

# Reducing the Number of Equations of a Multiple Trait MACE Model for International Bull Evaluation

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## Abstract

The multi-trait MACE model developed by Liu *et al.* (2004b) and implemented by Tarres *et al.* (2006) estimates additive genetic effects of animals for international evaluation in the same way as for national genetic evaluations, which guarantees minimal loss in the transfer of information from national to international evaluations. With more countries having moved to multiple trait models, the equation system of the multi-trait MACE model becomes much larger than the single trait MACE model, and the increase is even more dramatic with the use of sire and dam relationship. In this paper we absorbed the effects on foreign country scales for bulls without progeny in the bull evaluation. New equations were derived for effects of the non-parent bulls in home country and for effects of their sires and dams. The reduction of equations can be reached to 40% based on the information of a production trait MACE evaluation from Interbull, because a high percentage of bulls with national data have no progeny in the international bull evaluations. The efficiency of the within-animal absorption will be much higher for MACE models based on sire and maternal grandsire relationship than sire and dam relationship. This equation reduction technique does not cause any loss in accuracy, and it is easy to implement for routine evaluations. Validation of the within-bull absorption method can be done via simulation or with field data.

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## 1. Introduction

For international bull comparison, a multiple trait multiple country model developed by Liu *et al.* (2004b) evaluates daughter yield deviations (DYD) of bulls with associated effective daughter contribution (EDC), instead of deregressed proofs, in multiple across country evaluation (MACE, Schaeffer 1994). This multiple trait MACE (MT-MACE) model allows the same modelling of additive genetic effects in both national and international genetic evaluations (Tarres *et al.*, 2006), therefore it can better utilise the information derived from diverse national genetic evaluations. For instance, regression coefficients of DYD are defined as traits in international evaluation for a country applying a random regression test day model in national genetic evaluation, whereas a scalar DYD on mature equivalent 305-day lactation basis is the dependent variable for a country with a repeatability lactation model in national evaluation. Corresponding to DYD of a bull derived from a multi-trait national model, an EDC matrix needs to be considered in MT-MACE evaluation (Liu *et al.*, 2004a). In the

current single trait MACE (ST-MACE) model, each country is considered as a genetically distinct trait, thus the total number of traits per animal in current MACE is the number of countries. Because countries can have several correlated traits in the MT-MACE model, the number of effects per animal increases linearly with the number of traits within country. As a consequence, mixed model equations (MME) of the MT-MACE model become significantly larger than the equation system of the ST-MACE model. The objective of this study was to reduce the number of equations to be solved at no cost of accuracy.

## 2. Materials and Methods

### 2.1. A multiple trait international bull evaluation model

The international genetic evaluation model for a country is assumed to be identical to the statistical model in its national genetic evaluation, as far as additive genetic effects concerned. For a country *j* using a multiple trait model in national genetic evaluation, the

same model, including genetic and residual effects only, is applied to DYD of a bull  $i$  in international genetic evaluation:

$$\mathbf{q}_{ij} = \boldsymbol{\mu}_j + \mathbf{a}_{ij} + \boldsymbol{\varepsilon}_{ij} \quad [1]$$

where  $\mathbf{q}_{ij}$  is a vector of DYD of the  $i$ -th bull in country  $j$ ,  $\boldsymbol{\mu}_j$  is a vector of general means for traits of the  $j$ -th country,  $\mathbf{a}_{ij}$  is a vector of additive genetic effects of bull  $i$  in country  $j$ , and  $\boldsymbol{\varepsilon}_{ij}$  is a vector of residual effects. (Co)variance matrices for the random effects are:

$$\mathbf{G}_0 = \begin{bmatrix} \mathbf{G}_{0_{11}} & \mathbf{G}_{0_{12}} & \cdots & \mathbf{G}_{0_{1m}} \\ & \mathbf{G}_{0_{22}} & \cdots & \mathbf{G}_{0_{2m}} \\ & & \ddots & \vdots \\ \text{symm.} & & & \mathbf{G}_{0_{mm}} \end{bmatrix}, \text{ and } \mathbf{G}_0^{-1} = \begin{bmatrix} \mathbf{G}_0^{11} & \mathbf{G}_0^{12} & \cdots & \mathbf{G}_0^{1m} \\ & \mathbf{G}_0^{22} & \cdots & \mathbf{G}_0^{2m} \\ & & \ddots & \vdots \\ \text{symm.} & & & \mathbf{G}_0^{mm} \end{bmatrix}. \quad [3]$$

Let  $p_j$  represent the number of traits of country  $j$  in the MT-MACE model, then the total number of traits across all  $m$  countries is:

$$p = \sum_{j=1}^m p_j. \quad [4]$$

Denote the total number of bulls with data in any of all the countries as  $n_b$ . Furthermore, we differentiate the bulls with data according to the fact whether they have progeny in the MACE evaluation, let  $n_{b1}$  represent the number of the bulls having progeny and  $n_{b0}$  having no progeny. According to the theory of MACE where each country is treated as different trait, the total number of equations in the MT-MACE model is:

$$n_T = (n_{b1} + n_{b0} + n_o + n_g) \times p, \quad [5]$$

where  $n_o$  is the number of ancestors and  $n_g$  is the number of phantom parent groups.

$$\text{Var}(\mathbf{a}_{ij}) = \mathbf{G}_{0_{jj}}, \text{ and } [\text{Var}(\boldsymbol{\varepsilon}_{ij})]^{-1} = \boldsymbol{\Psi}_{ij}, \quad [2]$$

where  $\mathbf{G}_{0_{jj}}$  is genetic (co)variance matrix of country  $j$ , and  $\boldsymbol{\Psi}_{ij}$  is an EDC matrix associated with the DYD vector  $\mathbf{q}_{ij}$  (Liu *et al.*, 2004a). The above model can be simplified for yield deviations (YD) or DYD data from countries with a single trait model in national genetic evaluation, with all terms above becoming scalar. Denote genetic (co)variance matrix and its inverse of all  $m$  countries as:

## 2.2. Equations of bulls without progeny

Breeding values of an animal are determined by three sources of information: own data, parental averages and progeny contribution. In a typical international bull evaluation, only a low percentage of bulls have progeny that have also data in the bull comparison, as most progeny-tested bulls will not be used after the progeny test programme has completed. These bulls without progeny, i.e. non-parents, in the bull evaluation usually have data from only one country, with the exception of co-tested bulls. Their MACE proofs on other country scales are dependent on their parental averages of the foreign countries and daughter information from home country. Because of the dependency, we try to derive the equations of the non-parent bulls on foreign country scales by the parental averages and own data information from home country without actually solving the corresponding foreign equations. By doing so, the total number of equations to be solved is reduced to:

$$n_T^* = \sum_{j=1}^m n_{b0_j} * p_j + (n_{b1} + n_o + n_g) \times p, \quad [6]$$

where  $n_{b0_j}$  is the number of non-parent bulls in country  $j$ .

Assume that a non-parent bull  $i$  has data from country  $j^+$ , his proof vector is partitioned as:

$$\mathbf{a}_i' = [\mathbf{a}_{ij^+}' \quad \mathbf{a}_{ij^-}'] \quad [7]$$

where  $\mathbf{a}_{ij^+}$  represents the  $i$ -th bull's proofs from country  $j^+$  contributing data, and  $\mathbf{a}_{ij^-}$  represents the bull's proofs on foreign countries  $j^-$  where he does not have data. The inverse of genetic (co)variance matrix can be partitioned accordingly:

$$\mathbf{G}_0^{-1} = \begin{bmatrix} \mathbf{G}_0^{j^+j^+} & \mathbf{G}_0^{j^+j^-} \\ \mathbf{G}_0^{j^-j^+} & \mathbf{G}_0^{j^-j^-} \end{bmatrix} = \begin{bmatrix} \mathbf{G}_0^{j^+} \\ \mathbf{G}_0^{j^-} \end{bmatrix} \quad [8]$$

In the MME system of the MT-MACE model (Liu *et al.*, 2004b), left-hand-side (LHS) and right-hand-side (RHS) corresponding to the bull  $i$  are respectively:

$$\begin{bmatrix} \Psi_{ij^+} + a^{ii} \mathbf{G}_0^{j^+j^+} & a^{ii} \mathbf{G}_0^{j^+j^-} \\ a^{ii} \mathbf{G}_0^{j^-j^+} & a^{ii} \mathbf{G}_0^{j^-j^-} \end{bmatrix} \text{ and } \begin{bmatrix} \Delta_{ij^+} \\ \mathbf{0} \end{bmatrix}. \quad [9]$$

Because the bull  $i$  has no progeny in the bull evaluation, his equations for the foreign countries  $j^-$  are:

$$a^{ii} \mathbf{G}_0^{j^-j^+} \hat{\mathbf{a}}_{ij^+} + a^{ii} \mathbf{G}_0^{j^-j^-} \hat{\mathbf{a}}_{ij^-} - \frac{1}{2} d_i \mathbf{G}_0^{j^-} (\hat{\mathbf{s}} + \hat{\mathbf{d}}) = \mathbf{0}, \quad [10]$$

where  $\hat{\mathbf{s}}$  and  $\hat{\mathbf{d}}$  are estimated breeding values (EBV) of sire and dam of the bull  $i$ . From

$$\hat{\mathbf{a}}_{ij^-} = (\mathbf{G}_0^{j^-j^-})^{-1} \left[ \frac{1}{2} \frac{d_i}{a^{ii}} \mathbf{G}_0^{j^-} (\hat{\mathbf{s}} + \hat{\mathbf{d}}) - \mathbf{G}_0^{j^-j^+} \hat{\mathbf{a}}_{ij^+} \right]. \quad [11]$$

As the bull  $i$  does not have progeny,  $d_i = a^{ii}$ . By partitioning the sire and dam EBV vectors according to the data from home

Equation 10, EBV of the bull  $i$  on foreign country scales are obtained:

and foreign countries of the bull  $i$ , Equation 11 becomes:

$$\hat{\mathbf{a}}_{ij^-} = \frac{1}{2} (\hat{\mathbf{s}}_{j^-} + \hat{\mathbf{d}}_{j^-}) - (\mathbf{G}_0^{j^-j^-})^{-1} \mathbf{G}_0^{j^-j^+} \left[ \hat{\mathbf{a}}_{ij^+} - \frac{1}{2} (\hat{\mathbf{s}}_{j^+} + \hat{\mathbf{d}}_{j^+}) \right]. \quad [12]$$

It can be seen from Equation 12 that the bull's proofs on foreign country scales,  $j^-$ , are parental averages of the foreign countries and a function of Mendelian sampling effects of the bull of his home country  $j^+$ . Normally,

$\mathbf{G}_0^{j^-j^+}$  takes the opposite sign as  $(\mathbf{G}_0^{j^-j^-})^{-1}$  because of the positive definiteness of  $\mathbf{G}_0$ . This is illustrated with a 2 x 2 matrix:

$$\begin{pmatrix} x_{11} & x_{12} \\ x_{21} & x_{22} \end{pmatrix}^{-1} = \frac{1}{x_{11}x_{22} - x_{12}x_{21}} \begin{pmatrix} x_{22} & -x_{12} \\ -x_{21} & x_{11} \end{pmatrix}. \quad [13]$$

Therefore, the bull's proofs on foreign country scales are equal to the parental average on the foreign countries plus a function of Mendelian sampling estimates from own countries, as long as the bull itself does not

have progeny in the international bull evaluation.

Equations of the bull  $i$  on his own country scale are:

$$\Psi_{ij^+} \hat{\mu}_{j^+} + (\Psi_{ij^+} + a^{ii} \mathbf{G}_0^{j^+j^+}) \hat{\mathbf{a}}_{ij^+} + a^{ii} \mathbf{G}_0^{j^+j^-} \hat{\mathbf{a}}_{ij^-} - \frac{1}{2} d_i \mathbf{G}_0^{j^+j^+} (\hat{\mathbf{s}}_{j^+} + \hat{\mathbf{d}}_{j^+}) - \frac{1}{2} d_i \mathbf{G}_0^{j^+j^-} (\hat{\mathbf{s}}_{j^-} + \hat{\mathbf{d}}_{j^-}) = \Delta_{ij^+} \quad [14]$$

The foreign proofs of this bull,  $\hat{\mathbf{a}}_{ij^-}$ , can be absorbed into his proofs in own country, which is realised by replacing the term  $\hat{\mathbf{a}}_{ij^-}$  in

Equation 14 with Equation 12. The absorption leads to new equations for his proofs in own country:

$$\Psi_{ij^+} \hat{\mu}_{j^+} + (\Psi_{ij^+} + a^{ii} \mathbf{G}_{0^*}^{j^+j^+}) \hat{\mathbf{a}}_{ij^+} - \frac{1}{2} d_i \mathbf{G}_{0^*}^{j^+j^+} (\hat{\mathbf{s}}_{j^+} + \hat{\mathbf{d}}_{j^+}) = \Delta_{ij^+} \quad [15]$$

where

$$\mathbf{G}_{0^*}^{j^+j^+} = \mathbf{G}_0^{j^+j^+} - \mathbf{G}_0^{j^+j^-} (\mathbf{G}_0^{j^-j^-})^{-1} \mathbf{G}_0^{j^-j^+} = \mathbf{G}_0^{j^+j^+} - \mathbf{G}_{0^-}^{j^+j^+} \quad [16]$$

It can be seen from Equation 15 that the bull's  $j^+$  equations are not dependent on the  $j^-$  equations of his parents after the absorption.

### 2.3. Parental equations of the non-parent bulls

Due to the within-animal absorption of the non-informative effects of bull  $i$  on foreign country scales, equations of his sire and dam are changed. Because the dam has no data in the bull evaluation, her less complicated equations can be represented by the equations of the sire. Assume that the sire has own data in the MT-MACE evaluation, his equations are:

$$\Psi_s \hat{\mu} + (\Psi_s + a^{ss} \mathbf{G}_0^{-1}) \hat{\mathbf{s}} - \frac{1}{2} d_s \mathbf{G}_0^{-1} (\hat{\mathbf{s}}_s + \hat{\mathbf{d}}_s) - \sum_{k=1}^{n_s} \frac{1}{2} d_k \mathbf{G}_0^{-1} (\hat{\mathbf{a}}_k - \frac{1}{2} \hat{\mathbf{m}}_k) = \Delta_s \quad [17]$$

where  $\Psi_s$  represents EDC matrix of the sire  $s$ ,  $\hat{\mathbf{s}}_s$  and  $\hat{\mathbf{d}}_s$  represent EBV of sire and dam of the sire  $s$ ,  $k$  denotes progeny of the sire  $s$ ,  $n_s$  is the number of progeny of the sire  $s$ ,  $\hat{\mathbf{a}}_k$  is EBV vector of progeny  $k$  of the sire  $s$ ,  $\hat{\mathbf{m}}_k$  is proof vector of dam of progeny  $k$  or mate of the sire  $s$ ,  $\Delta_s$  represents RHS of the sire, and  $d_s$  ( $d_k$ ) is Mendelian sampling term of sire  $s$  (progeny

$k$ ) (Mrode, 2005). Note that

$$a^{ss} = d_s + \sum_{k=1}^{n_s} \frac{1}{4} d_k. \quad [18]$$

Equation 17 of the sire  $s$  can be partitioned according to the data of the progeny, bull  $i$ , in order to consider the effect of the absorption of foreign effects of the bull  $i$  on his sire. Take the bull  $i$  out of the progeny contribution term in Equation 17 of his sire and consider only the equations  $j^+$  of the sire:

$$\begin{aligned} & \Psi_{sj^+} \hat{\boldsymbol{\mu}}_{j^+} + (\Psi_{sj^+} + a^{ss} \mathbf{G}_0^{j^+j^+}) \hat{\boldsymbol{s}}_{j^+} + a^{ss} \mathbf{G}_0^{j^+j^-} \hat{\boldsymbol{s}}_{j^-} - \frac{1}{2} d_s \mathbf{G}_0^{j^+} (\hat{\boldsymbol{s}}_s + \hat{\boldsymbol{d}}_s) \\ & - \frac{1}{2} d_i \mathbf{G}_0^{j^+} (\hat{\boldsymbol{a}}_i - \frac{1}{2} \hat{\boldsymbol{d}}) - \sum_{k \neq i} \frac{1}{2} d_k \mathbf{G}_0^{j^+} (\hat{\boldsymbol{a}}_k - \frac{1}{2} \hat{\boldsymbol{m}}_k) = \Delta_{sj^+} \end{aligned} \quad [19]$$

Replacing the bull's non-informative effects,  $\hat{\boldsymbol{a}}_{ij^-}$ , with Equation 12 and collecting the same terms give:

$$\begin{aligned} & \Psi_{sj^+} \hat{\boldsymbol{\mu}}_{j^+} + \Psi_{sj^+} \hat{\boldsymbol{s}}_{j^+} + (a^{ss} \mathbf{G}_0^{j^+j^+} - \frac{1}{4} d_i \mathbf{G}_0^{j^+j^+}) \hat{\boldsymbol{s}}_{j^+} + (a^{ss} - \frac{1}{4} d_i) \mathbf{G}_0^{j^+j^-} \hat{\boldsymbol{s}}_{j^-} - \frac{1}{2} d_s \mathbf{G}_0^{j^+} (\hat{\boldsymbol{s}}_s + \hat{\boldsymbol{d}}_s) \\ & - \frac{1}{2} d_i \mathbf{G}_0^{j^+j^+} (\hat{\boldsymbol{a}}_{ij^+} - \frac{1}{2} \hat{\boldsymbol{d}}_{j^+}) - \sum_{k \neq i} \frac{1}{2} d_k \mathbf{G}_0^{j^+} (\hat{\boldsymbol{a}}_k - \frac{1}{2} \hat{\boldsymbol{m}}_k) = \Delta_{sj^+} \end{aligned} \quad [20]$$

Equation 20 shows that the covariance between the bull  $i$  and his sire  $s$  is reduced by  $\frac{1}{2} d_i \mathbf{G}_0^{j^+j^+} \hat{\boldsymbol{a}}_{ij^+}$ , the covariance between the sire  $s$  and the dam  $d$  by  $\frac{1}{4} d_i \mathbf{G}_0^{j^+j^+} \hat{\boldsymbol{d}}_{j^+}$ , and the variance of the sire  $s$  by  $\frac{1}{4} d_i \mathbf{G}_0^{j^+j^+} \hat{\boldsymbol{s}}_{j^+}$  as a result of the absorption of the non-informative

effects of the bull  $i$ . Equation 20 for the sire  $s$  is also valid for the dam of the  $i$ -th bull, when the sire  $s$  is replaced by dam  $d$ .

Corresponding to the non-informative effects of the bull  $i$ , the equations of his sire  $s$  are:

$$\begin{aligned} & \Psi_{sj^-} \hat{\boldsymbol{\mu}}_{j^-} + (\Psi_{sj^-} + a^{ss} \mathbf{G}_0^{j^-j^-}) \hat{\boldsymbol{s}}_{j^-} + a^{ss} \mathbf{G}_0^{j^-j^+} \hat{\boldsymbol{s}}_{j^+} - \frac{1}{2} d_s \mathbf{G}_0^{j^-} (\hat{\boldsymbol{s}}_s + \hat{\boldsymbol{d}}_s) \\ & - \frac{1}{2} d_i \mathbf{G}_0^{j^-} (\hat{\boldsymbol{a}}_i - \frac{1}{2} \hat{\boldsymbol{d}}) - \sum_{k \neq i} \frac{1}{2} d_k \mathbf{G}_0^{j^-} (\hat{\boldsymbol{a}}_k - \frac{1}{2} \hat{\boldsymbol{m}}_k) = \Delta_{sj^-} \end{aligned} \quad [21]$$

Similar to the manipulation of Equation 19, the non-informative effects of the bull  $i$  are replaced with Equation 12 and this leads to:

$$\begin{aligned} & \Psi_{sj^-} \hat{\boldsymbol{\mu}}_{j^-} + \Psi_{sj^-} \hat{\boldsymbol{s}}_{j^-} + (a^{ss} - \frac{1}{4} d_i) \mathbf{G}_0^{j^-} \hat{\boldsymbol{s}} - \frac{1}{2} d_s \mathbf{G}_0^{j^-} (\hat{\boldsymbol{s}}_s + \hat{\boldsymbol{d}}_s) \\ & - \sum_{k \neq i} \frac{1}{2} d_k \mathbf{G}_0^{j^-} (\hat{\boldsymbol{a}}_k - \frac{1}{2} \hat{\boldsymbol{m}}_k) = \Delta_{sj^-} \end{aligned} \quad [22]$$

Equation 22 shows that the bull  $i$  and his dam no longer contribute to the  $j^-$  effects of the sire due to the absorption process and the variance of the sire effects  $\hat{\boldsymbol{s}}_{j^-}$  is reduced by  $\frac{1}{4} d_i \mathbf{G}_0^{j^-} \hat{\boldsymbol{s}}$ .

#### 2.4. Modified procedure for updating pedigree contribution

Because the absorption process does not influence the EDC matrices or the least squares

part of LHS of the equations of the MT-MACE model, the updating procedure for calculation of data contribution using Formulas 6 and 7 in the paper by Liu *et al.* (2004b) remains valid. However, the formulas for updating pedigree contribution using Formulas 8, 9, and 10 in the paper by Liu *et al.* (2004b) must be modified according to Equations 15, 20, and 22.

For non-parent bulls with data, identify the absorbed effects  $\hat{\boldsymbol{a}}_{ij^-}$  for each of them. The absorbed effects are different for the non-parent bulls from different countries. In

general, co-tested, non-parent bulls can be handled in the same way as the non-parent bulls with data from one country. As in the regular way of updating pedigree contribution, pedigree file must be read sequentially to accumulate pedigree contribution. We assume that the pre-conditioned conjugate gradients algorithm is applied with the iteration on data technique to solve the equation system (Liu *et al.*, 2004b).

$$\mathbf{w}_i = \mathbf{w}_i + a^{ii} \mathbf{G}_0^{-1} \hat{\mathbf{z}}_i^{[t-1]} - \frac{1}{2} d_i \mathbf{G}_0^{-1} (\hat{\mathbf{z}}_s^{[t-1]} + \hat{\mathbf{z}}_d^{[t-1]}), \quad [23]$$

$$\mathbf{w}_s = \mathbf{w}_s - \frac{1}{2} d_i \mathbf{G}_0^{-1} \hat{\mathbf{z}}_i^{[t-1]} + \frac{1}{4} d_i \mathbf{G}_0^{-1} \hat{\mathbf{z}}_d^{[t-1]}, \quad [24]$$

$$\mathbf{w}_d = \mathbf{w}_d - \frac{1}{2} d_i \mathbf{G}_0^{-1} \hat{\mathbf{z}}_i^{[t-1]} + \frac{1}{4} d_i \mathbf{G}_0^{-1} \hat{\mathbf{z}}_s^{[t-1]}, \quad [25]$$

where  $\mathbf{w}_i(z_i)$ ,  $\mathbf{w}_s(z_s)$ , and  $\mathbf{w}_d(z_d)$  are sub-vectors of work vector  $\mathbf{w}$  (search direction vector  $\mathbf{z}$ ) for genetic effects of animal  $i$  and its sire  $s$  and dam  $d$ , respectively.

$$\mathbf{w}_{ij^+} = \mathbf{w}_{ij^+} + a^{ii} \mathbf{G}_{0^*}^{j^+j^+} \hat{\mathbf{z}}_{ij^+}^{[t-1]} - \frac{1}{2} d_i \mathbf{G}_{0^*}^{j^+j^+} (\hat{\mathbf{z}}_{sj^+}^{[t-1]} + \hat{\mathbf{z}}_{dj^+}^{[t-1]}). \quad [26]$$

For the contribution of the animal  $i$  to its sire  $s$ :

$$\mathbf{w}_{sj^+} = \mathbf{w}_{sj^+} - \frac{1}{4} d_i (\mathbf{G}_{0^-}^{j^+j^+} \hat{\mathbf{z}}_{sj^+}^{[t-1]} + \mathbf{G}_0^{j^+j^-} \hat{\mathbf{z}}_{sj^-}^{[t-1]}) - \frac{1}{2} d_i \mathbf{G}_{0^*}^{j^+j^+} \hat{\mathbf{z}}_{ij^+}^{[t-1]} + \frac{1}{4} d_i \mathbf{G}_{0^*}^{j^+j^+} \hat{\mathbf{z}}_{dj^+}^{[t-1]}, \quad [27]$$

$$\mathbf{w}_{sj^-} = \mathbf{w}_{sj^-} - \frac{1}{4} d_i \mathbf{G}_0^{j^-j^-} \hat{\mathbf{z}}_s^{[t-1]}. \quad [28]$$

And similarly for the contribution of the animal  $i$  to its dam  $d$ :

$$\mathbf{w}_{dj^+} = \mathbf{w}_{dj^+} - \frac{1}{4} d_i (\mathbf{G}_{0^-}^{j^+j^+} \hat{\mathbf{z}}_{dj^+}^{[t-1]} + \mathbf{G}_0^{j^+j^-} \hat{\mathbf{z}}_{dj^-}^{[t-1]}) - \frac{1}{2} d_i \mathbf{G}_{0^*}^{j^+j^+} \hat{\mathbf{z}}_{ij^+}^{[t-1]} + \frac{1}{4} d_i \mathbf{G}_{0^*}^{j^+j^+} \hat{\mathbf{z}}_{sj^+}^{[t-1]}, \quad [29]$$

$$\mathbf{w}_{dj^-} = \mathbf{w}_{dj^-} - \frac{1}{4} d_i \mathbf{G}_0^{j^-j^-} \hat{\mathbf{z}}_d^{[t-1]}. \quad [30]$$

### 3. Results

#### 3.1. Efficiency of the absorption method

From Formula 6, it can be seen that the efficiency of the within-bull absorption procedure depends mainly on the proportion of the non-parent bulls relative to the total number of animals in the MACE evaluation. In order to investigate the efficiency, data of nine major dairy countries from February 2006 Interbull evaluation were chosen (Table 1). Some relevant statistics for calculating the number of equations were derived from the data obtained from Interbull routine February 2006 production trait MACE evaluation (Fikse, 2006). A total of 91540 Holstein bulls with national proofs from 27

For animals other than the non-parent bulls, pedigree contribution is updated as described in the paper by Liu *et al.* (2004b). For animal  $i$  that is not a non-parent, its pedigree contribution to the multiplication of coefficient matrix of MME with search direction vector  $\mathbf{z}$  is:

If animal  $i$  is an non-parent bull with data in country  $j^+$ , then Formula 23 becomes:

countries/populations were considered in the Interbull evaluation, 6587 of them had proofs from more than one country, which means that 7.2% of the bulls were common bulls with 1.2% of them being sires of bulls. With the relationship of sire and maternal grandsire (MGS), 5427 ancestors without proofs were traced back, and which accounted for 5.6% of the total number of animals, 96 967, in the Interbull evaluation. The number of sires or MGS with national proofs were 2110, thus there were 89430 non-parent bulls with proofs, and which represented 97.7% of all bulls with proofs and 92.2% of all animals in the evaluation. In the joint French-German bull evaluation (Tarres *et al.*, 2006) there were 31361 bulls with DYD, 939 of them had data from both countries, 1633 of them were sires. Thus, the number of non-parent bulls was 29

728, representing 94.8% of all bulls with DYD. Due to the sire dam relationship used in the joint evaluation, 36 212 ancestors were found from Interbull pedigree file, which represented 53.6% of all animals in the joint evaluation. Based on the information from both the Interbull evaluation and the joint French-German evaluation, following assumptions were made: 1) 54% of all animals were ancestors having no data; 2) 97% of bulls with data were non-parents; and 3) 7% of bulls with data were common bulls as well as non-parents and this ratio was assumed to be equal for every country. Additionally, we assume that the number of phantom parent groups was 0.

In addition to the ST-MACE model currently used Interbull evaluation, two MT-MACE models were investigated, the first being termed as random regression MACE (RR-MACE) model, and the second as multiple lactation MACE (ML-MACE model). The two MT-MACE models differed with respect to the analysed data. The RR-MACE model evaluated the DYD expressed in random regression coefficients (Liu *et al.*, 2004a) and the ML-MACE model the DYD on 305-day lactation basis. Among the three MACE models, the RR-MACE model had the most equations, whereas the equation system of the ST-MACE model was smallest. The reduction of equations is c.a. 40% by the absorption technique across all the MACE models. Full pedigree information of bulls via sire and dam is assumed in this study. For bull pedigree including sire, MGS and MGD group, the reduction of equation is much more significant, because only a very small percentage of bulls with data have progeny in the bull evaluation.

### 3.2. Validation study

The developed within-bull absorption approach for reducing the number of equations of the MT-MACE model can be validated via simulation or using the field data. Currently, the validation via a small simulated data set is being under way. We will modify the Fortran 95 source code of our solver program to conduct a validation with field data. In either case, identical MACE proofs must be obtained from both the original MT-MACE model and

the MACE model with the within-bull absorption.

## 4. Discussion

The MT-MACE model (Liu *et al.*, 2004b, Tarres *et al.*, 2006) better uses the information coming from national evaluations with diverse genetic evaluation models, because the additive genetic effects for the MT-MACE evaluation are identical to the effects in national evaluations. The MT-MACE model does not condense national proofs into a function of the original proofs, since any condensation of the national proofs, e.g. combining proofs of regression coefficients to lactation basis, leads to loss of information. As MACE model in general, the MT-MACE model is flexible by treating countries as genetically distinct traits and it is not parsimonious, because every animal has effects on all country scales. Compared to ST-MACE, the higher accuracy of the MT-MACE model is associated with higher computing cost, as numerous countries have upgraded their national evaluation models from single trait to multiple trait models. Thus, there is a need to reduce the computing cost and maintain the accuracy at the same time.

The proposed reduction of equations involves only the non-parent bulls with national data. Their effects on foreign country scales, where there are no data available, are absorbed into their effects in own country. As a result of the absorption procedure, equations for the bulls' effects on home country scale and the equations of their sires and dams are changed accordingly. We derived the new equations for the non-parent bulls' effects in home country and their parents' respective effects. In addition, we developed a new procedure to update the pedigree contribution according to the within-bull absorption process. This within-animal absorption procedure is also valid for international cow genetic evaluation, although it will be less effective than for international bull evaluation due to a lower percentage of cows having no progeny in the international cow evaluation.

Based on the February 2006 Interbull production trait MACE evaluation (Fikse,

2006), we investigated the efficiency of this within-animal absorption procedure. A simpler version of the MT-MACE model, the multiple lactation MACE model ML-MACE, was considered additionally in comparison to the regression coefficients MACE model RR-MACE. Up to 40% of equations were eliminated when applying the within-bull absorption method for all of the three MACE models with the sire and dam relationship. For the current Interbull MACE model, a ST-MACE model using sire and MGS relationship, the reduction of equations will be much more efficient, because the proportion of non-parent bulls to the total number of animals is much higher than the three MACE models with sire and dam relationship. With more countries upgrading to multiple trait model for national evaluation, the absorption method will make the MT-MACE model even more efficient. The proposed within-bull absorption method is easy to implement and can be applied in routine MACE evaluation. So far a similar method has been used for parameter estimation in Interbull procedures. The proposed within-bull absorption method will be validated with a small simulated data set as well as with field data from routine evaluation.

## 5. Acknowledgement

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## 6. References

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**Table 1.** Comparison of the numbers of equations of the MACE models with and without the within-bull absorption based on the Holstein data of February 2006 Interbull evaluation for production traits ‡.

	No. of bulls with national data or no. of animals	No. of effects and equations of		
		MT-MACE with DYD regression coefficients (RR-MACE)	MT-MACE with 305-day DYD (ML-MACE)	ST-MACE model
Australia	4 601	1	1	1
Canada	6 429	15	3	1
Denmark	5 653	1	1	1
France	10 113	1	1	1
Germany	14 841	9	3	1
Italy	5 703	15	3	1
Netherlands	8 905	15	3	1
United Kingdom	4 012	9	3	1
United States	21 468	1	1	1
Sum	81 725	67	19	9
No. of ancestors without data and equations	89 223	5 977 941	1 695 237	803 007
No. of bulls being parents and equations	2 280	152 760	43 320	20 520
No. of non-parent bulls and equations	73 725	475 426	145 681	68 564
Total no. of animals and equations of MACE model with absorption	165 228	6 606 127	1 884 238	892 091
Total no. of animals and equations of the original MACE model	165 228	11 070 276	3 139 332	1 487 052
Equation reduction (%)		40.33	39.98	40.01

‡ Note that the relationship among animals is set up by sire and dam, instead of sire and MGS.