Guidelines for Approximating Genomic Reliabilities of the Single-Step Genomic Model

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Abstract

A genomic reliability method developed by the Interbull Working Group on Genomic Reliability Calculation approximated reliabilities of estimated genomic breeding values for the multi-step genomic model as well as the single-step genomic model. Several modifications and improvements have been made thereafter, with a main optimization of making the genomic reliability method feasible for large-scale national genomic evaluations. The calculation of exact reliabilities of direct genomic values was proven to be computational demanding for large, genotyped populations. Therefore, this step of the original genomic reliability method, along with other steps, is no longer required in routine genomic evaluation but it is still needed when a genomic model or a major change in the national model is introduced. Consequently, two guidelines have been developed separately for the routine national single-step genomic evaluation and for deriving genomic effective daughter contribution gain via the Interbull GEBV Test. Detailed technical steps have been described in the new guidelines to assist the countries in applying the methods to the routine single-step evaluation and the derivation of the genomic effective daughter contribution gain parameter in a genomic validation. These guidelines should harmonize the calculation of genomic reliabilities and make the genomic reliabilities of marketed genomic bulls comparable across countries.

Key words: genomic reliability, single-step model, genomic validation, dairy cattle evaluation

Introduction

For conventional evaluations without genomic information, accurate reliability calculation methods were developed and have been routinely used in dairy cattle evaluations, e.g. a single-trait reliability method by VanRaden and Wiggans (1991) for a repeatability animal model, and multi-trait reliability methods (Liu et al. 2002; Tier and Meyer 2004) for a multi-trait animal model. For all types of genetic evaluation models, including a maternal-effect model for calving traits, fairly accurate and highly efficient reliability methods have been utilized for national dairy cattle evaluations.

Soon after the introduction of genomic selection in 2008, diverse genomic reliability methods (Liu et al. 2010; Wiggans and VanRaden 2010) were developed to consider a bull reference population, which covered multi-step genomic models as well as single-step genomic models (Misztal et al. 2013). To make national genomic reliabilities comparable across countries, an Interbull working group was set up in 2016 aiming to develop a standard genomic reliability (GREL) method for dairy cattle evaluations (Liu et al. 2017). The standardized GREL method by the working group was applicable for both multi-step and single-step models. However, at that time large-

scale female animal genotyping just started in few countries and thus the number of genotyped animals was still manageable.

The aims of this study were 1) to develop guidelines for routine genomic evaluations with millions of genotyped animals; 2) to address technical issues related to routine reliability calculation, and 3) to identify topics for future research and development projects.

Interbull genomic reliability method for the single-step model

Main Features of the Genomic Reliability Calculation Method

The Interbull standardized genomic reliability method (Liu et al. 2017) has the following features:

1) Keep using traditional reliability methods for the conventional part of the single-step model (SSM), including the calculation of effective daughter contribution (EDC) of bulls or cows according to the Interbull standardized methods,
2) Genotype data are treated as a new source of information contributing to the total reliability,
3) Calculate exact reliability values of direct genomic values (DGV) using all genotypic data of all genotyped animals, and
4) Adjust theoretical genomic reliability level via a genomic validation test.

Complex statistical models have been used for many trait groups when calculating the conventional part of reliability, e.g., a multi-lactation random regression model for test-day traits, a maternal-effect model for calving traits, or a multi-parity multi-trait animal model for fertility traits. Young animals and all genotyped animals must be included in the step of calculating the conventional part of reliability. Having completed the conventional reliability calculation, a model containing a general mean and additive genetic effect is assumed to compute the genomic contribution to the total reliability.

In contrast to approximating genomic reliabilities of candidates based on genomic or pedigree relationship to reference animals (Liu et al. 2010; Wiggans and VanRaden 2010), exact DGV reliability values are calculated using all genotypic data of all animals, including those with own phenotypic data and young candidates via the software *snp_blup_rel* (Ben Zaabza et al. 2020a). A single-trait SNP BLUP model without a residual polygenic effect (RPG) was assumed here for the computation of the exact reliability values of DGV, being equal to genomic breeding values (GEBV) under the assumption of no RPG effect at this step. An overestimation of genomic reliability by ignoring the RPG effect will be accounted for in a later step of adjusting GREL via Interbull GEBV Test (Mäntysaari et al. 2010).

Need for A Downward Adjustment of the Theoretical Genomic Reliabilities for Large Genotyped Population

The Interbull genomic reliability method was applied to the single-step evaluations of four test-day traits and 25 conformation traits in German Holstein (Liu et al. 2023). Phenotypic, genotypic and pedigree data stemmed from German Holstein official evaluation in April 2023. Genotype data of 1,318,780 genotyped Holstein animals were evaluated jointly with 264 million of test-day records or deregressed MACE proofs of 13,528,444 cows and bulls for each of the four test-day traits. For the 25 conformation traits, the number of national cows and MACE bulls with own phenotypic data was 3,144,366. The size of reference population was 524,187 for the test-day trait protein yield and 386,062 for the conformation trait stature, respectively (See Table 1 in Liu et al. 2023). According to the exact DGV reliabilities of the genotyped Holstein AI bulls (Figures 5 and 6 in Liu et al. 2023), it was clear that the exact, theoretical DGV reliability for 1-year-old genomic AI bulls born in 2022 was

way too high, with an average of 0.97 for milk yield and 0.83 for the conformation trait angularity which was recently introduced with a new trait definition and had much less data than all the other conformation traits. The extremely large reference population of the German Holstein led to the exceedingly high level of the exact, theoretical DGV reliability for the young genomic AI bulls of just 1 year old. With more animals genotyped, the level of theoretical DGV reliability will keep increasing. Therefore, a downward adjustment for the theoretical genomic reliabilities (VanRaden and O'Connell 2018) is, in general, needed for large, genotyped populations.

Ignoring the Individual Variability in DGV Reliabilities for Large Genotyped Population

In addition to the level of DGV reliabilities, variation in theoretical DGV reliabilities was investigated for the German Holstein animals (Liu et al. 2023). Standard deviations of the DGV reliabilities by birth year were plotted for all the genotyped German Holstein AI bulls (Figures 7 and 8 in Liu et al. 2023). Both graphs clearly showed that the standard deviation of DGV reliabilities was extremely small for the young genomic AI bulls without daughters, being as low as 0.005 for all the four test-day traits and about 0.01 for the conformation traits, indicating that the theoretical DGV reliabilities of the young animals had little variation among themselves, probably caused by the very large genotyped population and a fairly complete list of ancestor animals in the reference population for the young animals. These two graphs suggested a constant value of genomic EDC may give a satisfactory approximation of the exact, theoretical DGV reliabilities which usually required considerable computing time to calculate even with the highly efficient software *snp_blup_rel* (Ben Zaabza et al. 2020a). The simplification of the genomic reliability calculation makes it feasible for routine single-step evaluation of millions of genotyped animals.

Results & Discussion

As the number of genotyped animals increased over time e.g. by a large-scale female animal genotyping program and reached a high level for the German Holstein population, the variation in theoretical DGV reliabilities or total genomic reliabilities became smaller among the young, genotyped animals without own phenotypic data, also due to more complete ancestry in the genomic reference population for the young animals. The level of genomic reliabilities for the young animals was more important to ascertain than accounting for the individual variation in the DGV reliabilities. Therefore, a constant value of genomic EDC gain may be safely assumed for all the genotyped animals, which needs to be determined via a genomic validation study.

Since the calculation of the exact, theoretical DGV reliabilities of the original genomic reliability method (Liu et al. 2017) took a considerably long time for the very large genotyped population like German Holstein and the consideration of individual DGV reliabilities became less important for the large genotyped population, the step of calculating theoretical DGV reliabilities via *snp_blup_rel* was moved from the routine single-step evaluation pipeline to the genomic validation test conducted usually with much less time pressure than the routine genomic evaluation. Therefore, two Guidelines were developed separately for the routine single-step evaluation and for the genomic validation test deriving the genomic EDC gain parameter (see Appendices for the two Guidelines). Both Guidelines were approved by the Interbull Steering Committee in April 2024.

The standardized Interbull genomic reliability method was successfully implemented in all 10 trait groups of the German Holstein single-step evaluation according to the two Guidelines (see Appendices).

Technical Issues Related to Implementing the Guidelines on Genomic Reliabilities

A Multi-Breed Genomic Evaluation Model

Some countries or dairy populations may evaluate multiple dairy breeds jointly in a single-step evaluation, with some of the breeds having genotype data. For instance, Jersey and Holstein breeds would be evaluated together in a joint system, with both breeds having own genotypic data. Due to the vast difference in the size of reference populations of the two breeds, it is expected that young candidates of the Jersey breed would have lower genomic reliabilities than those of the Holstein breed. Regardless how the genotypic data are modelled for the two breeds, separate populations of genotyped animals and reference animals need to be defined according to the Guidelines (see Appendices). In addition, the adjustment step for genomic reliabilities must be conducted for each breed separately. Following all the steps of the two Guidelines, different levels of genomic reliabilities between the Jersey and Holstein candidates are ensured.

Applicability to Small Genotyped or Reference Populations

The step of adjusting genomic reliabilities of the Interbull GREL method plays a key role in determining a proper level of genomic reliabilities for young candidates. Applicability of the GREL method is limited to whether the required Interbull GEBV Test (Sullivan 2024) can be conducted for a small population with a limited number of genotyped animals or reference animals, such as a small breed with a small number of genotyped animals or a new trait with a small number of reference animals. If enough validation bulls can be defined for the GEBV Test, then the GREL adjustment and derivation of the genomic EDC gain parameter can be done properly.

For new traits like dry matter intake that have no reasonable number of validation bulls available, further research is required to investigate how to use validation cows with low reliability for the GREL adjustment. If a genomic validation via forward prediction cannot be performed due to a small number of reference cows for a new trait like dry matter intake, new research will be needed to extend the GREL method for a different validation procedure such as cross-validation.

Some countries or populations may have trait groups containing sub-traits with similar heritability values and data structure, assuming the same GREL adjustment factor for all the sub-traits of the trait group might simplify the genomic reliability calculation steps under this circumstance.

Frequency for Updating the Parameter of Genomic EDC Gain

As stated above, the core parameter of genomic EDC gain is used in the routine genomic reliability calculation (see Guidelines I) and determined via the Interbull GEBV Test (see Guidelines II). Because the derivation of the genomic EDC gain parameter is linked to Interbull GEBV Test, an update of this parameter value needs to be done whenever a new GEBV Test is requested. According to the current validation rules by Interbull, the update will be mandatory when a new national evaluation model is implemented, major changes are introduced to a national evaluation, or a routine validation of every 2 years is called. The same phenotypic, genotypic and pedigree data are used for the derivation of the genomic EDC gain parameter as for the Interbull GEBV Test.

Level of Genomic Reliabilities in Case of an Inflated Prediction

A country or population may pass the Interbull GEBV Test for a given trait, even when an inflation of prediction exits, with a regression slope being evidently but not yet statistically significantly less than 1. A legitimate concern was raised, if the adjusted genomic reliabilities would be too high for this situation, as GEBV variance of the validation bulls in the truncated validation data set appeared to be too high.

With dependent variable being GEBV of a later full single-step evaluation, a linear regression test (Legarra and Reverter 2018) can be applied according to the Interbull GEBV Test (Sullivan 2024):

$$\hat{u}_L = b_0 + b_1 \hat{u}_E + \epsilon \quad [1]$$

where $\hat{u}_L$ and $\hat{u}_E$ represent GEBV of a validation bull from the later full evaluation and the early truncated evaluation, respectively; b_0 and b_1 denote the intercept and slope of the regression line; and ϵ is a residual. Let *r* denote the correlation of two sets of GEBV for the validation bulls. For the simple linear regression model 1, the regression slope and correlation have the following relationship:

$$b_1 = r \sqrt{var(\hat{u}_L)} / \sqrt{var(\hat{u}_E)} \quad [2]$$

and

$$var(\hat{u}_L) = \frac{b_1^2}{r^2} var(\hat{u}_E) \quad [3]$$

According to the Interbull GREL method (Formular 11 in Liu et al. 2017), variance of the difference between the two sets of GEBV of the validation is needed for adjusting the theoretical genomic reliabilities. It can be shown that the variance of GEBV differences is:

$$var(\hat{u}_E - \hat{u}_L) = var(\hat{u}_L) - (2b_1 - 1)var(\hat{u}_E). \quad [4]$$

The Interbull GREL method with an adjustment for genomic reliabilities uses $var(\hat{u}_E - \hat{u}_L)$ but not $var(\hat{u}_L) - var(\hat{u}_E)$. The two variance terms are equal:

$$var(\hat{u}_E - \hat{u}_L) = var(\hat{u}_L) - var(\hat{u}_E) \quad [5]$$

only when $b_1 = 1$ for the case of no over- or underprediction.

In case of an inflated prediction, $b_1 < 1$, we can show that:

$$var(\hat{u}_E - \hat{u}_L) > var(\hat{u}_L) - var(\hat{u}_E) \quad [6]$$

which indicates that the expected average reliability of the early truncated evaluation (Formula 12 in Liu et al. 2017) is lower than the case of $b_1 = 1$.

For the third case of an underprediction $b_1 > 1$, we can see that

$$var(\hat{u}_E - \hat{u}_L) < var(\hat{u}_L) - var(\hat{u}_E) \quad [7]$$

indicating that the expected average reliability of the early truncated evaluation of the validation bulls be higher than the scenario of $b_1 = 1$.

We can draw a conclusion that the genomic reliability adjustment method of the Interbull GREL method does not result in too high genomic reliabilities in case of an inflated prediction.

Future Research Topics

Most countries or populations apply *multi-trait models* for routine conventional or single-step evaluations. However, a simple univariate model with only additive genetic effects is assumed to model the genomic information by the Interbull GREL method (see the two Guidelines in Appendices). Logically, applying the multi-trait model to the genomic part of the Interbull GREL method should be envisioned. By assuming the multi-trait model at all steps of genomic reliability calculation, genomic reliabilities would be more consistent with the multi-trait GEBV of the single-step model.

To ascertain the genomic EDC gain, a SNP BLUP model was assumed ignoring the RPG effect. Ben Zaabza et al. (2020b) extended the *SNP BLUP model with the RPG effect* added and developed a Monte Carlo sampling-based approach. New research will be needed to further improve the computational efficiency of the SNP BLUP model with the RPG effect.

As shown in the two Guidelines (see Appendices I and II), *many steps* are required to be conducted to calculate accurate genomic reliabilities for all animals and particularly for young marketed genomic bulls whose genomic reliabilities must be comparable across

countries. Some of the steps may need to be merged to reduce the complexity of the genomic reliability method. The structure of left-hand-side of mixed model equations of the single-step genomic model may be further explored to make the genomic reliabilities even more accurate.

Conclusions

The Interbull genomic reliability method was further optimized and modified to allow an efficient implementation for routine single-step evaluation with millions of genotyped animals. Several steps of the original genomic reliability method, which required considerable computing time for large, genotyped populations, were no longer required for the routine evaluation. Instead, those steps were taken out only for the purpose of deriving the parameter of genomic EDC gain via Interbull GEBV Test. Therefore, two separate guidelines were developed for the routine single-step evaluation and for the derivation of the core parameter of genomic reliability calculation. The step of adjusting genomic reliabilities via Interbull GEBV Test ensured a realistic level of genomic reliabilities, especially for young, genotyped animals. All countries or evaluation populations are encouraged to apply the Interbull standardized genomic reliability method according to the two Guidelines.

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Appendix I:

Guidelines for Approximating Genomic Reliabilities of the Single-Step Genomic Model

A genomic reliability method (Liu et al., 2017) developed by the Interbull Working Group approximates reliabilities of estimated genomic breeding values (GEBV) for a multi-step or a single-step genomic model. Several modifications and improvements have been made thereafter. This document describes technical details of the calculation of genomic reliabilities (GREL) of the single-step genomic model.

The Interbull GREL method assumes that Interbull member countries applies an accurate method to calculating pedigree-based conventional reliabilities, by ignoring genotype data, for either a single-trait repeatability model (VanRaden and Wiggans, 1991) or a multi-trait animal model (Liu et al. 2004; Tier and Meyer 2004) such as a random regression test-day model for milk production traits or a maternal-effect model for calving traits. Besides animals with own phenotypic records, genotyped animals without own phenotypic records must also be included in the calculation of the conventional reliabilities.

The required data for approximating genomic reliabilities using the Interbull GREL method are:

1) A pedigree file which is used for the single-step genomic evaluation of an evaluated trait or a linear index of evaluated traits. The pedigree file must be sorted from the oldest to the youngest animals (or in the opposite order) and should include both genotyped and ungenotyped animals,
2) An estimate of the heritability (h^2) of the evaluated trait or index of interest,
3) Pedigree-based conventional reliability values of all animals in the pedigree file, including genotyped animals without own phenotypic records, for the evaluated trait or index of the evaluated traits, and
4) Genomic effective daughter contribution (EDC) gain (φ_c) for the evaluated trait or index of the evaluated traits, which was derived by the countries following the Interbull GREL procedure (see Appendix for the *Guidelines for Deriving Genomic Effective Daughter Contribution Gain*).

The technical steps for calculating the final GREL for genotyped and ungenotyped animals are given below:

1. *Propagation of genomic information of the genotyped animals to their non-genotyped relatives*
   In the propagation process the trait-specific constant of the genomic EDC gain φ_c is treated as weight on genotypic data for each of the genotyped animals to approximate genomic reliabilities of their non-genotyped relatives. The propagation involves two steps (VanRaden and Wiggans, 1991; Liu et al. 2004): 1) accumulating progeny contribution by passing the genomic information φ_c of the genotyped animals to their non-genotyped ancestors through the pedigree from the youngest to oldest animals (while skipping genotyped ancestors), and 2) then collecting parental contribution by passing the genomic information from the oldest to youngest animals through the pedigree (while skipping genotyped progeny). Having completed these two steps of propagation through the pedigree, the *i*-th non-genotyped relative receives a reliability value, $\mathfrak{R}_i^{propg}$. According to the concept of genotype confidence (Eding, 2022), $\mathfrak{R}_i^{propg}$ is then multiplied with

$$\mathfrak{R}_c = \frac{\varphi_c}{\varphi_c + \lambda} \qquad [1]$$

   where the variance ratio λ of the animal model is $\lambda = \frac{1-h^2}{h^2}$. Genomic EDC for the *i*-th non-genotyped relative is then converted from its reliability $\mathfrak{R}_i^{propg}\mathfrak{R}_c$ as

$$\varphi_i^{propg} = \lambda \frac{\Re_i^{propg}\Re_c}{1-\Re_i^{propg}\Re_c}. \qquad [2]$$

2. *Combining the genomic reliability gain with the conventional reliability to obtain final genomic reliability value for all animals in the pedigree*
   For a *i*-th animal included in the single-step genomic evaluation, its conventional reliability value $\Re_i^{conv}$ is converted to EDC with:

$$\varphi_i^{conv} = \lambda \frac{\Re_i^{conv}}{1-\Re_i^{conv}} \qquad [3]$$

   If the animal is genotyped, then its total EDC contributed by both the conventional and genomic information is:

$$\varphi_i^{total} = \varphi_i^{conv} + \varphi_c \qquad [4]$$

   Otherwise, a total EDC for the animal without genotype data is:

$$\varphi_i^{total} = \varphi_i^{conv} + \varphi_i^{propg} \qquad [5]$$

   The genomic reliability of the *i*-th animal contributed by phenotypic, pedigree and genomic data is then:

$$\Re_i = \frac{\varphi_i^{total}}{\varphi_i^{total}+\lambda} \qquad [6]$$

It is worth noting that the approximated genomic reliabilities depend on the genomic EDC gain φ_c, which should be derived following the *Guidelines for Deriving Genomic Effective Daughter Contribution Gain* (see Appendix II) and be regularly updated, e.g., when an Interbull member country implements the single-step model or introduces major changes to its national single-step genomic evaluation.

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Appendix II:

Guidelines for Deriving Genomic Effective Daughter Contribution Gain

The Interbull genomic reliability method (Liu et al., 2017) has been optimised to make the genomic reliability calculation feasible for routine single-step genomic evaluations with millions of genotyped animals (see the *Guidelines for Approximating Genomic Reliabilities of the Single-Step Model*). A parameter, called hereafter genomic effective daughter contribution gain (φ_c) and required by the Interbull genomic reliability method, must be derived for every trait evaluated by the Interbull member countries.

Conventional reliability values are assumed to be reasonably accurate using an accurate reliability method for a single-trait model like VanRaden and Wiggans (1991) and a multi-trait model like Liu et al. (2004) or Tier and Meyer (2004).

Genomic breeding values (GEBV) of a single-step evaluation using the full phenotypic, genotypic and pedigree data as well as GEBV of an early single-step evaluation using a sub-set of the phenotypic data are needed. According to VanRaden and O'Connell (2018), following data are required for deriving the genomic EDC gain parameter φ_c:

1) A pedigree file (PED_{full}) that is used for a single-step evaluation using the full phenotypic and genotypic data. This pedigree file should also include genotyped animals without own phenotypic records;
2) An extracted pedigree file containing only genotyped animals and their ancestors (PED_{geno});
3) Heritability value (h^2) of the evaluated trait or a linear index of breeding values of evaluated traits and variance ratio of the animal model $\lambda = \frac{1-h^2}{h^2}$;
4) Conventional reliability values of all animals, including genotyped animals without own phenotypic records;
5) A file containing effective daughter contribution (EDC) of genotyped bulls and/or effective record contribution (ERC) of genotyped cows. When a genotyped cow with phenotypic records and her sire are both genotyped, her sire's EDC must be adjusted for her contribution to avoid a double counting of her own phenotype information. Interbull proposed an adjustment method for EDC of bulls and technical details of the EDC adjustment are given in Interbull (2018);
6) A list of genotyped animals for the single-step evaluation;
7) A file of allele frequencies for all SNP markers used in the genomic evaluation;
8) A SNP genotype file for all the genotyped animals containing ID of the animals and genotype string of all the SNP markers;
9) A list of validation bulls for *Interbull GEBV test* (Mäntysaari et al. 2010); and
10) GEBV of the validation bulls from the single-step evaluation with the full data set and from the early evaluation with the truncated subset of data.

The technical steps for deriving the genomic EDC gain constant φ_c are given below. Steps 1 to 5 must be run for both the full evaluation and the truncated, early evaluation.

1. *Computing reliabilities of direct genomic values (DGV) for all genotyped animals via software snp_blup_rel* (Ben Zaabza et al. 2020)
   A SNP-BLUP model without a residual polygenic effect is assumed for computing reliability values of DGV or genomic breeding value estimates (GEBV = DGV), denoted as $\mathfrak{R}^{DGV}$. The software *snp_blup_rel* reads heritability value of the trait, ERC values of the genotyped cows with own phenotypic data and adjusted EDC values of genotyped bulls with daughters, SNP genotypes of all the genotyped animals, and the corresponding

allele frequencies. Multiple single-traits can be evaluated jointly to reduce the total clock time. Reliabilities of DGV will be calculated for all the genotyped animals, including those without own phenotypic records. As an option, the inverse matrix of left-hand-side of the mixed model equation of the SNP BLUP model may be saved in a file for later use.

2. *Computing reliabilities of conventional EBV for all the genotyped animals*
Ignoring genotype data of the genotyped animals, reliabilities of conventional EBV, denoted as $\mathfrak{R}^{A22}$, need to be approximated using the EDC / ERC of the genotyped bulls / cows and pedigree file for all the genotyped animals. The same genotyped animals with the same EDC or ERC values must be considered as in Step 1 of calculating reliabilities of DGV. In addition, the smaller pedigree for the genotyped animals, PED_{geno}, are used here for faster speed.

3. *Calculating theoretical genomic EDC gain for every genotyped animal*
For a genotyped animal *i*, its theoretical gain in genomic EDC can be calculated by comparing the reliabilities of DGV and conventional EBV:

$$\varphi_i = \lambda\left(\frac{\mathfrak{R}_i^{DGV}}{1-\mathfrak{R}_i^{DGV}} - \frac{\mathfrak{R}_i^{A22}}{1-\mathfrak{R}_i^{A22}}\right). \qquad [1]$$

If $\varphi_i < 0$ for any reason, set $\varphi_i = 0$. For all the genotyped animals, average of their theoretical genomic EDC gain is denoted as $\bar{\varphi}$. [2]

4. *Propagating the genomic information from the genotyped animals to their non-genotyped relatives*
Using the theoretical genomic EDC gain (φ_i) as input data of the genotyped animals, genomic reliabilities of their non-genotyped relatives can be computed by processing the full pedigree file, PED_{full}, containing all animals with or without genotypic data. Firstly, progeny contribution to every animal is accumulated by processing the full pedigree from the youngest to oldest animals, and secondly parental contribution to the animal is collected by processing the full pedigree from the oldest to youngest animals. For a non-genotyped relative *i*, its genomic reliability, $\mathfrak{R}_i^{propg}$, contributed by its genotyped relatives after the two steps, is converted to EDC as:

$$\varphi_i^{propg} = \lambda\,\mathfrak{R}_i^{propg}\bar{\mathfrak{R}}/(1-\mathfrak{R}_i^{propg}\bar{\mathfrak{R}}) \qquad [3]$$

where $\bar{\mathfrak{R}} = \bar{\varphi}/(\bar{\varphi}+\lambda)$.

5. *Combining genomic with conventional reliabilities for all animals*
If animal *i* is genotyped, then its total theoretical EDC, $\varphi_i^{T\_total}$, contributed by conventional and genomic information is calculated:

$$\varphi_i^{T\_total} = \varphi_i^{conv} + \varphi_i \qquad [4]$$

where φ_i^{conv} represents the *i*-th animal's EDC converted from its total, conventional reliability $\mathfrak{R}_i^{conv}$:

$$\varphi_i^{conv} = \lambda\,\mathfrak{R}_i^{conv}/(1-\mathfrak{R}_i^{conv}). \qquad [5]$$

Similarly for a non-genotyped animal, its total theoretical EDC is:

$$\varphi_i^{T\_total} = \varphi_i^{conv} + \varphi_i^{propg}. \qquad [6]$$

A total theoretical genomic reliability is finally calculated by converting the total EDC:

$$\mathfrak{R}_i^{T_{total}} = \varphi_i^{T\_total}/(\varphi_i^{T_{total}} + \lambda) \qquad [7]$$

6. *Deriving an adjustment factor for EDC using validation animals from Interbull GEBV test*
   Based on the same validation bulls used in Interbull GEBV test (Mäntysaari et al. 2010; Sullivan 2024), expected change in genomic reliability is calculated:

$$E(\Delta\Re) = var(\hat{u}_L - \hat{u}_E)/\sigma_u^2 \qquad [8]$$

where $\hat{u}_L$ and $\hat{u}_E$ represent GEBV of the validation bulls from the later evaluation with full data set and the early evaluation with truncated data, respectively; and σ_u^2 is additive genetic variance of the evaluated trait or the linear index of interest. Sire variance estimates provided in routine MACE evaluation by Interbull may be used here as the genetic variance of own country.

Denote average genomic reliability values of the validation bulls from the later full evaluation $\overline{\Re}_L$, which is assumed to be reasonably accurately approximated due to daughter phenotypic information of the validation bulls. Average genomic reliability of the validation bulls in the early, truncated evaluation is expected to be:

$$E(\Re_E) = \overline{\Re}_L - E(\Delta\Re) \qquad [9]$$

The expected average genomic reliability is then converted to EDC:

$$E(\varphi_E) = \lambda\ E(\Re_E)/(1 - E(\Re_E)) \qquad [10]$$

Let $\Re_{i\_E}^{T\_total}$ represent the theoretical genomic reliability of validation bull *i* from the early, truncated evaluation using Equation [7], the average of the theoretical EDC for all the validation bulls is then:

$$\bar{\varphi}_E = \frac{1}{n}\lambda\sum_1^n\left(\frac{\Re_{i\_E}^{T\_total}}{1-\Re_{i\_E}^{T\_total}}\right) \qquad [11]$$

where *n* is the number of validation bulls.

A ratio of the expected and theoretical EDC values is defined as an adjustment factor:

$$f = E(\varphi_E)/\bar{\varphi}_E \qquad [12]$$

The EDC adjustment factor $f < 1$ or $f > 1$ indicates an overestimation or underestimation of genomic reliabilities from the early evaluation, respectively.

7. *Repeating Step 3 of calculating genomic EDC gain for all the genotyped animals*
   For the genotyped animal *i*, its *adjusted* gain in genomic EDC can be calculated using their DGV and EBV reliabilities and the adjustment factor *f* :

$$\varphi_i^{adj} = \lambda\left(\frac{\Re_i^{DGV}}{1-\Re_i^{DGV}} * f\ - \frac{\Re_i^{A22}}{1-\Re_i^{A22}}\right). \qquad [13]$$

Average of the *adjusted* genomic EDC gain for the validation bulls can be used for genomic reliability calculation in routine single-step evaluation (see *Guidelines for Approximating Genomic Reliabilities of the Single-Step Model*):

$$\varphi_c = \frac{1}{n}\sum_1^n \varphi_i^{adj}. \qquad [14]$$

The Interbull genomic reliability method is linked to the new Interbull GEBV test (Sullivan 2024), i.e. countries need to develop a new adjustment factor for genomic EDC using Formula [8]. Every time a country is required to conduct a GEBV test for a particular trait, this country is automatically also required to perform the genomic reliability validation by deriving a new genomic EDC gain parameter for this trait.

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