

Package ‘MM4LMM’

September 27, 2021

Type Package

Title Inference of Linear Mixed Models Through MM Algorithm

Version 2.1.0

Date 2021-09-17

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Description The main function MMEst() performs (Restricted) Maximum Likelihood in a variance component mixed models using a Min-Max (MM) algorithm (Hunter, D. R., & Lange, K. (2004) <[doi:10.1198/0003130042836](https://doi.org/10.1198/0003130042836)>).

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Imports Rcpp (>= 0.12.13), Matrix, parallel, stats, MASS, utils

LinkingTo Rcpp, RcppEigen

NeedsCompilation yes

Depends R (>= 2.10)

Repository CRAN

Date/Publication 2021-09-27 14:10:18 UTC

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Description

This package provides a function to perform either ML or ReML estimation in a Variance Component Mixed Model. The optimization of the (possibly Restricted) log-likelihood is performed using the Min-Max algorithm described in Hunter et al. (2004). Depending on the number of variance components, different computational tricks are used to speed up inference. Additionally, the [AnovaTest](#) function provides Type I, Type III and Type III Kenward Roger approximation test series for fixed effects. The nullity of a specific linear combination can also be tested.

Details

Variance Component Mixed Models are mixed models of the form

$$Y = X\beta + \sum_{k=1}^K Z_k u_k$$

where Y is the response vector, X and β are respectively the incidence matrix and the coefficient vector associated with the fixed effects, u_k is the k th vector of random effects and corresponds to its associated incidence matrix. All random effect are assumed to be Gaussian with mean 0 and covariance $\sigma_k^2 R_k$, where R_k is a known correlation matrix and σ_k^2 is an unknown variance parameter. All random effects are assumed to be independent. In many applications the last random component corresponds to the error and therefore both Z_k and R_k correspond to the identity matrix.

In such models the inference of both the unknown variance components $\sigma_k^2, \dots, \sigma_K^2$ and the fixed effect β can be achieved through Maximum Likelihood (ML) or Restricted Maximum Likelihood (ReML) estimation. Neither ML nor ReML yield close form expressions of the estimates, consequently the maximization of the (restricted) log-likelihood has to be performed numerically. This package provides the user with Min-Max algorithms for the optimization. Efficient tricks such as profiling, MME trick and MM acceleration are implemented for computational efficiency (see Johnson et al. (1995), Varadhan et al. (2008) for details). The main function [MMEst](#) handles parallel inference of multiple models sharing the same set of correlation matrices - but possibly different fixed effects, an usual situation in GWAS analysis for instance.

Author(s)

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References

- Johnson, D. L., & Thompson, R. (1995). Restricted maximum likelihood estimation of variance components for univariate animal models using sparse matrix techniques and average information. *Journal of dairy science*, 78(2), 449-456.
- Hunter, D. R., & Lange, K. (2004). A tutorial on MM algorithms. *The American Statistician*, 58(1), 30-37.

Kenward, M. G., & Roger, J. H. (1997). Small sample inference for fixed effects from restricted maximum likelihood. *Biometrics*, 983-997.

Varadhan, R., & Roland, C. (2008). Simple and globally convergent methods for accelerating the convergence of any EM algorithm. *Scandinavian Journal of Statistics*, 35(2), 335-353.

Zhou, H., Hu, L., Zhou, J., & Lange, K. (2015). MM algorithms for variance components models. arXiv preprint arXiv:1509.07426.

AnovaTest

Type I and Type III Tests for mixed models.

Description

This function computes Type I and Type III tests for each fixed effect of a model, as displayed by the [MMEst](#) function. Alternatively, a specific linear combination of the fixed parameters may be tested (at 0).

Usage

```
AnovaTest(ResMMEst , TestedCombination=NULL , Type = "TypeIII" ,
          Cofactor = NULL , X = NULL , formula = NULL , VarList = NULL ,
          NbCores=1)
```

Arguments

ResMMEst	A list as displayed by the MMEst function.
TestedCombination	A contrast matrix or a list of contrast matrices C_m . Each matrix corresponds to a (set of) linear combination to be (jointly) tested at 0.
Type	"TypeI", "TypeIII" or "KR" (default is "TypeIII"). AnovaTest will compute tests of the given type for each fixed effect in the model. The option is ignored if a TestedCombination is provided. If Type is "KR" then AnovaTest will compute Type III test using Kenward Roger approximation, see Kenward and Roger (1997) for details.
Cofactor	The incidence matrix corresponding to fixed effects common to all models used in MMEst . If NULL, a single intercept is used as cofactor. This entry is needed when Type is "KR".
X	The incidence matrix or a list of incidence matrices corresponding to fixed effects specific to each model used in MMEst (default is NULL). This entry is needed when Type is "KR".
formula	The formula object specifying the fixed effect part of all models separated by + operators used in MMEst (default is NULL). This entry is needed when Type is "KR".
VarList	The list of correlation matrices associated with random and residual effects used in MMEst (default is NULL). This entry is needed when Type is "KR".
NbCores	The number of cores to be used.

Details

If no TestedCombination is provided, the function performs either Type I or Type III tests for each fixed effect in the model (default is Type III). If TestedCombination is provided, each linear combination in TestedCombination is tested at 0 using a Wald test. No check is performed regarding the estimability of the linear combination to be tested. If the dimension of the combination does not match with the dimension of ResMMEst, a NA is returned.

Value

The output of the function is a list with as many items as in the original input list ResMMEst. For each item of ResMMEst, a table is provided that contains the Wald test statistics, p-values and degrees of freedom for all tested hypotheses.

Author(s)

F. Laporte and T. Mary-Huard

References

Kenward, M. G., & Roger, J. H. (1997). Small sample inference for fixed effects from restricted maximum likelihood. *Biometrics*, 983-997.

Examples

```
require('MM4LMM')
data(QTLDetectionExample)
Pheno <- QTLDetectionExample$Phenotype
Geno <- QTLDetectionExample$Genotype
Kinship <- QTLDetectionExample$Kinship

##Build the VarList object
VL <- list(Additive = Kinship , Error = diag(1,length(Pheno)))

##Perform inference
Result <- MMEst(Y=Pheno , X = Geno , VarList = VL)

##Compute tests
AOV <- AnovaTest(Result,Type="TypeI")

##Test specific contrast matrix
TC = matrix(c(0,1),nrow=1)
AOV2 <- AnovaTest(Result, TestedCombination = TC)

AOV3 <- AnovaTest(Result, TestedCombination = TC , Type="KR" , X = Geno , VarList = VL)
```

MMEst

*MM inference method for variance component mixed models***Description**

This is the main function of the *MM4LMM* package. It performs inference in a variance component mixed model using a Min-Max algorithm. Inference in multiple models (e.g. for GWAS analysis) can also be performed.

Usage

```
MMEst(Y, Cofactor = NULL, X = NULL, formula=NULL, VarList, ZList = NULL, Method = "Reml",
Henderson=NULL, Init = NULL, CritVar = 0.001, CritLogLik = 0.001,
MaxIter = 100, NbCores = 1)
```

Arguments

Y	A vector of response values.
Cofactor	An incidence matrix corresponding to fixed effects common to all models to be adjusted. If NULL, a single intercept is used as cofactor.
X	An incidence matrix or a list of incidence matrices corresponding to fixed effects specific to each model. If X is a matrix, one model per column will be fitted. If X is a list, one model per element of the list will be fitted (default is NULL).
formula	A formula object specifying the fixed effect part of all models separated by + operators. To specify an interaction between Cofactor and X use the colnames of X when it is a list or use "Xeffect" when X is a matrix.
VarList	A list of covariance matrices associated with random and residual effects.
ZList	A list of incidence matrices associated with random and residual effects (default is NULL).
Method	The method used for inference. Available methods are "Reml" (Restricted Maximum Likelihood) and "ML" (Maximum Likelihood).
Henderson	If TRUE the Henderson trick is applied. If FALSE the Henderson trick is not applied. If NULL the algorithm chooses whether to use the trick or not.
Init	A vector of initial values for variance parameters (default is NULL)
CritVar	Value of the criterion for the variance components to stop iteration. (see Details)
CritLogLik	Value of the criterion for the log-likelihood to stop iteration. (see Details)
MaxIter	Maximum number of iterations per model.
NbCores	Number of cores to be used.

Details

If X is NULL, the following model is fitted:

$$Y = X_C \beta_C + \sum_{k=1}^K Z_k u_k$$

with X_C the matrix provided in Cofactor, β_C the unknown fixed effects, Z_k the incidence matrix provided for the k th component of ZList and u_k the k th vector of random effects. If ZList is unspecified, all incidence matrices are assumed to be the Identity matrix. Random effects are assumed to follow a Gaussian distribution with mean 0 and covariance matrix $R_k \sigma_k^2$, where R_k is the k th correlation matrix provided in VarList.

If X is not NULL, the following model is fitted for each i :

$$Y = X_C \beta_C + X_{[i]} \beta_{[i]} + \sum_{k=1}^K Z_k u_k$$

where $X_{[i]}$ is the incidence matrix corresponding to the i th component (i.e. column if X is a matrix, element otherwise) of X , and $\beta_{[i]}$ is the (unknown) fixed effect associated to $X_{[i]}$.

All models are fitted using the MM algorithm. If Henderson=TRUE, at each step the quantities required for updating the variance components are computed using the Mixed Model Equation (MME) trick. See Johnson et al. (1995) for details.

Value

The result is a list where each element corresponds to a fitted model. Each element displays the following:

Beta	Estimated values of β_C and β_i
Sigma2	Estimated values of $\sigma_1^2, \dots, \sigma_K^2$
VarBeta	Variance matrix of Beta
LogLik (Method)	The value of the (restricted, if Method is "Reml") log-likelihood
NbIt	The number of iterations required to reach the optimum
Method	The method used for the inference
attr	An integer vector with an entry for each element of Beta giving the term in Factors which gave rise to this element (for internal use in the function AnovaTest)
Factors	Names of each term in the formula

Author(s)

F. Laporte and T. Mary-Huard

References

- Johnson, D. L., & Thompson, R. (1995). Restricted maximum likelihood estimation of variance components for univariate animal models using sparse matrix techniques and average information. *Journal of dairy science*, 78(2), 449-456.
- Hunter, D. R., & Lange, K. (2004). A tutorial on MM algorithms. *The American Statistician*, 58(1), 30-37.
- Zhou, H., Hu, L., Zhou, J., & Lange, K. (2015). MM algorithms for variance components models. arXiv preprint arXiv:1509.07426.

Examples

```
require('MM4LMM')

#### Example 1: variance component analysis, 1 model
data(VarianceComponentExample)
DataHybrid <- VarianceComponentExample$Data
KinF <- VarianceComponentExample$KinshipF
KinD <- VarianceComponentExample$KinshipD

##Build incidence matrix for each random effect
Zf <- t(sapply(as.character(DataHybrid$CodeFlint), function(x)
  as.numeric(rownames(KinF)==x)))
Zd <- t(sapply(as.character(DataHybrid$CodeDent), function(x)
  as.numeric(rownames(KinD)==x)))

##Build the VarList and ZList objects
VL = list(Flint=KinF , Dent=KinD , Error = diag(1,nrow(DataHybrid)))
ZL <- list(Flint=Zf , Dent=Zd , Error = diag(1,nrow(DataHybrid)))

##Perform inference
#A first way to call MMEst
ResultVA <- MMEst(Y=DataHybrid$Trait , Cofactor = matrix(DataHybrid$Trial)
  , ZList = ZL , VarList = VL)
length(ResultVA)
print(ResultVA)

#A second way to call MMEst (same result)
Formula <- as.formula('~ Trial')
ResultVA2 <- MMEst(Y=DataHybrid$Trait , Cofactor = DataHybrid,
  formula = Formula
  , ZList = ZL , VarList = VL)
length(ResultVA2)
print(ResultVA2)

#### Example 2: Marker Selection with interaction between Cofactor and X matrix
Formula <- as.formula('~ Trial+Xeffect+Xeffect:Trial')
ResultVA3 <- MMEst(Y=DataHybrid$Trait , Cofactor = DataHybrid,
  X = VarianceComponentExample$Markers,
  formula = Formula
```

```

                                , ZList = ZL , VarList = VL)
length(ResultVA3)
print(ResultVA3[[1]])

#### Example 3: QTL detection with two variance components
data(QTLDetectionExample)
Pheno <- QTLDetectionExample$Phenotype
Geno <- QTLDetectionExample$Genotype
Kinship <- QTLDetectionExample$Kinship

##Build the VarList object
VLgd <- list(Additive=Kinship , Error=diag(1,length(Pheno)))

##Perform inference
ResultGD <- MMEst(Y=Pheno , X=Geno
                  , VarList=VLgd , CritVar = 10e-5)

length(ResultGD)
print(ResultGD[[1]])

```

MMVcov

Covariance Matrix for variance estimators.

Description

This function computes the covariance matrix of variance estimators using either the inverse of the Expected Hessian Matrix or the inverse of the Average Information Matrix.

Usage

```
MMVcov(ResMM , Y , Cofactor = NULL , formula = NULL,
       ZList = NULL , VarList , information="Expected")
```

Arguments

ResMM	A list as displayed by the MMEst function for a Variance Component Analysis (only the first element of the list will be analyzed).
Y	The vector of response values used in the function MMEst .
Cofactor	The incidence matrix corresponding to fixed effects common to all models to be adjusted used in the function MMEst . If NULL, a vector full of 1 is used.
formula	The formula object specifying the fixed effect part of all models separated by + operators used in the function MMEst (default is NULL).
ZList	The list of incidence matrices associated with random and residual effects used in the function MMEst (default is NULL).
VarList	The list of covariance matrices associated with random and residual effects used in the function MMEst .

information A string specifying the method used to approximate the covariance matrix. It can be either "Expected" (default) to use the Expected Hessian Matrix or "AI" to use the Average Information Matrix. The AI matrix is always computed using Reml estimates whereas the expected hessian matrix could also be used for ML estimates.

Details

If **information** is not specified then the algorithm computes the covariance matrix using the Expected matrix based on the inference method (Reml or ML) used in the first item of ResMM. If **information** is equal to "AI" then it computes the AI matrix to calculate the covariance matrix. Only the first item of ResMM is analyzed.

Value

The output of the function is a list:

vcov The covariance matrix of the variance estimators
SE The standard errors of the variance estimators (the square root of the covariance matrix diagonal)

Author(s)

F. Laporte and T. Mary-Huard

Examples

```
require('MM4LMM')
data(VarianceComponentExample)
DataHybrid <- VarianceComponentExample$Data
KinF <- VarianceComponentExample$KinshipF
KinD <- VarianceComponentExample$KinshipD

##Build incidence matrix for each random effect
Zf <- t(sapply(as.character(DataHybrid$CodeFlint), function(x)
as.numeric(rownames(KinF)==x)))
Zd <- t(sapply(as.character(DataHybrid$CodeDent), function(x)
as.numeric(rownames(KinD)==x)))

##Build the VarList and ZList objects
VL = list(Flint=KinF , Dent=KinD , Error = diag(1,nrow(DataHybrid)))
ZL <- list(Flint=Zf , Dent=Zd , Error = diag(1,nrow(DataHybrid)))

##Perform inference
#A first way to call MMEst
ResultVA <- MMEst(Y=DataHybrid$Trait , Cofactor = matrix(DataHybrid$Trial)
, ZList = ZL , VarList = VL)
Expected_vcov <- MMVcov(ResMM=ResultVA,Y=DataHybrid$Trait,
Cofactor = matrix(DataHybrid$Trial),
, ZList = ZL , VarList = VL)
AI_vcov <- MMVcov(ResMM=ResultVA,Y=DataHybrid$Trait,
```

```
Cofactor = matrix(DataHybrid$Trial),
, ZList = ZL , VarList = VL , information = "AI")
```

QTLDetectionExample *QTL Detection Example*

Description

This corresponds to (a sample of) the dataset presented in Rincent et al. (2014).

Usage

```
data("QTLDetectionExample")
```

Format

The format is: List of 3

Phenotype Named num [1:259]

Genotype int [1:259,1:10]

Kinship num [1:259,1:259]

Details

The list contains three elements:

- Phenotype: a numeric vector containing phenotypes of individuals
- Genotype: a matrix containing the genotypes of individuals over 10 biallelic markers
- Kinship: a matrix of simple relatedness coefficients between individuals

Source

<https://link.springer.com/article/10.1007%2Fs00122-014-2379-7>

References

Rincent, R., Nicolas, S., Bouchet, S., Altmann, T., Brunel, D., Revilla, P., ... & Schipprack, W. (2014). Dent and Flint maize diversity panels reveal important genetic potential for increasing biomass production. *Theoretical and applied genetics*, 127(11), 2313-2331.

Examples

```
data(QTLDetectionExample)
names(QTLDetectionExample)
## maybe str(QTLDetectionExample) ; plot(QTLDetectionExample) ...
```

VarianceComponentExample

Variance Component Example

Description

This corresponds to (a sample of) the dataset presented in Giraud et al. (2017).

Usage

```
data("VarianceComponentExample")
```

Format

The format is: List of 3

Data 'data.frame': 432 obs. of 5 variables

Trial a factor with 2 levels

CodeHybrid a factor with 177 levels

CodeDent a factor with 116 levels

CodeFlint a factor with 122 levels

Trait a numeric vector

KinshipD num [1:116,1:116]

KinshipF num [1:122,1:122]

Details

The list contains three elements:

- Data: a data frame containing the information about hybrids (trials, hybrid names, dent parental lines, flint parental lines and phenotypes)
- KinshipD: a matrix of simple relatedness coefficients between dent lines
- KinshipF: a matrix of simple relatedness coefficients between flint lines

Source

<https://www.genetics.org/content/207/3/1167.figures-only>

References

Giraud, H., Bauland, C., Falque, M., Madur, D., Combes, V., Jamin, P., ... & Blanchard, P. (2017). Reciprocal Genetics: Identifying QTL for General and Specific Combining Abilities in Hybrids Between Multiparental Populations from Two Maize (*Zea mays* L.) Heterotic Groups. *Genetics*, 207(3), 1167-1180.

Examples

```
data(VarianceComponentExample)
names(VarianceComponentExample)
## maybe str(VarianceComponentExample) ; plot(VarianceComponentExample) ...
```

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