

# Package ‘skewlmm’

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**Type** Package

**Title** Scale Mixture of Skew-Normal Linear Mixed Models

**Version** 0.2.3

**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, Lachos and Matos (2021) <doi:10.1002/sim.8870>.

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**BugReports** <https://github.com/fernandalschumacher/skewlmm/issues>

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**NeedsCompilation** no

**Author** Fernanda L. Schumacher [aut, cre]  
(<<https://orcid.org/0000-0002-5724-8918>>),  
Larissa A. Matos [aut] (<<https://orcid.org/0000-0002-2635-0901>>),  
Victor H. Lachos [aut] (<<https://orcid.org/0000-0002-7239-2459>>)

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

```
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 <a href="#">residuals.SMN</a> .
resType	"response", "normalized" (default), or "modified". An optional character string specifying which type of residual should be used. For details see <a href="#">residuals.SMN</a> .

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.
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

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*. doi: [10.1002/sim.8870](https://doi.org/10.1002/sim.8870).

### 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)

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

---

errorVar                      *Error scale matrix associated with times*

---

### 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*. doi: [10.1002/sim.8870](https://doi.org/10.1002/sim.8870).

### 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.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", tol = .0001)  
fitted(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, ...)
```

**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 Healy'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  $1/n, 2/n, \dots, n/n$  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.

**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*. doi: [10.1002/sim.8870](https://doi.org/10.1002/sim.8870).

**See Also**

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

**Examples**

```
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**

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

**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.
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**

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*. doi: [10.1002/sim.8870](https://doi.org/10.1002/sim.8870).

**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",tol=.0001)
lr.test(fm1, fm2)
```



---

mahalDist	<i>Mahalanobis distance from a smn.lmm or smsn.lmm object</i>
-----------	---

---

**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**

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*. doi: [10.1002/sim.8870](https://doi.org/10.1002/sim.8870).

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), fm1)
```

---

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

---

### Description

Fitted values versus residuals plot.

### Usage

```
## 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 <a href="#">residuals.SMN</a> . Default is "response", indicating raw residuals.
level	Level of residual that should be used. For details see <a href="#">residuals.SMN</a> . 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

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

---

plot.acfresid	<i>Plot ACF for smn.lmm or smsn.lmm residuals</i>
---------------	---

---

**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                      *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

```
## 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 <a href="#">mahalDist</a> .
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), 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**

```
## 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

**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 smsn.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**

<code>object</code>	an object inheriting from class <code>SMSN</code> , representing a fitted scale mixture skew-normal linear mixed model.
<code>newData</code>	a data frame for which response variable should be predicted, including covariates, <code>groupVar</code> and possibly <code>timeVar</code> .
<code>...</code>	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

**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.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

**See Also**

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

**Examples**

```
fm1 <- smsn.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**

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*. doi: [10.1002/sim.8870](https://doi.org/10.1002/sim.8870).



**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

**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)
```

---

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**

```
rsmsn.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 $\Sigma = \text{sigma2} * R$ .
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*. doi: [10.1002/sim.8870](https://doi.org/10.1002/sim.8870).

**See Also**

[smsn.lmm](#)

**Examples**

```
#generating a sample for 1 individual at 5 times
nj1<-5
rsmnsn.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) rsmnsn.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)
```

**Description**

It fits a scale mixture of normal linear mixed model with possible within-subject dependence structure, using an EM-type algorithm. It provides estimates and standard errors of parameters.

**Usage**

```
smn.lmm(data, formFixed, groupVar, formRandom = ~1, depStruct = "UNC",
         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, showCriterion=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. "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.
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.
showCriterion	A logical value indicating if the criterion should be shown at each iteration.

### 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 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.
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 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**

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*. doi: [10.1002/sim.8870](https://doi.org/10.1002/sim.8870).

**See Also**

[print.SMN](#), [summary.SMN](#), [predict.SMN](#), [residuals.SMN](#), [plot.SMN](#), [smsn.lmm](#)

**Examples**

```
#simple example
dat1 <- as.data.frame(nlme::Orthodont)
fm1 <- smn.lmm(dat1,formFixed=distance ~ age,groupVar="Subject",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)
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)
```

**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**

```
smsgn.lmm(data, formFixed, groupVar, formRandom = ~1, depStruct = "UNC",
  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, showCriterion=FALSE)
```

**Arguments**

<code>data</code>	A data frame containing the variables named in <code>formFixed</code> , <code>formRandom</code> , <code>groupVar</code> , and <code>timeVar</code> .
<code>formFixed</code>	A two-sided linear formula object describing the fixed effects part of the model, with the response on the left of a <code>~</code> operator and the covariates, separated by <code>+</code> operators, on the right.
<code>groupVar</code>	A character containing the name of the variable which represents the subjects or groups in data.
<code>formRandom</code>	A one-sided linear formula object describing the random effects part of the model, with the covariates, separated by <code>+</code> operators, on the right of a <code>~</code> operator. By default, a model with random intercept is considered.
<code>depStruct</code>	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).
<code>timeVar</code>	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.
<code>distr</code>	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.
<code>pAR</code>	If <code>depStruct="ARp"</code> , <code>pAR</code> indicates the order of the autoregressive process that should be used. Otherwise, it is meaningless.
<code>luDEC</code>	Optional. Upper limit for estimating the "damping" parameter for DEC covariance. If <code>luDEC&lt;=1</code> , only attenuation of the exponential decay can be obtained.
<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>initialValues</code>	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.
showCriterion	A logical value indicating if the criterium should be shown at each iteration.

### 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 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.
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

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*. doi: [10.1002/sim.8870](https://doi.org/10.1002/sim.8870).

## See Also

[print.SMSN](#), [summary.SMSN](#), [predict.SMSN](#), [residuals.SMSN](#), [plot.SMSN](#), [smn.lmm](#)

## Examples

```
#simple example
dat1 <- as.data.frame(nlme::Orthodont)
fm1 <- smsn.lmm(dat1,formFixed=distance ~ age,groupVar="Subject",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)
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)
```

---

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. 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 <a href="#">errorVar</a> 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

**See Also**

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

**Examples**

```
fm1 <- smn.lmm(distance ~ age + Sex, data = nlme::Orthodont, groupVar="Subject")
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. 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 <a href="#">errorVar</a> 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

**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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