Package: lmmlite (via r-universe)

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Title Simple LMM Fitter for QTL Mapping

Description A port of parts of 'pylmm' for fitting linear mixed models relevant to genome-wide association studies (GWAS) and quantitative trait locus (QTL) mapping.

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Depends R (>= 3.1.0)

Imports stats, Rcpp (>= 0.12.12)

Suggests testthat, devtools, roxygen2, knitr, rmarkdown

License AGPL-3

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BugReports https://github.com/kbroman/lmmlite/issues

LazyData true

VignetteBuilder knitr

LinkingTo Rcpp, RcppEigen

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ByteCompile true

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Contents

`calcLL` *Calculate log likelihood for a given heritability*

Description

Calculate the log likelihood for a given value of the heritability, `hsq`.

Usage

```
calcLL(hsq, Kva, y, X, reml = TRUE, use_cpp = TRUE)
```

Arguments

`hsq`	heritability
`Kva`	eigenvalues of K (calculated by `eigen_rotation()`)
`y`	rotated phenotypes (calculated by `eigen_rotation()`)
`X`	rotated covariate matrix (calculated by `eigen_rotation()`)
`reml`	If TRUE, use REML; otherwise use ordinary maximum likelihood.
`use_cpp`	= if TRUE, use c++ version of code

Value

The log likelihood value, with the corresponding estimates of `beta` and `sigmasq` included as attributes.

Examples

```
data(recla)
e <- eigen_rotation(recla$kinship, recla$pheno[,1], recla$covar)
loglik <- calcLL(0.5, e$Kva, e$y, e$X)
many_loglik <- calcLL(seq(0, 1, by=0.1), e$Kva, e$y, e$X)
```

`eigen_rotation` *eigen decomposition + rotation*

Description

Do eigen decomposition of kinship matrix and rotate `X` and `y` by that, i.e., pre-multiply by the transpose of the matrix of eigenvectors. If `Kva` and `Kve_t` provided, just do the "rotation".

Usage

```
eigen_rotation(K, y, X = NULL, Kva = NULL, Kve_t = NULL, use_cpp = TRUE)
```

Arguments

`K`	Kinship matrix (required if `use_cpp=TRUE`)
`y`	Phenotypes
`X`	Numeric matrix with covariates. If NULL, use a column of 1's (for intercept).
`Kva`	Eigenvalues of `K` (optional, ignored if `use_cpp=TRUE`)
`Kve_t`	= transposed eigenvectors of K (optional, ignored if `use_cpp=TRUE`)
`use_cpp`	= if TRUE, use c++ version of code

Value

List containing `Kva`, `Kve_t` and rotated `y` and `X`.

Examples

```
data(recla)
e <- eigen_rotation(recla$kinship, recla$pheno[,1], recla$covar)
```

`fitLMM` *Fit a linear mixed model*

Description

Fit a linear mixed model of the form y = Xb + e where e follows a multivariate normal distribution with mean 0 and variance matrix `sigmasq_g K + sigmasq_e I`, where `K` is a known kniship matrix and `I` is the identity matrix.

Usage

```
fitLMM(
  Kva,
  y,
  X,
  reml = TRUE,
  check_boundary = TRUE,
  tol = 0.0001,
  use_cpp = TRUE,
  compute_se = FALSE
)
```

Arguments

`Kva`	Eigenvalues of K (calculated by `eigen_rotation()`)
`y`	Rotated phenotypes (calculated by `eigen_rotation()`)
`X`	Rotated covariate matrix (calculated by `eigen_rotation()`)
`reml`	If TRUE, use REML; otherwise use ordinary maximum likelihood.
`check_boundary`	If TRUE, explicitly check log likelihood at 0 and 1.
`tol`	Tolerance for convergence
`use_cpp`	= if TRUE, use c++ version of code
`compute_se`	= if TRUE, return the standard error of the `hsq` estimate using the Fisher Information matrix of the MLE estimate. The standard error will be in an `attr` of `hsq` in the output. Currently requires `use_cpp = FALSE`, and so if `compute_se=TRUE` we take `use_cpp=FALSE`.

Value

List containing estimates of `beta`, `sigmasq`, `hsq`, `sigmasq_g`, and `sigmasq_e`, as well as the log likelihood (`loglik`). If `compute_se=TRUE`, the output also contains `hsq_se`.

Examples

```
data(recla)
e <- eigen_rotation(recla$kinship, recla$pheno[,1], recla$covar)
result <- fitLMM(e$Kva, e$y, e$X)

# also compute SE
wSE <- fitLMM(e$Kva, e$y, e$X, compute_se = TRUE, use_cpp=FALSE)
c(hsq=wSE$hsq, SE=wSE$hsq_se)
```

`getMLsoln` *Get MLEs for coefficients and variance*

Description

For a fixed value for `hsq`, the heritability, calculate the corresponding maximum likelihood estimates of `beta` and `sigmasq`, with the latter being the total variance, `sigmasq_g` + `sigmasq_e`.

Usage

```
getMLsoln(hsq, Kva, y, X, reml = TRUE, use_cpp = TRUE)
```

Arguments

`hsq`	heritability
`Kva`	eigenvalues of K (calculated by `eigen_rotation()`)
`y`	rotated phenotypes (calculated by `eigen_rotation()`)
`X`	rotated covariate matrix (calculated by `eigen_rotation()`)
`reml`	If TRUE, use REML; otherwise use ordinary maximum likelihood.
`use_cpp`	= if TRUE, use c++ version of code

Value

list containing `beta` and `sigmasq`, with residual sum of squares and (if `reml=TRUE`, `log det (XSX)`) as attributes.

Examples

```
data(recla)
e <- eigen_rotation(recla$kinship, recla$pheno[,1], recla$covar)
ml <- getMLsoln(0.5, e$Kva, e$y, e$X)
```

`recla` *Example kinship, phenotype, and covariate data*

Description

Estimated kinship matrix, phenotypes, and covariates for diversity outcross mice, taken from Recla et al. (2014) and Logan et al. (2013)

Format

A list with three components, `kinship`, `pheno`, and `covar`, each a matrix.

Details

These are data for a set of diversity outcross mice. The kinship matrix was calculated from MUGA array data, using the R/qtl2 package.

Source

QTL Archive, `https://phenome.jax.org/projects/Recla1`

References

Recla JM, Robledo RF, Gatti DM, Bult CJ, Churchill GA, Chesler EJ (2014) Precise genetic mapping and integrative bioinformatics in Diversity Outbred mice reveals Hydin as a novel pain gene. Mamm Genome 25:211-222

Logan RW, Robledo RF, Recla JM, Philip VM, Bubier JA, Jay JJ, Harwood C, Wilcox T, Gatti DM, Bult CJ, Churchill GA, Chesler EJ (2013) High-precision genetic mapping of behavioral traits in the diversity outbred mouse population. Genes Brain Behav 12:424-437

Examples

```
data(recla)
```

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