

# 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.

**Depends** R (>= 4.1.0)

**Imports** lme4 (>= 1.1-28)

**Suggests** nlme (>= 3.1-123), ggplot2 (>= 2.0.0), minqa

**License** GPL-3

**URL** <https://gitlab.com/iagogv/troudblme4solver>

**BugReports** <https://gitlab.com/iagogv/troudblme4solver/-/issues>

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dwmw

*Solver for (generalized) linear MM warnings*

## 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

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

## Arguments

|                               |  |
|-------------------------------|--|
| <code>lmmodel</code>          | The model of interest, output of either <code>lmer</code> or <code>glmer</code> , that is, an object of class <code>merMod</code> and <i>subclass</i> either <code>lmerMod</code> or <code>glmerMod</code> .     |
| <code>boundary_check</code>   | 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). |
| <code>scale</code>            | 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 <i>warning</i> or <i>message</i> .                           |
| <code>scale_info</code>       | 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.                          |
| <code>tol</code>              | A numeric value (default is 1e-4), tolerance under which to consider if a model is singular (see <code>boundary_check</code> argument).  |
| <code>max_message_iter</code> | A numeric value (default is 7), generally the maximum number of iterations allowed to update the model. For the exception, see the Details section.  |
| <code>pri_nAGQ</code>         | A length 1 boolean object (TRUE or FALSE [default]), determining if the function prioritizes incrising nAGQ over updating model start parameters when both are possible solutions to warned issues.              |
| <code>max_nAGQ</code>         | A numeric value (default is 6), maximum to which increase the nAGQ argument fitting <code>glmer</code> models.   |
| <code>next_optimizer</code>   | An optimizer (default is "bobyqa"), next to be used when model convergence is failing.   |

|              |  |
|--------------|--|
| next_optCtrl | A <a href="#">list</a> (default is <code>list(maxfun=2e5)</code> ) of additional arguments to be passed to the nonlinear optimizer (see <a href="#">Nelder_Mead</a> , <a href="#">bobyqa</a> ). In particular, both <code>Nelder_Mead</code> and <code>bobyqa</code> use <code>maxfun</code> to specify the maximum number of function evaluations they will try before giving up - in contrast to <code>optim</code> and <code>optimx</code> -wrapped optimizers, which use <code>maxit</code> . (Also see <a href="#">convergence</a> for details of stopping tolerances for different optimizers. |
| when_next    | A numeric value not greater than <code>max_message_iter - 1</code> (which is the default), specifying from which iteration a model convergence failing is approached with a new optimizer ( <code>next_optimizer</code> ) and with a new set of arguments to it ( <code>next_optCtrl</code> ).   |
| 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)"*-like 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 `lmmode1` 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 `lmmode1` argument. When all random effects are removed, an object of class `glm` or `lm` depending also on the input `lmmode1`.

### Author(s)

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### See Also

[lmer](#), [glmer](#), [merMod](#) [lmerControl](#), [convergence](#), [troubleshooting](#), [isSingular](#), [lm](#) and [glm](#).

### Examples

```
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 dmmw, we remove the singularity of the model
fmo1 <- dmmw(lmer(distance ~ age + (age|Subject) + (0+nsex|Subject) +
  (0 + nsexage|Subject), data = Orthodont))
summary(fmo1)

## It also can be used on the output object

fmo2 <- dmmw(fmo)
summary(fmo2)
}
```

---

|                |   |
|----------------|---|
| fly_parameters | <i>Data for the SO question <a href="https://stackoverflow.com/questions/23478792/warning-messages-when-trying-to-run-glmer-in-r">https://stackoverflow.com/questions/23478792/warning-messages-when-trying-to-run-glmer-in-r</a> messages when trying to run glmer in r.</i> |
|----------------|---|

---

## 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 <- dnmw(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 <a href="#">lmer</a> or <a href="#">glmer</a> , that is, an object of class <a href="#">merMod</a> and <i>subclass</i> either <a href="#">lmerMod</a> or <a href="#">glmerMod</a> . |
| 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**

```
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)
}
```

**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

Model is nearly unidentifiable: very large eigenvalue -  
Rescale variables?

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 <- dnmw(m1, scale = TRUE)  
summary(m2)
```

---

issue618large

*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

Model is nearly unidentifiable: very large eigenvalue -  
Rescale variables?

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 <- dnmw(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 [Rhrefhttps://stackoverflow.com/questions/60028673/lme4-error-boundary-singular-fit-see-issingularlme4](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.

Line a factor with levels Line1 Line10 Line11 Line12 Line13 Line14 Line15 Line16 Line17  
Line18 Line19 Line2 Line20 Line21 Line22 Line23 Line24 Line25 Line26 Line27 Line28  
Line29 Line3 Line30 Line31 Line32 Line33 Line34 Line35 Line36 Line37 Line38 Line39  
Line4 Line40 Line41 Line42 Line43 Line44 Line45 Line46 Line47 Line48 Line49 Line5  
Line50 Line51 Line52 Line53 Line54 Line55 Line56 Line57 Line58 Line59 Line6 Line60  
Line61 Line62 Line63 Line64 Line65 Line66 Line67 Line7 Line8 Line9

Rep a factor with levels 1 2

Weight a numeric vector

PLANT a factor with levels 1 2 3 4

X a factor with levels 24 12 21 11 13 14 22 23

**Source**

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

**Examples**

```
data(plants)
str(plants)

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

---

treatments

*Data for the Cross Validated question  
Rhref<https://stats.stackexchange.com/questions/575666/lme4-glmer-warning-messages-with-count-data-mixed-effects-model-and-how-to-prlme4-glmer-warning-messages-with-count-data-mixed-effects-model-and-how-to-proceed-with-model-fit>*

---

**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**

```
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 <- dnmw(glmm.1, verbose = TRUE)
summary(glmm.11)
```

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