

Package ‘BioMixModel’

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Type Package

Title Mixed Models for Biological, Clustered and Longitudinal Data

Version 1.0.0

Description Fits and interprets mixed-effects models for clustered, longitudinal and heterogeneous biological data. Provides variance partitioning, intraclass correlation, penalized likelihood summaries, a heterogeneous-data information criterion, model comparison, diagnostics, and ensemble-style summaries for multilevel data. The package is designed as a complementary, interpretable workflow around established mixed-model methods. Methods for intraclass correlation and variance partitioning are informed by Nakagawa and Schielzeth (2010) <[doi:10.1111/j.1469-185X.2010.00141.x](https://doi.org/10.1111/j.1469-185X.2010.00141.x)> and Nakagawa et al. (2017) <[doi:10.1098/rsif.2017.0213](https://doi.org/10.1098/rsif.2017.0213)>. Mixed-effects modeling approaches are described by Zuur et al. (2009) <[doi:10.1007/978-0-387-87458-6](https://doi.org/10.1007/978-0-387-87458-6)>.

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compare_biomix	<i>Compare BioMixModel fits</i>
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Description

Compare BioMixModel fits

Usage

compare_biomix(...)

Arguments

... biomix models.

Value

Comparison data frame.

diagnose_biomix	<i>Diagnose a BioMixModel fit</i>
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Description

Diagnose a BioMixModel fit

Usage

```
diagnose_biomix(model)
```

Arguments

model	A biomix model.
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Value

Diagnostic data frame.

fit_bayes_mix	<i>Fit a Bayesian mixed-effects model</i>
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Description

Fits a Bayesian mixed-effects model using **brms**.

Usage

```
fit_bayes_mix(formula, data, family = "gaussian", ...)
```

Arguments

formula	A model formula containing fixed and random effects.
data	A data frame.
family	Character family name or a brms family object.
...	Additional arguments passed to brms::brm() .

Value

An object of class biomix_bayes.

fit_biomix	<i>Fit a biological mixed model</i>
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Description

Fits either an ordinary linear model or a linear mixed-effects model.

Usage

```
fit_biomix(formula, data, random = NULL, method = c("REML", "ML"))
```

Arguments

formula	Model formula containing fixed effects.
data	Data frame.
random	Optional random-effects specification as a one-sided formula, e.g. <code>~ 1 subject</code> or <code>~ time subject</code> .
method	Estimation method: "REML" or "ML".

Value

An object of class `biomix`.

fit_gamm	<i>Fit a generalized additive mixed model</i>
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Description

Fits a generalized additive mixed model using **mgcv**.

Usage

```
fit_gamm(formula, data, random = NULL, ...)
```

Arguments

formula	A GAM formula.
data	A data frame containing the response and predictors.
random	Optional random-effects specification.
...	Additional arguments passed to <code>mgcv::gam()</code> or <code>mgcv::gamm()</code> .

Value

An object of class `biomix_gamm`.

fit_glmm

*Fit a generalized linear mixed-effects model***Description**

Fits generalized linear mixed-effects models using **glmmTMB**. Supported distributions include binomial, Poisson, and negative-binomial models. Zero-inflated models can be fitted using `zi` formula.

Usage

```
fit_glmm(
  formula,
  data,
  family = c("binomial", "poisson", "nbinom1", "nbinom2"),
  ziformula = ~0,
  dispformula = ~1,
  ...
)
```

Arguments

<code>formula</code>	A model formula containing fixed and random effects.
<code>data</code>	A data frame.
<code>family</code>	Distribution. Supported values are "binomial", "poisson", "nbinom1", and "nbinom2".
<code>ziformula</code>	Formula for the zero-inflation component. The default <code>~0</code> specifies no zero-inflation component.
<code>dispformula</code>	Formula for the dispersion component.
<code>...</code>	Additional arguments passed to <code>glmmTMB::glmmTMB()</code> .

Value

An object of class `biomix_glmm`.

Examples

```
dat <- data.frame(
  y = rpois(100, 5),
  x = rnorm(100),
  id = factor(rep(1:20, each = 5))
)

model <- fit_glmm(
  y ~ x + (1 | id),
  data = dat,
  family = "poisson"
)
```

fit_multivariate	<i>Fit a multivariate mixed-effects model</i>
------------------	---

Description

Fits a multivariate mixed-effects model using **brms**.

Usage

```
fit_multivariate(formulas, data, ...)
```

Arguments

formulas	A list of model formulas.
data	A data frame.
...	Additional arguments passed to <code>brms::brm()</code> .

Value

An object of class `biomix_multivariate`.

fit_nlme_biomix	<i>Fit a nonlinear mixed-effects model</i>
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Description

Fits a nonlinear mixed-effects model using **nlme**.

Usage

```
fit_nlme_biomix(formula, data, fixed, random, start, ...)
```

Arguments

formula	Nonlinear model formula.
data	Data frame containing the response, predictors, and grouping variables.
fixed	Fixed-effects specification for nonlinear parameters.
random	Random-effects specification for nonlinear parameters.
start	Starting values for the nonlinear parameters.
...	Additional arguments passed to <code>nlme::nlme()</code> .

Value

An object of class `biomix_nlmm`.

fit_nlmm

*Fit a nonlinear mixed-effects model***Description**

Fits nonlinear mixed-effects models using **nlme**.

Usage

```
fit_nlmm(
  model,
  data,
  fixed = NULL,
  random = NULL,
  start = NULL,
  method = c("REML", "ML"),
  ...
)
```

Arguments

model	Nonlinear model formula.
data	Data frame containing the response, predictors, and grouping variables.
fixed	Fixed-effects specification for the nonlinear parameters.
random	Random-effects specification for the nonlinear parameters.
start	Optional starting values for the nonlinear parameters.
method	Estimation method, "REML" or "ML".
...	Additional arguments passed to <code>nlme::nlme()</code> .

Value

An object of class `biomix_nlmm`.

fit_spatial_mix

*Fit a spatial mixed-effects model***Description**

Fits a spatial mixed-effects model using a user-specified spatial correlation structure.

Usage

```
fit_spatial_mix(formula, data, correlation = NULL, ...)
```

Arguments

formula	Model formula.
data	Data frame.
correlation	Spatial correlation structure.
...	Additional arguments passed to <code>nlme::lme()</code> .

Value

An object of class `biomix_spatial`.

<code>fit_survival_mix</code>	<i>Fit a survival mixed-effects model</i>
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Description

Fits frailty/mixed-effects Cox models using `coxme`.

Usage

```
fit_survival_mix(formula, data, ...)
```

Arguments

formula	A survival model formula.
data	Data frame.
...	Additional arguments passed to <code>coxme::coxme()</code> .

Value

An object of class `biomix_survival`.

<code>get_fit</code>	<i>Extract the fitted model</i>
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Description

Extract the fitted model

Usage

```
get_fit(model)
```

Arguments

model	A <code>BioMixModel</code> object.
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Value

The underlying fitted model.

haic

Heterogeneity-aware Akaike information criterion

Description

Calculates HAIC by adding a heterogeneity penalty to AIC.

Usage

```
haic(model)
```

Arguments

model A biomix model.

Value

Numeric HAIC.

icc_biomix

Intraclass correlation coefficient

Description

Calculates the proportion of variance attributable to random effects.

Usage

```
icc_biomix(model)
```

Arguments

model A biomix model.

Value

Numeric ICC.

model_summary	Compact model summary
Description	
Compact model summary	
Usage	
model_summary(model)	
Arguments	
model	A biomix model.
Value	
A list of model statistics.	
model_summary.biomix_nlmm	Summary for nonlinear mixed-effects BioMixModel

Description

Summary for nonlinear mixed-effects BioMixModel
Summarize a nonlinear mixed-effects model

Usage

```
## S3 method for class 'biomix_nlmm'  
model_summary(model)  
  
## S3 method for class 'biomix_nlmm'  
model_summary(model)
```

Arguments

model A biomix_nlmm model.

Value

A list containing nonlinear mixed-model statistics.
A list of model statistics.

plot_biomix	<i>Plot diagnostic residuals</i>
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Description

Plot diagnostic residuals

Usage

```
plot_biomix(model, type = c("residuals", "qq"))
```

Arguments

model	A biomix model.
type	Plot type, "residuals" or "qq".

Value

Invisibly returns the model.

variance_partition	<i>Variance partitioning</i>
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Description

Extracts variance components from a BioMixModel fit.

Usage

```
variance_partition(model)
```

Arguments

model	A biomix model.
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Value

Data frame containing variance components and proportions.

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