

Package ‘skewlmm’

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Type Package

Title Scale Mixture of Skew-Normal Linear Mixed Models

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Description It fits scale mixture of skew-normal linear mixed models using either an expectation-maximization (EM) type algorithm or its accelerated version (Damped Anderson Acceleration with Epsilon Monotonicity, DAAREM), including some possibilities for modeling the within-subject dependence. Details can be found in Schumacher, Lachos and Matos (2021) <doi:10.1002/sim.8870>.

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acfresid	<i>Autocorrelation function for smn.lmm or smsn.lmm residuals</i>
----------	---

Description

This function calculates the empirical autocorrelation function for the within-subject residuals from a smn.lmm or smsn.lmm fit. The autocorrelation values are calculated using pairs of residuals within-subjects. The autocorrelation function is useful for investigating serial correlation models for discrete-time data, preferably equally spaced.

Usage

```
acfresid(object, maxLag, resLevel = "marginal", resType = "normalized",
         calcCI = FALSE, levelCI, MCiter, seed)
```

Arguments

object	An object inheriting from class SMN or SMSN, representing a fitted scale mixture of (skew) normal linear mixed model.
maxLag	An optional integer giving the maximum lag for which the autocorrelation should be calculated. Defaults to maximum lag in the within-subject residuals.
resLevel	"marginal" (default) or "conditional". An optional character string specifying which residual should be used. For details see residuals.SMN .
resType	"response", "normalized" (default), or "modified". An optional character string specifying which type of residual should be used. For details see residuals.SMN .
calcCI	TRUE or FALSE (default). A logical value indicating if Monte Carlo confidence intervals should be computed for the conditionally independent model, which can be used for testing if the autocorrelations are zero.
levelCI	An optional numeric value in (0, 1) indicating the confidence level that should be used in the Monte Carlo confidence intervals. Default is 0.95.
MCiter	An optional discrete value indicating the number of Monte Carlo samples that should be used to compute the confidence intervals. Default is 300.
seed	An optional value used to specify seeds inside the function. Default is to use a random seed.

Value

A data frame with columns lag, ACF, and n.used representing, respectively, the lag between residuals within a pair, the corresponding empirical autocorrelation, and the number of pairs used. If calcCI=TRUE, the data frame has two extra columns containing the confidence intervals for the conditionally independent model. The returned value inherits from class acfresid.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

- Pinheiro, J. C. & Bates, D. M. (2000). Mixed-Effects Models in S and S-PLUS. Springer, New York, NY.
- Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[smn.lmm](#), [smsn.lmm](#), [plot.acfresid](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
acf1 = acfresid(fm1)
acf1
plot(acf1)

## computing simulated bands
acfCI = acfresid(fm1, calcCI=TRUE)
plot(acfCI)
```

boot_ci

Extract confidence intervals from lmmBoot object

Description

It extracts confidence intervals from parametric bootstrap results obtained using the `boot_par()` function.

Usage

```
boot_ci(object, conf = 0.95)
```

Arguments

object	An object containing the results of the <code>boot_par()</code> function.
conf	Confidence level to be considered.

Value

A matrix containing the confidence intervals.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

See Also

[boot_par](#), [smsn.lmm](#), [smn.lmm](#)

Examples

```
fm1 = smn.lmm(nlme::Orthodont, formFixed=distance ~ age+Sex, groupVar="Subject")
b1 = boot_par(fm1, B=100)
boot_ci(b1)
```

boot_par

Parametric bootstrap for SMSN/SMN objects

Description

It generates and estimates B Monte Carlo samples identical to the fitted model.

Usage

```
boot_par(object, B = 100, seed = 123)
```

Arguments

object	A smsn.lmm or smn.lmm object containing the fitted model to be updated.
B	Number of samples to be used.
seed	Seed to be used.

Details

This function provides an alternative for the asymptotic standard errors and confidence intervals given in summary, which may be helpful for small samples. Nevertheless, the computational cost is higher and it may take several minutes to get the results.

Value

A tibble of class lmmBoot with B lines, where each line contains the estimated parameters from a simulated sample.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

See Also

[boot_ci](#), [smsn.lmm](#), [smn.lmm](#)

Examples

```
fm1 = smn.lmm(nlme::Orthodont, formFixed=distance ~ age+Sex, groupVar="Subject")
b1 = boot_par(fm1, B=100)
boot_ci(b1)
```

coef

Extract coefficients from smsn.lmm, smn.lmm and smn.clmm objects

Description

It extracts estimated coefficients from smsn.lmm, smn.lmm and smn.clmm objects. The estimated coefficients are obtained by adding together the fixed and random effects estimates.

Usage

```
## S3 method for class 'SMN'
coef(object, ...)
## S3 method for class 'SMSN'
coef(object, ...)
## S3 method for class 'SMNclmm'
coef(object, ...)
```

Arguments

object	An object inheriting from class SMN, SMSN, or SMNclmm, representing a fitted scale mixture skew-normal linear mixed model.
...	Additional arguments

Value

Matrix of coefficients.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[smsn.lmm](#), [smn.lmm](#), [smn.clmm](#), [fitted.SMSN](#), [fitted.SMN](#), [fitted.SMNC1mm](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
coef(fm1)
```

confint	<i>Computes confidence intervals from smn.lmm and smsn.lmm fitted models</i>
---------	--

Description

Computes either asymptotical (based on normality from maximum likelihood estimators) or parametric bootstrapped confidence intervals from a model fit.

Usage

```
## S3 method for class 'SMN'
confint(object, parm, level = 0.95, method, ...)
## S3 method for class 'SMSN'
confint(object, parm, level = 0.95, method, ...)
```

Arguments

object	An object inheriting from class SMN or SMSN
parm	A character indicating for which parameter the intervals should be returned. Available options: "beta" for fixed effects, or "all" for all parameters. Default is "all".
level	Confidence level to be used.
method	A character indicating with method should be used. "asymptotic" refers to traditional confidence intervals based on asymptotical normality from maximum likelihood estimators; "bootstrap" performs a parametric bootstrap method based on B samples (100 by default), and is only recommended to small to moderate sample sizes.
...	Additional arguments to be passed to boot_par.

Value

A table containing the estimate and the respective confidence interval.

See Also

[smn.lmm](#), [smsn.lmm](#), [boot_par](#), [boot_ci](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
confint(fm1)
```

criteria	<i>Extracts criteria for model comparison of SMSN/SMN/SMNclmm objects</i>
----------	---

Description

It extracts criteria for model comparison of several SMSN-LMM, SMN-LMM and/or SMN-CLMM (for censored responses).

Usage

```
criteria(lobjects)
```

Arguments

lobjects A list containing the smsn.lmm, smn.lmm or smn.clmm objects to be compared.

Value

A data.frame containing for each model the maximum log-likelihood value, the number of parameters, the AIC, and the BIC.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[smsn.lmm](#), [smn.lmm](#), [smn.clmm](#)

Examples

```
fm_norm = smn.lmm(nlme::Orthodont, formFixed=distance~age+Sex, groupVar="Subject")
fm_t = update(fm_norm, distr="t")
fm_sn = smsn.lmm(nlme::Orthodont, formFixed=distance~age+Sex, groupVar="Subject")
fm_cens = smn.clmm(nlme::Orthodont, formFixed=distance~age+Sex, groupVar="Subject")
criteria(list(fm_norm=fm_norm, fm_t=fm_t, fm_sn=fm_sn, fm_cens=fm_cens))
```

errorVar	<i>Error scale matrix associated with times</i>
----------	---

Description

It returns a scale matrix associated with the error term at time `times`. Can be applied to a `smn.lmm` or `smsn.lmm` object or to a specific dependence structure with chosen parameter values.

Usage

```
errorVar(times, object = NULL, sigma2 = NULL, depStruct = NULL,
         phi = NULL)
```

Arguments

<code>times</code>	A vector containing the times for which the matrix should be calculated.
<code>object</code>	A <code>smn.lmm</code> or <code>smsn.lmm</code> object for which the variance should be extracted.
<code>sigma2</code>	Common variance parameter, such that $\Sigma = \text{sigma2} * R$. Only evaluated if <code>object</code> is <code>null(object)</code> .
<code>depStruct</code>	Dependence structure. "UNC" for conditionally uncorrelated ("CI" is also accepted), "ARp" for AR(p) – p is <code>length(phi)</code> –, "CS" for compound symmetry, "DEC" for DEC, and "CAR1" for continuous-time AR(1). Only evaluated if <code>object</code> is <code>null(object)</code> .
<code>phi</code>	Parameter vector indexing the dependence structure. Only evaluated if <code>object</code> is <code>null(object)</code> .

Value

Matrix of dimension `length(times)`.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[smsn.lmm](#), [smn.lmm](#)

Examples

```
fm1 = smsn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
errorVar(times=1:4, fm1)
#
errorVar(times=1:5, sigma2=1, depStruct="ARp", phi=.5)
errorVar(times=1:5, sigma2=1, depStruct="DEC", phi=c(.5,.8))
```

fitted.SMN

*Extract smn.lmm fitted values***Description**

The fitted values are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels.

Usage

```
## S3 method for class 'SMN'
fitted(object, ...)
```

Arguments

object	An object inheriting from class SMN, representing a fitted scale mixture normal linear mixed model.
...	Additional arguments.

Value

Vector of fitted values with length equal to `nrow(data)`.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

See Also

[smn.lmm](#), [predict.SMN](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
fitted(fm1)
```

fitted.SMNclmm	<i>Extract smn.clmm fitted values</i>
----------------	---------------------------------------

Description

The fitted values are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels.

Usage

```
## S3 method for class 'SMNclmm'
fitted(object, ...)
```

Arguments

object	An object inheriting from class SMNclmm, representing a fitted scale mixture normal linear mixed model with censored responses.
...	Additional arguments.

Value

Vector of fitted values with length equal to nrow(data).

Author(s)

Fernanda L. Schumacher, Larissa A. Matos, Victor H. Lachos and Katherine L. Valeriano

See Also

[smn.clmm](#), [predict.SMNclmm](#)

Examples

```
nj1 = 5; m = 30
time = rep(1:nj1, times=m)
groups = as.factor(rep(1:m, each=nj1))
dat1 = rmsn.clmm(time, groups, cbind(1,time), rep(1,m*nj1), sigma2=0.7,
                D=0.6*diag(1), beta=c(1,2), depStruct="UNC")

fm1 = smn.clmm(dat1, formFixed=y~x, groupVar="ind", depStruct="UNC",
               ci="ci", lcl="lcl", ucl="ucl", control=lmmControl(max.iter=30))
fitted(fm1)
```

fitted.SMSN	<i>Extract smsn.lmm fitted values</i>
-------------	---------------------------------------

Description

The fitted values are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels.

Usage

```
## S3 method for class 'SMSN'
fitted(object, ...)
```

Arguments

object	An object inheriting from class SMSN, representing a fitted scale mixture skew-normal linear mixed model.
...	Additional arguments.

Value

Vector of fitted values with length equal to `nrow(data)`.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

See Also

[smsn.lmm](#), [predict.SMSN](#)

Examples

```
fm1 = smsn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject",
               control=lmmControl(tol=.0001))
fitted(fm1)
```

fixef	<i>Extract estimated fixed effects from smsn.lmm, smn.lmm and smn.clmm objects</i>
-------	--

Description

It extracts fixed effects from smsn.lmm and smn.lmm objects.

Usage

```
## S3 method for class 'SMN'
fixef(object, ...)
## S3 method for class 'SMSN'
fixef(object, ...)
```

Arguments

object	An object inheriting from class SMN, SMSN, or SMNCens, representing a fitted scale mixture skew-normal linear mixed model.
...	Additional arguments

Value

Matrix of estimated random effects.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[smsn.lmm](#), [smn.lmm](#), [smn.clmm](#), [fitted.SMSN](#), [fitted.SMN](#), [fitted.SMNClmm](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
fixef(fm1)
```

formula	<i>Formula from an smn.lmm and smsn.lmm models</i>
---------	--

Description

It returns the formula used for both fixed and random terms of the linear mixed model represented by object.

Usage

```
## S3 method for class 'SMN'
formula(x, ...)
## S3 method for class 'SMSN'
formula(x, ...)
```

Arguments

x	An object inheriting from class SMN or SMSN
...	Additional arguments

Value

formFixed	Fixed effects formula
formRandom	Random effects formula
groupVar	Variable identified subjects or clusters

See Also

[smn.lmm](#), [smsn.lmm](#), [criteria](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
formula(fm1)
```

healy.plot	<i>Healy-type plot from a smn.lmm or smsn.lmm object</i>
------------	--

Description

It creates a Healy-type plot from a smn.lmm or smsn.lmm object, for goodness-of-fit assessment.

Usage

```
healy.plot(object, dataPlus = NULL, dotsize = 0.4, calcCI = FALSE,
           levelCI, MCiter, seed, ...)
```

Arguments

object	An object inheriting from class SMN or SMSN, representing a fitted scale mixture of (skew) normal linear mixed model.
dataPlus	Optional. Expanded dataset that should be used instead the one used for fitting. This is necessary for unbalanced datasets, since Haley's plot requires all subject to have the same number of observations.
dotsize	Optional. Dotsize used in ggplot.
calcCI	TRUE or FALSE (default). A logical value indicating if Monte Carlo confidence intervals should be computed for the conditionally independent model, which can be used for testing if the autocorrelations are zero.
levelCI	An optional numeric value in $(0, 1)$ indicating the confidence level that should be used in the Monte Carlo confidence intervals. Default is 0.95.
MCiter	An optional discrete value indicating the number of Monte Carlo samples that should be used to compute the confidence intervals. Default is 300.
seed	An optional value used to specify seeds inside the function. Default is to use a random seed.
...	Additional arguments.

Details

It constructs a Healy-type plot (Healy, 1968) by plotting the nominal probability values $1/n, 2/n, \dots, n/n$ against the theoretical cumulative probabilities of the ordered observed Mahalanobis distances. If the fitted model is appropriate, the plot should resemble a straight line through the origin with unit slope. If `calcCI=TRUE`, the plot presents two dashed blue lines containing approximated confidence intervals by considering that the fitted model is correct.

Value

A [ggplot](#) object.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

Healy, M. J. R. (1968). Multivariate normal plotting. *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 17(2), 157-161.

Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[ggplot](#), [smn.lmm](#), [smsn.lmm](#), [mahalDist](#), [acfresid](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
healy.plot(fm1)

## computing simulated bands
healy.plot(fm1, calcCI=TRUE)
```

lmmControl	<i>Control options for smsn.lmm(), smn.lmm() and smn.clmm()</i>
------------	---

Description

The values supplied in the function call replace the defaults and a list with all possible arguments is returned. The returned list has class "lmmControl" and is used as the control argument to the `smsn.lmm()`, `smn.lmm()` and `smn.clmm()` functions.

Usage

```
lmmControl(tol = 1e-06, max.iter = 300, calc.se = TRUE, lb = NULL,
           lu = NULL, luDEC = 10,
           initialValues = list(beta = NULL, sigma2 = NULL, D = NULL,
                                lambda = NULL, phi = NULL, nu = NULL),
           quiet = !interactive(), showCriterion = FALSE, algorithm = "DAAREM",
           parallelphi = NULL, parallelnu = NULL, ncores = NULL,
           control.daarem = list())
```

Arguments

<code>tol</code>	Tolerance for the convergence criterion. Default = 1e-6.
<code>max.iter</code>	Maximum number of iterations for the EM algorithm. Default = 200.
<code>calc.se</code>	A logical value indicating if standard errors should be calculated.
<code>lb</code>	Optional. Bottom limit for estimating nu.
<code>lu</code>	Optional. Upper limit for estimating nu.
<code>luDEC</code>	Optional. Upper limit for estimating the "damping" parameter for DEC covariance. If <code>luDEC</code> ≤ 1, only attenuation of the exponential decay can be obtained.
<code>initialValues</code>	Optional. A named list containing initial parameter values, with at most the following elements: <code>beta</code> , <code>sigma2</code> , <code>D</code> , <code>lambda</code> , <code>phi</code> , <code>nu</code> .
<code>quiet</code>	A logical value indicating if the iteration message should be suppressed. Useful when calling the function in R Markdown.
<code>showCriterion</code>	A logical value indicating if the criterion should be shown at each iteration.
<code>algorithm</code>	Algorithm to be used for estimation, either "DAAREM" (default) or "EM". DAAREM is an acceleration method and usually converges with fewer iterations, but it may result in numerical errors (in this case, please use the "EM" option).

<code>parallelphi</code>	A logical value indicating if parallel optimization should be used in the numerical update of the parameters related to the within-subject dependence structure. Default is TRUE if the data contains more than 30 subjects, and FALSE otherwise. Meaningless if <code>depStruct = "UNC"</code> .
<code>parallelnu</code>	A logical value indicating if parallel optimization should be used in the numerical update of <code>nu</code> . Meaningless if <code>distr="norm"</code> or <code>distr="sn"</code> .
<code>ncores</code>	Number of cores to be used for the parallel optimization. Meaningless if <code>parallelphi = FALSE</code> and <code>parallelnu = FALSE</code> .
<code>control.daarem</code>	List of control for the daarem algorithm. See <code>help(daarem, package = "daarem")</code> for details. Meaningless if <code>algorithm = "EM"</code>

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

Henderson, N.C. and Varadhan, R. (2019) Damped Anderson acceleration with restarts and monotonicity control for accelerating EM and EM-like algorithms, *Journal of Computational and Graphical Statistics*, Vol. 28(4), 834-846.

Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[smsn.lmm](#), [smn.lmm](#), [smn.clmm](#), [update](#)

Examples

```
lmmControl(algorithm = "EM")

fm1 = smn.lmm(nlme::Orthodont, formFixed=distance ~ age+Sex,
              groupVar="Subject", control=lmmControl(tol=1e-7))
```

logLik

Log-likelihood of an smn.lmm and smsn.lmm models

Description

It returns the log-likelihood value of the linear mixed model represented by object evaluated at the estimated coefficients.

Usage

```
## S3 method for class 'SMN'
logLik(object, ...)
## S3 method for class 'SMSN'
logLik(object, ...)
```

Arguments

`object` An object inheriting from class SMN or SMSN
`...` Additional arguments.

Value

The log-likelihood value of the model represented by `object` evaluated at the estimated coefficients.

See Also

[smn.lmm](#), [smsn.lmm](#), [criteria](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
logLik(fm1)
```

<code>lr.test</code>	<i>Likelihood-ratio test for SMSN/SMN objects</i>
----------------------	---

Description

It performs a likelihood-ratio test for two nested SMSN-LMM or SMN-LMM.

Usage

```
lr.test(obj1, obj2, level = 0.05)
```

Arguments

`obj1, obj2` `smsn.lmm` or `smn.lmm` objects containing the fitted models to be tested.
`level` The significance level that should be used. If `quiet = TRUE`, this is ignored.

Value

`statistic` The test statistic value.
`p.value` The p-value from the test.
`df` The degrees of freedom used on the test.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[smsn.lmm](#), [smn.lmm](#)

Examples

```
fm1 = smn.lmm(nlme::Orthodont, formFixed=distance ~ age+Sex, groupVar="Subject")
fm2 = smsn.lmm(nlme::Orthodont, formFixed=distance ~ age+Sex, groupVar="Subject",
               control=lmmControl(tol=.0001))
lr.test(fm1, fm2)
```

`mahalDist`

Mahalanobis distance from a smn.lmm or smsn.lmm object

Description

Returns the squared Mahalanobis distance from a fitted SMN-LMM or SMSN-LMM.

Usage

```
mahalDist(object, decomposed = FALSE, dataPlus = NULL)
```

Arguments

<code>object</code>	An object inheriting from class SMN or SMSN, representing a fitted scale mixture of (skew) normal linear mixed model.
<code>decomposed</code>	Logical. If TRUE, the Mahalanobis distance is decomposed in an error term and a random effect term. Default is FALSE.
<code>dataPlus</code>	Optional. Expanded dataset that should be used instead the one used for fitting, useful for using Healy's plot with missing data.

Value

A vector containing the Mahalanobis distance, if `decomposed = FALSE`, or a data frame containing the Mahalanobis distance and its decomposition in error term and random effect (b) term, if `decomposed = TRUE`.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

Zeller, C. B., Labra, F. V., Lachos, V. H. & Balakrishnan, N. (2010). Influence analyses of skew-normal/independent linear mixed models. *Computational Statistics & Data Analysis*, 54(5).

See Also

[smn.lmm](#), [smsn.lmm](#), [plot.mahalDist](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
mahalDist(fm1)
plot(mahalDist(fm1), nlabels=2)
```

`mahalDistCens`

Mahalanobis distance from a smn.clmm object

Description

Returns the squared Mahalanobis distance from a fitted SMN-CLMM. Censored values are imputed using their conditional expectation from the fitting algorithm.

Usage

```
mahalDistCens(object)
```

Arguments

<code>object</code>	An object inheriting from class <code>SMNclmm</code> , representing a fitted scale mixture of normal censored linear mixed model.
---------------------	---

Value

An object of class `mahalDistCens` containing the Mahalanobis distance.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos, Victor H. Lachos and Katherine L. Valeriano

References

Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

Zeller, C. B., Labra, F. V., Lachos, V. H. & Balakrishnan, N. (2010). Influence analyses of skew-normal/independent linear mixed models. *Computational Statistics & Data Analysis*, 54(5).

See Also

[smn.clmm](#), [plot.mahalDistCens](#)

Examples

```

nj1 = 5; m = 30
time = rep(1:nj1, times=m)
groups = as.factor(rep(1:m, each=nj1))
dat1 = rmsn.clmm(time, groups, cbind(1,time), rep(1,m*nj1), sigma2=0.7,
                D=0.5*diag(1), beta=c(1,2), depStruct="CS", phi=0.4)

# Estimation
fm1 = smn.clmm(dat1, formFixed=y~x, groupVar="ind", depStruct="CS", ci="ci",
               lcl="lcl", ucl="ucl", control=lmmControl(max.iter=30))
distance = mahalDistCens(fm1)
plot(distance, level=0.95, nlabels=2)

```

miceweight

*Data set for clinical trial measuring mice weight***Description**

Sintetic longitudinal data set based on a clinical trial designed to test two diet treatments in comparison to a control group. The weight of 52 mice (reported in grams) is measured weekly from baseline until week 10 of treatment.

Usage

```
data(miceweight)
```

Format

This data frame contains the following columns:

treat Treatment received (treatment 1 (T1), treatment 2 (T2), or control (C))

mouseID Mouse ID

week Week since treatment started

weight Mouse weight in grams

Details

Dietary supplementations were administered for groups T1 and T2 starting at week 5.

This dataset was created using minor perturbations from a real study for which the original data is not publicly available. Data features such as covariances and skewness were preserved.

See Also

[smsn.lmm](#)

Examples

```
library(ggplot2)

data(miceweight)
ggplot(miceweight) + geom_line(aes(x=week, y=weight, group=mouseID)) +
  facet_wrap(~treat) + theme_bw()
```

nobs	<i>Extract the number of observations from smn.lmm and smsn.lmm fitted models</i>
------	---

Description

Extract the total number of observations from a model fit (considering all repeated measurements from all subjects or clusters).

Usage

```
## S3 method for class 'SMN'
nobs(object, ...)
## S3 method for class 'SMSN'
nobs(object, ...)
```

Arguments

object	An object inheriting from class SMN or SMSN
...	Additional arguments.

Value

A single integer, expected to be equal to `nrow(data)`.

See Also

[smn.lmm](#), [smsn.lmm](#), [criteria](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
nobs(fm1)
```

plot	<i>Plot a smn.lmm or smsn.lmm object</i>
------	--

Description

Fitted values versus residuals plot.

Usage

```
## S3 method for class 'SMN'
plot(x, type = "response", level = "conditional",
     useweight = TRUE, alpha = 0.3, ...)

## S3 method for class 'SMSN'
plot(x, type = "response", level = "conditional",
     useweight = TRUE, alpha = 0.3, ...)
```

Arguments

x	An object inheriting from class SMN or SMSN, representing a fitted scale mixture of (skew) normal linear mixed model.
type	Type of residual that should be used. For details see residuals.SMN . Default is "response", indicating raw residuals.
level	Level of residual that should be used. For details see residuals.SMN . Default is "conditional".
useweight	A logical value indicating if the estimated weights should be used as color in the plot.
alpha	Transparency parameter to be used ($0 < \alpha < 1$). Meaningless if useweight = TRUE.
...	Additional arguments.

Value

A [ggplot](#) object.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

See Also

[ggplot](#), [smn.lmm](#), [smsn.lmm](#), [fitted.SMN](#), [fitted.SMSN](#), [residuals.SMN](#), [residuals.SMSN](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont,
              groupVar="Subject", distr="t")
plot(fm1)
plot(fm1, useweight=FALSE)

library(ggplot2)
plot(fm1) + ggtitle("t-LMM for orthodont data")
```

plot.acfresid

*Plot ACF for smn.lmm or smsn.lmm residuals***Description**

Plot method for objects of class "acfresid".

Usage

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

Arguments

x	An object inheriting from class acfresid, representing the empirical autocorrelation function from the residuals of a scale mixture of (skew) normal linear mixed model.
...	Additional arguments.

Value

A [ggplot](#) object.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

See Also

[ggplot](#), [acfresid](#), [smn.lmm](#), [smsn.lmm](#), [residuals.SMN](#), [residuals.SMSN](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
plot(acfresid(fm1))

acfCI = acfresid(fm1, calcCI=TRUE)
plot(acfCI)
```

plot.mahalDist	<i>Plot Mahalanobis distance for a fitted smn.lmm or smsn.lmm</i>
----------------	---

Description

Plot method for objects of class "mahalDist". For the total Mahalanobis distance, it gives a quantile for outlier detection, based on the Mahalanobis distance theoretical distribution.

Usage

```
## S3 method for class 'mahalDist'
plot(x, fitobject, type, level = 0.99, nlabels = 3, ...)
```

Arguments

x	An object inheriting from class mahalDist, representing the Mahalanobis distance from a fitted scale mixture of (skew) normal linear mixed model.
fitobject	Optional. An object inheriting from class SMN or SMSN, representing the fitted scale mixture of (skew) normal linear mixed model that was used for calculating the Mahalanobis distance.
type	Optional. Either "total" (default), for the standard Mahalanobis distance, "error", for the error term of the decomposition, or "b" for the random effect term of the decomposition. For details see mahalDist .
level	An optional numeric value in (0, 1) indicating the level of the quantile. It only has utility if type="total". Default is 0.99.
nlabels	Number of observations that should be labeled. Default is 3.
...	Additional arguments.

Value

A [ggplot](#) object, plotting the index versus the Mahalanobis distance, if all subject have the same number of observations; or plotting the number of observations per subject versus the Mahalanobis, otherwise.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

See Also

[ggplot](#), [mahalDist](#), [smn.lmm](#), [smsn.lmm](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
plot(mahalDist(fm1), nlabels=2)

#the estimated quantile is stored at the attribute "info" of the plot object
plotMD = plot(mahalDist(fm1))
attr(plotMD, "info")
```

plot.mahalDistCens	<i>Plot Mahalanobis distance for a fitted smn.clmm</i>
--------------------	--

Description

Plot method for objects of class "mahalDistCens". It also gives a quantile for outlier detection, based on the Mahalanobis distance theoretical distribution.

Usage

```
## S3 method for class 'mahalDistCens'
plot(x, fitobject, level = 0.99, nlabels = 3, ...)
```

Arguments

x	An object inheriting from class mahalDistCens, representing the Mahalanobis distance from a fitted scale mixture of normal censored linear mixed model.
fitobject	Optional. An object inheriting from class SMNc1mm, representing the fitted scale mixture of normal linear mixed model that was used for calculating the Mahalanobis distance.
level	An optional numeric value in (0, 1) indicating the level of the quantile. Default is 0.99.
nlabels	Number of observations that should be labeled. Default is 3.
...	Additional arguments.

Value

A [ggplot](#) object, plotting the index versus the Mahalanobis distance, if all subject have the same number of observations; or plotting the number of observations per subject versus the Mahalanobis, otherwise.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos, Victor H. Lachos and Katherine L. Valeriano

See Also

[ggplot](#), [mahalDistCens](#), [smn.clmm](#)

Examples

```

nj1 = 5; m = 30
time = rep(1:nj1, times=m)
groups = as.factor(rep(1:m, each=nj1))
dat1 = rmsn.clmm(time, groups, cbind(1,time), rep(1,m*nj1), sigma2=0.7,
                D=0.5*diag(1), beta=c(1,2), depStruct="CS", phi=0.4)

# Estimation
fm1 = smn.clmm(dat1, formFixed=y~x, groupVar="ind", depStruct="CS", ci="ci",
               lcl="lcl", ucl="ucl", control=lmmControl(max.iter=30))
distance = mahalDistCens(fm1)
plot(distance, level=0.95, nlabels=2)

```

plot.SMNclmm	<i>Plot a smn.clmm object</i>
--------------	-------------------------------

Description

Fitted values versus residuals plot. Censored values are imputed using their conditional expectation from the fitting algorithm.

Usage

```

## S3 method for class 'SMNclmm'
plot(x, level = "conditional", useweight = TRUE,
     alpha = 0.3, ...)

```

Arguments

x	An object inheriting from class SMNclmm, representing a fitted scale mixture of normal censored linear mixed model.
level	Level of residual that should be used. For details see residuals.SMNclmm . Default is "conditional".
useweight	A logical value indicating if the estimated weights should be used as color in the plot.
alpha	Transparency parameter to be used ($0 < \alpha < 1$). Meaningless if useweight = TRUE.
...	Additional arguments.

Value

A [ggplot](#) object.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos, Victor H. Lachos and Katherine L. Valeriano

See Also

[ggplot](#), [smn.clmm](#), [fitted.SMNclmm](#), [residuals.SMNclmm](#)

Examples

```
nj1 = 5; m = 30
time = rep(1:nj1, times=m)
groups = as.factor(rep(1:m, each=nj1))
dat1 = rmsn.clmm(time, groups, cbind(1,time), rep(1,m*nj1), sigma2=0.7,
                D=0.5*diag(1), beta=c(1,2), depStruct="UNC", distr="t", nu=4)
# Estimation
fm1 = smn.clmm(dat1, formFixed=y~x, groupVar="ind", depStruct="UNC", ci="ci",
               lcl="lcl", ucl="ucl", distr="t", control=lmmControl(max.iter=30))
plot(fm1)
```

predict.SMN

Prediction of future observations from an smn.lmm object

Description

Predicted values are obtained through conditional expectation. For details, see Schumacher, Lachos, and Matos (2021).

Usage

```
## S3 method for class 'SMN'
predict(object, newData, ...)
```

Arguments

object	An object inheriting from class SMN, representing a fitted scale mixture normal linear mixed model.
newData	A data frame for which response variable should be predicted, including co-variates, groupVar and possibly timeVar. If missing or NULL, fitted values are returned.
...	Additional arguments.

Value

A data frame with covariates, groupVar and ypred, where ypred contains the predicted values from the response variable.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[smn.lmm](#), [fitted.SMN](#)

Examples

```
dat1 = nlme::Orthodont
fm1 = smn.lmm(distance ~ age+Sex, data=subset(dat1, age<14), groupVar="Subject")
predict(fm1, subset(dat1, age==14))
```

predict.SMNclmm	<i>Prediction of future observations from an smn.clmm object</i>
-----------------	--

Description

Predicted values are obtained through conditional expectation. For details, see Schumacher, Lachos, and Matos (2021).

Usage

```
## S3 method for class 'SMNclmm'
predict(object, newData, ...)
```

Arguments

object	An object inheriting from class SMNclmm, representing a fitted scale mixture normal linear mixed model.
newData	A data frame for which response variable should be predicted, including covariates, groupVar and possibly timeVar. If missing or NULL, fitted values are returned.
...	Additional arguments.

Value

A data frame with covariates, groupVar and ypred, where ypred contains the predicted values from the response variable.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos, Victor H. Lachos and Katherine L. Valeriano

References

Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[smn.clmm](#), [fitted.SMNclmm](#)

Examples

```
# Simulated example: 20 individuals with 5 times for estimation and
# 1 time for prediction
set.seed(963)
nj1 = 6; m = 20
time = rep(1:nj1, times=m)
groups = as.factor(rep(1:m, each=nj1))
dat1 = rmsn.clmm(time, groups, cbind(1,time), rep(1,m*nj1), sigma2=0.4,
                D=0.6*diag(1), beta=c(1,2), depStruct="CS", phi=0.25)

# Estimation
fm1 = smn.clmm(subset(dat1,time<6), formFixed=y~x, groupVar="ind",
                depStruct="CS", ci="ci", lcl="lcl", ucl="ucl",
                control=lmmControl(max.iter=30, tol=1e-4))

# Prediction
pred = predict(fm1, subset(dat1,time==6))
# MSPE
mean((subset(dat1,time==6)$y - pred$ypred)^2)
```

predict.SMSN

Prediction of future observations from an smsn.lmm object

Description

Predicted values are obtained through conditional expectation. For details, see Schumacher, Lachos, and Matos (2021).

Usage

```
## S3 method for class 'SMSN'
predict(object, newData, ...)
```

Arguments

object	An object inheriting from class SMSN, representing a fitted scale mixture skew-normal linear mixed model.
newData	A data frame for which response variable should be predicted, including co-variates, groupVar and possibly timeVar. If missing or NULL, fitted values are returned.
...	Additional arguments.

Value

A data frame with covariates, groupVar and ypred, where ypred contains the predicted values from the response variable.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[smsn.lmm](#), [fitted.SMSN](#)

Examples

```
dat1 = nlme::Orthodont
fm1 = smsn.lmm(distance ~ age+Sex, data=subset(dat1, age<14), groupVar="Subject")
predict(fm1, subset(dat1, age==14))
```

print.SMN

Print a smn.lmm object

Description

Print a smn.lmm object.

Usage

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

Arguments

x	An object inheriting from class SMN, representing a fitted scale mixture normal linear mixed model.
...	Additional print arguments.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

See Also

[smn.lmm](#), [summary.SMN](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
fm1
```

print.SMNclmm	<i>Print a smn.clmm object</i>
---------------	--------------------------------

Description

Print a smn.clmm object.

Usage

```
## S3 method for class 'SMNclmm'
print(x, confint.level = 0.95, ...)
```

Arguments

x	An object inheriting from class SMNclmm, representing a fitted scale mixture normal linear mixed model with censored responses.
confint.level	Level of the approximate confidence intervals presented.
...	Additional print arguments.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos, Victor H. Lachos and Katherine L. Valeriano

See Also

[smn.clmm](#), [summary.SMNclmm](#)

Examples

```
nj1 = 5; m = 30
time = rep(1:nj1, times=m)
groups = as.factor(rep(1:m, each=nj1))
dat1 = rmsn.clmm(time, groups, cbind(1,time), rep(1,m*nj1), sigma2=0.7,
                D=0.6*diag(1), beta=c(1,2), depStruct="UNC")
fm1 = smn.clmm(dat1, formFixed=y~x, groupVar="ind", formRandom=~1,
                depStruct="UNC", ci="ci", lcl="lcl", ucl="ucl")
fm1
```

print.SMSN	<i>Print a smsn.lmm object</i>
------------	--------------------------------

Description

Print a smsn.lmm object.

Usage

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

Arguments

x	An object inheriting from class SMSN, representing a fitted scale mixture skew-normal linear mixed model.
...	Additional print arguments.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

See Also

[smsn.lmm](#), [summary.SMSN](#)

Examples

```
fm1 = smsn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
fm1
```

ranef	<i>Extract random effects from smsn.lmm, smn.lmm and smn.clmm objects</i>
-------	---

Description

It extracts random effects from smsn.lmm, smn.lmm and smn.clmm objects.

Usage

```
## S3 method for class 'SMN'
ranef(object, ...)
## S3 method for class 'SMSN'
ranef(object, ...)
## S3 method for class 'SMNclmm'
ranef(object, ...)
```

Arguments

`object` An object inheriting from class `SMN`, `SMSN`, or `SMNclmm`, representing a fitted scale mixture skew-normal linear mixed model.

`...` Additional arguments

Value

Matrix of estimated random effects.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[smsn.lmm](#), [smn.lmm](#), [smn.clmm](#), [fitted.SMSN](#), [fitted.SMN](#), [fitted.SMNclmm](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
ranef(fm1)
```

residuals

Extract model residuals from smn.lmm and smsn.lmm objects

Description

The conditional residuals are obtained by subtracting the fitted values from the response vector, while the marginal residuals are obtained by subtracting only the fixed effects from the response vector.

Usage

```
## S3 method for class 'SMN'
residuals(object, level = "conditional", type = "response", ...)

## S3 method for class 'SMSN'
residuals(object, level = "conditional", type = "response", ...)
```

Arguments

object	An object inheriting from class SMN or SMSN, representing a fitted scale mixture of (skew) normal linear mixed model.
level	Either "conditional", for obtaining conditional residuals, or "marginal", for marginal residuals.
type	An optional character string specifying the type of residuals to be used. If "response", as by default, the "raw" residuals (observed - fitted) are used; if "normalized", the standardized residuals (residuals pre-multiplied by the inverse square-root of the estimated variance matrix) are used; else, if "modified", modified residuals (residuals pre-multiplied by the inverse square-root of the estimated scale matrix) are used.
...	Additional arguments.

Details

Modified residuals are useful when the variance is not finite, such as when $\nu \leq 2$ for t or ST distributions, or when $\nu \leq 1$ for SL or SSL distributions.

Value

Vector with the residuals of length equal to `nrow(data)`.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

See Also

[smn.lmm](#), [smsn.lmm](#), [acfresid](#), [mahalDist](#), [healy.plot](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
residuals(fm1)
plot(fm1, useweight=FALSE)
```

residuals.SMNclmm

Extract model residuals from smn.clmm objects

Description

The conditional residuals are obtained by subtracting the fitted values from the response vector, while the marginal residuals are obtained by subtracting only the fixed effects from the response vector.

Censored values are imputed using their conditional expectation from the fitting algorithm.

Usage

```
## S3 method for class 'SMNclmm'
residuals(object, level = "conditional", ...)
```

Arguments

<code>object</code>	An object inheriting from class <code>SMNclmm</code> , representing a fitted scale mixture of normal censored linear mixed model.
<code>level</code>	Either <code>"conditional"</code> , for obtaining conditional residuals, or <code>"marginal"</code> , for marginal residuals.
<code>...</code>	Additional arguments.

Value

Vector with the residuals of length equal to `nrow(data)`.

Note

The residuals are computed after imputing the censored observations.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos, Victor H. Lachos and Katherine L. Valeriano

See Also

[smn.clmm](#), [mahalDistCens](#)

Examples

```
nj1 = 5; m = 30
time = rep(1:nj1, times=m)
groups = as.factor(rep(1:m, each=nj1))
dat1 = rmsn.clmm(time, groups, cbind(1,time), rep(1,m*nj1), sigma2=0.7,
                 D=0.6*diag(1), beta=c(1,2), depStruct="CS", phi=0.4)

fm1 = smn.clmm(dat1, formFixed=y~x, groupVar="ind", depStruct="CS", ci="ci",
               lcl="lcl", ucl="ucl", control=lmmControl(max.iter=30))
residuals(fm1)
```

rsmn.clmm

*Generate data from SMSN-CLMM with censored responses***Description**

It creates a simulated data set from SMSN-CLMM with several possible dependence structures, with an established censoring rate or a fixed limit of detection (LOD).

Usage

```
rsmn.clmm(time, ind, x, z, sigma2, D, beta, lambda=rep(0, nrow(D)),
           depStruct="UNC", phi=NULL, distr="norm", nu=NULL, type="left",
           pcens=0.10, LOD=NULL)
```

Arguments

time	Vector of length N containing times that should be used in data generation, where N indicates the total number of observations.
ind	Vector of length N containing the variable which represents the subjects or groups.
x	Design matrix for fixed effects of dimension $N \times p$.
z	Design matrix for random effects of dimension $N \times q$.
sigma2	Common variance parameter, such that $\Sigma = \sigma^2 * R$.
D	Variance matrix for random effects.
beta	Vector of fixed effects parameter.
lambda	Skewness parameter of random effects.
depStruct	Dependence structure. "UNC" for conditionally uncorrelated ("CI" is also accepted), "ARp" for AR(p) – p is length(phi)–, "CS" for compound symmetry, "DEC" for DEC, "CAR1" for continuous-time AR(1), and "MA1" for moving average of order 1.
phi	Parameter vector indexing the dependence structure.
distr	Distribution that should be used. "norm" for normal, "t" for Student-t, "sn" for skew-normal, and "st" for skew-t.
nu	Degrees of freedom for Student-t and skew-t distributions. It must be greater than 2.
type	left for left censoring and right for right censoring.
pcens	Desired censoring rate.
LOD	Desired limit of detection. If LOD is provided, then pcens will be discarded.

Value

A data frame containing time, the variable indicating groups (ind), the generated response variable (y), the censoring indicator variable (ci), the lower censoring limit (lc1), the upper censoring limit (uc1), and possible covariates.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos, Victor H. Lachos and Katherine L. Valeriano

References

Matos, L. A., Prates, M. O., Chen, M. H., and Lachos, V. H. (2013). Likelihood-based inference for mixed-effects models with censored response using the multivariate-t distribution. *Statistica Sinica* 23(3), 1323-1345.

Lachos, V. H., A. Matos, L., Castro, L. M., and Chen, M. H. (2019). Flexible longitudinal linear mixed models for multiple censored responses data. *Statistics in medicine*, 38(6), 1074-1102.

See Also

[smn.clmm](#)

Examples

```
library(ggplot2)

# Generating a sample for m=25 individuals with 5 times
nj1 = 5
m = 25
time = rep(1:nj1, times=m)
groups = as.factor(rep(1:m, each=nj1))

# Considering 10% of right censoring responses and normal distribution
dat1 = rsmsn.clmm(time, groups, cbind(1,time), rep(1,m*nj1), sigma2=.25,
                  D=0.5*diag(1), beta=c(1,2), depStruct="ARp", phi=0.5,
                  type="right")

head(dat1)
ggplot(dat1, aes(x=x, y=y, group=ind)) + geom_line() +
  stat_summary(aes(group=1), geom="line", fun=mean, col="blue", size=1.5) +
  geom_line(aes(x=x,y=lcl), color="red", linetype="dashed")

# Considering LOD=4, left censoring, and Student-t distribution
dat2 = rsmsn.clmm(time, groups, cbind(1,time), rep(1,m*nj1), sigma2=.25,
                  D=0.5*diag(1), beta=c(1,2), depStruct="CS", phi=0.2,
                  distr="t", nu=4, LOD=4)

mean(dat2$ci) #censoring rate
ggplot(dat2, aes(x=x, y=y, group=ind)) + geom_line() +
  stat_summary(aes(group=1), geom="line", fun=mean, col="blue", size=1.5) +
  geom_line(aes(x=x,y=ucl), color="red", linetype="dashed")
```

rsmsn.lmm

Generate data from SMSN-LMM

Description

It creates a simulated data set from SMSN-LMM (or from SMN-LMM, if $\lambda = 0$) with several possible dependence structures, for one subject.

Usage

```
rsmn.lmm(time1, x1, z1, sigma2, D1, beta, lambda, depStruct = "UNC",
          phi = NULL, distr = "sn", nu = NULL)
```

Arguments

time1	Vector containing times that should be used in data generation.
x1	Design matrix for fixed effects.
z1	Design matrix for random effects.
sigma2	Common variance parameter, such that $\Sigma = \sigma^2 * R$.
D1	Variance matrix for random effects.
beta	Vector of fixed effects parameter.
lambda	Skewness parameter of random effects.
depStruct	Dependence structure. "UNC" for conditionally uncorrelated ("CI" is also accepted), "ARp" for AR(p) – p is length(phi)–, "CS" for compound symmetry, "DEC" for DEC, and "CAR1" for continuous-time AR(1).
phi	Parameter vector indexing the dependence structure.
distr	Distribution that should be used. "sn" for skew-normal, "st" for skew-t, "ss" for skew-slash, and "scn" for skew-contaminated normal.
nu	Parameter vector indexing distr. Should be NULL for "sn", be a vector of length 1 for "st" and "ss", and of length 2 for "scn".

Value

A data frame containing time, the generated response variable (y), and possible covariates.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

- Lachos, V. H., P. Ghosh, and R. B. Arellano-Valle (2010). Likelihood based inference for skew-normal independent linear mixed models. *Statistica Sinica* 20, 303-322.
- Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[smsgn.lmm](#)

Examples

```
# Generating a sample for 1 individual at 5 times
nj1 = 5
rmsn.lmm(1:nj1, cbind(1, 1:nj1), rep(1, nj1), sigma2=.25, D1=diag(1),
         beta=c(1, 2), lambda=2, depStruct="ARp", phi=.5,
         distr="st", nu=5)

# Generating a sample for m=25 individuals with 5 times
library(dplyr)
library(purrr)
library(ggplot2)
nj1 = 5
m = 25
gendatList = map(rep(nj1, m),
                 function(nj) rmsn.lmm(1:nj, cbind(1, 1:nj), rep(1, nj),
                                       sigma2=.25, D1=.5*diag(1), beta=c(1, 2),
                                       lambda=2, depStruct="ARp", phi=.5))

gendat = bind_rows(gendatList, .id="ind")
ggplot(gendat, aes(x=x, y=y, group=ind)) + geom_line() +
  stat_summary(aes(group=1), geom="line", fun=mean, col="blue", size=2)
#
fm1 = smsn.lmm(y ~ x, data=gendat, groupVar="ind", depStruct="ARp",
              pAR=1)
summary(fm1)
```

sigma

Residual standard deviation from smn.lmm and smsn.lmm objects

Description

Extract the estimated residual standard deviation from smn.lmm and smsn.lmm objects.

Usage

```
## S3 method for class 'SMN'
sigma(object, ...)
## S3 method for class 'SMSN'
sigma(object, ...)
```

Arguments

object	An object inheriting from class SMN or SMSN
...	Additional arguments.

Value

A positive number.

See Also

[smn.lmm](#), [smsn.lmm](#), [criteria](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
sigma(fm1)
```

smn.clmm	<i>ML estimation of scale mixture of normal linear mixed models with censored responses</i>
----------	---

Description

It fits left, right, or interval censored scale mixture of normal linear mixed model with possible within-subject dependence structure, using the EM algorithm. It provides estimates and standard errors of parameters.

Usage

```
smn.clmm(data, formFixed, groupVar, formRandom = ~1, depStruct = "UNC",
          ci, lcl, ucl, timeVar = NULL, distr = "norm",
          nufix = FALSE, pAR = 1, control = lmmControl())
```

Arguments

data	A data frame containing the variables named in formFixed, formRandom, groupVar, timeVar, ci, lcl, and ucl.
formFixed	A two-sided linear formula object describing the fixed effects part of the model, with the response on the left of a ~ operator and the covariates, separated by + operators, on the right.
groupVar	A character containing the name of the variable which represents the subjects or groups in data.
formRandom	A one-sided linear formula object describing the random effects part of the model, with the covariates, separated by + operators, on the right of a ~ operator. By default, a model with random intercept is considered.
depStruct	A character indicating which dependence structure should be used. "UNC" for conditionally uncorrelated ("CI" is also accepted), "ARp" for AR(p) – p is length(phi)– , "CS" for compound symmetry, "DEC" for DEC, "CAR1" for continuous-time AR(1), and "MA1" for moving average of order 1.
ci	A character containing the name of the censoring indicator variable in data, which should be 1 if the respective observation is censored or missing, and 1 otherwise. If missing, it is assumed that none of the observations is censored.
lcl	A character containing the name of the lower censoring limit in data. If missing, it is assumed lcl=-Inf, i.e., no left limit.

ucl	A character containing the name of the upper censoring limit in data. If missing, it is assumed $ucl=Inf$, i.e., no right limit.
timeVar	A character containing the name of the variable which represents the time in data. Meaningless if <code>depStruct="UNC"</code> or <code>depStruct="CS"</code> . For other structures, if <code>is.null(timeVar)</code> the observations are considered equally spaced and ordered. If <code>depStruct="ARp"</code> , <code>timeVar</code> must be an index, preferably starting at 1.
distr	A character indicating which distribution should be used. "norm" for normal and "t" for Student-t.
nufix	TRUE or FALSE indicating if ν should be estimated for t distribution. If <code>nufix=TRUE</code> , ν must be specified through <code>lmmControl()</code> .
pAR	If <code>depStruct="ARp"</code> , <code>pAR</code> indicates the order of the autoregressive process that should be used (1 by default). Otherwise, it is meaningless.
control	An object resulting from the function <code>lmmControl()</code> , containing additional options for the estimation algorithm.

Details

It fits the model $Y_i = X_i\beta + Z_ib_i + \epsilon_i$, for $i = 1, \dots, n$, where Y_i is a vector with n_i observed continuous responses, $b_i \sim SMN(0, D; H)$ and $\epsilon_i \sim SMN(0, \Sigma_i; H)$, indexed by the same mixing distribution.

For details see Matos et al. (2013) and Lachos et al. (2019).

Value

An object of class "SMNclmm" representing the SMN-CLMM fit. Generic functions such as `print` and `summary` have methods to show the results of the fit. The functions `fitted` and `ranef` can be used to extract some of its components.

Specifically, the following components are returned:

theta	Named vector with parameter estimates.
iter	Number of iterations runned.
estimates	A named list containing parameter estimates.
yest	Imputed values in the response variable.
uhat	Estimated weights.
loglik.track	Vector containing the log-likelihood value from each iteration of the estimation procedure.
random.effects	Estimated random effects.
std.error	A vector with standard errors.
loglik	Value of the log-likelihood at last iteration.
elapsedTime	Time elapsed in processing, in seconds.
error	Convergence criterion at last iteration.
criteria	A list with AIC, BIC, and SIC criterion.

call	The smn.clmm call that produced the object.
data	The data frame used on smn.clmm call.
formula	A list containing the formulas used on smn.clmm call.
depStruct	A character indicating which dependence structure was used.
covRandom	A character indicating which structure was used for the random effects scale matrix.
distr	A character indicating which distribution was used.
N	The number of observations used.
n	The number of individuals/groups used.
groupVar	A character indicating the name of the grouping variable.
timeVar	A character indicating the name of the time variable, if any.
fitted	A vector of fitted values.

Author(s)

Larissa A. Matos, Victor H. Lachos, Katherine L. Valeriano and Fernanda L. Schumacher

References

- Henderson, N. C. and R. Varadhan (2019). Damped anderson acceleration with restarts and monotonicity control for accelerating EM and EM-like algorithms. *Journal of Computational and Graphical Statistics* 28(4), 834-846.
- Matos, L. A., Prates, M. O., Chen, M. H., and Lachos, V. H. (2013). Likelihood-based inference for mixed-effects models with censored response using the multivariate-t distribution. *Statistica Sinica* 23(3), 1323-1345.
- Lachos, V. H., A. Matos, L., Castro, L. M., and Chen, M. H. (2019). Flexible longitudinal linear mixed models for multiple censored responses data. *Statistics in medicine*, 38(6), 1074-1102.

See Also

[lmmControl](#), [update](#), [predict.SMNclmm](#), [residuals.SMNclmm](#), [plot.SMNclmm](#), [smn.lmm](#), [smsn.lmm](#)

Examples

```
# Generating a sample for m=30 individuals with 5 times
# Considering 10% of left censoring responses
# AR(1) and normal distribution
nj1 = 5
m = 30
time = rep(1:nj1, times=m)
groups = as.factor(rep(1:m, each=nj1))
dat1 = rmsn.clmm(time = time, ind = groups, x = cbind(1,time), z = rep(1,m*nj1),
                 sigma2=0.6, D=0.5*diag(1), beta=c(1,2), depStruct="ARp",
                 phi=0.4, pcens = .1, type = "left")

# Estimation using UNC
fm0 = smn.clmm(dat1, formFixed=y~x, groupVar="ind", ci="ci", ucl="ucl")
```

```
summary(fm0)

# Estimation using AR(1)
fm1 = update(fm0, depStruct="ARp")

# Estimation using AR(1) and t distribution
fm2 = update(fm1, distr="t")

# Comparing fitted models
criteria(list(fm0= fm0, fm1=fm1, fm2=fm2))
```

smn.lmm

ML estimation of scale mixture of normal linear mixed models

Description

It fits a scale mixture of normal linear mixed model with possible within-subject dependence structure, using an EM-type algorithm (via the DAAREM method, by default). It provides estimates and standard errors of parameters.

Usage

```
smn.lmm(data, formFixed, groupVar, formRandom = ~1, depStruct = "UNC",
         timeVar = NULL, distr = "norm", covRandom = "pdSymm",
         pAR = 1, control = lmmControl())
```

Arguments

data	A data frame containing the variables named in formFixed, formRandom, groupVar, and timeVar.
formFixed	A two-sided linear formula object describing the fixed effects part of the model, with the response on the left of a ~ operator and the covariates, separated by + operators, on the right.
groupVar	A character containing the name of the variable which represents the subjects or groups in data.
formRandom	A one-sided linear formula object describing the random effects part of the model, with the covariates, separated by + operators, on the right of a ~ operator. By default, a model with random intercept is considered.
depStruct	A character indicating which dependence structure should be used. "UNC" for conditionally uncorrelated ("CI" is also accepted), "ARp" for AR(p) – p is length(phi) – , "CS" for compound symmetry, "DEC" for DEC, and "CAR1" for continuous-time AR(1).
timeVar	A character containing the name of the variable which represents the time in data. Meaningless if depStruct="UNC" or depStruct="CS". For other structures, if is.null(timeVar) the observations are considered equally spaced and ordered. If depStruct="ARp", timeVar must be an index, preferably starting at 1.

distr	A character indicating which distribution should be used. "norm" for normal, "t" for t, "sl" for slash, and "cn" for contaminated normal.
covRandom	A character indicating which structure should be used for the random effects scale matrix (either "pdSymm" (default), for a general positive-definite matrix, or "pdDiag", for a diagonal matrix).
pAR	If depStruct="ARp", pAR indicates the order of the autoregressive process that should be used. Otherwise, it is meaningless.
control	An object resulting from the function <code>lmmControl()</code> , containing additional options for the estimation algorithm.

Details

It fits the model $Y_i = X_i\beta + Z_ib_i + \epsilon_i$, for $i = 1, \dots, n$, where Y_i is a vector with n_i observed continuous responses, $b_i \sim SMN(0, D; H)$ and $\epsilon_i \sim SMN(0, \Sigma_i; H)$, indexed by the same mixing distribution.

For efficiency, the DAAREM method is used for parameter estimation. In case of numerical errors, please try passing to `lmmControl(algorithm = "DAAREM")` to the control argument.

For details see Schumacher, Lachos & Matos (2021).

Value

An object of class "SMN" representing the SMN-LMM fit. Generic functions such as `print` and `summary` have methods to show the results of the fit. The functions `fitted` and `ranef` can be used to extract some of its components.

Specifically, the following components are returned:

theta	Named vector with parameter estimates.
iter	Number of iterations runned.
estimates	A named list containing parameter estimates.
uhat	Estimated weights.
loglik.track	Vector containing the log-likelihood value from each iteration of the estimation procedure.
random.effects	Estimated random effects.
std.error	A vector with standard errors.
loglik	Value of the log-likelihood at last iteration.
elapsedTime	Time elapsed in processing, in seconds.
error	Convergence criterion at last iteration.
call	The <code>smn.lmm</code> call that produced the object.
criteria	A list with AIC and BIC criterion.
data	The data frame used on <code>smn.lmm</code> call.
formula	A list containing the formulas used on <code>smn.lmm</code> call.
depStruct	A character indicating which dependence structure was used.

covRandom	A character indicating which structure was used for the random effects scale matrix.
distr	A character indicating which distribution was used.
N	The number of observations used.
n	The number of individuals/groups used.
groupVar	A character indicating the name of the grouping variable.
control	The control list used in the function's call.
timeVar	A character indicating the name of the time variable, if any.
fitted	A vector of fitted values, if calc.bi=TRUE.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

- Henderson, N. C. and R. Varadhan (2019). Damped anderson acceleration with restarts and monotonicity control for accelerating EM and EM-like algorithms. *Journal of Computational and Graphical Statistics* 28(4), 834-846.
- Lachos, V. H., P. Ghosh, and R. B. Arellano-Valle (2010). Likelihood based inference for skew-normal independent linear mixed models. *Statistica Sinica* 20, 303-322.
- Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[lmmControl](#), [update](#), [predict.SMN](#), [residuals.SMN](#), [plot.SMN](#), [smsn.lmm](#), [smn.clmm](#)

Examples

```
#simple example
dat1 = as.data.frame(nlme::Orthodont)
fm1 = smn.lmm(dat1, formFixed=distance ~ age, groupVar="Subject",
              control=lmmControl(max.iter=30))
fm1

#fitting for several distributions / dependence structures
fm1 = smn.lmm(dat1, formFixed=distance ~ age+Sex, groupVar="Subject")
fm2 = smn.lmm(dat1, formFixed=distance ~ age+Sex, groupVar="Subject",
              distr="t")
fm3 = smn.lmm(dat1, formFixed=distance ~ age+Sex, groupVar="Subject",
              distr="sl")
fm4 = smn.lmm(dat1, formFixed=distance ~ age+Sex, groupVar="Subject",
              depStruct="ARp", pAR=1)
criteria(list(fm1=fm1, fm2=fm2, fm3=fm3, fm4=fm4))
summary(fm3)

#some diagnostic tools
```

```

plot(fm3)
acf3 = acfresid(fm3, calcCI=TRUE, MCiter=100)
plot(acf3)
plot(mahalDist(fm3), nlabels=2)
healy.plot(fm3)

```

smsn.lmm

ML estimation of scale mixture of skew-normal linear mixed models

Description

It fits a scale mixture of skew-normal linear mixed model with possible within-subject dependence structure, using an EM-type algorithm (via the DAAREM method, by default). It provides estimates and standard errors of parameters.

Usage

```

smsn.lmm(data, formFixed, groupVar, formRandom = ~1, depStruct = "UNC",
          timeVar = NULL, distr = "sn", covRandom = "pdSymm",
          skewind, pAR = 1, control = lmmControl())

```

Arguments

data	A data frame containing the variables named in formFixed, formRandom, groupVar, and timeVar.
formFixed	A two-sided linear formula object describing the fixed effects part of the model, with the response on the left of a ~ operator and the covariates, separated by + operators, on the right.
groupVar	A character containing the name of the variable which represents the subjects or groups in data.
formRandom	A one-sided linear formula object describing the random effects part of the model, with the covariates, separated by + operators, on the right of a ~ operator. By default, a model with random intercept is considered.
depStruct	A character indicating which dependence structure should be used. "UNC" for conditionally uncorrelated ("CI" is also accepted), "ARp" for AR(p) – p is length(phi) – , "CS" for compound symmetry, "DEC" for DEC, and "CAR1" for continuous-time AR(1).
timeVar	A character containing the name of the variable which represents the time in data. Meaningless if depStruct="UNC" or depStruct="CS". For other structures, if is.null(timeVar) the observations are considered equally spaced and ordered. If depStruct="ARp", timeVar must be an index, preferably starting at 1.
distr	A character indicating which distribution should be used. "sn" for skew-normal, "st" for skew-t, "ssl" for skew-slash, and "scn" for skew-contaminated normal.

covRandom	A character indicating which structure should be used for the random effects scale matrix (either "pdSymm" (default), for a general positive-definite matrix, or "pdDiag", for a diagonal matrix).
skewind	A vector of length equal to the number of random effects, containing 0's and 1's, indicating which elements of the skewness parameter vector should be estimated (optional, default is an all-ones vector).
pAR	If depStruct="ARp", pAR indicates the order of the autoregressive process that should be used. Otherwise, it is meaningless.
control	An object resulting from the function <code>lmmControl()</code> , containing additional options for the estimation algorithm.

Details

It fits the model $Y_i = X_i\beta + Z_ib_i + \epsilon_i$, for $i = 1, \dots, n$, where Y_i is a vector with n_i observed continuous responses, $b_i \sim SMSN(c\Delta, D, \lambda; H)$ and $\epsilon_i \sim SMN(0, \Sigma_i; H)$, indexed by the same mixing distribution.

For efficiency, the DAAREM method is used for parameter estimation. In case of numerical errors, please try passing to `lmmControl(algorithm = "DAAREM")` to the control argument.

For details see Schumacher, Lachos & Matos (2021).

Value

An object of class "SMSN" representing the SMSN-LMM fit. Generic functions such as `print` and `summary` have methods to show the results of the fit. The functions `fitted` and `ranef` can be used to extract some of its components.

Specifically, the following components are returned:

theta	Named vector with parameter estimates.
iter	Number of iterations runned.
estimates	A named list containing parameter estimates.
uhat	Estimated weights.
loglik.track	Vector containing the log-likelihood value from each iteration of the estimation procedure.
random.effects	Estimated random effects.
std.error	A vector with standard errors.
loglik	Value of the log-likelihood at last iteration.
elapsedTime	Time elapsed in processing, in seconds.
error	Convergence criterion at last iteration.
call	The <code>smsn.lmm</code> call that produced the object.
criteria	A list with AIC and BIC criterion.
data	The data frame used on <code>smsn.lmm</code> call.
formula	A list containing the formulas used on <code>smsn.lmm</code> call.
depStruct	A character indicating which dependence structure was used.

covRandom	A character indicating which structure was used for the random effects scale matrix.
distr	A character indicating which distribution was used.
N	The number of observations used.
n	The number of individuals/groups used.
groupVar	A character indicating the name of the grouping variable.
control	The control list used in the function's call.
timeVar	A character indicating the name of the time variable, if any.
fitted	A vector of fitted values, if calc.bi=TRUE.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

Henderson, N. C. and R. Varadhan (2019). Damped anderson acceleration with restarts and monotonicity control for accelerating EM and EM-like algorithms. *Journal of Computational and Graphical Statistics* 28(4), 834-846.

Lachos, V. H., P. Ghosh, and R. B. Arellano-Valle (2010). Likelihood based inference for skew-normal independent linear mixed models. *Statistica Sinica* 20, 303-322.

Schumacher, F. L., Lachos, V. H., and Matos, L. A. (2021). Scale mixture of skew-normal linear mixed models with within-subject serial dependence. *Statistics in Medicine* 40(7), 1790-1810.

See Also

[lmmControl](#), [update](#), [predict.SMSN](#), [residuals.SMSN](#), [plot.SMSN](#), [smn.lmm](#), [smn.clmm](#)

Examples

```
#simple example
dat1 = as.data.frame(nlme::Orthodont)
fm1 = smsn.lmm(dat1, formFixed=distance ~ age, groupVar="Subject",
               control=lmmControl(max.iter=30))
fm1

#fitting for several distributions / dependence structures
fm1 = smsn.lmm(dat1, formFixed=distance ~ age+Sex, groupVar="Subject")
fm2 = smsn.lmm(dat1, formFixed=distance ~ age+Sex, groupVar="Subject",
               distr="st")
fm3 = smsn.lmm(dat1, formFixed=distance ~ age+Sex, groupVar="Subject",
               distr="ssl")
fm4 = smsn.lmm(dat1, formFixed=distance ~ age+Sex, groupVar="Subject",
               depStruct="ARp", pAR=1)
criteria(list(fm1=fm1, fm2=fm2, fm3=fm3, fm4=fm4))
summary(fm3)

#some diagnostic tools
```

```
plot(fm3)
acf3 = acfresid(fm3, calcCI=TRUE, MCiter=100)
plot(acf3)
plot(mahalDist(fm3), nlabels=2)
healy.plot(fm3)
```

summary.SMN

*Summary of a smn.lmm object***Description**

summary method for class "SMN".

Usage

```
## S3 method for class 'SMN'
summary(object, confint.level = 0.95, ...)
```

Arguments

object	An object inheriting from class SMN, representing a fitted scale mixture normal linear mixed model.
confint.level	Level of the approximate confidence intervals presented.
...	Additional arguments.

Value

varRandom	Estimated variance matrix from random effects (D).
varFixed	Parameter estimates of variance from random errors (Σ). For recovering the error variance matrix use errorVar function.
tableFixed	Estimated fixed effects, their standard errors and approximated confidence intervals.
criteria	Maximum log-likelihood value, AIC and BIC criteria.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

See Also

[boot_par](#), [smn.lmm](#), [errorVar](#), [plot.SMN](#), [residuals.SMN](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject")
summary(fm1)
```

summary.SMNclmm	<i>Summary of a smn.clmm object</i>
-----------------	-------------------------------------

Description

summary method for class "SMNclmm".

Usage

```
## S3 method for class 'SMNclmm'
summary(object, confint.level = 0.95, ...)
```

Arguments

object	An object inheriting from class SMNclmm, representing a fitted scale mixture normal linear mixed model with censored responses.
confint.level	Level of the approximate confidence intervals presented.
...	Additional arguments.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos, Victor H. Lachos and Katherine L. Valeriano

See Also

[smn.clmm](#), [plot.SMNclmm](#), [residuals.SMNclmm](#)

Examples

```
nj1 = 5; m = 30
time = rep(1:nj1, times=m)
groups = as.factor(rep(1:m, each=nj1))
dat1 = rmsn.clmm(time, groups, cbind(1,time), rep(1,m*nj1), sigma2=0.7,
                 D=0.5*diag(1), beta=c(1,2), depStruct="UNC")
fm1 = smn.clmm(dat1, formFixed=y~x, groupVar="ind", formRandom=~1,
               depStruct="UNC", ci="ci", lcl="lcl", ucl="ucl")
summary(fm1)
```

summary.SMSN

*Summary of a smsn.lmm object***Description**

summary method for class "SMSN".

Usage

```
## S3 method for class 'SMSN'
summary(object, confint.level = 0.95, ...)
```

Arguments

object	An object inheriting from class SMSN, representing a fitted scale mixture skew-normal linear mixed model.
confint.level	Level of the approximate confidence intervals presented.
...	Additional arguments.

Value

varRandom	Estimated variance matrix from random effects (D).
varFixed	Parameter estimates of variance from random errors (Σ). For recovering the error variance matrix use errorVar function.
tableFixed	Estimated fixed effects, their standard errors and approximated confidence intervals.
criteria	Maximum log-likelihood value, AIC and BIC criteria.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

See Also

[boot_par](#), [smsn.lmm](#), [errorVar](#), [plot.SMSN](#), [residuals.SMSN](#)

Examples

```
fm1 = smsn.lmm(distance ~ age+Sex, data=nlme::Orthodont, groupVar="Subject",
               control=lmmControl(tol=.0001))
summary(fm1)
```

update

*Update for SMSN/SMN/SMNclmm objects***Description**

It fits a SM(S)N-(C)LMM by updating a fitted object.

Usage

```
## S3 method for class 'SMN'
update(object, ..., evaluate = TRUE)

## S3 method for class 'SMSN'
update(object, ..., evaluate = TRUE)

## S3 method for class 'SMNclmm'
update(object, ..., evaluate = TRUE)
```

Arguments

object	A smsn.lmm, smn.lmm or smn.clmm object containing the fitted model to be updated.
...	Arguments to be changed.
evaluate	A logical value indicating if the new class should be evaluated. If FALSE, the call is returned.

Value

An object resulting from the smsm.lmm(), smn.lmm() or smn.clmm() function.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos, Victor H. Lachos and Katherine L. Valeriano

See Also

[smsn.lmm](#), [smn.lmm](#), [smn.clmm](#)

Examples

```
fm1 = smn.lmm(nlme::Orthodont, formFixed=distance ~ age+Sex, groupVar="Subject")
fm2 = update(fm1, distr="t")
fm2
```

UTIdata*Data set for Unstructured Treatment Interruption Study*

Description

Data set from a study of Unstructured Treatment Interruption in HIV-infected adolescents in four institutions in the USA. The main outcome is the HIV-1 RNA viral load, which is subject to censoring below the lower limit of detection of the assay (50 copies/mL). The censored observations are indicated by the variable RNAcens.

Usage

```
data(UTIdata)
```

Format

This data frame contains the following columns:

Patid patient ID

Days.after.TI days after treatment interruption

Fup follow-up months

RNA viral load RNA

RNAcens censoring indicator for viral load

Details

This dataset was copied from the `lmec` package, which was discontinued from CRAN in May 2022.

Source

Saitoh, A., Foca, M, et al. (2008), Clinical outcome in perinatally acquired HIV-infected children and adolescents after unstructured treatment interruption, *Pediatrics*, 121, e513-e521.

See Also

[smn.clmm](#)

Examples

```
library(ggplot2)

data(UTIdata)
ggplot(UTIdata) + geom_line(aes(x=Fup, y=log10(RNA), group=Patid)) +
  geom_hline(yintercept=log10(50), color="red", linetype="dashed") +
  geom_hline(yintercept=log10(400), color="red", linetype="dashed") +
  labs(x="Time", y=bquote(log["10"]("RNA"))) + theme_bw()

# Proportion of censoring
prop.table(table(UTIdata$RNAcens))
```

weight_plot	<i>Weight plot for smn.lmm or smsn.lmm object</i>
-------------	---

Description

Estimated weights versus Mahalanobis distance plot

Usage

```
weight_plot(object)
```

Arguments

object	An object inheriting from class SMN or SMSN, representing a fitted scale mixture of (skew) normal linear mixed model.
--------	---

Value

A [ggplot](#) object.

Author(s)

Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

See Also

[ggplot](#), [smn.lmm](#), [smsn.lmm](#), [fitted.SMN](#), [fitted.SMSN](#), [residuals.SMN](#), [residuals.SMSN](#)

Examples

```
fm1 = smn.lmm(distance ~ age+Sex, data=nlme::Orthodont,  
              groupVar="Subject", distr="t")  
weight_plot(fm1)
```

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