Supplementary material: Equivalent models

To derive a computationally efficient implementation of a regression algorithm exploiting codata for SNP markers for , we present equivalent models to the SNP-BLUP and show how the estimates of the effects, and their associated prediction error variances, can be transformed between these. Prediction error variances are important to compute since they are the basis for calculations of standard errors and effective number of parameters [2, 3]. Most of theory below is found in [10] but here the focus is on fitting a regression model for SNP-specific variances using codata on the SNP markers, and some minor typos of [10] have been corrected below.

Three different, but equivalent, specifications of the random effects will be used and will be referred to as the *SNP Model*, the *animal model* and the *Cholesky Model*. The SNP effects may have variances with different weights given by the diagonal matrix , and the residuals are assumed iid normal with variance :

**SNP Model**

(1)

**Animal model**

(2)

**Cholesky Model**

(3)

The use of equivalent LMMs in the research field of animal breeding and quantitative genetics is well established. The contribution here is to present how LMM theory can be used for heteroscedastic variance components, to show how the prediction error variances can be transformed between models, to implement the theory in a computationally efficient R package **CodataGS**, and to apply it to a model including external codata on the SNP genotypes presented further below.

Different mixed model equations for the equivalent models

For LMM Henderson's mixed model equations (MME) are used to estimate both the fixed and random effects for given variance components. They can also be used iteratively to estimate variance components as implemented in the R package **hglm** [9]. Although the models above are equivalent, the MME are different.

**SNP model**

For the SNP Model we have the MME

(4)

These MMEs are of size , where is the number of columns in . Hence, the size of the equations are very large for high-dimensional data.

**Animal model**

Let the random effects be individual effects for each observation and the correlation matrix between these. Then is relatively small () and the MME are

(5)

of size Hence, the size of these MME is much smaller than eq. 4 for

.

**Cholesky model**

In a third equivalent model we define (where has size ) and the random effects are individual independent random effects. The MME are

(6)

of size

Transformation of effects between equivalent models

For , the size of the MME in models (5) and (6) are much smaller than in model (4).

The random effects can be transformed between these equivalent models [6, 7] so that the estimated SNP effects can easily be calculated from the individual effects in model (5)

. (7)

Furthermore, we have so that

. (8)

The matrix is moderately large () but the transformation is a simple cross-product.

Hence, the calculations can be made in parts without reading all of into memory. They can also easily be parallelized if necessary.

Transformation of prediction error variances between equivalent models

Not only the estimates, but also the prediction error variances (*i.e.* the diagonal elements of ), are important to compute to allow for model checking and inference.

In the Cholesky model (eq. 6), let be

. (9)

Decompose the inverse of as

. (10)

Then the prediction covariance matrix is , see [1].

Denote the *j*:th diagonal element of as . Then these elements can be calculated separately as

(11)

where is the *j*:th row of the transformation matrix .

These computations are derived as follows. The prediction covariance matrix is

(12)

is the matrix transforming effects to in eq. (8), then

(13)

Combining these two equations, we get

(14)

*i.e.*

(15)

So

(16)

A simple relationship between hat values for random effects and the prediction error variance

Henderson's MME are equivalent to the solving an augmented model using weighted least squares [4, 8]. The augmented design matrix for the SNP model is

(17)

and the weight matrix is

(18)

and the *hat matrix* for this augmented model is .

Let be the lower right part of and the corresponding submatrix for the Cholesky model. Then the relationship between these submatrices and the prediction error variances are:

(19)

and

(20)

Consequently, the hat values for the SNP model (i.e. the *j*:th diagonal element in , ) can be computed efficiently from the prediction error variance of the Cholesky model.

(21)

where is the *j*:th row of the transformation matrix and is the j:th diagonal element of

Let be the vector of the diagonal elements in . In the R package **CodataGS**, is efficiently computed as , where is the sum of columns of , is the direct (elementwise) Hadamard product, and is a square root matrix of

computed using Singular Value Decomposition.

Fitting SNP variances using codata with a generalized linear model

Let be a design matrix with rows including covariates for the SNP markers. Then marker specific variances can be computed using a generalized linear model with a Gamma distribution and a log link function with response values and weights [4, 8], and linear predictor . An iterative procedure is applied where the diagonal elements in are updated using the fitted values: . This is the iterative reweighted least squares procedure for hierarchical generalized linear models derived in [3] and presented in [4] and [8].

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