

Package ‘lmmpar’

August 3, 2017

Title Parallel Linear Mixed Model

Version 0.1.0

Description Embarrassingly Parallel Linear Mixed Model calculations spread across local cores which repeat until convergence.

Encoding UTF-8

License MIT + file LICENSE

LazyData TRUE

Depends R (>= 3.2.2)

Imports MASS, matrixcalc, mnormt, plyr, doParallel, bigmemory

Suggests testthat

RoxygenNote 6.0.1

URL <https://github.com/fulyagokalp/lmmpar>

BugReports <https://github.com/fulyagokalp/lmmpar/issues>

NeedsCompilation no

Author Fulya Gokalp Yavuz [aut, cre],
Barret Schloerke [aut]

Maintainer Fulya Gokalp Yavuz <fulyagokalp@gmail.com>

Repository CRAN

Date/Publication 2017-08-03 15:17:37 UTC

R topics documented:

lmmpar	2
Index	4

lmmpar

*Parallel Linear Mixed Model***Description**

Embarrassingly Parallel Linear Mixed Model calculations spread across local cores which repeat until convergence. All calculations are currently done locally, but theoretically, the calculations could be extended to multiple machines.

Usage

```
lmmpar(Y, X, Z, subject, beta, R, D, sigma, maxiter = 500, cores = 8,
       verbose = TRUE)
```

Arguments

Y	matrix of responses with observations/subjects on column and repeats for each observation/subject on rows. It is (m x n) dimensional.
X	observed design matrices for fixed effects. It is (m*n x p) dimensional.
Z	observed design matrices for random effects. It is (m*n x q) dimensional.
subject	vector of positions that belong to each subject.
beta	fixed effect estimation vector with length p.
R	variance-covariance matrix of residuals.
D	variance-covariance matrix of random effects.
sigma	initial sigma value.
maxiter	the maximum number of iterations that should be calculated.
cores	the number of cores. Why not to use maximum?!
verbose	boolean that defaults to print iteration context

Examples

```
# Set up fake data
n <- 1000 # number of subjects
m <- 4    # number of repeats
N <- n * m # true size of data
p <- 15   # number of betas
q <- 2    # width of random effects

# Initial parameters
# beta has a 1 for the first value. all other values are ~N(10, 1)
beta <- rbind(1, matrix(rnorm(p, 10), p, 1))
R <- diag(m)
D <- matrix(c(16, 0, 0, 0.025), nrow = q)
sigma <- 1
```

```
# Set up data
subject <- rep(1:n, each = m)
repeats <- rep(1:m, n)

subj_x <- lapply(1:n, function(i) cbind(1, matrix(rnorm(m * p), nrow = m)))
X <- do.call(rbind, subj_x)
Z <- X[, 1:q]
subj_beta <- lapply(1:n, function(i) mnormt::rmnorm(1, rep(0, q), D))
subj_err <- lapply(1:n, function(i) mnormt::rmnorm(1, rep(0, m), sigma * R))

# create a known response
subj_y <- lapply(
  seq_len(n),
  function(i) {
    (subj_x[[i]] %% beta) +
      (subj_x[[i]][, 1:q] %% subj_beta[[i]]) +
      subj_err[[i]]
  }
)
Y <- do.call(rbind, subj_y)

# run the algorithm to recover the known betas
ans <- lmpar(
  Y,
  X,
  Z,
  subject,
  beta = beta,
  R = R,
  D = D,
  cores = 1, # increase for faster computation
  sigma = sigma,
  verbose = TRUE
)
str(ans)
```

Index

Impar, [2](#)