Package ‘rrBlupMethod6’

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Type Package

Title Re-parametrization of RR-BLUP to allow for a fixed residual variance

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Depends R (>= 2.11.0)

Description rrBlupMethod6 -- Re-parametrization of mixed model formulation to allow for a fixed residual variance when using RR-BLUP for genomwide estimation of marker effects and linear transformation of the adjusted means proposed by Piepho et al.(2011)

License GPL (>= 2)

LazyLoad yes

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rrBlupMethod6 – Re-parametrization of RR-BLUP to allow for a fixed residual variance.

Description

rrBlupMethod6 – Re-parametrization of the mixed model formulation of Kang et al. (2008), to allow for a fixed residual variance when using RR-BLUP for genomwide estimation of marker effects and linear transformation of the adjusted means proposed by Piepho et al. (2011).

Details

Package: rrBlupMethod6
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License: GNU General Public License Version 2, June 1991
LazyLoad: yes

Kang et al. (2008) describe an efficient mixed model formulation for the special case of only one random effect besides the error, which avoids any matrix computation in the REML estimation of variance components. Piepho et al. (2011) re-parametrize their formulation to allow for a fixed residual variance. This re-parametrization might be especially useful in a plant breeding context. Here, the phenotypes used for estimation of marker effects are commonly the adjusted (for all other random and fixed effects) entry means, obtained beforehand from a one- or two-step adjustment procedure, most likely a mixed-model analysis (Moehring and Piepho, 2009). From this analysis, good estimates of the residual variance are usually available, so that it is not necessary and even counterproductive to re-estimate this parameter in RR-BLUP (Moehring and Piepho, 2009). Please see Piepho et al. (2011) for details.

The method is restricted to the case where \( R = I \sigma^2 \), where \( R \) is the error variance-covariance matrix and \( \sigma^2 \) is the error variance. An independent estimate of \( R \) is often available from the analysis that yielded adjusted means. In case \( R \) does not meet this assumption, a linear transformation (rotation) can always be applied to ensure \( R = I \sigma^2 \) (Piepho et al., 2011, Schulz-Streeck et al., 2012), provided that \( R \) is known. Hence, we replace \( y \) by \( L_R y \) and \( Z \) by \( L_R Z \), where \( y \) is the vector with the adjusted means, \( R^{-1} = (L_R)^2 \) such that \( L_R \) is square and symmetric and \( Z \) is the matrix with marker information. \( L_R \) is easily obtained from a spectral decomposition of \( R^{-1} \). With these replacements, analysis can proceed assuming that \( R = I \sigma^2 \) with \( \sigma^2 = 1 \).

The package \texttt{rrBlupMethod6} implements the method denoted "Method 6" in Piepho et al. (2011). The original parametrization of Kang et al. (2008) was previously implemented in the R package \texttt{rrBLUP} (Endelman, 2011), available from CRAN under \url{http://cran.r-project.org/web/packages/rrBLUP/index.html}. We used parts of the code of an earlier version (1.1) of \texttt{rrBLUP} as a starting point for our implementation.
rrBlupM6

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References
Schulz-Streeck T, Ogutu JO, Piepho HP (2012) Comparisons of single-stage and two-stage approaches to genomic selection. Submitted

See Also
rrBlupM6, rrBlupRotation

Description
This function implements "Method 6" described in Piepho et al. (2011), a re-parametrization of Kang et al.'s (2008) mixed model formulation to allow for a fixed residual variance when using RR-BLUP for genomwide estimation of marker effects.

Usage
rrBlupM6(y, X = matrix(1,nrow=n,ncol=1), Z, sig2e, chunks = as.integer(1))

Arguments
y Numeric vector with phenotypic observations (for example the entry means).
X Design matrix of fixed effects, including the intercept. By default, this is an all 1 column vector for the intercept.
Matrix assigning marker genotypes to phenotypes in y. The dimension of the matrix must be no. phenotypes (rows) times no. markers (columns). The coding must be 1 and -1 for the two homozygous genotypes.

The value of the residual variance, numeric vector of length 1.

Integer giving the number of chunks into which to split the computation of ZZ'. Computing this matrix in chunks might have computational advantages when the number of markers and observations is very large and the available memory is low. The default is 1, which computes ZZ' directly (i.e. as Z %*% t(Z)).

Please see Piepho et al. (2011) for details on the re-parametrization and the computation of ZZ’ in chunks. Currently only bi-allelic markers are supported.

A list with three components

- `uhat` numeric vector with the BLUP marker effects,
- `betahat` numeric vector with the BLUE of the fixed effects and
- `sig2u` numeric vector of length 1 with the REML estimate of the marker effect variance

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Examples

```r
# simulate a small data set (250 observations, 300 markers)
set.seed(3421475)
N <- 250
M <- 300

Z <- matrix(sample(c(1,-1),N * M, replace = TRUE),
             nrow = N,
             ncol = M)

# marker effects
u <- rnorm(M, 0, sqrt(1/M))

sig2e <- 1
y <- Z %*% u + rnorm(N,0,sqrt(sig2e))

out <- rrBlupM6(Z = Z, y = y, sig2e = sig2e)
```
## rrBlupRotation

### rrBlupRotation – linear transformation for the adjusted means and the design matrices

#### Description

This function implements the rotation described in Piepho et al. (2011) thus the assumption of $R = I\sigma^2$ in function `rrBlupM6` is satisfied.

#### Usage

```
rrBlupRotation(y, X = matrix(1, nrow=n, ncol=1), Z, R)
```

#### Arguments

- `y`  
  Numeric vector with adjusted means of the genotypes.
- `X`  
  Design matrix of fixed effects, including the intercept. By default, this is an all 1 column vector for the intercept.
- `Z`  
  Matrix assigning marker genotypes to phenotypes in `y`. The dimension of the matrix must be no. phenotypes (rows) times no. markers (columns). The coding must be 1 and -1 for the two homozygous genotypes.
- `R`  
  Variance-covariance structure of the adjusted means

#### Details

Please see Piepho et al. (2011) and Schulz-Streeck et al. (2012) for details on the rotation approach. The variance-covariance structure $R$ can, for example, be obtained with the function `vcov` from fitted (`mer`) model objects, or with the output option `COV` for the LSMEANS statement in PROC MIXED in SAS.
Value

A list with three components

- **y_tilda** Numeric vector with the rotated adjusted means,
- **X_tilda** Rotated design matrix of the fixed effects and
- **Z_tilda** Rotated design matrix with the marker information

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See Also

`rrBlupMethod`, `rrBlupM6`

Examples

```r
## simulate a small data set (250 observations, 300 markers)
set.seed(3421475)
N <- 250
M <- 300

Z <- matrix(sample(c(1,-1),N * M, replace = TRUE),
             nrow = N,
             ncol = M)

## marker effects
u <- rnorm(M, 0, sqrt(1/M))
sig2e <- 1
y <- Z %*% u + rnorm(N,0,sqrt(sig2e))

## simulate a random variance-covariance structure of the adjusted means
## (Note that this is just for demonstration purposes, the values are
## non-sensical!)
R <- matrix(rnorm(N*N),N,N)
diag(R) <- abs(diag(R))
R <- R + t(R)

## rotate
out_r <- rrBlupRotation(y, Z = Z, R = R)

## use rotated y,X and Z for computing marker effects and set sig2e = 1
out_RRBLUP_m6_r <- rrBlupM6(y = out_r$y_tilda,
                           X = out_r$X_tilda,
                           Z = out_r$Z_tilda,
                           sig2e = 1,
                           chunks = 4)
```
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