Package ‘skewlmm’

September 18, 2021

Type Package

Title Scale Mixture of Skew-Normal Linear Mixed Models

Version 1.0.0

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>.

License MIT + file LICENSE

Depends R (>= 4.0), optimParallel

Encoding UTF-8

Imports dplyr, ggplot2, moments, mvtnorm, nlme, numDeriv, purrr, ggrepel, furrr, future, haven

URL `https://github.com/fernandalschumacher/skewlmm`

BugReports `https://github.com/fernandalschumacher/skewlmm/issues`

RoxygenNote 7.1.1

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`>)

Repository CRAN

Date/Publication 2021-09-18 04:40:02 UTC

R topics documented:

acfresid 2
boot_ci 4
boot_par 5
criteria 6

errorVar 7
fitted.SMN 8
fitted.SMSN 9
healy.plot 10
lmmControl 11
lr.test 13
mahalDist 14
plot 15
plot.acfresid 16
plot.mahalDist 17
predict.SMN 18
predict.SMSN 19
print.SMN 20
print.SMSN 21
ranef 21
residuals 22
rsmsn.lmm 23
smn.lmm 25
smsn.lmm 28
summary.SMN 31
summary.SMSN 32
update 33

Index **34**

`acfresid` *Autocorrelation function for smn.lmm or smsn.lmm residuals*

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 `boot_par()` 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)
```

`criteria` *Extracts criteria for model comparison of SMSN/SMN objects*

Description

It extracts criteria for model comparison of sereval SMSN-LMM and/or SMN-LMM.

Usage

```
criteria(lobjects)
```

Arguments

`lobjects`	A list containg the smsn.lmm or smn.lmm 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`

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")
criteria(list(fm_norm = fm_norm,fm_t = fm_t,fm_sn = fm_sn))
```

`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

`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 $\Sigma = sigma2 * R$. Only evaluated if object `is.null(object)`.
`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). Only evaluated if object `is.null(object)`.
`phi`	Parameter vector indexing the dependence structure. Only evaluated if object `is.null(object)`.

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.SMSN` *Extract smsn.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 '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)
```

`healy.plot` *Healy-type plot from a smn.lmm or smsn.lmm object*

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 $1/n, 2/n, ..., n/n$ 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` *Control options for* `smsn.lmm()` *and* `smn.lmm()`

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()` and `smn.lmm()` 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 = FALSE, showCriterium = FALSE, algorithm = "DAAREM",
           parallelphi = NULL, parallelnu = NULL, ncores = NULL,
           control.daarem = list())
```

Arguments

`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.

`luDEC`	Optional. Upper limit for estimating the "damping" parameter for DEC covariance. If `luDEC<=1`, only attenuation of the exponential decay can be obtained.
`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.
`algorithm`	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).
`parallelphi`	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 `depStruct = "UNC"`.
`parallelnu`	A logical value indicating if parallel optimization should be used in the numerical update of nu. Meaningless if `distr="norm"` or `distr="sn"`.
`ncores`	Number of cores to be used for the parallel optimization. Meaningless if `parallelphi = FALSE` and `parallelnu = FALSE`.
`control.daarem`	List of control for the daarem algorithm. See `help(daarem,package = "daarem")` for details. Meaningless if `algorithm = "EM"`

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`, `update`

Examples

```
lmmControl(algorithm = "EM")

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

`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)
```

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

`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 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)
```

`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",
     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` *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 = 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")
```

`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 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 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.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 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 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.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 40(7), 1790-1810.

See Also

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

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)
```

`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 $\Sigma = sigma2 * R$.
`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 40(7), 1790-1810.

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 with 5 times
library(dplyr)
```

```
library(purrr)
library(ggplot2)
nj1 <- 5
m <- 25
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 = mean, col = "blue", size = 2)
#
fm1 <- smsn.lmm(y ~ x, data = gendat, groupVar = "ind", depStruct = "ARp",
                pAR = 1)
summary(fm1)
```

`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 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.
`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 `lmmControl()`, containing additional options for the estimation algorithm.

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 ϵ_i $SMN(0, \Sigma_i; H)$, 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 `smn.lmm` call that produced the object.
`criteria`	A list with AIC and BIC criterion.

`data`	The data frame used on `smn.lmm` call.
`forumla`	A list containing the formulas used on `smn.lmm` 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`

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 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.
`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 `lmmControl()`, containing additional options for the estimation algorithm.

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 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 `smsn.lmm` call that produced the object.
`criteria`	A list with AIC and BIC criterion.

`data`	The data frame used on `smsn.lmm` call.
`forumla`	A list containing the formulas used on `smsn.lmm` 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`

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.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 objects*

Description

It fits a SM(S)N-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)
```

Arguments

`object`	A smsn.lmm or smn.lmm 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()` or `smn.lmm()` function.

Author(s)

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

See Also

`smsn.lmm`, `smn.lmm`

Examples

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

Index

∗ **datagen**
    `rsmsn.lmm`, 23
∗ **hplot**
    `plot`, 15
    `plot.acfresid`, 16
    `plot.mahalDist`, 17
∗ **htest**
    `boot_ci`, 4
    `boot_par`, 5
    `lr.test`, 13
∗ **models**
    `acfresid`, 2
    `criteria`, 6
    `errorVar`, 7
    `fitted.SMN`, 8
    `fitted.SMSN`, 9
    `healy.plot`, 10
    `lmmControl`, 11
    `mahalDist`, 14
    `predict.SMN`, 18
    `predict.SMSN`, 19
    `print.SMN`, 20
    `print.SMSN`, 21
    `ranef`, 21
    `residuals`, 22
    `smn.lmm`, 25
    `smsn.lmm`, 28
    `summary.SMN`, 31
    `summary.SMSN`, 32
    `update`, 33
∗ **robust**
    `smn.lmm`, 25
    `smsn.lmm`, 28
    `summary.SMSN`, 32
    `update`, 33

`acfresid`, 2, *11*, *16*, *23*

`boot_ci`, 4, *5*
`boot_par`, *4*, 5, *31, 32*

`criteria`, 6

`errorVar`, 7, *31, 32*

`fitted.SMN`, 8, *15*, *18*, *22*
`fitted.SMSN`, 9, *15*, *19*, *22*

`ggplot`, *11*, *15–17*

`healy.plot`, 10, *23*

`lmmControl`, 11, *26, 27*, *29, 30*
`lr.test`, 13

`mahalDist`, *11*, 14, *17*, *23*

`plot`, 15
`plot.acfresid`, *3*, 16
`plot.mahalDist`, *14*, 17
`plot.SMN`, *27*, *31*
`plot.SMSN`, *30*, *32*
`predict.SMN`, *8*, 18, *27*
`predict.SMSN`, *9*, 19, *30*
`print.SMN`, 20
`print.SMSN`, 21

`ranef`, 21
`residuals`, 22
`residuals.SMN`, *2, 3*, *15, 16*, *27*, *31*
`residuals.SMSN`, *15, 16*, *30*, *32*
`rsmsn.lmm`, 23

`smn.lmm`, *3–8*, *11–18*, *20*, *22, 23*, 25, *30, 31*, *33*
`smsn.lmm`, *3–7*, *9*, *11–17*, *19*, *21–24*, *27*, 28, *32, 33*
`summary.SMN`, *20*, 31
`summary.SMSN`, *21*, 32

`update`, *12*, *27*, *30*, 33