Package ‘lme4’

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Title Linear Mixed-Effects Models using ‘Eigen’ and S4
Contact LME4 Authors <lme4-authors@lists.r-forge.r-project.org>
Description Fit linear and generalized linear mixed-effects models.
   The models and their components are represented using S4 classes and
   methods. The core computational algorithms are implemented using the
   ‘Eigen’ C++ library for numerical linear algebra and ‘RcppEigen’ glue.
Depends R (>= 3.0.2), Matrix (>= 1.1.1), methods, stats
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Description

lme4 provides functions for fitting and analyzing mixed models: linear (\texttt{lmer})
generalized linear (\texttt{glmer}) and nonlinear (\texttt{nlmer}).
Differences between nlme and lme4

**lme4** covers approximately the same ground as the earlier **nlme** package. The most important differences are:

- **lme4** uses modern, efficient linear algebra methods as implemented in the Eigen package, and uses reference classes to avoid undue copying of large objects; it is therefore likely to be faster and more memory-efficient than **nlme**.
- **lme4** includes generalized linear mixed model (GLMM) capabilities, via the **glmer** function.
- **lme4** does not currently implement **nlme**’s features for modeling heteroscedasticity and correlation of residuals.
- **lme4** does not currently offer the same flexibility as **nlme** for composing complex variance-covariance structures, but it does implement crossed random effects in a way that is both easier for the user and much faster.
- **lme4** offers built-in facilities for likelihood profiling and parametric bootstrapping.
- **lme4** is designed to be more modular than **nlme**, making it easier for downstream package developers and end-users to re-use its components for extensions of the basic mixed model framework. It also allows more flexibility for specifying different functions for optimizing over the random-effects variance-covariance parameters.
- **lme4** is not (yet) as well-documented as **nlme**.

Differences between current (1.0.+) and previous versions of lme4

- [gn]lmer now produces objects of class **merMod** rather than class **mer** as before
- the new version uses a combination of S3 and reference classes (see ReferenceClasses, merPredD-class, and lmResp-class) as well as S4 classes; partly for this reason it is more interoperable with **nlme**
- The internal structure of [gn]lmer is now more modular, allowing finer control of the different steps of argument checking; construction of design matrices and data structures; parameter estimation; and construction of the final merMod object (see modular)
- profiling and parametric bootstrapping are new in the current version
- the new version of **lme4** does not provide an mcmcsamp (post-hoc MCMC sampling) method, because this was deemed to be unreliable. Alternatives for computing p-values include parametric bootstrapping (bootMer) or methods implemented in the pbkrtest package and leveraged by the lmerTest package and the Anova function in the car package (see pvalues for more details).

Caveats and trouble-shooting

- Some users who have previously installed versions of the RcppEigen and minqa packages may encounter segmentation faults (!!!); the solution is to make sure to re-install these packages before installing **lme4**. (Because the problem is not with the explicit version of the packages, but with running packages that were built with different versions of **Rcpp** in conjunction with each other, simply making sure you have the latest version, or using update.packages, will not necessarily solve the problem; you must actually re-install the packages. The problem is most likely with **minqa**.)
Arabidopsis clipping/fertilization data

Description
Data on genetic variation in responses to fertilization and simulated herbivory in *Arabidopsis*

Usage
data("Arabidopsis")

Format
A data frame with 625 observations on the following 8 variables.

- **reg**: region: a factor with 3 levels NL (Netherlands), SP (Spain), SW (Sweden)
- **popu**: population: a factor with the form n.R representing a population in region R
- **gen**: genotype: a factor with 24 (numeric-valued) levels
- **rack**: a nuisance factor with 2 levels, one for each of two greenhouse racks
- **nutrient**: fertilization treatment/nutrient level (1, minimal nutrients or 8, added nutrients)
- **amd**: simulated herbivory or "clipping" (apical meristem damage): unclipped (baseline) or clipped
- **status**: a nuisance factor for germination method (Normal, Petri.Plate, or Transplant)
- **totalNfruits**: total fruit set per plant (integer)

Source
From Josh Banta

References

Examples
data(Arabidopsis)
summary(Arabidopsis[,"total.fruits"])
table(gsub("\d-9\d\s","",levels(Arabidopsis[,"popu"])))
library(lattice)
stripplot(log(total.fruits+1) ~ amd|nutrient, data = Arabidopsis,
    groups = gen,
    strip=strip.custom(strip.names=c(TRUE,TRUE)),
    type=c('p','a'), ## points and panel-average value --
    ## see ?panel.xyplot
    scales=list(x=list(rot=90)),
    main="Panel: nutrient, Color: genotype")
Model-based (Semi-)Parametric Bootstrap for Mixed Models

Description

Perform model-based (Semi-)parametric bootstrap for mixed models.

Usage

```r
bootMer(x, FUN, nsim = 1, seed = NULL, use.u = FALSE, re.form=NA,
type = c("parametric", "semiparametric"),
verbose = FALSE, .progress = "none", PBargs = list(),
parallel = c("no", "multicore", "snow"),
ncpus = getOption("boot.ncpus", 1L), cl = NULL)
```

Arguments

- `x` a fitted `merMod` object: see `lmer`, `glmer`, etc.
- `FUN` a function taking a fitted `merMod` object as input and returning the statistic of interest, which must be a (possibly named) numeric vector.
- `nsim` number of simulations, positive integer; the bootstrap $B$ (or $R$).
- `seed` optional argument to `set.seed`.
- `use.u` logical, indicating whether the spherical random effects should be simulated / bootstrapped as well. If TRUE, they are not changed, and all inference is conditional on these values. If FALSE, new normal deviates are drawn (see Details).
- `re.form` formula, NA (equivalent to `use.u=FALSE`), or NULL (equivalent to `use.u=TRUE`): alternative to `use.u` for specifying which random effects to incorporate. See `simulate.merMod` for details.
- `type` character string specifying the type of bootstrap, "parametric" or "semiparametric"; partial matching is allowed.
- `verbose` logical indicating if progress should print output
- `.progress` character string - type of progress bar to display. Default is "none"; the function will look for a relevant `*ProgressBar` function, so "txt" will work in general; "tk" is available if the `tcltk` package is loaded; or "win" on Windows systems. Progress bars are disabled (with a message) for parallel operation.
- `PBargs` a list of additional arguments to the progress bar function (the package authors like `list(style=3)`).
- `parallel` The type of parallel operation to be used (if any). If missing, the default is taken from the option "boot.parallel" (and if that is not set, "no").
- `ncpus` integer: number of processes to be used in parallel operation: typically one would choose this to be the number of available CPUs.
- `cl` An optional `parallel` or `snow` cluster for use if `parallel = "snow"`. If not supplied, a cluster on the local machine is created for the duration of the boot call.
Details

The semi-parametric variant is only partially implemented, and we only provide a method for `lmer` and `glmer` results.

The working name for `bootMer()` was “simulestimate()”, as it is an extension of `simulate` (see `simulate.merMod`), but we want to emphasize its potential for valid inference.

- If `use.u` is FALSE and type is "parametric", each simulation generates new values of both the “spherical” random effects $u$ and the i.i.d. errors $\epsilon$, using `rnorm()` with parameters corresponding to the fitted model $x$.
- If `use.u` is TRUE and type=="parametric", only the i.i.d. errors (or, for GLMMs, response values drawn from the appropriate distributions) are resampled, with the values of $u$ staying fixed at their estimated values.
- If `use.u` is TRUE and type=="semiparametric", the i.i.d. errors are sampled from the distribution of (response) residuals. (For GLMMs, the resulting sample will no longer have the same properties as the original sample, and the method may not make sense; a warning is generated.) The semiparametric bootstrap is currently an experimental feature, and therefore may not be stable.
- The case where `use.u` is FALSE and type=="semiparametric" is not implemented; Morris (2002) suggests that resampling from the estimated values of $u$ is not good practice.

Value

an object of S3 class "boot", compatible with `boot` package’s `boot()` result.

References


See Also

- `confint.merMod`, for a more specific approach to bootstrap confidence intervals on parameters.
- `refit()`, or `PBmodcomp()` from the `pbkrtest` package, for parametric bootstrap comparison of models.
- `boot()`, and then `boot.ci`, from the `boot` package.
- `profile-methods`, for likelihood-based inference, including confidence intervals.
- `pvalues`, for more general approaches to inference and p-value computation in mixed models.

Examples

```r
fm91ML <- lmer(Yield ~ 1|Batch, Dyestuff, REML = FALSE)
## see ?profile-methods
mySumm <- function(.) { s <- sigma(.)
c(beta =getME(., "beta"), sigma = s, sig01 = unname(s * getME(., "theta"))) }
```
(t0 <- mySumm(fm01ML)) # just three parameters
## alternatively:
mySumm2 <- function(.) {
  c(beta=fixef(.), sigma=sigma(.), sig01=sqrt(unlist(VarCorr(.))))
}

set.seed(100)
## 3.8s (on a 5600 MIPS 64bit fast(year 2009) desktop "AMD Phenom(tm) II X4 925"):
system.time( boo1 <- bootMer(fm01ML, mySumm, nsim = 1000) )

## to "look" at it
require("boot") ## a recommended package, i.e. *must* be there
boo1
## note large estimated bias for sig01
## (~30% low, decreases _slightly_ for nsim = 1000)

## extract the bootstrapped values as a data frame ...
head(as.data.frame(boo1))

## ------ Bootstrap-based confidence intervals **************

## warnings about "Some ... intervals may be unstable" go away
## for larger bootstrap samples, e.g. nsim=500

## intercept
(bCI.1 <- boot.ci(boo1, index=1, type=c("norm", "basic", "perc"))) # beta

## Residual standard deviation - original scale:
(bCI.2 <- boot.ci(boo1, index=2, type=c("norm", "basic", "perc")))
## Residual SD - transform to log scale:
(bCI.2L <- boot.ci(boo1, index=2, type=c("norm", "basic", "perc"),
  h = log, hdot = function(.) 1/., hinv = exp))

## Among-batch variance:
(bCI.3 <- boot.ci(boo1, index=3, type=c("norm", "basic", "perc"))) # sig01

## Extract all CIs (somewhat awkward)
bCI.tab <- function(b, ind=length(b$t0), type="perc", conf=0.95) {
  btab0 <- t(sapply(as.list(seq(ind)), function(i)
    boot.ci(b, index=i, conf=conf, type=type)$percent))
  btab <- btab0[,4:5]
  rownames(btab) <- names(b$t0)
  a <- (1 - conf)/2
  a <- c(a, 1 - a)
  pct <- stats:::format.perc(a, 3)
  colnames(btab) <- pct
  return(btab)
}

bCI.tab(boo1)

## Graphical examination:
plot(boo1,index=3)
## Description

Data on the breakage angle of chocolate cakes made with three different recipes and baked at six different temperatures. This is a split-plot design with the recipes being whole-units and the different temperatures being applied to sub-units (within replicates). The experimental notes suggest that the replicate numbering represents temporal ordering.

## Format

A data frame with 270 observations on the following 5 variables.

- **replicate**: a factor with levels 1 to 15
- **recipe**: a factor with levels A, B and C
- **temperature**: an ordered factor with levels 175 < 185 < 195 < 205 < 215 < 225
- **angle**: a numeric vector giving the angle at which the cake broke.
- **temp**: numeric value of the baking temperature (degrees F).

## Details

The `replicate` factor is nested within the `recipe` factor, and `temperature` is nested within `replicate`.

## Source

Original data were presented in Cook (1938), and reported in Cochran and Cox (1957, p. 300). Also cited in Lee, Nelder and Pawitan (2006).

## References


Examples

```r
str(cake)
## 'temp' is continuous, 'temperature' an ordered factor with 6 levels

(fm1 <- lmer(angle ~ recipe * temperature + (1|recipe:replicate), cake, REML = FALSE))
(fm2 <- lmer(angle ~ recipe + temperature + (1|recipe:replicate), cake, REML = FALSE))
(fm3 <- lmer(angle ~ recipe + temp + (1|recipe:replicate), cake, REML = FALSE))
## and now "choose":
anova(fm3, fm2, fm1)
```

---

**cbpp**

*Contagious bovine pleuropneumonia*

---

**Description**

Contagious bovine pleuropneumonia (CBPP) is a major disease of cattle in Africa, caused by a mycoplasma. This dataset describes the serological incidence of CBPP in zebu cattle during a follow-up survey implemented in 15 commercial herds located in the Boji district of Ethiopia. The goal of the survey was to study the within-herd spread of CBPP in newly infected herds. Blood samples were quarterly collected from all animals of these herds to determine their CBPP status. These data were used to compute the serological incidence of CBPP (new cases occurring during a given time period). Some data are missing (lost to follow-up).

**Format**

A data frame with 56 observations on the following 4 variables.

- **herd** A factor identifying the herd (1 to 15).
- **incidence** The number of new serological cases for a given herd and time period.
- **size** A numeric vector describing herd size at the beginning of a given time period.
- **period** A factor with levels Q to T.

**Details**

Serological status was determined using a competitive enzyme-linked immuno-sorbent assay (cELISA).

**Source**

Examples

## response as a matrix
(m1 <- glmer(cbind(incidence, size - incidence) ~ period + (1 | herd),
 family = binomial, data = cbpp))

## response as a vector of probabilities and usage of argument "weights"
m1p <- glmer(incidence / size ~ period + (1 | herd), weights = size,
 family = binomial, data = cbpp)

## Confirm that these are equivalent:
stopifnot(all.equal(fixef(m1), fixef(m1p), tolerance = 1e-5),
 all.equal(ranef(m1), ranef(m1p), tolerance = 1e-5))

## GLMM with individual-level variability (accounting for overdispersion)

```r
cbpp$obs <- 1:nrow(cbpp)
(m2 <- glmer(cbind(incidence, size - incidence) ~ period + (1 | herd) + (1|obs),
 family = binomial, data = cbpp))
```

confint.merMod

Compute Confidence Intervals for Parameters of a [ng]lmer Fit

Description

Compute confidence intervals on the parameters of a *lmer()* model fit (of class "merMod").

Usage

```r
## S3 method for class 'merMod'
confint(object, parm, level = 0.95,
 method = c("profile", "Wald", "boot"), zeta,
 nsim = 500,
 boot.type = c("perc","basic","norm"),
 FUN = NULL, quiet = FALSE,
 oldNames = TRUE, ...)
```

Arguments

- **object**: a fitted [ng]lmer model
- **parm**: parameters for which intervals are sought. Specified by an integer vector of positions, character vector of parameter names, or (unless doing parametric bootstrapping with a user-specified bootstrap function) "theta_" or "beta_" to specify variance-covariance or fixed effects parameters only: see the which parameter of profile.
- **level**: confidence level < 1, typically above 0.90.
- **method**: a character string determining the method for computing the confidence intervals.
- **zeta**: (for method = "profile" only:) likelihood cutoff (if not specified, as by default, computed from level).
\texttt{nsim} \hspace{1cm} \text{number of simulations for parametric bootstrap intervals.}

\texttt{FUN} \hspace{1cm} \text{bootstrap function; if NULL, an internal function that returns the fixed-effect parameters as well as the random-effect parameters on the standard deviation/correlation scale will be used. See \texttt{bootMer} for details.}

\texttt{boot.type} \hspace{1cm} \text{bootstrap confidence interval type, as described in \texttt{boot.ci}. (Methods ‘stud’ and ‘bca’ are unavailable because they require additional components to be calculated.)}

\texttt{quiet} \hspace{1cm} \text{(logical) suppress messages about computationally intensive profiling?}

\texttt{oldNames} \hspace{1cm} \text{(logical) use old-style names for variance-covariance parameters, e.g. \textquote{.sig01}, rather than newer (more informative) names such as \textquote{sd_(Intercept)|Subject”? (See signames argument to profile).}

\texttt{...} \hspace{1cm} \text{additional parameters to be passed to \texttt{profile.merMod} or \texttt{bootMer}, respectively.}

### Details

Depending on the method specified, \texttt{confint()} computes confidence intervals by

- \textquote{profile”: computing a likelihood profile and finding the appropriate cutoffs based on the likelihood ratio test;
- \textquote{Wald”: approximating the confidence intervals (of fixed-effect parameters only; all variance-covariance parameters CIs will be returned as \texttt{NA}) based on the estimated local curvature of the likelihood surface;
- \textquote{boot”: performing parametric bootstrapping with confidence intervals computed from the bootstrap distribution according to \texttt{boot.type} (see \texttt{bootMer, boot.ci}).

### Value

A numeric table (\texttt{matrix} with column and row names) of confidence intervals; the confidence intervals are computed on the standard deviation scale.

### Note

The default method \textquote{profile” amounts to

\begin{verbatim}
\texttt{confint(profile(object, which=parm), signames=oldNames, ...), level, zeta)}
\end{verbatim}

where the \texttt{profile} method \texttt{profile.merMod} does almost all the computations. Therefore it is typically advisable to store the \texttt{profile(.) result, say in \texttt{pp}, and then use \texttt{confint(pp, level=*) e.g., for different levels.}

### Examples

\begin{verbatim}
fm1 <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy)
fm1W <- confint(fm1, method="Wald")# very fast, but ....
fm1W
testLevel <- if (nzchar(s <- Sys.getenv("LME4_TEST_LEVEL"))) as.numeric(s) else 1
\end{verbatim}
Assessing Convergence for Fitted Models

Description

The `lme4` package uses general-purpose nonlinear optimizers (e.g., Nelder-Mead or Powell’s BOBYQA method) to estimate the variance-covariance matrices of the random effects. Assessing reliably whether such algorithms have converged is difficult. For example, evaluating the Karush-Kuhn-Tucker conditions (convergence criteria which in the simplest case of non-constrained optimization reduce to showing that the gradient is zero and the Hessian is positive definite) is challenging because of the difficulty of evaluating the gradient and Hessian.

We (the `lme4` authors and maintainers) are still in the process of finding the best strategies for testing convergence. Some of the relevant issues are

- the gradient and Hessian are the basic ingredients of KKT-style testing, but when they have to be estimated by finite differences (as in the case of `lme4`; direct computation of derivatives based on analytic expressions may eventually be available for some special classes, but we have not yet implemented them) they may not be sufficiently accurate for reliable convergence testing.
- The Hessian computation in particular represents a difficult tradeoff between computational expense and accuracy. At present the Hessian computations used for convergence checking (and for estimating standard errors of fixed-effect parameters for GLMMs) follow the `ordinal` package in using a naive but computationally cheap centered finite difference computation (with a fixed step size of $10^{-4}$). A more reliable but more expensive approach is to use Richardson extrapolation, as implemented in the `numDeriv` package.
- it is important to scale the estimated gradient at the estimate appropriately; two reasonable approaches are
  1. don’t scale random-effects (Cholesky) gradients, since these are essentially already unitless (for LMMs they are scaled relative to the residual variance; for GLMMs they are scaled relative to the sampling variance of the conditional distribution); for GLMMs, scale fixed-effect gradients by the standard deviations of the corresponding input variable, or
  2. scale gradients by the inverse Cholesky factor of the Hessian, equivalent to scaling by the estimated Wald standard error of the estimated parameters. The latter approach is
used in the current version of \texttt{lme4}; it has the disadvantage that it requires us to estimate the Hessian (although the Hessian is required for reliable estimation of the fixed-effect standard errors for GLMMs in any case).

- Exploratory analyses suggest that (1) the naive estimation of the Hessian may fail for large data sets (number of observations greater than approximately $10^5$); (2) the magnitude of the scaled gradient increases with sample size, so that warnings will occur even for apparently well-behaved fits with large data sets.

If you do see convergence warnings, and want to trouble-shoot/double-check the results, the following steps are recommended (examples are given below):

- double-check the model specification and the data for mistakes
- center and scale continuous predictor variables (e.g. with \texttt{scale})
- check for singularity: if any of the diagonal elements of the Cholesky factor are zero or very small, the convergence testing methods may be inappropriate (see examples)
- double-check the Hessian calculation with the more expensive Richardson extrapolation method (see examples)
- restart the fit from the apparent optimum, or from a point perturbed slightly away from the optimum
- try all available optimizers (e.g. several different implementations of BOBYQA and Nelder-Mead, L-BFGS-B from \texttt{optim}, \texttt{nlminb}, ...) While this will of course be slow for large fits, we consider it the gold standard; if all optimizers converge to values that are practically equivalent, then we would consider the convergence warnings to be false positives.

To quote Douglas Adams, we apologize for the inconvenience.

\textbf{See Also}

\texttt{lmerControl}

\textbf{Examples}

```r
fm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)

## 1. center and scale predictors:
ss.CS <- transform(sleepstudy, Days=scale(Days))
fm1.CS <- update(fm1, data=ss.CS)

## 2. check singularity
diag.vals <- getME(fm1, "theta")[getME(fm1, "lower") == 0]
any(diag.vals < 1e-6) # FALSE

## 3. recompute gradient and Hessian with Richardson extrapolation
devfun <- update(fm1, devFunOnly=TRUE)
if (isLMM(fm1)) {
  pars <- getME(fm1, "theta")
} else {
  ## GLMM: requires both random and fixed parameters
  pars <- getME(fm1, c("theta","fixef"))
}
```
if (require("numDeriv")) {
  cat("hess:\n"); print(hess <- hessian(devfun, unlist(pars)))
  cat("grad:\n"); print(grad <- grad(devfun, unlist(pars)))
  cat("scaled gradient:\n")
  print(scgrad <- solve(chol(hess), grad))
}

## compare with internal calculations:
fm@optinfo$derivs

## 4. restart the fit from the original value or
## a slightly perturbed value:
fm1.restart <- update(fm1, start=pars)

## 5. try all available optimizers

source(system.file("utils", "allFit.R", package="lme4"))
fm1.all <- allFit(fm1)
ss <- summary(fm1.all)
ss$fixef    ## extract fixed effects
ss$llik     ## log-likelihoods
ss$sdcor    ## SDs and correlations
ss$theta    ## Cholesky factors
ss$which.OK ## which fits worked

---

**devcomp**  
*Extract the deviance component list*

### Description

Return the deviance component list

### Usage

```r
devcomp(x)
```

### Arguments

- `x`  
a fitted model of class `merMod`

### Details

A fitted model of class `merMod` has a `devcomp` slot as described in the value section.

### Value

- a list with components
  - `dims` a named integer vector of various dimensions
  - `cmp` a named numeric vector of components of the deviance
Note
This function is deprecated, use `getME(.) , "devcomp"`.

---

**drop1.merMod**

*Drop all possible single fixed-effect terms from a mixed effect model*

---

**Description**

Drop allowable single terms from the model: see `drop1` for details of how the appropriate scope for dropping terms is determined.

**Usage**

```r
## S3 method for class 'merMod'
drop1(object, scope, scale = 0,
    test = c("none", "Chisq", "user"),
    k = 2, trace = FALSE, sumFun, ...)
```

**Arguments**

- `object` a fitted `merMod` object.
- `scope` a formula giving the terms to be considered for adding or dropping.
- `scale` Currently ignored (included for S3 method compatibility)
- `test` should the results include a test statistic relative to the original model? The $\chi^2$ test is a likelihood-ratio test, which is approximate due to finite-size effects.
- `k` the penalty constant in AIC
- `trace` print tracing information?
- `sumFun` a summary function to be used when `test="user"`. It must allow arguments `scale` and `k`, but these may be ignored (e.g. specified in dots). The first two arguments must be `object`, the full model fit, and `objectDrop`, a reduced model. If `objectDrop` is missing, `sumFun` should return a vector of with the appropriate length and names (the actual contents are ignored).
- `...` other arguments (ignored)

**Details**

`drop1` relies on being able to find the appropriate information within the environment of the formula of the original model. If the formula is created in an environment that does not contain the data, or other variables passed to the original model (for example, if a separate function is called to define the formula), then `drop1` will fail. A workaround (see example below) is to manually specify an appropriate environment for the formula.

**Value**

An object of class `anova` summarizing the differences in fit between the models.
Examples

```r
# likelihood ratio tests
drop1(fm1, test="ChiSq")

# use Kenward-Roger corrected F test, or parametric bootstrap, to test the significance of each dropped predictor
if (require(pbkrtest) && packageVersion("pbkrtest") >= "0.3.8") {
  KRSumFun <- function(object, objectDrop, ...) {
    knames <- c("ndf", "ddf", "F.stat", "p.value", "F.scaling")
    r <- if (missing(objectDrop)) {
      setNames(rep(NA, length(knames)), knames)
    } else {
      ktest <- KRemodcomp(object, objectDrop)
      unlist(ktest$stats[knames])
    }
    attr(r, "method") <- c("Kenward-Roger via pbkrtest package")
    r
  }
  drop1(fm1, test="user", sumFun=KRSumFun)
}

if(lme4:::testLevel() >= 3) { # takes about 16 sec
  PBSumFun <- function(object, objectDrop, ...) {
    pbnames <- c("stat", "p.value")
    r <- if (missing(objectDrop)) {
      setNames(rep(NA, length(pbnames)), pbnames)
    } else {
      pbtest <- Pbmmodcomp(object, objectDrop, nsim=nsim)
      unlist(pbtest@test[2, pbnames])
    }
    attr(r, "method") <- c("Parametric bootstrap via pbkrtest package")
    r
  }
  system.time(drop1(fm1, test="user", sumFun=PBSumFun))
}

# workaround for creating a formula in a separate environment
createFormula <- function(resp, fixed, rand) {
  f <- reformulate(c(fixed, rand), response=resp)
  # use the parent (createModel) environment, not the environment of this function (which does not contain 'data')
  environment(f) <- parent.frame()
  f
}
createModel <- function(data) {
  mf.final <- createFormula("Reaction", "Days", "(Days|Subject)")
  lmer(mf.final, data=data)
}
drop1(createModel(data=sleepstudy))
```
**dummy**  

*Dummy variables (experimental)*

**Description**

Largely a wrapper for `model.matrix` that accepts a factor, `f`, and returns a dummy matrix with `nlevels(f)-1` columns (the first column is dropped by default). Useful whenever one wishes to avoid the behaviour of `model.matrix` of always returning an `nlevels(f)`-column matrix, either by the addition of an intercept column, or by keeping one column for all levels.

**Usage**

```r
dummy(f, levelsToKeep)
```

**Arguments**

- `f`  
  An object coercible to `factor`.

- `levelsToKeep`  
  An optional character vector giving the subset of `levels(f)` to be converted to dummy variables.

**Value**

A `model.matrix` with dummy variables as columns.

**Examples**

```r
data(Orthodont, package="nlme")
lmer(distance ~ age + (age|Subject) + 
      (0+dummy(Sex, "Female")|Subject), data = Orthodont)
```

---

**Dyestuff**  

*Yield of dyestuff by batch*

**Description**

The **Dyestuff** data frame provides the yield of dyestuff (Naphthalene Black 12B) from 5 different preparations from each of 6 different batches of an intermediate product (H-acid). The **Dyestuff2** data were generated data in the same structure but with a large residual variance relative to the batch variance.

**Format**

Data frames, each with 30 observations on the following 2 variables.

- **Batch** a factor indicating the batch of the intermediate product from which the preparation was created.
- **Yield** the yield of dyestuff from the preparation (grams of standard color).
Details
The Dyestuff data are described in Davies and Goldsmith (1972) as coming from “an investigation to find out how much the variation from batch to batch in the quality of an intermediate product (H-acid) contributes to the variation in the yield of the dyestuff (Naphthalene Black 12B) made from it. In the experiment six samples of the intermediate, representing different batches of works manufacture, were obtained, and five preparations of the dyestuff were made in the laboratory from each sample. The equivalent yield of each preparation as grams of standard colour was determined by dye-trial.”

The Dyestuff2 data are described in Box and Tiao (1973) as illustrating “the case where between-batches mean square is less than the within-batches mean square. These data had to be constructed for although examples of this sort undoubtably occur in practice, they seem to be rarely published.”

Source
O.L. Davies and P.L. Goldsmith (eds), Statistical Methods in Research and Production, 4th ed., Oliver and Boyd, (1972), section 6.4
G.E.P. Box and G.C. Tiao, Bayesian Inference in Statistical Analysis, Addison-Wesley, (1973), section 5.1.2

Examples

```r
require(lattice)
str(Dyestuff)
dotplot(reorder(Batch, Yield) ~ Yield, Dyestuff,
  ylab = "Batch", jitter.y = TRUE, aspect = 0.3,
  type = c("p", "a"))
dotplot(reorder(Batch, Yield) ~ Yield, Dyestuff2,
  ylab = "Batch", jitter.y = TRUE, aspect = 0.3,
  type = c("p", "a"))
(fm1 <- lmer(Yield ~ 1|Batch, Dyestuff))
(fm2 <- lmer(Yield ~ 1|Batch, Dyestuff2))
```

---

**expandDoubleVerts**

*Expand terms with ‘||’ notation into separate ‘|’ terms*

**Description**
From the right hand side of a formula for a mixed-effects model, expand terms with the double vertical bar operator into separate, independent random effect terms.

**Usage**

```r
expandDoubleVerts(term)
```

**Arguments**

- **term** a mixed-model formula
Value

the modified term

Note

Because || works at the level of formula parsing, it has no way of knowing whether a variable is a factor. It just takes the terms within a random-effects term and literally splits them into the intercept and separate no-intercept terms, e.g. (1+\(x+y|f\)) would be split into (1|f) + (0+\(x|f\)) + (0+\(y|f\)). However, || will fail to break up factors into separate terms; the dummy function can be useful in this case, although it is not as convenient as ||.

See Also

formula, model.frame, model.matrix, dummy.

Other utilities: mkRespMod, mkReTrms, nlformula, nobars, subbars

Examples

```r
m <- ~ x + (x || g)
expandDoubleVerts(m)
set.seed(101)
dd <- expand.grid(f=factor(letters[1:3]), g=factor(1:200), rep=1:3)
dd$y <- simulate(-f + (1|g) + (0+dummy(f,"b")|g) + (0+dummy(f,"c")|g),
                newdata=dd,
                newparams=list(beta=rep(0,3),
                                theta=c(1,2,1),
                                sigma=1),
                family=gaussian)[][]
ml <- lmer(y~f|g), data=dd)
VarCorr(ml)
ml2 <- lmer(y~f+1|g) + (0+dummy(f,"b")|g) + (0+dummy(f,"c")|g),
          data=dd)
VarCorr(ml2)
```
findbars

Arguments

x a formula
frloc a data frame
char.only (logical) convert only character variables to factors?

Value

a copy of the data frame with factors converted

Description

From the right hand side of a formula for a mixed-effects model, determine the pairs of expressions that are separated by the vertical bar operator. Also expand the slash operator in grouping factor expressions and expand terms with the double vertical bar operator into separate, independent random effect terms.

Usage

findbars(term)

Arguments

term a mixed-model formula

Value

pairs of expressions that were separated by vertical bars

Note

This function is called recursively on individual terms in the model, which is why the argument is called term and not a name like form, indicating a formula.

See Also

formula, model.frame, model.matrix.

Other utilities: mkRespMod, mkReTrms, nlformula, nobars, subbars
Examples

```r
findbars(f1 ~ Reaction ~ Days + (Days | Subject))
## => list( Days | Subject )
## These two are equivalent: % tests in ../inst/tests/test-doubleVertNotation.R
findbars(y ~ Days + (1 | Subject) + (0 + Days | Subject))
findbars(y ~ Days + (Days || Subject))
## => list of length 2: list ( 1 | Subject , 0 + Days | Subject)
findbars(~ 1 + (1 | batch / cask))
## => list of length 2: list ( 1 | cask:batch , 1 | batch)
```

fixef

**Extract fixed-effects estimates**

Description

Extract the fixed-effects estimates

Usage

```r
## S3 method for class 'merMod'
fixef(object, add.dropped=FALSE, ...)
```

Arguments

- `object`: any fitted model object from which fixed effects estimates can be extracted.
- `add.dropped`: for models with rank-deficient design matrix, reconstitute the full-length parameter vector by adding NA values in appropriate locations?
- `...`: optional additional arguments. Currently none are used in any methods.

Details

Extract the estimates of the fixed-effects parameters from a fitted model.

Value

A named, numeric vector of fixed-effects estimates.

Examples

```r
fixef(lmer(Reaction ~ Days + (1|Subject) + (0+Days|Subject), sleepstudy))
fm2 <- lmer(Reaction ~ Days + Days2 + (1|Subject),
            data=transform(sleepstudy,Days2=Days))
fixef(fm2,add.dropped=TRUE)
## first two parameters are the same ...
stopifnot(all.equal(fixef(fm2,add.dropped=TRUE)[1:2],
                   fixef(fm2)))
```
fortify

add information to data based on a fitted model

Description

add information to data based on a fitted model

Usage

fortify.merMod(model, data = getData(model), ...)

Arguments

model fitted model
data original data set, if needed
... additional arguments

Details

fortify is a function defined in the ggplot2 package, q.v. for more details. fortify is not defined here, and fortify.merMod is defined as a function rather than an S3 method, to avoid (1) inducing a dependency on ggplot2 or (2) masking methods from ggplot2. This is currently an experimental feature.

getME

Extract or Get Generalized Components from a Fitted Mixed Effects Model

Description

Extract (or “get”) “components” – in a generalized sense – from a fitted mixed-effects model, i.e., (in this version of the package) from an object of class ‘merMod’.

Usage

getME(object, name, ...)

## S3 method for class 'merMod'
getME(object,  
name = c("X", "Z", "Zt", "Ztlist", "mmList", "y", "mu", "u", "b",  
"A", "RX", "RZX", "sigma", "flist",  
"fixef", "beta", "theta", "ST", "REML", "is_REML",  
"n_rtrms", "n_rfacs", "N", "n", "p", "q"),
getME

"p_i", "l_i", "q_i", "k", "m_i", "m",
"cnms", "devcomp", "offset", "lower", "devfun", "glmer.nb.theta"),
...

Arguments

object a fitted mixed-effects model of class "merMod", i.e., typically the result of \texttt{lmer()}, \texttt{glmer()} or \texttt{nlmer()}.

name a character vector specifying the name(s) of the “component”. If \texttt{length(name) > 1} or if \texttt{name == "ALL"}, a named \texttt{list} of components will be returned. Possible values are:

"X": fixed-effects model matrix

"Z": random-effects model matrix

"Zt": transpose of random-effects model matrix. Note that the structure of Zt has changed since \texttt{lme4.0}; to get a backward-compatible structure, use \texttt{do.call(Matrix::rBind, getME(.,"Ztlist"))}

"Ztlist": list of components of the transpose of the random-effects model matrix, separated by individual variance component

"mmList": list of raw model matrices associated with random effects terms

"y": response vector

"mu": conditional mean of the response

"u": conditional mode of the “spherical” random effects variable

"b": conditional mode of the random effects variable

"Gp": groups pointer vector. A pointer to the beginning of each group of random effects corresponding to the random-effects terms, beginning with 0 and including a final element giving the total number of random effects

"Tp": theta pointer vector. A pointer to the beginning of the theta sub-vectors corresponding to the random-effects terms, beginning with 0 and including a final element giving the number of thetas.

"L": sparse Cholesky factor of the penalized random-effects model.

"Lambda": relative covariance factor \(\Lambda\) of the random effects.

"Lambdat": transpose \(\Lambda'\) of \(\Lambda\) above.

"Lind": index vector for inserting elements of \(\theta\) into the nonzeros of \(\Lambda\).

"Tlist": vector of template matrices from which the blocks of \(\Lambda\) are generated.

"A":Scaled sparse model matrix (class "dgCMatrix") for the unit, orthogonal random effects, \(U\), equal to \texttt{getME(.,"Zt") \%\% getME(.,"Lambdat")}

"RX": Cholesky factor for the fixed-effects parameters

"RZX": cross-term in the full Cholesky factor

"sigma": residual standard error; note that \texttt{sigma(object)} is preferred.

"flist": a list of the grouping variables (factors) involved in the random effect terms

"fixef": fixed-effects parameter estimates

"beta": fixed-effects parameter estimates (identical to the result of \texttt{fixef}, but without names)
"theta": random-effects parameter estimates: these are parameterized as the relative Cholesky factors of each random effect term

"ST": A list of S and T factors in the TSST' Cholesky factorization of the relative variance matrices of the random effects associated with each random-effects term. The unit lower triangular matrix, T, and the diagonal matrix, S, for each term are stored as a single matrix with diagonal elements from S and off-diagonal elements from T.

"n_rtrms": number of random-effects terms

"n_rfacs": number of distinct random-effects grouping factors

"N": number of rows of X

"n": length of the response vector, y

"p": number of columns of the fixed effects model matrix, X

"q": number of columns of the random effects model matrix, Z

"p_i": numbers of columns of the raw model matrices, mmList

"l_i": numbers of levels of the grouping factors

"q_i": numbers of columns of the term-wise model matrices, ZtList

"k": number of random effects terms

"m_i": numbers of covariance parameters in each term

"m": total number of covariance parameters

"cnms": the “component names”, a list.

"REML": 0 indicates the model was fitted by maximum likelihood, any other positive integer indicates fitting by restricted maximum likelihood

"is_REML": same as the result of isREML(.)

"devcomp": a list consisting of a named numeric vector, cmp, and a named integer vector, dims, describing the fitted model. The elements of cmp are:

- ldL2: twice the log determinant of L
- ldRX2: twice the log determinant of RX
- wrss: weighted residual sum of squares
- ussq: squared length of u
- pwrss: penalized weighted residual sum of squares, “wrss + ussq”
- drsum: sum of residual deviance (GLMMs only)
- dev: deviance criterion at optimum (models fit by ML only)
- sigmaML: ML estimate of residual standard deviation
- sigmaREML: REML estimate of residual standard deviation
- tolPwrss: tolerance for declaring convergence in the penalized iteratively weighted residual sum-of-squares (GLMMs only)

The elements of dims are:

- N: number of rows of X
- n: length of y
- p: number of columns of X
- nmp: n-p
getME

nth  length of theta
q    number of columns of Z
nAGQ see glmer
compDev see glmerControl
useSc TRUE if model has a scale parameter
reTrms number of random effects terms
REML  θ indicates the model was fitted by maximum likelihood, any other
      positive integer indicates fitting by restricted maximum likelihood
GLMM TRUE if a GLMM
NLMM TRUE if an NLMM
"offset": model offset
"lower": lower bounds on model parameters (random effects parameters only).
"devfun": deviance function (so far only available for LMMs)
"glmer.nb.theta": negative binomial θ parameter, only for glmer.nb.
"ALL": get all of the above as a list.
... currently unused in lme4, potentially further arguments in methods.

Details

The goal is to provide “everything a user may want” from a fitted “merMod” object as far as it is not
available by methods, such as fixef, ranef, vcov, etc.

Value

Unspecified, as very much depending on the name.

See Also

gcall(). More standard methods for “merMod” objects, such as ranef, fixef, vcov, etc.: see
methods(class="merMod")

Examples

## shows many methods you should consider *before* using getME():
methods(class = "merMod")

(fm1 <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy))
Z <- getME(fm1, "Z")
stopifnot(is(Z, "CsparseMatrix"),
c(100,36) == dim(Z),
all.equal(fixef(fm1), b1 <- getME(fm1, "beta"),
check.attributes=FALSE, tolerance = 0))

## A way to get *all* getME()s:
## internal consistency check ensuring that all work:
parts <- getME(fm1, "ALL")
str(parts, max=2)
stopifnot(identical(Z, parts $ Z),
identical(b1, parts $ beta))
GHrule

Univariate Gauss-Hermite quadrature rule

Description

Create a univariate Gauss-Hermite quadrature rule.

Usage

GHrule(ord, asMatrix = TRUE)

Arguments

ord      scalar integer between 1 and 25 - the order, or number of nodes and weights, in the rule. When the function being multiplied by the standard normal density is a polynomial of order 2k-1 the rule of order k integrates the product exactly.

asMatrix logical scalar - should the result be returned as a matrix. If FALSE a data frame is returned. Defaults to TRUE.

Details

This version of Gauss-Hermite quadrature provides the node positions and weights for a scalar integral of a function multiplied by the standard normal density.

Originally based on package SparseGrid’s hidden gqn().

Value

a matrix (or data frame, is asMatrix is false) with ord rows and three columns which are z the node positions, w the weights and ldnorm, the logarithm of the normal density evaluated at the nodes.

See Also

a different interface is available via GQdk().

Examples

(r5 <- GHrule(5, asMatrix=FALSE))
## second, fourth, sixth, eighth and tenth central moments of the standard Gaussian density
with(r5, sapply(seq(2, 10, 2), function(p) sum(w * z^p))))
Fitting Generalized Linear Mixed-Effects Models

Description

Fit a generalized linear mixed-effects model (GLMM). Both fixed effects and random effects are specified via the model formula.

Usage

```r
glmer(formula, data = NULL, family = gaussian, control = glmerControl(),
      start = NULL, verbose = 0L, nAGQ = 1L, subset, weights, na.action,
      offset, contrasts = NULL, mustart, etastart,
      devFunOnly = FALSE, ...)
```

Arguments

- `formula`: a two-sided linear formula object describing both the fixed-effects and fixed-effects part of the model, with the response on the left of a `~` operator and the terms, separated by `+` operators, on the right. Random-effects terms are distinguished by vertical bars (`|`) separating expressions for design matrices from grouping factors.
- `data`: an optional data frame containing the variables named in `formula`. By default the variables are taken from the environment from which `lmer` is called. While `data` is optional, the package authors strongly recommend its use, especially when later applying methods such as `update` and `drop1` to the fitted model (such methods are not guaranteed to work properly if `data` is omitted). If `data` is omitted, variables will be taken from the environment of `formula` (if specified as a formula) or from the parent frame (if specified as a character vector).
- `family`: a GLM family, see `glm` and `family`.
- `control`: a list (of correct class, resulting from `lmerControl()` or `glmerControl()` respectively) containing control parameters, including the nonlinear optimizer to be used and parameters to be passed through to the nonlinear optimizer, see the `lmerControl` documentation for details.
- `start`: a named list of starting values for the parameters in the model, or a numeric vector. A numeric start argument will be used as the starting value of theta. If `start` is a list, the theta element (a numeric vector) is used as the starting value for the first optimization step (default=1 for diagonal elements and 0 for off-diagonal elements of the lower Cholesky factor); the fitted value of theta from the first step, plus `start[["fixef"]`, are used as starting values for the second optimization step. If `start` has both `fixef` and `theta` elements, the first optimization step is skipped. For more details or finer control of optimization, see `modular`.
- `verbose`: integer scalar. If > 0 verbose output is generated during the optimization of the parameter estimates. If > 1 verbose output is generated during the individual PIRLS steps.
\textbf{Details}

Fit a generalized linear mixed model, which incorporates both fixed-effects parameters and random effects in a linear predictor, via maximum likelihood. The linear predictor is related to the conditional mean of the response through the inverse link function defined in the GLM family.

The expression for the likelihood of a mixed-effects model is an integral over the random effects space. For a linear mixed-effects model (LMM), as fit by \texttt{lmer}, this integral can be evaluated exactly. For a GLMM the integral must be approximated. The most reliable approximation for GLMMs is adaptive Gauss-Hermite quadrature, at present implemented only for models with a single scalar random effect. The \texttt{nAGQ} argument controls the number of nodes in the quadrature formula. A model with a single, scalar random-effects term could reasonably use up to 25 quadrature points per scalar integral.
Value

An object of class merMod (more specifically, an object of subclass glmerMod) for which many methods are available (e.g. methods(class="merMod"))

See Also

lmer (for details on formulas and parameterization); glm for Generalized Linear Models (without random effects). nlm for nonlinear mixed-effects models.
glmer.nb to fit negative binomial GLMMs.

Examples

```r
## generalized linear mixed model
library(lattice)
xyplot(incidence/size ~ period|herd, cbpp, type=c('g','p','l'),
       layout=c(3,5), index.cond = function(x,y)max(y))
(gm1 <- glmer(cbind(incidence, size - incidence) ~ period + (1 | herd),
              data = cbpp, family = binomial))
## using nAGQ=0 only gets close to the optimum
(gm1a <- glmer(cbind(incidence, size - incidence) ~ period + (1 | herd),
               cbpp, binomial, nAGQ = 0))
## using nAGQ = 9 provides a better evaluation of the deviance
## Currently the internal calculations use the sum of deviance residuals,
## which is not directly comparable with the nAGQ=0 or nAGQ=1 result.
(gm1a <- glmer(cbind(incidence, size - incidence) ~ period + (1 | herd),
               cbpp, binomial, nAGQ = 9))

## GLMM with individual-level variability (accounting for overdispersion)
## For this data set the model is the same as one allowing for a period:herd
## interaction, which the plot indicates could be needed.
cbpp$obs <- 1:nrow(cbpp)
(gm2 <- glmer(cbind(incidence, size - incidence) ~ period +
             (1 | herd) + (1|obs),
             family = binomial, data = cbpp))
anova(gm1,gm2)

## glmer and glm log-likelihoods are consistent
gm1Devfun <- update(gm1,devFunOnly=TRUE)
gm0 <- glm(cbind(incidence, size - incidence) ~ period,
          family = binomial, data = cbpp)
## evaluate GLMM deviance at RE variance=theta=0, beta=(GLM coeffs)
gm1Dev0 <- gm1Devfun(c(0,coef(gm0)))
## compare
stopifnot(all.equal(gm1Dev0,c(-2*logLik(gm0))))
## the toenail oncholysis data from Backer et al 1998
## these data are notoriously difficult to fit
## Not run:
if (require("HSAUR2")) {
  gm2 <- glmer(outcome~treatment*visit+(1|patientID),
              data=toenail,
              family=binomial,nAGQ=20)
}
```
Fitting Negative Binomial GLMMs

Description

Fits a generalized linear mixed-effects model (GLMM) for the negative binomial family, building on `glmer`, and initializing via `theta.ml` from MASS.

Usage

```r
glmer.nb(..., interval = log(th) + c(-3, 3),
  tol = 5e-5, verbose = FALSE, nb.control = NULL,
  initCtrl = list(limit = 20, eps = 2*tol, trace = verbose))
```

Arguments

- `...`: arguments as for `glmer(.)` such as formula, data, control, etc, but not family!
- `interval`: interval in which to start the optimization. The default is symmetric on log scale around the initially estimated theta.
- `tol`: tolerance for the optimization via `optimize`.
- `verbose`: logical indicating how much progress information should be printed during the optimization. Use `verbose = 2` (or larger) to enable `verbose=TRUE` in the `glmer()` calls.
- `nb.control`: optional list, like `glmerControl()`, used in `refit(*, control = control.nb)` during the optimization.
- `initCtrl`: (experimental, do not rely on this) a list with named components as in the default, passed to `theta.ml` (package MASS) for the initial value of the negative binomial parameter theta.

Value

An object of class `glmerMod`, for which many methods are available (e.g. `methods(class="glmerMod"))`, see `glmer`.

Note

For historical reasons, the shape parameter of the negative binomial and the random effects parameters in our (G)LMM models are both called theta (θ), but are unrelated here.

The negative binomial θ can be extracted from a fit `g <- glmer.nb()` by `getME(g, "glmer.nb.theta")`.

Parts of `glmer.nb()` are still experimental and methods are still missing or suboptimal. In particular, there is no inference available for the dispersion parameter θ, yet.
See Also

`glmer`; from package MASS, `negative.binomial` (which we re-export currently) and `theta.ml`, the latter for initialization of optimization.

The ‘Details’ of `pnbinom` for the definition of the negative binomial distribution.

Examples

```r
set.seed(101)
dd <- expand.grid(f1 = factor(1:3),
  f2 = LETTERS[1:2], g=1:9, rep=1:15,
  KEEP.OUT.ATTRS=FALSE)
summary(mu <- 5*(-4 + with(dd, as.integer(f1) + 4*as.numeric(f2))))
str(dd)
require("MASS")## and use its glm.nb() - as indeed we have zero random effect:
## Not run:
m.glm <- glm.nb(y ~ f1*f2, data=dd, trace=TRUE)
summary(m.glm)
m.nb <- glmer.nb(y ~ f1*f2 + (1|g), data=dd, verbose=TRUE)
m.nb
## The neg.binomial theta parameter:
getME(m.nb, "glmer.nb.theta")
LL <- logLik(m.nb)
## mixed model has 1 additional parameter (RE variance)
stopifnot(attr(LL,"df") == attr(logLik(m.glm),"df")+1)
plot(m.nb, resid(.) ~ g)# works, as long as data 'dd' is found

## End(Not run)
```

---

**glmerLaplaceHandle**

*Handle for glmerLaplace*

**Description**

Handle for calling the `glmerLaplace` C++ function. Not intended for routine use.

**Usage**

```r
glmerLaplaceHandle(pp, resp, nAGQ, tol, maxit, verbose)
```

**Arguments**

- `pp` *merPredD* object
- `resp` *lmResp* object
- `nAGQ` see `glmer`
- `tol` tolerance
- `maxit` maximum number of pwrss iterations
- `verbose` display optimizer progress
glmFamily

Value
Value of the objective function

glmFamily  
Generator object for the glmFamily class

Description
The generator object for the glmFamily reference class. Such an object is primarily used through its new method.

Usage
glmFamily(...)

Arguments
... Named argument (see Note below)

Methods
new(family=family) Create a new glmFamily object

Note
Arguments to the new method must be named arguments.

See Also
glmFamily

glmFamily-class  
Class "glmFamily" - a reference class for family

Description
This class is a wrapper class for family objects specifying a distribution family and link function for a generalized linear model (glm). The reference class contains an external pointer to a C++ object representing the class. For common families and link functions the functions in the family are implemented in compiled code so they can be accessed from other compiled code and for a speed boost.

Extends
All reference classes extend and inherit methods from "envRefClass".
golden-class

Note

Objects from this reference class correspond to objects in a C++ class. Methods are invoked on the C++ class using the external pointer in the Ptr field. When saving such an object the external pointer is converted to a null pointer, which is why there is a redundant field ptr that is an active-binding function returning the external pointer. If the Ptr field is a null pointer, the external pointer is regenerated for the stored family field.

See Also

family, glmFamily

Examples

str(glmFamily$new(family=poisson())

golden-class

Class "golden" and Generator for Golden Search Optimizer Class

Description

"golden" is a reference class for a golden search scalar optimizer, for a parameter within an interval. golden() is the generator for the "golden" class. The optimizer uses reverse communications.

Usage

golden(...)

Arguments

... (partly optional) arguments passed to new() must be named arguments. lower and upper are the bounds for the scalar parameter; they must be finite.

Extends

All reference classes extend and inherit methods from "envRefClass".

Examples

showClass("golden")

golden(lower= -100, upper= 1e100)
Sparse Gaussian / Gauss-Hermite Quadrature grid

Description

Generate the sparse multidimensional Gaussian quadrature grids.

Currently unused. See `GHRule()` for the version currently in use in package `lme4`.

Usage

```r
GQdk(d = 1L, k = 1L)
```

Arguments

- `d` integer scalar - the dimension of the function to be integrated with respect to the standard d-dimensional Gaussian density.
- `k` integer scalar - the order of the grid. A grid of order k provides an exact result for a polynomial of total order of $2k - 1$ or less.

Value

- `GQdk()` returns a matrix with $d + 1$ columns. The first column is the weights and the remaining d columns are the node coordinates.
- `GQN` is a list of lists, containing the non-redundant quadrature nodes and weights for integration of a scalar function of a d-dimensional argument with respect to the density function of the d-dimensional Gaussian density function.
  - The outer list is indexed by the dimension, d, in the range of 1 to 20. The inner list is indexed by k, the order of the quadrature.

Note

- `GQN` contains only the non-redundant nodes. To regenerate the whole array of nodes, all possible permutations of axes and all possible combinations of $\pm 1$ must be applied to the axes. This entire array of nodes is exactly what `GQdk()` reproduces.
- The number of nodes gets very large very quickly with increasing d and k. See the charts at [http://www.sparse-grids.de](http://www.sparse-grids.de).

Examples

```r
GQdk(2,5) # 53 x 3
GQN[[3]][[5]] # a 14 x 4 matrix
```
### Data on red grouse ticks from Elston et al. 2001

#### Description

Number of ticks on the heads of red grouse chicks sampled in the field (`grouseticks`) and an aggregated version (`grouseticks_agg`); see original source for more details.

#### Usage

```r
data(grouseticks)
```

#### Format

- **INDEX** (factor) chick number (observation level)
- **TICKS** number of ticks sampled
- **BROOD** (factor) brood number
- **HEIGHT** height above sea level (meters)
- **YEAR** year (-1900)
- **LOCATION** (factor) geographic location code
- **cHEIGHT** centered height, derived from **HEIGHT**
- **meanTICKS** mean number of ticks by brood
- **varTICKS** variance of number of ticks by brood

#### Details

`grouseticks_agg` is just a brood-level aggregation of the data.

#### Source

Robert Moss, via David Elston

#### References

### Examples

```r
data(grouseticks)
## Figure 1a from Elston et al
par(las=1,bty="1")
tvec <- c(0,1,2,5,20,40,80)
pvec <- c(4,1,3)
with(grouseticks_aggreg, plot(1+meanTICKS~HEIGHT, pch=pvec[factor(YEAR)],
log="y",axes=FALSE,
xlab="Altitude (m)",
ylab="Brood mean ticks"))
axis(side=1)
axis(side=2,at=tvec+1,label=tvec)
box()
abline(y=40, lty=2)
## Figure 1b
with(grouseticks_aggreg, plot(varTICKS~meanTICKS, pch=4,
 xlab="Brood mean ticks",
ylab="Within-brood variance"))
curve(1+x, from=0, to=70, add=TRUE)
## Model fitting
form <- TICKS~YEAR+HEIGHT+(1|BROOD)+(1|INDEX)+(1|LOCATION)
(full_mod) <- glmer(form, family="poisson", data=grouseticks)
```

---

### Description

Returns the values on the diagonal of the hat matrix, which is the matrix that transforms the response vector (minus any offset) into the fitted values (minus any offset). Note that this method should only be used for linear mixed models. It is not clear if the hat matrix concept even makes sense for generalized linear mixed models.

### Usage

```r
## S3 method for class 'merMod'
hatvalues(model, fullHatMatrix = FALSE, ...)
```

### Arguments

- `model`: An object of class `merMod`.
- `fullHatMatrix`: Return full hat matrix (not just diagonal values)?
- `...`: Not currently used

### Value

The diagonal elements of the hat matrix.
**Examples**

```r
m <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
hatvalues(m)
```

---

**Description**

University lecture evaluations by students at ETH Zurich, anonymized for privacy protection. This is an interesting “medium” sized example of a partially nested mixed effect model.

**Format**

A data frame with 73421 observations on the following 7 variables.

- `s`: a factor with levels `1:2972` denoting individual students.
- `d`: a factor with 1128 levels from `1:2160`, denoting individual professors or lecturers.
- `studage`: an ordered factor with levels `2 < 4 < 6 < 8`, denoting student’s “age” measured in the semester number the student has been enrolled.
- `lectage`: an ordered factor with 6 levels, `1 < 2 < ... < 6`, measuring how many semesters back the lecture rated had taken place.
- `service`: a binary factor with levels `0` and `1`; a lecture is a “service”, if held for a different department than the lecturer’s main one.
- `dept`: a factor with 14 levels from `1:15`, using a random code for the department of the lecture.
- `y`: a numeric vector of ratings of lectures by the students, using the discrete scale `1:5`, with meanings of ‘poor’ to ‘very good’.

Each observation is one student’s rating for a specific lecture (of one lecturer, during one semester in the past).

**Details**

The main goal of the survey is to find “the best liked prof”, according to the lectures given. Statistical analysis of such data has been the basis for a (student) jury selecting the final winners.

The present data set has been anonymized and slightly simplified on purpose.

**Examples**

```r
str(InstEval)
head(InstEval, 16)
xtabs(~ service + dept, InstEval)
```
isNested

Is f1 nested within f2?

Description

Does every level of f1 occur in conjunction with exactly one level of f2? The function is based on converting a triplet sparse matrix to a compressed column-oriented form in which the nesting can be quickly evaluated.

Usage

isNested(f1, f2)

Arguments

f1  factor 1
f2  factor 2

Value

TRUE if factor 1 is nested within factor 2

Examples

with(Pastes, isNested(cask, batch))  ## => FALSE
with(Pastes, isNested(sample, batch))  ## => TRUE

isREML

Check characteristics of models

Description

Check characteristics of models: whether a model fit corresponds to a linear (LMM), generalized linear (GLMM), or nonlinear (NLMM) mixed model, and whether a linear mixed model has been fitted by REML or not (isREML(x) is always FALSE for GLMMs and NLMMs).

Usage

isREML(x, ...)

isLMM(x, ...)

isNLMM(x, ...)

isGLMM(x, ...)

isreml

Check characteristics of models
Arguments

x                a fitted model.

...         additional, optional arguments. (None are used in the merMod methods)

Details

These are generic functions. At present the only methods are for mixed-effects models of class merMod.

Value

a logical value

See Also

glmer, nlmer, getME

Examples

fm1 <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy)
gm1 <- glmer(cbind(incidence, size - incidence) ~ period + (1 | herd),
             data = cbpp, family = binomial)
nml <- nlmer(circumference ~ SSlogis(age, Asym, xmid, scal) ~ Asym|Tree,
             data = orange, start = c(Asym = 200, xmid = 725, scal = 350))

isLMM(fm1)
isGLMM(gm1)

## check all:
is.MM <- function(x) c(LMM = isLMM(x), GLMM = isGLMM(x), NLMM = isNLMM(x))
stopifnot(cbind(is.MM(fm1), is.MM(gm1), is.MM(nml))
== diag(rep(TRUE,3)))
Arguments

formula

a two-sided linear formula object describing both the fixed-effects and random-effects part of the model, with the response on the left of a ~ operator and the terms, separated by + operators, on the right. Random-effects terms are distinguished by vertical bars (|) separating expressions for design matrices from grouping factors. Two vertical bars (||) can be used to specify multiple uncorrelated random effects for the same grouping variable. (Because of the way it is implemented, the ||-syntax works only for design matrices containing numeric (continuous) predictors; to fit models with independent categorical effects, see dummy or the lmer_alt function from the afex package.)

data

an optional data frame containing the variables named in formula. By default the variables are taken from the environment from which lmer is called. While data is optional, the package authors strongly recommend its use, especially when later applying methods such as update and drop1 to the fitted model (such methods are not guaranteed to work properly if data is omitted). If data is omitted, variables will be taken from the environment of formula (if specified as a formula) or from the parent frame (if specified as a character vector).

REML

logical scalar - Should the estimates be chosen to optimize the REML criterion (as opposed to the log-likelihood)?

control

a list (of correct class, resulting from lmerControl() or glmerControl() respectively) containing control parameters, including the nonlinear optimizer to be used and parameters to be passed through to the nonlinear optimizer, see the *lmerControl documentation for details.

start

a named list of starting values for the parameters in the model. For lmer this can be a numeric vector or a list with one component named "theta".

verbose

integer scalar. If > 0 verbose output is generated during the optimization of the parameter estimates. If > 1 verbose output is generated during the individual PIRLS steps.

subset

an optional expression indicating the subset of the rows of data that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

weights

an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or a numeric vector. Prior weights are not normalized or standardized in any way. In particular, the diagonal of the residual covariance matrix is the squared residual standard deviation parameter sigma times the vector of inverse weights. Therefore, if the weights have relatively large magnitudes, then in order to compensate, the sigma parameter will also need to have a relatively large magnitude.

na.action

a function that indicates what should happen when the data contain NAs. The default action (na.omit, inherited from the 'factory fresh' value of getOption("na.action")) strips any observations with any missing values in any variables.

offset

this can be used to specify an a priori known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more offset terms can be included in the
formula instead or as well, and if more than one is specified their sum is used. See `model.offset`.

contrasts an optional offset. See the contrasts.arg of `model.matrix.default`.

devFunOnly logical - return only the deviance evaluation function. Note that because the deviance function operates on variables stored in its environment, it may not return exactly the same values on subsequent calls (but the results should always be within machine tolerance).

... other potential arguments. A method argument was used in earlier versions of the package. Its functionality has been replaced by the `REML` argument.

Details

- If the `formula` argument is specified as a character vector, the function will attempt to coerce it to a formula. However, this is not recommended (users who want to construct formulas by pasting together components are advised to use `as.formula` or `reformulate`); model fits will work but subsequent methods such as `drop1`, `update` may fail.

- When handling perfectly collinear predictor variables (i.e. design matrices of less than full rank), `lmer` is not quite as sophisticated as some simpler modeling frameworks such as `lm` and `glm`. While it does automatically drop collinear variables (with a message rather than a warning), it does not automatically fill in NA values for the dropped coefficients; these can be added via `fixef(fitted.model, add.dropped=TRUE)`. This information can also be retrieved via `attr(getME(fitted.model,"X"),"col.dropped")`.

- the deviance function returned when `devFunOnly` is `TRUE` takes a single numeric vector argument, representing the theta vector. This vector defines the scaled variance-covariance matrices of the random effects, in the Cholesky parameterization. For models with only simple (intercept-only) random effects, theta is a vector of the standard deviations of the random effects. For more complex or multiple random effects, running `getME(.,"theta")` to retrieve the theta vector for a fitted model and examining the names of the vector is probably the easiest way to determine the correspondence between the elements of the theta vector and elements of the lower triangles of the Cholesky factors of the random effects.

Value

An object of class `merMod` (more specifically, an object of subclass `lmerMod`), for which many methods are available (e.g. `methods(class="merMod")`)

See Also

`lm` for linear models; `glmer` for generalized linear; and `nlmer` for nonlinear mixed models.

Examples

```r
## linear mixed models - reference values from older code
(fm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy))
summary(fm1)# (with its own print method; see class?merMod % ./merMod-class.Rd

str(terms(fm1))
stopifnot(identical(terms(fm1, fixed.only=FALSE),

```
lmerControl

Control of Mixed Model Fitting

Description

Construct control structures for mixed model fitting. All arguments have defaults, and can be grouped into

- general control parameters, most importantly optimizer, further restart_edge, etc;
- model- or data-checking specifications, in short “checking options”, such as check.nobs.vs.rankZ, or check.rankX (currently not for nlmerControl);
- all the parameters to be passed to the optimizer, e.g., maximal number of iterations, passed via the optCtrl list argument.

Usage

lmerControl(optimizer = "bobyqa",
            restart_edge = TRUE,
            boundary.tol = 1e-5,
            calc.derivs=TRUE,
            use.last.params=FALSE,
            sparseX = FALSE,
            ## input checking options
            check.nobs.vs.rankZ = "ignore",
            check.nobs.vs.nlev = "stop",
            check.nlev.gtreq.5 = "ignore",}
check.nlev.gtr.1 = "stop",
check.nobs.vs.nRE="stop",
check.rankX = c("message+drop.cols", "silent.drop.cols", "warn+drop.cols",
                 "stop.deficient", "ignore"),
check.scaleX = c("warning","stop","silent.rescale",
                 "message+rescale","warn+rescale","ignore"),
check.formula.LHS = "stop",
## convergence checking options
check.conv.grad = .makeCC("warning", tol = 2e-3, relTol = NULL),
check.conv.singular = .makeCC(action = "ignore", tol = 1e-4),
check.conv.hess = .makeCC(action = "warning", tol = 1e-6),
## optimizer args
optCtrl = list()

glmerControl(optimizer = c("bobyqa", "Nelder_Mead"),
              restart.edge = FALSE,
              boundary.tol = 1e-5,
              calc.derivs=TRUE,
              use.last.params=FALSE,
              sparseX = FALSE,
              tolPwrss=1e-7,
              compDev=TRUE,
              nAGQ0initStep=TRUE,
              ## input checking options
check.nobs.vs.rankZ = "ignore",
check.nobs.vs.nlev = "stop",
check.nlev.gtrq.5 = "ignore",
check.nlev.gtr.1 = "stop",
check.nobs.vs.nRE="stop",
check.rankX = c("message+drop.cols", "silent.drop.cols", "warn+drop.cols",
                 "stop.deficient", "ignore"),
check.scaleX = "warning",
check.formula.LHS = "stop",
check.response.not.const = "stop",
## convergence checking options
check.conv.grad = .makeCC("warning", tol = 1e-3, relTol = NULL),
check.conv.singular = .makeCC(action = "ignore", tol = 1e-4),
check.conv.hess = .makeCC(action = "warning", tol = 1e-6),
## optimizer args
optCtrl = list()
nlmerControl(optimizer = "Nelder_Mead", tolPwrss = 1e-10,
              optCtrl = list())

.makeCC(action, tol, relTol, ...)
Arguments

- **optimizer**: character - name of optimizing function(s). A character vector or list of functions: length 1 for lmer or glmer, possibly length 2 for glmer). The built-in optimizers are **Nelder_Mead** and **bobyqa** (from the **minqa** package). Any minimizing function that allows box constraints can be used provided that it

  1. takes input parameters fn (function to be optimized), par (starting parameter values), lower (lower bounds) and control (control parameters, passed through from the control argument) and

  2. returns a list with (at least) elements par (best-fit parameters), fval (best-fit function value), conv (convergence code, equal to zero for successful convergence) and (optionally) message (informational message, or explanation of convergence failure).

Special provisions are made for **bobyqa**, **Nelder_Mead**, and optimizers wrapped in the **optimx** package; to use the **optimx** optimizers (including **lMbfgsMb** from base **optim** and **nlminb**), pass the method argument to **optim** in the optCtrl argument (you may also need to load the **optimx** package manually using `library(optimx)` or `require(optimx)`).

For glmer, if `length(optimizer)` == 2, the first element will be used for the preliminary (random effects parameters only) optimization, while the second will be used for the final (random effects plus fixed effect parameters) phase. See **modular** for more information on these two phases.

- **calc.derivs**: logical - compute gradient and Hessian of nonlinear optimization solution?

- **use.last.params**: logical - should the last value of the parameters evaluated (TRUE), rather than the value of the parameters corresponding to the minimum deviance, be returned? This is a "backward bug-compatibility" option; use TRUE only when trying to match previous results.

- **sparseX**: logical - should a sparse model matrix be used for the fixed-effects terms? Currently inactive.

- **restart_edge**: logical - should the optimizer attempt a restart when it finds a solution at the boundary (i.e. zero random-effect variances or perfect +/−1 correlations)? (Currently only implemented for lmerControl.)

- **boundary.tol**: numeric - within what distance of a boundary should the boundary be checked for a better fit? (Set to zero to disable boundary checking.)

- **tolPwrss**: numeric scalar - the tolerance for declaring convergence in the penalized iteratively weighted residual sum-of-squares step.

- **compDev**: logical scalar - should compiled code be used for the deviance evaluation during the optimization of the parameter estimates?

- **nAGQ@initStep**: do one initial run with nAGQ = 0.

- **check.nlev.gtre.5**: character - rules for checking whether all random effects have >= 5 levels. See action.

- **check.nlev.gtr.1**: character - rules for checking whether all random effects have > 1 level. See action.
check.nobs vs. rankZ
character - rules for checking whether the number of observations is greater than (or greater than or equal to) the rank of the random effects design matrix (Z), usually necessary for identifiable variances. As for action, with the addition of "warningSmall" and "stopSmall", which run the test only if the dimensions of Z are < 1e6. nobs > rank(Z) will be tested for LMMs and GLMMs with estimated scale parameters; nobs >= rank(Z) will be tested for GLMMs with fixed scale parameter. The rank test is done using the method="qr" option of the rankMatrix function.

check.nobs vs. nlev
character - rules for checking whether the number of observations is less than (or less than or equal to) the number of levels of every grouping factor, usually necessary for identifiable variances. As for action.

check.nobs vs. nRE
character - rules for checking whether the number of observations is greater than (or greater than or equal to) the number of random-effects levels for each term, usually necessary for identifiable variances. As for check.nobs vs. nlev.

check.conv.grad
rules for checking the gradient of the deviance function for convergence. A list as returned by .makeCC, or a character string with only the action.

check.conv.singular
rules for checking for a singular fit, i.e. one where some parameters are on the boundary of the feasible space (for example, random effects variances equal to 0 or correlations between random effects equal to +/- 1.0); as for check.conv.grad above.

check.conv.hess
rules for checking the Hessian of the deviance function for convergence.; as for check.conv.grad above.

check.rankX
character - specifying if rankMatrix(X) should be compared with ncol(X) and if columns from the design matrix should possibly be dropped to ensure that it has full rank. Sometimes needed to make the model identifiable. The options can be abbreviated; the three "*.drop.cols" options all do drop columns, "stop.deficient" gives an error when the rank is smaller than the number of columns where "ignore" does no rank computation, and will typically lead to less easily understandable errors, later.

check.scaleX
character - check for problematic scaling of columns of fixed-effect model matrix, e.g. parameters measured on very different scales.

check.formula.LHS
check whether specified formula has a left-hand side. Primarily for internal use within simulate.merMod; use at your own risk as it may allow the generation of unstable merMod objects

check.response.not.const
character - check that the response is not constant.

optCtrl
a list of additional arguments to be passed to the nonlinear optimizer (see Nelder_Mead, bobyqa). In particular, both Nelder_Mead and bobyqa use maxfun
to specify the maximum number of function evaluations they will try before giving up - in contrast to optim and optimx-wrapped optimizers, which use maxit.

action character - generic choices for the severity level of any test. "ignore": skip the test. "warning": warn if test fails. "stop": throw an error if test fails.

tol numeric - tolerance for check

relTol numeric - tolerance for checking relative variation

... other elements to include in check specification

Details

Note that (only!) the pre-fitting “checking options” (i.e., all those starting with "check." but not including the convergence checks ("check.conv.*") or rank-checking ("check.rank*") options) may also be set globally via options. In that case, (g)lmerControl will use them rather than the default values, but will not override values that are passed as explicit arguments.

For example, options(lmerControl=list(check.nobs.vs.rankZ = "ignore")) will suppress warnings that the number of observations is less than the rank of the random effects model matrix Z.

Value

The *Control functions return a list (inheriting from class "merControl") containing

1. general control parameters, such as optimizer, restart_edge;

2. (currently not for nlmerControl:) "checkControl", a list of data-checking specifications, e.g., check.nobs.vs.rankZ;

3. parameters to be passed to the optimizer, i.e., the optCtrl list, which may contain maxiter.

.makeCC returns a list containing the check specification (action, tolerance, and optionally relative tolerance).

See Also

convergence

Examples

str(lmerControl())
str(glmmerControl())

## Not run:

## fit with default "bobyqa" algorithm ...
fm0 <- lmer(Reaction ~ Days + ( 1 | Subject), sleepstudy)
fm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)

## or with "Nelder_Mead" (the previous default) ...
fm1_bobyqa <- update(fm1, control = lmerControl(optimizer="Nelder_Mead"))

## or with the nlminb function used in older (<1.0) versions of lme4;
## this will usually replicate older results
require(optimx)
fm1_nlminb <- update(fm1,
control = lmerControl(optimizer = "optimx"),
...
lmList

Fit List of lm Objects with a Common Model

Description

Fit a list of lm objects with a common model for different subgroups of the data.
Usage

`lmList(formula, data, family, subset, weights, na.action, offset, pool = TRUE, ...)`

Arguments

- **formula**: a linear formula object of the form `y ~ x1+...+xn | g`. In the formula object, `y` represents the response, `x1,...,xn` the covariates, and `g` the grouping factor specifying the partitioning of the data according to which different `lm` fits should be performed.
- **family**: an optional family specification for a generalized linear model.
- **pool**: logical scalar, should the variance estimate pool the residual sums of squares
- **data**: an optional data frame containing the variables named in `formula`. By default the variables are taken from the environment from which `lmer` is called. See Details.
- **subset**: an optional expression indicating the subset of the rows of `data` that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
- **weights**: an optional vector of ‘prior weights’ to be used in the fitting process. Should be NULL or a numeric vector.
- **na.action**: a function that indicates what should happen when the data contain NAs. The default action (na.omit, inherited from the ‘factory fresh’ value of `getOption("na.action")`) strips any observations with any missing values in any variables.
- **offset**: this can be used to specify an *a priori* known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more `offset` terms can be included in the `formula` instead or as well, and if more than one is specified their sum is used. See `model.offset`.

Details

- While data is optional, the package authors strongly recommend its use, especially when later applying methods such as `update` and `drop1` to the fitted model (*such methods are not guaranteed to work properly if data is omitted*). If data is omitted, variables will be taken from the environment of `formula` (if specified as a formula) or from the parent frame (if specified as a character vector).

Value

An object of class `lmList` (see there, notably for the `methods` defined).

See Also

`lmList`
Examples

```r
fm.plm <- lmList(Reaction ~ Days | Subject, sleepstudy)
coef(fm.plm)
fm.2 <- update(fm.plm, pool = FALSE)
## coefficients are the same, "pooled or unpooled":
stopifnot( all.equal(coef(fm.2), coef(fm.plm)) )

(ci <- confint(fm.plm)) # print and rather *see* :
plot(ci) # how widely they vary for the individuals
```

Description

Class "lmList4" is an S4 class with basically a list of objects of class `lm` with a common model (but different data); see `lmList()` which returns these.

Package `nlme`'s `lmList()` returns objects of S3 class "lmList" and provides methods for them, on which our methods partly build.

Objects from the Class

Objects can be created by calls of the form `new("lmList4", ...)` or, more commonly, by a call to `lmList()`.

Methods

A dozen methods are provided. Currently, S4 methods for `show`, coercion (as(...)) and others inherited via "list", and S3 methods for `coef`, `confint`, `fitted`, `fixef`, `formula`, `logLik`, `pairs`, `plot`, `predict`, `print`, `qqnorm`, `ranef`, `residuals`, `sigma`, `summary`, and `update`.

`sigma(object)` returns the standard deviation $\hat{\sigma}$ (of the errors in the linear models), assuming a common variance $\sigma^2$ by pooling (even when pool = FALSE was used in the fit).

See Also

`lmList`

Examples

```r
if(getRversion() >= "3.2.0") {
  (mm <- methods(class = "lmList4"))
  ## The S3 ("not S4") ones :
  mm[attr(mm,"info")[,"isS4"]]
}
## For more examples: example(lmList) i.e., ?.lmList
```
Description

The generator objects for the `lmResp`, `lmerResp`, `glmResp` and `nlsResp` reference classes. Such objects are primarily used through their `new` methods.

Usage

`lmResp(...)`

Arguments

`...`  List of arguments (see Note).

Methods

`new(y=y)`: Create a new `lmResp` or `lmerResp` object.

`new(family=family, y=y)`: Create a new `glmResp` object.

`new(y=y, nlmod=nlmod, nlenv=nlenv, pnames=pnames, gam=gam)`: Create a new `nlsResp` object.

Note

Arguments to the `new` methods must be named arguments.

- `y` the numeric response vector
- `family` a `family` object
- `nlmod` the nonlinear model function
- `nlenv` an environment holding data objects for evaluation of `nlmod`
- `pnames` a character vector of parameter names
- `gam` a numeric vector - the initial linear predictor

See Also

`lmResp, lmerResp, glmResp, nlsResp`
Reference Classes for Response Modules,

Description

Reference classes for response modules, including linear models, "lmResp", generalized linear models, "glmResp", nonlinear models, "nlsResp" and linear mixed-effects models, "lmerResp". Each reference class is associated with a C++ class of the same name. As is customary, the generator object for each class has the same name as the class.

Extends

All reference classes extend and inherit methods from "envRefClass". Furthermore, "glmResp", "nlsResp" and "lmerResp" all extend the "lmResp" class.

Note

Objects from these reference classes correspond to objects in C++ classes. Methods are invoked on the C++ classes using the external pointer in the ptr field. When saving such an object the external pointer is converted to a null pointer, which is why there are redundant fields containing enough information as R objects to be able to regenerate the C++ object. The convention is that a field whose name begins with an upper-case letter is an R object and the corresponding field whose name begins with the lower-case letter is a method. Access to the external pointer should be through the method, not through the field.

See Also

lmer, glmer, n1mer, merMod.

Examples

```
s getClass("lmResp")
str(lmResp$new(y=1:4))
showClass("glmResp")
str(glmResp$new(family=poisson(), y=1:4))
showClass("nlsResp")
showClass("lmerResp")
str(lmerResp$new(y=1:4))
```
Class "merMod" of Fitted Mixed-Effect Models

Description

A mixed-effects model is represented as a merPred object and a response module of a class that inherits from class lmResp. A model with a lmerResp response has class lmerMod; a glmResp response has class glmerMod; and a nlsResp response has class nlmerMod.

Usage

```r
## S3 method for class 'merMod'
anova(object, ..., refit = TRUE, model.names=NULL)
## S3 method for class 'merMod'
coef(object, ...)
## S3 method for class 'merMod'
deviance(object, REML = NULL, ...)
## S3 method for class 'merMod'
REMLcrit(object)
## S3 method for class 'merMod'
extractAIC(fit, scale = 0, k = 2, ...)
## S3 method for class 'merMod'
family(object, ...)
## S3 method for class 'merMod'
formula(x, fixed.only = FALSE, random.only = FALSE, ...)
## S3 method for class 'merMod'
fitted(object, ...)
## S3 method for class 'merMod'
logLik(object, REML = NULL, ...)
## S3 method for class 'merMod'
nobs(object, ...)
## S3 method for class 'merMod'
gngrps(object, ...)
## S3 method for class 'merMod'
terms(x, fixed.only = TRUE, random.only = FALSE, ...)
## S3 method for class 'merMod'
vcov(object, correlation = TRUE, sigm = sigma(object),
use.hessian = NULL, ...)
## S3 method for class 'merMod'
model.frame(formula, fixed.only = FALSE, ...)
## S3 method for class 'merMod'
model.matrix(object, type = c("fixed", "random", "randomListRaw"), ...)
## S3 method for class 'merMod'
print(x, digits = max(3, getOption("digits") - 3),
       correlation = NULL, symbolic.cor = FALSE,
       signif.stars = getOption("show.signif.stars"), ranef.comp = "Std.Dev.", ...)
```

```r
## S3 method for class 'merMod'
```
### Args

**object**
- An R object of class `merMod`, i.e., as resulting from `lmer()`, or `glmer()`, etc.

**x**
- An R object of class `merMod` or `summary.merMod`, respectively, the latter resulting from `summary(<merMod>)`.

**fit**
- An R object of class `merMod`.

**formula**
- In the case of `model.frame`, a `merMod` object.

**refit**
- Logical indicating if objects of class `lmerMod` should be refitted with ML before comparing models. The default is `TRUE` to prevent the common mistake of inappropriately comparing REML-fitted models with different fixed effects, whose likelihoods are not directly comparable.

**model.names**
- Character vectors of model names to be used in the anova table.

**scale**
- Not currently used (see `extractAIC`).

**k**
- See `extractAIC`.

**REML**
- Logical. If `TRUE`, return the restricted log-likelihood rather than the log-likelihood. If `NULL` (the default), set `REML` to `isREML(object)` (see `isREML`).

**fixed.only**
- Logical indicating if only the fixed effects components (terms or formula elements) are sought. If `false`, all components, including random ones, are returned.

**random.only**
- Complement of `fixed.only`; indicates whether random components only are sought. (Trying to specify `fixed.only` and `random.only` at the same time will produce an error.)

**correlation**
- (Logical) for vcov, indicates whether the correlation matrix as well as the variance-covariance matrix is desired; for `summary.merMod`, indicates whether the correlation matrix should be computed and stored along with the covariance; for `print.summary.merMod`, indicates whether the correlation matrix of the fixed-effects parameters should be printed. In the latter case, when `NULL` (the default), the correlation matrix is printed when it has been computed by `summary(.)`, and when \( p < 20 \).

**use.hessian**
- (Logical) indicates whether to use the finite-difference Hessian of the deviance function to compute standard errors of the fixed effects, rather estimating based on internal information about the inverse of the model matrix (see `getME(.,”RX”)`). The default is to use the Hessian whenever the fixed effect parameters are arguments to the deviance function (i.e. for GLMMs with `nAGQ>0`), and to use...
Objects from the Class

Objects of class merMod are created by calls to \texttt{lmer}, \texttt{glmer} or \texttt{nlmer}.

S3 methods

The following S3 methods with arguments given above exist (this list is currently not complete):

\texttt{anova}: returns the sequential decomposition of the contributions of fixed-effects terms or, for multiple arguments, model comparison statistics. For objects of class \texttt{merMod} the default behavior is to refit the models with LM if fitted with \texttt{REML = TRUE}, this can be controlled via the \texttt{refit} argument. See also \texttt{anova}.

\texttt{coef}: Computes the sum of the random and fixed effects coefficients for each explanatory variable for each level of each grouping factor.

\texttt{extractAIC}: Computes the (generalized) Akaike An Information Criterion. If isREML(fit), then fit is refitted using maximum likelihood.

\texttt{family}: \texttt{family} of fitted GLMM. (Warning: this accessor may not work properly with customized families/link functions.)

\texttt{fitted}: Fitted values, given the conditional modes of the random effects. For more flexible access to fitted values, use \texttt{predict.merMod}.
logLik: Log-likelihood at the fitted value of the parameters. Note that for GLMMs, the returned value is only proportional to the log probability density (or distribution) of the response variable. See logLik.

model.frame: returns the frame slot of merMod.

model.matrix: returns the fixed effects model matrix.

nobs, ngrps: Number of observations and vector of the numbers of levels in each grouping factor. See ngrps.

summary: Computes and returns a list of summary statistics of the fitted model, the amount of output can be controlled via the print method, see also summary.

print.summary: Controls the output for the summary method.

vcov: Calculate variance-covariance matrix of the fixed effect terms, see also vcov.

update: See update.

Deviance and log-likelihood of GLMMs

One must be careful when defining the deviance of a GLM. For example, should the deviance be defined as minus twice the log-likelihood or does it involve subtracting the deviance for a saturated model? To distinguish these two possibilities we refer to absolute deviance (minus twice the log-likelihood) and relative deviance (relative to a saturated model, e.g. Section 2.3.1 in McCullagh and Nelder 1989). With GLMMs however, there is an additional complication involving the distinction between the likelihood and the conditional likelihood. The latter is the likelihood obtained by conditioning on the estimates of the conditional modes of the spherical random effects coefficients, whereas the likelihood itself (i.e. the unconditional likelihood) involves integrating out these coefficients. The following table summarizes how to extract the various types of deviance for a glmerMod object:

<table>
<thead>
<tr>
<th></th>
<th>conditional</th>
<th>unconditional</th>
</tr>
</thead>
<tbody>
<tr>
<td>relative deviance</td>
<td>object@resp$aic()</td>
<td>NA in lme4</td>
</tr>
<tr>
<td>absolute deviance</td>
<td>-2*logLik(object)</td>
<td>-2*logLik(object)</td>
</tr>
</tbody>
</table>

This table requires two caveats:

- If the link function involves a scale parameter (e.g. Gamma) then object@resp$aic() - 2 * getME(object, "deviance") is required for the absolute-conditional case.
- If adaptive Gauss-Hermite quadrature is used, then logLik(object) is currently only proportional to the absolute-unconditional log-likelihood.

For more information about this topic see the misc/logLikGLMM directory in the package source.

Slots

resp: A reference class object for an lme4 response module (lmResp-class).

Gp: See getME.

call: The matched call.

frame: The model frame containing all of the variables required to parse the model formula.
See Also

lmer, glmer, nlmer, merPredD, lmerResp, glmResp, nlsResp

Other methods for merMod objects documented elsewhere include: fortify.merMod, drop1.merMod, isLMM.merMod, isGLMM.merMod, isNLMM.merMod, isREML.merMod, plot.merMod, predict.merMod, profile.merMod, ranef.merMod, refit.merMod, refitML.merMod, residuals.merMod, sigma.merMod, simulate.merMod, summary.merMod.

Examples

showClass("merMod")
methods(class="merMod")## over 30 (S3) methods available

## -> example(lmer) for an example of vcov.merMod()

---

**merPredD**

*Generator object for the merPredD class*

**Description**

The generator object for the merPredD reference class. Such an object is primarily used through its new method.

**Usage**

merPredD(...)  

**Arguments**

...  

List of arguments (see Note).
Note

`merPredD(...)` is a short form of `new("merPredD", ...)` to create a new `merPredD` object and the ... must be named arguments, `(X, Zt, Lambdat, Lind, theta, n):`

- **X**: dense model matrix for the fixed-effects parameters, to be stored in the `X` field.
- **Zt**: transpose of the sparse model matrix for the random effects. It is stored in the `Zt` field.
- **Lambdat**: transpose of the sparse lower triangular relative variance factor (stored in the `Lambdat` field).
- **Lind**: integer vector of the same length as the `x` slot in the `Lambdat` field. Its elements should be in the range 1 to the length of the `theta` field.
- **theta**: numeric vector of variance component parameters (stored in the `theta` field).
- **n**: sample size, usually `nrow(X)`.

See Also

The class definition, `merPredD`, also for examples.

merPredD-class  
Class "merPredD" - a Dense Predictor Reference Class

Description

A reference class (see mother class definition “envRefClass” for a mixed-effects model predictor module with a dense model matrix for the fixed-effects parameters. The reference class is associated with a C++ class of the same name. As is customary, the generator object, `merPredD`, for the class has the same name as the class.

Note

Objects from this reference class correspond to objects in a C++ class. Methods are invoked on the C++ class object using the external pointer in the `Ptr` field. When saving such an object the external pointer is converted to a null pointer, which is why there are redundant fields containing enough information as R objects to be able to regenerate the C++ object. The convention is that a field whose name begins with an upper-case letter is an R object and the corresponding field, whose name begins with the lower-case letter is a method. References to the external pointer should be through the method, not directly through the `Ptr` field.

See Also

`lmer`, `glmer`, `nlmer`, `merPredD`, `merMod`.

Examples

```r
showClass("merPredD")
pp <- slot(lmer(Yield ~ 1|Batch, Dyestuff), "pp")
stopifnot(is(pp, "merPredD"))
str(pp) # an overview of all fields and methods' names.
```
Description

From a merMod object create an R function that takes a single argument, which is the new parameter value, and returns the deviance.

Usage

mkdevfun(rho, nAGQ = 1L, maxit = 100, verbose = 0, control = list())

Arguments

rho an environment containing pp, a prediction module, typically of class merPredD and resp, a response module, e.g., of class lmerResp.

nAGQ scalar integer - the number of adaptive Gauss-Hermite quadrature points. A value of 0 indicates that both the fixed-effects parameters and the random effects are optimized by the iteratively reweighted least squares algorithm.

maxit scalar integer, currently only for GLMMs: the maximal number of Pwrss update iterations.

verbose scalar logical: print verbose output?

control list of control parameters, a subset of those specified by lmerControl (tolPwrss and compDev for GLMMs, tolPwrss for NLMMs)

Details

The function returned by mkdevfun evaluates the deviance of the model represented by the predictor module, pp, and the response module, resp.

For lmer model objects the argument of the resulting function is the variance component parameter, theta, with lower bound. For glmer or nlmer model objects with nAGQ = 0 the argument is also theta. However, when nAGQ > 0, the argument is c(theta, beta).

Value

A function of one numeric argument.

See Also

lmer, glmer and nlmer

Examples

(dd <- lmer(Yield ~ 1|Batch, Dyestuff, devFunOnly=TRUE))
dd(0.8)
minqa::bobyqa(1, dd, 0)
mkMerMod

Create a 'merMod' Object

Description

Create an object of (a subclass of) class merMod from the environment of the objective function and the value returned by the optimizer.

Usage

mkMerMod(rho, opt, reTrms, fr, mc, lme4conv = NULL)

Arguments

rho          the environment of the objective function
opt          the optimization result returned by the optimizer (a list: see lmerControl for required elements)
reTrms       random effects structure from the calling function (see mkReTrms for required elements)
fr           model frame (see model.frame)
mc           matched call from the calling function
lme4conv     lme4-specific convergence information (results of checkConv)

Value

an object from a class that inherits from merMod.

mkRespMod

Create an lmerResp, glmResp or nlsResp instance

Description

Create an lmerResp, glmResp or nlsResp instance

Usage

mkRespMod(fr, REML = NULL, family = NULL, nlenv = NULL, nlmod = NULL, ...)

Arguments

- fr: a model frame
- REML: logical scalar, value of REML for an lmerResp instance
- family: the optional glm family (glmResp only)
- nlenv: the nonlinear model evaluation environment (nlsResp only)
- nlmod: the nonlinear model function (nlsResp only)
- ...: where to look for response information if fr is missing. Can contain a model response, y, offset, offset, and weights, weights.

Value

- an lmerResp or glmResp or nlsResp instance

See Also

- Other utilities: findbars, mkReTrms, nlformula, nobars, subbars

Description

From the result of findbars applied to a model formula and the evaluation frame fr, create the model matrix Zt, etc, associated with the random-effects terms.

Usage

mkReTrms(bars, fr, drop.unused.levels=TRUE)

Arguments

- bars: a list of parsed random-effects terms
- fr: a model frame in which to evaluate these terms
- drop.unused.levels: (logical) drop unused factor levels? (experimental)

Value

- a list with components

  - Zt: transpose of the sparse model matrix for the random effects
  - theta: initial values of the covariance parameters
  - Lind: an integer vector of indices determining the mapping of the elements of the theta vector to the "x" slot of Lambdat
  - Gp
lower bounds on the covariance parameters
Lambdat transpose of the sparse relative covariance factor
flist list of grouping factors used in the random-effects terms
cnms a list of column names of the random effects according to the grouping factors
Ztlist list of components of the transpose of the random-effects model matrix, separated by random-effects term

See Also
Other utilities: findbars, mkRespMod, nlformula, nobars, subbars. getME can retrieve these components from a fitted model, although their values and/or forms may be slightly different in the final fitted model from their original values as returned from mkReTrms.

Examples
```
data("Pixel", package="nlme")
mform <- pixel ~ day + I(day^2) + (day | Dog) + (1 | Side/Dog)
(bar.f <- findbars(mform)) # list with 3 terms
mf <- model.frame(subbars(mform), data=Pixel)
rt <- mkReTrms(bar.f, mf)
names(rt)
```

mkSimulateTemplate Make templates suitable for guiding mixed model simulations

Description
Make data and parameter templates suitable for guiding mixed model simulations, by specifying a model formula and other information (EXPERIMENTAL). Most useful for simulating balanced designs and for getting started on unbalanced simulations.

Usage
```
mkParsTemplate(formula, data)
mkDataTemplate(formula, data, nGrps = 2, nPerGrp = 1, rfunc = NULL, ...)
```

Arguments
```
formula A mixed model formula (see lmer).
data A data frame containing the names in formula.
nGrps Number of levels of a grouping factor.
nPerGrp Number of observations per level.
rfunc Function for generating covariate data (e.g. rnorm).
... Additional parameters for rfunc.
```

See Also
These functions are designed to be used with simulate.merMod.
makVarCorr

Make Variance and Correlation Matrices from theta

Description
Make variance and correlation matrices from theta

Usage
makVarCorr(sc, cnms, nc, theta, nms)

Arguments
sc
scale factor (residual standard deviation).
cnms
component names.
nc
numeric vector: number of terms in each RE component.
theta
theta vector (lower-triangle of Cholesky factors).
nms
component names (FIXME: nms/cnms redundant: nms=names(cnms)?)

Value
A matrix

See Also
VarCorr

modular
Modular Functions for Mixed Model Fits

Description
Modular functions for mixed model fits

Usage
lFormula(formula, data = NULL, REML = TRUE, subset,
weights, na.action, offset, contrasts = NULL,
control = lmerControl(), ...)

mkLmerDevfun(fr, X, reTrms, REML = TRUE, start = NULL,
verbose = 0, control = lmerControl(), ...)

optimizeLmer(devfun,
optimizer = formals(lmerControl)$optimizer,
Arguments

- **formula**: a two-sided linear formula object describing both the fixed-effects and random-effects parts of the model, with the response on the left of a ~ operator and the terms, separated by + operators, on the right. Random-effects terms are distinguished by vertical bars ("|") separating expressions for design matrices from grouping factors.

- **data**: an optional data frame containing the variables named in formula. By default the variables are taken from the environment from which lmer is called. While data is optional, the package authors strongly recommend its use, especially when later applying methods such as update and drop1 to the fitted model (such methods are not guaranteed to work properly if data is omitted). If data is omitted, variables will be taken from the environment of formula (if specified as a formula) or from the parent frame (if specified as a character vector).

- **REML**: (logical) indicating to fit restricted maximum likelihood model.

- **subset**: an optional expression indicating the subset of the rows of data that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

- **weights**: an optional vector of ‘prior weights’ to be used in the fitting process. Should be NULL or a numeric vector.

- **na.action**: a function that indicates what should happen when the data contain NAs. The default action (na.omit, inherited from the 'factory fresh' value of getOption("na.action")) strips any observations with any missing values in any variables.

- **offset**: this can be used to specify an a priori known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more offset terms can be included in the
modular

formula instead or as well, and if more than one is specified their sum is used. See `model.offset`.

**contrasts**
an optional list. See the contrasts.arg of `model.matrix.default`.

**control**
a list giving

for `[g]lFormula`: all options for running the model, see `lmerControl`;
for `mkLmerDevFun`, `mkGlmerDevFun`: options for the inner optimization step;
for `optimizeLmer` and `optimizeGlmer`: control parameters for nonlinear optimizer (typically inherited from the ... argument to `lmerControl`).

**fr**
A model frame containing the variables needed to create an `lmerResp` or `glmResp` instance.

**X**
fixed-effects design matrix

**reTrms**
information on random effects structure (see `mkReTrms`).

**start**
starting values (see `lmer`)

**verbose**
print output?

**maxit**
maximal number of Pwrss update iterations.

**devfun**
a deviance function, as generated by `mkLmerDevFun`.

**nAGQ**
number of Gauss-Hermite quadrature points

**stage**
opimization stage (1: nAGQ=0, optimize over theta only; 2: nAGQ possibly >0, optimize over theta and beta)

**optimizer**
character - name of optimizing function(s). A character vector or list of functions: length 1 for `lmer` or `glmer`, possibly length 2 for `glmer`. The built-in optimizers are "Nelder_Mead" and "bobyqa" (from the `minqa` package). Any minimizing function that allows box constraints can be used provided that it

1. takes input parameters `fn` (function to be optimized), `par` (starting parameter values), `lower` (lower bounds) and `control` (control parameters, passed through from the `control` argument) and
2. returns a list with (at least) elements `par` (best-fit parameters), `fval` (best-fit function value), `conv` (convergence code) and (optionally) `message` (informational message, or explanation of convergence failure).

Special provisions are made for `bobyqa`, `Nelder_Mead`, and optimizers wrapped in the `optimx` package; to use `optimx` optimizers (including L-BFGS-B from base `optim` and `nlminb`), pass the `method` argument to `optim` in the `control` argument.

For `glmer`, if length(`optimizer`) == 2, the first element will be used for the preliminary (random effects parameters only) optimization, while the second will be used for the final (random effects plus fixed effect parameters) phase. See `modular` for more information on these two phases.

**restart_edge**
see `lmerControl`

**boundary.tol**
see `lmerControl`

**family**
a GLM family; see `glm` and `family`.

**mustart**
optional starting values on the scale of the conditional mean; see `glm` for details.
etastart optional starting values on the scale of the unbounded predictor; see glm for details.

... other potential arguments; for optimizeLmer and optimizeGlmer, these are passed to internal function optwrap, which has relevant parameters calc.derivs and use.last.params (see lmerControl).

Details

These functions make up the internal components of an [gn]lmer fit.

- [g]lFormula takes the arguments that would normally be passed to [g]lmer, checking for errors and processing the formula and data input to create a list of objects required to fit a mixed model.
- mk(Gl|L)merDevfun takes the output of the previous step (minus the formula component) and creates a deviance function
- optimize(Gl|L)mer takes a deviance function and optimizes over theta (or over theta and beta, if stage is set to 2 for optimizeGlmer
- updateGlmerDevfun takes the first stage of a GLMM optimization (with nAGQ=0, optimizing over theta only) and produces a second-stage deviance function
- mkMerMod takes the environment of a deviance function, the results of an optimization, a list of random-effect terms, a model frame, and a model all and produces a [g]lmerMod object.

Value

lFormula and glFormula return a list containing components:

fr model frame
X fixed-effect design matrix
reTrms list containing information on random effects structure: result of mkReTrms
REML (lFormula only): logical indicating if restricted maximum likelihood was used (Copy of argument.)

mkLmerDevfun and mkGlmerDevfun return a function to calculate deviance (or restricted deviance) as a function of the theta (random-effect) parameters. updateGlmerDevfun returns a function to calculate the deviance as a function of a concatenation of theta and beta (fixed-effect) parameters. These deviance functions have an environment containing objects required for their evaluation. CAUTION: The environment of functions returned by mk(Gl|L)merDevfun contains reference class objects (see ReferenceClasses, merPredD-class, lmResp-class), which behave in ways that may surprise many users. For example, if the output of mk(Gl|L)merDevfun is naively copied, then modifications to the original will also appear in the copy (and vice versa). To avoid this behavior one must make a deep copy (see ReferenceClasses for details).

optimizeLmer and optimizeGlmer return the results of an optimization.
Examples

### Fitting a linear mixed model in 4 modularized steps

#### 1. Parse the data and formula:

```r
lmod <- lFormula(Reaction ~ Days + (Days|Subject), sleepstudy)
names(lmod)
```

#### 2. Create the deviance function to be optimized:

```r
(devfun <- do.call(mklmerdevfun, lmod))
ls(environment(devfun)) # the environment of 'devfun' contains objects
# required for its evaluation
```

#### 3. Optimize the deviance function:

```r
opt <- optimizeLmer(devfun)
opt[1:3]
```

#### 4. Package up the results:

```r
mkMerMod(environment(devfun), opt, lmod$reTrms, fr = lmod$fr)
```

### Same model in one line

```r
lmer(Reaction ~ Days + (Days|Subject), sleepstudy)
```

### Fitting a generalized linear mixed model in six modularized steps

#### 1. Parse the data and formula:

```r
glmod <- glFormula(cbind(incidence, size - incidence) ~ period + (1 | herd),
data = cbpp, family = binomial)
names(glmod)
```

#### 2. Create the deviance function for optimizing over theta:

```r
(devfun <- do.call(mkGlmerDevfun, glmod))
ls(environment(devfun)) # the environment of devfun contains lots of info
```

#### 3. Optimize over theta using a rough approximation (i.e. nAGQ = 0):

```r
(opt <- optimizeGlmer(devfun))
```

#### 4. Update the deviance function for optimizing over theta and beta:

```r
(devfun <- updateGlmerDevfun(devfun, glmod$reTrms))
```

#### 5. Optimize over theta and beta:

```r
opt <- optimizeGlmer(devfun, stage=2)
opt[1:3]
```

#### 6. Package up the results:

```r
mkMerMod(environment(devfun), opt, glmod$reTrms, fr = glmod$fr)
```

### Same model in one line

```r
glmer(cbind(incidence, size - incidence) ~ period + (1 | herd),
data = cbpp, family = binomial)
```

---

**NelderMead**

*Nelder-Mead Optimization of Parameters, Possibly (Box) Constrained*

**Description**

Nelder-Mead optimization of parameters, allowing optimization subject to box constraints (contrary to the default, method = "Nelder-Mead", in R’s optim()), and using reverse communications.
Usage

Nelder_Mead(fn, par, lower = rep.int(-Inf, n), upper = rep.int(Inf, n),
control = list())

Arguments

fn a function of a single numeric vector argument returning a numeric scalar.
par numeric vector of starting values for the parameters.
lower numeric vector of lower bounds (elements may be -Inf).
upper numeric vector of upper bounds (elements may be Inf).
control a named list of control settings. Possible settings are

\textit{iprint} numeric scalar - frequency of printing evaluation information. Defaults
to 0 indicating no printing.
\textit{maxfun} numeric scalar - maximum number of function evaluations allowed
(default:10000).
\textit{FtolAbs} numeric scalar - absolute tolerance on change in function values (de-
fault: 1e-5)
\textit{FtolRel} numeric scalar - relative tolerance on change in function values (default:1e-
15)
\textit{XtolRel} numeric scalar - relative tolerance on change in parameter values (de-
fault: 1e-7)
\textit{MinMax} numeric scalar - maximum value of the minimum (default: .Ma-
chine$double.xmin)
\textit{xst} numeric vector of initial step sizes to establish the simplex - all elements
must be non-zero (default: rep(0.02,length(par)))
\textit{xt} numeric vector of tolerances on the parameters (default: xst*5e-4)
\textit{verbose} numeric value: 0=no printing, 1=print every 20 evaluations, 2=print
every 10 evalutions, 3=print every evaluation. Sets \textit{iprint}, if specified, but
does not override it.
\textit{warnOnly} a logical indicating if non-convergence (codes -1,-2,-3) should not
\textit{stop}(.), but rather only call \texttt{warning} and return a result which might in-
spected. Defaults to FALSE, i.e., stop on non-convergence.

Value

a \texttt{list} with components

\textit{fval} numeric scalar - the minimum function value achieved
\textit{par} numeric vector - the value of x providing the minimum
\textit{convergence} integer valued scalar, if not 0, an error code:
-4 nm_evals: maximum evaluations reached
-3 nm_forced: ?
-2 nm_nofeasible: cannot generate a feasible simplex
-1 nm_xnotfeasible: initial x is not feasible (?)
NelderMead-class

Class of Nelder-Mead optimizers and its Generator

Description

Class "NelderMead" is a reference class for a Nelder-Mead simplex optimizer allowing box constraints on the parameters and using reverse communication. The NelderMead() function conveniently generates such objects.

Usage

NelderMead(...)

Arguments

... Argument list (see Note below).

Methods

NelderMead$new(lower, upper, xst, x0, xt)

Create a new NelderMead object.

0 successful convergence

message a string specifying the kind of convergence.

control the list of control settings after substituting for defaults.

feval the number of function evaluations.

See Also

The NelderMead class definition and generator function.

Examples

fr <- function(x) {  # Rosenbrock Banana function
  x1 <- x[1]
  x2 <- x[2]
  100 * (x2 - x1 * x1)^2 + (1 - x1)^2
}

p0 <- c(-1.2, 1)

oo <- optim(p0, fr)  # also uses Nelder-Mead by default

o. <- Nelder_Mead(fr, p0)

o.1 <- Nelder_Mead(fr, p0, control=list(verb=1))  # some iteration output
  stopifnot(identical(o.[1:4], o.1[1:4]),
            all.equal(o.$par, oo$par, tolerance=1e-3))
  diff: 0.003865

o.2 <- Nelder_Mead(fr, p0, control=list(verb=3, XtolRel=1e-15, FtolAbs= 1e-14))

all.equal(o.2[-5], o.1[-5], tolerance=1e-15)  # TRUE, unexpectedly
Extends

All reference classes extend and inherit methods from "envRefClass".

Note

This is the default optimizer for the second stage of \texttt{glmer} and \texttt{nlmer} fits. We found that it was more reliable and often faster than more sophisticated optimizers.

Arguments to \texttt{NelderMead()} and the \texttt{new} method must be named arguments:

\begin{itemize}
  \item \texttt{lower} numeric vector of lower bounds - elements may be -\texttt{Inf}.
  \item \texttt{upper} numeric vector of upper bounds - elements may be \texttt{Inf}.
  \item \texttt{xst} numeric vector of initial step sizes to establish the simplex - all elements must be non-zero.
  \item \texttt{x0} numeric vector of starting values for the parameters.
  \item \texttt{xt} numeric vector of tolerances on the parameters.
\end{itemize}

References

Based on code in the NLopt collection.

See Also

\texttt{Nelder_Mead}, the typical “constructor”. Further, \texttt{glmer}, \texttt{nlmer}

Examples

\begin{verbatim}
showClass("NelderMead")
\end{verbatim}

---

\texttt{ngrps} \hspace{1cm} \textit{Number of Levels of a Factor or a "merMod" Model}

Description

Returns the number of levels of a \texttt{factor} or a set of factors, currently e.g., for each of the grouping factors of \texttt{lmer()}, \texttt{glmer()}, etc.

Usage

\begin{verbatim}
ngrps(object, ...)
\end{verbatim}

Arguments

\begin{itemize}
  \item \texttt{object} an R object, see Details.
  \item \texttt{...} currently ignored.
\end{itemize}
Details

Currently there are methods for objects of class `merMod`, i.e., the result of `lmer()` etc, and `factor` objects.

Value

The number of levels (of a factor) or vector of number of levels for each “grouping factor” of a

Examples

```r
ngrps(factor(seq(1,10,2)))
ngrps(lmer(Reaction ~ 1|Subject, sleepstudy))
```

### A named vector if there's more than one grouping factor :
```r
ngrps(lmer(strength ~ (1|batch/cask), Pastes))
```

```r
## cask:batch batch
## 30 10
```

`methods(ngrps) # -> "factor" and "merMod"

---

**nlformula**  
*Manipulate a Nonlinear Model Formula*

Description

Check and manipulate the formula for a nonlinear model, such as specified in `nlmer`.

Usage

```r
nlformula(mc)
```

Arguments

- `mc`  
  matched call from the calling function, typically `nlmer()`. Should have arguments named

  - **formula**: a formula of the form `resp ~ nlmod ~ meform` where `resp` is an expression for the response, `nlmod` is the nonlinear model expression and `meform` is the mixed-effects model formula. `resp` can be omitted when, e.g., optimizing a design.

  - **data**: a data frame in which to evaluate the model function

  - **start**: either a numeric vector containing initial estimates for the nonlinear model parameters or a list with components

    - `nlpars`: the initial estimates of the nonlinear model parameters

    - `theta`: the initial estimates of the variance component parameters
Details

The model formula for a nonlinear mixed-effects model is of the form \( \text{resp} \sim \text{nlmod} \sim \text{mixed} \) where \( \text{resp} \) is an expression (usually just a name) for the response, \( \text{nlmod} \) is the call to the nonlinear model function, and \( \text{mixed} \) is the mixed-effects formula defining the linear predictor for the parameter matrix. If the formula is to be used for optimizing designs, the \( \text{resp} \) part can be omitted.

Value

a list with components

- "respMod" a response module of class "nlsResp"
- "frame" the model frame, including a terms attribute
- "X" the fixed-effects model matrix
- "reTrms" the random-effects terms object

See Also

Other utilities: findbars, mkRespMod, mkReTrms, nobars, subbars

---

nlmer

Fitting Nonlinear Mixed-Effects Models

Description

Fit a nonlinear mixed-effects model (NLMM) to data, via maximum likelihood.

Usage

\[
\text{nlmer(formula, data = NULL, control = nlmerControl, start = NULL, verbose = 0L, nAGQ = 1L, subset, weights, na.action, offset, contrasts = NULL, devFunOnly = FALSE, ...)}
\]

Arguments

- formula a three-part “nonlinear mixed model” formula, of the form \( \text{resp} \sim \text{Nonlin}(\ldots) \sim \text{fixed} + \text{random} \), where the third part is similar to the RHS formula of, e.g., \text{lmer}.
- data an optional data frame containing the variables named in formula. By default the variables are taken from the environment from which \text{lmer} is called. While data is optional, the package authors strongly recommend its use, especially when later applying methods such as \text{update} and \text{drop1} to the fitted model (such methods are not guaranteed to work properly if data is omitted). If data is omitted, variables will be taken from the environment of formula (if specified as a formula) or from the parent frame (if specified as a character vector).
control a list (of correct class, resulting from `lmerControl()` or `glmerControl()` respectively) containing control parameters, including the nonlinear optimizer to be used and parameters to be passed through to the nonlinear optimizer, see the `lmerControl` documentation for details.

start starting estimates for the nonlinear model parameters, as a named numeric vector or as a list with components

- nlpars required numeric vector of starting values for the nonlinear model parameters
- theta optional numeric vector of starting values for the covariance parameters

verbose integer scalar. If > 0 verbose output is generated during the optimization of the parameter estimates. If > 1 verbose output is generated during the individual PIRLS steps.

nAGQ integer scalar - the number of points per axis for evaluating the adaptive Gauss-Hermite approximation to the log-likelihood. Defaults to 1, corresponding to the Laplace approximation. Values greater than 1 produce greater accuracy in the evaluation of the log-likelihood at the expense of speed. A value of zero uses a faster but less exact form of parameter estimation for GLMMs by optimizing the random effects and the fixed-effects coefficients in the penalized iteratively reweighted least squares step.

subset an optional expression indicating the subset of the rows of data that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.

weights an optional vector of ‘prior weights’ to be used in the fitting process. Should be `NULL` or a numeric vector.

na.action a function that indicates what should happen when the data contain `NA`s. The default action (`na.omit`, inherited from the ‘factory fresh’ value of `getOption("na.action")`) strips any observations with any missing values in any variables.

offset this can be used to specify an a priori known component to be included in the linear predictor during fitting. This should be `NULL` or a numeric vector of length equal to the number of cases. One or more offset terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See `model.offset`.

contrasts an optional `list`. See the contrasts.arg of `model.matrix.default`.

devFunOnly logical - return only the deviance evaluation function. Note that because the deviance function operates on variables stored in its environment, it may not return exactly the same values on subsequent calls (but the results should always be within machine tolerance).

... other potential arguments. A method argument was used in earlier versions of the package. Its functionality has been replaced by the nAGQ argument.

Details

Fit nonlinear mixed-effects models, such as those used in population pharmacokinetics.
**Note**

Adaptive Gauss-Hermite quadrature \( nAGQ>1 \) is not currently implemented for `nlmer`. Several other methods, such as simulation or prediction with new data, are unimplemented or very lightly tested.

**Examples**

```r
## nonlinear mixed models --- 3-part formulas ---
## 1. basic nonlinear fit. Use stats::SSlogis for its
## implementation of the 3-parameter logistic curve.
## "SS" stands for "self-starting logistic", but the
## "self-starting" part is not currently used by nlmer ... 'start' is
## necessary
startvec <- c(Asym = 200, xmid = 725, scal = 350)
(nml <- nlmer(circumference ~ SSlogis(age, Asym, xmid, scal) ~ Asym|Tree,
               Orange, start = startvec))
## 2. re-run with "quick and dirty" PIRLS step
(nmla <- update(nml, nAGQ = 0L))

## 3. Fit the same model with a user-built function:
## a. Define formula
nform <- ~Asym/(1+exp((xmid-input)/scal))
## b. Use deriv() to construct function:
nfun <- deriv(nform, namevec=c("Asym","xmid","scal"),
               function.arg=c("input","Asym","xmid","scal"))
(nmlb <- update(nml, circumference ~ nfun(age, Asym, xmid, scal) ~ Asym | Tree))

## 4. User-built function without using derivs():
## derivatives could be computed more efficiently
## by pre-computing components, but these are essentially
## the gradients as one would derive them by hand
nfun2 <- function(input, Asym, xmid, scal) {
  value <- Asym/(1+exp((xmid-input)/scal))
  grad <- cbind(Asym=1/(1+exp((xmid-input)/scal)),
               xmid=-Asym/(1+exp((xmid-input)/scal))*2*1/scal*
               exp((xmid-input)/scal),
               scal=-Asym/(1+exp((xmid-input)/scal))*2*
               -(xmid-input)/scal^2*exp((xmid-input)/scal))
  attr(value,"gradient") <- grad
  value
}
stopifnot(all.equal(attr(nfun(2,1,3,4),"gradient"),
                   attr(nfun(2,1,3,4),"gradient")))
nmlc <- update(nml, circumference ~ nfun2(age, Asym, xmid, scal) ~ Asym | Tree)
```

---

**nloptwrap**

*Wrappers for additional optimizers*
**Description**

Wrappers to allow use of alternative optimizers, from NLopt library or elsewhere, for nonlinear optimization stage

**Usage**

```r
nloptwrap(par, fn, lower, upper, control=list(),...)
nlminbwrap(par, fn, lower, upper, control=list(),...)
```

**Arguments**

- `par` starting parameter vector
- `fn` objective function
- `lower` vector of lower bounds
- `upper` vector of upper bounds
- `control` list of control parameters
- `...` additional arguments to be passed to objective function

**Details**

Using alternative optimizers is an important trouble-shooting tool for mixed models. These wrappers provide convenient access to the optimizers provided by Steven Johnson’s NLopt library (via the nloptr R package), and to the nlminb optimizer from base R. (nlminb is also available via the optimx package; this wrapper provides access to nlminb without the need to install/link the package, and without the additional post-fitting checks that are implemented by optimx (see examples below).

One important difference between the nloptr-provided implementation of BOBYQA and the minqa-provided version accessible via optimizer="bobyqa" is that it provides simpler access to optimization tolerances. minqa::bobyqa provides only the `rhoend` parameter ("[t]he smallest value of the trust region radius that is allowed"), while nloptr provides a more standard set of tolerances for relative or absolute change in the objective function or the parameter values (ftol_rel, ftol_abs, xtol_rel, xtol_abs).

**Value**

- `par` estimated parameters
- `fval` objective function value at minimum
- `feval` number of function evaluations
- `conv` convergence code (0 if no error)
- `message` convergence message

**Author(s)**

Gabor Grothendieck (nlminbwrap)
Examples

```r
environment(nloptwrap)$defaultControl
library(lme4)
fm1 <- lmer(Reaction+Days+(Days|Subject), sleepstudy)
## BOBYQA (default)
fm1_nloptr <- update(fm1, control=lmerControl(optimizer="nloptwrap"))
## Nelder-Mead
fm1_nloptr_NM <- update(fm1, control=lmerControl(optimizer="nloptwrap",
                         optCtrl=list(algorithm="NLOPT_LN_NELDERMEAD")))
## other nlopt algorithm options include NLOPT_LN_COBYLA, NLOPT_LN_SBPLX
fm1_nlminb <- update(fm1, control=lmerControl(optimizer="nlminbwrap"))
if (require(optimx)) {
  fm1_nlminb2 <- update(fm1, control=lmerControl(optimizer="optimx",
                                                  optCtrl=list(method="nlminb", kkt=FALSE)))
}
```

**Description**

Omit terms separated by vertical bars in a formula

**Usage**

```
nobars(term)
```

**Arguments**

- `term` the right-hand side of a mixed-model formula

**Value**

the fixed-effects part of the formula

**Note**

This function is called recursively on individual terms in the model, which is why the argument is called `term` and not a name like `form`, indicating a formula.

**See Also**

`formula, model.frame, model.matrix`

Other utilities: `findbars, mkRespMod, mkReTrms, nlformula, subbars`

**Examples**

```
nobars(Reaction ~ Days + (Days|Subject)) ## => Reaction ~ Days
```
Pastes

Paste strength by batch and cask

Description

Strength of a chemical paste product; its quality depending on the delivery batch, and the cask within the delivery.

Format

A data frame with 60 observations on the following 4 variables.

- **strength**: paste strength.
- **batch**: delivery batch from which the sample was sample. A factor with 10 levels: ‘A’ to ‘J’.
- **cask**: cask within the delivery batch from which the sample was chosen. A factor with 3 levels: ‘a’ to ‘c’.
- **sample**: the sample of paste whose strength was assayed, two assays per sample. A factor with 30 levels: ‘A:a’ to ‘J:c’.

Details

The data are described in Davies and Goldsmith (1972) as coming from “deliveries of a chemical paste product contained in casks where, in addition to sampling and testing errors, there are variations in quality between deliveries ... As a routine, three casks selected at random from each delivery were sampled and the samples were kept for reference. ... Ten of the delivery batches were sampled at random and two analytical tests carried out on each of the 30 samples”.

Source

O.L. Davies and P.L. Goldsmith (eds), *Statistical Methods in Research and Production, 4th ed.*, Oliver and Boyd, (1972), section 6.5

Examples

```r
str(Pastes)
require(lattice)
dotplot(cask ~ strength | reorder(batch, strength), Pastes,
       strip = FALSE, strip.left = TRUE, layout = c(1, 10),
       ylab = "Cask within batch",
       xlab = "Paste strength", jitter.y = TRUE)
## Modifying the factors to enhance the plot
Pastes <- within(Pastes, batch <- reorder(batch, strength))
Pastes <- within(Pastes, sample <- reorder(sample, strength),
                 as.numeric(batch)))
dotplot(sample ~ strength | batch, Pastes,
        strip = FALSE, strip.left = TRUE, layout = c(1, 10),
        scales = list(y = list(relation = "free")),
        ylab = "Sample within batch")
```
Penicillin

Variation in penicillin testing

Description

Six samples of penicillin were tested using the *B. subtilis* plate method on each of 24 plates. The response is the diameter (mm) of the zone of inhibition of growth of the organism.

Format

A data frame with 144 observations on the following 3 variables.

- **diameter**: diameter (mm) of the zone of inhibition of the growth of the organism.
- **plate**: assay plate. A factor with levels ‘a’ to ‘x’.
- **sample**: penicillin sample. A factor with levels ‘A’ to ‘F’.

Details

The data are described in Davies and Goldsmith (1972) as coming from an investigation to “assess the variability between samples of penicillin by the *B. subtilis* method. In this test method a bulk-inoculated nutrient agar medium is poured into a Petri dish of approximately 90 mm. diameter, known as a plate. When the medium has set, six small hollow cylinders or pots (about 4 mm. in diameter) are cemented onto the surface at equally spaced intervals. A few drops of the penicillin solutions to be compared are placed in the respective cylinders, and the whole plate is placed in an incubator for a given time. Penicillin diffuses from the pots into the agar, and this produces a clear circular zone of inhibition of growth of the organisms, which can be readily measured. The diameter of the zone is related in a known way to the concentration of penicillin in the solution.”

Source

O.L. Davies and P.L. Goldsmith (eds), *Statistical Methods in Research and Production, 4th ed.*, Oliver and Boyd, (1972), section 6.6
Examples

str(Penicillin)
require(lattice)
dotplot(reorder(plate, diameter) ~ diameter, Penicillin, groups = sample,
ylab = "Plate", xlab = "Diameter of growth inhibition zone (mm)",
type = c("p", "a"), auto.key = list(columns = 3, lines = TRUE,
title = "Penicillin sample")
(fm1 <- lmer(diameter ~ (1|plate) + (1|sample), Penicillin))

L <- getME(fm1, "L")
Matrix::image(L, main = "L",
sub = "Penicillin: Structure of random effects interaction")

plot.lmList4 plots for lmList4 objects

Description
diagnostic and confidence-interval plots for lmList fits

Usage

## S3 method for class 'lmList4'
plot(x, form, abline, id, idLabels, grid, ...)
## S3 method for class 'lmList4.confint'
plot(x, y, order, ...)
1 − value/2 quantile of the standard normal distribution are identified in the plot using idLabels. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.

idLabels: an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the observations identified according to id. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified observations. Default is getGroups(x).

grid: an optional logical value indicating whether a grid should be added to plot. Default depends on the type of Trellis plot used: if xyplot defaults to TRUE, else defaults to FALSE.

order: which coefficient to order the results by

...: optional arguments passed to the Trellis plot function.

Details

The plot method for lmlist objects is copied from that for lmList objects; see plot.lmList for details.

Author(s)

Original versions in nlme package by Jose Pinheiro and Douglas Bates

Examples

fm.plm <- lmList(Reaction ~ Days | Subject, sleepstudy)
## diagnostic plot: standardized residuals vs. fitted
plot(fm.plm, id=0.05)
ci <- confint(fm.plm)
## plot CIs, ordered by slope (coefficient 2)
plot(ci, order=2, ylab="Subject")

plot.merMod: diagnostic plots for merMod fits

diagnostic plots for merMod fits

Usage

## S3 method for class 'merMod'
plot(x,  
form = resid(. , type = "pearson") ~ fitted(. ), abline,  
id = NULL, idLabels = NULL, grid, ...)
## S3 method for class 'merMod'
qqmath( x, id = NULL, idLabels = NULL, ...)

plot.merMod
Arguments

\texttt{x} \quad \text{a fitted [nl]mer model}

\texttt{form} \quad \text{an optional formula specifying the desired type of plot. Any variable present in the original data frame used to obtain x can be referenced. In addition, x itself can be referenced in the formula using the symbol \".\". Conditional expressions on the right of a | operator can be used to define separate panels in a lattice display. Default is resid(., type = "pearson") ~ fitted(.), corresponding to a plot of the standardized residuals versus fitted values.}

\texttt{abline} \quad \text{an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.}

\texttt{id} \quad \text{an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized, or normalized residuals. Observations with absolute standardized (normalized) residuals greater than the 1 − value/2 quantile of the standard normal distribution are identified in the plot using \texttt{idlabels}. If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.}

\texttt{idLabels} \quad \text{an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the observations identified according to \texttt{id}. If given as a vector, it is converted to character and used to label the observations identified according to \texttt{id}. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified observations. Default is the interaction of all the grouping variables in the data frame. The special formula \texttt{idLabels =~ obs} will label the observations according to observation number.}

\texttt{grid} \quad \text{an optional logical value indicating whether a grid should be added to plot. Default depends on the type of lattice plot used: if \texttt{xypplot} defaults to \texttt{TRUE}, else defaults to \texttt{FALSE}.}

... \quad \text{optional arguments passed to the lattice plot function.}

Details

Diagnostic plots for the linear mixed-effects fit are obtained. The \texttt{form} argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a | operator) always implies that different panels are used for each level of the conditioning factor, according to a lattice display. If \texttt{form} is a one-sided formula, histograms of the variable on the right hand side of the formula, before a | operator, are displayed (the lattice function \texttt{histogram} is used). If \texttt{form} is two-sided and both its left and right hand side variables are numeric, scatter plots are displayed (the lattice function \texttt{xypplot} is used). Finally, if \texttt{form} is two-sided and its left had side variable is a factor, box-plots of the right hand side variable by the levels of the left hand side variable are displayed (the lattice function \texttt{bwplot} is used).

\texttt{qqmath} produces a Q-Q plot of the residuals (see \texttt{link\{qqmath\ranef\mer\}} for Q-Q plots of the conditional mode values).
**Author(s)**

original version in nlme package by Jose Pinheiro and Douglas Bates

**Examples**

```r
data(Orthodont, package="nlme")
fm1 <- lmer(distance ~ age + (age|Subject), data=Orthodont)
## standardized residuals versus fitted values by gender
plot(fm1, resid(.), scaled=TRUE) ~ fitted(.) | Sex, abline = 0)
## box-plots of residuals by Subject
plot(fm1, Subject ~ resid(.), scaled=TRUE))
## observed versus fitted values by Subject
plot(fm1, distance ~ fitted(.) | Subject, abline = c(0,1))
## residuals by age, separated by Subject
plot(fm1, resid(.), scaled=TRUE) ~ age | Sex, abline = 0)
require("lattice")
qqmath(fm1, id=0.05)
if (require("ggplot2") {  
  ## we can create the same plots using ggplot2 and the fortify() function
  fmIf <- fortify(fm1)
  ggplot(fmIf, aes(.fitted,.resid)) + geom_point(colour="blue") +
  facet_grid(.~Sex) + geom_hline(yintercept=0)
  ## note: Subjects are ordered by mean distance
  ggplot(fmIf, aes(Subject,.resid)) + geom_boxplot() + coord_flip()
  ggplot(fmIf, aes(.fitted,distance)) + geom_point(colour="blue") +
  facet_wrap(~Subject) + geom_abline(intercept=0,slope=1)
  ggplot(fmIf, aes(age,.resid)) + geom_point(colour="blue") + facet_grid(.~Sex) +
  geom_hline(yintercept=0)+geom_line(aes(group=Subject),alpha=0.4)+geom_smooth(method="loess")
  ## (warnings about loess are due to having only 4 unique x values)
  detach("package:ggplot2")
}
```

---

**Mixed-Effects Profile Plots (Regular / Density / Pairs)**

**Description**

Xyplot, Densityplot, and Pairs plot methods for a mixed-effects model profile.

- `xyplot()` draws “zeta diagrams”, also visualizing confidence intervals and their asymmetry.
- `densityplot()` draws the profile densities.
- `splom()` draws profile pairs plots. Contours are for the marginal two-dimensional regions (i.e. using df = 2).

**Usage**

```r
## S3 method for class 'thpr'
xyplot(x, data = NULL,  
  levels = sqrt(qchisq(pmax.int(0, pmin.int(1, conf)), df = 1)),
```
conf = c(50, 80, 90, 95, 99)/100,
absVal = FALSE, scales=NULL,
which = 1:nptot, ...)

## S3 method for class 'thpr'
densityplot(x, data, ...)

## S3 method for class 'thpr'
splom(x, data,
  levels = sqrt(qchisq(pmax.int(0, pmin.int(1, conf)), 2)),
  conf = c(50, 80, 90, 95, 99)/100, which = 1:nptot,
  draw.lower = TRUE, draw.upper = TRUE, ...)

Arguments

- **x**: a mixed-effects profile, i.e., of class "thpr", typically resulting from `profile(fm)` where `fm` is a fitted model from `lmer` (or its generalizations).
- **data**: unused - only for compatibility with generic.
- **levels**: the contour levels to be shown; usually derived from `conf`.
- **conf**: numeric vector of confidence levels to be shown as contours.
- **absVal**: logical indicating if `abs()`olute values should be plotted, often preferred for confidence interval visualization.
- **scales**: plotting options to be passed to `xyplot`
- **which**: integer or character vector indicating which parameters to profile: default is all parameters (see `profile-methods` for details).
- **draw.lower** (logical) draw lower-triangle (zeta scale) panels?
- **draw.upper** (logical) draw upper-triangle (standard dev/cor scale) panels?
- **...**: further arguments passed to `xyplot`, `densityplot`, or `splom` from package `lattice`, respectively.

Value

- **xyplot**: a density plot, a "trellis" object (`lattice` package) which when `print()`ed produces plots on the current graphic device.
- **densityplot**: a density plot, a "trellis" object, see above.
- **splom**: a pairs plot, aka `scatterplot` matrix, a "trellis" object, see above.

See Also

- `profile`, notably for an example.

Examples

## see example("profile.merMod")
predict.merMod

Predictions from a model at new data values

Description

The predict method for merMod objects, i.e. results of lmer(), glmer(), etc.

Usage

## S3 method for class 'merMod'
predict(object, newdata = NULL, newparams = NULL,
re.form = NULL, ReForm, REform, REform, terms = NULL,
type = c("link", "response"), allow.new.levels = FALSE,
na.action = na.pass, ...)

Arguments

object a fitted model object
newdata data frame of for which to evaluate predictions.
newparams new parameters to use in evaluating predictions, specified as in the start parameter for lmer or glmer – a list with components theta and/or (for GLMMs) beta.
re.form formula for random effects to condition on. If NULL, include all random effects; if NA or ~0, include no random effects
ReForm, REform allowed for backward compatibility: re.form is now the preferred argument name.
terms a terms object - unused at present.
type character string - either "link", the default, or "response" indicating the type of prediction object returned.
allow.new.levels logical if new levels (or NA values) in newdata are allowed. If FALSE (default), such new values in newdata will trigger an error; if TRUE, then the prediction will use the unconditional (population-level) values for data with previously unobserved levels (or NAs).
na.action function determining what should be done with missing values for fixed effects in newdata. The default is to predict NA: see na.pass.
...

Value

a numeric vector of predicted values
Note

There is no option for computing standard errors of predictions because it is difficult to define an efficient method that incorporates uncertainty in the variance parameters; we recommend bootMer for this task.

Examples

```r
(gm1 <- glmer(cbind(incidence, size - incidence) ~ period + (1 | herd), cbpp, binomial))
str(p0 <- predict(gm1))  # fitted values
str(p1 <- predict(gm1, re.form=NA))  # fitted values, unconditional (level-0)
newdata <- with(cbpp, expand.grid(period=unique(period), herd=unique(herd)))
str(p2 <- predict(gm1, newdata))  # new data, all RE
str(p3 <- predict(gm1, newdata, re.form=NA))  # new data, level-0
str(p4 <- predict(gm1, newdata, re.form= ~(1|herd)))  # explicitly specify RE
stopifnot(identical(p2, p4))
```

### profile-methods

**Profile method for merMod objects**

**Description**

Methods for `profile()` of `lmer` fitted models.

The `log()` method and the more flexible `logProf()` utility transform a lmer profile into one where logarithms of standard deviations are used; see Details.

**Usage**

```
## S3 method for class 'merMod'
profile(fitted, which = NULL, alphamax = 0.01,
        maxpts = 100, delta = NULL,
        delta.cutoff = 1/8, verbose = 0, devtol = 1e-09,
        maxmult = 10, startmethod = "prev", optimizer = NULL,
        control=NULL, signames = TRUE,
        parallel = c("no", " multicore", "snow"),
        ncpus =getOption("profile.ncpus", 1L), cl = NULL, ...)
## S3 method for class 'thpr'
as.data.frame(x, ...)
## S3 method for class 'thpr'
log(x, base = exp(1))
logProf(x, base = exp(1), ranef = TRUE,
        sigIni = if(ranef) "sig" else "sigma")
```
Arguments

fitted  a fitted model, e.g., the result of `lmer()`.
which  NULL value, integer or character vector indicating which parameters to profile: default (NULL) is all parameters. For integer, i.e., indexing, the parameters are ordered as follows:
(1) random effects (theta) parameters; these are ordered as in `getME(., "theta")`, i.e., as the lower triangle of a matrix with standard deviations on the diagonal and correlations off the diagonal.
(2) residual standard deviation (or scale parameter for GLMMs where appropriate).
(3) fixed effect (beta) parameters.
Alternatively, which may be a character, containing "beta_" or "theta_" denoting the fixed or random effects parameters, respectively, or also containing parameter names, such as ".sigma" or "(Intercept)".
alphamax  a number in (0, 1), such that 1 - alphamax is the maximum alpha value for likelihood ratio confidence regions; used to establish the range of values to be profiled.
maxpts  maximum number of points (in each direction, for each parameter) to evaluate in attempting to construct the profile.
delta  stepping scale for deciding on next point to profile. The code uses the local derivative of the profile at the current step to establish a change in the focal parameter that will lead to a step of delta on the square-root-deviance scale. If NULL, the delta.cutoff parameter will be used to determine the stepping scale.
delta.cutoff  stepping scale (see delta) expressed as a fraction of the target maximum value of the profile on the square-root-deviance scale. Thus a delta.cutoff setting of 1/n will lead to a profile with approximately 2*n calculated points for each parameter (i.e., n points in each direction, below and above the estimate for each parameter).
verbose  level of output from internal calculations.
devtol  tolerance for fitted deviances less than baseline (supposedly minimum) deviance.
maxmult  maximum multiplier of the original step size allowed, defaults to 10.
startmethod  method for picking starting conditions for optimization (STUB).
optimizer  (character or function) optimizer to use (see lmer for details); default is to use the optimizer from the original model fit.
control  a list of options controlling the profiling (see lmerControl): default is to use the control settings from the original model fit.
signames  logical indicating if abbreviated names of the form .sigNN should be used; otherwise, names are more meaningful (but longer) of the form (sd|cor)_(effects)|(group). Note that some code for profile transformations (e.g., log() or varianceProf) depends on signames==TRUE.
...  potential further arguments for various methods.
x  an object of class thpr (i.e., output of profile)
base  the base of the logarithm. Defaults to natural logarithms.
<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>ranef</code></td>
<td>logical indicating if the sigmas of the random effects should be log() transformed as well. If false, only $\sigma$ (standard deviation of errors) is transformed.</td>
</tr>
<tr>
<td><code>sigIni</code></td>
<td>character string specifying the initial part of the sigma parameters to be log transformed.</td>
</tr>
<tr>
<td><code>parallel</code></td>
<td>The type of parallel operation to be used (if any). If missing, the default is taken from the option &quot;profile.parallel&quot; (and if that is not set, &quot;no&quot;).</td>
</tr>
<tr>
<td><code>ncpus</code></td>
<td>integer: number of processes to be used in parallel operation: typically one would choose this to be the number of available CPUs.</td>
</tr>
<tr>
<td><code>cl</code></td>
<td>An optional parallel or snow cluster for use if parallel = &quot;snow&quot;. If not supplied, a cluster on the local machine is created for the duration of the profile call.</td>
</tr>
</tbody>
</table>

**Details**

The log method and the more flexible logProf() function transform the profile into one where $\log(\sigma)$ is used instead of $\sigma$. By default all sigmas including the standard deviations of the random effects are transformed i.e., the methods return a profile with all of the .sigNN parameters replaced by .lsigNN. If ranef is false, only ".sigma", the standard deviation of the errors, is transformed (as it should never be zero, whereas random effect standard deviations (.sigNN) can be reasonably be zero).

The forward and backward splines for the log-transformed parameters are recalculated.

Methods for function profile (package stats), here for profiling (fitted) mixed effect models.

**Value**

profile(merMod) returns an object of S3 class "thpr", which is data.frame-like. Notable methods for such a profile object confint(), which returns the confidence intervals based on the profile, and three plotting methods (which require the lattice package), xyplot, densityplot, and splom.

In addition, the log() (see above) and as.data.frame() methods can transform "thpr" objects in useful ways.

**See Also**

The plotting methods xyplot etc, for class "thpr"; varianceProf for transformation (from st.dev.) to variance scale.

For (more expensive) alternative confidence intervals: bootMer.

**Examples**

```r
fm01ML <- lmer(Yield ~ 1|Batch, Dyestuff, REML = FALSE)
system.time(
  tpr <- profile(fm01ML, optimizer="Nelder_Mead", which="beta_")
)# fast; as only *one* beta parameter is profiled over
## full profiling (default which means 'all) needs
## ~2.6s (on a 2010 Macbook Pro)
system.time( tpr <- profile(fm01ML))
## ~1s, + possible warning about bobyqa convergence
```
(confint(tpr) -> CIpr)

stopifnot(all.equal(unname(CIpr),
array(c(12.1985292, 38.2299848, 1486.4515,
84.0630513, 67.6576964, 1568.54849), dim = 3:2),
tol= 1e-07))# 1.37e-9 (64b)

library("lattice")
xyplot(tpr)

xyplot(tpr, absVal=TRUE) # easier to see conf.int.s (and check symmetry)
xyplot(tpr, conf = c(0.95, 0.99), # (instead of all five 50, 80,...)
      main = "95% and 99% profile() intervals")

xyplot(logProf(tpr, ranef=FALSE),
      main = expression("lmer profile()s"~~ log(sigma)x" (only log())")

densityplot(tpr, main="densityplot( profile(lmer(..)) )")

densityplot(varianceProf(tpr), main=" varianceProf( profile(lmer(..)) )")

splom(tpr)
splom(logProf(tpr, ranef=FALSE))
doMore <- !me4::testLevel() > 1

if(doMore) { # not typically, for time constraint reasons
  ## Batch and residual variance only
  system.time(tpr2 <- profile(fm01ML, which=1:2, optimizer="Nelder_Mead")
  print( xyplot(tpr2) )
  print( xyplot(log(tpr2)) ) # log(sigma) is better
  print( xyplot(logProf(tpr2, ranef=FALSE)) )

  ## GLMM example
gm1 <- glmer(cbind(incidence, size ~ incidence) ~ period + (1 | herd),
            data = cbpp, family = binomial)

  ## running ~ 10-12 seconds on a modern machine (-> "verbose" while you wait):
  print( system.time(pr4 <- profile(gm1, verbose=TRUE)) )
  print( xyplot(pr4, layout=c(5,1), as.table=TRUE) )
  print( xyplot(log(pr4), absVal=TRUE) ) # log(sigma_1)
  print( splom(pr4) )
  print( system.time( # quicker: only sig01 and one fixed effect
                     pr2 <- profile(gm1, which=c("theta_{1}"), "period2")))
  print( confint(pr2) )

  ## delta... higher underlying resolution, only for 'sigma_1':
  print( system.time(
                     pr4.hr <- profile(gm1, which="theta_{1}", delta.cutoff=1/16))
  print( xyplot(pr4.hr) )
}

---

**prt-utilities**

*Print and Summary Method Utilities for Mixed Effects*

**Description**

The `print`, `summary` methods (including the `print` for the `summary()` result) in `lme4` are modular, using about ten small utility functions. Other packages, building on `lme4` can use the same utilities for ease of programming and consistency of output.
Notably see the Examples.

`likAIC()` extracts the log likelihood, AIC, and related statics from a Fitted LMM.

`formatVC()` “format()”s the `VarCorr` matrix of the random effects – for `print()`ing and `show()`ing; it is also the “workhorse” of .prt.VC(), and returns a character matrix.

`.prt.*()` all use `cat` and `print` to produce output.

**Usage**

```r
likAIC(object, devianceFUN = devCrit, chkREML = TRUE,
       devcomp = object@devcomp)
```

```r
methTitle(dims)
```

```r
.prt.methTit(mt, class)
.prt.family (famL)
.prt.resids (resids, digits, title = "Scaled residuals: ", ...)  
.prt.call (call, long = TRUE)
.prt.aictab (aictab, digits = 1)
.prt.grps (ngrps, nobs)
.prt.warn (optinfo, summary = FALSE, ...)
```

```r
.prt.VC (varcor, digits, comp, formatter = format, ...)
formatVC(varcor, digits = max(3, getOption("digits") - 2),
        comp = "Std. Dev.", formatter = format,
        useScale = attr(varcor, "useSc"), ...)
```

**Arguments**

- `object` a LMM model fit
- `devianceFUN` the function to be used for computing the deviance; should not be changed for `lme4` created objects.
- `chkREML` optional logical indicating if object maybe a REML fit.
- `devcomp` for `lme4` always the equivalent of `object@devcomp`; here a list
- `dims` for `lme4` always the equivalent of `object@devcomp$dims`, a named vector or list with components "GLMM", "NLMM", "REML", and "nAGQ" of which the first two are logical scalars, and the latter two typically are FALSE or numeric.
- `mtit` the result of `methTitle(object)`
- `class` typically `class(object)`.
- `famL` a list with components family and link, each a character string; note that standard R family objects can be used directly, as well.
- `resids` numeric vector of model `residuals`
- `digits` non-negative integer of (significant) digits to print minimally.
- `title` character string.
- `...` optional arguments passed on, e.g., to `residuals()`.
call the call of the model fit; e.g., available via (generic) function `getCall()`.

long logical indicating if the output may be long, e.g., printing the control part of the call if there is one.

aictab typically the AICtab component of the result of `llikAIC()`.

varcor typically the result of `VarCorr()`.

comp optional ...

formatter a function used for formatting the numbers.

ngrps integer (vector), typically the result of `ngrps(object)`.

nobs integer; the number of observations, e.g., the result of `nobs`.

optinfo typically object @ optinfo, the optimization infos, including warnings if there were.

summary logical

useScale (logical) whether the parent model estimates a scale parameter

Value

`llikAIC()` returns a list with components

- `logLik` which is `logLik(object)`, and
- `AICtab` a “table” of `AIC, BIC, logLik, deviance` and `df.residual()` values.

Examples

```r
## Create a few "lme4 standard" models -----------------------------
fm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
fmM <- update(fm1, REML=FALSE) # -> Maximum Likelihood

gm1 <- glmer(glmcbind(incidence, size ~ incidence) ~ period + (1 | herd),
data = cbpp, family = binomial)
gmA <- update(gm1, nAGQ = 5)

(lA1 <- llikAIC(fm1))
(lAM <- llikAIC(fmM))
(lAg <- llikAIC(gmA))

(m1 <- methTitle(fm1 @ devcomp $ dims))
(mM <- methTitle(fmM @ devcomp $ dims))
(mG <- methTitle(gm1 @ devcomp $ dims))
(mA <- methTitle(gmA @ devcomp $ dims))

.prt.methTit(m1, class(fm1))
.prt.methTit(mA, class(gmA))

.prt.family(gaussian())
.prt.family(binomial())
.prt.family(poisson())
```
pvalues

Getting p-values for fitted models

Description

One of the most frequently asked questions about lme4 is "how do I calculate p-values for estimated parameters?" Previous versions of lme4 provided the mcmcsamp function, which efficiently generated a Markov chain Monte Carlo sample from the posterior distribution of the parameters, assuming flat (scaled likelihood) priors. Due to difficulty in constructing a version of mcmcsamp that was reliable even in cases where the estimated random effect variances were near zero (e.g. https://stat.ethz.ch/pipermail/r-sig-mixed-models/2009q4/003115.html), mcmcsamp has been withdrawn (or more precisely, not updated to work with lme4 versions >=1.0.0).

Many users, including users of the aovlmer.fnc function from the languageR package which relies on mcmcsamp, will be deeply disappointed by this lacuna. Users who need p-values have a variety of options. In the list below, the methods marked MC provide explicit model comparisons; CI denotes confidence intervals; and P denotes parameter-level or sequential tests of all effects in a model. The starred (*) suggestions provide finite-size corrections (important when the number of groups is <50); those marked (+) support GLMMs as well as LMMs.
- likelihood ratio tests via anova or drop1 (MC, +)
- profile confidence intervals via `profile.merMod` and `confint.merMod` (CI, +)
- parametric bootstrap confidence intervals and model comparisons via `bootMer` (or PBmodcomp in the pbkrtest package) (MC/CI, *+, +)
- for random effects, simulation tests via the RLRsim package (MC, *)
- for fixed effects, F tests via Kenward-Roger approximation using `krmodcomp` from the pbkrtest package (MC, *)
- `car::Anova` and `lmerTest::anova` provide wrappers for Kenward-Roger-corrected tests using pbkrtest. `lmerTest::anova` also provides t tests via the Satterthwaite approximation (P, *)
- `afex::mixed` is another wrapper for pbkrtest and anova providing "Type 3" tests of all effects (P, *+, +)

`arm::sim`, or `bootMer`, can be used to compute confidence intervals on predictions.

For glmer models, the summary output provides p-values based on asymptotic Wald tests (P); while this is standard practice for generalized linear models, these tests make assumptions both about the shape of the log-likelihood surface and about the accuracy of a chi-squared approximation to differences in log-likelihoods.

When all else fails, don’t forget to keep p-values in perspective: http://www.phdcomics.com/comics/archive.php?comicid=905

---

**ranef**

*Extract the modes of the random effects*

---

**Description**

A generic function to extract the conditional modes of the random effects from a fitted model object. For linear mixed models the conditional modes of the random effects are also the conditional means.

**Usage**

```r
## S3 method for class 'merMod'
ranef(object, condVar = FALSE,
       drop = FALSE, whichel = names(ans), postVar=FALSE, ...)

## S3 method for class 'ranef.mer'
dotplot(x, data, main=TRUE, ...)
## S3 method for class 'ranef.mer'
qqmath(x, data, main=TRUE, ...)
```

**Arguments**

- `object` an object of a class of fitted models with random effects, typically a `merMod` object.
- `condVar` an optional logical argument indicating if the conditional variance-covariance matrices of the random effects should be added as an attribute.
drop should components of the return value that would be data frames with a single column, usually a column called ‘(Intercept)’, be returned as named vectors instead?

whichel character vector of names of grouping factors for which the random effects should be returned.

postVar a (deprecated) synonym for condVar

x a random-effects object (of class ranef.mer) produced by ranef

main include a main title, indicating the grouping factor, on each sub-plot?

data This argument is required by the dotplot and qqmath generic methods, but is not actually used.

... some methods for these generic functions require additional arguments.

Details

If grouping factor i has k levels and j random effects per level the ith component of the list returned by ranef is a data frame with k rows and j columns. If condVar is TRUE the "postVar" attribute is an array of dimension j by j by k. The kth face of this array is a positive definite symmetric j by j matrix. If there is only one grouping factor in the model the variance-covariance matrix for the entire random effects vector, conditional on the estimates of the model parameters and on the data will be block diagonal and this j by j matrix is the kth diagonal block. With multiple grouping factors the faces of the "postVar" attributes are still the diagonal blocks of this conditional variance-covariance matrix but the matrix itself is no longer block diagonal.

Value

An object of class ranef.mer composed of a list of data frames, one for each grouping factor for the random effects. The number of rows in the data frame is the number of levels of the grouping factor. The number of columns is the dimension of the random effect associated with each level of the factor.

If condVar is TRUE each of the data frames has an attribute called "postVar" which is a three-dimensional array with symmetric faces; each face contains the variance-covariance matrix for a particular level of the grouping factor. (The name of this attribute is a historical artifact, and may be changed to condVar at some point in the future.)

When drop is TRUE any components that would be data frames of a single column are converted to named numeric vectors.

Note

To produce a (list of) “caterpillar plots” of the random effects apply dotplot to the result of a call to ranef with condVar = TRUE; qqmath will generate a list of Q-Q plots.

Examples

require(lattice)
fm1 <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy)
fm2 <- lmer(Reaction ~ Days + (1|Subject) + (0+Days|Subject), sleepstudy)
fm3 <- lmer(diameter ~ (1|plate) + (1|sample), Penicillin)
refit

Refit a (merMod) Model with a Different Response

Description

Refit a model, possibly after modifying the response vector. This makes use of the model representation and directly goes to the optimization.

Usage

refit(object, newresp, ...)

## S3 method for class 'merMod'
refit(object, newresp = NULL, rename.response = FALSE,
       maxit = 100, ...)

Arguments

- **object**: a fitted model, usually of class `merMod`, to be refit with a new response.
- **newresp**: an (optional) numeric vector providing the new response, of the same length as the original response (see Details for information on NA handling). May also be a data frame with a single numeric column, e.g. as produced by `simulate(object)`.
- **rename.response**: when refitting the model, should the name of the response variable in the formula and model frame be replaced with the name of `newresp`?
- **maxit**: scalar integer, currently only for GLMMs: the maximal number of Pwrss update iterations.
- **...**: optional additional parameters. For the `merMod` method, `control`.

Details

Refit a model, possibly after modifying the response vector. This could be done using `update()`, but the `refit()` approach should be faster because it bypasses the creation of the model representation and goes directly to the optimization step.
Setting `rename.response = TRUE` may be necessary if one wants to do further operations (such as `update`) on the fitted model. However, the refitted model will still be slightly different from the equivalent model fitted via `update`; in particular, the `terms` component is not updated to reflect the new response variable, if it has a different name from the original.

If `newresp` has an `na.action` attribute, then it is assumed that NA values have already been removed from the numeric vector; this allows the results of `simulate(object)` to be used even if the original response vector contained NA values. Otherwise, the length of `newresp` must be the same as the original length of the response.

**Value**

an object like `x`, but fit to a different response vector `Y`.

**See Also**

`update.merMod` for more flexible and extensive model refitting; `refitML` for refitting a REML fitted model with maximum likelihood (`'ML'`).

**Examples**

```r
## Ex. 1: using refit() to fit each column in a matrix of responses -------
set.seed(101)
Y <- matrix(rnorm(1000), ncol=10)
## combine first column of responses with predictor variables
d <- data.frame(y=Y[,1], x=rnorm(100), f=rep(1:10,10))
## (use check.conv.grad="ignore" to disable convergence checks because we
## are using a fake example)
## fit first response
fit1 <- lmer(y ~ x+(1|f), data = d,
            control= lmerControl(check.conv.grad="ignore",
            check.conv.hess="ignore"))
## combine fit to first response with fits to remaining responses
res <- c(fit1,lapply(as.data.frame(Y[-1]), refit, object=fit1))

## Ex. 2: refitting simulated data using data that contain NA values -------
sleepstudyNA <- sleepstudy
sleepstudyNA$Reaction[1:3] <- NA
fm0 <- lmer(Reaction ~ Days + (1|Subject), sleepstudyNA)
## the special case of refitting with a single simulation works ...
ss0 <- refit(fm0, simulate(fm0))
## ... but if simulating multiple responses (for efficiency),
## need to use na.action=na.exclude in order to have proper length of data
fm1 <- lmer(Reaction ~ Days + (1|Subject), sleepstudyNA, na.action=na.exclude)
ss <- simulate(fm1, 5)
res2 <- refit(fm1, ss[[5]])
```
refitML 

Refit a Model by Maximum Likelihood Criterion

Description

Refit a (merMod) model using the maximum likelihood criterion.

Usage

refitML(x, ...)
## S3 method for class 'merMod'
refitML(x, optimizer = "bobyqa", ...)

Arguments

x a fitted model, usually of class "1merMod", to be refit according to the maximum likelihood criterion.
... optional additional parameters. None are used at present.
optimizer a string indicating the optimizer to be used.

Details

This function is primarily used to get a maximum likelihood fit of a linear mixed-effects model for an anova comparison.

Value

an object like x but fit by maximum likelihood

See Also

refit and update.merMod for more extensive refitting.

repos

Generator object for the rePos (random-effects positions) class

Description

The generator object for the rePos class used to determine the positions and orders of random effects associated with particular random-effects terms in the model.

Usage

repos(...)
rePos-class

Arguments

... Argument list (see Note).

Methods

new(mer=mer) Create a new rePos object.

Note

Arguments to the new methods must be named arguments. mer, an object of class "merMod", is the only required/expected argument.

See Also

rePos

---

rePos-class  Class "rePos"

Description

A reference class for determining the positions in the random-effects vector that correspond to particular random-effects terms in the model formula.

Extends

All reference classes extend and inherit methods from "envRefClass".

Examples

showClass("rePos")

---

residuals.merMod  residuals of merMod objects

Description

residuals of merMod objects
Usage

### S3 method for class 'merMod'
residuals(object,
  type = if (isGLMM(object)) "deviance" else "response",
  scaled = FALSE, ...)

### S3 method for class 'lmResp'
residuals(object,
  type = c("working", "response", "deviance", "pearson", "partial"),
  ...)

### S3 method for class 'glmResp'
residuals(object,
  type = c("deviance", "pearson", "working", "response", "partial"),
  ...)

Arguments

- **object**: a fitted [g]lmer (merMod) object
- **type**: type of residuals
- **scaled**: scale residuals by residual standard deviation (=scale parameter)?
- **...**: additional arguments (ignored: for method compatibility)

Details

- The default residual type varies between lmerMod and glmerMod objects: they try to mimic residuals.lm and residuals.glm respectively. In particular, the default type is "response", i.e. (observed-fitted) for lmerMod objects vs. "deviance" for glmerMod objects. type="partial" is not yet implemented for either type.
- Note that the meaning of "pearson" residuals differs between residuals.lm and residuals.lme. The former returns values scaled by the square root of user-specified weights (if any), but not by the residual standard deviation, while the latter returns values scaled by the estimated standard deviation (which will include the effects of any variance structure specified in the weights argument). To replicate lme behaviour, use type="pearson", scaled=TRUE.

---

**sigma**

*Extract Residual Standard Deviation 'Sigma'*

Description

Extract the estimated standard deviation of the errors, the “residual standard deviation” (also mis-named the “residual standard error”), from a fitted model.

Usage

### S3 method for class 'merMod'
sigma(object, ...)

sigma
Arguments

object a fitted model.

... additional, optional arguments, passed from or to methods. (None currently in our two methods.)

Details

Package *lme4* provides methods for mixed-effects models of class *merMod* and lists of linear models, *lmlist4*.

Value

Typically a number, the estimated standard deviation of the errors (“residual standard deviation”) for Gaussian models, and - less interpretably - the square root of the residual deviance per degree of freedom in more general models.

Examples

methods(sigma)# from R 3.3.0 on, shows methods from pkgs 'stats' *and* 'lme4'

---

**simulate.merMod**

*Simulate Responses From merMod Object*

Description

Simulate responses from a "merMod" fitted model object, i.e., from the model represented by it.

Usage

```r
## S3 method for class 'merMod'
simulate(object, nsim = 1, seed = NULL,
         use.u = FALSE, re.form = NA, ReForm, REform, REform,
         newdata=NULL, newparams=NULL, family=NULL,
         allow.new.levels = FALSE, na.action = na.pass, ...)
```

```r
## S3 method for class 'formula'
simulate(object, nsim = 1, seed = NULL,
         family, weights=NULL, offset=NULL, ...)
```

```r
.simulateFun(object, nsim = 1, seed = NULL, use.u = FALSE,
             re.form = NA, ReForm, REform, REform,
             newdata=NULL, newparams=NULL,
             formula=NULL, family=NULL, weights=NULL, offset=NULL,
             allow.new.levels = FALSE, na.action = na.pass, ...)
```
Arguments

object (for simulate.merMod) a fitted model object or (for simulate.formula) a (one-sided) mixed model formula, as described for `lmer`.

nsim positive integer scalar - the number of responses to simulate.

seed an optional seed to be used in `set.seed` immediately before the simulation so as to generate a reproducible sample.

use.u (logical) if TRUE, generate a simulation conditional on the current random-effects estimates; if FALSE generate new Normally distributed random-effects values. (Redundant with `re.form`, which is preferred: TRUE corresponds to `re.form = NULL` (condition on all random effects), while FALSE corresponds to `re.form = ~0` (condition on none of the random effects).)

re.form formula for random effects to condition on. If NULL, condition on all random effects; if NA or ~0, condition on no random effects. See Details.

ReForm, REform, REformL deprecated: `re.form` is now the preferred argument name.

newdata data frame for which to evaluate predictions.

newparams new parameters to use in evaluating predictions, specified as in the start parameter for `lmer` or `glmer` – a list with components theta and beta and (for LMMs or GLMMs that estimate a scale parameter) sigma.

formula a (one-sided) mixed model formula, as described for `lmer`.

family a GLM family, as in `glmer`.

weights prior weights, as in `lmer` or `glmer`.

offset offset, as in `glmer`.

allow.new.levels (logical) if FALSE (default), then any new levels (or NA values) detected in `newdata` will trigger an error; if TRUE, then the prediction will use the unconditional (population-level) values for data with previously unobserved levels (or NAs).

na.action what to do with NA values in new data: see `na.fail`

... optional additional arguments: none are used at present.

Details

- ordinarily `simulate` is used to generate new values from an existing, fitted model (`merMod` object): however, if `formula`, `newdata`, and `newparams` are specified, `simulate` generates the appropriate model structure to simulate from.

- The `re.form` argument allows the user to specify how the random effects are incorporated in the simulation. All of the random effects terms included in `re.form` will be conditioned on - that is, the conditional modes of those random effects will be included in the deterministic part of the simulation. (If new levels are used (and `allow.new.levels` is TRUE), the conditional modes for these levels will be set to the population mode, i.e. values of zero will be used for the random effects.) Conversely, the random effect terms that are not included in `re.form` will be simulated from - that is, new values will be chosen for each group based on the estimated random-effects variances.
The default behaviour (using `re.form=NA`) is to condition on none of the random effects, simulating new values for all of the random effects.

- For Gaussian fits, `sigma` specifies the residual standard deviation; for Gamma fits, it specifies the shape parameter (the rate parameter for each observation is calculated as `shape/mean(i)`). For negative binomial fits, the overdispersion parameter is specified via the family, e.g. `simulate(..., family=negative.binomial)`.  

See Also

`bootMer` for “simulestimate”, i.e., where each simulation is followed by refitting the model.

Examples

```r
## test whether fitted models are consistent with the
## observed number of zeros in CBPP data set:
gml <- glmer(cbind(incidence, size - incidence) ~ period + (1 | herd),
             data = cbpp, family = binomial)
gg <- simulate(gml,1000)
zeros <- sapply(gg,function(x) sum(x[,"incidence"]>=0))
plot(table(zeros))
abline(v=sum(cbpp$incidence==0),col=2)
##
## simulate from a non-fitted model; in this case we are just
## replicating the previous model, but
params <- list(theta=0.5,beta=c(2,-1,-2,-3))
simdat <- with(cbpp,expand.grid(herd=levels(herd),period=factor(1:4)))
simdat$size <- 15
simdat$incidence <- sample(0:1,size=nrow(simdat),replace=TRUE)
form <- formula(gml)[-2]
simulate(form,newdata=simdat,family=binomial,
         newparams=params)
```

sleepstudy

Reaction times in a sleep deprivation study

Description

The average reaction time per day for subjects in a sleep deprivation study. On day 0 the subjects had their normal amount of sleep. Starting that night they were restricted to 3 hours of sleep per night. The observations represent the average reaction time on a series of tests given each day to each subject.

Format

A data frame with 180 observations on the following 3 variables.

Reaction  Average reaction time (ms)
Days  Number of days of sleep deprivation
Subject  Subject number on which the observation was made.
Details

These data are from the study described in Belenky et al. (2003), for the sleep-deprived group and for the first 10 days of the study, up to the recovery period.

References


Examples

```r
str(sleepstudy)
require(lattice)
xyplot(Reaction ~ Days | Subject, sleepstudy, type = c("g","p","r"),
   index = function(x,y) coef(lm(y ~ x))[1],
   xlab = "Days of sleep deprivation",
   ylab = "Average reaction time (ms)", aspect = "xy")
(fm1 <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy))
(fm2 <- lmer(Reaction ~ Days + (1|Subject) + (0+Days|Subject), sleepstudy))
```

---

### subbars

"Substitute Bars"

#### Description

Substitute the `+` function for the `|` function in a mixed-model formula, recursively (hence the argument name `term`). This provides a formula suitable for the current `model.frame` function.

#### Usage

```r
subbars(term)
```

#### Arguments

- `term`  
  a mixed-model formula

#### Value

the formula with all `|` operators replaced by `+`

#### See Also

- `formula`, `model.frame`, `model.matrix`
- Other utilities: `findbars`, `nobars`, `mkRespMod`, `mkReTrms`, `nlformula`
Basic troubleshooting

This page attempts to summarize some of the common problems with fitting \texttt{glmer} models and how to troubleshoot them.

- **failure to converge in (xxxx) evaluations** The optimizer hit its maximum limit of function evaluations. To increase this, use the \texttt{optControl} argument of \texttt{glmerControl} – for \texttt{Nelder-Mead} and \texttt{bobyqa} the relevant parameter is \texttt{maxfun}; for \texttt{optim} and \texttt{optimx}-wrapped optimizers, including \texttt{nlsminbwrap}, it’s \texttt{maxit}; for \texttt{nloptwrap}, it’s \texttt{maxeval}.

- **Model failed to converge with max$|\text{grad}|$** … The scaled gradient at the fitted (RE)ML estimates is worryingly large. Try
  - refitting the parameters starting at the current estimates: getting consistent results (with no warning) suggests a false positive
  - switching optimizers: getting consistent results suggests there is not really a problem; getting a similar log-likelihood with different parameter estimates suggests that the parameters are poorly determined (possibly the result of a misspecified or overfitted model)
  - compute values of the deviance in the neighbourhood of the estimated parameters to double-check that \texttt{lme4} has really found a local optimum.

- **Hessian is numerically singular: parameters are not uniquely determined** The Hessian (inverse curvature matrix) at the maximum likelihood or REML estimates has a very large eigenvalue, indicating that (within numerical tolerances) the surface is completely flat in some direction. The model may be misspecified, or extremely badly scaled (see "Model is nearly unidentifiable").

- **Model is nearly unidentifiable** … Rescale variables? The Hessian (inverse curvature matrix) at the maximum likelihood or REML estimates has a large eigenvalue, indicating that the surface is nearly flat in some direction. Consider centering and/or scaling continuous predictor variables.

- **Contrasts can be applied only to factors with 2 or more levels** One or more of the categorical predictors in the model has fewer than two levels. This may be due to user error when converting these predictors to factors prior to modeling, or it may result from some factor levels being eliminated due to NAs in other predictors. Double-check the number of data points in each factor level to see which one is the culprit: \texttt{lapply(na.omit(df[,vars]), table)} (where \texttt{df} is the data frame and \texttt{vars} are the column names of your predictor variables).
Description

This function calculates the estimated variances, standard deviations, and correlations between the random-effects terms in a mixed-effects model, of class `merMod` (linear, generalized or nonlinear). The within-group error variance and standard deviation are also calculated.

Usage

```R
## S3 method for class 'merMod'
VarCorr(x, sigma=1, ...)

## S3 method for class 'VarCorr.merMod'
as.data.frame(x, row.names = NULL,
   optional = FALSE, order = c("cov.last", "lower.tri"), ...)

## S3 method for class 'VarCorr.merMod'
print(x, digits = max(3,getOption("digits") - 2),
   comp = "Std.Dev.", formatter = format, ...)
```

Arguments

- `x` for `VarCorr`: a fitted model object, usually an object inheriting from class `merMod`. For `as.data.frame`, a `VarCorr.merMod` object returned from `VarCorr`.
- `sigma` an optional numeric value used as a multiplier for the standard deviations.
- `digits` an optional integer value specifying the number of digits
- `order` arrange data frame with variances/standard deviations first and covariances/correlations last for each random effects term ("cov.last"), or in the order of the lower triangle of the variance-covariance matrix ("lower.tri")?
- `row.names`, optional
  Ignored: necessary for the `as.data.frame` method.
- `...` Ignored for the `as.data.frame` method; passed to other `print()` methods for the `print()` method.
- `comp` a character vector, specifying the components to be printed; simply passed to `formatVC()`.
- `formatter` a function for formatting the numbers; simply passed to `formatVC()`.

Details

The `print` method for `VarCorr.merMod` objects has optional arguments `digits` (specify digits of precision for printing) and `comp`: the latter is a character vector with any combination of "Variance" and "Std.Dev.", to specify whether variances, standard deviations, or both should be printed.
Value

An object of class `VarCorr` from package `nlme`, by Jose Pinheiro and Douglas Bates. See Also `lmer`, `nlmer` Examples

```r
data(Orthodont, package="nlme")
fm1 <- lmer(distance ~ age + (age|Subject), data = Orthodont)
(vc <- VarCorr(fm1))
## both variance and std.dev.
print(vc, comp=c("Variance","Std.Dev."), digits=2)
## variance only
print(vc, comp=c("Variance"))
as.data.frame(vc)
as.data.frame(vc, order="lower.tri")
```

Description

Transform a mixed-effects profile, i.e. conceptually, `x <- profile(lmer(...), ..)` from standard deviation to the variance scale.

Usage

`varianceProf(x, ranef = TRUE)`
Arguments

x  a mixed-effects model profile.
ranef  logical indicating if all sigmas should be transformed, see logProf.

Value

a transformed mixed-effects model profile

See Also

profile and methods, notably, logProf for log transformation of the sigmas; also for nice examples including graphics.

vcconv  Convert between representations of (co-)variance structures

Description

Convert between representations of (co-)variance structures (EXPERIMENTAL). See source code for details.

Usage

mlist2vec(L)
vec2mlist(v, n = NULL, symm = TRUE)
vec2STlist(v, n = NULL)
sdcov2cov(m)
cov2sdcor(V)
Vv_to_Cv(v, n = NULL, s = 1)
Sv_to_Cv(v, n = NULL, s = 1)
Cv_to_Vv(v, n = NULL, s = 1)
Cv_to_Sv(v, n = NULL, s = 1)

Arguments

L  List of symmetric, upper-triangular, or lower-triangular square matrices.
v  Concatenated vector containing the elements of the lower-triangle (including the diagonal) of a symmetric or triangular matrix.
n  Number of rows (and columns) of the resulting matrix.
symm  Return symmetric matrix if TRUE or lower-triangular if FALSE.
m  Standard deviation-correlation matrix.
V  Covariance matrix.
s  Scale parameter.
Details

- `mlist2vec` Convert list of matrices to concatenated vector of lower triangles with an attribute that gives the dimension of each matrix in the original list. This attribute may be used to reconstruct the matrices. Returns a concatenation of the elements in one triangle of each matrix. An attribute "clen" gives the dimension of each matrix.
- `vec2mlist` Convert concatenated vector to list of matrices (lower triangle or symmetric). These matrices could represent Cholesky factors, covariance matrices, or correlation matrices (with standard deviations on the diagonal).
- `vec2Stlist` Convert concatenated vector to list of ST matrices.
- `sdcor2cov` Standard deviation-correlation matrix to covariance matrix convert 'sdcor' format (std dev on diagonal, cor on off-diag) to and from variance-covariance matrix.
- `cov2sdcor` Covariance matrix to standard deviation-correlation matrix (i.e. standard deviations on the diagonal and correlations off the diagonal).
- `Vv_to_Cv` Variance-covariance to relative covariance factor. Returns a vector of elements from the lower triangle of a relative covariance factor.
- `Sv_to_Cv` Standard-deviation-correlation to relative covariance factor. Returns a vector of elements from the lower triangle of a relative covariance factor.
- `Cv_to_Vv` Relative covariance factor to variance-covariance. From unscaled Cholesky vector to (possibly scaled) variance-covariance vector. Returns a vector of elements from the lower triangle of a variance-covariance matrix.
- `Cv_to_Sv` Relative covariance factor to standard-deviation-correlation. From unscaled Chol to sd-cor vector. Returns a vector of elements from the lower triangle of a standard-deviation-correlation matrix.

Value

(Co-)variance structure

Examples

```r
vec2mlist(1:6)
mvec2mlist(vec2mlist(1:6)) # approximate inverse
```

**VerbAgg**

Verbal Aggression item responses

Description

These are the item responses to a questionnaire on verbal aggression. These data are used throughout De Boeck and Wilson, *Explanatory Item Response Models* (Springer, 2004) to illustrate various forms of item response models.
Format

A data frame with 7584 observations on the following 13 variables.

Anger  the subject’s Trait Anger score as measured on the State-Trait Anger Expression Inventory (STAXI)
Gender  the subject’s gender - a factor with levels M and F
item  the item on the questionnaire, as a factor
resp  the subject’s response to the item - an ordered factor with levels no < perhaps < yes
id  the subject identifier, as a factor
btype  behavior type - a factor with levels curse, scold and shout
situ  situation type - a factor with levels other and self indicating other-to-blame and self-to-blame
mode  behavior mode - a factor with levels want and do
r2  dichotomous version of the response - a factor with levels N and Y

Source

http://bear.soe.berkeley.edu/EIRM/

References


Examples

```r
str(VerbAgg)
## Show how r2 := h(resp) is defined:
with(VerbAgg, stopifnot( identical(r2, {
  r <- factor(resp, ordered=FALSE); levels(r) <- c("N","Y","Y"); r))))

xtabs(~ item + resp, VerbAgg)
xtabs(~ btype + resp, VerbAgg)
round(100 * ftable(prop.table(xtabs(~ situ + mode + resp, VerbAgg), 1:2), 1))
person <- unique(subset(VerbAgg, select = c(id, Gender, Anger)))
require(lattice)
densityplot(~ Anger, person, groups = Gender, auto.key = list(columns = 2),
  xlab = "Trait anger score (STAXI)"

if(lme4:::testLevel() >= 3) { ## takes about 15 sec
  print(fmVA <- glmer(r2 ~ (Anger + Gender + btype + situ)^2 +
    (1|id) + (1|item), family = binomial, data = VerbAgg), corr=FALSE)
}

## much faster but less accurate
print(fmVA0 <- glmer(r2 ~ (Anger + Gender + btype + situ)^2 +
  (1|id) + (1|item), family = binomial, data = VerbAgg, nAGQ=0), corr=FALSE)
```
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