Calculation of Weighting Factors for the Canadian Test Day Model

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Interbull has designed a new procedure to calculate weighting factors for use in international genetic evaluations. The procedure as described consists of two steps. Step 1 calculates the reliability based on an animal's own performance records. Step 2 uses this reliability on progeny and mates to calculate a weight for each bull.

Although Interbull provides two alternatives for Step 1, neither method can be applied to the random regression test day model implemented in Canada. The first method given is for a single trait model, and the Canadian test day model (CTDM) is a multiple trait model. The second method uses a P matrix that is the sum of genetic and residual covariances. However in the CTDM, observations and residual covariances are for test day yields while breeding values and genetic covariances are for parameters in a curve. The genetic and residual covariances for the CTDM cannot be added since they are on different scales.

Therefore, a procedure was developed to calculate reliabilities for a random regression test day model that could be used in Step 1 of the Interbull weighting factor calculation. The new procedure accounted for the same effects that were considered in the Step 1 methods presented by Interbull. The new Step 1 procedure was based on the domestic reliability calculation (Jamrozik et al., 2000) as currently implemented in Canada.

Step 1 for a Random Regression Test-Day Model

The breeding value sent to Interbull can be calculated as:

$$EBV_i = \mathbf{k'a_i}$$

$$V(EBV_i) = g_i = \mathbf{k'G_0k}$$

For each animal:

Form the coefficient matrix corresponding to the animal's genetic regressions:

$$\mathbf{C_i = Z_i' R^{*}_i{}^{-1} Z_i + G_0^{-1}}$$

Absorb equations for permanent environmental regression coefficients into $\mathbf{C_i}$:

$$\mathbf{D_i = [C_i - Z_i' R^{*}_i{}^{-1} Z_i (Z_i' R^{*}_i{}^{-1} Z_i + P_0^{-1}) Z_i' R^{*}_i{}^{-1} Z_i]^{-1}}$$

Calculate the prediction error variance as:

$$m_i = \mathbf{k' D_i k}$$

Calculate the reliability based on data as:

$$R_i(o) = 1 - m_i/g_i$$

where:

$\mathbf{a_i}$ is a vector of genetic random regression coefficients for animal i,

k is a vector with coefficients used to calculate a trait of interest,

$\mathbf{G_0}$ is the genetic (regression coefficients) covariance matrix,

$\mathbf{R^*_i}$ is a matrix with modified residual covariances among observed traits,

$\mathbf{Z_i}$ is a vector assigning genetic regressions of animal i to observations, and

$\mathbf{P_0}$ is the permanent environmental (regression coefficients) covariance matrix.

In the Canadian domestic reliability calculation $\mathbf{R^*_i}$ is equal to the residual covariance matrix ($\mathbf{R_i}$). The use of $\mathbf{R_i}$ accounts for differences in weights placed on records, but does not account for the effects of contemporary group size. The $\mathbf{R_i}$ matrix is block diagonal with non-zero covariances between traits measured on the same day (milk, fat, protein and somatic cell score) and zero covariances between observations on different days. In order to account for contemporary group size, each block diagonal is pre-multiplied by a scalar w_{ij}, defined for animal i in group j as:

$$w_{ij} = CGS_j / [CGS_j - 1]$$

where:

CGS_j is the number of animals tested in the same lactation (first vs. later) on the same day in the same herd.

Application of the Procedure for Canadian Protein Yield

The above procedure was applied to Canadian Holstein Protein data (August, 2000), by lactation and for combined protein across lactations. Weighting factors for combined protein increased by approximately 17% relative to number of daughters, for bulls with the highest accuracies. For first lactation protein, the comparative increase was 34%. These were modest increases relative to those observed for several other countries that have implemented the new Interbull procedure (Interbull, 2000*a*). The procedure was also applied without the adjustment for contemporary group size, and gave very similar increases (18% and 37% for combined and 1st lactation protein, respectively).

To investigate the effect of adjusting for CG size, Step 1 reliabilities were examined for both the Canadian test day model (using the new Step 1 procedure) and for a single trait repeatability model (using the Interbull (2000*b*) Step 1 procedure), with and without the CG size adjustment.

Reliabilities for the single-trait repeatability model were calculated using the following assumptions:

h^2 = .36 (same as in the CTDM for Holsteins),

r = .68 (assuming that half the non-genetic variance is permanent environmental), contemporary group size = 10 (similar to the Holstein data in the CTDM), number of daughters of the sire in the contemporary group = 1, and weights within each contemporary group are equal (same as in the CTDM).

Table 1. Effect of accounting for contemporary group size on reliability based on the data

Number of test-day records	% Decrease in reliability when accounting for contemporary group size in a single-trait repeatability model	% Decrease in reliability when accounting for contemporary group size in the Canadian test day model
1	3.43	4.79
2	2.07	2.59
3	1.48	2.11
4	1.16	2.03
5	0.95	1.92
6	0.80	1.73
7	0.70	1.45
8	0.61	1.18
9	0.55	1.13
10	0.50	1.08
11	0.45	0.87
12	0.42	0.88
13	0.39	0.81
14	0.36	0.74
15	0.34	0.67
16	0.32	0.60

The impact of CG size decreased rapidly for both types of models as the number of TD records increased. The impact of the CG size adjustment was small when an animal has 15 TD records which is the average number of test day records for Canadian Holstein cows with observations.

The contemporary group size adjustment proposed for the CTDM had a small impact on reliabilities and subsequently on weighting factors of sires, but a larger impact than would be expected compared to a single-trait repeatability model using the Interbull Step 1 procedures.

References

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