

Package ‘bmco’

March 10, 2026

Title Bayesian Analysis for Multivariate Categorical Outcomes

Version 0.1.0

Description Provides Bayesian methods for comparing groups on multiple binary outcomes. Includes basic tests using multivariate Bernoulli distributions, subgroup analysis via generalized linear models, and multilevel models for clustered data.

For statistical underpinnings, see Kavelaars, Mulder, and Kaptein (2020) <[doi:10.1177/0962280220922256](https://doi.org/10.1177/0962280220922256)>, Kavelaars, Mulder, and Kaptein (2024) <[doi:10.1080/00273171.2024.2337340](https://doi.org/10.1080/00273171.2024.2337340)>, and Kavelaars, Mulder, and Kaptein (2023) <[doi:10.1186/s12874-023-02034-z](https://doi.org/10.1186/s12874-023-02034-z)>.

An interactive shiny app to perform sample size computations is available.

License GPL (>= 3)

Encoding UTF-8

LazyData TRUE

LazyDataCompression xz

RoxygenNote 7.3.3

Imports abind, coda, MCMCpack, msm, pgdraw, tcltk, Rdpack, stats

Suggests knitr, rmarkdown, testthat, RefManageR

Config/testthat/edition 3

VignetteBuilder knitr

RdMacros Rdpack

URL <https://github.com/XynthiaKavelaars/bmco>,
<https://xynthia-kavelaars.shinyapps.io/bmco-pwr/>

BugReports <https://github.com/XynthiaKavelaars/bmco/issues>

Depends R (>= 3.5)

NeedsCompilation no

Author Xynthia Kavelaars [aut, cre] (ORCID:

<<https://orcid.org/0000-0003-1600-3153>>),

Joris Mulder [ths] (ORCID: <<https://orcid.org/0000-0001-7007-3086>>),

Maurits Kaptein [ths] (ORCID: <<https://orcid.org/0000-0002-6316-7524>>),

Dutch Research Council [fnd] (Grant no. 406.18.505)

Maintainer Xynthia Kavelaars <xynthia.kavelaars@ou.nl>

Repository CRAN

Date/Publication 2026-03-10 11:30:07 UTC

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bmco-package

bmco: Bayesian Analysis for Multivariate Categorical Outcomes

Description

Provides Bayesian methods for comparing groups on multiple binary outcomes, including basic tests, regression adjustment, and multilevel models.

Main functions

- **bmvb**: Bayesian test using multivariate Bernoulli
- **bglm**: Subgroup analysis using Bayesian logistic regression analysis
- **bglmm**: Multilevel data using Bayesian multilevel logistic regression analysis

Author(s)

Maintainer: Xynthia Kavelaars <xynthia.kavelaars@ou.nl> ([ORCID](#))

Other contributors:

- Joris Mulder ([ORCID](#)) [thesis advisor]
- Maurits Kaptein ([ORCID](#)) [thesis advisor]
- Dutch Research Council (Grant no. 406.18.505) [funder]

References

Kavelaars X, Mulder J, Kaptein M (2020). “Decision-making with multiple correlated binary outcomes in clinical trials.” *Statistical Methods in Medical Research*, **29**(11), 3265–3277. doi:[10.1177/0962280220922256](https://doi.org/10.1177/0962280220922256).

Kavelaars X, Mulder J, Kaptein M (2024). “Bayesian Multivariate Logistic Regression for Superiority and Inferiority Decision-Making under Observable Treatment Heterogeneity.” *Multivariate Behavioral Research*, **59**(4), 859–882. doi:[10.1080/00273171.2024.2337340](https://doi.org/10.1080/00273171.2024.2337340).

Kavelaars X, Mulder J, Kaptein M (2023). “Bayesian multilevel multivariate logistic regression for superiority decision-making under observable treatment heterogeneity.” *BMC Medical Research Methodology*, **23**(1). doi:[10.1186/s1287402302034z](https://doi.org/10.1186/s1287402302034z).

See Also

Useful links:

- <https://github.com/XynthiaKavelaars/bmco>
- <https://xynthia-kavelaars.shinyapps.io/bmco-pwr/>
- Report bugs at <https://github.com/XynthiaKavelaars/bmco/issues>

bglm

Bayesian Generalized Linear Model

Description

Perform a Bayesian test for differences between two (sub)groups on multiple binary outcomes using multinomial logistic regression as described in Kavelaars et al. (2024).

Usage

```
bglm(  
  data,  
  grp,  
  grp_a,  
  grp_b,  
  x_var,  
  y_vars,
```

```

x_method = c("Empirical", "Analytical", "Value"),
x_def = c(-Inf, Inf),
test = c("right_sided", "left_sided"),
rule = c("All", "Any", "Comp"),
w = NULL,
b_mu0 = NULL,
b_sigma0 = NULL,
n_burn = 10000,
n_it = 20000,
n_thin = 1,
n_chain = 2,
start = c(0.5, 1),
return_diagnostics = TRUE,
return_diagnostic_plots = FALSE,
return_samples = FALSE
)

```

Arguments

| | |
|-----------------------|---|
| <code>data</code> | Data frame containing the data. |
| <code>grp</code> | Character string. Name of the grouping variable (will be treated as factor). |
| <code>grp_a</code> | Value of <code>grp</code> indicating first group. |
| <code>grp_b</code> | Value of <code>grp</code> indicating second group. |
| <code>x_var</code> | Character string. Name of covariate variable (currently supports single continuous or binary covariate) |
| <code>y_vars</code> | Character vector. Names of outcome variables (currently supports 2 outcomes). |
| <code>x_method</code> | Character. Method for handling covariate: "Analytical" (numerical integration), "Empirical" (empirical marginalization), or "Value" (specific value). Default is "Empirical". |
| <code>x_def</code> | Numeric vector. Defines subpopulation: length-2 vector <code>c(lower, upper)</code> for "Analytical"/"Empirical", or scalar for "Value". Default is <code>c(-Inf, Inf)</code> . |
| <code>test</code> | Character. Direction of test: "left_sided" for $P(A>B)$ or "right_sided" for $P(B>A)$. Default is "right_sided". |
| <code>rule</code> | Character. Decision rule: "All" (all outcomes favor hypothesis), "Any" (at least one outcome favors hypothesis), or "Comp" (weighted combination). Default is "All". |
| <code>w</code> | Numeric vector. Weights for compensatory rule. Only used if <code>rule = "Comp"</code> . If <code>NULL</code> and <code>rule = "Comp"</code> , equal weights are used. Default is <code>NULL</code> . |
| <code>b_mu0</code> | Vector of prior means of fixed regression coefficients. Default is <code>rep(0, P)</code> , where <code>P</code> refers to the number of columns in the model matrix. |
| <code>b_sigma0</code> | Prior covariance matrix ($P \times P$) of regression coefficients. Default is <code>diag(1e-2, P)</code> , where <code>P</code> refers to the number of columns in the model matrix. |
| <code>n_burn</code> | Integer. Number of burn-in iterations. Default is 10000. |
| <code>n_it</code> | Integer. Number of MCMC iterations. Default is 20000. |

`n_thin` Integer. Thinning interval. Default is 1.

`n_chain` Integer. Number of MCMC chains to be sampled. Default is 2.

`start` Numeric vector. Starting values for chains. Should have length `n_chain`. Default is `c(0.5, 1)`.

`return_diagnostics` Logical. Return MCMC diagnostics? Default is TRUE.

`return_diagnostic_plots` Logical. Should MCMC chains for diagnostic plots (traceplots, autocorrelation, density) be returned? Default is FALSE. If TRUE, diagnostics are returned by default.

`return_samples` Logical. Should posterior samples be returned? Default is FALSE.

Value

An object of class `bglm`, a list containing:

estimates A list with posterior means and standard deviations of group probabilities (`mean_a`, `mean_b`, `sd_a`, `sd_b`), as well as posterior means (`b`) and standard deviations (`b_sd`) of the regression coefficients.

sample_sizes A list with group sample sizes (`n_a`, `n_b`).

delta A list with posterior mean differences (`mean_delta`), posterior standard errors (`se_delta`), posterior probability of the hypothesis (`pop`), and, if `rule = "Comp"`, the weighted difference (`w_delta`).

info A list with prior specifications, test settings, group labels, covariate handling method, and subpopulation definition.

diags If diagnostics are requested, a list with MCMC diagnostic results for the regression coefficients.

samples If `return_samples = TRUE`, a list containing posterior draws of `theta_a`, `theta_b`, `delta`, and regression coefficients.

References

Kavelaars X, Mulder J, Kaptein M (2024). "Bayesian Multivariate Logistic Regression for Superiority and Inferiority Decision-Making under Observable Treatment Heterogeneity." *Multivariate Behavioral Research*, **59**(4), 859–882. doi:10.1080/00273171.2024.2337340.

Examples

```
# Example with simulated data
# Generate data
set.seed(123)
n <- 100

data <- data.frame(
  group = rep(c("A", "B"), each = n/2),
  x = rnorm(n),
  stringsAsFactors = FALSE
```

```

)

p1 <- p2 <- rep(NA, n)

for (i in 1:n) {
  grpB <- ifelse(data$group[i] == "B", 1, 0)

  p1[i] <- plogis(-0.50 + 0.75 * grpB + 0.10 * data$x[i] + 0.20 * grpB * data$x[i])
  p2[i] <- plogis(-0.50 + 0.80 * grpB + 0.05 * data$x[i] + 0.15 * grpB * data$x[i])

  data$y1[i] <- rbinom(1, 1, p1[i])
  data$y2[i] <- rbinom(1, 1, p2[i])
}

# Analyze
result <- bglm(
  data = data,
  grp = "group",
  grp_a = "A",
  grp_b = "B",
  x_var = "x",
  y_vars = c("y1", "y2"),
  x_method = "Empirical",
  x_def = c(-Inf, Inf),
  test = "right_sided",
  rule = "All",
  n_burn = 100, # Too low for proper MCMC sampling
  n_it = 500 # Too low for proper MCMC sampling
)

print(result)

```

bglmm

Bayesian Generalized Linear Mixed Model

Description

Perform a Bayesian test for differences between two (sub)groups on multiple binary outcomes using multilevel multinomial logistic regression, as described in Kavelaars et al. (2023).

Usage

```

bglmm(
  data,
  grp,
  grp_a = NULL,
  grp_b = NULL,
  id_var,
  x_var,

```

```

y_vars,
x_method = c("Empirical", "Analytical", "Value"),
x_def = c(-Inf, Inf),
test = c("right_sided", "left_sided"),
rule = c("All", "Any", "Comp"),
w = NULL,
n_burn = 10000,
n_it = 50000,
start = c(0.5, 1),
fixed = NULL,
random = NULL,
b_mu0 = NULL,
b_sigma0 = NULL,
g_mu0 = NULL,
g_sigma0 = NULL,
nu0 = NULL,
tau0 = NULL,
n_chain = 2,
return_thinned = TRUE,
n_thin = 10,
return_diagnostics = TRUE,
return_diagnostic_plots = FALSE,
return_samples = FALSE
)

```

Arguments

| | |
|----------|--|
| data | Data frame containing the data. |
| grp | Character string. Name of the grouping variable. |
| grp_a | Value of grp indicating first group (will be determined from factor levels if NULL). |
| grp_b | Value of grp indicating second group (will be determined from factor levels if NULL). |
| id_var | Character string. Name of cluster/ID variable. |
| x_var | Character string. Name of covariate variable. |
| y_vars | Character vector. Names of outcome variables (currently supports 2 outcomes). |
| x_method | Character. Method for handling covariate. Default is "Empirical". |
| x_def | Numeric. Defines subpopulation. Default is $c(-Inf, Inf)$. |
| test | Character. Direction of test: "left_sided" for $P(A>B)$ or "right_sided" for $P(B>A)$. Default is "right_sided". |
| rule | Character. Decision rule: "All" (all outcomes favor hypothesis), "Any" (at least one outcome favors hypothesis), or "Comp" (weighted combination). Default is "All". |
| w | Numeric vector. Weights for compensatory rule. Only used if rule = "Comp". If NULL and rule = "Comp", equal weights are used. Default is NULL. |

| | |
|--------------------------------------|--|
| <code>n_burn</code> | Integer. Number of burn-in iterations. Default is 10000. |
| <code>n_it</code> | Integer. Number of MCMC iterations. Default is 50000 (takes long running time!). |
| <code>start</code> | Numeric vector. Starting values for chains. Default is <code>c(0.5, 1)</code> . |
| <code>fixed</code> | Character vector. Names of fixed effect variables. Default is <code>c(x_var, grp_x_var)</code> . |
| <code>random</code> | Character vector. Names of random effect variables. Default is <code>c("Intercept", grp)</code> . |
| <code>b_mu0</code> | Numeric vector. Prior means for fixed effects. Default is <code>rep(0, length(fixed))</code> . |
| <code>b_sigma0</code> | Matrix. Prior covariance for fixed effects. Default is <code>diag(0.1, length(fixed))</code> . |
| <code>g_mu0</code> | Numeric vector. Prior means for random effects. Default is <code>rep(0, length(random))</code> . |
| <code>g_sigma0</code> | Matrix. Prior covariance for random effects. Default is <code>diag(0.1, length(random))</code> . |
| <code>nu0</code> | Numeric. Prior degrees of freedom for inverse-Wishart. Default is <code>length(random)</code> . |
| <code>tau0</code> | Matrix. Prior scale matrix of dimension <code>length(random) x length(random)</code> for inverse-Wishart. Default is <code>diag(1e-1, length(random))</code> . |
| <code>n_chain</code> | Integer. Number of MCMC chains. Default is 2. |
| <code>return_thinned</code> | Logical. Return thinned chains? Default is TRUE. |
| <code>n_thin</code> | Integer. Thinning interval. Default is 10. |
| <code>return_diagnostics</code> | Logical. Return MCMC diagnostics? Default is TRUE. |
| <code>return_diagnostic_plots</code> | Logical. Should MCMC chains for diagnostic plots (traceplots, autocorrelation, density) be returned? Default is FALSE. If TRUE, diagnostics are returned by default. |
| <code>return_samples</code> | Logical. Return posterior samples? Default is FALSE. |

Value

An object of class `bglmm`, a list containing:

estimates A list with posterior means and standard deviations of group probabilities (`mean_a`, `mean_b`, `sd_a`, `sd_b`). If estimated, posterior means and standard deviations of fixed effects (`b`, `b_sd`) and random effects and variance components (`g`, `g_sd`, `tau`, `tau_sd`) are included.

sample_sizes A list with group sample sizes (`n_a`, `n_b`) and the number of clusters (`J`).

delta A list with posterior mean differences (`mean_delta`), posterior standard errors (`se_delta`), posterior probability of the hypothesis (`pop`), and, if `rule = "Comp"`, the weighted difference (`w_delta`).

info A list with prior specifications, model structure (fixed and random effects), test settings, group labels, covariate handling method, and subpopulation definition.

diags If diagnostics are requested, a list with MCMC diagnostic results for fixed effects, random effects, and variance components.

samples If `return_samples = TRUE`, a list containing posterior draws of group probabilities, differences, fixed effects, random effects, and variance components (if applicable).

References

Kavelaars X, Mulder J, Kaptein M (2023). “Bayesian multilevel multivariate logistic regression for superiority decision-making under observable treatment heterogeneity.” *BMC Medical Research Methodology*, **23**(1). doi:10.1186/s1287402302034z.

Examples

```
# Example with simulated data
# Generate data
set.seed(123)
J <- 20 # No. clusters
nJ <- 15 # Sample size per cluster

# Generate random intercepts
uj_1 <- rnorm(J)
uj_2 <- rnorm(J)
data <- data.frame(
  id = factor(rep(1:J, each = nJ)),
  group = rep(rep(c("A", "B"), each = J/2), each = nJ),
  x = rnorm(J * nJ),
  stringsAsFactors = FALSE
)

p1 <- p2 <- rep(NA, J * nJ)

for (i in 1:(J * nJ)) {
  j <- as.numeric(data$id[i])
  grpB <- ifelse(data$group[i] == "B", 1, 0)

  p1[i] <- plogis(-0.50 + 0.75 * grpB + 0.10 * data$x[i] + 0.20 * grpB * data$x[i] + uj_1[j])
  p2[i] <- plogis(-0.50 + 0.80 * grpB + 0.05 * data$x[i] + 0.15 * grpB * data$x[i] + uj_2[j])

  data$y1[i] <- rbinom(1, 1, p1[i])
  data$y2[i] <- rbinom(1, 1, p2[i])
}

# Analyze
result <- bglmm(
  data = data,
  grp = "group",
  grp_a = "A",
  grp_b = "B",
  id_var = "id",
  x_var = "x",
  y_vars = c("y1", "y2"),
  x_method = "Empirical",
  x_def = c(-Inf, Inf),
  fixed = c("group", "x", "group_x"),
  random = c("Intercept"), # Random intercept model
  test = "right_sided",
  rule = "All",
  n_burn = 100, # Too low for proper MCMC sampling
```

```

n_it = 500 # Too low for proper MCMC sampling
)

print(result) # Warnings due to low number of MCMC iterations (n_burn and n_it)

```

bglmm_data

Simulated Multilevel Clinical Trial Data

Description

A simulated dataset representing a two-arm clinical trial with 300 subjects nested within 20 clusters (e.g., hospitals), one continuous covariate, and two binary outcomes. It serves as the underlying data for `bglmm_fit` and can be used to illustrate `bglmm`.

Usage

```
bglmm_data
```

Format

A data frame with 300 rows and 5 columns:

id Factor with 20 levels (1–20). Cluster identifier (e.g., hospital). Each cluster contains 15 subjects.

group Character. Treatment arm: "placebo" (clusters 1–10) or "drug" (clusters 11–20).

age Numeric. Continuous covariate drawn from $N(50, 10^2)$.

y1 Integer (0/1). First binary outcome.

y2 Integer (0/1). Second binary outcome.

Details

Data were generated with `set.seed(2024)` using logistic models with cluster-specific random intercepts $u_{j1}, u_{j2} \sim N(0, 0.25)$:

$$P(y_1 = 1) = \text{logit}^{-1}(-0.50 + 0.75 \text{ drug} + 0.10 \text{ age}/10 + u_{j1})$$

$$P(y_2 = 1) = \text{logit}^{-1}(-0.50 + 0.80 \text{ drug} + 0.05 \text{ age}/10 + u_{j2})$$

where `drug` is 1 for the drug arm and 0 for placebo. See `data-raw/generate_examples.R` for the full script.

See Also

[bglmm](#), [bglmm_fit](#), [bglm_data](#)

Examples

```

head(bglmm_data)
table(bglmm_data$group, bglmm_data$id)

```

`bglmm_fit`*Pre-computed bglmm Example Fit*

Description

A fitted `bglmm` object estimated on `bglmm_data`. Used in package examples and tests so that `print`, `summary`, and `plot` examples run in well under 5 seconds without re-running the MCMC sampler.

Usage

```
bglmm_fit
```

Format

An object of class `bglmm` as returned by `bglmm`. See the **Value** section of `bglmm` for a full description of the list components. Key settings: `n_burn = 10000`, `n_it = 50000`, `n_thin = 10`, `n_chain = 2`, `return_diagnostics = TRUE`, `return_samples = TRUE`.

Details

Generated with `set.seed(2024)`. See `data-raw/generate_examples.R` for the full reproducible script.

See Also

[bglmm](#), [bglmm_data](#), [bglm_fit](#)

Examples

```
print(bglmm_fit)
summary(bglmm_fit)
```

`bglm_data`*Simulated Single-Level Clinical Trial Data*

Description

A simulated dataset representing a two-arm clinical trial with 200 subjects, one continuous covariate, and two binary outcomes. It serves as the underlying data for `bglm_fit` and can be used to illustrate `bglm`.

Usage

```
bglm_data
```

Format

A data frame with 200 rows and 4 columns:

group Character. Treatment arm: "placebo" (n = 100) or "drug" (n = 100).

age Numeric. Continuous covariate drawn from $N(50, 10^2)$.

y1 Integer (0/1). First binary outcome.

y2 Integer (0/1). Second binary outcome.

Details

Data were generated with `set.seed(2024)` using logistic models:

$$P(y_1 = 1) = \text{logit}^{-1}(-0.50 + 0.75 \text{ drug} + 0.10 \text{ age}/10)$$

$$P(y_2 = 1) = \text{logit}^{-1}(-0.50 + 0.80 \text{ drug} + 0.05 \text{ age}/10)$$

where drug is 1 for the drug arm and 0 for placebo. See `data-raw/generate_examples.R` for the full script.

See Also

[bglm](#), [bglm_fit](#), [bglmm_data](#)

Examples

```
head(bglm_data)
table(bglm_data$group, bglm_data$y1)
```

bglm_fit

Pre-computed bglm Example Fit

Description

A fitted `bglm` object estimated on `bglm_data`. Used in package examples and tests so that `print`, `summary`, and `plot` examples run in well under 5 seconds without re-running the MCMC sampler.

Usage

```
bglm_fit
```

Format

An object of class `bglm` as returned by `bglm`. See the **Value** section of `bglm` for a full description of the list components. Key settings: `n_burn = 10000`, `n_it = 20000`, `n_chain = 2`, `return_diagnostics = TRUE`, `return_samples = TRUE`.

Details

Generated with `set.seed(2024)`. See `data-raw/generate_examples.R` for the full reproducible script.

See Also

[bglm](#), [bglm_data](#), [bglmm_fit](#)

Examples

```
print(bglm_fit)
summary(bglm_fit)
```

bmvb

Bayesian Multivariate Bernoulli Test

Description

Perform a Bayesian test for differences between two groups on multiple binary outcomes using a Multivariate Bernoulli distribution, as described in Kavelaars et al. (2020).

Usage

```
bmvb(
  data,
  grp,
  grp_a,
  grp_b,
  y_vars,
  test = c("right_sided", "left_sided"),
  rule = c("All", "Any", "Comp"),
  w = NULL,
  prior_a = 0.5,
  prior_b = 0.5,
  n_it = 10000,
  return_samples = FALSE
)
```

Arguments

| | |
|---------------------|---|
| <code>data</code> | Data frame containing the data. |
| <code>grp</code> | Character string. Name of the grouping variable. |
| <code>grp_a</code> | Value of <code>grp</code> indicating first group. |
| <code>grp_b</code> | Value of <code>grp</code> indicating second group. |
| <code>y_vars</code> | Character vector. Names of outcome variables (currently supports 2 outcomes). |

| | |
|----------------|--|
| test | Character. Direction of test: "left_sided" for $P(A>B)$ or "right_sided" for $P(B>A)$. Default is "right_sided". |
| rule | Character. Decision rule: "All" (all outcomes favor hypothesis), "Any" (at least one outcome favors hypothesis), or "Comp" (weighted combination). Default is "All". |
| w | Numeric vector. Weights for compensatory rule. Only used if rule = "Comp". If NULL and rule = "Comp", equal weights are used. Default is NULL. |
| prior_a | Numeric. Prior hyperparameter (Dirichlet) for group A. Default is 0.5 (Jeffreys' prior) |
| prior_b | Numeric. Prior hyperparameter (Dirichlet) for group B. Default is 0.5 (Jeffreys' prior). |
| n_it | Integer. Number of MCMC iterations. Default is 10000. |
| return_samples | Logical. Should posterior samples be returned? Default is FALSE. |

Value

An object of class `bmvb`, a list containing:

estimates A list with posterior means (`mean_a`, `mean_b`) and standard deviations (`sd_a`, `sd_b`) of the category probabilities for both groups.

sample_sizes A list with group sample sizes (`n_a`, `n_b`).

delta A list with posterior mean differences (`mean_delta`), posterior standard errors (`se_delta`), posterior probability of the hypothesis (`pop`), and, if rule = "Comp", the weighted difference (`w_delta`).

info A list with test specifications, including the decision rule, test direction, group labels, and weights (if applicable).

samples If `return_samples = TRUE`, a list containing posterior draws of `theta_a`, `theta_b`, and `delta`.

References

Kavelaars X, Mulder J, Kaptein M (2020). "Decision-making with multiple correlated binary outcomes in clinical trials." *Statistical Methods in Medical Research*, **29**(11), 3265–3277. doi:[10.1177/0962280220922256](https://doi.org/10.1177/0962280220922256).

Examples

```
# Example with simulated data
# Generate data
set.seed(123)
data <- data.frame(
  treatment = rep(c("control", "drug"), each = 50),
  outcome1 = rbinom(100, 1, 0.5),
  outcome2 = rbinom(100, 1, 0.5)
)

# Analyze
```

```
result <- bmvb(  
  data = data,  
  grp = "treatment",  
  grp_a = "control",  
  grp_b = "drug",  
  y_vars = c("outcome1", "outcome2"),  
  n_it = 10000  
)  
  
print(result)
```

plot.bglm

Plot Method for bglm Objects

Description

Plot Method for bglm Objects

Usage

```
## S3 method for class 'bglm'  
plot(x, type = "all", parameters = NULL, ...)
```

Arguments

| | |
|------------|--|
| x | A bglm object returned by bglm(). |
| type | Character. Type of plot: "trace", "density", "autocorr", or "all". Default is "all". |
| parameters | Character vector. Which parameters to plot. Default is NULL (all parameters). |
| ... | Additional arguments passed to plotting functions. |

Value

Invisibly returns NULL (plots are displayed).

Examples

```
# Uses the pre-computed example object shipped with the package.  
# Plot trace plots for the fixed-effect regression coefficients:  
plot(bglm_fit, type = "trace")
```

plot.bglmm *Plot Method for bglmm Objects*

Description

Plot Method for bglmm Objects

Usage

```
## S3 method for class 'bglmm'
plot(x, type = "all", which = "fixed", parameters = NULL, ...)
```

Arguments

| | |
|------------|--|
| x | A bglmm object returned by bglmm(). |
| type | Character. Type of plot: "trace", "density", "autocorr", or "all". Default is "all". |
| which | Character. Which component to plot: "fixed" (b), "random" (g), "variance" (tau), or "all". Default is "fixed". |
| parameters | Character vector. Which parameters to plot. Default is NULL (all parameters). |
| ... | Additional arguments passed to plotting functions. |

Value

Invisibly returns NULL (plots are displayed).

Examples

```
# Uses the pre-computed example object shipped with the package.
# Trace plots for the fixed-effect regression coefficients:
plot(bglmm_fit, type = "trace", which = "fixed")

# Trace plots for the random-effect variance components:
plot(bglmm_fit, type = "trace", which = "variance")
```

print.bglm *Print Method for bglm Objects*

Description

Print Method for bglm Objects

Usage

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

Arguments

| | |
|--------|--|
| x | A bglm object. |
| digits | Number of digits to display. Default is 3. |
| ... | Additional arguments (not used). |

Value

Invisibly returns the input object.

See Also

[summary.bglm](#)

Examples

```
# Uses the pre-computed example object shipped with the package:  
print(bglm_fit)
```

`print.bglmm` *Print Method for bglmm Objects*

Description

Print Method for bglmm Objects

Usage

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

Arguments

| | |
|--------|--|
| x | A bglmm object. |
| digits | Number of digits to display. Default is 3. |
| ... | Additional arguments (not used). |

Value

Invisibly returns the input object.

See Also

[summary.bglmm](#)

Examples

```
# Uses the pre-computed example object shipped with the package:
print(bglm_fit)
```

print.bmvb

Print Method for bmvb Objects

Description

Print Method for bmvb Objects

Usage

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

Arguments

| | |
|--------|--|
| x | A bmvb object. |
| digits | Number of digits to display. Default is 3. |
| ... | Additional arguments (not used). |

Value

Invisibly returns the input object.

See Also

[summary.bmvb](#)

Examples

```
set.seed(2024)
trial_data <- data.frame(
  treatment = rep(c("placebo", "drug"), each = 50),
  y1 = rbinom(100, 1, rep(c(0.40, 0.60), each = 50)),
  y2 = rbinom(100, 1, rep(c(0.50, 0.70), each = 50))
)
fit <- bmvb(
  data = trial_data, grp = "treatment",
  grp_a = "placebo", grp_b = "drug",
  y_vars = c("y1", "y2"), n_it = 1000
)
print(fit)
```

print.summary.bglm *Print Method for summary.bglm Objects*

Description

Print Method for summary.bglm Objects

Usage

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

Arguments

| | |
|--------|--|
| x | A summary.bglm object returned by summary.bglm . |
| digits | Number of digits to display. Default is 3. |
| ... | Additional arguments (not used). |

Value

Invisibly returns x.

See Also

[summary.bglm](#), [print.bglm](#)

Examples

```
# Uses the pre-computed example object shipped with the package:  
print(summary(bglm_fit))
```

print.summary.bglmm *Print Method for summary.bglmm Objects*

Description

Print Method for summary.bglmm Objects

Usage

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

Arguments

x A `summary.bglmm` object returned by `summary.bglmm`.
digits Number of digits to display. Default is 3.
... Additional arguments (not used).

Value

Invisibly returns x.

See Also

[summary.bglmm](#), [print.bglmm](#)

Examples

```
# Uses the pre-computed example object shipped with the package:  
print(summary(bglmm_fit))
```

print.summary.bmvb *Print Method for summary.bmvb Objects*

Description

Print Method for `summary.bmvb` Objects

Usage

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

Arguments

x A `summary.bmvb` object returned by `summary.bmvb`.
digits Number of digits to display. Default is 3.
... Additional arguments (not used).

Value

Invisibly returns x.

See Also

[summary.bmvb](#), [print.bmvb](#)

Examples

```

set.seed(2024)
trial_data <- data.frame(
  treatment = rep(c("placebo", "drug"), each = 50),
  y1 = rbinom(100, 1, rep(c(0.40, 0.60), each = 50)),
  y2 = rbinom(100, 1, rep(c(0.50, 0.70), each = 50))
)
fit <- bmvb(
  data = trial_data, grp = "treatment",
  grp_a = "placebo", grp_b = "drug",
  y_vars = c("y1", "y2"), n_it = 1000,
  return_samples = TRUE
)
print(summary(fit))

```

summary.bglm

*Summary Method for bglm Objects***Description**

Provides a comprehensive summary of a `bglm` analysis, including the regression coefficient table, prior specification, MCMC diagnostics (effective sample sizes and \hat{R} per parameter), and, when the model was fitted with `return_samples = TRUE`, credible intervals.

Usage

```

## S3 method for class 'bglm'
summary(object, prob = 0.95, ...)

```

Arguments

| | |
|---------------------|--|
| <code>object</code> | A <code>bglm</code> object returned by <code>bglm</code> . |
| <code>prob</code> | Numeric. Coverage probability for credible intervals. Default is 0.95. |
| <code>...</code> | Additional arguments (not used). |

Value

An object of class `summary.bglm`, a list containing:

- estimates** Posterior means and SDs of group probabilities and regression coefficients.
- sample_sizes** Group sample sizes.
- delta** Posterior mean differences, SEs, and posterior probability.
- info** Prior specification, test settings, and marginalization details.
- credible_intervals** If posterior samples are available: credible interval matrices for `theta_a`, `theta_b`, and `delta`.
- effective_n** If posterior samples are available: effective sample sizes for `theta_a`, `theta_b`, and `delta`.
- mcmc_diags** MCMC diagnostics for the regression coefficients (effective sample sizes and \hat{R}).

See Also

[bglm](#), [print.bglm](#)

Examples

```
# Uses the pre-computed example object shipped with the package:
summary(bglm_fit)
```

| | |
|---------------|---|
| summary.bglmm | <i>Summary Method for bglmm Objects</i> |
|---------------|---|

Description

Provides a comprehensive summary of a [bglmm](#) analysis, including fixed and random effect tables, variance component estimates, multilevel structure, and MCMC convergence diagnostics.

Usage

```
## S3 method for class 'bglmm'
summary(object, prob = 0.95, ...)
```

Arguments

| | |
|--------|--|
| object | A bglmm object returned by bglmm . |
| prob | Numeric. Coverage probability for credible intervals. Default is 0.95. |
| ... | Additional arguments (not used). |

Value

An object of class `summary.bglmm`, a list containing:

estimates Posterior means and SDs of group probabilities, fixed effects, random effects, and variance components.

sample_sizes Group sample sizes and number of clusters.

delta Posterior mean differences, SEs, and posterior probability.

info Prior specification, model structure, test settings, and marginalization details.

credible_intervals If posterior samples are available: credible interval matrices for `theta_a`, `theta_b`, and `delta`.

effective_n If posterior samples are available: effective sample sizes for `theta_a`, `theta_b`, and `delta`.

mcmc_diags MCMC convergence diagnostics (ESS, \hat{R} , MPSRF) for fixed effects, random effects, and variance components.

See Also

[bglmm](#), [print.bglmm](#)

Examples

```
# Uses the pre-computed example object shipped with the package:
summary(bglmm_fit)
```

summary.bmvb

Summary Method for bmvb Objects

Description

Provides a comprehensive summary of a [bmvb](#) analysis. When the model was fitted with `return_samples = TRUE`, credible intervals and effective sample sizes are included.

Usage

```
## S3 method for class 'bmvb'
summary(object, prob = 0.95, ...)
```

Arguments

| | |
|---------------------|--|
| <code>object</code> | A bmvb object returned by bmvb . |
| <code>prob</code> | Numeric. Coverage probability for credible intervals. Default is 0.95. |
| <code>...</code> | Additional arguments (not used). |

Value

An object of class `summary.bmvb`, a list containing all fields of `object` plus:

credible_intervals If posterior samples are available: a list with `prob` and credible interval matrices for `theta_a`, `theta_b`, and `delta`.

effective_n If posterior samples are available: a list with effective sample sizes for `theta_a`, `theta_b`, and `delta`.

See Also

[bmvb](#), [print.bmvb](#)

Examples

```
set.seed(2024)
trial_data <- data.frame(
  treatment = rep(c("placebo", "drug"), each = 50),
  y1 = rbinom(100, 1, rep(c(0.40, 0.60), each = 50)),
  y2 = rbinom(100, 1, rep(c(0.50, 0.70), each = 50))
)
fit <- bmvb(
  data = trial_data, grp = "treatment",
  grp_a = "placebo", grp_b = "drug",
  y_vars = c("y1", "y2"), n_it = 1000,
  return_samples = TRUE
)
summary(fit)
```

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