

# Package ‘merTools’

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**Title** Tools for Analyzing Mixed Effect Regression Models

**Version** 0.5.2

**Description** Provides methods for extracting results from mixed-effect model objects fit with the 'lme4' package. Allows construction of prediction intervals efficiently from large scale linear and generalized linear mixed-effects models.

**Depends** R (>= 3.0.2), arm, lme4 (>= 1.1-11), methods

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**Imports** dplyr, mvtnorm, foreach, shiny, abind, ggplot2, blme, broom.mixed,

**License** GPL (>= 2)

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**VignetteBuilder** knitr

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---

averageObs	<i>Find the average observation for a merMod object</i>
------------	---

---

### Description

Extract a data frame of a single row that represents the average observation in a merMod object. This function also allows the user to pass a series of conditioning argument to calculate the average observation conditional on other characteristics.

### Usage

```
averageObs(merMod, varList = NULL, origData = NULL, ...)
```

### Arguments

merMod	a merMod object
varList	optional, a named list of conditions to subset the data on
origData	(default=NULL) a data frame containing the original, untransformed data used to call the model. This MUST be specified if the original variables used in formula function calls are NOT present as 'main effects'.
...	not used currently

### Details

Each character and factor variable in the data.frame is assigned to the modal category and each numeric variable is collapsed to the mean. Currently if mode is a tie, returns a "." Uses the collapseFrame function.

### Value

a data frame with a single row for the average observation, but with full factor levels. See details for more.

---

collapseFrame	<i>Collapse a dataframe to a single average row</i>
---------------	---

---

### Description

Take an entire dataframe and summarize it in one row by using the mean and mode.

### Usage

```
collapseFrame(data)
```

**Arguments**

data            a data.frame

**Details**

Each character and factor variable in the data.frame is assigned to the modal category and each numeric variable is collapsed to the mean. Currently if mode is a tie, returns a "."

**Value**

a data frame with a single row

---

draw	<i>Draw a single observation out of an object matching some criteria</i>
------	--

---

**Description**

Draw is used to select a single observation out of an R object. Additional parameters allow the user to control how that observation is chosen in order to manipulate that observation later. This is a generic function with methods for a number of objects.

**Usage**

```
draw(object, type = c("random", "average"), varList = NULL, seed = NULL, ...)

## S3 method for class 'merMod'
draw(object, type = c("random", "average"), varList = NULL, seed = NULL, ...)
```

**Arguments**

object            the object to draw from

type              what kind of draw to make. Options include random or average

varList           a list specifying filters to subset the data by when making the draw

seed              numeric, optional argument to set seed for simulations, ignored if type="average"

...               additional arguments required by certain methods

**Details**

In cases of tie, ".", may be substituted for factors.

**Value**

a data.frame with a single row representing the desired observation

**Examples**

```
fm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
# Random case
draw(fm1, type = "random")
# Average
draw(fm1, type = "average")
# Subset
draw(fm1, type = "average", varList = list("Subject" = "308"))
```

---

expectedRank	<i>Calculate the expected rank of random coefficients that account for uncertainty.</i>
--------------	---

---

**Description**

expectedRank calculates the expected rank and the percentile expected rank of any random term in a merMod object. A simple ranking of the estimated random effects (as produced by [ranef](#)) is not satisfactory because it ignores any amount of uncertainty.

**Usage**

```
expectedRank(merMod, groupFctr = NULL, term = NULL)
```

**Arguments**

merMod	An object of class merMod
groupFctr	An optional character vector specifying the name(s) the grouping factor(s) over which the random coefficient of interest varies. This is the variable to the right of the pipe,  , in the [g]lmer formula. This parameter is optional. If none is specified all terms will be returned.
term	An optional character vector specifying the name(s) of the random coefficient of interest. This is the variable to the left of the pipe,  , in the [g]lmer formula. Partial matching is attempted on the intercept term so the following character strings will all return rankings based on the intercept ( <i>provided that they do not match the name of another random coefficient for that factor</i> ): c("(Intercept)", "Int", "intercep", ...).

**Details**

Inspired by Lingsma et al. (2010, see also Laird and Louis 1989), expectedRank sums the probability that each level of the grouping factor is greater than every other level of the grouping factor, similar to a two-sample t-test.

The formula for the expected rank is:

$$ExpectedRank_i = 1 + \sum \phi((\theta_i - \theta_k) / \sqrt{var(\theta_i) + var(\theta_k)})$$

where  $\phi$  is the standard normal distribution function,  $\theta$  is the estimated random effect and  $var(\theta)$  is the posterior variance of the estimated random effect. We add one to the sum so that the minimum rank is one instead of zero so that in the case where there is no overlap between the variances of the random effects (or if the variances are zero), the expected rank equals the actual rank. The ranks are ordered such that the winners have ranks that are greater than the losers.

The formula for the percentile expected rank is:

$$100 * (ExpectedRank_i - 0.5) / N_{grps}$$

where  $N_{grps}$  is the number of grouping factor levels. The percentile expected rank can be interpreted as the fraction of levels that score at or below the given level.

NOTE: expectedRank will only work under conditions that lme4::ranef will work. One current example of when this is *not* the case is for models when there are multiple terms specified per factor (e.g. uncorrelated random coefficients for the same term, e.g. `lmer(Reaction ~ Days + (1 | Subject) + (0 + Days | Subject), data = sleepstudy)`)

### Value

A data.frame with the following five columns:

**groupFctr** a character representing name of the grouping factor

**groupLevel** a character representing the level of the grouping factor

**term** a character representing the formula term for the group

**estimate** effect estimate from `lme4::ranef(, condVar=TRUE)`.

**std.error** the posterior variance of the estimate random effect (from `lme4::ranef(, condVar=TRUE)`); named "term"\_var.

**ER** The expected rank.

**pctER** The percentile expected rank.

### References

Laird NM and Louis TA. Empirical Bayes Ranking Methods. *Journal of Education Statistics*. 1989;14(1)29-46. Available at <http://www.jstor.org/stable/1164724>.

Lingsma HF, Steyerberg EW, Eijkemans MJC, et al. Comparing and ranking hospitals based on outcome: results from The Netherlands Stroke Survey. *QJM: An International Journal of Medicine*. 2010;103(2):99-108. doi:10.1093/qjmed/hcp169

### Examples

```
#For a one-level random intercept model
m1 <- lmer(Reaction ~ Days + (1 | Subject), sleepstudy)
(m1.er <- expectedRank(m1))
```

```
#For a one-level random intercept model with multiple random terms
m2 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
#ranked by the random slope on Days
(m2.er1 <- expectedRank(m2, term="Days"))
```

```

#ranked by the random intercept
(m2.er2 <- expectedRank(m2, term="int"))

#For a two-level model with random intercepts
m3 <- lmer(y ~ service * dept + (1|s) + (1|d), InstEval)
#Ranked by the random intercept on 's'
(m3.er1 <- expectedRank(m3, groupFctr="s", term="Intercept"))

```

---

famlink	<i>Find link function family</i>
---------	----------------------------------

---

### Description

Find link function family

### Usage

```
famlink(object, resp = object@resp)
```

### Arguments

object	a merMod object
resp	the response vector

### Value

the link function and family

---

fastdisp	<i>fastdisp: faster display of model summaries</i>
----------	--

---

### Description

Display model fit summary of x or x like objects, fast

### Usage

```

fastdisp(x, ...)

## S3 method for class 'merMod'
fastdisp(x, ...)

## S3 method for class 'merModList'
fastdisp(x, ...)

```

**Arguments**

`x` a model object  
`...` additional arguments to pass to `arm::display` including number of digits

**Details**

Faster than the implementation in the `arm` package because it avoids refitting  
 The time saving is only noticeable for large, time-consuming (g)lmer fits.

**Value**

A printed summary of a `x` object

**See Also**

[display](#)

**Examples**

```
#Compare the time for displaying this modest model
require(arm)
m1 <- lmer(y ~ lectage + studage + (1|d) + (1|s), data=InstEval)
system.time(display(m1))
system.time(fastdisp(m1))
```

---

FEsim

*Simulate fixed effects from merMod FEsim simulates fixed effects from merMod object posterior distributions*

---

**Description**

Simulate fixed effects from merMod FEsim simulates fixed effects from merMod object posterior distributions

**Usage**

```
FEsim(merMod, n.sims = 200, oddsRatio = FALSE, seed = NULL)
```

**Arguments**

`merMod` a merMod object from the lme4 package  
`n.sims` number of simulations to use  
`oddsRatio` logical, should parameters be converted to odds ratios?  
`seed` numeric, optional argument to set seed for simulations

**Details**

Use the Gelman sim technique to build fixed effect estimates and confidence intervals. Uses the sim function in the arm package

**Value**

a data frame with the following columns

term Name of fixed term (intercept/coefficient)

mean Mean of the simulations

median Median of the simulations

sd Standard deviation of the simulations, NA if oddsRatio=TRUE

**Examples**

```
require(lme4)
m2 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
fe2 <- FESim(m2, 25)
head(fe2)
```

---

fetch.merMod.msgs      *Extract all warning msgs from a merMod object*

---

**Description**

Extract all warning msgs from a merMod object

**Usage**

```
fetch.merMod.msgs(x)
```

**Arguments**

x                    a merMod object

---

findFormFuns	findFormFuns used by <i>averageObs</i> to calculate proper averages
--------------	---

---

### Description

The purpose is to properly derive data for the average observation in the data by being 'aware' of formulas that contain interactions and/or function calls. For example, in the old behavior, if the formula contained a square term specified as  $I(x^2)$ , we were returning the mean of  $x^2$  not the square of  $\text{mean}(x)$ .

### Usage

```
findFormFuns(merMod, origData = NULL)
```

### Arguments

merMod	the merMod object from which to draw the average observation
origData	(default=NULL) a data frame containing the original, untransformed data used to call the model. This MUST be specified if the original variables used in formula function calls are NOT present as 'main effects'.

### Value

a data frame with a single row for the average observation, but with full factor levels. See details for more.

---

fixef.merModList	Extract fixed-effects estimates for a merModList
------------------	--

---

### Description

Extract fixed-effects estimates for a merModList

### Usage

```
## S3 method for class 'merModList'
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 list of fitted merMod models. Takes the mean of the individual fixef objects for each of the component models in the merModList.

**Value**

a named, numeric vector of fixed-effects estimates.

**Examples**

```
sim_list <- replicate(n = 10,  
  expr = sleepstudy[sample(row.names(sleepstudy), 180),],  
  simplify=FALSE)  
fml <- "Reaction ~ Days + (Days | Subject)"  
mod <- lmerModList(fml, data = sim_list)  
fixef(mod)
```

---

hasWeights	<i>Identify if a merMod has weights</i>
------------	---

---

**Description**

Identify if a merMod has weights

**Usage**

```
hasWeights(merMod)
```

**Arguments**

merMod            the merMod object to test for weights

**Value**

TRUE or FALSE for whether the model has weights

---

hsb	<i>A subset of data from the 1982 High School and Beyond survey used as examples for HLM software</i>
-----	---

---

**Description**

A key example dataset used for examples in the HLM software manual. Included here for use in replicating HLM analyses in R.

**Usage**

hsb

**Format**

A data frame with 7,185 observations on the following 8 variables.

schid a numeric vector, 160 unique values

mathach a numeric vector for the performance on a standardized math assessment

female a numeric vector coded 0 for male and 1 for female

ses a numeric measure of student socio-economic status

minority a numeric vector coded 0 for white and 1 for non-white students

sctype a numeric vector coded 0 for public and 1 for private schools

meansas a numeric, the average SES for each school in the data set

size a numeric for the number of students in the school

**Details**

The data file used for this presentation is a subsample from the 1982 High School and Beyond Survey and is used extensively in Hierarchical Linear Models by Raudenbush and Bryk. It consists of 7,185 students nested in 160 schools.

**Source**

Data made available by UCLA Institute for Digital Research and Education (IDRE) online: <https://stats.idre.ucla.edu/other/hlm/hlm-mlm/introduction-to-multilevel-modeling-using-hlm>

**References**

Stephen W. Raudenbush and Anthony S. Bryk (2002). Hierarchical Linear Models: Applications and Data Analysis Methods (2nd ed.). SAGE.

**Examples**

```
data(hsb)
head(hsb)
```

---

ICC	<i>Calculate the intraclass correlation using mixed effect models</i>
-----	---

---

**Description**

Calculate the intraclass correlation using mixed effect models

**Usage**

```
ICC(outcome, group, data, subset = NULL)
```

**Arguments**

outcome	a character representing the variable of the outcome
group	a character representing the name of the grouping term
data	a data.frame
subset	an optional subset

**Value**

a numeric for the intraclass correlation

**Examples**

```
data(sleepstudy)
ICC(outcome = "Reaction", group = "Subject", data = sleepstudy)
```

---

lmerModList	<i>Apply a multilevel model to a list of data frames</i>
-------------	--

---

**Description**

Apply a multilevel model to a list of data frames  
 Apply a Bayesian multilevel model to a list of data frames  
 Apply a generalized linear multilevel model to a list of data frames  
 Apply a Bayesian generalized linear multilevel model to a list of data frames

**Usage**

```
lmerModList(formula, data, parallel = FALSE, ...)
blmerModList(formula, data, parallel = FALSE, ...)
glmerModList(formula, data, parallel = FALSE, ...)
bglmerModList(formula, data, parallel = FALSE, ...)
```

**Arguments**

formula	a formula to pass through compatible with merMod
data	a list object with each element being a data.frame
parallel	logical, should the models be run in parallel? Default FALSE. If so, the 'future_lapply' function from the 'future.apply' package is used. See details.
...	additional arguments to pass to the estimating function

**Details**

Parallel computing is provided by the 'futures' package, and its extension the 'future.apply' package to provide the 'future\_lapply' function for easy parallel computations on lists. To use this package, simply register a parallel backend using the 'plan()' function from 'futures' - an example is to use 'plan(multisession)'

**Value**

a list of fitted merMod objects of class merModList  
 a merModList  
 a merModList  
 a merModList

**Examples**

```
sim_list <- replicate(n = 10,
  expr = sleepstudy[sample(row.names(sleepstudy), 180),],
  simplify=FALSE)
fml <- "Reaction ~ Days + (Days | Subject)"
mod <- lmerModList(fml, data = sim_list)
summary(mod)
```

---

merTools

---

*merTools: Provides methods for extracting and exploring results from merMod objects in the lme4 package.*


---

**Description**

The merTools package contains convenience tools for extracting useful information from and exploring the implications of merMod objects created by the lme4 package. These convenience functions are especially useful for merMod objects that take a long time to estimate due to their complexity or because they are estimated on very large samples.

**Details**

See the vignettes for usage examples

**merMod extraction/utility functions**

- [fastdisp](#)
- [superFactor](#)
- [REextract](#)
- [REsim](#)
- [FESim](#)
- [RMSE.merMod](#)
- [thetaExtract](#)
- [REquantile](#)

**merMod exploration functions**

- [plotREsim](#)
- [plotFESim](#)
- [draw](#)
- [wiggle](#)
- [subBoot](#)
- [predictInterval](#)
- [expectedRank](#)
- [REimpact](#)
- [shinyMer](#)

---

modelFixedEff	<i>Extract averaged fixed effect parameters across a list of merMod objects</i>
---------------	---

---

**Description**

Extract averaged fixed effect parameters across a list of merMod objects

**Usage**

```
modelFixedEff(modList, ...)
```

**Arguments**

modList	an object of class merModList
...	additional arguments to pass to <a href="#">tidy</a>

**Details**

The Rubin correction for combining estimates and standard errors from Rubin (1987) is applied to adjust for the within and between imputation variances.

**Value**

a data.frame of the averaged fixed effect parameters

**Examples**

```
sim_list <- replicate(n = 10,  
  expr = sleepstudy[sample(row.names(sleepstudy), 180),],  
  simplify=FALSE)  
fml <- "Reaction ~ Days + (Days | Subject)"  
mod <- lmerModList(fml, data = sim_list)  
modelFixedEff(mod)
```

---

modelInfo

*Extract model information from a merMod*

---

**Description**

Extract model information from a merMod

**Usage**

```
modelInfo(object)
```

**Arguments**

object            a merMod object

**Value**

Simple summary information about the object, number of observations, number of grouping terms, AIC, and residual standard deviation

**Examples**

```
sim_list <- replicate(n = 10,  
  expr = sleepstudy[sample(row.names(sleepstudy), 180),],  
  simplify=FALSE)  
fml <- "Reaction ~ Days + (Days | Subject)"  
mod <- lmerModList(fml, data = sim_list)  
modelInfo(mod[[1]])  
lapply(mod, modelInfo)
```

---

modelRandEffStats	<i>Extract data.frame of random effect statistics from merMod List</i>
-------------------	--

---

**Description**

Extract data.frame of random effect statistics from merMod List

**Usage**

```
modelRandEffStats(modList)
```

**Arguments**

modList            a list of multilevel models

**Value**

a data.frame

**Examples**

```
sim_list <- replicate(n = 10,  
  expr = sleepstudy[sample(row.names(sleepstudy), 180),],  
  simplify=FALSE)  
fml <- "Reaction ~ Days + (Days | Subject)"  
mod <- lmerModList(fml, data = sim_list)  
modelRandEffStats(mod)
```

---

plotFESim	<i>Plot the results of a simulation of the fixed effects</i>
-----------	--

---

**Description**

Plot the simulated fixed effects on a ggplot2 chart

**Usage**

```
plotFESim(  
  data,  
  level = 0.95,  
  stat = "median",  
  sd = TRUE,  
  intercept = FALSE,  
  sigmaScale = NULL,  
  oddsRatio = FALSE  
)
```

**Arguments**

data	a data.frame generated by <code>FESim</code> with simulations of the fixed effects of a <code>merMod</code>
level	the width of the confidence interval
stat	a character value indicating the variable name in data of the midpoint of the estimated interval, e.g. "mean" or "median"
sd	logical, indicating whether or not to plot error bars around the estimates (default is TRUE). Calculates the width of the error bars based on level and the variable named "sd" in data
intercept	logical, should the intercept be included, default is FALSE
sigmaScale	a numeric value to divide the estimate and the standard deviation by in the case of doing an effect size calculation
oddsRatio	logical, should the parameters be converted to odds ratios before plotting

**Value**

a `ggplot2` plot of the coefficient effects

**Examples**

```
fm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
(p1 <- plotFESim(FESim(fm1)))
```

---

plotREsim

*Plot the results of a simulation of the random effects*

---

**Description**

Plot the simulated random effects on a `ggplot2` chart. Points that are distinguishable from zero (i.e. the confidence band based on level does not cross the red line) are highlighted. Currently, the plots are ordered according to the grouping factor.

**Usage**

```
plotREsim(
  data,
  level = 0.95,
  stat = "median",
  sd = TRUE,
  sigmaScale = NULL,
  oddsRatio = FALSE,
  labs = FALSE,
  facet = TRUE
)
```

**Arguments**

data	a data.frame generated by <code>REsim</code> with simulations of the random effects of a <code>merMod</code>
level	the width of the confidence interval
stat	a character value indicating the variable name in data of the midpoint of the estimated interval, e.g. "mean" or "median"
sd	a logical indicating whether or not to plot error bars around the estimates (default is TRUE). Calculates the width of the error bars based on level and the variable named "sd" in data
sigmaScale	a numeric value to divide the estimate and the standard deviation by in the case of doing an effect size calculation
oddsRatio	logical, should the parameters be converted to odds ratios before plotting
labs	logical, include the labels of the groups on the x-axis
facet	Accepts either logical (TRUE) or list to specify which random effects to plot. If TRUE, facets by both groupFctr and term. If list selects the panel specified by the named elements of the list

**Value**

a ggplot2 plot of the coefficient effects

**Examples**

```
fm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
(p1 <- plotREsim(REsim(fm1)))
#Plot just the random effects for the Days slope
(p2 <- plotREsim(REsim(fm1), facet= list(groupFctr= "Subject", term= "Days")))
```

---

plot\_sim\_error\_chks *Extract all warning msgs from a merMod object*

---

**Description**

Extract all warning msgs from a merMod object

**Usage**

```
plot_sim_error_chks(
  type = c("FE", "RE"),
  level = 0.95,
  stat = c("mean", "median"),
  sd = TRUE,
  sigmaScale = NULL,
```

```

oddsRatio = FALSE,
labs = FALSE,
facet = TRUE
)

```

### Arguments

type	check a fixed or random effect
level	the width of the confidence interval
stat	a character value indicating the variable name in data of the midpoint of the estimated interval, e.g. "mean" or "median"
sd	a logical indicating whether or not to plot error bars around the estimates (default is TRUE). Calculates the width of the error bars based on level and the variable named "sd" in data
sigmaScale	a numeric value to divide the estimate and the standard deviation by in the case of doing an effect size calculation
oddsRatio	logical, should the parameters be converted to odds ratios before plotting
labs	logical, include the labels of the groups on the x-axis
facet	Accepts either logical (TRUE) or list to specify which random effects to plot. If TRUE, facets by both groupFctr and term. If list selects the panel specified by the named elements of the list

---

predictInterval

*Predict from merMod objects with a prediction interval*

---

### Description

This function provides a way to capture model uncertainty in predictions from multi-level models fit with lme4. By drawing a sampling distribution for the random and the fixed effects and then estimating the fitted value across that distribution, it is possible to generate a prediction interval for fitted values that includes all variation in the model except for variation in the covariance parameters, theta. This is a much faster alternative than bootstrapping for models fit to medium to large datasets.

### Usage

```

predictInterval(
  merMod,
  newdata,
  which = c("full", "fixed", "random", "all"),
  level = 0.8,
  n.sims = 1000,
  stat = c("median", "mean"),
  type = c("linear.prediction", "probability"),
  include.resid.var = TRUE,
  returnSims = FALSE,

```

```

    seed = NULL,
    .parallel = FALSE,
    .paropts = NULL,
    fix.intercept.variance = FALSE,
    ignore.fixed.terms = NULL
  )

```

## Arguments

<code>merMod</code>	a <code>merMod</code> object from <code>lme4</code>
<code>newdata</code>	a <code>data.frame</code> of new data to predict
<code>which</code>	a character specifying what to return, by default it returns the full interval, but you can also select to return only the fixed variation or the random component variation. If full is selected the resulting <code>data.frame</code> will be <code>nrow(newdata) * number of model levels long</code>
<code>level</code>	the width of the prediction interval
<code>n.sims</code>	number of simulation samples to construct
<code>stat</code>	take the median or mean of simulated intervals
<code>type</code>	type of prediction to develop
<code>include.resid.var</code>	logical, include or exclude the residual variance for linear models
<code>returnSims</code>	logical, should all <code>n.sims</code> simulations be returned?
<code>seed</code>	numeric, optional argument to set seed for simulations
<code>.parallel,</code>	logical should parallel computation be used, default is <code>FALSE</code>
<code>.paropts,</code>	-NOT USED: Caused issue #54- a list of additional options passed into the <code>foreach</code> function when parallel computation is enabled. This is important if (for example) your code relies on external data or packages: use the <code>.export</code> and <code>.packages</code> arguments to supply them so that all cluster nodes have the correct environment set up for computing.
<code>fix.intercept.variance</code>	logical; should the variance of the intercept term be adjusted downwards to roughly correct for its covariance with the random effects, as if all the random effects are intercept effects?
<code>ignore.fixed.terms</code>	a numeric or string vector of indexes or names of fixed effects which should be considered as fully known (zero variance). This can result in under-conservative intervals, but for models with random effects nested inside fixed effects, holding the fixed effects constant intervals may give intervals with closer to nominal coverage than the over-conservative intervals without this option, which ignore negative correlation between the outer (fixed) and inner (random) coefficients.

## Details

To generate a prediction interval, the function first computes a simulated distribution of all of the parameters in the model. For the random, or grouping, effects, this is done by sampling from a

multivariate normal distribution which is defined by the BLUP estimate provided by `raneF` and the associated variance-covariance matrix for each observed level of each grouping terms. For each grouping term, an array is build that has as many rows as there are levels of the grouping factor, as many columns as there are predictors at that level (e.g. an intercept and slope), and is stacked as high as there are number of simulations. These arrays are then multiplied by the new data provided to the function to produce a matrix of `yhat` values. The result is a matrix of the simulated values of the linear predictor for each observation for each simulation. Each grouping term has such a matrix for each observation. These values can be added to get the estimate of the fitted value for the random effect terms, and this can then be added to a matrix of simulated values for the fixed effect level to come up with `n.sims` number of possible `yhat` values for each observation.

The distribution of simulated values is cut according to the interval requested by the function. The median or mean value as well as the upper and lower bounds are then returned. These can be presented either on the linear predictor scale or on the response scale using the link function in the `merMod`.

### Value

a `data.frame` with three columns:

`fit` The center of the distribution of predicted values as defined by the `stat` parameter.

`lwr` The lower prediction interval bound corresponding to the quantile cut defined in `level`.

`upr` The upper prediction interval bound corresponding to the quantile cut defined in `level`.

If `returnSims = TRUE`, then the individual simulations are attached to this `data.frame` in the attribute `sim.results` and are stored as a matrix.

### Note

`merTools` includes the functions `subBoot` and `thetaExtract` to allow the user to estimate the variability in `theta` from a larger model by bootstrapping the model fit on a subset, to allow faster estimation.

### Examples

```
m1 <- lmer(Reaction ~ Days + (1 | Subject), sleepstudy)
regFit <- predict(m1, newdata = sleepstudy[11, ]) # a single value is returned
intFit <- predictInterval(m1, newdata = sleepstudy[11, ]) # bounded values
# Can do glmer
d1 <- cbpp
d1$y <- d1$incidence / d1$size
gm2 <- glmer(y ~ period + (1 | herd), family = binomial, data = d1,
            nAGQ = 9, weights = d1$size)
regFit <- predict(gm2, newdata = d1[1:10, ])
# get probabilities
regFit <- predict(gm2, newdata = d1[1:10, ], type = "response")
intFit <- predictInterval(gm2, newdata = d1[1:10, ], type = "probability")
intFit <- predictInterval(gm2, newdata = d1[1:10, ], type = "linear.prediction")
```

---

print.merModList      *Summarize a merMod list*

---

**Description**

Summarize a merMod list

**Usage**

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

**Arguments**

x                    a modList of class merModList  
...                  additional arguments

**Value**

a summary object of model information

**Examples**

```
sim_list <- replicate(n = 10,  
                      expr = sleepstudy[sample(row.names(sleepstudy), 180),],  
                      simplify=FALSE)  
fml <- "Reaction ~ Days + (Days | Subject)"  
mod <- lmerModList(fml, data = sim_list)  
summary(mod)
```

---

print.summary.merModList  
                          *Print the summary of a merMod list*

---

**Description**

Print the summary of a merMod list

**Usage**

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

**Arguments**

x                    a summary of amerModList object  
 ...                 additional arguments

**Value**

summary content printed to console

---

randomObs	<i>Select a random observation from model data</i>
-----------	--

---

**Description**

Select a random observation from the model frame of a merMod

**Usage**

```
randomObs(merMod, varList, seed = NULL)
```

**Arguments**

merMod             an object of class merMod  
 varList            optional, a named list of conditions to subset the data on  
 seed                numeric, optional argument to set seed for simulations

**Details**

Each factor variable in the data frame has all factor levels from the full model.frame stored so that the new data is compatible with predict.merMod

**Value**

a data frame with a single row for a random observation, but with full factor levels. See details for more.

---

ranef.merModList	<i>Extract random-effects estimates for a merModList</i>
------------------	--

---

## Description

Extract random-effects estimates for a merModList

## Usage

```
## S3 method for class 'merModList'  
ranef(object, ...)
```

## Arguments

object	an object of a class of fitted models with random effects, typically a <a href="#">merMod</a> object.
...	some methods for these generic functions require additional arguments.

## Details

Extract the estimates of the random-effects parameters from a list of fitted merMod models. Takes the mean of the individual ranef objects for each of the component models in the merModList.

## Value

a named, numeric vector of random-effects estimates.

## Examples

```
sim_list <- replicate(n = 10,  
  expr = sleepstudy[sample(row.names(sleepstudy), 180),],  
  simplify=FALSE)  
fml <- "Reaction ~ Days + (Days | Subject)"  
mod <- lmerModList(fml, data = sim_list)  
ranef(mod)
```

---

REcorrExtract	<i>Extract the correlations between the slopes and the intercepts from a model</i>
---------------	--

---

**Description**

Extract the correlations between the slopes and the intercepts from a model

**Usage**

```
REcorrExtract(model)
```

**Arguments**

model                    an object that inherits from class merMod

**Value**

a numeric vector of the correlations among the effects

**Examples**

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

---

REextract	<i>Extracts random effects</i>
-----------	--------------------------------

---

**Description**

Extracts random effect terms from an lme4 model

**Usage**

```
REextract(merMod)
```

**Arguments**

merMod                    a merMod object from the lme4 package

**Value**

a data frame with the following columns

**groupFctr** The name of the grouping factor associated with the random effects

**groupID** The level of the grouping factor associated with the random effects

**'term'** One column per random effect, the name is derived from the merMod

**'term'\_se** One column per random effect, the name is derived from the merMod

**Examples**

```
m2 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
rfx <- REextract(m2)
#Note the column names
head(rfx)
```

---

REimpact	<i>Calculate the weighted mean of fitted values for various levels of random effect terms.</i>
----------	--

---

**Description**

REimpact calculates the average predicted value for each row of a new data frame across the distribution of [expectedRank](#) for a merMod object. This allows the user to make meaningful comparisons about the influence of random effect terms on the scale of the response variable, for user-defined inputs, and accounting for the variability in grouping terms.

**Usage**

```
REimpact(merMod, newdata, groupFctr = NULL, term = NULL, breaks = 3, ...)
```

**Arguments**

merMod	An object of class merMod
newdata	a data frame of observations to calculate group-level differences for
groupFctr	The name of the grouping factor over which the random coefficient of interest varies. This is the variable to the right of the pipe,  , in the [g]lmer formula. This parameter is optional, if not specified, it will perform the calculation for the first effect listed by ranef.
term	The name of the random coefficient of interest. This is the variable to the left of the pipe,  , in the [g]lmer formula. Partial matching is attempted on the intercept term so the following character strings will all return rankings based on the intercept ( <i>provided that they do not match the name of another random coefficient for that factor</i> ): c("(Intercept)", "Int", "intercep", ...).
breaks	an integer representing the number of bins to divide the group effects into, the default is 3; alternatively it can specify breaks from 0-100 for how to cut the expected rank distribution
...	additional arguments to pass to <a href="#">predictInterval</a>

**Details**

The function predicts the response at every level in the random effect term specified by the user. Then, the expected rank of each group level is binned to the number of bins specified by the user. Finally, a weighted mean of the fitted value for all observations in each bin of the expected ranks is calculated using the inverse of the variance as the weight – so that less precise estimates are

downweighted in the calculation of the mean for the bin. Finally, a standard error for the bin mean is calculated.

This function uses the formula for variance of a weighted mean recommended by Cochran (1977).

### Value

A data.frame with all unique combinations of the number of cases, rows in the newdata element, and number of bins:

**case** The row number of the observation from newdata.

**bin** The ranking bin for the expected rank, the higher the bin number, the greater the expected rank of the groups in that bin.

**AvgFitWght** The weighted mean of the fitted values for case i in bin k

**AvgFitWghtSE** The standard deviation of the mean of the fitted values for case i in bin k.

**nobs** The number of group effects contained in that bin.

### References

Gatz, DF and Smith, L. The Standard Error of a Weighted Mean Concentration. I. Bootstrapping vs other methods. *Atmospheric Environment*. 1995;11(2)1185-1193. Available at <http://www.sciencedirect.com/science/article/pii/135223109400210C>

Cochran, WG. 1977. *Sampling Techniques* (3rd Edition). Wiley, New York.

### See Also

[expectedRank](#), [predictInterval](#)

### Examples

```
#For a one-level random intercept model
m1 <- lmer(Reaction ~ Days + (1 | Subject), sleepstudy)
m1.er <- REimpact(m1, newdata = sleepstudy[1, ], breaks = 2)
#For a one-level random intercept model with multiple random terms
m2 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
#ranked by the random slope on Days
m2.er1 <- REimpact(m2, newdata = sleepstudy[1, ],
  groupFctr = "Subject", term="Days")
#ranked by the random intercept
m2.er2 <- REimpact(m2, newdata = sleepstudy[1, ],
  groupFctr = "Subject", term="int")

# You can also pass additional arguments to predictInterval through REimpact
g1 <- lmer(y ~ lectage + studage + (1|d) + (1|s), data=InstEval)
zed <- REimpact(g1, newdata = InstEval[9:12, ], groupFctr = "d", n.sims = 50,
  include.resid.var = TRUE)
zed2 <- REimpact(g1, newdata = InstEval[9:12, ], groupFctr = "s", n.sims = 50,
  include.resid.var = TRUE)
zed3 <- REimpact(g1, newdata = InstEval[9:12, ], groupFctr = "d", breaks = 5,
  n.sims = 50, include.resid.var = TRUE)
```

---

REmargins	<i>Calculate the predicted value for each observation across the distribution of the random effect terms.</i>
-----------	---

---

### Description

REmargins calculates the average predicted value for each row of a new data frame across the distribution of [expectedRank](#) for a merMod object. This allows the user to make meaningful comparisons about the influence of random effect terms on the scale of the response variable, for user-defined inputs, and accounting for the variability in grouping terms.

### Usage

```
REmargins(
  merMod,
  newdata = NULL,
  groupFctr = NULL,
  term = NULL,
  breaks = 4,
  .parallel = FALSE,
  ...
)
```

### Arguments

merMod	An object of class merMod
newdata	a data frame of observations to calculate group-level differences for
groupFctr	The name of the grouping factor over which the random coefficient of interest varies. This is the variable to the right of the pipe,  , in the [g]lmer formula. This parameter is optional, if not specified, it will perform the calculation for the first effect listed by ranef. If the length is > 1 then the combined effect of all listed groups will be calculated and marginalized over co-occurrences of those groups if desired.
term	The name of the random coefficient of interest. This is the variable to the left of the pipe,  , in the [g]lmer formula. Partial matching is attempted on the intercept term so the following character strings will all return rankings based on the intercept ( <i>provided that they do not match the name of another random coefficient for that factor</i> ): c("(Intercept)", "Int", "intercep", ...).
breaks	an integer representing the number of bins to divide the group effects into, the default is 3.
.parallel,	logical should parallel computation be used, default is TRUE
...	additional arguments to pass to <a href="#">predictInterval</a>

## Details

The function simulates the

The function predicts the response at every level in the random effect term specified by the user. Then, the expected rank of each group level is binned to the number of bins specified by the user. Finally, a weighted mean of the fitted value for all observations in each bin of the expected ranks is calculated using the inverse of the variance as the weight – so that less precise estimates are downweighted in the calculation of the mean for the bin. Finally, a standard error for the bin mean is calculated.

## Value

A data.frame with all unique combinations of the number of cases, rows in the newdata element:

... The columns of the original data taken from newdata

**case** The row number of the observation from newdata. Each row in newdata will be repeated for all unique levels of the grouping\_var, term, and breaks.

**grouping\_var** The grouping variable the random effect is being marginalized over.

**term** The term for the grouping variable the random effect is being marginalized over.

**breaks** The ntile of the effect size for grouping\_var and term

**original\_group\_level** The original grouping value for this case

**fit\_combined** The predicted value from predictInterval for this case simulated at the Nth ntile of the expected rank distribution of grouping\_var and term

**upr\_combined** The upper bound of the predicted value.

**lwr\_combined** The lower bound of the predicted value.

**fit\_XX** For each grouping term in newdata the predicted value is decomposed into its fit components via predictInterval and these are all returned here

**upr\_XX** The upper bound for the effect of each grouping term

**lwr\_XX** The lower bound for the effect of each grouping term

**fit\_fixed** The predicted fit with all the grouping terms set to 0 (average)

**upr\_fixed** The upper bound fit with all the grouping terms set to 0 (average)

**lwr\_fixed** The lower bound fit with all the grouping terms set to 0 (average)

## References

Gatz, DF and Smith, L. The Standard Error of a Weighted Mean Concentration. I. Bootstrapping vs other methods. *Atmospheric Environment*. 1995;11(2)1185-1193. Available at <http://www.sciencedirect.com/science/article/pii/135223109400210C>

Cochran, WG. 1977. *Sampling Techniques* (3rd Edition). Wiley, New York.

## See Also

[expectedRank](#), [predictInterval](#)

**Examples**

```

fm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
mf1 <- REMargins(merMod = fm1, newdata = sleepstudy[1:10,])

# You can also pass additional arguments to predictInterval through REimpact
g1 <- lmer(y ~ lectage + studage + (1|d) + (1|s), data=InstEval)
margin_df <- REMargins(g1, newdata = InstEval[20:25, ], groupFctr = c("s"),
                       breaks = 4)
margin_df <- REMargins(g1, newdata = InstEval[20:25, ], groupFctr = c("d"),
                       breaks = 3)

```

REquantile

*Identify group level associated with RE quantile***Description**

For a user specified quantile (or quantiles) of the random effect terms in a merMod object. This allows the user to easily identify the observation associated with the nth percentile effect.

**Usage**

```
REquantile(merMod, quantile, groupFctr, term = "(Intercept)")
```

**Arguments**

merMod	a merMod object with one or more random effect levels
quantile	a numeric vector with values between 0 and 100 for quantiles
groupFctr	a character of the name of the random effect grouping factor to extract quantiles from
term	a character of the random effect to extract for the grouping factor specified. Default is the intercept.

**Value**

a vector of the level of the random effect grouping term that corresponds to each quantile

**Examples**

```

fm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
REquantile(fm1, quantile = 0.25, groupFctr = "Subject")
REquantile(fm1, quantile = 0.25, groupFctr = "Subject", term = "Days")

```

---

REsdExtract	<i>Extract the standard deviation of the random effects from a merMod object</i>
-------------	--

---

**Description**

Extract the standard deviation of the random effects from a merMod object

**Usage**

```
REsdExtract(model)
```

**Arguments**

model            an object that inherits from class merMod

**Value**

a numeric vector for standard deviations of the random effects

**Examples**

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

---

REsim	<i>Simulate random effects from merMod REsim simulates random effects from merMod object posterior distributions</i>
-------	--

---

**Description**

Simulate random effects from merMod REsim simulates random effects from merMod object posterior distributions

**Usage**

```
REsim(merMod, n.sims = 200, oddsRatio = FALSE, seed = NULL)
```

**Arguments**

merMod            a merMod object from the lme4 package  
n.sims            number of simulations to use  
oddsRatio        logical, should parameters be converted to odds ratios?  
seed              numeric, optional argument to set seed for simulations

**Details**

Use the Gelman sim technique to build empirical Bayes estimates. Uses the sim function in the arm package

**Value**

a data frame with the following columns

groupFctr Name of the grouping factor

groupID Level of the grouping factor

term Name of random term (intercept/coefficient)

mean Mean of the simulations

median Median of the simulations

sd Standard deviation of the simulations, NA if oddsRatio=TRUE

**Examples**

```
require(lme4)
m2 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
re2 <- REsim(m2, 25)
head(re2)
```

---

RMSE.merMod

*Estimate the Root Mean Squared Error (RMSE) for a lmerMod*


---

**Description**

Extract the Root Mean Squared Error for a lmerMod object

**Usage**

```
RMSE.merMod(merMod, scale = FALSE)
```

**Arguments**

merMod a lmerMod object from the lme4 package

scale logical, should the result be returned on the scale of response variable standard deviations?

**Value**

a numeric which represents the RMSE

**Examples**

```
require(lme4)
m2 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy)
RMSE.merMod(m2)
```

---

sanitizeNames	<i>Clean up variable names in data frames</i>
---------------	---

---

**Description**

Strips out transformations from variable names in data frames

**Usage**

```
sanitizeNames(data)
```

**Arguments**

data            a data.frame

**Value**

a data frame with variable names cleaned to remove factor() construction

---

setup_parallel	<i>Set up parallel environment</i>
----------------	------------------------------------

---

**Description**

Set up parallel environment

**Usage**

```
setup_parallel()
```

**Value**

Nothing

---

`shinyMer`*Launch a shiny app to explore your merMod interactively*

---

**Description**

`shinyMer` launches a shiny app that allows you to interactively explore an estimated `merMod` using functions from `merTools`.

**Usage**

```
shinyMer(merMod, simData = NULL, pos = 1)
```

**Arguments**

<code>merMod</code>	An object of class "merMod".
<code>simData</code>	A data.frame to make predictions from (optional). If NULL, then the user can only make predictions using the data in the frame slot of the merMod object.
<code>pos</code>	The position of the environment to export function arguments to. Defaults to 1, the global environment, to allow shiny to run.

**Value**

A shiny app

---

`shuffle`*Randomly reorder a dataframe*

---

**Description**

Randomly reorder a dataframe by row

**Usage**

```
shuffle(data)
```

**Arguments**

<code>data</code>	a data frame
-------------------	--------------

**Value**

a data frame of the same dimensions with the rows reordered randomly

---

stripAttributes	<i>Remove attributes from a data.frame</i>
-----------------	--

---

**Description**

Strips attributes off of a data frame that come with a merMod model.frame

**Usage**

```
stripAttributes(data)
```

**Arguments**

data	a data.frame
------	--------------

**Value**

a data frame with variable names cleaned to remove all attributes except for names, row.names, and class

---

subBoot	<i>Bootstrap a subset of an lme4 model</i>
---------	--

---

**Description**

Bootstrap a subset of an lme4 model

**Usage**

```
subBoot(merMod, n = NULL, FUN, R = 100, seed = NULL, warn = FALSE)
```

**Arguments**

merMod	a valid merMod object
n	the number of rows to sample from the original data in the merMod object, by default will resample the entire model frame
FUN	the function to apply to each bootstrapped model
R	the number of bootstrap replicates, default is 100
seed	numeric, optional argument to set seed for simulations
warn	logical, if TRUE, warnings from lmer will be issued, otherwise they will be suppressed default is FALSE

**Details**

This function allows users to estimate parameters of a large merMod object using bootstraps on a subset of the data.

**Value**

a data.frame of parameters extracted from each of the R replications. The original values are appended to the top of the matrix.

**Examples**

```
(fm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy))
resultMatrix <- subBoot(fm1, n = 160, FUN = thetaExtract, R = 20)
```

---

subsetList

*Subset a data.frame using a list of conditions*

---

**Description**

Split a data.frame by elements in a list

**Usage**

```
subsetList(data, list)
```

**Arguments**

data	a data.frame
list	a named list of splitting conditions

**Value**

a data frame with values that match the conditions in the list

---

 sum.mm

*Title*


---

**Description**

Title

**Usage**

```
## S3 method for class 'mm'
sum(
  object,
  correlation = (p <= getOption("lme4.summary.cor.max")),
  use.hessian = NULL,
  ...
)
```

**Arguments**

object	a merMod object
correlation	optional p value
use.hessian	logical
...	additional arguments to pass through

**Value**

a summary of the object

---

summary.merModList

*Print the results of a merMod list*


---

**Description**

Print the results of a merMod list

**Usage**

```
## S3 method for class 'merModList'
summary(object, ...)
```

**Arguments**

object	a modList of class merModList
...	additional arguments

**Value**

summary content printed to console

**Examples**

```
sim_list <- replicate(n = 10,  
  expr = sleepstudy[sample(row.names(sleepstudy), 180),],  
  simplify=FALSE)  
fml <- "Reaction ~ Days + (Days | Subject)"  
mod <- lmerModList(fml, data = sim_list)  
print(mod)
```

---

superFactor

*Create a factor with unobserved levels*

---

**Description**

Create a factor variable and include unobserved levels for compatibility with model prediction functions

**Usage**

```
superFactor(x, fullLev)
```

**Arguments**

x                    a vector to be converted to a factor  
fullLev             a vector of factor levels to be assigned to x

**Value**

a factor variable with all observed levels of x and all levels of x in fullLev

**Examples**

```
regularFactor <- c("A", "B", "C")  
regularFactor <- factor(regularFactor)  
levels(regularFactor)  
# Now make it super  
newLevs <- c("D", "E", "F")  
regularFactor <- superFactor(regularFactor, fullLev = newLevs)  
levels(regularFactor) # now super
```

---

thetaExtract	<i>Extract theta parameters from a merMod model</i>
--------------	---

---

**Description**

A convenience function that returns the theta parameters for a `merMod` object.

**Usage**

```
thetaExtract(merMod)
```

**Arguments**

`merMod` a valid `merMod` object

**Value**

a vector of the covariance, theta, parameters from a `merMod`

**See Also**

`merMod`

**Examples**

```
(fm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy))
thetaExtract(fm1) #(a numeric vector of the covariance parameters)
```

---

VarCorr.merModList	<i>Extract the variances and correlations for random effects from a merMod list</i>
--------------------	---

---

**Description**

Extract the variances and correlations for random effects from a `merMod` list

**Usage**

```
## S3 method for class 'merModList'
VarCorr(x, sigma = 1, rdig = 3L)
```

**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.

`rdig` the number of digits to round to, integer

**Value**

a list with two elements "stddev" and "correlation" for the standard deviations and correlations averaged across models in the list

**Examples**

```
sim_list <- replicate(n = 10,
  expr = sleepstudy[sample(row.names(sleepstudy), 180),],
  simplify=FALSE)
fml <- "Reaction ~ Days + (Days | Subject)"
mod <- lmerModList(fml, data = sim_list)
VarCorr(mod)
```

---

 wiggle

*Assign an observation to different values*


---

**Description**

Creates a new data.frame with copies of the original observation, each assigned to a different user-specified value of a variable. Allows the user to look at the effect on predicted values of changing either a single variable or multiple variables.

**Usage**

```
wiggle(data, varlist, valueslist)
```

**Arguments**

data	a data frame with one or more observations to be reassigned
varlist	a character vector specifying the name(s) of the variable to adjust
valueslist	a list of vectors with the values to assign to var

**Details**

If the variable specified is a factor, then wiggle will return it as a character.

**Value**

a data.frame with each row assigned to the one of the new variable combinations. All variable combinations are returned, eg wiggling two variables with 3 and 4 variables respectively will return a new dataset with  $3 * 4 = 12$  observations.

**Examples**

```
data(iris)
wiggle(iris[3,], varlist = "Sepal.Width", valueslist = list(c(1, 2, 3, 5)))
wiggle(iris[3:5,], "Sepal.Width", valueslist = list(c(1, 2, 3, 5)))
wiggle(iris[3,], c("Sepal.Width", "Petal.Length"), list(c(1,2,3,5), c(3,5,6)))
wiggle(iris[3:5,], c("Sepal.Width", "Petal.Length"), list(c(1,2,3,5), c(3,5,6)))
```

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