# Simple Method to Incorporate Univariate Interbeef Evaluations for Weaning Weight into National Multi-Variate Models

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## Abstract

Interbeef evaluations for weaning weight ( WWT) is based on a single trait model while the UK fits a multi-trait model with 9 other traits. The lack of correlated traits in Interbeef evaluations for WWT implies these could be less accurate. The paper presents a mixed method approach to incorporate contributions from the correlated traits into Interbeef evaluations without double counting. An approach to incorporate the correlated information for foreign animals and that accumulates increases in accuracy in WWT resulting from Interbeef evaluation and that from correlated traits at the national level is also presented.

## Introduction

The current Interbeef model for weaning weight (WWT) is an across country single trait evaluation. It involves the analysis of WWT phenotypic records from 8 countries, with observations from each country treated as different traits. The process involves the estimation of genetic correlations among the various countries in addition to the estimation of individual country heritabilities. The advantages of such across country evaluation is estimated breeding values (EBVs) are more accurate compared to national evaluations as there is additional information coming from other countries through pedigree links. However, most countries implement multi-trait models for WWT in combination with other traits. For instance, in the UK, the EBV published for WWT is from a multi-trait analysis involving 9 other traits. Thus the EBVs for WWT from Interbeef could be less accurate than those produced from national evaluations due to the lack of information from these traits. Thus a methodology that would combine Interbeef EBVs with national EBVs such that there is no double counting and accumulates increases in accuracy in WWT resulting from Interbeef across country evaluation with those from the national multi-trait model seems an optimum option.

Also, the Interbeef heritability estimates for a country is at times different from current estimates applied in the national evaluation. This could result in differences in the scale of national and Interbeef evaluations.

This paper therefore examines a method to combine Interbeef evaluation with the UK national evaluations without double counting. It also an present s an approach to harness the increases in accuracy in WWT resulting from Interbeef across country evaluation with those from correlated traits in the national multi-trait model.

## Material and Methods

Firstly the usual multi-trait model of the analysis of WWT (analysis 1)and the other 9 traits : birth weight (BWT), 400-day weight(400WT), muscle score(MSC), fat depth(FD), muscle depth(MD), gestation length (GL) , calving ease(CE) , docility (DOC) and scrotal size(SC) , was implemented on the data set sent to Interbeef for the 2013 January run. The multi-trait model employed for the analysis is :

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Zm} + \mathrm{W}\mathbf{pe} + \mathrm{e} \qquad [1]$$

where **y** is the vector of records for 10 traits, **b** is vector of solutions for fixed effects consisting of month of birth fitted for all traits apart from MSC, FD and FD, sex of calf for BWT, WWT and GL, birth types for all traits, dam breed at birth and embryo transfer status for WWT, GL, and CE , dam breed at weaning for all traits apart from BWT, GL and CE, dam age fitted as covariate for BWT, WWT, 400WT and GL, age at scanning fitted for MSC,MD and FD, age at measurement fitted for DOC and SC, dam parity fitted for

DOC only, and dam parity by sex of calf fitted for CE only.; **u** is the vector of random animal effects , **m** and **pe** are the vector of direct maternal and permanent environmental effects respectively for BWT, WWT, GL and CCE only and e is the random error term.

Secondly, the multi-trait analysis (analysis 2)was repeated but with records for WWT omitted for the animals whose observations have been sent to Interbeeef. The EBVs for WWT from this run result from the correlations between WWT and other traits in the model and have been termed correlated EBVs. Thirdly a univariate analysis of WWT (analysis 3)was undertaken with the model outlined in equation 1. The heritability used was 0.36 compared with the Interbeef estimate of 0.19.

In order to avoid doubling counting of information, an approach for incorporating the EBVs from analysis 2 with those from Interbeef using mixed model approach was examined. The methodology was tested by comparing combined EBVs from analysis 2 and 3 with those from analysis 1. The equations for animal solutions from the usual MME for a multi-trait analysis ( Mrode, 2005) are:

$$\left(\mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z}+\mathbf{A}^{-1}\mathbf{G}^{-1}\right)\hat{\mathbf{a}}=(\mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z})\mathbf{YD} \qquad (2)$$

where YD is the vector of yield deviations and $\mathbf{YD}=\left(\mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z}\right)^{-1}\left(\mathbf{Z}'\mathbf{R}^{-1}\left(\mathbf{y}-\mathbf{X}\hat{\mathbf{b}}\right)\right)$

Transferring the left non-diagonal terms of $\mathbf{A}^{-1}$ in equation (2) to the right side of the equation (VanRaden and Wiggans, 1991) gives:

$$\left(\mathbf{Z'R}^{-1}\mathbf{Z}+\mathbf{G}^{-1}\alpha_{\mathrm{anim}}\right)\hat{\mathbf{a}}_{\mathbf{anim}}=\mathbf{G}^{-1}\alpha_{\mathrm{par}}\left(\hat{\mathbf{a}}_{\mathbf{sire}}+\hat{\mathbf{a}}_{\mathbf{dam}}\right)+\left(\mathbf{Z'R}^{-1}\mathbf{Z}\right)\mathbf{YD}+\mathbf{G}^{-1}\sum\alpha_{\mathrm{prog}}\left(\mathbf{a}_{\mathrm{prog}}-0.5\hat{\mathbf{a}}_{mate}\right)$$

where $\alpha_{\mathrm{par}}$ = 1, 2/3 or ½ if both, one or neither parents are known respectively and $\alpha_{\mathrm{prog}}$ = 1 if animal's mate is known and 2/3 if unknown. Note that $\alpha_{\mathrm{anim}} = 2\,\alpha_{\mathrm{par}} + 0.5\,\alpha_{\mathrm{prog}}$. The above equation can be expressed as:

$$(\mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z}+\mathbf{G}^{-1}\alpha_{\mathbf{anim}})\hat{\mathbf{a}}_{\mathbf{anim}}=2\mathbf{G}^{-1}\alpha_{\mathbf{par}}(\mathbf{PA})+(\mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z})\mathbf{YD}+0.5\mathbf{G}^{-1}\sum\alpha_{\mathbf{prog}}(2\hat{\mathbf{a}}_{\mathbf{prog}}-\hat{\mathbf{a}}_{\mathbf{mate}})$$

where **PA** = parent average.

Pre-multiplying both sides of the equation by $(\mathbf{Z'R}^{-1}\mathbf{Z}+\mathbf{G}^{-1}\alpha_{\mathrm{anim}})^{-1}$ gives:

$$\hat{\mathbf{a}}_{\mathbf{anim}}=\mathbf{W}_1\mathbf{PA}+\mathbf{W}_2\mathbf{YD}+\mathbf{W}_3\mathbf{PC} \qquad (3)$$

with $\mathbf{PC}=\sum\alpha_{\mathbf{prog}}(2\hat{\mathbf{a}}_{\mathbf{prog}}-\hat{\mathbf{a}}_{\mathbf{mate})}/\sum\alpha_{\mathbf{prog}}$.

The weights $\mathbf{W}_1$, $\mathbf{W}_2$, and $\mathbf{W}_3$ = **I**, with $\mathbf{W}_1$ = $(\mathbf{DIAG})^{-1}2\mathbf{G}^{-1}\alpha_{\mathrm{par}}$, $\mathbf{W}_2 = (\mathbf{DIAG})^{-1}(\mathbf{Z'R}^{-1}\mathbf{Z})$, and $\mathbf{W}_3$ = $(\mathbf{DIAG})^{-1}0.5\mathbf{G}^{-1}\Sigma\alpha_{\mathrm{prog}}$ where $(\mathbf{DIAG}) = (\mathbf{Z'R}^{-1}\mathbf{Z}+\mathbf{G}^{-1}\alpha_{\mathrm{anim}})$.

From [3], the equation for an animal for trait I, can be written as

$$\mathbf{a}_{\mathrm{i-anim}}=\mathbf{W_1}(\mathbf{YD_j}-\mathbf{PA_j})+\mathbf{W_1PA_i}+\mathbf{W_2YD_i} \qquad (4)$$

If the trait i was missing from the multi-trait analysis, then [3] becomes:

$$\mathbf{a}_{\text{i-anim-cr}} = \mathbf{W_1(YD_j - PA_j) + W_1PA_i} \qquad (5)$$

A similar equation for the EBV of an animal from a univariate analysis is

$$\mathbf{a}_{\text{i-anim-uni}} = \mathbf{W_1PA_i + W_2YD_i} \qquad (6)$$

Thus equivalent solutions to [3] can be obtained by combining [5] and [6]. Thus

$$\mathbf{a}_{\text{i-anim-combined}} = \mathbf{a}_{\text{i-anim-cr}} + \mathbf{a}_{\text{i-anim-u}\textit{ni}} - \mathbf{W_1PA_i}$$

which equals

$$\mathbf{a}_{\text{i-anim-combined}} = \mathbf{W_1(YD_j - PA_j) + W_1PA_i + W_2YD_i} \qquad (7)$$

where the first term in the right hand side is the Mendelian Sampling (MS) contribution from correlated traits. Thus

$$\text{MS}_{\text{i-anim}} = \; = \mathbf{W_1(YD_j - PA_j)} \qquad = G_{jj}^{-1}G_{i,j}(a_{j\,\text{-anim}} - PA_j).$$

The application of [7] to combined correlated EBVs and univariate EBVs when the i^th^ trait was missing compared to an equivalent multi-trait indicated it resulted in over-prediction. Therefore [7] was modified as :

$$\mathbf{a}_{\text{i-anim-combined}} = \mathbf{W^*_1\,(YD_j - PA_j) + W_1PA_i + W_2YD_i} \qquad (8)$$

$$\mathbf{a}_{\text{i-anim-combined}} = \text{MS}^* + \mathbf{W_1PA_i + W_2YD_i} \qquad (9)$$

where $W^*_1$ was the $W_1$ in equation [5], corrected the over prediction and

$$\text{MS}^* = \mathbf{W^*_1\,(YD_j - PA_j)}$$

Equation [8] was used to combine Interbeef EBVs for WWT for about 7000 UK animals with correlated EBVs for WWT from analysis 2. Similarly EBVs for the same animals were combined for analyses 2 and 3. Both sets of combined EBVs were compared with the official EBVs for WWT for the animals.

## Results and Discussion

The distribution of Interbeef EBVs for WWT and those from the multi-trait model in the UK using model [1] is presented in Figure 1. A similar distribution but with UK WWT EBVs estimated from correlated traits (analysis 2) in shown in Figure 2 or with UK WWT EBVs estimated with a univariate model is shown in Figure 3. The marked difference in the distribution of UK WWT and Interbeef EBVs is well demonstrated in Figures 1 and 2 but this difference almost disappears in Figure 3. This indicates that the major source of differences in the Interbeef and UK national EBVs is the correlated information contributed to WWT evaluations in the multi-trait evaluation. This is further confirmed in Table 1 which shown a summary of the distribution of the different evaluations.

A standard deviation (std) of the EBVS from analysis 1, combined EBVs from analysis 2 and 3, and analysis 2 and Interbeef EBVs using equation (8) were 12.53, 12.93 and 14.440kg$^2$ respectively. This indicates the similarity in std between the official published EBVs for WWT and the combined EBVs. The slightly higher std for combined EBVs using Interbeef EBVs is expected due to the additional information from Interbeef evaluations. The distributions for the combined EBVs and the multi-trait EBVS are shown in Figures 4 and 5, confirming the similarity in the variance of the combined EBVS and EBVs from analysis 1. The correlation between the Interbeef evaluations with the UK official EBVs was 0.85 but this increased to 0.91 after the incorporating correlated information into Interbeef EBVs.

Combined reliabilities for the combined EBVs from analysis 2 and Interbeef evaluations could be computed as: Combined reliabilities = $DE_{itb}$ + $DE_{relnopa}$ , where DE refers to daughter equivalents computed from the Interbeef reliabilities and reliability from analysis corrected for parent contribution.

The combination procedure outlined can however be applied to foreign animals that have no records in the UK. The contribution of correlated traits to foreign animals could be approximated from the relationship between the correlated EBVS of UK animals with no records in analysis 2 ( a situation similar to foreign animals) and the MS* in equation (9). Thus a linear regression of MS* on Interbeef EBVs for this group of animals provides a means to update the Interbeef EBVs of foreign animals for correlated information from other traits in the UK. Similarly, the increase in reliabilities for foreign animals could be computed as $rg^2 * REL_{relnopa}$ , where is the $rg^2$ is the genetic correlation between WWT and the $i^{th}$ correlated trait and $REL_{relnopa}$ is the reliability for the correlated in analysis 2 corrected for parental contribution.

## Conclusion

The incorporation of correlated information from the UK multi-trait model into evaluations from Interbeef is necessary in order to gain the benefits of contributions from correlated traits and other countries. The combination method based the mixed model approach seems an appropriate method

## References

Mrode, R. 2005. *Linear models for the prediction of animal breeding values.* $2^{nd}$ edition CABI publishing Wallingford, UK.

**Table 1.** Summary statistics of estimated breeding values (EBVs) from the various models .

| ModeL | Mean | Standard Deviation | Minimum | Maximum |
|---|---|---|---|---|
| UK- multi-trait EBV | 10.692 | 12.905 | -46.017 | 66.082 |
| UK-Correlated EBV | 8.746 | 11.479 | -47.568 | 61.679 |
| UK-Univariate EBV | 3.812 | 11.486 | -42.727 | 52.882 |
| Interbeef EBV | 3.181 | 7.359 | -25.306 | 33.201 |

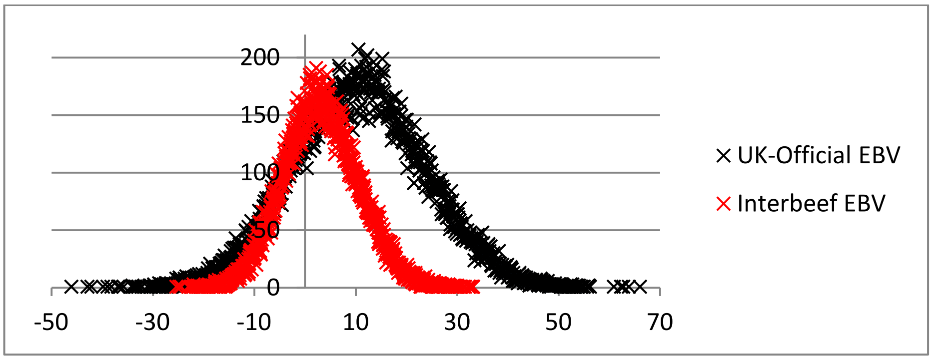

**Figure 1.** Distribution of weaning weight estimated breeding values (EBVs) for UK official multi-trait model and EBVS from Interbeef evaluations

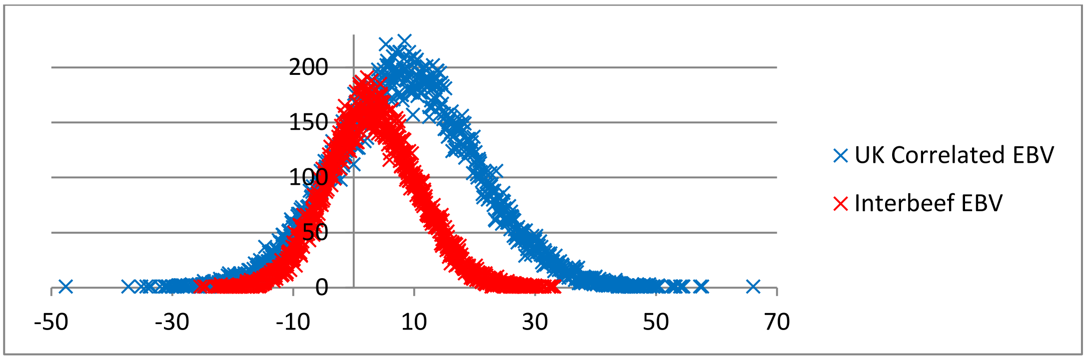

**Figure 2.** Distribution of weaning weight (WWT) correlated estimated breeding values (EBVs) from UK official multi-trait model with records for WWT omitted and EBVS from Interbeef evaluations.

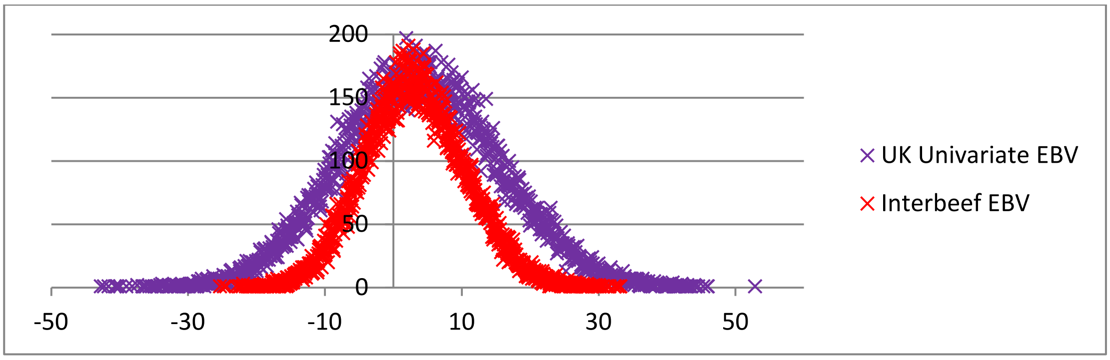

**Figure 3.** Distribution of weaning weight (WWT) estimated breeding values (EBVs) from UK univariate model and EBVS from Interbeef evaluations.

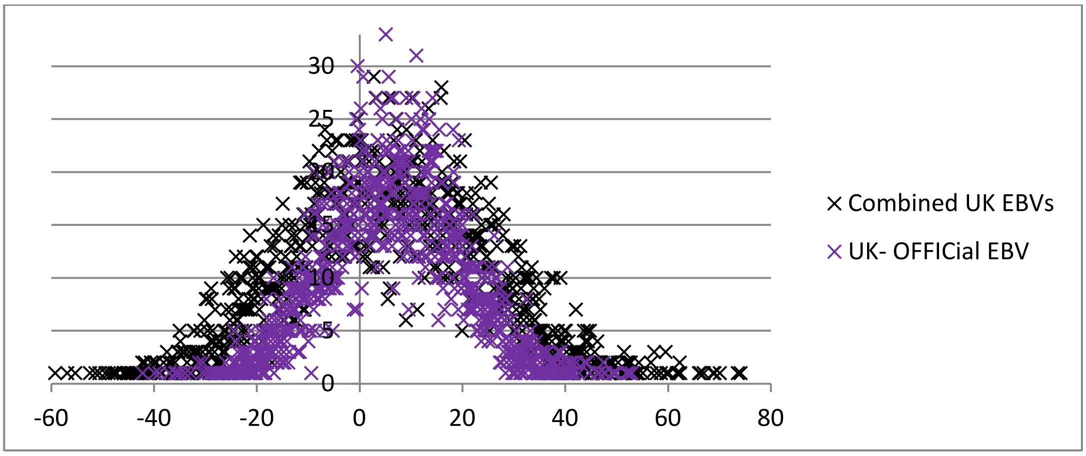

**Figure 4.** Distribution of combined estimated breeding values (EBVs) from UK univariate model and multi-trait with records for WWT omitted and the official EBVs from full multi-trait model.

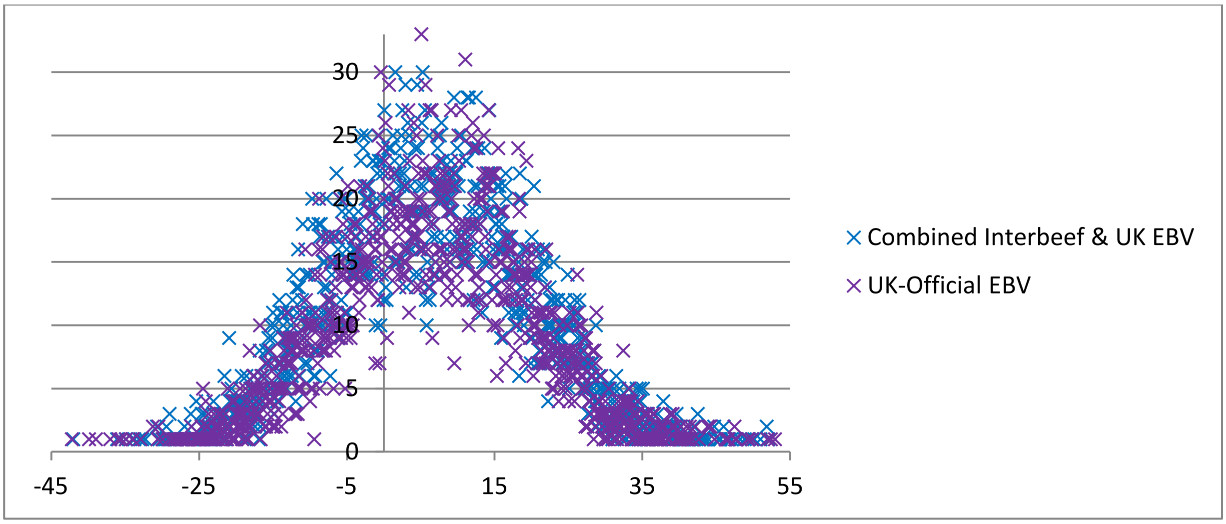

**Figure 5.** Distribution of combined estimated breeding values (EBVs) from Interbeef and multi-trait with records for WWT omitted and the official EBVs from full multi-trait model.