Package ‘trouBBlme4SolveR’

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Title Troubles Solver for 'lme4'
Description The main function of the package aims to update 'lmer()'/glmer()' models depending on their warnings, so trying to avoid convergence and singularity problems.
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Suggests nlme (>= 3.1-123), ggplot2 (>= 2.0.0), minqa
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Description

Updates a (possibly generalized) linear mixed model computed with the library `lme4` functions `lmer` or `glmer`, in order to elude some singularity or convergence problems informed by distinct warnings or messages.

Usage

```r
dwmw(lmmodel, boundary_check = TRUE, scale = FALSE, scale_info = TRUE, 
tol = 1e-4, max_message_iter = 7, max_nAGQ = 6, 
next_optimizer = "bobyqa", next_optCtrl = list(maxfun = 2e5), 
when_next = max_message_iter - 1, verbose = FALSE)
```

Arguments

- **lmmodel**: The model of interest, output of either `lmer` or `glmer`, that is, an object of class `merMod` and subclass either `lmerMod` or `glmerMod`.
- **boundary_check**: A length 1 boolean object (TRUE [default] or FALSE), determining if the function removes those random effects which make the model singular (in the simplest situation, those with standard deviation almost 0).
- **scale**: A length 1 boolean object (TRUE or FALSE [default]), determining if the function must rescale the numeric predictors when this action is asked in a warning or message.
- **scale_info**: A length 1 boolean object (TRUE [default] or FALSE), determining if the function should cat a message when some predictor variables are on very different scales, but are not rescaled.
- **tol**: A numeric value (default is 1e-4), tolerance under which to consider if a model is singular (see boundary_check argument).
- **max_message_iter**: A numeric value (default is 7), generally the maximum number of iterations allowed to update the model. For the exception, see the Details section.
- **max_nAGQ**: A numeric value (default is 6), maximum to which increase the nAGQ argument fitting `glmer` models.
- **next_optimizer**: An optimizer (default is "bobyqa"), next to be used when model convergence is failing.
- **next_optCtrl**: A list (default is `list(maxfun=2e5)`) 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`. (Also see convergence for details of stopping tolerances for different optimizers.)
A numeric value not greater than max_message_iter - 1 (which is the default), specifying from which iteration a model convergence failing is approached with a new optimizer (next_optimizer) and with a new set of arguments to it (next_optCtrl).

verbose A length 1 boolean object (TRUE or FALSE [default]) specifying if function iterations and model updating should be verbose.

Details

If the model does not generate any warning or message, dwmw returns itself. The function rescales numeric predictors if some warning or message suggests it and the scale argument is TRUE. If the model fails to converge, it only updates the starting values for the parameters in the model through the first when_next - 1 iterations, while it also updates the optimizer and their arguments through the next iterations.

If the model is singular (there is a "boundary (singular)"-alike message) and boundary_check is TRUE, the formula is updated removing the random effects which cause the model to be singular. If all the random effects are removed, a linear or generalized linear model is computed according to the lmmodel object.

If the model has subclass glmerMod, a single scalar random effect and converges but it is nearly unidentifiable with a very large eigenvalue, then nAGQ is increased one unity while nAGQ <= max_nAGQ (and only in this case, allowing the iterations to exceed max_message_iter until nAGQ == max_nAGQ).

Value

Generally, an object of class merMod, being either an object of subclass glmerMod or an object of subclass lmerMod, corresponding to the input lmmodel argument. When all random effects are removed, an object of class glm or lm depending also on the input lmmodel.

Author(s)

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See Also

lmer, glmer, merMod lmerControl, convergence, troubleshooting, isSingular, lm and glm.

Examples

```r
if(requireNamespace("nlme")){
  library(lme4)
  data(Orthodont, package = "nlme")
  Orthodont$nsex <- as.numeric(Orthodont$Sex == "Male")
  Orthodont$nsexage <- with(Orthodont, nsex*age)
  ## Without using dwmw, the next model is singular
  fmo <- lmer(distance ~ age + (age|Subject) + (0+nsex|Subject) +
              (0 + nsexage|Subject), data = Orthodont)
  summary(fmo)

  ## Using dwmw, we remove the singularity of the model
  fmo1 <- dwmw(lmer(distance ~ age + (age|Subject) + (0+nsex|Subject) +
```
fly_parameters

(0 + nsexage|Subject), data = Orthodont))
summary(fmo1)

### It also can be used on the output object

fmo2 <- dwmw(fmo)
summary(fmo2)
}

fly_parameters


Description

Two integer variables (ValidDetections and FalseDetections) to build an outcome, two factor variables to be used as clusters for the random effects (SUR.ID and Day), three factor variables to be used as fixed effects (tm, Area and replicate), five numeric variables to be used as fixed effects (c.distance, c.tm.depth, c.receiver.depth, c.temp and c.wind) and a pair of variables extra, allowing to build a model which fails to converge.

Usage

data("fly_parameters")

Format

A data frame with 220 observations on the following 14 variables.

SUR.ID  a factor with levels 10185 10186 10250
tm  a factor with levels CT PT-04
ValidDetections a numeric vector
CountDetections a numeric vector
FalseDetections a numeric vector
replicate a factor with levels 1 2
Area  a factor with levels Drug Channel Finger
Day  a factor with levels 03/06/13 2/22/13 2/26/13 2/27/13 3/14/13
R.det  a numeric vector
c.receiver.depth a numeric vector
c.tm.depth  a numeric vector
c.temp  a numeric vector
c.wind  a numeric vector
c.distance  a numeric vector
Source

warning messages when trying to run glmer in r

Examples

data(fly_parameters)
str(fly_parameters)
df <- fly_parameters
df$SUR.ID <- factor(df$SUR.ID)
df$replicate <- factor(df$replicate)
Rdet <- cbind(df$ValidDetections,df$FalseDetections)
Unit <- factor(1:length(df$ValidDetections))

library(lme4)
m1 <- glmer(Rdet ~ tm:Area + tm:c.distance +
  c.distance:Area + c.tm.depth:Area +
  c.receiver.depth:Area + c.temp:Area +
  c.wind:Area +
  c.tm.depth + c.receiver.depth +
  c.temp + c.wind + tm + c.distance + Area +
  replicate +
  (1|SUR.ID) + (1|Day) + (1|Unit),
data = df, family = binomial(link="logit"))
summary(m1)
m1_new <- dwmm(m1, scale = TRUE, max_message_iter = 3)
summary(m1_new)

fstruction

Formula removal of singular random effects

Description

Removes those random effects from a model formula making the model to be singular.

Usage

fstruction(model, tol = 1e-4)

Arguments

model The model of interest, output of either lmer or glmer, that is, an object of class lmerMod and subclass either lmerMod or glmerMod.
tol A numeric value (default is 1e-4), tolerance under which to determine if the random effects make the model to be singular.
Value

A list with a string component dstring which is the formula as character updated (to be used by update) after removing the singular random effects and, when no all the random effects are removed two other string components:

- betchar: a character vector with the random effect terms removed from the formula.
- inchar: a character vector having the same length as betchar with the corresponding groups (aggregate levels) for which the random effects are removed.

Author(s)

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See Also

formula, update

Examples

```r
if(requireNamespace("nlme")){
  library(lme4)
  data(Orthodont, package = "nlme")
  Orthodont$nsex <- as.numeric(Orthodont$Sex == "Male")
  Orthodont$nsexage <- with(Orthodont, nsex*age)
  ## The next model is singular
  fmo <- lmer(distance ~ age + (age|Subject) + (0+nsex|Subject) +
              (0 + nsexage|Subject), data = Orthodont)
  summary(fmo)

  ## Let's see the formula updated (as a string)
  fstruction(fmo)
}
```

Data example github issue 618 on the lme4 repository

Description

Three variables, being one dichotomous, other continuous and the last, categorical. Data for the first reproducible example for issue 618 on the lme4 Github-repository, making glmer to produce a warning for the model outcome_dead ~ AGE + (1|ZIP).

Usage

data("issue618")
Format
A data frame with 1000 observations on the following 3 variables.

outcome_dead an integer vector
AGE an integer vector
ZIP an integer vector

Source
convergence issues with continuous variables in model

Examples

data(issue618)
str(issue618)

library(lme4)
m1 <- glmer(outcome_dead ~ AGE + (1|ZIP), family = binomial, data = issue618)
summary(m1)
m2 <- dmmw(m1, scale = TRUE)
summary(m2)

Description
Three variables, being one dichotomous, other continuous and the last, categorical. Data for the first reproducible example for issue 618 on the lme4 Github-repository, making glmer to produce a warning for the model outcome_dead ~ AGE + (1|ZIP).

Usage
data("issue618")

Format
A data frame with 1000 observations on the following 3 variables.

outcome_dead an integer vector
AGE an integer vector
ZIP an integer vector
Source

convergence issues with continuous variables in model

Examples

data(issue618large)
str(issue618large)
library(lme4)
m1 <- glmer(outcome_dead ~ AGE + (1|ZIP), family = binomial, data = issue618large)
summary(m1)
m2 <- dwmw(m1, scale = TRUE)
summary(m2)
m3 <- glmer(outcome_dead ~ scale(AGE) + (1|ZIP), family = binomial, data = issue618large,
nAGQ=20)
aa <- allFit(m3)
ss <- summary(aa)
ss$msgs ## all NULL

plants

Data for the SO question [R](https://stackoverflow.com/questions/60028673/lme4-error-boundary-singular-fit-see-issingularlme4) error: boundary (singular) fit; see ?isSingular.

Description

Five variables, being one continuous to use as outcome (Weight), and four factors, of which two (Rep and PLANT) are used as clusters for the random effects of a singular linear mixed model (Weight ~ 1 + (1|Rep:PLANT)).

Usage

data("plants")

Format

A data frame with 536 observations on the following 5 variables.

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rep</td>
<td>a factor with levels 1 2</td>
</tr>
<tr>
<td>Weight</td>
<td>a numeric vector</td>
</tr>
<tr>
<td>PLANT</td>
<td>a factor with levels 1 2 3 4</td>
</tr>
<tr>
<td>X</td>
<td>a factor with levels 24 12 21 11 13 14 22 23</td>
</tr>
</tbody>
</table>
**treatments**

**Source**

lme4 error: boundary (singular) fit: see ?isSingular

**Examples**

```r
data(plants)
str(plants)

library(lme4)
fit <- lmer(Weight ~ 1 + (1|PLANT:Rep), data = plants)
summary(fit)
fit2 <- dwmw(fit)
summary(fit2)
```

---

**treatments**

<table>
<thead>
<tr>
<th>Data for the Cross Validated question</th>
</tr>
</thead>
</table>

**Description**

A continuous variable to be used as outcome (total_no), another to be used as predictor (week), two factor variables to be used as predictors (treatment and fzone) and another factor to be used as cluster for the random effects (plot) of a Poisson model failing to converge, and an extra variable.

**Usage**

```r
data("treatments")
```

**Format**

A data frame with 142 observations on the following 7 variables.

- `plot` a numeric vector
- `date` a character vector
- `total_no` a numeric vector
- `zone` a character vector
- `treatment` a character vector
- `week` a numeric vector
- `fzone` a character vector
Source

lme4: glmer() warning messages with count data mixed-effects model and how to proceed with model fit

Examples

data(treatments)
str(treatments)

library(lme4)
glmm.1 <- glmer(total_no ~ week*treatment*fzone + (1|plot), data = treatments,
                       family = poisson)
summary(glmm.1)
glmm.11 <- dwmw(glmm.1, verbose = TRUE)
summary(glmm.11)
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