

Package: TestREnlme (via r-universe)

July 3, 2026

Type Package

Title Nonparametric Tests for Random Effects in Linear and Nonlinear Mixed-Effects Models

Version 0.1.0

Description Provides nonparametric permutation tests for testing all or any subset of random effects in linear and nonlinear mixed-effects models, without requiring normality or other distributional assumptions on random effects or errors. Three distribution-free variance-component estimators are implemented: Variance Least Squares ('VLS'), Method of Moments ('MM'), and Method of Moments with First-Order Approximation ('MMF'). A permutation procedure is used to obtain finite-sample p-values. Plotting functions support data exploration, model evaluation, and communication of results. Methods are described in Uwimpuhwe, Drikvandi, and Blozis (2026) <[doi:10.1002/sim.70605](https://doi.org/10.1002/sim.70605)>.

License GPL (>= 3)

Encoding UTF-8

LazyData true

RoxygenNote 8.0.0

Depends R (>= 4.1.0)

Imports nlme (>= 3.1-150), Matrix (>= 1.3-0), MASS (>= 7.3-54), mgsub (>= 1.7.3), matrixcalc (>= 1.0-5), nls.multstart (>= 2.0.0), ggplot2 (>= 3.3.5), expm (>= 0.999-6), withr (>= 3.0.2), stats, utils, rlang

Suggests knitr, rmarkdown, ggpubr (>= 0.4.0), testthat (>= 3.0.0), reshape2 (>= 1.4.4)

VignetteBuilder knitr

URL <https://github.com/germaine86/TestREnlme>

BugReports <https://github.com/germaine86/TestREnlme/issues>

Config/testthat/edition 3

NeedsCompilation no

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

Date/Publication 2026-07-03 12:00:15 UTC

RemoteUrl <https://github.com/cran/TestREnlme>

RemoteRef HEAD

RemoteSha f061c1d5b68c7503c485fd5dfbccd2038af371d5

Contents

Beta_hat	2
bootstrap_se	3
Dhypothesis_test	5
Dmethod	7
MM_base	10
plot.Dmethod	12
plot.Dtest	12
plot_condition	13
plot_fitted	13
plot_perm_hist	14
plot_profiles	15
plot_residuals	16
plot_variance	16
SkillAcq	17
Tstat	19
ZandYPred	19

Index **21**

Beta_hat	<i>Estimate fixed effects by nonlinear least squares</i>
----------	--

Description

Estimates the fixed-effects parameter vector by unweighted NLS (first attempt via [nls](#)), or by weighted NLS via [nlminb](#) when `weights` is supplied or when the unweighted NLS fails. Used both for initial unweighted estimation and for GLS re-estimation at the end of VLS using the estimated variance components.

Usage

```
Beta_hat(data, Expr, start, weights = NULL, group = NULL, verbose = 1)
```

Arguments

data	A data.frame containing all model variables.
Expr	A two-sided formula specifying the nonlinear model.
start	A named numeric vector of starting values. See the start argument of <code>Dmethod</code> for details, including automatic computation via <code>nls.multstart::nls_multstart()</code> when not supplied.
weights	Either NULL (default, unweighted), a numeric vector of weights, or a named list of per-subject inverse covariance matrices (used for GLS re-estimation after variance components are estimated).
group	Character. Name of the grouping variable, required when weights is a list.
verbose	Integer (0, 1, or 2). Default 1.

Value

A named numeric vector of estimated fixed effects.

Examples

```
Expr <- conc ~ Dose * exp(ai2 + ai3 - ai1) *
      (exp(-Time * exp(ai3)) - exp(-Time * exp(ai2))) /
      (exp(ai2) - exp(ai3))
start <- c(ai1 = -3.22, ai2 = 0.47, ai3 = -2.45)
Beta_hat(as.data.frame(Theoph), Expr, start)
```

bootstrap_se

Bootstrap standard errors for variance component estimates

Description

Computes bootstrap standard errors for the fixed effects $\hat{\beta}$, random effect variance components \hat{D}_* , and error variance $\hat{\sigma}^2$ using one of two bootstrap strategies documented in the literature for mixed-effects models.

Usage

```
bootstrap_se(
  Dobj,
  nboot = 200,
  type = c("case", "residual"),
  seed = NULL,
  verbose = 1
)
```

Arguments

Dobj	An object of class "Dmethod" returned by <code>Dmethod</code> . The estimation method (default "VLS") is inherited from Dobj.
nboot	Positive integer. Number of bootstrap samples. Default 200.
type	Character. Bootstrap strategy: "case" Resample subjects with replacement (default). Valid under minimal assumptions. Recommended for general use Thai et al. (2013). "residual" Keep subjects fixed, resample marginal residuals $\hat{\epsilon}_i = Y_i - \hat{f}_i$ with replacement. Assumes i.i.d. residuals. See Carpenter et al. (2003), Thai et al. (2013).
seed	Optional integer seed for reproducibility. Default NULL.
verbose	Integer (0, 1, or 2). Default 1.

Value

A list of class "Dboot" with components:

Beta Matrix with columns Estimate and SE for the fixed effects.

Dhat Matrix with columns Estimate and SE for each variance/covariance component (flattened via row:column naming).

Sigma2 Matrix with columns Estimate and SE for the error variance.

Boot_Beta Matrix of bootstrap fixed-effects estimates (nboot x length(Beta)).

Boot_Dhat Array of bootstrap variance component matrices (k x k x nboot).

Boot_Sigma2 Numeric vector of bootstrap error variance estimates (length nboot).

type The bootstrap strategy used.

nboot Number of bootstrap samples requested.

nfail Number of bootstrap samples that failed.

References

Carpenter, J.R., Goldstein, H. and Rasbash, J. (2003). A novel bootstrap procedure for assessing the relationship between class size and achievement. *Journal of the Royal Statistical Society C*, **52**, 431–443.

Thai, H.T., Mentre, F., Holford, N.H.G., Veyrat-Follet, C. and Comets, E. (2013). A comparison of bootstrap approaches for estimating uncertainty of parameters in linear mixed-effects models. *Pharmaceutical Statistics*, **12**, 129–140.

Examples

```
d <- as.data.frame(Theoph)
Expr <- conc ~ Dose * exp(ai2 + ai3 - ai1) *
      (exp(-Time * exp(ai3)) - exp(-Time * exp(ai2))) /
      (exp(ai2) - exp(ai3))
start <- c(ai1 = -3.22, ai2 = 0.47, ai3 = -2.45)
random <- c("ai1 ~ B1 + bi1", "ai2 ~ B2 + bi2", "ai3 ~ B3 + bi3")
```

```
DVLS <- Dmethod(d, Expr, group = "Subject",
               random = random, start = start, method = "VLS")
DVLS[c("Dhat", "Sigma2", "Beta")]

BootSE <- bootstrap_se(DVLS, nboot = 20, type = "case", seed = NULL, verbose = 1)
```

Dhypothesis_test	<i>Permutation test for random effects in linear and nonlinear mixed-effects models</i>
------------------	---

Description

Performs a nonparametric permutation test for all random effects or any user-specified subset, using the test statistic of Drikvandi et al. (2013) adapted for nonlinear mixed-effects models in Uwimpuhwe (2026).

Usage

```
Dhypothesis_test(
  data,
  Expr,
  group,
  random,
  start = NULL,
  bi_out = NULL,
  method = c("VLS", "MM", "MMF"),
  Dhatt = NULL,
  Thatt = NULL,
  MM_base_obj = NULL,
  nperm = 200,
  seed = NULL,
  sig_alpha = 0.05,
  kappa_max = 10000,
  RR_catof = "kappa",
  verbose = 1,
  perm_freq = 10
)
```

Arguments

data	A data.frame containing all model variables.
Expr	A two-sided formula specifying the nonlinear model $f_i(a_i, \gamma)$. The left-hand side is the response variable and the right-hand side defines the nonlinear function using the subject-specific parameter names (e.g., ai1, ai2, ai3) that appear in start and random.

group	Character. Name of the grouping variable.
random	A character vector of two-sided formula strings, one per parameter in $a_i = A_i\beta + b_i$, mapping each subject-specific parameter (left-hand side, matching Expr and start) to its fixed-effects expression plus random effect (right-hand side). For example, <code>c("ai1 ~ B1 + bi1", "ai2 ~ B2 + bi2", "ai3 ~ B3 + bi3")</code> specifies that $ai1 = B1 + bi1$, $ai2 = B2 + bi2$, $ai3 = B3 + bi3$.
start	A named numeric vector of starting values for all parameters in Expr. Names must match those used in Expr (e.g., ai1, ai2, ai3). If NULL (the default), Dmethod attempts to compute starting values automatically using <code>nls.multstart::nls_multstart()</code> , searching over multiple initial values within a specified range (e.g. ± 10) for each parameter. If this step fails, provide start manually, or fit <code>nls_multstart()</code> or <code>nls()</code> separately with different starting values, search bounds, or optimisation settings, and use the resulting coefficients as starting values.
bi_out	Optional character vector naming the random effects to test. If NULL (default) all random effects are tested jointly (Algorithm 1). Otherwise, only the named effects are tested conditionally on the rest being retained.
method	Character. One of "VLS" (default), "MM", or "MMF".
Dhatt	Optional pre-computed "Dmethod" object. When supplied, variance estimation is skipped. This is the recommended approach when running multiple tests on the same data, since \hat{D}_* only needs to be computed once and can be reused.
Thatt	Optional pre-computed observed test statistic from Tstat.
MM_base_obj	Optional pre-computed "MM_base" object. Only used when method is "MM" or "MMF" and Dhatt is NULL.
nperm	Positive integer. Number of permutations B . Default 200. Use 1000 or more for publication results.
seed	Optional integer seed for reproducibility. Default NULL.
sig_alpha	Significance level for the reject/do-not-reject decision. Default 0.05.
kappa_max	Condition-number threshold for MM/MMF. Default 1e4.
RR_catof	Exclusion criterion passed to MM_base. Either "kappa" (default), which uses the condition-number threshold kappa_max, or a user-specified numeric threshold applied directly.
verbose	Integer (0, 1, or 2). Controls message output: 0 Completely silent. 1 Prints summary: subjects used/excluded, observed statistic, p -value, and decision (default). 2 Also prints every perm_freq permutation counter.
perm_freq	Integer. When verbose = 2, print a permutation progress message every perm_freq permutations. Default 10.

Value

An object of class "Dtest", a list with components:

Decision Character, "Reject H_0 " or "Do not reject H_0 ".

`pvalue` The empirical permutation p -value.
`Tobs` The observed test statistic T_{obs} .
`Tperm` Numeric vector of length `nperm` containing the permutation statistics $T^{(1)}, \dots, T^{(B)}$.
`Dhatt` The `Dmethod` object used.
`bi_out` The random effects tested.
`plot` A **ggplot2** histogram of the permutation null distribution with T_{obs} annotated.

References

Uwimpuhwe, G., Drikvandi, R., and Blozis, S.A. (2026). Testing random effects in nonlinear mixed-effects models. *Statistics in Medicine*. doi:10.1002/sim.70605

Uwimpuhwe, G., Drikvandi, R. and Blozis, S. A. (in preparation). TestREnlme: An R Package for Testing Random Effects in Nonlinear Mixed-Effects Models. *Journal of Statistical Software*.

Demidenko, E. (2013). *Mixed Models: Theory and Applications with R* (2nd ed.). Wiley.

Drikvandi, R., Verbeke, G., Khodadadi, A. and Nia, V. P. (2013). Testing multiple variance components in linear mixed-effects models. *Biostatistics*, **14** (1), 144–159.

Examples

```
d      <- as.data.frame(Theoph)
Expr   <- conc ~ Dose * exp(ai2 + ai3 - ai1) *
        (exp(-Time * exp(ai3)) - exp(-Time * exp(ai2))) /
        (exp(ai2) - exp(ai3))
start  <- c(ai1 = -3.22, ai2 = 0.47, ai3 = -2.45)
random <- c("ai1 ~ B1 + bi1", "ai2 ~ B2 + bi2", "ai3 ~ B3 + bi3")
DVLS   <- Dmethod(d, Expr, group = "Subject",
                 random = random, start = start)

## Permutation test (slow -- use nperm = 200 minimum for real use)
H      <- Dhypothesis_test(d, Expr, group = "Subject",
                          random = random, start = start,
                          Dhatt = DVLS, nperm = 20, seed = 1)

H$pvalue
H$plot
```

Dmethod	<i>Non-parametric approach to estimate variance components in a linear and nonlinear mixed-effects model</i>
---------	--

Description

Computes the scaled variance covariance matrix \hat{D}_* and the error variance $\hat{\sigma}^2$ using one of three nonparametric estimators: Variance Least Squares ("VLS"), Method of Moments ("MM"), or Method of Moments with First-Order Approximation ("MMF"). The method also estimate weighted fixed effects

Usage

```
Dmethod(
  data,
  Expr,
  group,
  random,
  start = NULL,
  method = c("VLS", "MM", "MMF"),
  MM_base_obj = NULL,
  kappa_max = 10000,
  RR_catof = "kappa",
  Beta_nls = NULL,
  verbose = 1,
  is_permuting = FALSE
)
```

Arguments

data	A data.frame containing all model variables.
Expr	A two-sided formula specifying the nonlinear model $f_i(a_i, \gamma)$. The left-hand side is the response variable and the right-hand side defines the nonlinear function using the subject-specific parameter names (e.g., ai1, ai2, ai3) that appear in start and random.
group	Character. Name of the grouping variable in data.
random	A character vector of two-sided formula strings, one per parameter in $a_i = A_i\beta + b_i$, mapping each subject-specific parameter (left-hand side, matching Expr and start) to its fixed-effects expression plus random effect (right-hand side). For example, <code>c("ai1 ~ B1 + bi1", "ai2 ~ B2 + bi2", "ai3 ~ B3 + bi3")</code> specifies that $ai1 = B1 + bi1$, $ai2 = B2 + bi2$, $ai3 = B3 + bi3$.
start	A named numeric vector of starting values for all parameters in Expr. Names must match those used in Expr (e.g., ai1, ai2, ai3). If NULL (the default), Dmethod attempts to compute starting values automatically using <code>nls.multstart::nls_multstart()</code> , searching over multiple initial values within a specified range (e.g. ± 10) for each parameter. If this step fails, provide start manually, or fit <code>nls_multstart()</code> or <code>nls()</code> separately with different starting values, search bounds, or optimisation settings, and use the resulting coefficients as starting values.
method	Character. One of "VLS" (default), "MM", or "MMF" estimation method.
MM_base_obj	An optional pre-computed object of class "MM_base" returned by <code>MM_base</code> . When NULL (default) and method is "MM" or "MMF", <code>MM_base()</code> is called internally. Supplying a pre-computed object avoids repeating the expensive first-stage NLS fits when calling both "MM" and "MMF" on the same data.
kappa_max	Positive numeric. Condition-number threshold for excluding subjects in MM/MMF. Default 1e4.
RR_catof	Exclusion criterion passed to <code>MM_base</code> . Either "kappa" (default), which uses the condition-number threshold <code>kappa_max</code> , or a user-specified numeric threshold applied directly.

Beta_nls	Optional named numeric vector of pre-computed fixed-effects estimates. If NULL (default), estimated internally via Beta_hat .
verbose	Integer (0, 1, or 2). 0 = silent; 1 = summary messages (default); 2 = full progress.
is_permuting	Logical. Internal flag set to TRUE during the permutation procedure, where the GLS-weighted refit of fixed effects is not needed and Beta_nls is used instead. Default FALSE.

Value

An object of class "Dmethod", a list with components:

Dhat The estimated scaled covariance matrix of random effects \hat{D}_* .

Sigma2 The estimated error variance $\hat{\sigma}^2$.

Beta The estimated fixed-effects vector $\hat{\beta}$.

method The estimation method used.

R Per-subject Jacobian matrices $R_i(\hat{\theta}_0)$.

Ypred Per-subject fitted values under fixed effects only.

residuals Per-subject residuals \hat{e}_i .

IDconvergence Subject inclusion/exclusion summary (MM/MMF only; NULL otherwise).

Additional internal objects are stored as an "internal" attribute (`attr(object, "internal")`) and used by package methods. They are not part of the user interface.

References

Uwimpuhwe, G., Drikvandi, R., and Blozis, S.A. (2026). Testing random effects in nonlinear mixed-effects models. *Statistics in Medicine*. doi:10.1002/sim.70605

Uwimpuhwe, G., Drikvandi, R. and Blozis, S. A. (in preparation). TestREnlme: An R Package for Testing Random Effects in Nonlinear Mixed-Effects Models. *Journal of Statistical Software*.

Demidenko, E. (2013). *Mixed Models: Theory and Applications with R* (2nd ed.). John Wiley & Sons

Drikvandi, R., Verbeke, G., Khodadadi, A. and Nia, V. P. (2013). Testing multiple variance components in linear mixed-effects models. *Biostatistics*, **14** (1), 144–159.

Examples

```
d      <- as.data.frame(Theoph)
Expr   <- conc ~ Dose * exp(ai2 + ai3 - ai1) *
        (exp(-Time * exp(ai3)) - exp(-Time * exp(ai2))) /
        (exp(ai2) - exp(ai3))
start  <- c(ai1 = -3.22, ai2 = 0.47, ai3 = -2.45)
random <- c("ai1 ~ B1 + bi1", "ai2 ~ B2 + bi2", "ai3 ~ B3 + bi3")
DVLS   <- Dmethod(d, Expr, group = "Subject",
                 random = random, start = start)
## method defaults to VLS; explicit: method = "VLS"
DVLS[c("Dhat", "Sigma2", "Beta")]
```

MM_base

*Compute first-stage quantities for MM and MMF estimators***Description**

Performs the first-stage nonlinear least squares (NLS) fit for each subject individually, and computes the per-subject Jacobian matrices $R_i^T R_i$ and condition numbers κ_i . The returned object can be passed to `Dmethod` via the `MM_base_obj` argument to avoid recomputing the first stage when calling both `method = "MM"` and `method = "MMF"` on the same data.

Usage

```
MM_base(
  data,
  Expr,
  group,
  random,
  start = NULL,
  kappa_max = 10000,
  RR_catof = "kappa",
  verbose = 1
)
```

Arguments

<code>data</code>	A <code>data.frame</code> containing all variables.
<code>Expr</code>	A two-sided formula specifying the nonlinear model $f_i(a_i, \gamma)$. The left-hand side is the response variable and the right-hand side defines the nonlinear function using the subject-specific parameter names (e.g., <code>ai1</code> , <code>ai2</code> , <code>ai3</code>) that appear in <code>start</code> and <code>random</code> .
<code>group</code>	Character. Name of the grouping (subject) variable.
<code>random</code>	A character vector of two-sided formula strings, one per parameter in $a_i = A_i\beta + b_i$, mapping each subject-specific parameter (left-hand side, matching <code>Expr</code> and <code>start</code>) to its fixed-effects expression plus random effect (right-hand side). For example, <code>c("ai1 ~ B1 + bi1", "ai2 ~ B2 + bi2", "ai3 ~ B3 + bi3")</code> specifies that $ai1 = B1 + bi1$, $ai2 = B2 + bi2$, $ai3 = B3 + bi3$.
<code>start</code>	A named numeric vector of starting values for all parameters in <code>Expr</code> . Names must match those used in <code>Expr</code> (e.g., <code>ai1</code> , <code>ai2</code> , <code>ai3</code>). If <code>NULL</code> (the default), <code>Dmethod</code> attempts to compute starting values automatically using
<code>kappa_max</code>	Positive numeric. Subjects whose per-subject Jacobian condition number exceeds this threshold are excluded from MM/MMF second-stage estimation. Default <code>1e4</code> .
<code>RR_catof</code>	Character. Exclusion criterion: <code>"kappa"</code> (default) uses the condition-number threshold <code>kappa_max</code> ; or a user-specified numeric threshold on the $R_i^T R_i$.
<code>verbose</code>	Integer (0, 1, or 2). 0 = silent; 1 = prints a summary of subjects retained and excluded (default); 2 = additionally prints per-subject convergence messages.

Value

A list of class "MM_base" with components:

`data` The (re-ordered, group-renumbered) `data.frame` used internally.

`group` Name of the grouping variable.

`start` The starting values used.

`Beta_nls` Named numeric vector of pooled (first-pass) fixed-effects estimates from [Beta_hat](#).

`random` The random formulas, aligned with `start`.

`re_names` Named character vector mapping random-effect names to subject-specific parameter names.

`Tmatrix` Matrix of per-subject scaled covariance terms (one row per subject, k^2 columns).

`Ti` List of per-subject $k \times k$ covariance matrices derived from `Tmatrix`.

`ddi` List of per-subject $k \times k$ second-stage deviation outer-product matrices (eq.~8.20).

`Lamda` Minimum eigenvalue of the standardised scatter matrix, used to bias-correct the MM/MMF variance estimates.

`sigma2` Pooled residual variance across retained subjects.

`Beta_GB` Named numeric vector of non-random-effect fixed-effects estimates.

`m` Total number of second-stage fixed-effects parameters ($k * ncol(Q)$).

`k` Number of random-effects parameters.

`id, uid, nud` Subject index vector, unique subject IDs, and number of unique subjects.

`IDworks` Integer vector of subject IDs retained after filtering.

`Q` Subject-level design matrix.

`Aai` List with elements A_i (per-subject design matrices) and a_{0i} (per-subject parameter estimates).

`kappa` Named numeric vector of per-subject condition numbers.

`IDconvergence` List with elements `ID_all`, `ID_used`, and `ID_supressed` (itself a list with `highRR` and `Unconverged`).

Examples

```
d      <- as.data.frame(Theoph)
Expr   <- conc ~ Dose * exp(ai2 + ai3 - ai1) *
        (exp(-Time * exp(ai3)) - exp(-Time * exp(ai2))) /
        (exp(ai2) - exp(ai3))
start  <- c(ai1 = -3.22, ai2 = 0.47, ai3 = -2.45)
random <- c("ai1 ~ B1 + bi1", "ai2 ~ B2 + bi2", "ai3 ~ B3 + bi3")
mb     <- MM_base(d, Expr, group = "Subject", random = random, start = start)
```

plot.Dmethod	<i>Plot method for Dmethod objects</i>
--------------	--

Description

By default all relevant diagnostic plots are produced and arranged in a grid. Use the `which` argument to select specific plots.

Usage

```
## S3 method for class 'Dmethod'
plot(x, time, which = NULL, ...)
```

Arguments

<code>x</code>	A "Dmethod" object.
<code>time</code>	Character. Name of the time variable (required).
<code>which</code>	Integer vector specifying which plots to show: 1 = individual profiles, 2 = fitted vs observed, 3 = residuals vs fitted (response), 4 = standardised residuals, 5 = condition numbers (MM/MMF only). Default: all applicable plots.
<code>...</code>	Additional arguments passed to individual plot functions.

Value

Invisibly returns a list of ggplot2 objects.

plot.Dtest	<i>Plot method for Dtest objects</i>
------------	--------------------------------------

Description

Displays the permutation null distribution histogram with the observed test statistic annotated.

Usage

```
## S3 method for class 'Dtest'
plot(x, ...)
```

Arguments

<code>x</code>	A "Dtest" object.
<code>...</code>	Additional arguments passed to plot_perm_hist .

Value

Invisibly returns the ggplot2 object.

plot_condition	<i>Plot per-subject condition numbers</i>
----------------	---

Description

Displays the condition numbers κ_i from a "MM_base" object or the MM_base_obj slot of a "Dmethod" object, sorted in decreasing order. A horizontal reference line at kappa_max marks the exclusion threshold.

Usage

```
plot_condition(Dobj, kappa_max = 10000, log_scale = TRUE)
```

Arguments

Dobj	A "MM_base_obj" object from MM_base , or a "Dmethod" object (for MM/MMF methods only).
kappa_max	Numeric. Exclusion threshold to highlight on the plot. Default 1e4.
log_scale	Logical. If TRUE (default), the y -axis is on the \log_{10} scale.

Value

A ggplot2 object.

plot_fitted	<i>Plot fitted curves overlaid on observed data</i>
-------------	---

Description

Draws the model-predicted trajectories on top of the observed data for each subject. When a "Dmethod" object is supplied, subject-specific EBLUP-adjusted predictions are used; otherwise only the population fixed-effects curve is shown.

Usage

```
plot_fitted(Dobj, time, subjects = NULL, overlay = TRUE, ncol = 4)
```

Arguments

Dobj	An object of class "Dmethod" returned by Dmethod .
time	Character. Name of the time variable in Dobj\$data.
subjects	Optional character or integer vector of subject IDs to plot. If NULL (default) all subjects are plotted.
overlay	Logical. If TRUE (default) observed and fitted curves are drawn in the same panel per subject. If FALSE, separate facets are used.
ncol	Integer. Number of columns for the subject facets. Default 4.

Value

A ggplot2 object.

plot_perm_hist	<i>Histogram of the permutation null distribution</i>
----------------	---

Description

Regenerates or customises the permutation histogram stored in a "Dtest" object. The observed statistic T_{obs} is shown as a vertical dashed line, and the empirical p -value and rejection decision are annotated on the plot.

Usage

```
plot_perm_hist(
  Htest,
  bins = 30,
  fill = "steelblue",
  line_col = "red",
  title = NULL
)
```

Arguments

Htest	An object of class "Dtest" returned by Dhypothesis_test .
bins	Integer. Number of histogram bins. Default 30.
fill	Character. Fill colour for the histogram bars. Default "steelblue".
line_col	Character. Colour for the T_{obs} line. Default "red".
title	Character. Plot title. If NULL a default title is generated.

Value

A ggplot2 object.

plot_profiles	<i>Plot raw individual trajectories</i>
---------------	---

Description

Produces a spaghetti plot of the raw observed trajectories for all subjects (or a selected subset), with an optional group-level mean profile and subject highlighting.

Usage

```
plot_profiles(  
  data,  
  group,  
  time,  
  response,  
  subjects = NULL,  
  mean_profile = TRUE,  
  highlight = NULL,  
  title = "Individual profiles"  
)
```

Arguments

data	A data.frame containing the data.
group	Character. Name of the grouping variable.
time	Character. Name of the time variable.
response	Character. Name of the response variable.
subjects	Optional character or integer vector of subject IDs to plot. If NULL (default) all subjects are plotted.
mean_profile	Logical. Whether to superimpose the group-level mean trajectory as a bold line. Default TRUE.
highlight	Optional character or integer vector of subject IDs to draw in a contrasting colour (e.g., subjects excluded by the condition-number filter).
title	Character. Plot title. Default "Individual profiles".

Value

A ggplot2 object.

Examples

```
d <- as.data.frame(Theoph)  
plot_profiles(d, group = "Subject", time = "Time", response = "conc")
```

plot_residuals	<i>Plot residuals versus fitted values</i>
----------------	--

Description

Produces a residuals-versus-fitted-values scatter plot with a horizontal reference line at zero and a loess smoother to aid detection of systematic misfit or heteroscedasticity.

Usage

```
plot_residuals(Dobj, time, type = c("response", "standardised", "subject"))
```

Arguments

Dobj	An object of class "Dmethod".
time	Character. Name of the time variable.
type	Character. Type of residuals: "response" (default) for raw residuals $Y_{ij} - \hat{Y}_{ij}$; "standardised" for residuals divided by $\hat{\sigma}$; "subject" for subject-level mean residuals.

Value

A ggplot2 object.

plot_variance	<i>Compare variance component estimates across methods</i>
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Description

Produces a side-by-side dot plot (or bar chart) of the estimated variance components \hat{d}_{*jj} for each random effect, comparing results from multiple estimation methods.

Usage

```
plot_variance(
  Dhatt_list,
  component = c("diagonal", "full"),
  title = "Variance component estimates"
)
```

Arguments

Dhatt_list	A named list of "Dmethod" objects, one per method. For example, list(VLS = DVLS, MM = DMM, MMF = DMMF).
component	Character. "diagonal" (default) plots only the variance terms \hat{d}_{*jj} ; "full" additionally includes the covariance terms.
title	Character. Plot title.

Value

A ggplot2 object.

SkillAcq

Skill acquisition data

Description

Response latency data from a study of quantitative skill acquisition on a learning task (Blozis 2004). Log-transformed response latencies are recorded for $N = 204$ subjects across $J = 11$ trial blocks, stored in wide format. Used to illustrate fitting a nonlinear mixed-effects model with a subject-level covariate (working memory) incorporated through the second-stage model, and to demonstrate reshaping wide-format longitudinal data into the long format required by [Dmethod](#) and [Dhypothesis_test](#).

Usage

SkillAcq

Format

A data frame with 204 rows (one per subject) and 13 columns:

- id** Subject identifier.
- ly1** Log-transformed response latency at trial block 1.
- ly2** Log-transformed response latency at trial block 2.
- ly3** Log-transformed response latency at trial block 3.
- ly4** Log-transformed response latency at trial block 4.
- ly5** Log-transformed response latency at trial block 5.
- ly6** Log-transformed response latency at trial block 6.
- ly7** Log-transformed response latency at trial block 7.
- ly8** Log-transformed response latency at trial block 8.
- ly9** Log-transformed response latency at trial block 9.
- ly10** Log-transformed response latency at trial block 10.
- ly11** Log-transformed response latency at trial block 11.
- wm2** Subject-level working-memory covariate.

Details

SkillAcq is stored in wide format, as commonly encountered in practice. Before use with `Dmethod` it must be reshaped to long format, with one row per subject-trial observation; see **Examples** below.

The nonlinear mixed-effects model used for this dataset is

$$Y_{ij} = a_{i1} - (a_{i1} + a_{i0}) \exp(a_{i2}T_{ij}) + \varepsilon_{ij},$$

with

$$a_{ik} = \beta_{0k} + \beta_{1k}wm2_i + b_{ik}, \quad k \in \{0, 1, 2\},$$

where a_{i0} , a_{i1} , and a_{i2} represent, respectively, the subject-specific initial performance offset, lower asymptote, and learning rate, each with a regression component on `wm2` and a subject-specific random effect. The questions of interest are whether all three random effects are necessary, and whether one or more can be removed to obtain a more parsimonious model; see `Dhypothesis_test`.

Source

Blozis, S. A. (2004). Structured latent curve models for the study of change in multivariate repeated measures. *Psychological Methods*, **9**(3), 334–353. <https://doi.org/10.1037/1082-989X.9.3.334>

Used as a worked example in Uwimpuhwe, G., Drikvandi, R. and Blozis, S. A. (in preparation). TestREnlme: An R Package for Testing Random Effects in Nonlinear Mixed-Effects Models. *Journal of Statistical Software*.

Examples

```
## Reshape from wide (ly1..ly11) to long format
qrt <- data.frame(SkillAcq)
qrt1 <- reshape2::melt(qrt, id.vars = c("id", "wm2"),
  variable.name = "ly", value.name = "Y")
qrt1$t <- as.numeric(sub("ly", "", qrt1$ly))

## Model: Y_ij = ai1 - (ai1 + ai0) * exp(ai2 * t_ij) + e_ij
## with aik = B0k + B1k * wm2_i + bik, k in {0, 1, 2}
Expr_learn <- Y ~ ai1 - (ai1 + ai0) * exp(ai2 * t)
random_learn <- c("ai0 ~ B00 + B10 * wm2 + bi0",
  "ai1 ~ B01 + B11 * wm2 + bi1",
  "ai2 ~ B02 + B12 * wm2 + bi2")

## Estimate variance components (VLS) and test all three random effects
DVLS_learn <- Dmethod(qrt1, Expr_learn, group = "id",
  random = random_learn, start = NULL)
DVLS_learn[c("Dhat", "Sigma2", "Beta")]

H_learn <- Dhypothesis_test(qrt1, Expr_learn, group = "id",
  random = random_learn, start = NULL,
  Dhatt = DVLS_learn, nperm = 200, seed = 1)

H_learn$pvalue
```

Tstat *Compute the observed test statistic*

Description

Computes $T_{\text{obs}} = N^{-1} \sum_i \text{tr}(R_i \hat{D}_* R_i^T)$ from a fitted [Dmethod](#) object.

Usage

```
Tstat(Dobj, bi_out = NULL)
```

Arguments

Dobj An object of class "Dmethod" returned by [Dmethod](#).

bi_out Optional character vector of random-effect names to test. If NULL (default) all random effects are included.

Value

A scalar, the value of T_{obs} .

ZandYPred *Compute Jacobian matrix and fixed-effects predicted values*

Description

Evaluates the Jacobian $R_i(\hat{\theta}_0)$ of the nonlinear model function with respect to the random-effects parameters, and computes fitted values under the fixed-effects-only model.

Usage

```
ZandYPred(data, Expr, group, random, Beta_nls = NULL, start = NULL)
```

Arguments

data A data.frame.

Expr A two-sided formula for the nonlinear model.

group Character name of the grouping variable.

random A named list or vector of one-sided formulas mapping each parameter to its random-effect expression, e.g. `c(B1 ~ B1 + bi1, B2 ~ B2 + bi2)`.

Beta_nls Named numeric vector of fixed-effects estimates from [Beta_hat](#).

start A named numeric vector of starting values. See the `start` argument of [Dmethod](#) for details, including automatic computation via `nls.multstart::nls_multstart()` when not supplied.

Value

A list with components:

`R` Named list of per-subject Jacobian matrices $R_i(\hat{\theta}_0)$.

`Ypred` Named list of per-subject predicted vectors $f_i(A_i\hat{\beta}, \hat{\gamma})$.

`residuals` Named list of per-subject residual vectors $\hat{e}_i = Y_i - f_i$.

Index

* datasets

SkillAcq, [17](#)

Beta_hat, [2](#), [9](#), [11](#), [19](#)

bootstrap_se, [3](#)

Dhypothesis_test, [5](#), [14](#), [17](#), [18](#)

Dmethod, [3](#), [4](#), [7](#), [10](#), [13](#), [17–19](#)

MM_base, [6](#), [8](#), [10](#), [13](#)

nlminb, [2](#)

nls, [2](#)

plot.Dmethod, [12](#)

plot.Dtest, [12](#)

plot_condition, [13](#)

plot_fitted, [13](#)

plot_perm_hist, [12](#), [14](#)

plot_profiles, [15](#)

plot_residuals, [16](#)

plot_variance, [16](#)

SkillAcq, [17](#)

Tstat, [6](#), [19](#)

ZandYPred, [19](#)