

Package ‘metaGLMM’

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Title Aggregate-Data Meta-Analysis with Generalized Linear Mixed Models

Version 1.0.0

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Description Extends traditional random-effects meta-analysis by embedding it within a generalized linear mixed-effects model framework. The package supports covariate adjustment and non-normal responses using aggregate data, and provides likelihood-based inference with computationally efficient likelihood evaluation. The underlying methodology is described in Hanada and Sugimoto (2026) <[doi:10.1093/biomtc/ujag148](https://doi.org/10.1093/biomtc/ujag148)>.

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as.data.frame.metaGLMM
<i>Convert a metaGLMM Fit to Aggregate-Row Data</i>

Description

Convert a metaGLMM Fit to Aggregate-Row Data

Usage

```
## S3 method for class 'metaGLMM'  
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

Arguments

x	A fitted metaGLMM object.
row.names	Optional row names.
optional	Unused.
...	Unused.

Value

A data frame containing the model frame and standardized diagnostic columns prefixed with a dot.

as_metafor_data	Create Study-Level Data for metafor Workflows
-----------------	---

Description

Create Study-Level Data for metafor Workflows

Usage

```
as_metafor_data(object, estimate = NULL, vi = NULL, labels = NULL)
```

Arguments

- object A fitted metaGLMM object.
- estimate Optional study-level estimates on the link scale.
- vi Optional study-level sampling variances on the link scale.
- labels Optional study labels.

Details

`forest.metaGLMM()` uses this conversion for its study rows. Automatic conversion is conservative; supply display estimates explicitly when the arm-level data do not identify one unambiguous study effect.

Value

A plain data frame with columns `yi`, `vi`, and `slab`. No metafor model class is assigned.

chu2020	dataset of Chu et al. (2020)
---------	------------------------------

Description

dataset of Chu et al. (2020)

Usage

```
chu2020
```

Format

A data.frame for binary distributed outcome with 7 studies:

Study Study ID

x1 COVID-19 events in the longer-distance group

n1 Number of participants in the longer-distance group

x0 COVID-19 events in the shorter-distance group

n0 Number of participants in the shorter-distance group

Source

Chu, D. K., Akl, E. A., Duda, S., Solo, K., Yaacoub, S., Schuenemann, H. J., et al. (2020). Physical distancing, face masks, and eye protection to prevent person-to-person transmission of SARS-CoV-2 and COVID-19: a systematic review and meta-analysis. *The Lancet*, 395(10242), 1973-1987. Data used under the terms of the Creative Commons Attribution IGO 3.0 License (CC BY 3.0 IGO): <https://creativecommons.org/licenses/by/3.0/igo/>

ci_metaGLMM

Legacy Confidence-Interval Dispatcher

Description

Legacy Confidence-Interval Dispatcher

Usage

```
ci_metaGLMM(
  object,
  parm = .default_ci_parm(object),
  method = "PLSBC",
  level = 0.95,
  rene.c = 30,
  correction = c("corrected", "noma"),
  ...
)
```

Arguments

object	A fitted metaGLMM or legacy mle2 object.
parm	Parameter names.
method	One of "AN", "PL", "SBC", or the legacy alias "PLSBC".
level	Confidence level.
reng.c	Maximum profile bracket expansions.
correction	SBC correction option.
...	Additional low-level arguments.

Value

A confidence-interval matrix.

confint.metaGLMM	<i>Confidence Intervals for a metaGLMM Fit</i>
------------------	--

Description

Confidence Intervals for a metaGLMM Fit

Usage

```
## S3 method for class 'metaGLMM'
confint(
  object,
  parm = names(stats::coef(object)),
  level = 0.95,
  method = "wald",
  ...
)
```

Arguments

- object A fitted metaGLMM object.
- parm Fixed-effect parameter names. The default is all fixed effects.
- level Confidence level.
- method One of "wald", "profile", or "SBC", matched without regard to case. SBC denotes the simple Bartlett-corrected profile method.
- ... Additional arguments passed to the low-level interval method.

Details

SBC is available for built-in and custom families with estimated heterogeneity. The correction uses the supplied study-level variances and the heterogeneity estimate under the profile constraint, so v_i must represent an appropriate sampling variance on the link scale. Profile and SBC intervals can be substantially more computationally expensive than Wald intervals.

Value

A matrix with lower and upper columns.

confint_AN	<i>Wald Confidence Intervals</i>
------------	----------------------------------

Description

Wald Confidence Intervals

Usage

```
confint_AN(object, parm = .default_ci_parm(object), level = 0.95, ...)
```

Arguments

object	A fitted metaGLMM or legacy mle2 object.
parm	Parameter names.
level	Confidence level.
...	Unused.

Value

A two-column confidence-interval matrix.

confint_GSBC	<i>Experimental Godambe-Calibrated Bartlett Intervals</i>
--------------	---

Description

This low-level method is retained for compatibility and remains experimental. It is intentionally not available through `confint.metaGLMM()`.

Usage

```
confint_GSBC(
  object,
  parm = .default_ci_parm(object),
  level = 0.95,
  rene.c = 30,
  silent = FALSE,
  ...
)
```

Arguments

object	A fitted metaGLMM or legacy mle2 object.
parm	Parameter names.
level	Confidence level.
range.c	Maximum number of geometric bracket expansions.
silent	Logical; return infinite endpoints instead of warning when a profile root cannot be bracketed.
...	Unused.

Value

A two-column confidence-interval matrix.

confint_PL	<i>Profile-Likelihood Confidence Intervals</i>
------------	--

Description

Profile-Likelihood Confidence Intervals

Usage

```
confint_PL(
  object,
  parm = .default_ci_parm(object),
  level = 0.95,
  range.c = 30,
  silent = FALSE,
  ...
)
```

Arguments

object	A fitted metaGLMM or legacy mle2 object.
parm	Parameter names.
level	Confidence level.
range.c	Maximum number of geometric bracket expansions.
silent	Logical; return infinite endpoints instead of warning when a profile root cannot be bracketed.
...	Unused.

Value

A two-column confidence-interval matrix.

confint_SBC	<i>Simple Bartlett-Corrected Confidence Intervals</i>
-------------	---

Description

Simple Bartlett-Corrected Confidence Intervals

Usage

```
confint_SBC(
  object,
  parm = .default_ci_parm(object),
  level = 0.95,
  rene.c = 30,
  silent = FALSE,
  correction = c("corrected", "noma"),
  ...
)
```

Arguments

object	A fitted metaGLMM or legacy mle2 object.
parm	Parameter names.
level	Confidence level.
reng.c	Maximum number of geometric bracket expansions.
silent	Logical; return infinite endpoints instead of warning when a profile root cannot be bracketed.
correction	Either "corrected" or the legacy value "noma".
...	Unused.

Value

A two-column confidence-interval matrix.

forest	<i>Forest Plots for metaGLMM Fits</i>
--------	---------------------------------------

Description

Forest Plots for metaGLMM Fits

Usage

```
forest(x, ...)
```


Arguments

`x` A fitted metaGLMM object.

`...` Arguments passed to a method.

Value

The value returned by the dispatched method. For a metaGLMM object, the function draws a forest plot as a side effect and invisibly returns the plotting data described in [forest.metaGLMM\(\)](#).

forest.metaGLMM	<i>Draw a Forest Plot</i>
-----------------	---------------------------

Description

Draw a Forest Plot

Usage

```
## S3 method for class 'metaGLMM'
forest(
  x,
  estimate = NULL,
  vi = NULL,
  labels = NULL,
  parm = NULL,
  contrast = NULL,
  random_scale = 1,
  level = 0.95,
  type = c("link", "exp"),
  ci_methods = NULL,
  prediction = TRUE,
  ci_args = list(),
  annotate = TRUE,
  digits = 2L,
  header = NULL,
  xlab = NULL,
  pch = 15,
  cex = 0.9,
  summary_cex = max(1.1, cex * 1.2),
  diamond_height = 0.18,
  left_margin = NULL,
  right_margin = NULL,
  ...
)
```

Arguments

<code>x</code>	A fitted metaGLMM object.
<code>estimate</code>	Optional study-level estimates on the link scale.
<code>vi</code>	Optional study-level sampling variances on the link scale.
<code>labels</code>	Optional study labels.
<code>parm</code>	Fixed-effect name for the pooled result.
<code>contrast</code>	Optional fixed-effect contrast; used instead of <code>parm</code> .
<code>random_scale</code>	Loading of heterogeneity for the pooled prediction interval.
<code>level</code>	Confidence and prediction level.
<code>type</code>	Either "link" or "exp".
<code>ci_methods</code>	One or more fixed-effect confidence-interval methods: "wald", "profile", or "SBC". Matching is case-insensitive and the displayed order follows this vector. The default uses SBC when it is available and Wald otherwise.
<code>prediction</code>	Logical; include a prediction interval?
<code>ci_args</code>	Optional list of additional arguments passed to <code>confint.metaGLMM()</code> for profile and SBC calculations.
<code>annotate</code>	Logical; show forest-plot-style column headers and formatted estimates with confidence limits in the right margin?
<code>digits</code>	Number of digits after the decimal point in annotations.
<code>header</code>	Optional two-element character vector for the left and right column headers.
<code>xlab</code>	Optional horizontal-axis label.
<code>pch</code>	Plotting symbol for studies.
<code>cex</code>	Expansion factor for study labels and symbols.
<code>summary_cex</code>	Expansion factor for pooled and prediction labels and symbols.
<code>diamond_height</code>	Half-height of the pooled confidence-interval diamond in plot-row units.
<code>left_margin</code>	Optional left margin in inches. The default measures the rendered labels and enlarges the current device margin when necessary.
<code>right_margin</code>	Optional right margin in inches. The default measures the formatted annotations when <code>annotate = TRUE</code> .
<code>...</code>	Additional arguments passed to <code>graphics::plot.default()</code> .

Details

With omitted display vectors, study estimates and variances are obtained through `as_metafor_data()`. Automatic extraction is used only when the fitted data unambiguously define one estimate per independent study. Otherwise, `estimate`, `vi`, and optionally `labels` must be supplied. For a grouped treatment-slope model, the pooled coefficient is selected automatically when exactly one model-matrix column represents the random-effect treatment loading. Display estimates are conceptually separate from the likelihood used for fitting. Selected fixed-effect confidence intervals and the plug-in prediction interval are drawn as filled diamonds. Profile and SBC intervals require `parm`; arbitrary contrast values are supported only for Wald intervals. The prediction interval is the package's Wald-type plug-in interval, not a profile- or Bartlett-corrected prediction interval. Plot margins are enlarged automatically for labels, headers, and numeric annotations.

Value

Invisibly, a data frame containing the data used to draw the plot, with one row for each study, requested pooled confidence interval, and optional prediction interval. The columns are kind (the row type: "study", "pooled", or "prediction"), label (the displayed row label), estimate (the point estimate), lower and upper (the interval limits), and method (the confidence-interval method, "prediction", or NA for study rows). Estimates and limits are on the link scale when type = "link" and are exponentiated when type = "exp". The forest plot is drawn as a side effect.

likelihood

*Evaluate the aggregate-data GLMM negative log likelihood.***Description**

Evaluate the aggregate-data GLMM negative log likelihood.

Usage

```
likelihood(
  formula,
  data,
  vi,
  ni,
  beta,
  tau2,
  family = stats::binomial(link = "logit"),
  tau2.min = 1e-06,
  re_group = NULL,
  trt = NULL,
  rstdnorm = stats::qnorm((qrng::sobol(5000, d = 1, scrambling = 1) * 4999 + 0.5)/5000)
)
```

Arguments

formula	Model formula.
data	Data frame or model frame containing the response and covariates.
vi	Sampling variances.
ni	Information multipliers (sample sizes for binomial/Poisson aggregate data).
beta	Fixed-effect coefficient vector.
tau2	Between-row/group variance.
family	A stats family or <code>metaGLMM_family()</code> object.
tau2.min	Lower numerical bound used while estimating tau2.
re_group	Optional grouping variable for a shared random slope.
trt	Optional name of a binary treatment/loading column.
rstdnorm	Standard-normal quadrature or quasi-Monte Carlo draws.

Value

A scalar negative log likelihood.

long2020	<i>dataset of Long et al. (2020)</i>
----------	--------------------------------------

Description

dataset of Long et al. (2020)

Usage

long2020

Format

A data.frame for gamma distributed outcome with 5 studies:

Study Study ID

mi Mean of intensive care unit (ICU) length of stay (LoS)

sdi Standard deviation of ICU LoS

ni Number of subjects

trt Treatment indicator: 1 for treatment and 0 for control

Source

Long, R., Tian, J., Wu, S., Li, Y., Yang, X., & Fei, J. (2020). Clinical efficacy of surgical versus conservative treatment for multiple rib fractures: a meta-analysis of randomized controlled trials. *International Journal of Surgery*, 83, 79-88. Data used under the terms of the Creative Commons Attribution 4.0 International License (CC BY 4.0): <https://creativecommons.org/licenses/by/4.0/>

make_ll_fun	<i>Build the quasi-Monte Carlo likelihood function used by metaGLMM().</i>
-------------	--

Description

The formal argument names are exactly the columns of `model.matrix()` (plus `tau2` when it is estimated), which makes factor and interaction models safe for optimizers such as [bbmle::mle2\(\)](#).

Usage

```
make_ll_fun(
  formula,
  data,
  vi,
  ni,
  tau2,
  family,
  tau2_var = FALSE,
  tau2.min = 1e-06,
  re_group = NULL,
  trt = NULL,
  rstdnorm = stats::qnorm((qrng::sobol(5000, d = 1, scrambling = 1) * 4999 + 0.5)/5000),
  ...
)
```

Arguments

formula	Model formula.
data	Model data.
vi	Sampling variances.
ni	Information multipliers.
tau2	Fixed or starting between-study variance.
family	A stats family or <code>metaGLMM_family()</code> object.
tau2_var	Whether tau2 is an optimizer parameter.
tau2.min	Numerical lower bound for estimated tau2.
re_group	Optional grouping variable.
trt	Optional binary loading column name.
rstdnorm	Standard-normal quasi-Monte Carlo draws.
...	Additional compatibility arguments (including offset).

Value

A function suitable for `bbmle::mle2()`.

make_ll_fun.fast	<i>Build the fast likelihood function using Gaussian closed form or GHQ.</i>
------------------	--

Description

Custom families intentionally use the QMC path (`fast = FALSE`) so their callback remains the single source of truth for the likelihood.

Usage

```
make_ll_fun.fast(  
  formula,  
  data,  
  vi,  
  ni,  
  tau2,  
  family,  
  tau2_var = FALSE,  
  tau2.min = 1e-06,  
  re_group = NULL,  
  trt = NULL,  
  ghq_Q = 1000L,  
  ...  
)
```

Arguments

formula	Model formula.
data	Model data.
vi	Sampling variances.
ni	Information multipliers.
tau2	Fixed or starting between-study variance.
family	A stats family or <code>metaGLMM_family()</code> object.
tau2_var	Whether tau2 is an optimizer parameter.
tau2.min	Numerical lower bound for estimated tau2.
re_group	Optional grouping variable.
trt	Optional binary loading column name.
ghq_Q	Number of Gauss-Hermite quadrature nodes.
...	Additional compatibility arguments (including <code>offset</code>).

Value

A function suitable for `bbmle::mle2()`.

metaGLMM	<i>Fit an Aggregate-Data Generalized Linear Mixed-Effects Meta-Analysis</i>
----------	---

Description

Fits the aggregate-data generalized linear mixed model described by Hanada and Sugimoto (2026). The optimizer is provided by `bbmle::mle2()`, but the returned object has a stable metaGLMM S3 interface.

Usage

```

metaGLMM(
  formula,
  data,
  vi,
  ni,
  tau2 = NA_real_,
  family = stats::gaussian(),
  tau2_var = TRUE,
  re_group = NULL,
  trt = NULL,
  rstdnorm = NULL,
  skip.hessian = FALSE,
  fast = TRUE,
  ghq_Q = 1000L,
  method_opt = NULL,
  start_beta = NULL,
  start_tau2 = NULL,
  tau2_param = c("tau2", "log_tau2"),
  control = NULL,
  ...
)

```

Arguments

formula	A model formula.
data	A data frame containing the variables in formula.
vi	A numeric vector of aggregate-data variances or dispersion values.
ni	A numeric vector of sample sizes, denominators, or exposures.
tau2	A fixed between-study variance when <code>tau2_var = FALSE</code> . Use 0 for a model without a random effect. It is ignored when <code>tau2_var = TRUE</code> .
family	A supported <code>stats::family()</code> object or an object created by <code>metaGLMM_family()</code> .
tau2_var	Logical; estimate the between-study variance?
re_group	Optional grouping vector. When supplied, observations in a group share the scalar random treatment effect defined by <code>trt</code> . Every group must contain both normalized loadings 0 and 1.
trt	Optional single column name in data containing a binary random- effect loading. It is required when <code>re_group</code> is supplied.
rstdnorm	Optional numeric integration points on the standard-normal scale for quasi-Monte Carlo integration.
skip.hessian	Logical; skip calculation of the Hessian?
fast	Logical; use closed-form Gaussian integration or compiled Gauss-Hermite quadrature for built-in families?
ghq_Q	Positive integer number of Gauss-Hermite quadrature points.

method_opt	Optional optimizer name passed to <code>bbmle::mle2()</code> .
start_beta	Optional numeric vector or list of fixed-effect starts. Named values must exactly match <code>colnames(model.matrix(formula, data))</code> . Unnamed values are interpreted in model-matrix column order.
start_tau2	Starting value for the between-study variance.
tau2_param	Internal parameterization for estimated heterogeneity: either "tau2" or "log_tau2".
control	Optional optimizer control list.
...	Additional arguments passed to <code>bbmle::mle2()</code> .

Details

Construction fails before optimization for empty, non-finite, or rank-deficient model designs and for invalid grouped random-effect or custom-family contracts. Non-convergence produces a warning; boundary heterogeneity and unavailable Hessian or covariance information remain available as object diagnostics.

Value

An object of class `metaGLMM`. Its integration component records the integration method and QMC provenance without storing the integration vector. Its convergence component records optimizer, Hessian, covariance, and boundary diagnostics.

References

Hanada, K. and Sugimoto, T. (2026). Random-effects meta-analysis via generalized linear mixed models: A Bartlett-corrected approach for few studies. *Biometrics*. doi:10.1093/biomtc/ujag148.

metaGLMM_family	<i>Create a custom aggregate-data family specification.</i>
-----------------	---

Description

Create a custom aggregate-data family specification.

Usage

```
metaGLMM_family(
  name,
  link = "identity",
  loglik,
  validate = NULL,
  initialize = NULL
)
```


Arguments

name	Family name used in printed output.
link	A link name accepted by <code>stats::make.link()</code> or a compatible link object.
loglik	A function with arguments <code>y</code> , <code>eta</code> , <code>vi</code> , and <code>ni</code> . It must return one aggregate log-likelihood contribution for every value of <code>eta</code> .
validate	Optional function used to validate response and design inputs.
initialize	Optional family-specific initialization function.

Details

The link callbacks and `loglik` must be vectorized and free of side effects. `metaGLMM()` probes the callbacks at its deterministic starting linear predictor before optimization and rejects non-numeric, incorrectly sized, or non-finite results.

Value

An object inheriting from `metaGLMM_family` and `family`.

mle2_fit	<i>Extract the Internal mle2 Fit</i>
----------	--------------------------------------

Description

Extract the Internal mle2 Fit

Usage

```
mle2_fit(object)
```

Arguments

object	A fitted metaGLMM object.
--------	---------------------------

Value

The internal `bbmle::mle2()` object.

predict.metaGLMM	<i>Predict from a metaGLMM Fit</i>
------------------	------------------------------------

Description

Predict from a metaGLMM Fit

Usage

```
## S3 method for class 'metaGLMM'
predict(
  object,
  newdata = NULL,
  type = c("link", "response", "exp"),
  interval = c("none", "confidence", "prediction"),
  level = 0.95,
  contrast = NULL,
  random_scale = NULL,
  ...
)
```

Arguments

object	A fitted metaGLMM object.
newdata	Optional data frame of covariate patterns.
type	Output scale: "link", "response", or "exp". The last exponentiates a log- or logit-scale result.
interval	One of "none", "confidence", or "prediction".
level	Confidence or prediction level.
contrast	Optional numeric contrast vector or matrix against the fixed effects. It cannot be combined with newdata or type = "response".
random_scale	Optional loading of the future scalar random effect.
...	Unused.

Details

A prediction interval targets a future underlying study-specific true effect. It combines fixed-effect uncertainty with τ^2 ; it does not add the sampling variance of a future observed estimator.

Value

A numeric vector when interval = "none"; otherwise a data frame with fit, lower, and upper columns.

`profile_ll`*Evaluate a Profile-Likelihood Ratio*

Description

Evaluate a Profile-Likelihood Ratio

Usage

```
profile_ll(value, object, parm)
```

Arguments

<code>value</code>	Numeric parameter values.
<code>object</code>	A fitted metaGLMM or legacy mle2 object.
<code>parm</code>	One fixed-effect parameter name.

Value

Profile likelihood-ratio statistics.

`profile_ll_sbc`*Evaluate a Simple Bartlett-Corrected Profile Ratio*

Description

Evaluate a Simple Bartlett-Corrected Profile Ratio

Usage

```
profile_ll_sbc(value, object, parm, correction = c("corrected", "noma"))
```

Arguments

<code>value</code>	Numeric parameter values.
<code>object</code>	A fitted metaGLMM or legacy mle2 object.
<code>parm</code>	One fixed-effect parameter name.
<code>correction</code>	Either "corrected" or "noma".

Value

Corrected profile likelihood-ratio statistics.

rutter2021	<i>dataset of Rutter et al. (2021)</i>
------------	--

Description

dataset of Rutter et al. (2021)

Usage

```
rutter2021
```

Format

A data.frame for Poisson distributed outcome with 11 studies:

Study Study ID

Year Publishing year

Sex Sex (Female or Male)

Events Number of events

Time Total observation time

Source

Rutter, M., Bowley, J., Lanyon, P. C., Grainge, M. J., & Pearce, F. A. (2021). A systematic review and meta-analysis of the incidence rate of Takayasu arteritis. *Rheumatology*, 60(11), 4982-4990. Data used under the terms of the Creative Commons Attribution 4.0 International License (CC BY 4.0): <https://creativecommons.org/licenses/by/4.0/>

summary.metaGLMM	<i>Summarize a metaGLMM Fit</i>
------------------	---------------------------------

Description

Summarize a metaGLMM Fit

Usage

```
## S3 method for class 'metaGLMM'
summary(object, ...)
```

Arguments

object	A fitted metaGLMM object.
...	Unused.

Value

An object of class summary.metaGLMM.

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