Package ‘skewlmm’

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Type    Package
Title   Scale Mixture of Skew-Normal Linear Mixed Models
Version 0.2.2
Maintainer Fernanda L. Schumacher <fernandalschumacher@gmail.com>
Description It fits scale mixture of skew-normal linear mixed models using an expectation–
maximization (EM) type algorithm, including some possibilities for modeling the within-
subject dependence. Details can be found in Schumacher, La-
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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

```r
acfresid(object, maxLag, resLevel = "marginal", resType = "normalized", calcCI = FALSE, IClevel, 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.
**acfresid**

IClevel  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**


**See Also**

smn.lmm, smsn.lmm, plot.acfresid

**Examples**

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

acfCI<- acfresid(fm1,calcCI=TRUE)
plot(acfCI)
```
errorVar  

**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**

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

**Arguments**

- `times`: A vector containing the times for which the matrix should be calculated.
- `object`: A smn.lmm or smsn.lmm object for which the variance should be extracted.
- `sigma2`: Common variance parameter, such that $\Sigma = \sigma^2 \cdot R$. Only evaluated if `object` is `NULL`.
- `depStruct`: Dependence structure. "CI" for conditional independence, "ARp" for AR(p) – p is `length(phi)`–, "CS" for compound symmetry, "DEC" for DEC, and "CAR1" for continuous-time AR(1). Only evaluated if `object` is `NULL`.
- `phi`: Parameter vector indexing the dependence structure. Only evaluated if `object` is `NULL`.

**Value**

Matrix of dimension `length(times)`.

**Author(s)**

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

**References**


**See Also**

`smsn.lmm`, `smn.lmm`
Examples

```r
fm1 <- smn.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**

```r
## 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

**References**


**See Also**

`smn.lmm`, `predict.SMN`
Examples

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

---

**fitted.SMSN**

*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**

```r
## 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

**References**


**See Also**

`smsn.lmm, predict.SMSN`

**Examples**

```r
fm1 <- smsn.lmm(distance ~ age + Sex, data = nlme::Orthodont, groupVar="Subject", tol = .0001)
fitted(fm1)
```
healy.plot

Healy-type plot from a smn.lmm or smsg.lmm object

Description

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

Usage

healy.plot(object, dataPlus=NULL, dotsize=0.4, ...)

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.

...

Additional arguments.

Details

It constructs a Healy-type plot (Healy, 1968) by plotting the nominal probability values 1/n, 2/n, ..., 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.

Value

A ggplot object.

Author(s)

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

References


See Also

ggplot, smn.lmm, smsg.lmm, mahalDist, acfresid
Examples

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

---

**lr.test**

*Likelihood-ratio test for SMSN/SMN objects*

### Description

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

### Usage

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

### Arguments

- `obj1, obj2` smn.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.
- `quiet` A logical value indicating if the result message should be suppressed. Default is FALSE.

### 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


### See Also

`smn.lmm`, `smn.lmm`

### Examples

```r
fm1 <- smn.lmm(nlme::Orthodont, formFixed=distance ~ age+Sex, groupVar="Subject")
fm2 <- smn.lmm(nlme::Orthodont, formFixed=distance ~ age+Sex, groupVar="Subject", tol=.0001)
lr.test(fm1,fm2)
```
mahalDist  

Mahalanobis distance from a smm.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

- `object`: An object inheriting from class SMN or SMSN, representing a fitted scale mixture of (skew) normal linear mixed model.
- `decomposed`: Logical. If TRUE, the Mahalanobis distance is decomposed in an error term and a random effect term. Default is FALSE.
- `dataPlus`: 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


See Also

smm.lmm, smsn.lmm, plot.mahalDist

Examples

```r
fm1 <- smm.lmm(distance ~ age + Sex, data = nlme::Orthodont, groupVar="Subject")
mahalDist(fm1)
plot(mahalDist(fm1),fm1)
```
plot  

*Plot a smn.lmm or smsn.lmm object*

---

**Description**

Fitted values versus residuals plot.

**Usage**

```r
## S3 method for class 'SMN'
plot(x,type="response",level="conditional",alpha=.3,...)

## S3 method for class 'SMSN'
plot(x,type="response",level="conditional",alpha=.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".
- **alpha**: Transparency parameter to be used (0<alpha<1).
- **...**: Additional arguments.

**Value**

A ggplot object.

**Author(s)**

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

**References**


**See Also**

ggplot, smn.lmm, smsn.lmm, fitted.SMN, fitted.SMSN, residuals.SMN, residuals.SMSN
Examples

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

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

plot.acfresid

Plot ACF for smn.lmm or smsn.lmm residuals

Description

Plot method for objects of class "acfresid".

Usage

```r
## 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

References


See Also

`ggplot, acfresid, smn.lmm, smsn.lmm, residuals.SMN, residuals.SMSN`
Examples

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

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

---

**plot.mahalDist**  
*Plot Mahalanobis distance for a fitted smn.lmm or smsn.lmm*

---

**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**

```r
## S3 method for class 'mahalDist'
plot(x, fitobject, type, level=.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`  
  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
predict.SMN

References


See Also

ggplot, mahalDist, smn.lmm, smsn.lmm

Examples

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

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

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 (2020).

Usage

```r
## 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 covariates, groupVar and possibly timeVar.
- **...**: 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


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.SMSN

Prediction of future observations from an smn.lmm object

Description

Predicted values are obtained through conditional expectation. For details, see Schumacher, Lachos, and Matos (2020).

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 covariates, groupVar and possibly timeVar.

... 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


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

References

print.SMSN

See Also

smn.lmm, summary.SMN

Examples

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

print.SMSN  Print a smsn.lmm object

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

References


See Also

smn.lmm, summary.SMN

Examples

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

Extract random effects from smsn.lmm and smn.lmm objects

Description

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

Usage

ranef(object)

Arguments

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

Value

Matrix of estimated random effects.

Author(s)

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

References


See Also

smsn.lmm, smn.lmm, fitted.SMSN, fitted.SMN

Examples

fm1 <- smsn.lmm(distance ~ age + Sex, data = nlme::Orthodont, groupVar="Subject", tol = .0001)
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
References

See Also
smn.lmm, smsn.lmm, acfresid, mahalDist, healy.plot

Examples
```r
fm1 <- smn.lmm(distance ~ age + Sex, data = nlme::Orthodont, groupVar="Subject")
residuals(fm1)
plot(fm1)
```

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
```r
rsmsn.lmm(time1, x1, z1, sigma2, D1, beta, lambda, depStruct = "CI",
          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 $\Sigma = \sigma^2 \cdot R$.
- `D1`: Variance matrix for random effects.
- `beta`: Vector of fixed effects parameter.
- `lambda`: Skewness parameter of random effects.
- `depStruct`: Dependence structure. "CI" for condcional independence, "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


See Also

smsn.lmm

Examples

# generating a sample for 1 individual at 5 times
nj1<-5
rsmsn.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=20 individuals at 5 times
library(dplyr)
library(purrr)
library(ggplot2)
nj1<-5
m<-50
gendatList<- map(rep(nj1,m), function(nj) rsmsn.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.y = mean, col="blue",size=2)
#
fm1 <- smsn.lmm(y ~ x, data = gendat, groupVar="ind", depStruct="ARp", pAR=1)
summary(fm1)
smn.lmm

Usage

```
smn.lmm(data, formFixed, groupVar, formRandom = ~1, depStruct = "CI",
timeVar = NULL, distr = "norm", pAR = 1, luDEC = 10,
tol = 1e-06, max.iter = 200, calc.se = TRUE, lb = NULL,
lu = NULL, initialValues = list(beta = NULL, sigma2 = NULL,
    D = NULL, phi = NULL, nu = NULL), quiet = FALSE, showCriterium=FALSE)
```

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. "CI" for conditional independence, "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="CI" or depStruct="CS". For other structures, if is.null(timeVar) the observations are considered equally spaced and ordered. If depStruct="ARp", timeVar must the 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.

pAR
If depStruct="ARp", pAR indicates the order of the autoregressive process that should be used. Otherwise, it is meaningless.

luDEC
Optional. Upper limit for estimating the "damping" parameter for DEC covariance. If luDEC<=1, only attenuation of the exponential decay can be obtained.

tol
Tolerance for the convergence criterion. Default=1e-6.

max.iter
Maximum number of iterations for the EM algorithm. Default=200.

calc.se
A logical value indicating if standard errors should be calculated.

lb
Optional. Bottom limit for estimating nu.

lu
Optional. Upper limit for estimating nu.

initialValues
Optional. A named list containing initial parameter values, with at most the following elements: beta, sigma2, D, phi, nu.

quiet
A logical value indicating if the iteration message should be suppressed. Useful when calling the function in R Markdown.

showCriterium
A logical value indicating if the criterium should be shown at each iteration.
Details

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

For details see Schumacher, Matos & Lachos (2020+).

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.
- **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 `smn.lmm` call that produced the object.
- **criteria**: A list with AIC and BIC criterion.
- **data**: The data frame used on `smn.lmm` call.
- **formula**: A list containing the formulas used on `smn.lmm` call.
- **depStruct**: A character indicating which depedence structure was used.
- **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, if `calc.bi=TRUE`.

Author(s)

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

References


smsg.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. It provides estimates and standard errors of parameters.

Usage

smsg.lmm(data, formFixed, groupVar, formRandom = ~1, depStruct = "CI",
         timeVar = NULL, distr = "sn", pAR = 1, luDEC = 10,
         tol = 1e-06, max.iter = 200, calc.se = TRUE, lb = NULL,
         lu = NULL, initialValues = list(beta = NULL, sigma2 = NULL,
         D = NULL, lambda = NULL, phi = NULL, nu = NULL), quiet = FALSE,
         showCriterium=FALSE)

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. "CI" for conditional independence, "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="CI" or depStruct="CS". For other structures, if is.null(timeVar) the observations are considered equally spaced and ordered. If depStruct="ARp", timeVar must the 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.

pAR  If depStruct="ARp", pAR indicates the order of the autoregressive process that should be used. Otherwise, it is meaningless.

l uDEC  Optional. Upper limit for estimating the "damping" parameter for DEC covariance. If luDEC<=1, only attenuation of the exponential decay can be obtained.

tol  Tolerance for the convergence criterion. Default=1e-6.

max.iter  Maximum number of iterations for the EM algorithm. Default=200.

calc.se  A logical value indicating if standard errors should be calculated.

lb  Optional. Bottom limit for estimating nu.

lu  Optional. Upper limit for estimating nu.

initialValues  Optional. A named list containing initial parameter values, with at most the following elements: beta, sigma2, D, lambda, phi, nu.

quiet  A logical value indicating if the iteration message should be suppressed. Useful when calling the function in R Markdown.

showCriterium  A logical value indicating if the criterium should be shown at each iteration.

Details

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

For details see Schumacher, Matos & Lachos (2020+).

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.

**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 `smsn.lmm` call that produced the object.

**criteria**  
A list with AIC and BIC criterion.

**data**  
The data frame used on `smsn.lmm` call.

**formula**  
A list containing the formulas used on `smsn.lmm` call.

**depStruct**  
A character indicating which dependence structure was used.

**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, if `calc.bi=TRUE`.

**Author(s)**

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

**References**


**See Also**

`print.SMSN`, `summary.SMSN`, `predict.SMSN`, `residuals.SMSN`, `plot.SMSN`, `smn.lmm`

**Examples**

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

#fitting for several distributions / dependence structures
fml1 <- smsn.lmm(dat1,formFixed=distance ~ age+Sex,groupVar="Subject")
```
\begin{verbatim}
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)
rbind(fm1$criteria,fm2$criteria,fm3$criteria,fm4$criteria)
summary(fm3)

#some diagnostic tools
plot(fm1)
acf1<- acfresid(fm1,calcCI=TRUE,MCiter=100)
plot(acf1)
plot(mahalDist(fm1),fm1,nlabels=2)
healy.plot(fm1)
\end{verbatim}

\section*{summary.SMN \quad \textit{Summary of a smn.lmm object}}

\subsection*{Description}
summary method for class "SMN".

\subsection*{Usage}
\begin{verbatim}
## S3 method for class 'SMN'
summary(object, confint.level = 0.95, ...)
\end{verbatim}

\subsection*{Arguments}
\begin{description}
\item[object] an object inheriting from class SMN, representing a fitted scale mixture normal linear mixed model.
\item[confint.level] Level of the approximate confidence intervals presented. Default=0.95.
\end{description}

\subsection*{Value}
\begin{description}
\item[varRandom] estimated variance matrix from random effects ($D$).
\item[varFixed] parameter estimates of variance from random errors ($\Sigma$). For recovering the error variance matrix use errorVar function.
\item[tableFixed] estimated fixed effects, their standard errors and approximated confidence intervals.
\item[criteria] Log-likelihood value from MLE, AIC and BIC criteria.
\end{description}

\subsection*{Author(s)}
Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos
References


See Also

smn.lmm, errorVar, plot.SMN, residuals.SMN

Examples

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

summary.SMSN

Summary of a smn.lmm object

Description

summary method for class "SMSN".

Usage

```r
## 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. Default=0.95.
- `...`: Additional arguments.

Value

- `varRandom`: estimated variance matrix from random effects ($D$).
- `varFixed`: parameter estimates of variance from random errors ($\Sigma$). For recovering the error variance matrix use `errorVar` function.
- `tableFixed`: estimated fixed effects, their standard errors and approximated confidence intervals.
- `criteria`: Log-likelihood value from MLE, AIC and BIC criteria.
Author(s)
Fernanda L. Schumacher, Larissa A. Matos and Victor H. Lachos

References

See Also
smsn.lmm, errorVar, plot.SMSN, residuals.SMSN

Examples
fm1 <- smsn.lmm(distance ~ age + Sex, data = nlme::Orthodont, groupVar="Subject", tol=.0001)
summary(fm1)
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