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A technical document on derivation and application of adjustment factor for genomic reliability values

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Theoretical genomic reliabilities depend on model assumptions of conventional or genomic models, they tend to be higher than those realized reliabilities which are calculated from validation R^2 values derived from genomic validation with truncated data (Harris et al. 2015a and 2015b). Therefore, those theoretical model genomic reliabilities must be adjusted to the level of the realised ones. An adjustment procedure for genomic reliability values (Liu et al. 2017) has been developed using genomic validation results following Interbull's *GEBV Test* (Mäntysaari et al. 2010).

Derivation of adjustment factor for genomic reliabilities

According to the *GEBV Test* (Mäntysaari et al. 2010), two sets of GEBV are available for validation bulls: u_L for a later, complete genomic evaluation with daughters' phenotypes included, u_E for an early, truncated genomic evaluation with no daughters available yet. We can derive an expected change in genomic reliabilities based on the two sets of GEBV of the validation bulls:

$$E(\Delta\Re) = \mathrm{var}(\hat{u}_L - \hat{u}_E)/\sigma_u^2 . \qquad [1]$$

Let us define average genomic reliability of the validation bulls from the later, complete evaluation as $\overline{\Re}_L$, then genomic reliability of the early evaluation for the validation population is expected, on average, to be:

$$E(\Re_E) = \overline{\Re}_L - E(\Delta\Re) . \qquad [2]$$

Denote $\Re_{E\_i}$ as a model genomic reliability of the early, truncated evaluation for a validation bull *i*, we convert the early genomic reliability to EDC for all the validation bulls to obtain an average of the EDC:

$$\overline{\varphi}_E = \frac{1}{n}\lambda \sum_{i=1}^{n} \Re_{E\_i}/(1-\Re_{E\_i}) \qquad [3]$$

where *n* is the number of validation bulls. The expected genomic reliability from the early evaluation $E(\Re_E)$ is converted to EDC:

$$E(\varphi_E) = \lambda\ E(\Re_E)/(1 - E(\Re_E)) . \qquad [4]$$

Using the two EDC values we can derive an adjustment factor for converting the theoretical model to realized genomic EDC:

$$f = E(\varphi_E)/\overline{\varphi}_E . \qquad [5]$$

The genomic EDC adjustment factor $f < 1$ or $f > 1$ indicates an overestimation or underestimation of the early genomic EDC/reliabilities, respectively. This multiplicative adjustment procedure affects not only average but also variance of the final, realized genomic reliability values.

In fact, this adjustment procedure is applicable to any two genomic evaluations, as long as the GEBV are validated e.g. via Interbull's *GEBV Test* (Mäntysaari et al. 2010).

Application of the adjustment procedure for genomic reliabilities

For approximating genomic reliability values for national evaluation, Interbull has developed a procedure comprising seven steps (Liu et al. 2017). Step 3 of the procedure describes how to adjust theoretical EDC of DGV using the adjustment factor *f*.

For calculating theoretical reliabilities of DGV, two separate formulae were proposed by Liu et al. (2017) for candidates and reference animals ([16] and [17] in Liu et al. (2017)). Furthermore, the DGV reliability formula [17] in Liu et al. (2017) does not result in differentiated reliabilities for reference bulls with higher and reference cows with lower conventional reliability values. Based on the findings of Erbe et al. (2018) and Charfeddine et al. (2018), an unified formula for calculating DGV reliabilities is proposed here for candidates as well as reference animals with varying reliability values:

$$\Re_i^{DGV} = r_{IMP}^2 (1-k)\Re_i^{SNP} + k\Re_i^{dat} \qquad [6]$$

where $\Re_i^{dat}$ represents reliability contributed by own phenotype data of animal *i*. The other variables in Equation [6] were all described in the paper by Liu et al. (2017). For a reference bull with daughters or a reference cow with own phenotype records:

$$\Re_i^{dat} = n_e / (n_e + \lambda) \qquad [7]$$

where n_e is effective daughter contribution (EDC) for the reference bull or effective record contribution (ERC) for the reference cow. Both EDC and ERC are expressed here on an animal model basis, not on a sire model basis, and thus $\lambda = (1-h^2)/h^2$. For genotyped candidates that are not included in the genomic reference population:

$$\Re_i^{dat} = 0 . \qquad [8]$$

Therefore, for the genotyped animals Equation [6] reduces to Equation [16] in the paper by Liu et al. (2017).

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