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S. A. Greenhalgh  
*Cornell University*

R. L. Quaas  
*Cornell University*

L. Dale Van Vleck  
*University of Nebraska-Lincoln, dvan-vleck1@unl.edu*

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# Approximating Prediction Error Variances for Multiple Trait Sire Evaluations

S. A. GREENHALGH, R. L. QUAAS,  
and L. D. VAN VLECK  
Department of Animal Science  
Cornell University  
Ithaca, NY 14853

## ABSTRACT

The coefficient matrix for multiple trait (milk, fat, and protein) mixed model equations may be too large to obtain prediction error variances from inverse elements. The commonly used reciprocals of diagonal elements may not be accurate approximations when sire relationships or multiple traits are included since much information is contained in offdiagonal elements. Approximations incorporating increased information from coefficient matrix were compared with actual prediction error variances for multiple trait evaluations for milk, fat, protein, and dollar value (relationships included) of 229 Ayrshire and 248 Brown Swiss bulls. Six approximations were selection index using number of daughter records, inverses of individual sire diagonal blocks, inverses of group and individual sire blocks, and inverses of all diagonal blocks and offdiagonal blocks associated with individual sires. All approximations underestimated actual prediction error variances, but most, except selection index, were highly correlated (.90 to .99) with actual prediction error variances of sire evaluations for milk yield and product value for contemporary bulls. The approximation incorporating most information from the coefficient matrix is recommended for use on basis of high correlation with and closeness to actual prediction error variances.

## INTRODUCTION

Indicators of accuracy of genetic evaluation such as the confidence range published in the Multiple Trait Northeast Artificial Insemination Sire Comparison (MT-NEAISC) provide a statistical measure of the reliability of a sire's genetic evaluation. The confidence range represents a multiple of the standard error of prediction (SEP) of a sire's true value, e.g., there is a 68% chance that a sire's true value is within  $\pm 1$  SEP of his predicted value. The SEP is the square root of the prediction error variance (PEV), which is a function of the diagonal elements of the inverse of the coefficient matrix (3).

Because inverses of large coefficient matrices often are difficult or impossible to obtain, PEV is commonly approximated by the reciprocal of the diagonal element of the coefficient matrix after absorption of herd-year-season equations. From regression of actual PEV on this approximation of PEV, Ufford et al. (7) computed a regression equation that predicted PEV from the reciprocal of the diagonal element for single trait Ayrshire, Brown Swiss, Jersey, and Guernsey sire evaluations. Their regression equation improved approximation of PEV for that analysis but may not be generally applicable to other data or models.

Following the precedent of Ufford et al. (7), Weller et al. (9) examined several approximations of PEV for single and multiple trait (first three lactations) Ayrshire sire evaluations with and without relationships among sires included. A function of the reciprocal of the diagonal element of the coefficient matrix less the contribution due to relationships was the best predictor of PEV for the single trait models both with and without relationships. In the multiple trait case, PEV is a matrix of variances and covariances relating to the multiple trait solutions for an individual sire. The PEV for dollar value in the multiple trait case was determined by premultiplying and post-

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multiplying each sire's  $3 \times 3$  diagonal block of the inverse of the coefficient matrix by a vector of economic weights. No satisfactory approximation of PEV for dollar value was found (9).

In a more general approach to approximation of PEV, Van Raden and Freeman (8) computed bounds for the diagonal elements of the inverse coefficient matrix. For a single trait model with one fixed effect (absorbed) and one random effect, bounds approaching actual PEV were formulated using partitioned matrix methods and quadratic forms of the coefficient matrix. Based on the results of their study, Van Raden and Freeman (8) suggested that bound procedures might be successfully extended to larger data sets and more complex models.

Incorporation of multiple traits in increasingly sophisticated models has necessitated further study of approximation of PEV. The purpose of this study was to examine approximations of PEV for use in computing confidence ranges for Northeast sire evaluations. The PEV is currently approximated by the inverse of a sire's diagonal block of the coefficient matrix.

#### METHODS

Sire evaluations were computed using first lactation records of Northeast cows in a multiple trait (milk, fat, and protein) analysis including relationships among sires. The PEV were determined from elements of the inverses of coefficient matrices for the two breeds in the Northeast with the smallest number of sires (Ayrshire and Brown Swiss). Approximations included varying amounts of information from the original coefficient matrix.

The PEV for group plus sire solutions (sire comparisons) and for within-group sire solutions were examined for milk and protein yield as well as for dollar value. The PEV for dollar value was obtained by premultiplying and postmultiplying a sire's  $3 \times 3$  diagonal block of the inverse of the coefficient matrix by a vector of economic values. Approximate PEV of dollar value was obtained by premultiplying and postmultiplying approximations of the elements of the inverse corresponding to the sire blocks by economic values. Approximations were evaluated by linear regression of PEV on approximate PEV.

Data consisted of two coefficient matrices of order 795 for Ayrshires and 855 for Brown

Swiss. Matrices were computed by R. W. Everett using the MT-NEAISC model for sire evaluation, which includes relationships among sires and maternal grandsire (MGS) effects to account for the quality of a daughter's dam (1, 4). The matrices contained information on 17,807 daughters of 229 Ayrshire sires and 5843 daughters of 248 Brown Swiss sires. The mixed model equations were formulated using the transformation for sire models with groups described in (5). Following the notation of Quaas and Pollak (5), the model was defined as:

$$y = Xh + ZQg + Zs + e \quad [1]$$

where:

$y$  = a vector of first lactation milk, fat, and protein records adjusted for days open and age-season of freshening ordered by trait within cow,

$h$  = a vector of fixed herd-year-season (HYS) effects,

$X$  = a known incidence matrix relating effects of HYS to cow records,

$s$  = a vector of random sire effects ordered by trait within sire,

$Z$  = a known incidence matrix relating effects of sires and MGS to cow records,

$g$  = a vector of fixed group effects,

$ZQ$  = a known incidence matrix relating group of sires and MGS to cow records, and

$e$  = a vector of random residual effects associated with cow records.

Means and variances of random effects were:

$$E \begin{bmatrix} s \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix} \quad \text{and:}$$

$$V \begin{bmatrix} s \\ e \end{bmatrix} = \begin{bmatrix} A*S & 0 \\ 0 & I*R \end{bmatrix}$$

where  $S$  is the  $3 \times 3$  variance-covariance matrix of sire effects for the three traits,  $A$  is the numerator relationship matrix for all sires represented in  $s$ , and  $R$  is the  $3 \times 3$  residual variance-covariance matrix (see Tables 1 and 2 for a

TABLE 1. Variance-covariance matrices of sire (S) and residual (R) effects for Ayrshire and Brown Swiss (kg<sup>2</sup>).<sup>1</sup>

Breed	Trait	Sire effects			Residual effects		
		Milk	Fat	Protein	Milk	Fat	Protein
Ayrshire	Milk	61,076	2058	1483	729,220	26,119	19,043
	Fat		103	52		1355	746
	Protein			51			905
Brown Swiss	Milk	109,999	3807	2776	1,309,348	48,331	36,322
	Fat		196	100		2584	1493
	Protein			99			1765

<sup>1</sup> R. W. Everett, 1984, personal communication.

priori estimates of these effects). The asterisk denotes the direct product operator.

Following absorption of HYS effects, the mixed model equations (MME) were:

$$\begin{bmatrix} Q'Z'MZQ & Q'Z'MZ \\ Z'MZQ & Z'MZ + L^{-1} \end{bmatrix} \begin{bmatrix} \hat{g} \\ \hat{s} \end{bmatrix} = \begin{bmatrix} Q'Z'My \\ Z'My \end{bmatrix} \quad [2]$$

where  $M = I - X[X'(I^*R^{-1})X]^{-1}X'$  and  $L^{-1} = A^{-1} * S^{-1}$ .

Transformation of [2] leads to the form:

$$\begin{bmatrix} Q'L^{-1}Q & -Q'L^{-1} \\ -L^{-1}Q & Z'MZ + L^{-1} \end{bmatrix} \begin{bmatrix} \hat{g} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} 0 \\ Z'My \end{bmatrix} \quad [3]$$

with  $\hat{u} = Q\hat{g} + \hat{s}$  (5).

A set of three LaGrange multiplier equations was added to each matrix, imposing a 1982 genetic base for sire comparison. The resulting coefficient matrices were inverted directly using a computer subroutine written by C. R. Henderson for obtaining a generalized inverse. The PEV of  $u$ ,  $[V(\hat{u} - u)]$ , was obtained from the diagonal elements of the inverse of the coefficient matrix. The PEV of  $s$ ,  $[V(\hat{s} - s)]$ , was computed as  $[V(Q\hat{g}) - 2Cov(Q\hat{g}, \hat{u} - u) + V(\hat{u} - u)]$ .

Partitioned matrix formulae were used to invert matrices containing increased information from the original coefficient matrix. The six PEV approximations included a selection index approximation based on number of records for each sire (SI), inverses of each sire's diagonal block of the coefficient matrix (DB), inverses of group and individual sire blocks of the coefficient

matrix (G1 and G2), and inverses of approximate coefficient matrices composed of all diagonal blocks of the coefficient matrix and the offdiagonal blocks associated with each individual sire (Q1 and Q2). Let  $P$  be the coefficient matrix in [3], representing information on  $n$  sires in  $k$  groups.

$$P = \begin{bmatrix} B & C \\ C' & D \end{bmatrix} \text{ and } P^{-1} = \begin{bmatrix} B^* & C^* \\ C'^* & D^* \end{bmatrix}$$

inverse elements can be obtained by (6):

$$D^* = D^{-1} + D^{-1}C'B^*CD^{-1} \quad [4a]$$

$$D^* = (D^{-1} - C'B^{-1}C)^{-1} \quad [4b]$$

For the  $j$ th sire in the  $i$ th group, let  $D_{jj}$  be the 3 x 3 diagonal block of the coefficient matrix corresponding to the  $j$ th sire, let  $B_{ii}$  be the

TABLE 2. Heritabilities,<sup>1</sup> genetic correlations,<sup>2</sup> and residual correlations<sup>3</sup> for Ayrshire and Brown Swiss sire evaluations (2).

	Milk	Fat	Protein
Milk	.31	.82	.82
Fat	.85	.28	.77
Protein	.88	.79	.21

<sup>1</sup> Diagonal elements.

<sup>2</sup> Above the diagonal.

<sup>3</sup> Below the diagonal.

diagonal block of the coefficient matrix corresponding to the  $i^{\text{th}}$  sire group, and let  $C_{ji}$  and  $C_{ij}$  be the corresponding offdiagonal blocks. The six approximations of  $D_{ij}$ , the diagonal block of the inverse of the coefficient matrix corresponding to the  $j^{\text{th}}$  sire, may be noted as:

$$S1 = (Z'_{jj}R^{-1}Z_{jj} + I_3 * S^{-1})^{-1}, \text{ where } Z_{jj} \text{ is the portion of } Z \text{ in [3] corresponding to the } j^{\text{th}} \text{ sire,}$$

$$DB = D_{jj}^{-1} \text{ where } D_{jj} \text{ is the diagonal block of [3] associated with the } j^{\text{th}} \text{ sire,}$$

$$G1 = (D_{jj}^{-1} - C_{ji}B_{ii}^{-1}C_{ij})^{-1}, \text{ using [4b], assuming that for the } j^{\text{th}} \text{ sire in the } i^{\text{th}} \text{ group, } P \text{ contains only the sire's group diagonal block } (B_{ii}), \text{ the sire's diagonal block } (D_{jj}), \text{ and corresponding offdiagonal blocks } (C_{ji}) \text{ and } (C_{ij}),$$

$$G2 = (D_{jj}^{-1} - \sum_{i=1}^k \sum_{m=1}^k C_{jm}B_{m1}^{-1}C_{ij})^{-1}, \text{ using [4b], assuming that } P \text{ contains the entire group block of the coefficient matrix } (Q'L^{-1}Q \text{ of [3]), the sire's diagonal block } (D_{jj}), \text{ and the offdiagonal blocks associated with all groups for the } j^{\text{th}} \text{ sire } (C_{jm} \text{ and } C_{ij} \text{ for } i = 1, k \text{ and } m = 1, k),$$

$$Q1 = D_{jj}^{-1} + D_{jj}^{-1} \left[ \sum_{i=1}^k C_{ji}B_{ii}^{-1}C_{ij} + \sum_{m=1}^n C_{jm}D^{mm}C_{mj} \right] D_{jj}^{-1}, \text{ using [4a] assuming that } P \text{ contains all } k \text{ group and } n \text{ sire diagonal blocks of the coefficient matrix and all offdiagonal blocks associated with the } j^{\text{th}} \text{ sire, and}$$

$$Q2 = (D_{jj}^{-1} - \left[ \sum_{i=1}^k C_{ji}B_{ii}^{-1}C_{ij} + \sum_{m=1}^n C_{jm}D^{mm}C_{mj} \right])^{-1}, \text{ using [4b] assuming } P \text{ identical to } P \text{ in } Q1.$$

The diagonal elements of  $D_{ij}$  represent PEV for milk, fat, and protein yield sire solutions. The PEV for dollar value were computed by premultiplying and postmultiplying  $D_{ij}$  by a vector,  $v$ , of economic values such that  $v_1 = .02565$ ,  $v_2 = 1.65$ , and  $v_3 = 1.30$  (values are based on a price of \$.275/kg milk, \$.165/point of fat test from 3.5% and \$.130/point of protein test from 3.2%).

Actual PEV was regressed on approximate PEV for sire comparisons across groups,  $[V(\hat{u} - u)]$ , and for within-group sire deviations,  $[V(\hat{s} - s)]$ . These comparisons were made for all

bulls in the evaluation; a subset of bulls containing sires with daughters with records (excluding base bulls included in the evaluation only for their pedigree information) and a subset of bulls containing sires in the last five genetic groups (recent or currently available sires).

## RESULTS AND DISCUSSION

Linear regression analysis showed that PEV of within group deviations  $[V(\hat{s} - s)]$  for milk and fat production were better approximated than PEV of across group sire comparisons  $[V(\hat{u} - u)]$  over all sires in the evaluation (Figure 1). Perfect prediction of PEV is illustrated by a reference line intercepting the Y axis at 0 with a slope of 1.00. Points falling above this line represent underestimates of PEV, and points falling below are overestimates of PEV. The regression line depicting the relationship between actual and approximate PEV for within group sire deviations is closer to the reference line ( $R^2 = .99$ ,  $(MSE)^{-5} = 198$ ) where  $R^2$  is the squared correlation coefficient and MSE is the mean squared error than the regression line associated with across group sire comparisons [ $R^2 = .88$ ,  $(MSE)^{-5} = 794$ ], indicating that within-group PEV is more accurately approximated than across group PEV for all sires in the evaluation. Figure 1

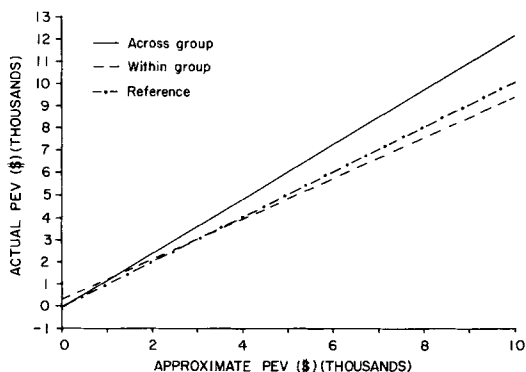


Figure 1. Regression of prediction error variance (PEV) for dollar value on Q1 approximation of PEV for dollar value for within group sire deviations and across group sire comparisons for all Ayrshire bulls. The Q1 approximation is based on inverse of approximate coefficient matrices of all diagonal and off-diagonal blocks of the coefficient matrices associated with each individual sire.

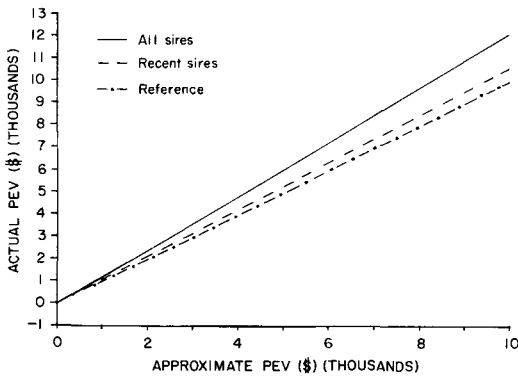


Figure 2. Regression of prediction error variance (PEV) for dollar value on Q1 approximation of PEV for dollar value for across group sire comparisons for all and for recent Ayrshire bulls. The Q1 approximation is based on inverse of approximate coefficient matrices of all diagonal and corresponding offdiagonal blocks of the coefficient matrices associated with each individual sire.

shows this result for the Q1 approximation in Ayrshires; all approximations are predicted within group PEV more accurately than across group PEV for both breeds.

The PEV of sire comparisons for the subsets

of bulls with progeny and recent bulls (bulls in the last five genetic groups) were well-approximated (Figure 2) for milk and fat production, suggesting that the variance of group effect estimates was poorly approximated for base bulls included in the evaluation strictly for their pedigree information. Slight improvement in approximation of PEV for across group sire comparisons for all bulls with progeny to bulls in the most recent genetic groups may reflect a decrease in the variance between group effects over time. This would be expected because more information is included in estimates of more recent group effects.

The PEV of sire comparisons for protein yield were not well approximated except for bulls with 20 or more daughters with protein records. Table 3 contains the coefficients associated with regression of actual PEV of protein yield on approximate PEV of across group sire comparisons for recent sires and sires with 20 or more daughters with protein records for the Ayrshire breed. The PEV for protein yield of sire comparisons were approximated with less error in the Brown Swiss breed ( $R^2 < .93$ ;  $53 < (MSE)^{-5} < 101$ ), apparently

TABLE 3. Regression of prediction error variances for protein yield for across group sire comparisons on prediction error variance approximations.<sup>1</sup>

Approximation <sup>2</sup>	R <sup>2</sup>	Intercept	Slope	(MSE) <sup>-5</sup>	
For recent Ayrshires sires (n = 121)					
			$\bar{X}$	SE	
SI	.50	1	1.43	.13	97
DB	.67	-8	1.66	.11	102
G1	.67	-7	1.61	.10	93
G2	.67	-8	1.61	.10	93
Q1	.67	-16	1.60	.10	89
Q2	.66	-22	1.61	.11	88
For Ayrshire sires with 20 or more daughters with protein records (n = 21)					
SI	.93	-5	1.15	.08	8
DB	.98	3	.98	.04	4
G1	.98	3	.97	.03	4
G2	.98	3	.97	.03	4
Q1	.98	2	.94	.03	4
Q2	.98	2	.94	.03	4

<sup>1</sup> R<sup>2</sup> is squared correlation coefficient; MSE is mean squared error.

<sup>2</sup> Selection index approximation based on the number of records for each sire (SI); inverses of each sire's diagonal block of the coefficient matrix (DB), inverses of group and individual sire and corresponding offdiagonal blocks of the coefficient matrix (G1 and G2); and inverses of approximate coefficient matrices composed of all diagonal blocks of the coefficient matrix and the offdiagonal blocks associated with each individual sire (Q1 and Q2).

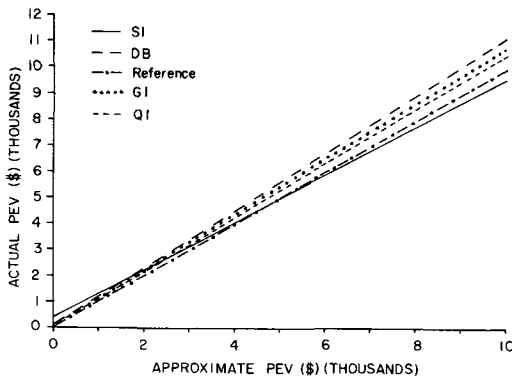


Figure 3. Regression of prediction error variance (PEV) for dollar value on SI, DB, G1, and Q1 approximations of PEV for across group sire comparisons for recent Ayrshire bulls. Selection index approximation based on the number of records for each sire (SI); inverses of each sire's diagonal block of the coefficient matrix (DB); inverses of group and individual sire and corresponding offdiagonal blocks of the coefficient matrix (G1 and G2); and inverses of approximate coefficient matrices composed of all diagonal blocks of the coefficient matrix and the off-diagonal blocks associated with each individual sire (Q1 and Q2).

because less protein information was missing for Brown Swiss daughters (92% of Ayrshire and 80% of Brown Swiss daughters were

missing protein information). Good approximations for PEV of sire comparisons were found for milk yield and dollar value, reflecting the heavy emphasis on milk in the pricing scheme used. The PEV of sire comparisons for dollar value may be even more accurately approximated for breeds with more protein information.

Of primary interest in this study was approximation of PEV of dollar value for recent or currently available sires. Figure 3 depicts the relationships of four approximations of PEV for dollar value for recent Ayrshire bulls with actual dollar value PEV. Results for recent Brown Swiss bulls were similar. The regression equations associated with these lines are in Table 4. Because G1 and G2 performed nearly identically in PEV approximation, only the G1 result is shown in Figure 3. The Q2 produced PEV approximations similar to those computed using the Q1 method for Ayrshire bulls. However, Q2 provided very poor PEV approximations ( $R^2 = .422$ ,  $(MSE)^5 = 2184$ ) for Brown Swiss bulls and is not depicted in Figure 3. No factor could be found to account for the poor performance of Q2 in approximating PEV for Brown Swiss bulls. Regression equations to predict PEV from approximate PEV were

TABLE 4. Regression of prediction error variances for dollar value for across group sire comparisons on prediction error variance approximations for recent Ayrshire and Brown Swiss sires.<sup>1</sup>

Approximation <sup>2</sup>	R <sup>2</sup>	Intercept	Slope		(MSE) <sup>5</sup>
Ayrshire (n = 121)					
			$\bar{X}$	SE	
SI	.85	393	.92	.04	550
DB	.97	77	1.11	.02	330
G1	.97	90	1.07	.02	298
G2	.97	88	1.07	.02	293
Q1	.97	53	1.05	.02	243
Q2	.97	45	1.05	.02	234
Brown Swiss (n = 106)					
SI	.93	1088	.88	.02	861
DB	.91	313	1.22	.04	1329
G1	.92	321	1.18	.03	1198
G2	.93	282	1.18	.03	1152
Q1	.97	57	1.13	.02	773
Q2	.42	2620	.48	.06	2184

<sup>1</sup> R<sup>2</sup> is squared correlation coefficient; MSE is mean squared error.

<sup>2</sup> Selection index approximation based on the number of records for each sire (SI); inverses of each sire's diagonal block of the coefficient matrix (DB); inverses of group and individual sire and corresponding offdiagonal blocks of the coefficient matrix (G1 and G2); and inverses of approximate coefficient matrices composed of all diagonal blocks of the coefficient matrix and the offdiagonal blocks associated with each individual sire (Q1 and Q2).

different for Ayrshire and Brown Swiss bulls for dollar value. Although functions of approximations, as studied by Ufford et al. (7) and Weller et al. (9) are expected to be better predictors of PEV than the approximations alone, they have limited applicability in that each different data set or model considered must be analyzed separately to obtain the appropriate regression equations.

Approximations also may be considered in terms of the amount of information they incorporate from the coefficient matrix. The Q1 incorporated the most information from the coefficient matrix and performed consistently well in terms of  $R^2$ , linear regression coefficients and uniform closeness to actual PEV. Thus, Q1 appears to be the method of choice for approximating PEV. Although Q2 incorporated the same information as Q1, it is not recommended for use to approximate PEV due to poor performance in approximating PEV for Brown Swiss bulls for dollar value. The G1 and G2 follow Q1 and Q2 in amount of information used, followed by the inverse of the diagonal block and the selection index approximation.

All approximations were easy to compute because none required much calculation or large amounts of computer storage. The PEV of sire comparisons computed using relationships among sires for milk yield and dollar value were well-approximated in this study of two breeds with little protein information. For breeds with more protein information, PEV for dollar value may be even more accurately approximated by methods outlined in this project.

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