

# Package ‘robustlmm’

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**Type** Package

**Title** Robust Linear Mixed Effects Models

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**Description** A method to fit linear mixed effects models robustly.  
Robustness is achieved by modification of the scoring equations  
combined with the Design Adaptive Scale approach.

**License** GPL-2

**URL** <https://github.com/kollerma/robustlmm>

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robustlmm-package	<i>Robust linear mixed effects models</i>
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### Description

robustlmm provides functions for estimating linear mixed effects models in a robust way.

The main workhorse is the function `rlmer`; it is implemented as direct robust analogue of the popular `lmer` function of the `lme4` package. The two functions have similar abilities and limitations. A wide range of data structures can be modeled: mixed effects models with hierarchical as well as complete or partially crossed random effects structures are possible. While the `lmer` function is optimized to handle large datasets efficiently, the computations employed in the `rlmer` function are more complex and for this reason also more expensive to compute. The two functions have the same limitations in the support of different random effect and residual error covariance structures. Both support only diagonal and unstructured random effect covariance structures.

The `robustlmm` package implements most of the analysis tool chain as is customary in R. The usual functions such as `summary`, `coef`, `resid`, etc. are provided as long as they are applicable for this type of models (see `rlmerMod-class` for a full list). The functions are designed to be as similar as possible to the ones in the `lme4` package to make switching between the two packages easy.

Details on the implementation and example analyses are provided in the package vignette available via `vignette("rlmer")` (Koller 2016).

### References

- Manuel Koller (2016). `robustlmm`: An R Package for Robust Estimation of Linear Mixed-Effects Models. *Journal of Statistical Software*, 75(6), 1-24. doi:10.18637/jss.v075.i06
- Manuel Koller (2013). Robust estimation of linear mixed models. (Doctoral dissertation, Diss., Eidgenössische Technische Hochschule ETH Zürich, Nr. 20997, 2013).

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chgDefaults	<i>Change default arguments</i>
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**Description**

Change the default arguments for a PsiFunction instance.

**Usage**

```
## S4 method for signature 'Rcpp_SmoothPsi'
chgDefaults(object, ...)
## S4 method for signature 'Rcpp_HuberPsi'
chgDefaults(object, ...)
## S4 method for signature 'Rcpp_PsiFunction'
chgDefaults(object, ...)
## S4 method for signature 'Rcpp_PsiFunctionToPropIIPsiFunctionWrapper'
chgDefaults(object, ...)
```

**Arguments**

object	PsiFunction instance to convert
...	arguments to change

**Note**

Note that names of named arguments are ignored. Only the order of the arguments is considered when assigning new arguments.

**Examples**

```
sPsi <- chgDefaults(smoothPsi, k=2)
curve(smoothPsi$psi(x), 0, 3)
curve(sPsi$psi(x), 0, 3, color="blue", add=TRUE)
```

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compare	<i>Create comparison charts for multiple fits</i>
---------	---

---

**Description**

Use compare to quickly compare the estimated parameters of the fits of multiple lmerMod or rlmerMod objects.

The functions `xtable.comparison.table` and `print.xtable.comparison.table` are wrapper functions for the respective `xtable` and `print.xtable` functions.

The function `getInfo` is internally used to prepare object for producing a comparison chart in `compare`.

**Usage**

```

compare(..., digits = 3, dnames = NULL,
        show.rho.functions = TRUE)

## S3 method for class 'comparison.table'
xtable(x, caption = NULL,
       label = NULL, align = NULL, digits = NULL,
       display = NULL, ...)

## S3 method for class 'xtable.comparison.table'
print(x,
      add.hlines = TRUE, latexify.namescol = TRUE,
      include.rownames = FALSE, ...)

getInfo(object, ...)

## S3 method for class 'lmerMod'
getInfo(object, ...)

## S3 method for class 'rmlmerMod'
getInfo(object, ...)

```

**Arguments**

...	objects to compare, or, for the <code>xtable</code> functions: passed to the respective <code>xtable</code> function.
<code>digits</code>	number of digits to show in output
<code>dnames</code>	names of objects given as arguments (optional)
<code>show.rho.functions</code>	whether to show rho functions in output.
<code>x</code>	object of class "comparison.table" or "xtable.comparison.table"
<code>caption</code>	see <code>xtable</code> .
<code>label</code>	see <code>xtable</code> .
<code>align</code>	see <code>xtable</code> .
<code>display</code>	see <code>xtable</code> .
<code>add.hlines</code>	replace empty lines in comparison table by hlines. Supersedes <code>hline.after</code> argument of <code>print.xtable</code> .
<code>latexify.namescol</code>	replace "sigma" and "x" in the first column by latex equivalents.
<code>include.rownames</code>	include row numbers (the object returned by <code>xtable.comparison.table</code> includes names in the first column)
<code>object</code>	object

**Value**

getInfo returns alist with estimated coefficients, estimated variance components, sigma, deviance and parameter configuration used to fit.

**See Also**

[xtable](#)  
[print.xtable](#)

**Examples**

```
## Not run:
fm1 <- lmer(Yield ~ (1|Batch), Dyestuff)
fm2 <- rlmr(Yield ~ (1|Batch), Dyestuff)
compare(fm1, fm2)
require(xtable)
xtable(compare(fm1, fm2))
str(getInfo(fm1))

## End(Not run)
```

getME

*Extract or Get Generalize Components from a Fitted Mixed Effects Model*

**Description**

Extract (or “get”) “components” – in a generalized sense – from a fitted mixed-effects model, i.e. from an object of class “[rlmerMod](#)” or “[merMod](#)”.

The function theta is short for getME(, “theta”).

**Usage**

```
## S3 method for class 'rlmerMod'
getME(object,
  name = c("X", "Z", "Zt", "Ztlist", "y", "mu",
    "u", "b.s", "b", "Gp", "Tp", "Lambda",
    "Lambdat", "A", "U_b", "Lind", "sigma",
    "flist", "beta", "theta", "n_rtrms",
    "n_rfacs", "cnms", "devcomp", "offset",
    "lower", "rho_e", "rho_b", "rho_sigma_e",
    "rho_sigma_b", "M", "w_e", "w_b",
    "w_b_vector", "w_sigma_e", "w_sigma_b",
    "w_sigma_b_vector", "is_REML"), ...)

theta(object)
```

**Arguments**

**object** a fitted mixed-effects model of class "r1merMod", i.e. typically the result of `r1mer()`.

**name** a character string specifying the name of the "component". Possible values are:

**X** fixed-effects model matrix

**Z** random-effects model matrix

**Zt** transpose of random-effects model matrix

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

**y** response vector

**mu** conditional mean of the response

**u** conditional mode of the "spherical" random effects variable

**b.s** synonym for "u"

**b** onditional 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.

**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 total number of random effects

**Lambda** relative covariance factor of the random effects.

**U\_b** synonym for "Lambda"

**Lambdat** transpose of the relative covariance factor of the random effects.

**Lind** index vector for inserting elements of  $\theta$  into the nonzeros of  $\Lambda$

**A** Scaled sparse model matrix (class "dgCMatrix") for the unit, orthogonal random effects,  $U$ , equal to `getME(.,"Zt") %% getME(.,"Lambdat")`

**sigma** residual standard error

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

**beta** fixed-effects parameter estimates (identical to the result of `fixef`, but without names)

**theta** random-effects parameter estimates: these are parameterized as the relative Cholesky factors of each random effect term

**n\_rtrms** number of random-effects terms

**n\_rfacs** number of distinct random-effects grouping factors

**cnms** the "component names", a 'list'.

**devcomp** a list consisting of a named numeric vector, "cmp", and a named integer vector, "dims", describing the fitted model

**offset** model offset

**lower** lower bounds on model parameters (random effects parameters only)

**rho\_e** rho function used for the residuals

**rho\_b** list of rho functions used for the random effects

**rho\_sigma\_e** rho function used for the residuals when estimating sigma

**rho\_sigma\_b** list of rho functions used for the random effects when estimating the covariance parameters

**M** list of matrices, blocks of the Henderson's equations and the matrices used for computing the linear approximations of the estimates of beta and spherical random effects.

**w\_e** robustness weights associated with the observations

**w\_b** robustness weights associated with the spherical random effects, returned in the same format as [ranef\(\)](#)

**w\_b\_vector** robustness weights associated with the spherical random effects, returned as one long vector

**w\_sigma\_e** robustness weights associated with the observations when estimating sigma

**w\_sigma\_b** robustness weights associated with the spherical random effects when estimating the covariance parameters, returned in the same format as [ranef\(\)](#)

**w\_sigma\_b\_vector** robustness weights associated with the spherical random effects when estimating the covariance parameters, returned as one long vector

**is\_REML** returns TRUE for `rlmerMod`-objects (for compatibility with `lme4`)

... potentially further arguments passed to and from methods; none here at the moment.

## Details

The goal is to provide “everything a user may want” from a fitted “`rlmerMod`” 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

[getCall\(\)](#); more standard methods for `rlmerMod` objects, such as [ranef](#), [fixef](#), [vcov](#), etc.: see `methods(class="rlmerMod")`

## Examples

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

## doFit = FALSE to speed up example
(fm1 <- rlmer(Reaction ~ Days + (Days|Subject), sleepstudy,
             method="DASvar", doFit=FALSE))
Z <- getME(fm1, "Z")
stopifnot(is(Z, "CsparseMatrix"),
          c(180,36) == dim(Z),
          all.equal(fixef(fm1), getME(fm1, "beta"),
                   check.attributes=FALSE, tolerance = 0))
```

```
## All that can be accessed [potentially ..]:
(nmME <- eval(formals(robustlmm:::getME.rlmerMod)$name))
% dont..
stopifnot(all.equal(theta(fm1), getME(fm1, "theta")))
```

---

other

*Other methods*

---

## Description

Other miscellaneous utilities for instances of the PsiFunction class.

## Usage

```
## S4 method for signature 'Rcpp_SmoothPsi'
show(object)
## S4 method for signature 'Rcpp_HuberPsi'
show(object)
## S4 method for signature 'Rcpp_PsiFunction'
show(object)
## S4 method for signature 'Rcpp_PsiFunctionToPropIIPsiFunctionWrapper'
show(object)
```

## Arguments

object            instance of class PsiFunction to be plotted

## Examples

```
show(smoothPsi)
```

---

plot-methods

*Plot an Object of the "Psi Function" Class*

---

## Description

The `plot` method objects of class PsiFunction simply visualizes the  $\rho()$ ,  $\psi()$ , and weight functions and their derivatives.



**Usage**

```
## S4 method for signature 'Rcpp_SmoothPsi'
plot(x, y,
     which = c("rho", "psi", "Dpsi", "wgt", "Dwgt"),
     main = "full",
     col = c("black", "red3", "blue3", "dark green", "light green"),
     leg.loc = "right", ...)
## S4 method for signature 'Rcpp_HuberPsi'
plot(x, y,
     which = c("rho", "psi", "Dpsi", "wgt", "Dwgt"),
     main = "full",
     col = c("black", "red3", "blue3", "dark green", "light green"),
     leg.loc = "right", ...)
## S4 method for signature 'Rcpp_PsiFunction'
plot(x, y,
     which = c("rho", "psi", "Dpsi", "wgt", "Dwgt"),
     main = "full",
     col = c("black", "red3", "blue3", "dark green", "light green"),
     leg.loc = "right", ...)
## S4 method for signature 'Rcpp_PsiFunctionToPropIIPsiFunctionWrapper'
plot(x, y,
     which = c("rho", "psi", "Dpsi", "wgt", "Dwgt"),
     main = "full",
     col = c("black", "red3", "blue3", "dark green", "light green"),
     leg.loc = "right", ...)
```

**Arguments**

x	instance of class <code>PsiFunction</code> to be plotted
y	(optional) vector of abscissa values (to plot object at).
which	<a href="#">character</a> vector of slots to be included in plot; by default, all of the slots are included
main	string or logical indicating the kind of plot title; either "full", "short" or FALSE which chooses a full, a short or no main title at all.
col	colors to be used for the different slots
leg.loc	legend placement, see also x argument of <a href="#">legend</a>
...	passed to <a href="#">matplot</a>

**Note**

If you want to specify your own title, use `main=FALSE`, and a subsequent `title(...)` call.

**See Also**

[psi-functions](#).

**Examples**

```

plot(huberPsiRcpp)
plot(huberPsiRcpp, which=c("psi", "Dpsi", "wgt"),
     main="short", leg = "topleft")

plot(smoothPsi)
## Plotting aspect ratio = 1:1 :
plot(smoothPsi, asp=1, main="short",
     which = c("psi", "Dpsi", "wgt", "Dwgt"))

```

---

plot.rlmerMod	<i>Plot Method for "rlmerMod" objects.</i>
---------------	--

---

**Description**

Diagnostic plots for objects of class `rlmerMod` and `lmerMod`.

**Usage**

```

## S3 method for class 'rlmerMod'
plot(x, y = NULL, which = 1:4,
     title = c("Fitted Values vs. Residuals",
              "Normal Q-Q vs. Residuals",
              "Normal Q-Q vs. Random Effects",
              "Scatterplot of Random Effects for Group \"%s\""),
     multiply.weights = FALSE, ...)

## S3 method for class 'rlmerMod_plots'
print(x,
      ask = interactive() & length(x) > 1, ...)

```

**Arguments**

<code>x</code>	an object as created by <code>rlmer</code> or <code>lmer</code> ; or an object as created by <code>plot.rlmerMod</code>
<code>y</code>	currently ignored.
<code>which</code>	integer number between 1 and 4 to specify which plot is desired.
<code>title</code>	Titles for the different plots. The fourth item can be a format string passed to <code>sprintf</code> to add the name of the current group.
<code>multiply.weights</code>	multiply the residuals / random effects with the robustness weights when producing the Q-Q plots.
<code>ask</code>	waits for user input before displaying each plot.
<code>...</code>	currently ignored.

**Details**

The robustness weights for estimating the fixed and random effects are used in the plots, e.g., the ones returned by `getME(object, "w_e")` and `getME(object, "w_b")`.

**Value**

a list of plots of class `ggplot` that can be used for further modification before plotting (using `print`).

**See Also**

[getME](#), [ggplot](#)

**Examples**

```
## Not run:
rfm <- rlmr(Yield ~ (1|Batch), Dyestuff)
plot(rfm)
fm <- lmer(Reaction ~ Days + (Days|Subject), sleepstudy)
plot.rlmrMod(fm)

## End(Not run)
```

---

psi-functions

*Classical, Huber and smoothed Huber psi- or rho-functions*


---

**Description**

$\psi$ -functions are used by `rlmer` in the estimating equations and to compute robustness weights. Change tuning parameters using `chgDefaults` and convert to squared robustness weights using the `psi2propII` function.

**Details**

The “**classical**”  $\psi$ -function `cPsi` can be used to get a non-robust, i.e., classical, fit. The `psi` slot equals the identity function, and the `rho` slot equals quadratic function. Accordingly, the robustness weights will always be 1 when using `cPsi`.

The **Huber**  $\psi$ -function `huberPsiRcpp` is identical to the one in the package `robustbase`. The `psi` slot equals the identity function within  $\pm k$  (where  $k$  is the tuning parameter). Outside this interval it is equal to  $\pm k$ . The `rho` slot equals the quadratic function within  $\pm k$  and a linear function outside.

The **smoothed Huber**  $\psi$ -function is very similar to the regular Huber  $\psi$ -function. Instead of a sharp bend like the Huber function, the smoothed Huber function bends smoothly. The first tuning constant,  $k$ , can be compared to the tuning constant of the original Huber function. The second tuning constant,  $s$ , determines the smoothness of the bend.

**See Also**

[chgDefaults](#) and [psi2propII](#) for changing tuning parameters; [psi\\_func-class](#) for a more detailed description of the slots; `PsiFunction` C++ class for a base class to create custom  $\psi$ -functions.

**Examples**

```

plot(cPsi)
plot(huberPsiRcpp)
plot(smoothPsi)
curve(cPsi$psi(x), -3, 3)
curve(smoothPsi$psi(x), -3, 3, add=TRUE, col="red")
curve(huberPsiRcpp$psi(x), -3, 3, add=TRUE, col="blue")

```

---

psi2propII

*Convert to Proposal II weight function*


---

**Description**

Converts the PsiFunction instance into one that corresponds to Proposal II, i.e., a function of the squared weights. The other elements of the PsiFunction instance are adapted accordingly.

**Usage**

```

## S4 method for signature 'Rcpp_SmoothPsi'
psi2propII(object, ...)
## S4 method for signature 'Rcpp_HuberPsi'
psi2propII(object, ...)
## S4 method for signature 'Rcpp_PsiFunction'
psi2propII(object, ...)
## S4 method for signature 'Rcpp_PsiFunctionToPropIIPsiFunctionWrapper'
psi2propII(object, ...)

```

**Arguments**

object	PsiFunction instance to convert
...	optional, new default arguments passed to chgDefaults.

**Examples**

```

par(mfrow=c(2,1))
plot(smoothPsi)
plot(psi2propII(smoothPsi))

```

---

residuals.rlmerMod      *Get residuals*


---

**Description**

The per-observation residuals are returned, i.e., the difference of the observation and the fitted value including random effects. With type one can specify whether the weights should be used or not.

**Usage**

```
## S3 method for class 'rlmerMod'
residuals(object,
  type = c("response", "weighted"), scaled = FALSE, ...)
```

**Arguments**

object	rlmerMod object
type	type of residuals
scaled	scale residuals by residual standard deviation (=scale parameter)?
...	ignored

**Examples**

```
## Not run:
fm <- rlmer(Yield ~ (1|Batch), Dyestuff)
stopifnot(all.equal(resid(fm, type="weighted"),
  resid(fm) * getME(fm, "w_e")))

## End(Not run)
```

---

rlmer      *Robust linear mixed models*


---

**Description**

Robust estimation of linear mixed effects models, for hierarchical nested and non-nested, e.g., crossed, datasets.

The `lmerNoFit` function can be used to get trivial starting values. This is mainly used to verify the algorithms to reproduce the fit by `lmer` when starting from trivial initial values.

**Usage**

```
rLmer(formula, data, ..., method = "DAStau",
      rho.e = smoothPsi, rho.b = smoothPsi, rho.sigma.e,
      rho.sigma.b, rel.tol = 1e-08,
      max.iter = 40 * (r + 1)^2, verbose = 0, doFit = TRUE,
      init)

lmerNoFit(formula, data = NULL, ..., initTheta)
```

**Arguments**

formula	a two-sided linear formula object describing the fixed-effects part of the model, with the response on the left of a <code>~</code> operator and the terms, separated by <code>+</code> operators, on the right. The vertical bar character <code> </code> separates an expression for a model matrix and a grouping factor.
data	an optional data frame containing the variables named in formula. By default the variables are taken from the environment from which <code>lmer</code> is called.
...	Additional parameters passed to <code>lmer</code> to find the initial estimates. See <a href="#">lmer</a> .
method	method to be used for estimation of theta and sigma, see <a href="#">Details</a> .
rho.e	object of class <code>psi_func</code> , specifying the functions to use for the huberization of the residuals.
rho.b	object of class <code>psi_func</code> or list of such objects (see <a href="#">Details</a> ), specifying the functions to use for the huberization of the random effects.
rho.sigma.e	object of class <code>psi_func</code> , specifying the weight functions to use for the huberization of the residuals when estimating the variance components, use the <a href="#">psi2propII</a> function to specify squared weights and custom tuning parameters.
rho.sigma.b	(optional) object of class <code>psi_func</code> or list of such objects, specifying the weight functions to use for the huberization of the random effects when estimating the variance components (see <a href="#">Details</a> ). Use <a href="#">psi2propII</a> to specify squared weights and custom tuning parameters or <a href="#">chgDefaults</a> for regular weights for variance components including correlation parameters.
rel.tol	relative tolerance used as criteria in the fitting process.
max.iter	maximum number of iterations allowed.
verbose	verbosity of output. Ranges from 0 (none) to 3 (a lot of output)
doFit	logical scalar. When <code>doFit = FALSE</code> the model is not fit but instead a structure with the model matrices for the random-effects terms is returned (used to speed up tests). When <code>doFit = TRUE</code> , the default, the model is fit immediately.
init	optional <code>lmerMod</code> - or <code>rLmerMod</code> -object to use for starting values, a list with elements <code>'fixef'</code> , <code>'u'</code> , <code>'sigma'</code> , <code>'theta'</code> , or a function producing an <code>lmerMod</code> object.
initTheta	parameter to initialize theta with (optional)

## Details

**Overview:** This function implements a robust approach of fitting linear mixed effect models. It can be used much like the function `lmer` in the package `lme4`. The supported models are the same as for `lmer` (gaussian family only). The robust approach used is based on the robustification of the scoring equations and an application of the Design Adaptive Scale approach.

Example analyses and theoretical details on the method are available in the vignette (see `vignette("r1mer")`).

Models are specified using the `formula` argument, using the same syntax as for `lmer`. Additionally, one also needs to specify what robust scoring or weight functions are to be used (arguments starting with `rho.`). By default a smoothed version of the Huber function is used. Furthermore, the `method` argument can be used to speed up computations at the expense of accuracy of the results.

**Computation methods:** Currently, there are two different methods available for fitting models. They only differ in how the consistency factors for the Design Adaptive Scale estimates are computed. Available fitting methods for `theta` and `sigma.e`:

- `DAStau` (default): For this method, the consistency factors are computed using numerical quadrature. This is slower but yields more accurate results. This is the direct analogue to the DAS-estimate in robust linear regression.
- `DASvar`: This method computes the consistency factors using a direct approximation which is faster but less accurate. For complex models with correlated random effects with more than one correlation term, this is the only method available.

**Weight functions:** The tuning parameters of the weight functions “rho” can be used to adjust robustness and efficiency of the resulting estimates (arguments `rho.e`, `rho.b`, `rho.sigma.e` and `rho.sigma.b`). Better robustness will lead to a decrease of the efficiency. By default, the tuning parameters are set to yield estimates with approximately 95% efficiency for the fixed effects. The variance components are estimated with a lower efficiency but better robustness properties.

One has to use different weight functions and tuning parameters for simple variance components and for such including correlation parameters. By default, they are chosen appropriately to the model at hand. However, when using the `rho.sigma.e` and `rho.sigma.b` arguments, it is up to the user to specify the appropriate function.

- For simple variance components and the residual error scale use the function `psi2propII` to change the tuning parameters. This is similar to Proposal II in the location-scale problem (i.e., using the squared robustness weights of the location estimate for the scale estimate; otherwise the scale estimate is not robust).
- For random effects modeled with correlation parameters (referred to as nondiagonal case below), use the `chgDefaults` function to change the tuning parameters. The parameter estimation problem is multivariate, unlike the case without correlation where the problem was univariate. For the employed estimator, this amounts to switching from simple scale estimates to estimating correlation matrices. Therefore different weight functions have to be used. Squaring of the weights (using the function `psi2propII`) is no longer necessary. To yield estimates with the same efficiency, the tuning parameters for the nondiagonal are generally larger than for the simple case. As a rule of thumb, one may use the squared tuning parameters of the simple case for the nondiagonal case.

Tables of tuning factors are given in the vignette (`vignette("r1mer")`). For the smoothed Huber function the tuning parameters to get approximately 95% efficiency are  $k = 2.28$  for

simple variance components and  $k = 5.11$  for variance components including correlation parameters.

**Specifying (multiple) weight functions:** If custom weight functions are specified using the argument `rho.b` (`rho.e`) but the argument `rho.sigma.b` (`rho.sigma.e`) is missing, then the squared weights are used for simple variance components and the regular weights are used for variance components including correlation parameters. The same tuning parameters will be used, to get higher efficiency one has to specify the tuning parameters by hand using the [psi2propII](#) and [chgDefaults](#) functions.

To specify separate weight functions `rho.b` and `rho.sigma.b` for different variance components, it is possible to pass a list instead of a `psi_func` object. The list entries correspond to the groups as shown by `VarCorr(.)` when applied to the model fitted with `lmer`. A set of correlated random effects count as just one group.

### Value

object of class `rlmerMod`.

### Author(s)

Manuel Koller, with thanks to Vanda Lourenço for improvements.

### See Also

[lmer](#), [vignette\("rlmer"\)](#)

### Examples

```
## dropping of VC
system.time(print(rlmer(Yield ~ (1|Batch), Dyestuff2, method="DASvar")))

## Not run:
## Default method "DAStau"
system.time(rfm.DAStau <- rlmer(Yield ~ (1|Batch), Dyestuff))
summary(rfm.DAStau)
## DASvar method (faster, less accurate)
system.time(rfm.DASvar <- rlmer(Yield ~ (1|Batch), Dyestuff,
                               method="DASvar"))

## compare the two
compare(rfm.DAStau, rfm.DASvar)

## Fit variance components with higher efficiency
## psi2propII yields squared weights to get robust estimates
rlmer(diameter ~ 1 + (1|plate) + (1|sample), Penicillin,
      rho.sigma.e = psi2propII(smoothPsi, k = 2.28),
      rho.sigma.b = psi2propII(smoothPsi, k = 2.28))

## use chgDefaults for variance components including
## correlation terms (regular, non squared weights suffice)
rlmer(Reaction ~ Days + (Days|Subject), sleepstudy,
      rho.sigma.e = psi2propII(smoothPsi, k = 2.28),
      rho.sigma.b = chgDefaults(smoothPsi, k = 5.11, s=10))
```



```
r1mer(Yield ~ (1|Batch), Dyestuff, init = lmerNoFit)
## End(Not run)
```

---

r1merMod-class	<i>r1merMod Class</i>
----------------	-----------------------

---

## Description

Class "r1merMod" of Robustly Fitted Mixed-Effect Models

## Details

A robust mixed-effects model as returned by [r1mer](#).

## Objects from the Class

Objects are created by calls to [r1mer](#).

## Methods

Almost all methods available from objects returned from [lmer](#) are also available for objects returned by [r1mer](#). They usage is the same.

It follows a list of some the methods that are exported by this package:

- [coef](#)
- [deviance](#) (disabled, see below)
- [extractAIC](#) (disabled, see below)
- [family](#)
- [fitted](#)
- [fixef](#)
- [formula](#)
- [getInfo](#)
- [isGLMM](#)
- [isLMM](#)
- [isNLMM](#)
- [isREML](#)
- [logLik](#) (disabled, see below)
- [model.frame](#)
- [model.matrix](#)
- [nobs](#)
- [plot](#)

- [predict](#)
- [ranef](#) (only partially implemented)
- [residuals](#)
- [sigma](#)
- [summary](#)
- [terms](#)
- [update](#)
- [VarCorr](#)
- [vcov](#)
- [weights](#)

### Disabled methods

A log likelihood or even a pseudo log likelihood is not defined for the robust estimates returned by [r1mer](#). Methods that depend on the log likelihood are therefore not available. For this reason the methods `deviance`, `extractAIC` and `logLik` stop with an error if they are called.

### See Also

[r1mer](#); corresponding class in package `lme4`: [merMod](#)

### Examples

```
showClass("r1merMod")

## convert an object of type 'lmerMod' to 'r1merMod'
## to use the methods provided by robustlmm
fm <- lmer(Yield ~ (1|Batch), Dyestuff)
rfm <- as(fm, "r1merMod")
compare(fm, rfm)
```

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