma_reg(n = 1000, y, x, prior_list = prior_list)
print(sim2)

##### Start of rGamma_reg examples #####
## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.
ctl <- c(4.17, 5.58, 5.18, 6.11, 4.50, 4.61, 5.17, 4.53, 5.33, 5.14)

```

```

trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)

## Set up prior hyperparameters (shape/rate) and model matrix via Prior_Setup
ps <- Prior_Setup(weight ~ group, family = gaussian())
y <- ps$y
x <- as.matrix(ps$x)

## rGamma_reg uses a dGamma-style prior on dispersion with fixed beta.
## Use coefficients from Prior_Setup (full-model GLM MLE by default).
prior_list <- list(beta = ps$coefficients, shape = ps$shape, rate = ps$rate)

out <- rGamma_reg(n = 1000, y = y, x = x, prior_list = prior_list, family = gaussian())
summary(out)

```

SimulationPipeline

Low-Level Simulation Pipeline for Bayesian GLMs

Description

A detailed overview of the low-level simulation pipeline used by `rglmb()` and related functions. These routines implement the optimization -> standardization -> envelope sizing -> envelope construction -> sampling -> back-transformation workflow described in (Nygren and Nygren 2006).

Details

(summaries of each step)

References

Nygren K~N, Nygren L~M (2006). "Likelihood Subgradient Densities." *Journal of the American Statistical Association*, **101**(475), 1144–1156. doi:10.1198/016214506000000357.

Examples

```

##### Start of rNormalGLM_std examples #####
data(menarche, package="MASS")

summary(menarche)
plot(Menarche/Total ~ Age, data=menarche)

Age2=menarche$Age-13

x<-matrix(as.numeric(1.0),nrow=length(Age2),ncol=2)
x[,2]=Age2

y=menarche$Menarche/menarche$Total
wt=menarche$Total

```

```

mu<-matrix(as.numeric(0.0),nrow=2,ncol=1)
mu[2,1]=(log(0.9/0.1)-log(0.5/0.5))/3

V1<-1*diag(as.numeric(2.0))

# 2 standard deviations for prior estimate at age 13 between 0.1 and 0.9
## Specifies uncertainty around the point estimates

V1[1,1]<-((log(0.9/0.1)-log(0.5/0.5))/2)^2
V1[2,2]=(3*mu[2,1]/2)^2 # Allows slope to be up to 1 times as large as point estimate

famfunc<-glmbfamfunc(binomial(logit))

f1<-famfunc$f1
f2<-famfunc$f2 # Used in optim and glmsim_cpp
f3<-famfunc$f3 # Used in optim
f5<-famfunc$f5
f6<-famfunc$f6

dispersion2<-as.numeric(1.0)
start <- mu
offset2=rep(as.numeric(0.0),length(y))
P=solve(V1)
n=1000

##### Adjust weight for dispersion

wt2=wt/dispersion2

##### Shift mean vector to offset so that adjusted model has 0 mean

alpha=x%*as.vector(mu)+offset2
mu2=0*as.vector(mu)
P2=P
x2=x

##### Optimization step to find posterior mode and associated Precision

parin=start-mu

opt_out=optim(parin,f2,f3,y=as.vector(y),x=as.matrix(x),mu=as.vector(mu2),
              P=as.matrix(P),alpha=as.vector(alpha),wt=as.vector(wt2),
              method="BFGS",hessian=TRUE
)

bstar=opt_out$par ## Posterior mode for adjusted model
bstar
bstar+as.vector(mu) # mode for actual model
A1=opt_out$hessian # Approximate Precision at mode

## Standardize Model

```

```

Standard_Mod=glmb_Standardize_Model(y=as.vector(y), x=as.matrix(x),P=as.matrix(P),
                                     bstar=as.matrix(bstar,ncol=1), A1=as.matrix(A1))

bstar2=Standard_Mod$bstar2
A=Standard_Mod$A
x2=Standard_Mod$x2
mu2=Standard_Mod$mu2
P2=Standard_Mod$P2
L2Inv=Standard_Mod$L2Inv
L3Inv=Standard_Mod$L3Inv

Env2=EnvelopeBuild(as.vector(bstar2), as.matrix(A),y, as.matrix(x2),
                   as.matrix(mu2,ncol=1),as.matrix(P2),as.vector(alpha),as.vector(wt2),
                   family="binomial",link="logit",Gridtype=as.integer(3),
                   n=as.integer(n),sortgrid=TRUE)

## These now seem to match

Env2

# The low-level sampler is called below with explicit type coercions.

### Note: getting the types correct here is important but potentially difficult for users
### May be better to call an R function wrapper that checks (and converts when possible)
## to correct types

sim=rNormalGLM_std(n=as.integer(n),y=as.vector(y),x=as.matrix(x2),mu=as.matrix(mu2,ncol=1),
                  P=as.matrix(P2),alpha=as.vector(alpha),wt=as.vector(wt2),
                  f2=f2,Envelope=Env2,family="binomial",link="logit",as.integer(0))

out=L2Inv%*%L3Inv%*%t(sim$out)

for(i in 1:n){
  out[,i]=out[,i]+mu
}

summary(t(out))
mean(sim$draws)

```

Description

These functions are [methods](#) for class "mrglmb" or "summary.mrglmb" objects produced by [multi_rindepNormalGamma_reg](#), [multi_rNormalGamma_reg](#), [multi_rNormal_reg](#), or [multi_rlmb](#).

Usage

```
## S3 method for class 'mrglmb'
summary(object, ...)

## S3 method for class 'summary.mrglmb'
print(x, digits = max(3, getOption("digits") - 3), ...)
```

Arguments

object	An object of class "mrglmb".
x	An object of class "summary.mrglmb" for which printed output is desired.
digits	The number of significant digits to use when printing.
...	Additional optional arguments passed to summary.rglmb or print.summary.rglmb .

Details

Mirrors the behavior of [summary.mlm](#): each response column is summarized independently using [summary.rglmb](#) and printed with a "Response <name> :" header.

Value

summary.mrglmb returns a named list of "summary.rglmb" objects (one per response column), with class "summary.mrglmb". The names match names(object).

See Also

[multi_rlm](#), [multi_rNormalGamma_reg](#), [multi_rNormal_reg](#), [multi_rindepNormalGamma_reg](#), [summary.rglmb](#)

summary.rGamma_reg	<i>Summarizing Bayesian gamma_reg Distribution Functions</i>
--------------------	--

Description

These functions are all [methods](#) for class rGamma_reg or summary.rGamma_reg objects.

Usage

```
## S3 method for class 'rGamma_reg'
summary(object, ...)

## S3 method for class 'summary.rGamma_reg'
print(x, digits = max(3, getOption("digits") - 3), ...)
```

Arguments

object	an object of class "rGamma_reg" for which a summary is desired.
x	an object of class "summary.rGamma_reg" for which a printed output is desired.
digits	the number of significant digits to use when printing.
...	Additional optional arguments

Value

summary.rGamma_reg() returns an object of class "summary.rGamma_reg", a list containing summaries of posterior draws for the dispersion and precision parameters. Components include:

call	the matched call from the fitted object.
n	number of posterior draws.
coefficients1	matrix of prior means and standard deviations for precision and dispersion.
coefficients	matrix of posterior means, posterior standard deviations, Monte Carlo errors, and empirical tail probabilities.
Percentiles	matrix of posterior percentiles for dispersion draws.
implied_disp_point	dispersion point estimate implied by the Gamma prior on precision, computed as rate / shape.

print.summary.rGamma_reg() prints the summary object and returns x invisibly.

Examples

```
## summary.rGamma_reg: dGamma prior (dispersion-only; coefficients fixed)
## All three functions (rGamma_reg, rglmb, rlmb) use summary.rGamma_reg when
## prior is dGamma.
##
## This example uses the Boston data: Prior_Setup() for hyperparameters and
## ps$coefficients as fixed beta for dGamma / rGamma_reg-style runs.
data("Boston", package = "MASS")

predictors <- setdiff(names(Boston), "medv")
Boston_centered <- Boston
Boston_centered[predictors] <- scale(Boston[predictors], center = TRUE, scale = FALSE)

form <- medv ~
  crim + zn +
  indus + chas + nox + age + dis + rad + tax + ptratio + black + lstat + rm

ps.boston <- Prior_Setup(form, gaussian(), data = Boston_centered)
rate_dg <- if (!is.null(ps.boston$rate_gamma)) ps.boston$rate_gamma else ps.boston$rate

y <- ps.boston$y
x <- as.matrix(ps.boston$x)
wt <- rep(1, length(y))

## 1. rGamma_reg
```

```

out1 <- rGamma_reg(
  n = 1000,
  y = y,
  x = x,
  prior_list = list(beta = ps.boston$coefficients, shape = ps.boston$shape, rate = rate_dg),
  offset = rep(0, length(y)),
  weights = wt,
  family = gaussian()
)
summary(out1)

## 2. rglmb
out2 <- rglmb(n = 1000, y = y, x = x,
  pfamily = dGamma(shape = ps.boston$shape, rate = rate_dg, beta = ps.boston$coefficients),
  weights = wt, family = gaussian())
summary(out2)

## 3. rlmb
out3 <- rlmb(n = 1000, y = y, x = x,
  pfamily = dGamma(shape = ps.boston$shape, rate = rate_dg, beta = ps.boston$coefficients),
  weights = wt)
summary(out3)

```

summary.rglmb

Summarizing Bayesian Generalized Linear Model Distribution Functions

Description

These functions are all [methods](#) for class `rglmb`, `rlmb`, or `summary.rglmb` objects.

Usage

```

## S3 method for class 'rglmb'
summary(object, ...)

## S3 method for class 'rlmb'
summary(object, ...)

## S3 method for class 'summary.rglmb'
print(x, digits = max(3, getOption("digits") - 3), ...)

```

Arguments

<code>object</code>	an object of class <code>"rglmb"</code> or <code>"rlmb"</code> for which a summary is desired.
<code>x</code>	an object of class <code>"summary.rglmb"</code> for which a printed output is desired.
<code>digits</code>	the number of significant digits to use when printing.
<code>...</code>	Additional optional arguments

Details

`summary.rglmb` summarizes output from `rglmb` or `rlmb`. For dGamma rate-prior Poisson fits, it delegates to `summary.rGamma_reg`.

Value

`summary.rglmb` returns an object of class `"summary.rglmb"`, a list with posterior summaries, DIC-related quantities, and tables suitable for `print.summary.rglmb`.

See Also

`rglmb`, `rlmb`, `summary.rGamma_reg`, `summary.glm`, `summary.lm`.

Examples

```
data(menarche, package = "MASS")

summary(menarche)

Age2 <- menarche$Age - 13

x <- matrix(as.numeric(1.0), nrow = length(Age2), ncol = 2)
x[, 2] <- Age2

y <- menarche$Menarche / menarche$Total
wt <- menarche$Total

mu <- matrix(as.numeric(0.0), nrow = 2, ncol = 1)
mu[2, 1] <- (log(0.9 / 0.1) - log(0.5 / 0.5)) / 3

V1 <- 1 * diag(as.numeric(2.0))

V1[1, 1] <- ((log(0.9 / 0.1) - log(0.5 / 0.5)) / 2)^2
V1[2, 2] <- (3 * mu[2, 1] / 2)^2

out <- rglmb(
  n = 1000, y = y, x = x, pfamily = dNormal(mu = mu, Sigma = V1),
  weights = wt, family = binomial(logit)
)
summary(out)
```

two_block_align_b_to_xhyper

Align random-effect vector to X_hyper row order

Description

Maps one column of Block~1 random effects (b, in group_levels order) to the row order of X_hyper[[k]] for Block~2 pseudo-response y. See `inst/ARCHITECTURE_glmrb.md`.

Usage

```
two_block_align_b_to_xhyper(b_vec, X_k, group_levels)
```

```
two_block_align_b_to_xhyper_cpp(b_vec, X_k, group_levels)
```

Arguments

b_vec Length-J vector for one RE component (named by `group_levels` or positional).
X_k Group-level design matrix ($J \times q_k$).
group_levels Character vector defining Block~1 row order of `b`.

Value

Numeric vector of length `nrow(X_k)` in `X_hyper` row order.

```
two_block_block2_one_chain
```

One-chain Block 2 update (fixed effects, τ^2 , iteration counts)

Description

Given current random effects for replicate chain `i`, update fixed effects (and ING dispersion) via one `rglmb()` call per RE component.

Usage

```
two_block_block2_one_chain(
  i,
  b,
  fixef,
  tau2,
  iters,
  re_names,
  group_levels,
  design,
  pfamily_list,
  ptypes
)
```

Arguments

i Chain index (1 . . n).
b $J \times p_{re} \times n$ array of random effects (read-only).
fixef Named list of fixed-effect matrices ($n \times p_k$ per RE block).
tau2 $n \times p_{re}$ matrix of random-effect variances.

iters	n x p_re matrix of Block~2 iteration counts.
re_names	Character vector of random-effect block names.
group_levels	Character vector of group level labels.
design	Model design list (X_hyper, etc.).
pfamily_list	Named list of Block~2 pfamily objects.
ptypes	Named character vector of pfamily types.

Value

List with fixef, tau2, and iters (each fully updated for chain i).

See Also

[two_block_block2_one_chain_cpp](#), [rGLMM_sweep](#)

two_block_block2_one_chain_cpp

Block 2 one-chain update via C++ (native align + rglmb)

Description

Same semantics as [two_block_block2_one_chain](#); b is aligned to X_hyper rows in C++ before each rglmb() call.

Usage

```
two_block_block2_one_chain_cpp(
  i,
  b,
  fixef,
  tau2,
  iters,
  re_names,
  group_levels,
  design,
  pfamily_list,
  ptypes
)
```

Arguments

i	Chain index (1 . . n).
b	J x p_re x n array of random effects (read-only).
fixef	Named list of fixed-effect matrices (n x p_k per RE block).
tau2	n x p_re matrix of random-effect variances.

iters	n x p_re matrix of Block~2 iteration counts.
re_names	Character vector of random-effect block names.
group_levels	Character vector of group level labels.
design	Model design list (X_hyper, etc.).
pfamily_list	Named list of Block~2 pfamily objects.
ptypes	Named character vector of pfamily types.

Value

List with fixef, tau2, and iters.

two_block_optimize_pilot_cost

Pilot / main chain cost calibration for two-block GLMM sampling

Description

Tools for the pilot-vs-main trade-off in non-Gaussian two-block GLMM paths: certificate the start distance when main chains begin at a pilot mean, calibrate m_convergence from Nygren TV bounds, evaluate total inner-sweep cost, and search for a cost-optimal n_pilot.

Usage

```
two_block_d0_pilot_start(n_pilot, p, pilot_start_tol = 0.95)
```

```
two_block_m_convergence_for_pilot_start(
  rate,
  n_pilot,
  tv_tol,
  p,
  pilot_start_tol = 0.95,
  method = c("theorem3", "corollary1")
)
```

```
two_block_pilot_sampling_cost(
  n,
  n_pilot,
  rate,
  tv_tol,
  m_convergence_pilot,
  p,
  pilot_start_tol = 0.95,
  method = c("theorem3", "corollary1")
)
```

```

two_block_optimize_pilot_cost(
  n,
  rate,
  tv_tol,
  m_convergence_pilot,
  p,
  pilot_start_tol = 0.95,
  method = c("theorem3", "corollary1"),
  n_pilot_min = 1L,
  n_pilot_max = NULL
)

```

Arguments

n_pilot	Number of pilot replicate chains (positive integer).
p	Dimension of the Block~2 hyper vector (positive integer).
pilot_start_tol	One-sided chi-squared quantile in $(0, 1)$ for the D_0 certificate (default 0.95).
rate	Object from two_block_rate .
tv_tol	Target total-variation tolerance in $(0, 1)$ passed to two_block_l_for_tv when calibrating m_convergence.
method	"theorem3" (exact terms) or "corollary1" (geometric envelope).
n	Number of main-stage stored draws.
m_convergence_pilot	Inner Gibbs sweeps per pilot stored draw (m_p).
n_pilot_min, n_pilot_max	Integer bounds for the n_pilot search in two_block_optimize_pilot_cost (inclusive). When n_pilot_max is NULL, defaults to $\max(10000L, 10L * n)$.

Details

The functions form a bottom-up stack:

1. [two_block_d0_pilot_start](#): $D_0 = \chi_{p,\alpha}^2 / n_{\text{pilot}}$ for a pilot-mean start.
2. [two_block_m_convergence_for_pilot_start](#): main-stage m_convergence at that D_0 (via [two_block_l_for_tv](#)).
3. [two_block_pilot_sampling_cost](#): $C = n_{\text{pilot}} m_p + n m_{\text{conv}}(n_{\text{pilot}})$.
4. [two_block_optimize_pilot_cost](#): minimize C over n_pilot (advisory unless wired into [rGLMM_reg](#)).

This is the Gibbs analogue of [EnvelopeOpt](#)'s build-plus-sample cost.

Value

Non-negative scalar D_0 .

List with m_convergence (integer sweeps per main draw), m_min (mode-start minimum), delta_m, D_0, and n_pilot.

List with total_cost, pilot_cost, main_cost, m_convergence, and the fields returned by two_block_m_convergence_for

List with n_pilot_opt, m_convergence_opt, total_cost_opt, cost_at_opt, and cost_curve (data frame of evaluated n_pilot values near the optimum).

Functions

- `two_block_d0_pilot_start()`: Squared standardized start distance from a pilot mean start: $D_0 = \chi_{p,\alpha}^2 / n_{\text{pilot}}$.
- `two_block_m_convergence_for_pilot_start()`: Main-stage inner sweeps for a pilot-mean chain start. When n_pilot is large, D_0 is small and the result approaches the mode-start minimum m_min.
- `two_block_pilot_sampling_cost()`: Total inner-sweep cost for a pilot / main sampling plan: $C = n_{\text{pilot}} m_p + n m_{\text{conv}}(n_{\text{pilot}})$.
- `two_block_optimize_pilot_cost()`: Search over candidate n_pilot values for the minimum of `two_block_pilot_sampling_cost`. The returned optimum is advisory only unless wired into the sampler.

See Also

`two_block_rate`, `two_block_l_for_tv`, `EnvelopeOpt`, `rGLMM_reg`

glmbayes Simulation Functions `multi_rNormal_reg()`, `multi_rlmb()`, `rGLMM_Re_Draw()`, `rGLMM_reg()`, `rGLMM_sweep()`, `rLMM_reg`, `rinddepNormalGamma_reg_with_envelope()`, `simfuncs`, `two_block_rNormal_reg()`, `two_block_rate()`, `two_block_tv_bound()`

two_block_rate

Two-block Gibbs sampler convergence rate (Remark 8 eigenvalues)

Description

Computes the eigenvalues of $A = P_{11}^{-1/2} P_{12} P_{22}^{-1} P_{21} P_{11}^{-1/2}$ for the joint Gaussian posterior targeted by `two_block_rNormal_reg` with `family = gaussian()` and fixed variance components. The maximal eigenvalue λ^* is the geometric contraction rate of the two-block Gibbs sampler (Nygren 2020, Claim 2 / Remark 8 / Corollary 1): the total variation distance between the l -step kernel and the target decays like $(\lambda^*)^l$.

Usage

```
two_block_rate(
  x,
  block,
  x_hyper,
  prior_list_block1,
  prior_list_block2,
  weights = NULL,
  family = gaussian(),
  group_levels = levels(block),
```

```

    warn_slow = TRUE
  )

  ## S3 method for class 'two_block_rate'
  print(x, tols = c(0.01, 0.001, 1e-06), ...)

  two_block_rate_from_pfamily_list(
    x,
    block,
    x_hyper,
    prior_list_block1,
    pfamily_list,
    weights = NULL,
    family = gaussian(),
    group_levels = levels(block),
    warn_slow = TRUE
  )

```

Arguments

<code>x</code>	Object of class "two_block_rate".
<code>block</code>	Grouping factor or block partition of length 12.
<code>x_hyper</code>	Named list of group-level design matrices X_k ($J \times q_k$), one per column of <code>x</code> .
<code>prior_list_block1</code>	Block 1 prior: P or Sigma ($p_{re} \times p_{re}$); dispersion required for <code>gaussian()</code> when <code>weights</code> is NULL.
<code>prior_list_block2</code>	Named list of Block 2 prior lists (each with P or Sigma, $q_k \times q_k$).
<code>weights</code>	Optional per-observation working weights (length 1 or 12). Default for <code>gaussian()</code> : $1 / \text{prior_list_block1}\$dispersion$. Required for non-Gaussian families.
<code>family</code>	Response family (default <code>gaussian()</code>).
<code>group_levels</code>	Character vector defining group order (default <code>levels(block)</code>); must match the row order of <code>x_hyper</code> when rownames are absent.
<code>warn_slow</code>	If TRUE (default), issue a <code>warning()</code> when <code>lambda_star</code> exceeds 0.95 (strong cross-block coupling and potentially slow convergence). Set FALSE for repeated internal rate evaluations (e.g. pilot upper-bound scans).
<code>tol</code>	Numeric vector of TV tolerances for the implied <code>m_convergence</code> table.
<code>...</code>	Ignored.
<code>pfamily_list</code>	Named list of <code>pfamily</code> objects (one per RE component), as in two_block_rNormal_reg .

Details

Block convention: the paper's x_1 (the block updated second in each sweep) is the Block 2 hyper vector γ of dimension $q = \sum_k q_k$; the paper's x_2 is the Block 1 random-effect stack. A is therefore $q \times q$ and is computed without ever forming the $J_{p_{re}} \times J_{p_{re}}$ Block 1 precision: per group only $p_{re} \times p_{re}$ solves are needed, followed by a single $q \times q$ symmetric eigendecomposition.

For non-Gaussian families the joint posterior is not normal; supplying IRLS-style weights evaluated at the posterior mode (via the internal `two_block_mode_weights()` helper used by `rGLMM_reg`) yields a local-Gaussian heuristic rate (no theorem applies).

Value

Object of class "two_block_rate": a list with `lambda_star` (the Remark 8 rate), eigenvalues (full spectrum $a_1 \geq \dots \geq a_q$ in $[0, 1)$), `m_for_tol` (function: iterations needed so that $(\lambda^*)^m \leq \text{tol}$), $S(P_{12}P_{22}^{-1}P_{21})$, `P11`, `dims`, `re_names`, `gamma_names`, `group_levels`, `family`, `weights_source`, and `call`.

`x` invisibly.

Functions

- `two_block_rate_from_pfamily_list()`: Convergence rate from a `pfamily_list` Block~2 spec: thin wrapper that accepts Block~2 priors as `pfamily` objects. For `dNormal` components the fixed dispersion is used; for `dIndependent_Normal_Gamma` components the conservative `disp_lower` plug-in is used (the rate is then an upper bound over the truncated τ^2 range).

References

Nygren, K. (2020). *On the total variation distance between multivariate normal densities with applications to two-block Gibbs samplers*. Unpublished manuscript.

See Also

[two_block_tv_bound](#), [two_block_rNormal_reg](#)

glmbayes Simulation Functions [multi_rNormal_reg\(\)](#), [multi_rlmb\(\)](#), [rGLMM_Re_Draw\(\)](#), [rGLMM_reg\(\)](#), [rGLMM_sweep\(\)](#), [rLMM_reg](#), [rindepNormalGamma_reg_with_envelope\(\)](#), [simfuncs](#), [two_block_optimize_pilot_cost](#), [two_block_rNormal_reg\(\)](#), [two_block_tv_bound\(\)](#)

`two_block_rNormal_reg` *Two-block Gibbs sampler with pfamily Block 2 priors*

Description

Runs the coupled Block~1 / Block~2 Gibbs sampler for two-block mixed models. Block~1 draws group-level random effects b_j ; Block~2 updates hyper means γ_k via `pfamily$simfun` (always Gaussian).

Usage

```
two_block_rNormal_reg(
  n,
  y,
  x,
  block,
  x_hyper,
  prior_list_block1,
  pfamily_list,
  fixef_start,
  re_coef_names = colnames(x),
  group_levels = levels(block),
  group_name = NULL,
  m_convergence = 10L,
  sampling = c("replicate", "chain"),
  family = gaussian(),
  offset = NULL,
  weights = 1,
  Gridtype = 2L,
  n_envopt = NULL,
  use_parallel = TRUE,
  use_openc1 = FALSE,
  verbose = FALSE,
  progbar = TRUE
)
```

Arguments

n	Number of stored draws.
y	Response vector of length nrow(x).
x	Level-1 design matrix Z (12 x p_re).
block	Grouping factor or block partition of length 12.
x_hyper	Named list of group-level design matrices X_k (J x q_k), one per column of x.
prior_list_block1	Prior for Block~1: P or Sigma, dispersion (required for gaussian()), optional ddef. mu is updated internally.
pfamily_list	Named list of pfamily objects, one per column of x: dNormal or dIndependent_Normal_Gamma .
fixef_start	Named list of hyper-parameter vectors at which each inner chain is initialised.
re_coef_names	Character vector naming columns of x.
group_levels	Character vector defining row order of Block~1 draws.
group_name	Name for the grouping column in coefficients.
m_convergence	Number of inner Gibbs steps per stored draw.
sampling	Sampling scheme; only "replicate" is implemented.
family	Response family for Block~1 (default gaussian()). Block~2 always uses gaussian().

offset, weights Passed to Block~1 (length 12 or recycled).
 Gridtype, n_envopt, use_parallel, use_opengl, verbose
 Passed to Block~1 when family is not Gaussian.
 progbars Logical; show a text progress bar.

Details

Each component of `pfamily_list` may be a [dNormal](#) prior (conjugate γ_k draw at fixed dispersion) or a [dIndependent_Normal_Gamma](#) prior, in which case Block~2 makes a joint (γ_k , τ^2_k) draw via the likelihood-subgradient envelope sampler (the same path as `rglmb` with an ING `pfamily`) and the sampled τ^2_k is fed back into the Block~1 prior precision on the next inner step. ING components must supply both `disp_lower` and `disp_upper`: every τ^2_k draw is hard-truncated to that window, and requiring both bounds keeps the window fixed across sweeps (one-sided specifications would fall back to a per-sweep surrogate-posterior window inside the envelope code, making the truncation state-dependent).

Value

Object of class "two_block_rNormal_reg" with fields `fixef_draws`, `coefficients`, `fixef_last`, `b_last`, `mu_all_last`, `family`, `n`, `m_convergence`, `sampling`, `fixef_start`, `re_coef_names`, `group_levels`, `group_name`, `call`, plus `dispersion_fixef_draws`: an $n \times p_{re}$ matrix of the Block~2 dispersion (τ^2_k) at each stored draw (constant columns for `dNormal` components), and `iters_fixef_draws`: an $n \times p_{re}$ matrix of the total number of Block~2 candidates generated per stored draw, summed over the `m_convergence` inner sweeps (mirrors `iters` in `rglmb`-style samplers; `dIndependent_Normal_Gamma` components count envelope accept-reject candidates until acceptance, `dNormal` components count exactly 1 conjugate draw per sweep, so their column equals `m_convergence`; divide by `m_convergence` for the average number of candidates per accepted draw).

See Also

[rGLMM_sweep](#), [rGLMM_reg](#), [rLMMNormal_reg](#), [dNormal](#), [dIndependent_Normal_Gamma](#)

glmbayes Simulation Functions [multi_rNormal_reg\(\)](#), [multi_rlmb\(\)](#), [rGLMM_Re_Draw\(\)](#), [rGLMM_reg\(\)](#), [rGLMM_sweep\(\)](#), [rLMM_reg](#), [rindepNormalGamma_reg_with_envelope\(\)](#), [simfuncs](#), [two_block_optimize_pilot_cost](#), [two_block_rate\(\)](#), [two_block_tv_bound\(\)](#)

<code>two_block_tv_bound</code>	<i>Total-variation bound for the two-block Gibbs sampler</i>
---------------------------------	--

Description

Evaluates the bound on the total variation distance between the l -step kernel of the two-block Gibbs sampler and its target (Nygren 2020), from the eigenvalue spectrum computed by [two_block_rate](#).

Usage

```
two_block_tv_bound(rate, l, method = c("theorem3", "corollary1"), D0 = 0)

two_block_l_for_tv(
  rate,
  tol,
  method = c("theorem3", "corollary1"),
  D0 = 0,
  l_max = 1000000L,
  warn = TRUE
)
```

Arguments

rate	Object from two_block_rate .
l	Integer vector of sweep counts (each ≥ 1).
method	"theorem3" (exact terms) or "corollary1" (geometric envelope).
D0	Optional squared standardized distance of the starting point from the posterior mean, $(x^{(0)} - \mu)^\top \Sigma_{11}^{-1} (x^{(0)} - \mu)$. Default 0 (start at the posterior mean).
tol	Target total-variation tolerance in (0, 1).
l_max	Search cap for the doubling/bisection search only; not used as the returned sweep count when certification fails.
warn	If TRUE (default), emit a single warning when the fallback path is taken. Set FALSE for repeated internal calls (e.g. pilot cost optimization) to avoid warning spam.

Details

method = "theorem3" evaluates the exact Theorem 3 terms $d_i^{(l)}$ using the closed form $\text{erf}_n(x) = P(\chi_n^2 \leq 2x^2)$ with $r_i^{(l)} = (1 - a_{i-1}^{2l}) / (1 - a_i^{2l})$. method = "corollary1" evaluates the looser geometric envelope of Corollary 1 (via Remarks 5 and 17), which decays like a_i^{2l} with explicit constants.

When the chain is started at the exact posterior mean (as `lmerb` does), $D0 = 0$ and the mean term of both bounds vanishes identically; only the variance-convergence sum remains. The returned bound is capped at 1.

Note the bound applies to the block updated *second* in each sweep (the Block 2 hyper vector γ); the stored Block 1 draw lags by a half-step, so evaluate at $l - 1$ when calibrating `m_convergence` for the random-effect draws.

Value

Numeric vector of TV bounds, one per element of `l`, capped at 1.

Integer: the required number of sweeps, or an uncertified fallback (see Details) with a warning when certification fails.

Functions

- `two_block_l_for_tv()`: Smallest l such that `two_block_tv_bound(rate, l, method, D0) <= tol`. The bound is decreasing in l , so a doubling search followed by bisection is exact. If the bound does not reach `tol` within `l_max` sweeps (near-degenerate `rate$lambda_star`, close to 1), a `warning()` is issued (when `warn = TRUE`) and the uncertified geometric proxy l from `rate$m_for_tol(tol)` is returned (not `l_max`). If `lambda_star >= 1 - .two_block_lambda_star_one_tol()`, `two_block_rate` stops before sweep calibration proceeds.

References

Nygren, K. (2020). *On the total variation distance between multivariate normal densities with applications to two-block Gibbs samplers*. Unpublished manuscript.

See Also

`two_block_rate`

glmbayes Simulation Functions `multi_rNormal_reg()`, `multi_rlmb()`, `rGLMM_Re_Draw()`, `rGLMM_reg()`, `rGLMM_sweep()`, `rLMM_reg`, `rinddepNormalGamma_reg_with_envelope()`, `simfuncs`, `two_block_optimize_pilot_cost`, `two_block_rNormal_reg()`, `two_block_rate()`

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