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Breeding value reliabilities for multiple-trait single-step genomic best linear unbiased predictor

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ABSTRACT

Approximate multistep methods to calculate reliabilities for estimated breeding values in large genetic evaluations were developed for single-trait (ST-R^2A) and multitrait (MT-R^2A) single-step genomic BLUP (ssGBLUP) models. First, a traditional animal model was used to estimate the amount of nongenomic information for the genotyped animals. Second, this information was used with genomic data in a genomic BLUP model (genomic BLUP/SNP-BLUP) to approximate the total amount of information and ssGBLUP reliabilities for the genotyped animals. Finally, reliabilities for the nongenotyped animals were calculated using a traditional animal model where the increased information due to genomic data for the genotyped animals is accounted for by including pseudo-record counts for the genotyped animals. The approaches were tested using a multiple-trait ssGBLUP model on 2 data sets. The first data set (data 1) was small enough such that exact ssGBLUP model reliabilities could be computed by inversion and compared with the approximation method reliabilities. Data 1 had 46,535 first-, 35,290 second-, and 23,780 third-lactation 305-d milk yield records from 47,124 Finnish Red dairy cows. The pedigree comprised 64,808 animals, of which 19,757 were genotyped. We examined the efficiency of the MT-R^2A approximation on a large data set (data 2) derived from the joint Nordic (Danish, Finnish, and Swedish) Holstein dairy cattle data. Data 2 had 17.8 million 305-d milk records from 8.3 million cows and first 3 lactations. The pedigree had 11 million animals of which 274,145 were genotyped on 46,342 SNP markers. For data 1, correlations between the exact ssGBLUP model and the ST-R^2A for the genotyped (nongenotyped) animals were 0.995 (0.987), 0.965 (0.984), and 0.950 (0.983) for first, second, and third lactation, respectively. Correspondingly, correlations between exact ssGBLUP reliabilities and MT-R^2A for the genotyped (nongenotyped) animals were 0.995 (0.993), 0.992 (0.991), and 0.990 (0.990) for first, second, and third lactation, respectively. The regression coefficients (b_1) of ssGBLUP reliability on ST-R^2A for the genotyped (nongenotyped) animals ranged from 0.87 (0.94) for first lactation to 0.68 (0.93) for third lactation, whereas for MT-R^2A they were between 0.91 (0.99) for first lactation to 0.89 (0.99) for third lactation. Correspondingly, the intercepts varied from 0.11 (0.05) to 0.3 (0.06) for ST-R^2A and from 0.06 (0.01) to 0.07 (0.02) for MT-R^2A. The computing time for the approximation method was approximately 12% of that required by the direct exact approach. In conclusion, the developed approximate approach allows calculating estimated breeding value reliabilities in the ssGBLUP model even for large data sets.

Key words: dairy cattle, genomic evaluation, breeding value, effective record contributions, reliability

INTRODUCTION

Single-step genomic BLUP (**ssGBLUP**) allows including genomic information into a model simultaneously with phenotypic and pedigree information from both genotyped and nongenotyped individuals for calculating genomic enhanced breeding values (**GEBV**) (Legarra et al., 2009; Aguilar et al., 2010; Christensen and Lund, 2010). One of the main advantages of ssGBLUP is its prediction accuracy, which is as high as, if not greater than, any other method (Legarra et al., 2014). The simple framework to account for genomic information even for complicated models is computationally challenging but many approaches have been presented to solve GEBV efficiently (Mäntysaari et al., 2020; Misztal et al., 2020; Koivula et al., 2021). However, calculation of individual GEBV accuracies is computationally more challenging and only few approaches have been proposed.

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Reliability (or accuracy) of GEBV measures the precision of GEBV and, thus, the potential response to selection (Gorjanc et al., 2015). Computationally the most challenging component in the calculation of GEBV reliability is due to prediction error variance (**PEV**), which is a function of elements of the inverse of the coefficient matrix of mixed model equations (**MME**). Even though the reliability calculated from the inverse of the MME can deviate from the squared correlation between true and EBV (Bijma, 2012), it is widely used in genetic evaluations. Because the inverse cannot be computed for large MME, approximation methods need to be used. Several approaches have been proposed to approximate reliabilities for the animal model without genomic information (Misztal and Wiggans, 1988; Harris and Johnson, 1998; Jamrozik et al., 2000; Tier and Meyer, 2004). For simple genomic models like GBLUP/SNP-BLUP, direct and Monte Carlo approaches have been proposed (Ben Zaabza et al., 2020, 2021). None of these methods are directly suitable for ssGBLUP.

Genomic information in ssGBLUP is propagated to all animals (genotyped and nongenotyped) using a combined relationship matrix that has both pedigree-based (**A**) and genomic (**G**) relationship matrices (Legarra et al., 2009; Christensen and Lund, 2010). The inverse relationship matrix is used in MME. Misztal et al. (2013) presented 2 approximate approaches to calculate the reliability of GEBV for the genotyped animals in ssGBLUP. Both approaches first calculate reliability in an animal model without genomic information. In the second step the calculated reliabilities are combined with genomic information. The authors reported that their methods are computationally feasible for populations of up to 100,000 genotyped animals. Liu et al. (2017) developed a multistep genomic reliability method, namely Interbull genomic reliability. The method was applied in a single-trait model. Using a single-step SNP-based model, known as single-step Bayesian regression developed by Fernando et al. (2014), Gao et al. (2018) used Markov chain Monte Carlo in the calculations to estimate PEV of EBV to 305-d production traits accurately for a Finnish Red dairy cattle population. Based on the single-step Bayesian regression model, Edel et al. (2019) presented a multistep approach which approximates GEBV reliabilities in ssGBLUP for all animals. First, the GEBV reliability of the genotyped animals is approximated using deregression weights and genomic information. The increased reliability due to genomics is used to increase record weights for the genotyped animals in the final step to approximate GEBV reliability for the nongenotyped animals. Both approaches allow the use of multitrait reliability approximation methods for the nongenomic information. However, inclusion of correlated information increases the computational challenges considerably unless the correlations are ignored in some steps.

We present and test a ssGBLUP reliability approximation method for a multiple-trait model. The objectives of this research were (1) to present an approximation approach for the GEBV reliabilities, and (2) to compare the approximate GEBV reliabilities with corresponding GEBV reliabilities obtained from the inverse of the MME coefficient matrix in animal and ssGBLUP models. We use a 3-trait milk yield model and data from dairy cattle where both bulls and cows can have genotypes.

MATERIALS AND METHODS

No animals were used in this study, and ethical approval for the use of animals was thus deemed unnecessary.

Multiple-Trait Model

A simple multiple-trait (**MT**) ssGBLUP model can be defined as

$$\begin{bmatrix}\mathbf{y}_1\\ \mathbf{y}_2\\ \vdots\\ \mathbf{y}_t\end{bmatrix}=\begin{bmatrix}\mathbf{X}_1 & 0 & \cdots & 0\\ 0 & \mathbf{X}_2 & \dots & 0\\ \vdots & \vdots & \ddots & \vdots\\ 0 & 0 & \cdots & \mathbf{X}_t\end{bmatrix}\begin{bmatrix}\mathbf{b}_1\\ \mathbf{b}_2\\ \vdots\\ \mathbf{b}_t\end{bmatrix}+\begin{bmatrix}\mathbf{W}_1 & 0 & \cdots & 0\\ 0 & \mathbf{W}_2 & \dots & 0\\ \vdots & \vdots & \ddots & \vdots\\ 0 & 0 & \cdots & \mathbf{W}_t\end{bmatrix}\begin{bmatrix}\mathbf{u}_1\\ \mathbf{u}_2\\ \vdots\\ \mathbf{u}_t\end{bmatrix}+\begin{bmatrix}\mathbf{e}_1\\ \mathbf{e}_2\\ \vdots\\ \mathbf{e}_t\end{bmatrix}, \quad [1]$$

where vector $\mathbf{y}_j$ has phenotypes for trait j; vector $\mathbf{b}_j$ has fixed effects affecting trait j; vector $\mathbf{u}_j$ has individual additive genetic values trait j, and vector $\mathbf{e}_j$ has the residuals for trait j. Matrices $\mathbf{X}$ and $\mathbf{W}$, with subscripts 1, 2, and t, are known incidence matrices relating fixed and additive genetic effects to each trait, respectively, where t is the number of traits.

The model can also be written as

$$\mathbf{y}=\mathbf{Xb}+\mathbf{Wu}+\mathbf{e}, \quad [2]$$

where

$$\mathbf{y}=\begin{bmatrix}\mathbf{y}_1\\ \mathbf{y}_2\\ \vdots\\ \mathbf{y}_t\end{bmatrix},\ \mathbf{X}=\begin{bmatrix}\mathbf{X}_1 & 0 & \cdots & 0\\ 0 & \mathbf{X}_2 & \dots & 0\\ \vdots & \vdots & \ddots & \vdots\\ 0 & 0 & \cdots & \mathbf{X}_t\end{bmatrix},$$

$$\mathbf{b}=\begin{bmatrix}\mathbf{b}_1\\ \mathbf{b}_2\\ \vdots\\ \mathbf{b}_t\end{bmatrix},\ \mathbf{W}=\begin{bmatrix}\mathbf{W}_1 & 0 & \cdots & 0\\ 0 & \mathbf{W}_2 & \cdots & 0\\ \vdots & \vdots & \ddots & \vdots\\ 0 & 0 & \cdots & \mathbf{W}_t\end{bmatrix},$$

$$\mathbf{u}=\begin{bmatrix}\mathbf{u}_1\\ \mathbf{u}_2\\ \vdots\\ \mathbf{u}_t\end{bmatrix},\ \text{and}\ \mathbf{e}=\begin{bmatrix}\mathbf{e}_1\\ \mathbf{e}_2\\ \vdots\\ \mathbf{e}_t\end{bmatrix}.$$

It is assumed that $\mathbf{u} \sim N\left(0, \mathbf{G}_0 \otimes \mathbf{H}\right)$, where

$$\mathbf{G}_0=\begin{bmatrix}\sigma^2_{u_1} & \sigma_{u_{12}} & \cdots & \sigma_{u_{1t}}\\ \sigma_{u_{12}} & \sigma^2_{u_2} & \cdots & \sigma_{u_{2t}}\\ \vdots & \vdots & \ddots & \vdots\\ \sigma_{u_{1t}} & \sigma_{u_{2t}} & \cdots & \sigma^2_{u_t}\end{bmatrix}$$

is the matrix of genetic covariance across traits and $\mathbf{H}$ is the joint relationship matrix of genotyped and nongenotyped animals. For simplicity of presentation here, we assume that each animal has either no observations or observations on all traits. Thus, we assume $\mathbf{e} \sim N\left(0, \mathbf{R}_0 \otimes \mathbf{I}\right)$, where

$$\mathbf{R}_0=\begin{bmatrix}\sigma^2_{e_1} & \sigma_{e_{12}} & \cdots & \sigma_{e_{1t}}\\ \sigma_{e_{12}} & \sigma^2_{e_2} & \cdots & \sigma_{e_{2t}}\\ \vdots & \vdots & \ddots & \vdots\\ \sigma_{e_{1t}} & \sigma_{e_{2t}} & \cdots & \sigma^2_{e_t}\end{bmatrix}$$

is the matrix of residual covariance across traits and $\mathbf{I}$ is the identity matrix.

The MME for ssGBLUP for a MT model [2] can be written as

$$\begin{bmatrix}\mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{W}\\ \mathbf{W}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{W}'\mathbf{R}^{-1}\mathbf{W}+\mathbf{G}_0^{-1}\otimes\mathbf{H}^{-1}\end{bmatrix}\begin{bmatrix}\hat{\mathbf{b}}\\ \hat{\mathbf{u}}\end{bmatrix}=\begin{bmatrix}\mathbf{X}'\mathbf{R}^{-1}\mathbf{y}\\ \mathbf{W}'\mathbf{R}^{-1}\mathbf{y}\end{bmatrix}, \quad [3]$$

and the inverse of the relationship matrix $\mathbf{H}$ as

$$\mathbf{H}^{-1}=\mathbf{A}^{-1}+\begin{bmatrix}0 & 0\\ 0 & \mathbf{G}_w^{-1}-\mathbf{A}_{22}^{-1}\end{bmatrix},$$

where $\mathbf{A}$ ($\mathbf{A}_{22}$) is the pedigree-based numerator relationship matrix for all (genotyped) animals and $\mathbf{G}_w$ is the genomic relationship matrix. We assume that $\mathbf{G}_w=(1-w)\mathbf{G}+w\mathbf{A}_{22}$, where w is the polygenic proportion of genetic variance.

Denote the coefficient matrix of the MME by $\mathbf{C}_{\text{MT}}$ and its inverse matrix elements as

$$\mathbf{C}^{-1}_{\text{MT}}=\begin{bmatrix}\mathbf{C}^{\text{bb}}_{\text{MT}} & \mathbf{C}^{\text{bu}}_{\text{MT}}\\ \mathbf{C}^{\text{bu}}_{\text{MT}} & \mathbf{C}^{\text{uu}}_{\text{MT}}\end{bmatrix},$$

where

$$\mathbf{C}^{\text{uu}}_{\text{MT}}=\begin{bmatrix}\mathbf{V}_{11} & \mathbf{V}_{12} & \cdots & \mathbf{V}_{1t}\\ \mathbf{V}_{21} & \mathbf{V}_{22} & \cdots & \mathbf{V}_{2t}\\ \vdots & \vdots & \ddots & \vdots\\ \mathbf{V}_{t1} & \mathbf{V}_{t2} & \cdots & \mathbf{V}_{tt}\end{bmatrix}$$

is the prediction error covariance (**PEC**) matrix of GEBV. The GEBV reliability of animal i and trait j can be calculated as

$$r^2_{ij}=1-\frac{\left\{\mathbf{V}_{jj}\right\}_{ii}}{\mathbf{H}_{ii}\sigma^2_j}, \quad [4]$$

where $\{\mathbf{V}_{jj}\}_{ii}$ and $\mathbf{H}_{ii}$ are the diagonal elements of the PEC and $\mathbf{H}$ matrices pertaining to animal i and trait j, and σ^2_j is genetic variance of trait j.

Reliability Approximation

Reliabilities were approximated separately for genotyped and nongenotyped animals (Figure 1). We first describe the general approach and present technical details in the following section. The calculation of GEBV reliability for the genotyped animals included 3 main steps. First, we approximated the amount of nongenomic information in the genotyped animals using approximate reliability $\left(r^2_a\right)$ in a pedigree-based animal model. Full pedigree and phenotypic data were included into this animal model where all the nongenetic effects were absorbed into the additive genetic effect. Second, to approximate GEBV reliability for the genotyped animals, the already calculated reliabilities r^2_a for the genotyped animals were used to calculate effective record contributions (**ERC**) for the genotyped animals based on an approach called reverse reliability estimation ($\mathbf{ERC}_{\mathbf{rev}}$), which allows accounting for information from the nongenotyped animals using the pedigree relationship structure and the multitrait covariance structure. Third, we approximated the GEBV reliability r^2_g for the genotyped animals, using MT GBLUP model with the calculated ERC_{rev} as weights. This step can be done by

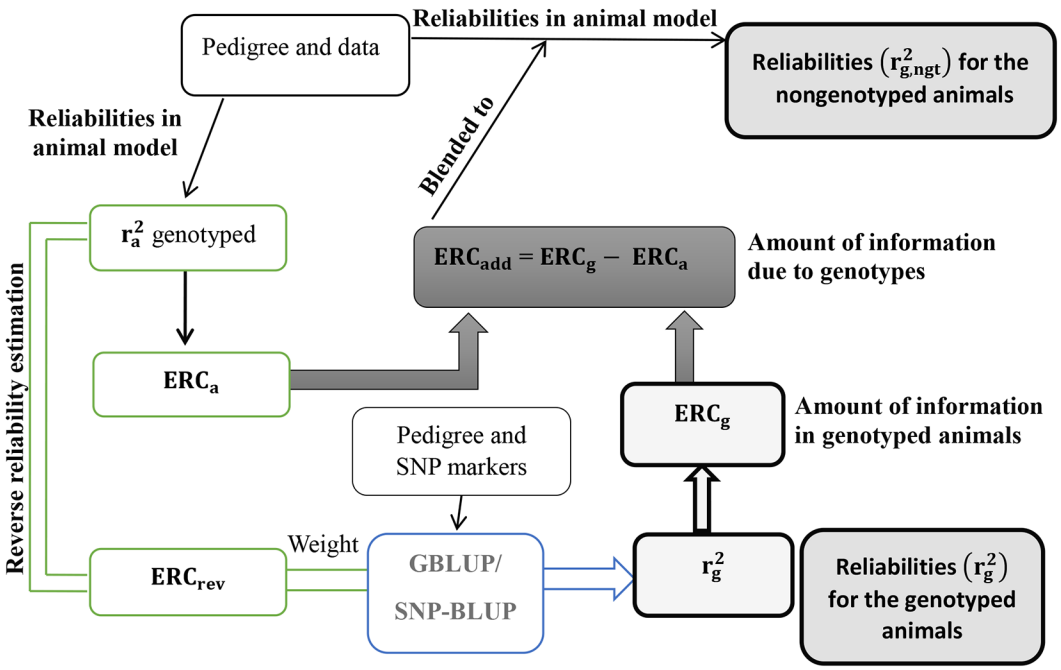

Figure 1. Steps in approximating genomic estimated breeding value reliabilities for the genotyped $\left(r^2_g\right)$ and nongenotyped $\left(r^2_{ngt}\right)$ animals. GBLUP = genomic BLUP. ERC = effective record contributions; ERC_a = ERC, counting for nongenomic information in animal model; ERC_{rev} = ERC-based on reverse reliability estimation in animal model; ERC_g = ERC counting for genomic information in genomic model; and ERC_{add} = added genomic information.

an equivalent MT SNP-BLUP model more efficiently than GBLUP when the number of genotyped animals is larger than the number of SNP markers.

Reliabilities for the nongenotyped animals needed 4 additional steps. First, the already obtained reliabilities r_a^2 for the genotyped animals were transformed into effective record contributions ($\mathbf{ERC_a}$), which are used to measure the amount of nongenomic information. Second, the approximate ssGBLUP reliabilities r_g^2 were converted into ERC_g, which are the measure of the total information. Third, we calculated the contribution due to the genomic information: $ERC_{add} = ERC_g - ERC_a$. Finally, the estimated genomic information of the genotyped animals ERC_{add} were included into the evaluation model as pseudo-record weights corresponding to the additional information for the pedigree-based animal model. Thus, we computed the approximate ssGBLUP reliabilities for the nongenotyped animals by adding the contribution of genomic information to the genotyped animals through pseudo-observations in a standard pedigree-based animal model GEBV.

Reliabilities for the Nongenomic Model

Reliabilities for EBV by a pedigree-based animal model can be approximated by many approaches. Tier and Meyer (2004) is a MT approach, which is why we used it as a basis in the ERC calculation to estimate the amount of nongenomic information for genotyped animals. (see Effective Record Contributions section). The method of Tier and Meyer (2004) has 3 main steps: (1) determining the amount of information from the animal's own records, (2) processing the pedigree from youngest to oldest (upwards) and accumulating the number of the records on each animal's progeny, and (3) processing the pedigree from oldest to youngest to combine the values of parents, ancestors, and collateral relatives for each animal. The last step, in turn, involves 2 steps: removing the animal's own contribution from the parent reliability and then combining the contributions for each animal from all sources of information (parents, progeny, and its own records). See Tier and Meyer (2004) for more details.

Effective Record Contributions

The ERC were used to indicate the amount of information that a genotyped animal had at 3 different steps of the approach (Figure 1). The ERC can be computed in several ways, and we used 2 types of ERC approaches. A simple ERC for an animal was based on the formula

$$ERC = \frac{r^2}{\left(1-r^2\right)} \times \frac{\left(1-h^2\right)}{h^2},$$

where h^2 is heritability and r^2 is reliability. This simple ERC was used in 2 of the steps: for the amount of nongenomic information in the nongenomic animal model ($\mathbf{ERC_a}$) and for the amount of total information with genomic information ($\mathbf{ERC_g}$) of the genotyped animals. For ERC_a, the reliability was calculated by the method of Tier and Meyer (2004) method, but for ERC_g, the approximate GEBV reliability of genotyped animals was used.

An alternative to the simple ERC calculation is based on the so-called reverse reliability estimation, which was applied to obtain ERC_{rev}. We used it to quantify the nongenomic information and as a weight in the calculation to approximate genomic reliability for the genotyped animals. The reverse reliability estimation approach attempts to account for the double counting of information that is present in the simple ERC-based weights. For example, when a genotyped bull has a genotyped daughter with an observation, the simple ERC formula will include the daughter observation in the daughter ERC as well as in the sire ERC through the increased sire reliability. The reverse reliability estimation approach approximates ERC from a given value of reliability by reversing the method of Tier and Meyer (2004). When the original Tier and Meyer (2004) algorithm estimates animal model reliability using ERC, the reverse estimation approach estimates $\widehat{\text{ERC}}$, which gives the same PEV as the original PEV*, where the asterisk stands for the initial value of prediction error variance. When the PEV* is from the full data with records on all animals, but ERC_{rev} is solved for only a subset of (genotyped) animals, the approach automatically adds the information from the nongenotyped relatives to the genotyped animals. The calculation of the $\widehat{\text{ERC}}$ involves the accumulation of information from progeny and parents using pedigree information as in the original Tier and Meyer (2004) approach. In the Tier and Meyer (2004) reliability estimation, each animal will receive a t by t PEC matrix having the diagonals (PEV) used in the estimation of the reliabilities. However, in our reverse reliability estimation, with a given $ERC^{[k]}$ for all animals, we estimate $PEV^{[k]}$, and if it does not correspond to PEV*, we search for a new $ERC^{[k+1]}$ that will give $PEV^{[k+1]}$ closer to PEV*, where k represents the iteration number. Because the ERC of each animal affects others, this approach needs to be repeated iteratively, unlike the method of Tier and Meyer (2004), which can be done by only 2 passes through the pedigree, from youngest to oldest (upwards) and from oldest to youngest (downwards). Appendix 1 has a pseudo-code for the reverse reliability approach.

The new $ERC^{[k+1]}$ was solved animal-wise from a nonlinear equation:

$$\left\{\left[\mathbf{G}_i^{-1} + \mathbf{E}(\mathbf{c})\mathbf{R}_0^{-1}\mathbf{E}(\mathbf{c})\right]^{-1}\right\}_{jj} = \{\mathbf{y}\}_j, \quad [5]$$

where $\{\mathbf{y}\}_j = \{\mathbf{V}_{jj}\}_{ii}$ are the original PEV* of animal i and trait j, $\mathbf{G}_i^{-1}$ contains $\mathbf{G}_0^{-1}$ and contributions from animal's offspring and ancestors, and $\mathbf{R}_0$ is the between-trait residual variance-covariance matrix recorded for animal i. When an animal has missing observations for some of the traits, these traits have no ERC, and there is a missing ERC pattern. For these missing ERC patterns, submatrices of $\mathbf{R}_0$ were used by deleting rows and columns corresponding to the missing ERC. The ERC values are in the diagonal $\mathbf{E}(\mathbf{c})$ matrix, $\{\mathbf{E}(\mathbf{c})\}_{jj} = \sqrt{\mathbf{c}_j}$, where $\mathbf{c}_j$ is the ERC for trait j to be solved. We implemented a Newton-Raphson-based algorithm for solving the ERC_{rev} for each individual (see Appendix 2).

The calculation of GBLUP/SNP-BLUP reliability is illustrated in the following example. Consider a 3-trait ($t = 3$) GBLUP model:

$$\mathbf{y} = \begin{bmatrix}\mathbf{y}_1\\ \mathbf{y}_2\\ \vdots\\ \mathbf{y}_t\end{bmatrix} = \begin{bmatrix}\mathbf{1}\mu_1\\ \mathbf{1}\mu_2\\ \vdots\\ \mathbf{1}\mu_t\end{bmatrix} + \begin{bmatrix}\mathbf{u}_1\\ \mathbf{u}_2\\ \vdots\\ \mathbf{u}_t\end{bmatrix} + \begin{bmatrix}\mathbf{e}_1\\ \mathbf{e}_2\\ \vdots\\ \mathbf{e}_t\end{bmatrix}, \quad [6]$$

where $\mathbf{y}_j$ is the vector of observations for trait j; μ_j is the general means for trait j, and $\mathbf{1}$ is vector of ones; and $\mathbf{e}_j$ has the residuals for trait j. It is assumed that

$$\begin{bmatrix}\mathbf{u}_1\\ \mathbf{u}_2\\ \vdots\\ \mathbf{u}_t\end{bmatrix} \sim \boldsymbol{N}\left(0, \mathbf{G}_0 \otimes \mathbf{G}\right),$$

where $\mathbf{G}_0$ is the $t \times t$ between-trait genetic covariance matrix and $\mathbf{G}$ is the genomic relationship matrix (VanRaden, 2008). Residuals between individuals are assumed uncorrelated. Observations for an individual are correlated with a residual covariance structure $\left[\mathbf{E}(\mathbf{c})\right]^{-1}\mathbf{R}_0\left[\mathbf{E}(\mathbf{c})\right]^{-1}$, where $\mathbf{E}(\mathbf{c})$ is a diagonal matrix having the square roots of ERC_{rev} values for the individual. The GEBV reliability of animal i and trait j can be calculated as

$$r_{ij}^2 = 1 - \frac{\mathbf{PEV}_{ij}}{\mathbf{G}_{ii}\sigma_j^2}, \quad [7]$$

where $\mathbf{PEV}_{ij}$ is the diagonal element of the MME coefficient matrix pertaining to animal i and trait j and $\mathbf{G}_{ii}$ is a diagonal genomic relationship matrix element for animal i. Because we are interested in computing reliability or PEV, the vector of observations is not used in the computations.

Reliabilities for the Nongenotyped Animals

We approximated reliabilities for the nongenotyped animals by "blending" the increased genomic information of the genotyped animals into a traditional animal model. In this approach, each genotyped animal will have additional record counts or pseudo-observations to each of the original traits. Unlike the original records, pseudo-observations have only a fixed general mean in addition to the additive genetic effect with a weight ERC_{add}. The pseudo-observations have the same additive genetic and residual variances as the original model traits.

Data

The performance of the approximation was tested on real data from the Finnish Red dairy cattle provided by Nordic Cattle Genetic Evaluations (**NAV**). The data set, called data 1, was constructed to be small enough so that the exact ssGBLUP model reliabilities could be computed by inversion and compared with the approximation method reliabilities. The data set comprised 46,535 first-, 35,290 second-, and 23,780 third-lactation 305-d milk yield records from 47,124 Finnish Red dairy cows, with 64,808 animals in the pedigree. The genotypes included 46,914 SNP markers for 19,757 animals. A description of the data is given in Table 1. Heritabilities for 305-d milk yield by parity and correlations between parities are shown in Table 2. To demonstrate the efficiency of the proposed approximation, we applied the method to a larger data set (data 2), which had 8.10 million first-, 5.97 million second-, and 3.72 million third-lactation 305-d milk yield records from 8.28 million Nordic (Danish, Finnish, and Swedish) Holstein dairy cows. The pedigree comprised up to 11 million animals, of which 274,145 were genotyped on 46,342 SNP markers.

The MT model was

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Wu} + \mathbf{e},$$

Table 1. Description of data 1 for 305-d milk lactations 1, 2, and 3

305-d milk lactation	Genotyped	Nongenotyped	All[1]	All missing[2]
1	15,698	30,837	46,535	589
2	10,387	24,888	35,275	11,834
3	6,077	17,701	23,778	23,344

[1]Number of animals with observations for the whole population.
[2]Number of animals with missing observations for the whole population.

where $\mathbf{y}$ is the vector of phenotypic values, $\mathbf{b}$ is the vector of fixed effects including herd-year of calving, year-season of calving, and age at calving. $\mathbf{X}$ is the incidence matrix associating $\mathbf{b}$ with $\mathbf{y}$, $\mathbf{W}$ is the incidence matrix relating breeding values to the phenotypes, $\mathbf{u}$ is a vector of random additive genetic values, and $\mathbf{e}$ represents the residual effects. An extra polygenic effect with 10% of total genetic variance was included.

Study Design

We calculated the exact reliabilities in the ssGBLUP model, to which the single-trait multistep genomic reliability approximation (**ST-R^{2}A**) and multitrait multistep genomic reliability approximation (**MT-R^{2}A**) were compared. Even though a comparison of reliabilities from exact ssGBLUP and from exact animal model (**AM**) is outside the scope of this article, it can be interesting to investigate the usefulness of the approximation methods by comparing their performance to that achieved by AM reliabilities. Thus, we report the correlation, the maximum absolute difference, and the mean squared error (**MSE**) between model reliabilities from exact ssGBLUP and ST-R^{2}A, and from exact ssGBLUP and MT-R^{2}A. In addition, the linear regression of the exact ssGBLUP model reliability on the ST-R^{2}A and MT-R^{2}A was fitted.

Computations

For the computations we used a multicore computer with 2 Intel Xeon E5–2680 v.2 processors (2.8 GHz; Intel Corp.) and limited them to 10 CPU cores. Com-

Table 2. Additive genetic correlations (above diagonal), heritabilities (diagonal), and phenotypic correlations (below diagonal) for 305-d milk production in lactations 1, 2, and 3

305-d milk lactation	1	2	3
1	**0.443**	0.796	0.710
2	0.540	**0.323**	0.978
3	0.443	0.619	**0.336**

putation of the exact ssGBLUP and GBLUP reliabilities by inverting the left-hand side of the MME were done using exa99 from the software package MiX99 (Strandén and Lidauer, 1999). Computation of $\mathbf{A}_{22}$ matrix was done using RelaX2 (Strandén and Vuori, 2006). Matrix $\mathbf{G}_{w}^{-1} - \mathbf{A}_{22}^{-1}$ was computed by the Hginv program (Strandén and Mäntysaari, 2018). Base population allele frequencies were calculated using the Bpop program (Strandén and Mäntysaari, 2020). We computed the Tier and Meyer (2004) reliability approximation using apax99 from MiX99. For the reverse reliability approximations, a program was written in Fortran 95.

RESULTS

Reliability for Genotyped Animals

Correlations between the reliabilities from exact ssGBLUP and ST-R^{2}A, and from exact ssGBLUP and MT-R^{2}A, for 3 groups of genotyped animals are summarized in Table 3. The first group includes all the genotyped animals (19,757); the second group, a subgroup called young candidates, has young genotyped bulls with no daughter information and cows without records (born in or after 2015); and the third group has genotyped bulls with daughter information. Correlations between the reliabilities from the exact ssGBLUP and ST-R^{2}A for the first group, which includes all of the genotyped animals, ranged from 0.995 for the first lactation to 0.950 for the third lactation (Table 3). An improvement of 0.02 for the second lactation and of 0.04 for the third lactation was observed in the correlations between reliabilities from exact ssGBLUP and MT-R^{2}A as compared with ST-R^{2}A. However, no improvement in the correlations was observed for first lactation by using MT-R^{2}A. This could be expected because fewer records were missing for first lactation and the correlation was already very high: 0.995. With ST-R^{2}A, the MSE ranged from 0.0004 for the first lactation to 0.0186 for the third lactation.

The use of MT-R^{2}A resulted in a lower MSE for second and third lactations than the ST-R^{2}A (Table 3). However, the MSE for the first lactation remained almost identical, 0.0001, with MT-R^{2}A compared with ST-R^{2}A. The regression coefficients (b_1) of ssGBLUP reliability on ST-R^{2}A ranged from 0.87 (first lactation) to 0.68 (third lactation), whereas for MT-R^{2}A they were between 0.91 (first lactation) to 0.89 (third lactation). The general mean varied from 0.11 to 0.30 for ST-R^{2}A and from 0.06 to 0.07 for MT-R^{2}A, indicating that MT-R^{2}A resulted in less difference between the true and approximated reliabilities (i.e., bias) for all considered traits.

Table 3. Correlation (r), maximum absolute difference (max), and mean squared error (MSE) between reliabilities from exact single-step genomic BLUP (ssGBLUP) and single-trait multistep genomic reliability approximation (ST-R^{2}A), and from exact ssGBLUP and multitrait multistep genomic reliability approximation (MT-R^{2}A), and regression coefficients (b_1) and intercepts (b_0) of the linear regression of exact ssGBLUP reliabilities on approximations by ST-R^{2}A and MT-R^{2}A for all genotyped animals, young candidates, and genotyped bulls with daughters[1]

Group	305-d milk lactation	ST-R^{2}A					MT-R^{2}A				
		r	Max	MSE	b_1	b_0	r	Max	MSE	b_1	b_0
All genotyped animals	1	0.995	0.12	0.0004	0.87	0.11	0.995	0.05	0.0001	0.91	0.06
	2	0.965	0.27	0.0102	0.72	0.26	0.992	0.07	0.0002	0.89	0.07
	3	0.950	0.35	0.0186	0.68	0.30	0.990	0.07	0.0002	0.89	0.07
Young candidates	1	0.981	0.03	0.0002	0.899	0.082	0.981	0.03	0.00008	0.94	0.04
	2	0.866	0.20	0.0180	0.493	0.397	0.981	0.03	0.00009	0.92	0.05
	3	0.882	0.24	0.0316	0.599	0.355	0.980	0.03	0.0001	0.92	0.04
Genotyped bulls with daughters	1	0.997	0.122	0.0009	0.904	0.089	0.998	0.05	0.0001	0.94	0.05
	2	0.983	0.267	0.0127	0.818	0.210	0.997	0.07	0.0003	0.92	0.06
	3	0.974	0.354	0.170	0.811	0.224	0.991	0.07	0.0003	0.92	0.06

[1]Intercept (b_0) and slope (b_1) were calculated from a linear model of the exact single-step genomic BLUP reliabilities on approximate reliabilities.

For the young candidates subgroup, correlations between reliabilities from exact ssGBLUP and ST-R^2A ranged from 0.981 for the first lactation to 0.866 for the second lactation. These estimates are generally lower than those achieved in the group of all genotyped animals and the subgroup of the genotyped bulls with daughters (Table 3). Interestingly, using MT-R^2A instead of the ST-R^2A in the young candidates group gave a substantial increase in correlation for the second and third lactations, (0.12), which is higher than for the other 2 groups. For example, use of MT-R^2A led to only slightly increased correlations within the subgroup of bulls with daughter records. This could be expected, in part because the correlation achieved by the ST-R^2A was already high, between 0.997 for the first lactation and 0.974 for the third lactation.

A perfect approximation of exact ssGBLUP reliabilities can be illustrated by a reference line intercepting the y-axis at 0 with a regression coefficient (slope) of 1. The points below this line are overestimates (upwards) of exact ssGBLUP reliabilities, and those falling above the line represent underestimates (downwards) of exact ssGBLUP reliabilities. Figure 2 shows the plots of exact ssGBLUP versus MT-R^2A reliabilities for 305-d milk yield for first, second, and third lactations. The fit of the MT-R^2A approximation for first lactation was better than for second and third lactations, although the approximated reliabilities deviated from the truth to both sides. For all traits, the underestimation occurred for animals with lower exact reliability (<0.5). However, the MT approximation slightly overestimated the reliabilities for animals with high exact reliabilities.

Table 4 shows the correlations of reliabilities from exact ssGBLUP and AM for the first 3 lactations for the genotyped animals, as well as the regression coefficients and intercepts of ssGBLUP on AM reliabilities. The correlation estimates between reliabilities from exact ssGBLUP and AM were nearly identical for all traits (0.95). The use of ST-R^2A instead of AM increased the correlation estimates by up to 4%.

The ST-R^2A showed lower bias than AM for all traits as indicated by the MSE values (Table 4). In fact, the MSE estimates from exact AM were higher for all traits than those associated with ST-R^2A. Additionally, the regression coefficients and intercepts obtained by AM agreed reasonably well with the high MSE estimates, and deviated from 1 and 0, respectively, more than the comparable estimates obtained by using ST-R^2A. For example, the estimated regression coefficients from AM were 0.50, 0.52, and 0.54 for first, second, and third lactation, respectively, and were smaller than those obtained from ST-R^2A: 0.87, 0.72, and 0.68, respectively. Furthermore, the use of MT-R^2A gave the highest correlations with the true ssGBLUP reliabilities and

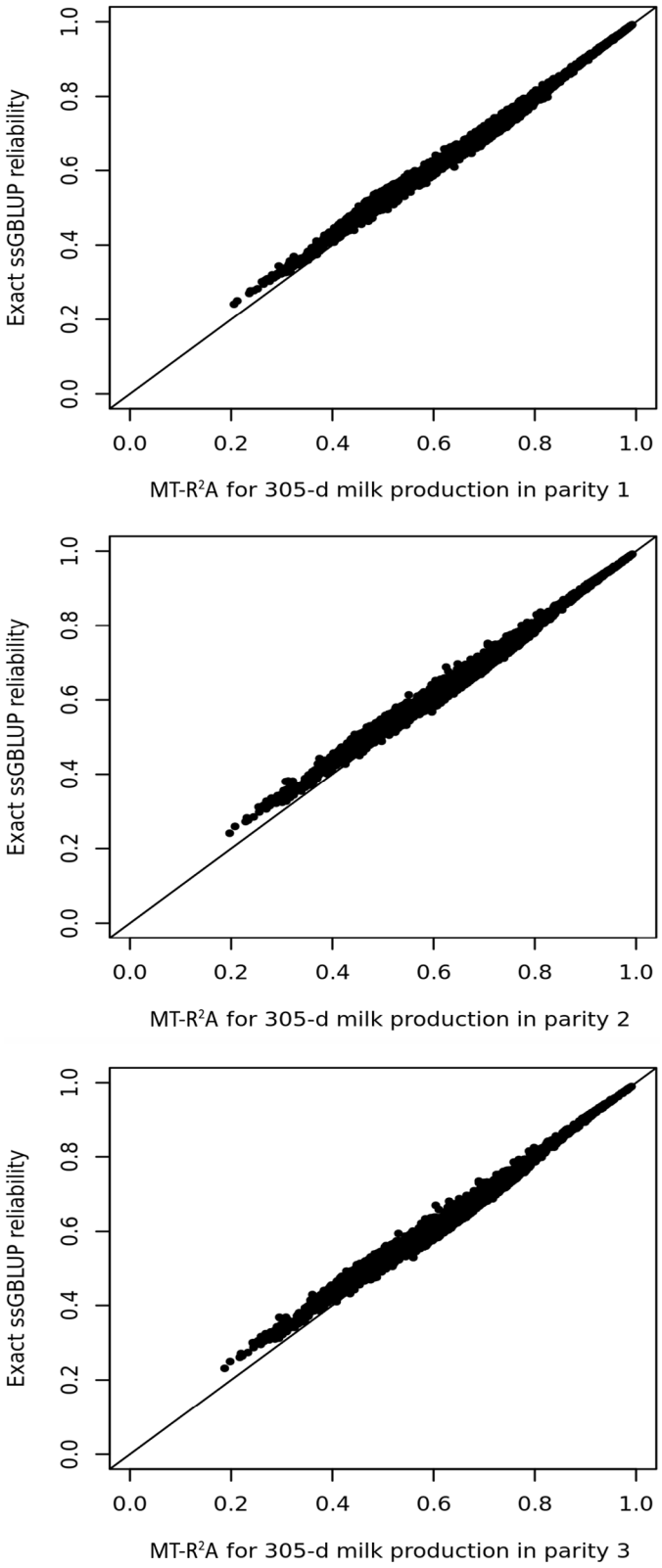

Figure 2. Reliabilities for all genotyped animals by exact single-step genomic BLUP (ssGBLUP) versus multitrait multistep genomic reliability approximation (MT-R^2A) for 305-d milk in lactations 1, 2, and 3.

Table 4. Correlation (r), maximum difference (max), and mean squared error (MSE) between reliabilities from exact single-step genomic BLUP (ssGBLUP) and exact animal models (AM), and regression coefficients (b_1) and intercepts (b_0) of the linear regression of exact ssGBLUP reliabilities on exact AM reliabilities for genotyped animals[1]

305-d milk lactation	r	Max	MSE	b_1	b_0
1	0.953	0.55	0.0376	0.50	0.45
2	0.950	0.53	0.0392	0.52	0.42
3	0.951	0.51	0.0386	0.54	0.40

[1]Intercept (b_0) and slope (b_1) of regression were calculated from a linear model of the ssGBLUP on AM reliabilities.

delivered the least bias, especially for second and third lactations when compared with AM reliabilities.

Reliability for Nongenotyped Animals

The correlations and differences between reliabilities calculated from exact ssGBLUP and ST-R^{2}A and MT-R^{2}A for the nongenotyped animals are in Table 5. Agreement between EBV reliability calculated by exact ssGBLUP and by both ST-R^{2}A and MT-R^{2}A was generally excellent in terms of correlations for the different traits. For example, correlations between exact ssGBLUP and ST-R^{2}A reliabilities ranged from 0.987 for first lactation to 0.983 for third lactation. Correlation between exact ssGBLUP and MT-R^{2}A was higher than that between exact ssGBLUP and ST-R^{2}A for the first lactation. An improvement of 0.06 in the correlations between reliabilities from exact ssGBLUP and MT-R^{2}A was observed for second and third lactations. The use of the MT-R^{2}A method led to a significant reduction in the MSE in comparison to ST-R^{2}A. For example, the MSE associated with MT-R^{2}A were almost 4 times smaller than those obtained from ST-R^{2}A, (0.0005 vs. 0.0020) for third lactation and (0.0005 vs. 0.0018) for second lactation. This could be expected because there were more missing observations in second and third lactations (Table1).

Figure 3 illustrates the reliabilities from exact ssGBLUP versus those from MT-R^{2}A for nongenotyped animals. The points depicting the relationship between the true ssGBLUP and approximated reliabilities for nongenotyped animals were generally close to the reference line. No clear upward or downward biases can be seen. However, reliabilities were approximated with less error for animals with high exact ssGBLUP reliabilities, although significant deviations from the reference line could be observed for some animals with high exact reliabilities (Figure 3).

Table 6 gives the correlations between reliabilities from exact ssGBLUP and AM reliabilities, as well as the regression coefficients and intercepts of ssGBLUP on AM reliabilities for 305-d milk yield in the first 3 lactations for the nongenotyped animals. A good improvement was achieved using ST-R^{2}A compared with exact AM. However, the reliabilities from MT-R^{2}A were as good as or better than those from ST-R^{2}A and gave an additional improvement in correlations and accuracy. For example, the correlation estimates between exact ssGBLUP and MT-R^{2}A were 0.993, 0.991, and 0.990, for 305-d milk yield in first, second, and third lactation, respectively, and were higher than those between exact ssGBLUP and exact AM reliabilities: 0.981, 0.979, and 0.978.

The MSE values associated with MT-R^{2}A for nongenotyped animals were 0.0004, 0.0005, and 0.0005 for 305-d milk yield for first, second, and third lactation (Table 5), respectively, and were almost 5 times smaller than the MSE of 0.0018, 0.0017, and 0.0016 from AM reliabilities (Table 6). In contrast, the MSE of ST-R^{2}A was close to AM. The regression coefficients were closer to 1 and the intercepts to 0 with MT-R^{2}A than with AM for all studied traits. In fact, slopes as high as 0.99 (intercept 0.01), 0.99 (intercept 0.02), and 0.99 (intercept 0.02) were obtained with MT-R^{2}A for first, second, and third lactation, respectively. The corresponding slopes for AM reliabilities were 0.88 (intercepts 0.07) for lactations 1 through 3, respectively, showing that MT-R^{2}A significantly outperformed the AM reliabilities over all

Table 5. Correlation (r), maximum absolute difference (max), and mean squared error (MSE) between reliabilities from exact single-step genomic BLUP (ssGBLUP) and single-trait multistep genomic reliability approximation (ST-R^{2}A), and from exact ssGBLUP and multitrait multistep genomic reliability approximation (MT-R^{2}A), and regression coefficients (b_1) and intercepts (b_0) of the linear regression of exact ssGBLUP reliabilities on approximations by ST-R^{2}A and MT-R^{2}A for nongenotyped animals[1]

305-d milk lactation	Single-trait model approximation					Multiple-trait model approximation				
	r	Max	MSE	b_1	b_0	r	Max	MSE	b_1	b_0
1	0.987	0.24	0.0014	0.94	0.05	0.993	0.23	0.0004	0.99	0.01
2	0.984	0.23	0.0018	0.93	0.06	0.991	0.22	0.0005	0.99	0.02
3	0.983	0.24	0.0020	0.93	0.06	0.990	0.21	0.0005	0.99	0.02

[1]Intercept (b_0) and slope (b_1) of regression of correct reliability from ssGBLUP on approximation by the multiple-trait weighted genomic BLUP model.

Table 6. Correlation (r), maximum difference (max), and mean squared error (MSE) between reliabilities from exact single-step genomic BLUP (ssGBLUP) and exact animal model (AM), and regression coefficients (b_1) and intercepts (b_0) of the linear regression of exact ssGBLUP reliabilities on exact AM reliabilities for nongenotyped animals[1]

305-d milk lactation	r	Max	MSE	b_1	b_0
1	0.981	0.41	0.0018	0.88	0.07
2	0.979	0.36	0.0017	0.88	0.07
3	0.978	0.35	0.0016	0.88	0.07

[1]Intercept (b_0) and slope (b_1) of regression were calculated from a linear model of ssGBLUP on AM reliabilities.

traits considered in this analysis. The regression coefficients for ST-R^{2}A were close to those by MT-R^{2}A. The exact AM reliabilities were closer to those by ssGBLUP for animals with high reliabilities (results not shown) than by MT-R^{2}A, possibly because genomic information had less impact for animals already having high reliabilities.

Computing Times

Table 7 gives the wall clock times and memory requirements to perform the calculation of reliabilities for ssGBLUP and MT-R^{2}A. The time requirement with MT-R^{2}A was up to 0.1 h. However, the computing times for the exact ssGBLUP model reliabilities including the computing time for the calculation of the diagonal of **H** matrix were considerably higher (>3 h). Inversion of the MME was the most expensive task in calculating the exact GEBV reliabilities. In ssGBLUP model reliabilities, the MME had 212,169 equations, which required 335 GB of RAM. In MT-R^{2}A, calculating the genomic reliabilities in the multiple-trait GBLUP model involved inversion of a system with 59,274 equations, i.e., $t(1 + n_g)$ equations with t the number of traits and n_g the number of genotyped animals. When the coefficient matrix was stored in double precision, it took 26 GB of RAM. The inversion was the most time-consuming step. However, all of the other steps in MT-R^{2}A were performed in seconds and did not require as much memory.

DISCUSSION

We developed and tested a method of approximating GEBV reliabilities in ssGBLUP using a single-trait and a multitrait multistep genomic reliability approximation (ST-R^{2}A and MT-R^{2}A). The approximation method was based on a separate calculation of reliabilities for genotyped and nongenotyped animals. This involved calculating the amount of nongenomic information for the genotyped animals in a conventional pedigree-based

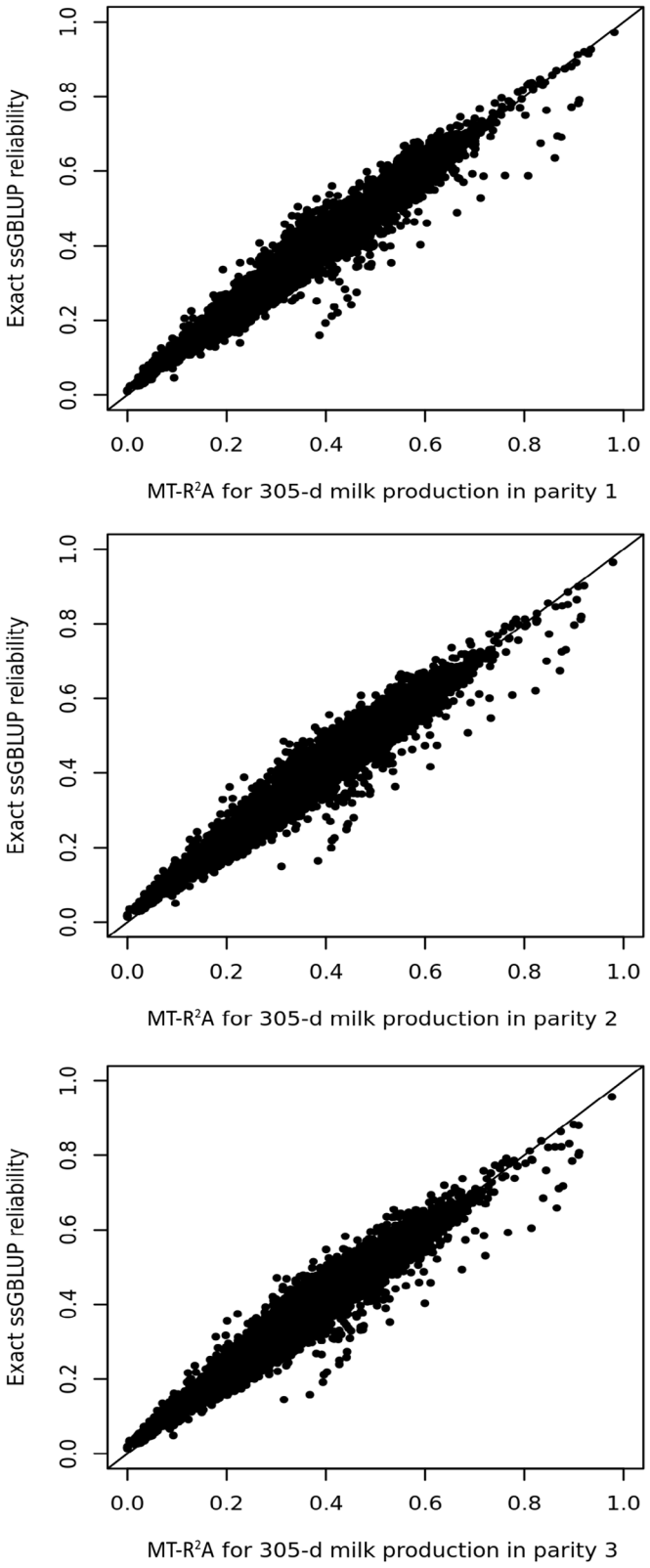

Figure 3. Reliabilities for nongenotyped animals by exact single-step genomic BLUP (ssGBLUP) versus multitrait multistep genomic reliability approximation (MT-R^{2}A) for 305-d milk production in lactations 1, 2, and 3.

AM, and then including the genomic information to estimate the total information in ssGBLUP model reliability. Reliabilities for the nongenotyped animals were obtained by adding the increased genomic contribution to the genotyped animals in a pedigree-based reliability approximation.

The results suggest that the approximations corresponded well to the exact ssGBLUP reliabilities calculated by the direct inverse of the left-hand side of the MME. However, there was a slight upward bias in the reliabilities of genotyped animals with high reliability (>0.6). This may be due to the cumulative assumptions and approximations inherent in our multistep procedure. In the first step we calculated reliability in an AM using the approximation method of Tier and Meyer (2004), who also reported an upward bias at the higher reliabilities (>0.5) with their approximation method. In the second step, we used the reliabilities from the first step to quantify the nongenomic pedigree-based information ERC_{rev} for the genotyped animals by reverse approximation. The reliabilities for the genotyped animals were calculated by the GBLUP/SNP-BLUP model using ERC_{rev} as weights. Thus, the approximated reliability for the genotyped animals had at least 2 sources for error: the first step reliabilities and ERC_{rev}. The presented reverse reliability approximation is a MT approach, whereas the GEBV reliability r_g^2 for the genotyped animals was calculated by MT and ST models using the ERC_{rev} as weights. Thus, this could generate more bias in the ST approach.

The results from the approximation method for nongenotyped animals were as good as or better than those obtained for genotyped animals. Indeed, the correlations between the exact reliabilities from ssGBLUP and the corresponding approximations were above 0.990 and the regression coefficients were close to unity for nongenotyped animals across all traits. However, for a few outliers with high exact reliabilities, the approximation deviated from the exact ssGBLUP reliability.

Various other multistep procedures have been proposed based on the idea of transferring genomic information from genotyped to nongenotyped animals (Taskinen et al., 2013, 2014; Liu et al., 2017; Edel et al., 2019). Our method is similar to the multistep procedure developed by Liu et al. (2017), the so-called Interbull genomic reliability method in a single-trait model. This method consists of 6 steps: (1) calculating the reliabilities of SNP genotypes; (2) calculating the reliability of direct genomic value (**DGV**); (3) adjusting the theoretical reliabilities to the realized reliabilities; (4) calculating the genomic gain from effective daughter contribution (**EDC**); (5) propagating the genomic information to nongenotyped individuals; and (6) calculating the final reliabilities enhanced with genomic information. The main difference between the aforementioned method and ours is that the Interbull genomic reliability method is a single-trait approach, whereas our method is a MT approach. In addition, a difference lies in step 2, where we determined the ERC_{rev} by reverse approximation of pedigree-based AM reliabilities by the method of Tier and Meyer (2004). Liu et al. (2017) calculated the ERC based on absorbing the block of fixed effects and nongenetic effects in such a way that all cows with phenotypic data get an ERC value. Moreover, our multistep procedure does not include adjustment of theoretical genomic reliabilities.

Our results are in line with the reliabilities approximated using the Interbull standardized genomic reliability procedure in Erbe et al. (2018), who reported correlations of 0.99 between the approximated and true ssGBLUP reliabilities for genotyped animals, and slightly less accurate results for nongenotyped animals. The authors also noted that the bias for the genotyped animals depended on how the reference population is defined and on the weights given to the reference animals. However, they did not explicitly specify the reasons for the bias observed in the reliability of GEBV for nongenotyped animals.

Edel et al. (2019) developed 2 approximation methods for calculating reliabilities in ssGBLUP. They used the single-step marker effect model developed by Fernando et al. (2014), which has an extra model effect called imputation residual for nongenotyped animals. The approach calculates PEV for SNP marker effects, and then approximates the imputation residuals either by diagonal approximation of the imputation residual subblock or by reducing the nongenotyped animals to those with relevant contributions. Edel et al. (2019) combined the 2 approximations to calculate genomic reliabilities for genotyped animals and proposed to propagate the increased reliability due to genomic information to nongenotyped animals. The approach is similar to ours in the steps to approximate reliabilities for the nongenotyped animals, but it differs in details. For example, Edel et al. (2019) calculated the increase due to genomics in the reliability scale, whereas we used the ERC scale. We transformed the reliability increase

Table 7. Computing time (wall clock time in h) and peak memory use (in GB) for single-step genomic BLUP (ssGBLUP), multiple-trait multistep genomic reliability approximation (MT-R^2A), and single-trait multistep genomic reliability approximation (ST-R^2A) on data 1

Method	Peak memory (GB)	Wall clock time (h)
ssGBLUP	335	3.15
MT-R^2A	26	0.10
ST-R^2A	3	0.06

into ERC weights similarly as they did. However, they added the ERC increase directly to the "conventional" weight used in the pedigree-based AM to estimate reliability. In our approach, the increased weight was considered for a new pseudo-observation and did not increase information to estimate fixed effects.

We assessed the bias of the approximation methods using regression of the ssGBLUP reliabilities computed by inverting the left-hand side MME on those from ST-R^2A and MT-R^2A. The regression coefficient estimates for the approximate reliabilities for the nongenotyped animals were generally in line with those reported by Edel et al. (2019). For the genotyped animals, in contrast, our results were less in agreement with the same study. In this context, statistics on exact ssGBLUP versus exact AM reliabilities obtained in Edel et al. (2019) were slightly higher than those in the present study. It is possible that the difference between the results of our study from those of Edel et al. (2019) may be due to the different data structure. For example, we had many more genotyped animals and a large proportion of them were females with phenotypes (Table 1).

The correlations between the exact ssGBLUP and approximated reliabilities in our study were high (>0.98) for genotyped animals over all traits using MT-R^2A, even for the subgroup of young candidates. These values are comparable to the value of 0.99 obtained using the first approximation of Misztal et al. (2013). The correlations in our study were higher than those achieved by the second approximation in their study. Note that the first approximation of Misztal et al. (2013) requires computing the inverse of a matrix which includes the matrices $\mathbf{G}^{-1}$ and $\mathbf{A}_{22}^{-1}$, making it computationally demanding for a large number of genotyped animals. Our approach allows using either SNP-BLUP or GBLUP such that the memory and computational requirements can be chosen to be equal or less than in their approach. The second approach in Misztal et al. (2013) uses only diagonals of $\mathbf{G}^{-1}$ and $\mathbf{A}_{22}^{-1}$. In practice, our method should be at least as good as the first approximation of Misztal et al. (2013) for single-trait models but better for MT models because our approach uses MT reverse reliability and allows the use of a MT model for the approximation of reliability for genotyped animals.

The results of our study imply that the highest correlation and lowest bias can be achieved by applying MT approximation rather than by analyzing the traits separately in a single-trait approximation. The MT approximation is associated with fewer biases compared with ST approximation, especially for traits with high missing phenotype records. In fact, for the group comprising all the genotyped animals, gains of 0.01 to 0.06 on correlation estimates were achieved by MT-R^2A compared with ST-R^2A over the 3 traits, particularly for traits with a large number of missing phenotype records (Table 1). We examined the gain from using the MT-R^2A over ST-R^2A for the subgroup of young candidates and observed a relatively large improvement by MT-R^2A compared with the group of all genotyped animals. However, the effect of missing traits on the observed gain due to MT-R^2A was not clear, especially for the second and third lactations.

The MSE associated with MT approximation were up to 5 times smaller than in ST approximation, particularly for nongenotyped animals. This improvement derives from the fact that traits with a high amount of missing phenotype records acquire extra information from correlations. Numerous studies have identified the benefit of multitrait model reliabilities over single-trait reliabilities when traits are correlated. Strabel et al. (2001) found that MT approximation lessened the bias of the approximation compared with a ST-based method in the approximation of reliabilities for a MT model with maternal effects on Senepol cattle data. In the MT model, the correlated information can be accounted for, but it is not in the ST model reliabilities. This can lead to a downward trend in ST model reliabilities from the correct level. Further, the use of a MT model is more beneficial than a ST model for a trait with low heritability when a correlated trait with high heritability is available. In our study, all 3 traits had practically the same heritability values (Table 2). However, the second and third lactations included a large amount of missing phenotypic data, and the MT model proved highly beneficial for these lactations, whereas the first lactation gained only negligibly. Quite the contrary, for the 305-d milk yield in the first lactation for genotyped animals, we found that the correlation between reliability from MT approximation and the exact ssGBLUP reliability was of the same magnitude as that between ST approximation and exact ssGBLUP reliability.

The computing time for calculating model reliability for MT-R^2A was less than that for ssGBLUP. In MT-R^2A, the most time was spent in the calculation of genomic reliabilities using the multiple-trait GBLUP model. Note that the MME in MT GBLUP was determined by the number of traits t and the number of genotyped animals n_g.

The use of a MT GBLUP can be infeasible in practice when the number of genotyped animals is very high. The computational cost of inverting the MME is a cubic function $O[(tn_g)^3]$, where O is a theoretical measure of the execution of an algorithm, and the memory requirement is a quadratic function $O[n_g(m + t^2 n_g)]$, where m is the number of SNP markers. Thus, the cost

is upper bounded by a cubic or quadratic function times a constant (Knuth, 1976). The memory requirement for MME for the 3-trait GBLUP model reliability with around 20,000 genotyped animals was 26 GB. Extrapolating, such memory requirements would be around 670 GB for 100,000 genotyped animals and 3 traits, which can present a considerable computational burden. Using an equivalent MT SNP-BLUP model would lead to a system of equations of size $t(1 + m)$, where m is the number SNP markers. Computation of MT SNP-BLUP has a cost of $O[(tm)^3]$ for computing time and $O[m(n_g + t^2m)]$ for memory requirement, which is lower than for GBLUP when the number of genotyped animals n_g is more than the number of SNP markers m.

Including the residual polygenic (**RPG**) effect in SNP-BLUP model would increase the computational cost of inverting the MME in SNP-BLUP from $O[(tm)^3]$ to $O[t(m + n_g)]^3$, which is computationally challenging with an increasing number of genotyped animals. To overcome the potential computational problem, Ben Zaabza et al. (2020) proposed a Monte Carlo (**MC**)-based sampling method to estimate the SNP-BLUP model reliability with an RPG effect (MC-SNP-BLUP), where the MME size depends on the number of markers (m) and MC samples (n_{mc}) instead of ($m + n_g$). Further, Ben Zaabza et al. (2021) extended the MC-SNP-BLUP to another (MC)-based sampling method called full-MC-SNP-BLUP, where the size of the MME is determined by n_{mc}. This method has a cost of $O[(tn_{mc})^3]$ for computing times and $O[n_{mc}(n_g + t^2n_{mc})]$ for memory. When m is less than n_g and n_g is large, the full MC approach is computationally less demanding than the exact GBLUP, which involves the time-consuming task of making and inverting the **G** matrix (see Ben Zaabza et al., 2021). The full-MC approach was reported to be computationally efficient for large data sets and to provide good approximation to the exact values with only a small upward bias. A drawback of the full-MC approach is its tendency to overestimate reliability for animals with low reliability. Moreover, a small MC and high RPG effects are associated with overestimation. The authors recommended that the RPG proportion, the number of genotyped animals, and the population structure should be considered when determining the number of MC samples. In practice, a reasonable compromise should be made between accuracy of the reliability and the length of the computing time when using any MC approach.

We examined the efficiency of our multistep procedure using the full-MC approach (Ben Zaabza et al., 2021) in the intermediate step for approximating reliabilities of the genotyped animals on the largest data (data 2). We used MC sample sizes of 120,000 and 160,000 for data 2. The required computing times in the full-MC-SNP-BLUP were 347 min and 527 min for 120,000 and 160,000 MC samples (Table 8), respectively. These computing times are less than required by GBLUP (3,090 min) using a data of a comparable size, containing 240,000 genotyped animals and 50,000 SNP markers (see Ben Zaabza et al., 2021). Memory requirements for making MME were 115 GB with 120,000 and 204 GB with 160,000 MC samples. If exact SNP-BLUP had been used, 822 GB would have been needed, which exceeded the RAM available on our computer. The computing times for inverting MME coefficient matrix were 32 min with 120,000 MC samples and 73 min with 160,000 MC samples. Assuming computing time increases cubically by MME size, inverting the exact SNP-BLUP reliability with RPG would require more than 10 h. For more details on the different steps in the full-MC-SNP-BLUP reliability calculation, see Ben Zaabza et al. (2021).

Table 8. Computing time (wall clock, in min) for calculating model reliability in the full Monte Carlo (MC)-SNP-BLUP model

	Sample size	
Method[1]	120,000	160,000
MC-marker-effects	20	25
MC-RPG	188	252
Making MME	47	82
Inversion	32	73
PEV computation	60	95
Total	347	527

[1]RPG = residual polygenic; MME = mixed model equations; PEV = prediction error variance.

CONCLUSIONS

This paper outlines a method for the estimation of GEBV reliabilities in a single-step genomic model. Our results indicate that ssGBLUP reliabilities can be approximated satisfactorily both for genotyped and nongenotyped animals. We conclude that the proposed method is efficient in terms of computing time and memory requirements and can be applied even for large data sets. This method is particularly efficient when using an equivalent MT SNP-BLUP model when the number of genotyped animals is more than the number of SNP markers.

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APPENDIX 1

We give a pseudo code for 2 functions needed in the ERC calculation by the reverse reliability estimation approach. The main function (ERC_rev) has an iterative loop for calculating ERC. This function calls function TierMeyer, which calculates new ERC values. Iteration in the main function ends when the ERC values no longer change or when the number of iterations has reached maximum ($\boldsymbol{k}_{\max}$). For the change in ERC values, we used a tolerance of 10^{-6} for ε. When the vector of trait-wise ERC value changes $\left(\mathbf{n}_{\mathbf{d}}^{[k]}\right.$ at iteration $k\left.\right)$ was less than or equal to ε for every trait, the iteration was terminated.

In the code, we use the following notations: $||\cdot||_2$ is the column-wise vector 2-norm over animals, $Diag(\mathbf{v})$ gives the diagonal matrix from the argument vector $\mathbf{v}$, and $Diag(\mathbf{M})$ returns the diagonal vector of the argument matrix $\mathbf{M}$. Augmented assignment operations "+=" and "−=" were used to shorten the notation. For example, $\mathbf{M}$ += $\mathbf{C}$ is the same as $\mathbf{M} = \mathbf{M} + \mathbf{C}$. The ERC_rev function is called with the following arguments: the genetic covariance matrix $\mathbf{G}_0$, the residual covariance matrix $\mathbf{R}_0$, the prediction error variances ($\mathbf{PEV}$) of genotyped animals for all traits, the reliabilities r^2 of genotyped animals for all traits, the heritabilities h^2 of all traits, and the maximum number of iterations $k_{\max}$. PEV and r^2 for the nongenotyped animals are set to zero, and the full pedigree is used. The ERC_rev function returns ERC for the genotyped animals.

function ERC_rev($\mathbf{G}_0$, $\mathbf{R}_0$, PEV, $\mathbf{r}^2$, $\mathbf{h}^2$, $\mathbf{k}_{\max}$)
  $n_{\mathbf{d}}^{[0]} = 2\varepsilon$; $n_{\mathbf{d}}^{[1]} = 2\varepsilon$
  $\mathbf{ERC}_{ij}^{[0]} = \lambda_j \mathbf{r}_{ij}^2 \Big/ \left(1 - \mathbf{r}_{ij}^2\right)$, all animals i, $\lambda_j = \dfrac{1 - h_j^2}{h_j^2}$, $j = 1, \ldots,$ traits.
  k = 0
  while $\left\{\left[\left(k < k_{\max}\right)\right]\ \text{AND}\ \left[\text{any}\left(n_{\mathbf{d}}^{[k]} > \varepsilon\right)\right]\right\}$
    restrict = restrict OR $\left[\text{any}\left(n_{\mathbf{d}}^{[k+1]} > n_{\mathbf{d}}^{[k]}\right)\right]$ OR $\left(k > k_{\max}/2\right)$
    k = k + 1
    $\mathbf{ERC}^{[k]}$ = TierMeyer($\mathbf{G}_0$, $\mathbf{R}_0$, $\mathbf{ERC}^{[k-1]}$, PEV, restrict)
    $\mathbf{d}^{[k]}$ = $\mathbf{ERC}^{[k]}$ − $\mathbf{ERC}^{[k-1]}$
    $n_{\mathbf{d}}^{k} = ||\,\mathbf{d}^{[k]}\,||_2 \big/ ||\,\mathbf{ERC}^{[k-1]}\,||_2$
  end while
  return ($\mathbf{ERC}^{[k]}$)
end ERC_reverse

function TierMeyer($\mathbf{G}_0$, $\mathbf{R}_0$, $\mathbf{ERC}^{[k-1]}$, PEV, restrict)
  if (restrict) then ω = 0.35 else ω = 0.70
  $\mathbf{F}$ = 0; $\mathbf{C}$ = 0
  do i from youngest to oldest animal
    $\mathbf{E}_i = Diag\left(\sqrt{\mathbf{ERC}_i^{[k-1]}}\right)$
    $\mathbf{F}_i$ += $\mathbf{E}_i \mathbf{R}_0^{-1} \mathbf{E}_i$
    $\mathbf{C}_i = \dfrac{1}{3}\mathbf{G}_0^{-1} - \dfrac{4}{9}\mathbf{G}_0^{-1}\left(\mathbf{F}_i + \dfrac{4}{3}\mathbf{G}_0^{-1}\right)^{-1}\mathbf{G}_0^{-1}$
    if ($sire\ of\ i$ exists) $\mathbf{F}_{\text{sire of } i}$ += $\mathbf{C}_i$
    if ($dam\ of\ i$ exists) $\mathbf{F}_{\text{dam of } i}$ += $\mathbf{C}_i$
  end do
  do i from oldest to youngest
    if ($sire\ of\ i$ exists) $\mathbf{F}_i$ += $\dfrac{1}{3}\mathbf{G}_0^{-1} - \dfrac{4}{9}\mathbf{G}_0^{-1}\left(\mathbf{F}_{sire\ of\ i} - \mathbf{C}_i + \dfrac{4}{3}\mathbf{G}_0^{-1}\right)^{-1}\mathbf{G}_0^{-1}$
    if ($dam\ of\ i$ exists) $\mathbf{F}_i$ += $\dfrac{1}{3}\mathbf{G}_0^{-1} - \dfrac{4}{9}\mathbf{G}_0^{-1}\left(\mathbf{F}_{\text{dam of}i} - \mathbf{C}_i + \dfrac{4}{3}\mathbf{G}_0^{-1}\right)^{-1}\mathbf{G}_0^{-1}$

```
    if (any (ERC_i^[k-1] >0)) then
F_i −= E_i R_0^-1 E_i
G_i^-1 = F_i + G_0^-1
use Newton-Raphson to solve vector c in Diag((G_0^-1 + E_i R_0^-1 E_i)^-1) = PEV_i
where E_i = Diag(√c) with starting value c = ERC_i^[k-1].
ERC_i^[k] = ERC_i^[k-1] + ω(c − ERC_i^[k-1])
E_i = Diag(√ERC_i^[k])
F_i += E_i R_0^-1 E_i
    endif
  end do
  return(ERC^[k])
end TierMeyer
```

APPENDIX 2

We implemented a Newton-Raphson–based algorithm for solving from a nonlinear equation:

$$\boldsymbol{f}(\mathbf{c}) = \mathbf{y},$$

where $\mathbf{c}$ is a $t \times 1$ vector of effective record contributions (ERC) and t is the number of traits. The left-hand side, $\boldsymbol{f}(\mathbf{c})$, are the diagonals of inverse matrix $\mathbf{M}^{-1}$, $\{\boldsymbol{f}(\mathbf{c})\}_j = \{\mathbf{M}^{-1}\}_{jj}$, $j = 1, \ldots, t$, where $\mathbf{M}$ is a $t \times t$ matrix:

$$\mathbf{M} = \mathbf{G}_i^{-1} + \mathbf{E}\mathbf{R}_0^{-1}\mathbf{E},$$

where $\mathbf{E}$ is a diagonal matrix containing the square roots of vector $\mathbf{c}$ on the diagonal, $\{\mathbf{E}(\mathbf{c})\}_{jj} = \sqrt{\mathbf{c}_j}$, $\mathbf{G}_i^{-1}$ contains the inverse of the genetic covariance matrix $\mathbf{G}_0^{-1}$ and contributions from offspring and ancestors of animal i, and $\mathbf{R}_0$ is the residual covariance matrix. The right-hand side has the prediction error variances (PEV) of individual: $\{\mathbf{y}\}_j = \{\mathbf{V}_{jj}\}_{ii}$ that are the diagonal elements of the prediction error co-variance (PEC) matrix pertaining to animal i and trait j.

The solving method attempts to find the root of the multivariate function $\mathbf{F}(\mathbf{c}) = \mathbf{0}$, where $\mathbf{F}(\mathbf{c}) = \boldsymbol{f}(\mathbf{c}) - \mathbf{y}$. As the root may not exist in all cases, a location $\mathbf{c}$ that minimizes $||\mathbf{F}||$ is the actual target. First, an initial value for the $\mathbf{c}$ vector is chosen denoted $\mathbf{c}^{[0]}$. In every iteration k, the method calculates new location for $\mathbf{c}$ by

$$\mathbf{c}^{[k+1]} = \mathbf{c}^{[k]} - \alpha\mathbf{J}\left(c^{[k]}\right)^{-1}\mathbf{F}\left(\mathbf{c}^{[k]}\right),$$

where $\mathbf{F}\left(\mathbf{c}^{[k]}\right)$ and Jacobian $\mathbf{J}\left(c^{[k]}\right)$ are evaluated at the current values of ERC. As negative ERC are not allowed, $\mathbf{c}$ has constraints that are handled by projection onto the positive side. A simple line search is performed starting from $\alpha = 1$ and halving it until $\left\|\mathbf{F}\left(\mathbf{c}^{[k+1]}\right)\right\|$ is smaller than (or equal to) previous $\left\|\mathbf{F}\left(\mathbf{c}^{[k]}\right)\right\|$. Convergence is achieved when the improvement in $||\mathbf{F}||$ is small enough compared to a given tolerance.

The t by t Jacobian matrix $\mathbf{J}$ has the first-order derivatives of the vector valued multi-variate function $\mathbf{F}$:

$$\mathbf{J}(\mathbf{c}) = \begin{pmatrix} \frac{\partial \mathbf{F}_1}{\partial \mathbf{c}_1} & \cdots & \frac{\partial \mathbf{F}_1}{\partial \mathbf{c}_t} \\ \vdots & \ddots & \vdots \\ \frac{\partial \mathbf{F}_t}{\partial \mathbf{c}_1} & \cdots & \frac{\partial \mathbf{F}_t}{\partial \mathbf{c}_t} \end{pmatrix},$$

Because the $\mathbf{y}$ vector in $\mathbf{F}(\mathbf{c})$ is constant, the components of the Jacobian matrix are

$$\mathbf{J}_{jl} = \frac{\partial\left(f(c)_j\right)}{\partial c_l} = \frac{\partial\left(\left\{\mathbf{M}^{-1}\right\}_{jj}\right)}{\partial c_l}.$$

For example, let $\mathbf{c}$ contain 3 traits ($t = 3$) such that $\mathbf{M}$ is a 3×3 matrix. Then, the first-order derivative of diagonal j of the $\mathbf{M}^{-1}$ matrix with respect to trait l of $\mathbf{c}$ is equal to

$$\begin{aligned}\mathbf{J}_{jl} &= \left\{\frac{\partial \mathbf{M}^{-1}}{\partial c_l}\right\}_{jj} = -\left\{\mathbf{M}^{-1}\frac{\partial \mathbf{M}}{\partial c_l}\mathbf{M}^{-1}\right\}_{jj}, \text{ where } \frac{\partial \mathbf{M}}{\partial c_l} = \frac{\partial}{\partial c_l}\left(\mathbf{G}_i^{-1} + \mathbf{E}\mathbf{R}_0^{-1}\mathbf{E}\right)\\ &= \left(\frac{\partial \mathbf{E}}{\partial c_l}\right)\mathbf{R}_0^{-1}\mathbf{E} + \mathbf{E}\left(\frac{\partial \mathbf{R}_0^{-1}}{\partial c_l}\right)\mathbf{E} + \mathbf{E}\mathbf{R}_0^{-1}\left(\frac{\partial \mathbf{E}}{\partial c_l}\right)\\ &= \left(\frac{\partial \mathbf{E}}{\partial c_l}\right)\mathbf{R}_0^{-1}\mathbf{E} + \mathbf{E}\mathbf{R}_0^{-1}\left(\frac{\partial \mathbf{E}}{\partial c_l}\right).\end{aligned}$$

We illustrate the computation of the Jacobian matrix by differentiating the $\mathbf{M}$ matrix with respect to the first trait $\mathbf{c}_1$:

$$\begin{aligned}\frac{\partial \mathbf{M}}{\partial \mathbf{c}_1} &= \frac{\partial}{\partial \mathbf{c}_1}\left[\begin{pmatrix} c_1^{0.5} & 0 & 0\\ 0 & c_2^{0.5} & 0\\ 0 & 0 & c_3^{0.5}\end{pmatrix}\begin{pmatrix} r^{11} & r^{12} & r^{13}\\ r^{12} & r^{22} & r^{23}\\ r^{13} & r^{23} & r^{33}\end{pmatrix}\begin{pmatrix} c_1^{0.5} & 0 & 0\\ 0 & c_2^{0.5} & 0\\ 0 & 0 & c_3^{0.5}\end{pmatrix}\right]\\ &= \frac{\partial}{\partial \mathbf{c}_1}\left[\begin{pmatrix} c_1^{0.5} & 0 & 0\\ 0 & c_2^{0.5} & 0\\ 0 & 0 & c_3^{0.5}\end{pmatrix}\right]\begin{pmatrix} r^{11} & r^{12} & r^{13}\\ r^{12} & r^{22} & r^{23}\\ r^{13} & r^{23} & r^{33}\end{pmatrix}\begin{pmatrix} c_1^{0.5} & 0 & 0\\ 0 & c_2^{0.5} & 0\\ 0 & 0 & c_3^{0.5}\end{pmatrix}\\ &+ \begin{pmatrix} c_1^{0.5} & 0 & 0\\ 0 & c_2^{0.5} & 0\\ 0 & 0 & c_3^{0.5}\end{pmatrix}\begin{pmatrix} r^{11} & r^{12} & r^{13}\\ r^{12} & r^{22} & r^{23}\\ r^{13} & r^{23} & r^{33}\end{pmatrix}\frac{\partial}{\partial \mathbf{c}_1}\left[\begin{pmatrix} c_1^{0.5} & 0 & 0\\ 0 & c_2^{0.5} & 0\\ 0 & 0 & c_3^{0.5}\end{pmatrix}\right]\\ &= \begin{pmatrix} \frac{1}{2}c_1^{-0.5} & 0 & 0\\ 0 & 0 & 0\\ 0 & 0 & 0\end{pmatrix}\begin{pmatrix} r^{11} & r^{12} & r^{13}\\ r^{12} & r^{22} & r^{23}\\ r^{13} & r^{23} & r^{33}\end{pmatrix}\begin{pmatrix} c_1^{0.5} & 0 & 0\\ 0 & c_2^{0.5} & 0\\ 0 & 0 & c_3^{0.5}\end{pmatrix} + \begin{pmatrix} c_1^{0.5} & 0 & 0\\ 0 & c_2^{0.5} & 0\\ 0 & 0 & c_3^{0.5}\end{pmatrix}\begin{pmatrix} r^{11} & r^{12} & r^{13}\\ r^{12} & r^{22} & r^{23}\\ r^{13} & r^{23} & r^{33}\end{pmatrix}\begin{pmatrix} \frac{1}{2}c_1^{-0.5} & 0 & 0\\ 0 & 0 & 0\\ 0 & 0 & 0\end{pmatrix}.\end{aligned}$$

Thus, the first derivative of $\mathbf{M}$ with respect to $\mathbf{c}_1$ is

$$\frac{\partial \mathbf{M}}{\partial \mathbf{c}_1} = \begin{pmatrix} r^{11} & \frac{1}{2}c_1^{-0.5}r^{12}c_2^{0.5} & \frac{1}{2}c_1^{-0.5}r^{13}c_3^{0.5}\\ \frac{1}{2}c_1^{-0.5}r^{12}c_2^{0.5} & 0 & 0\\ \frac{1}{2}c_1^{-0.5}r^{13}c_3^{0.5} & 0 & 0\end{pmatrix}.$$