Outline of a Procedure to Calculate Weighting Factors for Models with Maternal Effects

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Abstract

A procedure to calculate weighting factors for bulls to be used in international genetic evaluation for linear models with direct and maternal effects have earlier been presented by Liu *et al.* (2003). Small updates to this paper as well as illustration of similarities between calculation of reliabilities and effective daughter contributions in single trait and multiple trait models are shown in this paper.

Introduction

Pilot studies of international genetic evaluations for calving traits have been performed for 10 Holstein populations (Jakobsen *et al.,* 2003; Pasman & Reinhardt, 2002; Pasman *et al.,* 2003). These studies showed feasibility of international genetic evaluations for calving traits. Breeding values for the pilot run have been weighted with number of born calves/number of calving daughters. For the routine evaluation to come in place issues regarding effective daughter contributions (EDC) have been raised. The currently used procedure to calculate EDC's for international genetic evaluation of linear traits (Interbull, 2000) is valid for single trait models. Limitations in the current procedure have been indicated when it comes to multitrait models (Liu *et al.,* 2002). A procedure to calculate EDC's for multitrait linear models was developed and described by Liu *et al.* (2001*b*) and the procedure was applied to test day data by Liu *et al.* (2001*a*). Developments in this procedure was proceeded to include linear models with both direct and maternal effects (Liu *et al.,* 2003).

However, limitations due to double counting of dam and progeny contributions as well as no account for permanent environment of own birth records were identified. The purpose of this paper was therefore, to indicate these limitations and also, in the appendix to show the similarities between the single trait and the multiple trait calculation of reliabilities and EDC's.

Methods

A linear model with maternal effects can be written as:

$$\mathbf{Y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Wm} + \mathbf{Wp} + \mathbf{e} \qquad [1]$$

And the variance of $\mathbf{Y}$ can be written as:

$$V(\mathbf{Y}) = V(\mathbf{Zu}) + V(\mathbf{Wm}) +$$

$$COV(\mathbf{Zu}, \mathbf{Wm}) + V(\mathbf{Wp}) + V(\mathbf{e})$$

$$= \begin{bmatrix} \mathbf{Z} & \mathbf{W} \end{bmatrix} \begin{bmatrix} \mathbf{G_o^{-1}} \otimes \mathbf{A^{-1}} \end{bmatrix} \begin{bmatrix} \mathbf{Z} \\ \mathbf{W} \end{bmatrix}$$

$$+ \mathbf{I}\sigma_{pe}^2 + \mathbf{I}\,\sigma_e^2 \qquad [2]$$

where $\mathbf{Y}$ is a vector of observations, $\mathbf{X}$, $\mathbf{Z}$, and $\mathbf{W}$ are incidence matrices, and $\mathbf{b}$, $\mathbf{u}$, $\mathbf{m}$, $\mathbf{p}$, and $\mathbf{e}$, are vectors of fixed effects, direct additive genetic effects, maternal additive genetic effects, permanent environmental effects, and random residuals, respectively. $\mathbf{A}$ is the relationship matrix, $\mathbf{G_o}$ is the genetic (co)variance matrix, $\mathbf{I}$ is the identity matrix, σ_{pe}^2 is the permanent environmental variance, and σ_e^2 is the residual variance.

We want to calculate the weighting factor (W_{sire}) for the sire to be used for international genetic evaluation. To do so, we first need to

calculate the sum of EDC-contributions $\left(\varepsilon_{final}\right)$ and reliability $\left(\Re_{sire}\right)$ of the bull.

Apart from Step 1 and Step 2 the calculations follows the procedure by Liu *et al.* (2003).

Step 1

Absorb fixed effects, permanent environmental effects, and maternal effects into direct genetic effects. Then absorb fixed effects, permanent environmental, and direct genetic effects into maternal effects.

Step 2

The absorption of direct effects into maternal effects and maternal effects into direct effects as well as the calculation of EDC's for own records are the main steps that deviate from Liu *et al.* (2003). Previously, there was an overestimation for both direct and maternal effect of EDC contribution for own data. And also, the permanent environmental effects of own birth records were neglected earlier. The main reason for the elements of ε_o (equation 4) to change is the absorption performed under Step 1. All matrices for all animals are 2 x 2 matrices. Similarities between the EDC from the single trait model and the EDC from the multi-trait model can be seen in Appendix 1.

The EDC-matrix for own records $\left(\varepsilon_o\right)$ of direct and maternal effects can be calculated as:

$$\varepsilon_o = \begin{bmatrix} \delta - \dfrac{\delta^2}{\delta + G^{mm}} & 0 \\ 0 & \delta_q - \displaystyle\sum_{all\_calves} \dfrac{\delta^2}{\delta + G^{dd}} \end{bmatrix}$$

[4]

where

$$\mathbf{G_o^{-1}} = \begin{bmatrix} G^{dd} & G^{dm} \\ G^{md} & G^{mm} \end{bmatrix},$$

$$\delta = n_j \sigma_e^{-2} \frac{n_{q'} - n_j + \lambda}{n_{q'} + \lambda} \qquad [5]$$

$$\delta_q = \sigma_e^{-2} \frac{n_q \lambda}{n_q + \lambda} \qquad [6]$$

$$\lambda = \frac{\sigma_e^2}{\sigma_{pe}^2} \qquad [7]$$

n_j is related to the birth record of the animal and is calculated as $n_j = 1 - \dfrac{1}{h_j}$, where h_j is number of calves in contemporary group, $n_{q'} = \displaystyle\sum_{i=1}^m n_{ij}$, where i is number of calves of the same dam, n_q is related to the q-th calving record in case the animal being a dam and is calculated as $n_q = 1 - \dfrac{1}{h_q}$, where h_q is number of calves in contemporary group for calving record of the cow.

The value in the upper left corner of equation 4 is the EDC of own birth record (individual identified as a calf), while the EDC in the lower right corner is the EDC of calving records.

Information loss due to multiple calves of a sire in the same contemporary group can be accounted for as shown in Interbull (2000). The slightly modified formula can be written as:

$$w_{ijk} = \left(\sum_{i=1}^n x_{ij} - \sum_{i=1}^n x_{ijk} \right) / \sum_{i=1}^n x_{ij} \qquad [8]$$

where w_{ijk} is the weight of the *i'th* calving record in the *j'th* contemporary group, of the *k'th* sire, $\displaystyle\sum_{i=1}^n x_{ij}$ is the total sum over calving records in the *j'th* contemporary group, and $\displaystyle\sum_{i=1}^n x_{ijk}$ is total sum over calving records by the *k'th* sire in the *j'th* contemporary group.

Step 3

Calculate reliability for own data

$$\Re_y = \mathbf{I} - \left(\boldsymbol{\varepsilon}_o \mathbf{G}_o + \mathbf{I}\right)^{-1} \qquad [9]$$

Step 4

Calculate reliabilities for progeny adjusted for mate $\left(\Re_{P-M}\right)$

$$\Re_{P-M} = \frac{1}{4}\left[\mathbf{E} - \mathbf{E}(\mathbf{E} + (\mathbf{I} - \frac{1}{4}\Re_M^*)^{-1})^{-1}\mathbf{E} \right] \qquad [10]$$

where

$$\mathbf{E} = \left(\mathbf{I} - \Re_y\right)^{-1} - \mathbf{I} \qquad [11]$$

$\Re_M^*$ is reliability of mate, and $\Re_p^*$ is reliability of progeny.

Step 5

Calculate EDC of each progeny adjusted for mate $\boldsymbol{\varepsilon}_{P-M}$

$$\boldsymbol{\varepsilon}_{P-M} = 4 * \left[\left(\mathbf{I} - \Re_{P-M}\right)^{-1} - \mathbf{I}\right]\mathbf{G}_o^{-1} \qquad [12]$$

Step 6

Calculate the final EDC for the sire $\left(\boldsymbol{\varepsilon}_{final}\right)$

$$\boldsymbol{\varepsilon}_{final} = \sum_{i=1}^{n} \boldsymbol{\varepsilon}_{P-M_i} \qquad [13]$$

Step 7

And the reliability $\left(\Re_{sire}\right)$ for each of these sires can be calculated as

$$\Re_{sire} = \mathbf{I} - \left(\frac{1}{4}\boldsymbol{\varepsilon}_{final}\mathbf{G}_o + \mathbf{I}\right)^{-1} \qquad [14]$$

The reliability of each of these sires can be transferred to real reliabilities using formula 15.

$$\Re_{sire} = \begin{bmatrix} \dfrac{\mathbf{v}_1'\mathbf{G}_o\Re_{total}\mathbf{v}_1}{\mathbf{v}_1'\mathbf{G}_o\mathbf{v}_1} & \dfrac{\mathbf{v}_1'\mathbf{G}_o\Re_{total}\mathbf{v}_2}{\mathbf{v}_1'\mathbf{G}_o\mathbf{v}_2} \\[3mm] \dfrac{\mathbf{v}_2'\mathbf{G}_o\Re_{total}\mathbf{v}_1}{\mathbf{v}_2'\mathbf{G}_o\mathbf{v}_1} & \dfrac{\mathbf{v}_2'\mathbf{G}_o\Re_{total}\mathbf{v}_2}{\mathbf{v}_2'\mathbf{G}_o\mathbf{v}_2} \end{bmatrix}$$

$$[15]$$

where

$$\mathbf{v}_1 = \begin{bmatrix} 1 \\ 0 \end{bmatrix} \text{ and } \mathbf{v}_2 = \begin{bmatrix} 0 \\ 1 \end{bmatrix}$$

Step 8

Final weighting factors $\left(W_{direct} \text{ and } W_{maternal}\right)$ are calculated trait wise for each bull:

$$W_{direct} = k_{direct} * \frac{\Re_{final[d:d,d:d]}}{1 - \Re_{final[d:d,d:d]}} \qquad [16]$$

and

$$W_{maternal} = k_{maternal} * \frac{\Re_{final[m:m,m:m]}}{1 - \Re_{final[m:m,m:m]}} \qquad [17]$$

where:

$\Re_{final[d:d,d:d]}$ and $\Re_{final[m:m,m:m]}$ are the parts of the final reliability matrix for direct and maternal effects, respectively.

$$k_{direct} = \frac{\sigma_e^2 + \dfrac{3}{4}\sigma_d^2}{\dfrac{1}{4}\sigma_d^2} = \frac{\left(4 - h_d^2\right) - 4\left(\sigma_{pe}^2 + \sigma_d^2 + \sigma_{dm}\right)/\sigma_P^2}{h_d^2} \qquad [18]$$

and calculation of $k_{maternal}$ follows with exchange of σ_d^2 to σ_m^2 the procedure for calculation of k_{direct}.

The phenotypic variance is calculated as:

$$\sigma_P^2 = \sigma_d^2 + \sigma_m^2 + \sigma_{dm} + \sigma_{pe}^2 + \sigma_e^2$$

As described by Liu *et al.* (2003) these *k*-values are slightly different from the k-values or variance ratios $\left(k = \dfrac{4 - h^2}{h^2} \right)$ used in the Interbull single trait method for EDC-calculation. The difference is due to the correlation between direct and maternal effects.

Discussion

We have here outlined a procedure to calculate weights for linear models with maternal effects. This procedure should suit national animal models for calving traits. Of the ten countries participating in the pilot-studies for calving traits for the Holstein populations only Canada and Germany are currently using an animal model. Model formulation and parameters differ between sire-MGS models and animal models. Therefore, formulas may be revised to suit the linear sire-MGS models for calving traits. Also, France and USA are using threshold models for their national evaluations. It still needs to be investigated if we can adapt the proposed EDC-procedure to underlying liabilities.

Conclusion

We have here outlined a possible procedure for calculation of weights for linear animal models with maternal effects. The procedure is the matrix equivalent to a single trait procedure and is appealing in that sense. Also, it is only necessary to go through data once and the EDC-matrix for each animal can be set up directly. A small example calculation has shown a slight bias in reliability calculations. This small bias could be caused by the non-parsimoniousness of the model used on a small data set. So the next step will be to try the procedure on a large data set.

References

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Appendix:
Reliability and EDC equivalents in multiple trait and single trait models

	Single Trait	Multiple Trait
Reliability	$\mathfrak{R}_s = 1 - \dfrac{1}{\sigma_s^2} * \dfrac{1}{(n_{ej}+k)}$	$\mathfrak{R}_s = \mathbf{I} - \mathbf{G_s^{-1}C}$
Effective Daughter Contribution	$\varepsilon_s = \left[\dfrac{1}{1-\mathfrak{R}_s} - 1 \right] * \dfrac{1}{\sigma_s^2}$	$\boldsymbol{\varepsilon_s} = \left[\left(\mathbf{I} - \mathfrak{R}_s\right)^{-1} - \mathbf{I} \right] \mathbf{G_s^{-1}}$

$\mathfrak{R}_s$ is reliability of a sire, $\mathbf{I}$ is identity matrix, $\mathbf{G_s^{-1}}$ is the inverted sire-(co)variance matrix, $\mathbf{C}$ is the sub-matrix of the inverted coefficient matrix of the mixed model equations, $\boldsymbol{\varepsilon_s}$ is the effective daughter contribution of the sire, σ_s^2 is the sire-variance, σ_e^2 is the residual variance, n_{ej} is effective number of daughters, and $k = \dfrac{\sigma_e^2}{\sigma_s^2}$.