Package 'robustBLME'

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Type Package

Title Robust Bayesian Linear Mixed-Effects Models using ABC

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Depends R (>= 3.0.0), lme4 (>= 1.1.12)

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Description Bayesian robust fitting of linear mixed effects models though weighted likelihood equations and approximate Bayesian computation.

Suggests devtools

License GPL-3

LazyData TRUE

Imports Rcpp (>= 0.12.1), numDeriv, mvtnorm, utils, parallel, doParallel, foreach, iterators, stats

LinkingTo Rcpp, RcppArmadillo

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RoxygenNote 6.0.1

NeedsCompilation yes

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emp_FSBT *Full Significance Bayesian Testing*

Description

Performs Full Significance Bayesian Testing (FSBT) for univariate sharp null hypothesis based on a posterior sample. The marginal posterior density is obtained by kernel density estimation from the posterior sample provided through the `sample` argument.

Usage

```
emp_FSBT(H0, sample)
```

Arguments

`H0`	The value under the null hypothesis.
`sample`	A monte Carlo sample from the marginal posterior distribution.

Value

double

References

Pereira, C. A. d. B., Stern, J. M. and Wechsler, S. (2008) Can a significance test be genuinely Bayesian? *Baysian Analysis* **3**, 79-100.

emp_hpd *Empirical Highest Posterior Density Interval*

Description

Computes empirical Highest Posterior Density (HPD) interval from a posterior sample. Works only for scalar marginal posteriors.

Usage

```
emp_hpd(x, prob = 0.95)
```

Arguments

`x`	a univariata or marginal posterior sample.
`prob`	the required posterior probability content.

`rblme` *Fits robust Bayesian linear mixed-effects models (BLMM) to data via robust REML estimating functions.*

Description

This is the main function of the package which implements the method of Ruli et al. (2017). It fits robust Bayesian LMMs to data, via robust REML estimating functions. The robust estimating functions are those proposed by Richardson & Welsh (1995), which are robust versions of restricted maximum likelihood (REML) estimating equations. An ABC-MCMC algorithm is used and the data are summarised through a rescaled version of the aforementioned estimating functions. See Ruli et al. (2017) for the details of the method. The current version (0.1.2) supports only models a single random effects. An extension for more general settings will be provided in the near future.

Usage

```
rblme(nabc, h.obj,
        chain.control = list(trace.init = NULL, thin.by = NULL),
        n.cores = 1)
```

Arguments

`nabc`	the number of posterior samples to be drawn.
`h.obj`	a list of objects as returned by the `tune.h` function.
`chain.control`	parameters for tracing and thinning the chain.
`n.cores`	the number of cores for parallel computation.

Value

list

References

Ruli E., Sartori N. & Ventura L. (2017) Robust approximate Bayesian inference with an application to linear mixed models. http://arxiv.org/abs/?? Richardson A. M. & Welsh A. H. (1995) Robust restricted maximum likelihood in mixed linear models. *Biometrics* **51**, 1429-1439.

Examples

```
x <- 1:3
y <- x^2

## Not run:
```

tune.h *Tune ABC distance bandwidth*

Description

Tunes the bandwidth h of the ABC distance to get the desired level of acceptance rate specified via acc.rate. Besides tuning h, the function also gets the relevant quantities need for running ABC-MCMC by a preliminary run of the lmer command.

Usage

```
tune.h(formula, data, ..., n.samp = 1e+5, n.sim.HJ = 500, acc.rate, grid.h, prior,
       cHub = 1.345, cHub2 = 2.07,
       init, n.cores = 1, use.h)
```

Arguments

formula	a two-sided linear formula object describing the fixed-effects part of the model, with the response on the left of a ~ operator and the terms, separated by + operators on the right. The "|" character 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 of lmer called internally.
...	other aruments to be passed to lmer(). Currently none is used.
n.samp	the number of pilot posterior samples to be drawn with ABC for each value of grid.h.
n.sim.HJ	the number of simulations to be used for computing the sensitivity and variabiliy matrices.
acc.rate	the desired acceptance rate of the ABC-MCMC algorithm.
grid.h	a grid of h values within which the "optimal" value is to be found.
prior	A named list of user-defined prior hyper-parameters. See "Details" below.
cHub	The tunnin constant of the Huber function for the location parameter.
cHub2	The tunnin constant of the Huber proposal 2 function for the scale parameter.
init	optional object to use for starting values. Currently ignored as initial values are taken from lmer.
n.cores	the number of cores for parallel computation.
use.h	a bandwidth to be used for the ABC distance. If provided, no tuning for h is performed and acc.rate argument is ingored.

Details

Given a specifiction of the formula and data the function calls internally rlmer to get the REML estimates and extracts from the resulting object the necesary quantites. Then proceeds by finding the solution of the REML II robust estimating equations and computes the sensitiviy and the variability matrices. Finally for each value of codegrid.h draws n.samp posterior samples with the ABC-MCMC algorithm and saves the acceptance rate. Finally a functions is built by a smoothing spline the acceptance rates vs grid.h. The "optimal" value of h in grid.h is found by inverting the spline function at acc.rate. Currently, the prior for the fixed effects is the product of scalar normals

with mean zero and user-specified variance. All fixed parameters are assumed to have equal prior variance. For the variance components the prior is halfCauchy with user-specified scale. Both variance parameters are assumed to have equal prior scale.

Value

a list.

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