Estimation of Sampling (Co)variances of the REML Estimators for Variance Components in a Mixed Linear Model

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SUMMARY

We derive an expression of sampling (co)variances of the restricted maximum likelihood estimators of variance components in a mixed linear model with one random effect except for the residual term. The given matrix describing the sampling (co)variances is not a log likelihood-based one, but is rather developed noticing the equivalence between the restricted maximum likelihood estimators and the corresponding estimators by a minimum variance quadratic unbiased estimation in which the prior information for the variance ratio is based on the restricted maximum likelihood estimators of variance components. The current approach takes account of the exact (co)variances of the quadratics for the minimum variance quadratic unbiased estimation under normality, and the matrix derived is different from the inverse of the so-called information matrix which represents the large-sample, asymptotic dispersion matrix of the restricted maximum likelihood estimators. A numerical comparison is conducted to confirm the validity of our approach.

1. Introduction

Numerous methods for estimating variance components have been proposed until now. Of the methods, the restricted maximum likelihood procedure (REML; Patterson and Thompson, 1971) is considered by animal breeders as one of the most desirable methods for the breeding applications, when observations are normally distributed. The likelihood-based methods such as REML and the maximum likelihood procedure (ML; Hartley and Rao, 1967) give the estimators which are, for example, consistent, efficient and asymptotically normal and so on, as described for ML by Miller (1973). Additionally, the REML estimators take account of the loss in degree of freedom resulting from the estimation of fixed effects. Furthermore, from the viewpoint of animal breeding and genetics, the (RE)ML estimators are known to be free of some forms of selection bias (e.g., Thompson, 1973; Meyer and Thompson, 1984).

For the (RE)ML estimation, one of the other attractive features is that a dispersion matrix of the estimators is always available. The matrix is given as the inverse of the so-called information matrix. The estimated sampling (co)variances of the REML estimators are important to obtain standard errors of genetic parameter estimates which are calculated as non-linear functions of (co)variance components estimated by REML. Also, the estimated sampling (co)variances are effectively used to assess the degree of connectedness in mixed linear models for genetic evaluation. Of course, for these purposes, we can utilize the inverse of the information matrix. However, the sampling (co)variances provided by the information matrix approach are known to be the large-sample, asymptotic ones as

Key words: Mixed linear model; REML estimator; Sampling variance; Variance component.

the number of observations approaches infinity.

In this paper, we describe another estimation procedure, which is not based on the likelihood, of the sampling (co)variances of the REML estimators, by noticing the equivalence between the REML estimators and the minimum variance quadratic unbiased estimators (MIVQUE; LaMotte, 1970, 1971, 1973; Rao, 1971) for which the prior variance ratio is based on the REML estimators.

2. A Mixed Linear Model

Consider the following mixed linear model with one random effect except for the residual term

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{e} \quad (1)$$

where $\mathbf{y}$ is a $(N \times 1)$ vector of observations, $\boldsymbol{\beta}$ is a $(p \times 1)$ vector of fixed effects, $\mathbf{u}$ is a $(q \times 1)$ vector of random effects such as the effects of animals or sires in animal breeding applications, $\mathbf{e}$ is a $(N \times 1)$ vector of random residuals, and $\mathbf{X}$ and $\mathbf{Z}$ are $(N \times p)$ and $(N \times q)$ known incidence matrices, respectively. We assume that

$$\mathbb{E} \begin{pmatrix} \mathbf{y} \\ \mathbf{u} \\ \mathbf{e} \end{pmatrix} = \begin{pmatrix} \mathbf{X}\boldsymbol{\beta} \\ \mathbf{0} \\ \mathbf{0} \end{pmatrix} \quad (2)$$

and

$$\text{Var} \begin{pmatrix} \mathbf{u} \\ \mathbf{e} \end{pmatrix} = \begin{pmatrix} \mathbf{A} & \mathbf{0} \\ \mathbf{0} & \mathbf{I} \end{pmatrix} \boldsymbol{\theta} \quad (3)$$

with $\boldsymbol{\theta} = (\sigma_u^2 \ \sigma_e^2)'$, where σ_u^2 and σ_e^2 are the variance components, and $\mathbf{A}$ is the symmetric matrix like additive relationship matrix in animal breeding applications. Under the assumptions above, the dispersion matrix of $\mathbf{y}$ is given by

$$\text{Var}(\mathbf{y}) = \mathbf{Z}\mathbf{A}\mathbf{Z}'\sigma_u^2 + \mathbf{I}\sigma_e^2 \equiv \mathbf{V}. \quad (4)$$

3. REML Estimators by the EM Algorithm and the Asymptotic Dispersion Matrix

The mixed model equations (Henderson, 1973, 1975, 1984a) are expressed as

$$\begin{pmatrix} \mathbf{X}'\mathbf{X} & \mathbf{X}'\mathbf{Z} \\ \mathbf{Z}'\mathbf{X} & \mathbf{Z}'\mathbf{Z} + \mathbf{A}^{-1}\alpha \end{pmatrix} \begin{pmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}} \end{pmatrix} = \begin{pmatrix} \mathbf{X}'\mathbf{y} \\ \mathbf{Z}'\mathbf{y} \end{pmatrix} \quad (5)$$

for the model (1), where α is the true variance ratio, that is, $\alpha = \sigma_e^2/\sigma_u^2$. Then the empirical mixed model equations for REML estimation are given by replacing α in eq.(5) by its estimate $\tilde{\alpha}$ (Patterson and Thompson, 1971). For the empirical equations, using a projection matrix

$$\mathbf{M} = \mathbf{I} - \mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}', \quad (6)$$

absorbing fixed effects from eq.(5), and solving the resulting equations gives

$$\begin{aligned} \hat{\mathbf{u}} &= (\mathbf{Z}'\mathbf{M}\mathbf{Z} + \mathbf{A}^{-1}\tilde{\alpha})^{-1}\mathbf{Z}'\mathbf{M}\mathbf{y} \\ &\equiv \mathbf{C}\mathbf{Z}'\mathbf{M}\mathbf{y}. \end{aligned} \quad (7)$$

Then, one of the iteration formulae for the REML estimation by the EM algorithm (Dempster et al., 1977) can be written as

$$\tilde{\boldsymbol{\theta}} = \begin{pmatrix} \tilde{\sigma}_u^2 \\ \tilde{\sigma}_e^2 \end{pmatrix} = \begin{pmatrix} q & -\text{tr}(\mathbf{A}^{-1}\mathbf{C}) \\ 0 & N - r(\mathbf{X}) \end{pmatrix}^{-1} \begin{pmatrix} \mathbf{y}'\mathbf{Q}_1\mathbf{y} \\ \mathbf{y}'\mathbf{Q}_2\mathbf{y} \end{pmatrix}, \quad (8)$$

where tr is the trace operator, $r(\mathbf{X})$ is the rank of $\mathbf{X}$, and the two quadratic forms of $\mathbf{y}$ are given by

$$\begin{pmatrix} \mathbf{y}'\mathbf{Q}_1\mathbf{y} \\ \mathbf{y}'\mathbf{Q}_2\mathbf{y} \end{pmatrix} = \begin{pmatrix} \mathbf{y}'\mathbf{M}\mathbf{Z}\mathbf{C}\mathbf{A}^{-1}\mathbf{C}\mathbf{Z}'\mathbf{M}\mathbf{y} \\ \mathbf{y}'\mathbf{M}(\mathbf{I} - \mathbf{Z}\mathbf{C}\mathbf{Z}')\mathbf{M}\mathbf{y} \end{pmatrix} \equiv \mathbf{s}. \quad (9)$$

Iterating on eq.(8) with eq.(7), with a pre-assigned initial value for α , yields the REML estimates at the convergence.

As discussed, e.g., by Corbeil and Searle (1976), the large-sample, asymptotic dispersion matrix of the REML estimators $\tilde{\boldsymbol{\theta}}$ is always available and is given by the inverse of the information matrix ($\mathbf{I}(\boldsymbol{\theta})$), as follows

$$\text{Var}(\tilde{\boldsymbol{\theta}}) \simeq [\mathbf{I}(\boldsymbol{\theta})]^{-1} \quad (10)$$

with

$$\mathbf{I}(\boldsymbol{\theta}) = \mathbf{E} \left(\frac{\partial^2 l}{\partial \boldsymbol{\theta} \partial \boldsymbol{\theta}'} \right) \quad (11)$$

where l represents the log-likelihood function not involving $\boldsymbol{\beta}$.

4. MIVQUE Estimators

For the MIVQUE of variance components (LaMotte, 1970, 1971, 1973; Rao, 1971) under the model (1), one of the estimation formulae based on expectations of the two quadratic forms given in eq.(9) is written as

$$\hat{\boldsymbol{\theta}} = \begin{pmatrix} \hat{\sigma}_u^2 \\ \hat{\sigma}_e^2 \end{pmatrix} = \mathbf{H}^{-1}\mathbf{s} = \{h_{ij}\}^{-1}\mathbf{s}, \quad (12)$$

where

$$\begin{aligned} h_{11} &= \text{tr}(\mathbf{Z}'\mathbf{M}\mathbf{Z}\mathbf{C}\mathbf{A}^{-1}\mathbf{C}\mathbf{Z}'\mathbf{M}\mathbf{Z}\mathbf{A}), \\ h_{12} &= \text{tr}(\mathbf{Z}'\mathbf{M}\mathbf{Z}\mathbf{C}\mathbf{A}^{-1}\mathbf{C}), \\ h_{21} &= \text{tr}(\mathbf{Z}'\mathbf{M}\mathbf{Z}\mathbf{A}) - \text{tr}(\mathbf{Z}'\mathbf{M}\mathbf{Z}\mathbf{C}\mathbf{Z}'\mathbf{M}\mathbf{Z}\mathbf{A}), \end{aligned}$$

and

$$h_{22} = N - r(\mathbf{X}) - \text{tr}(\mathbf{Z}'\mathbf{M}\mathbf{Z}\mathbf{C}),$$

as stated by Henderson (1984b).

The MIVQUE approach by eq.(12) requires information of the matrix $\mathbf{A}$ in addition to its inverse $\mathbf{A}^{-1}$. Then eliminating $\mathbf{A}$ from eq.(12) and rearranging the resulting equations leads to a more simplified form with only $\mathbf{A}^{-1}$ and $\mathbf{C}$ matrices included in the trace operation, which is given by

$$\hat{\boldsymbol{\theta}} = \mathbf{T}^{-1}\mathbf{s} = \{t_{ij}\}^{-1}\mathbf{s}, \quad (13)$$

where, with a guessed value γ for α ,

$$\begin{aligned} t_{11} &= q - 2\text{tr}(\mathbf{A}^{-1}\mathbf{C})\gamma + \text{tr}\{(\mathbf{A}^{-1}\mathbf{C})^2\}\gamma^2, \\ t_{12} &= \text{tr}(\mathbf{A}^{-1}\mathbf{C}) - \text{tr}\{(\mathbf{A}^{-1}\mathbf{C})^2\}\gamma, \\ t_{21} &= q\gamma - \text{tr}(\mathbf{A}^{-1}\mathbf{C})\gamma^2, \end{aligned}$$

and

$$t_{22} = N - r(\mathbf{X}) - q + \text{tr}(\mathbf{A}^{-1}\mathbf{C})\gamma.$$

Whereas eq.(13) with $\gamma = \alpha$ give **the** MIVQUE, the equation with a prior information $\gamma(\neq \alpha)$ provides **a** MIVQUE.

5. Proposed Dispersion Matrix

In this section, we derive another matrix whose elements represent information for sampling (co)variances of REML estimators, which is developed utilizing the equivalence existing between the REML estimator and the estimator by the iterative version of MIVQUE (I-MIVQUE) that has essentially been suggested and/or discussed by, e.g., LaMotte (1970), Rao (1972), Hocking and Kutner (1975), Harville (1977), and Rao (1979). For (I-)MIVQUE and REML under normality, we have the relationships that a first iterate of REML with a pre-assigned initial value for the variance ratio is equal to a MIVQUE, and that I-MIVQUE is identical to REML, provided that the I-MIVQUE estimates converged are all positive (for a review, see, e.g., Searle, 1979).

Now, for the model (1), consider MIVQUE estimators($\hat{\boldsymbol{\theta}}$) for which the prior variance ratio is based on REML estimators($\tilde{\boldsymbol{\theta}}$). Then, we have

$$\text{Var}(\tilde{\boldsymbol{\theta}}) = \text{Var}(\hat{\boldsymbol{\theta}}) \quad (14)$$

with $\hat{\boldsymbol{\theta}} = \tilde{\boldsymbol{\theta}}$, and therefore $\text{Var}(\tilde{\boldsymbol{\theta}})$ would be expressed by

$$\text{Var}(\tilde{\boldsymbol{\theta}}) = \begin{pmatrix} \text{Var}(\tilde{\sigma}_u^2) & \text{Cov}(\tilde{\sigma}_u^2, \tilde{\sigma}_e^2) \\ \text{Sym.} & \text{Var}(\tilde{\sigma}_e^2) \end{pmatrix} = \mathbf{T}^{-1} \text{Var}(\mathbf{s}) \mathbf{T}^{-1'} \quad (15)$$

where $\text{Var}(\mathbf{s})$ is the covariance matrix for the two quadratic forms given by eq.(9), that is,

$$\text{Var}(\mathbf{s}) = \begin{pmatrix} \text{Var}(\mathbf{y}'\mathbf{Q}_1\mathbf{y}) & \text{Cov}(\mathbf{y}'\mathbf{Q}_1\mathbf{y}, \mathbf{y}'\mathbf{Q}_2\mathbf{y}) \\ \text{Sym.} & \text{Var}(\mathbf{y}'\mathbf{Q}_2\mathbf{y}) \end{pmatrix}. \quad (16)$$

For eq.(16), considering the distributional properties of a quadratic form $\mathbf{y}'\mathbf{Q}\mathbf{y}$ where $\mathbf{y}$ follows $N(\mathbf{X}\boldsymbol{\beta}, \mathbf{V})$, the r^{th} cumulant of $\mathbf{y}'\mathbf{Q}\mathbf{y}$ is given by

$$K_r(\mathbf{y}'\mathbf{Q}\mathbf{y}) = 2^{r-1}(r-1)! \left[\text{tr}\{(\mathbf{Q}\mathbf{V})^r\} + r\boldsymbol{\beta}'\mathbf{X}'\mathbf{Q}(\mathbf{V}\mathbf{Q})^{r-1}\mathbf{X}\boldsymbol{\beta} \right], \quad (17)$$

and then, with $r = 2$, we have

$$\text{Var}(\mathbf{y}'\mathbf{Q}\mathbf{y}) = 2\text{tr}\{(\mathbf{Q}\mathbf{V})^2\} + 4\boldsymbol{\beta}'\mathbf{X}'\mathbf{Q}\mathbf{V}\mathbf{Q}\mathbf{X}\boldsymbol{\beta}. \quad (18)$$

Similarly, from the properties for bilinear forms under multivariate normality, the covariance between the two different quadratic forms in the same vector $\mathbf{y}$, $\mathbf{y}'\mathbf{Q}_1\mathbf{y}$ and $\mathbf{y}'\mathbf{Q}_2\mathbf{y}$, is expressed as

$$\text{Cov}(\mathbf{y}'\mathbf{Q}_1\mathbf{y}, \mathbf{y}'\mathbf{Q}_2\mathbf{y}) = 2\text{tr}(\mathbf{Q}_1\mathbf{V}\mathbf{Q}_2\mathbf{V}) + 4\boldsymbol{\beta}'\mathbf{X}'\mathbf{Q}_1\mathbf{V}\mathbf{Q}_2\mathbf{X}\boldsymbol{\beta}. \quad (19)$$

From $4\beta'X'QVQX\beta = 0$ and $4\beta'X'Q_1VQ_2X\beta = 0$ because of $MX = 0$, we have the following

$$\begin{pmatrix} \text{Var}(y'Q_1y) \\ \text{Cov}(y'Q_1y, y'Q_2y) \\ \text{Var}(y'Q_2y) \end{pmatrix} = \begin{pmatrix} 2\text{tr}\{(Q_1V)^2\} \\ 2\text{tr}(Q_1VQ_2V) \\ 2\text{tr}\{(Q_2V)^2\} \end{pmatrix} = Wv, \quad (20)$$

where W is a (3×3) matrix and $v = (\sigma_u^4 \ \sigma_u^2\sigma_e^2 \ \sigma_e^4)'$. After certain matrix operations, the elements w_{ij} of W in eq.(20) are finally given as

$$\begin{aligned} w_{11} &= 2[q - 4\text{tr}(A^{-1}C)\tilde{\alpha} + 6\text{tr}\{(A^{-1}C)^2\}\tilde{\alpha}^2 - 4\text{tr}\{(A^{-1}C)^3\}\tilde{\alpha}^3 \\ &\quad + \text{tr}\{(A^{-1}C)^4\}\tilde{\alpha}^4] \\ w_{12} &= 4[\text{tr}(A^{-1}C) - 3\text{tr}\{(A^{-1}C)^2\}\tilde{\alpha} + 3\text{tr}\{(A^{-1}C)^3\}\tilde{\alpha}^2 \\ &\quad - \text{tr}\{(A^{-1}C)^4\}\tilde{\alpha}^3] \\ w_{13} &= 2[\text{tr}\{(A^{-1}C)^2\} - 2\text{tr}\{(A^{-1}C)^3\}\tilde{\alpha} + \text{tr}\{(A^{-1}C)^4\}\tilde{\alpha}^2] \\ w_{21} &= 2[q\tilde{\alpha} - 3\text{tr}(A^{-1}C)\tilde{\alpha}^2 + 3\text{tr}\{(A^{-1}C)^2\}\tilde{\alpha}^3 - \text{tr}\{(A^{-1}C)^3\}\tilde{\alpha}^4] \\ w_{22} &= 4[\text{tr}(A^{-1}C)\tilde{\alpha} - 2\text{tr}\{(A^{-1}C)^2\}\tilde{\alpha}^2 + \text{tr}\{(A^{-1}C)^3\}\tilde{\alpha}^3] \\ w_{23} &= 2[\text{tr}\{(A^{-1}C)^2\}\tilde{\alpha} - \text{tr}\{(A^{-1}C)^3\}\tilde{\alpha}^2] \\ w_{31} &= 2[q\tilde{\alpha}^2 - 2\text{tr}(A^{-1}C)\tilde{\alpha}^3 + \text{tr}\{(A^{-1}C)^2\}\tilde{\alpha}^4] \\ w_{32} &= 4[\text{tr}(A^{-1}C)\tilde{\alpha}^2 - \text{tr}\{(A^{-1}C)^2\}\tilde{\alpha}^3] \end{aligned}$$

and

$$w_{33} = 2[N - r(X) - q + \text{tr}\{(A^{-1}C)^2\}\tilde{\alpha}^2],$$

with $\tilde{\alpha} = \tilde{\sigma}_e^2/\tilde{\sigma}_u^2$. Note that of course the true values of variance components are involved in eq.(20).

6. A Numerical Comparison

Our approach given in Section 5 was tested by a Monte Carlo simulation. An unbalanced-data structure was simulated with a cross-classified mixed linear model containing herd, sire and residual effects, and the generated data were analyzed by the same model as assumed for generating the data. Herd effects were regarded as fixed, and sire and residual effects random. The numbers of herds, sires and progeny per sire were ten, thirty and fifteen, respectively. Progeny of sires, using an uniform distribution, were assigned randomly to herds. Herd effects were generated as normal random variables and were treated as fixed effects in the analyses. The proportion of variation due to herd factor to total one was assumed to be fifty percent. Sire and residual effects were assumed to follow normal distributions with zero means and variances σ_s^2 and σ_e^2 , respectively. The true values of σ_s^2 and σ_e^2 were set to 1 and 7, respectively, so that the true heritability (h^2) was assumed to be .5 with

$$h^2 = \sigma_A^2/(\sigma_A^2 + \sigma_E^2) = 4\sigma_s^2/(\sigma_s^2 + \sigma_e^2)$$

Table 1
Sampling (co)variances estimated by Procedure I*

No. of replicates	$\tilde{\sigma}_s^2$				$\tilde{\sigma}_e^2$				Cov.
	Ave.	Max.	Min.	Var.	Ave.	Max.	Min.	Var.	
300	1.002	1.961	.115	.135	7.010	8.259	5.732	.218	-.020
3,000	1.000	2.543	.065	.159	7.008	8.670	5.229	.234	-.014

* The true values of σ_s^2 and σ_e^2 were 1 and 7, respectively.

Table 2
**Sampling (co)variances estimated
by Procedures II* and III***

Procedure	Value	/	Var($\tilde{\sigma}_s^2$)	Var($\tilde{\sigma}_e^2$)	Cov($\tilde{\sigma}_s^2, \tilde{\sigma}_e^2$)
II	Average		.152	.238	-.016
	Maximum		.152	.238	-.016
	Minimum		.152	.239	-.016
	Range		.000	.000	.000
III	Average		.182	.238	-.019
	Maximum		2.325	.238	-.159
	Minimum		.103	.238	-.007
	Range		2.222	.000	.152

* The number of replicates was 300.

where σ_A^2 and σ_E^2 represent additive genetic and environmental variances, respectively.

For REML estimation, the initial value of residual to sire variance ratio was always set to 7 ($= \sigma_e^2 / \sigma_s^2$). Convergence was assumed when change of the variance ratio between two successive iterations was less than $10^{-6}\%$. A total of three hundred replicates, using different random seed numbers, were conducted.

Values for sampling (co)variances of REML estimators, for the given data structure, were obtained; as the (co)variances calculated from actual three hundred estimates for each of sire and residual components (denoted as Procedure I), as the average of three hundred values based on our equation (15) with $\tilde{\alpha}$ and ν (Procedure II), and as the average of three hundred values computed by eq.(10) with $\tilde{\alpha}$ and the true variance components assumed (Procedure III). Note that Procedure III was also carried out just for a comparison.

The results by Procedure I are shown in Table 1, and those by Procedures II and III are given in Table 2. The actual REML estimates for three hundred replicates ranged from 1.961 to .115 for σ_s^2 and from 8.259 to 5.732 for σ_e^2 . The values of Var($\tilde{\sigma}_s^2$), Var($\tilde{\sigma}_e^2$) and Cov($\tilde{\sigma}_s^2, \tilde{\sigma}_e^2$) that were estimated by Procedure I were .135, .218 and -.020, respectively. The values obtained by Procedure II (our approach) were .152, .238 and -.016 for Var($\tilde{\sigma}_s^2$), Var($\tilde{\sigma}_e^2$) and Cov($\tilde{\sigma}_s^2, \tilde{\sigma}_e^2$), respectively. For the replicates, values for Var($\tilde{\sigma}_s^2$), Var($\tilde{\sigma}_e^2$) and Cov($\tilde{\sigma}_s^2, \tilde{\sigma}_e^2$) by eq.(15) were quite stable, and the ranges were all under 1×10^{-3} .

Although for the number of replicates there was a considerable agreement found between the corresponding values by Procedures I and II, we furthermore carried out Procedure I conducting additional three thousand replicates to further clarify the true sampling (co)variances. Then, as would be expected, the differences between the observed values by Procedure I and the corresponding values by Procedure II became much smaller (see Table 1), showing the validity of our approach under the consideration of a still limited number of replicates. The values of $\text{Var}(\tilde{\sigma}_s^2)$, $\text{Var}(\tilde{\sigma}_e^2)$ and $\text{Cov}(\tilde{\sigma}_s^2, \tilde{\sigma}_e^2)$ estimated by Procedure III were .182, .238 and -.019, respectively, so that $\text{Var}(\tilde{\sigma}_s^2)$ was overestimated by Procedure III.

7. Discussion

The REML and ML estimation of variance components in mixed linear models with unbalanced data requires iterated solutions to a constrained, non-linear system of equations. Therefore, it has been considered that deriving exact sampling (co)variances of the estimators is quite intractable or nearly impossible. Most statistical textbooks such as Kendall and Stuart (1973) consider the properties and distribution of ML estimators for large samples. It is shown that the ML estimator of the parameter asymptotically follows a normal distribution with lower bound dispersion matrix which equals minus the inverse of the information matrix, i.e., the matrix of expected values of second partial derivatives of the log-likelihood function. The large sample theory, for ML estimation of variance components, has been discussed by Hartley and Rao (1967). The theory is valid for the REML estimation, too. Thus the conventional approach to the estimation of sampling (co)variances for the REML estimators is the use of the inverse of the information matrix which is always available.

In this paper, we have described another expression for sampling (co)variances of the REML estimators, which is in a form different from that of the inverse of the information matrix. The current approach has been developed, noticing that a MIVQUE in which the prior information for the variance ratio is based on the REML estimators yields the same estimators as for REML and taking advantage of working with such a MIVQUE procedure which is not based on the likelihood function and is not an iterative method. The proposed approach would be applicable to more general mixed models with more than two random effects except for the residual effect. However, it would be a quite tremendous work to actually have the current dispersion matrices for the general models, and then we have dealt with the simplest model as assumed in eq.(1).

Following LaMotte (1971), the MIVQUE expectations of quadratic forms involve both the matrices $\mathbf{A}$ and $\mathbf{A}^{-1}$, as given in eq.(12). The matrix $\mathbf{A}$, however, is eliminated in the $\mathbf{T}$ matrix in eqs.(13) and (15). This point is important from the viewpoint of animal breeding applications. In the applications, $\mathbf{A}$ would typically be the matrix for additive genetic relationships among animals such as sires, dams or individuals, and it is often computationally very demanding or impossible in some cases to construct $\mathbf{A}$ from pedigree information (and $\mathbf{A}^{-1}$ from $\mathbf{A}$) for usual large datasets. However, fortunately, $\mathbf{A}^{-1}$ can be constructed directly and more easily from pedigree information without forming $\mathbf{A}$ itself (Henderson, 1976; Quaas, 1976). Accordingly, we have presented the $\mathbf{W}$ matrix in eq.(20) also in a form involving (the traces of) only the product of $\mathbf{A}^{-1}$ and $\mathbf{C}$.

For the model (1), the sampling variance of an estimator is proportional to a particular

quadratic function of the inverse of the true variance ratio α , where the coefficients depend on the incidence matrices $\mathbf{X}$ and $\mathbf{Z}$ (and $\tilde{\alpha}$). Those for the EM-REML estimators would be characterized by the specific equations (15) and (20) in such a way that the (co)variances of the corresponding MIVQUE quadratics under normality are exactly taken account of. As a result, for the model (1), whereas the EM-REML point estimation of variance components requires $\text{tr}(\mathbf{A}^{-1}\mathbf{C})$ and the certain elements of (the inverse of) the information matrix include $\text{tr}\{(\mathbf{A}^{-1}\mathbf{C})^2\}$ in addition to $\text{tr}(\mathbf{A}^{-1}\mathbf{C})$, the current dispersion matrix given as eq.(15) involves the traces of $(\mathbf{A}^{-1}\mathbf{C})^k$ with $k = 1 \sim 4$. For our approach, considering a limited number of replicates, the simulation study conducted seems to well demonstrate the validity of the proposed dispersion matrix. However, the theoretical relationship between the current matrix and the inverse of the information matrix is not thoroughly known to the authors in this stage. A further theoretical investigation on this point is definitely needed as a next step.

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