Improved Validation Tools - Dairy

Introduction

Interbull Centre has developed a set of validation tools to assure that data provided by the national genetic centers (NGEC) are as unbiased as possible and obtained by statistically sound models. The tools available have been developed for conventional EBVs (four different tests available: 3 trend tests and 1 Mendelian Sampling Variance test) as well as genomic breeding values (GEBVs) via the GEBV test.

The ***GEBV test*** will be applied to validate national models used to compute GEBV that NGECs publish and will eventually submit to Interbull for international genetic evaluations including genomic information. The *GEBV test* can also be considered a quality assurance assessment for national genomic evaluations.

During the course of the 2023-2024 EURC working programme, the GEBV test has been reviewed and improved to make it more robust to handle genomic pre-selection variance.

Aim of the **GEBV test** is to evaluates:

1. the unbiasedness of the genomic evaluations through the evaluation of
    1. the consistency of the genetic trend captured by GEBV,
    2. the consistency of bull rankings before versus after having progeny, and
    3. the consistency of the variation of GEBV relative to EBV;
2. the improvement in selection accuracy from the use of GEBV instead of EBV.

A time-oriented cross-validation is used to test how well genomic evaluations of young bull calves, using current models and phenotypic data from 4 years ago, can predict current progeny performance. The NGEC shall re-run their current evaluation software while excluding the most recent 4 years of daughter phenotypes, to obtain reduced-data genetic (EBVr) and genomic (GEBVr) evaluations. The software will then test if the ranking and variance of bull GEBVr match statistical and genetic expectations relative to ranking and variance of the bull comparisons based on current progeny differences, as an indication of unbiasedness. Furthermore, if the GEBVr are more highly correlated than EBVr with the current progeny phenotypes, it is an indication of accuracy improvement with GEBV.

Linear regression models are used for the validation test, where the expected value of regression slopes equals 1 if validation bulls are an unselected group, and a value less than 1 if only a selected subgroup of the most recent proven bulls have been genotyped. The expected slope is lower with selective genotyping due to effects of selection on variances and co-variances used to compute the validation slope. The software will account for effects of selective genotyping on expected slopes, using estimates of selection differential from the differences between average EBV of the genotyped bulls versus all proven bulls born in the period considered for validation testing. Bootstrapping is used for all significance testing, and a combination of statistical and biological limits of tolerance is used by Interbull to assign an overall assessment of pass or fail.

New Methodology

The improved GEBV test is now based on VanRaden's de-regressed GEBV (described in the 2021 Interbull bulletin paper, https://journal.interbull.org/index.php/ib/article/view/82) as the official prediction target. The VanRaden dGEBV replaces the previously used dEBV target described by Mantysaari et al (2010). Predicting later GEBV or dGEBV from earlier GEBV is conceptually easier to understand and to verify than predictions of dEBV. The new tests are also more suitable for validating single-step models, where genomic preselection effects are properly accounted in new input files GEBVf, GEBVr and dGEBV, whereas the previous input file, dEBV, would include genomic preselection bias.

With the implementation of a new validation target, the de-regression method has now been internationally standardized because the dGEBV are derived directly from values based on official publication rules in the same way for all countries.

The software will make sure that full and reduced-data evaluations are on the same genetic base of expression by adjusting the mean and variance of reduced-data evaluations to match the base of expression of full-data evaluations. These adjustments to align the evaluation scales are based on bulls already progeny-proven in the reduced data who have expected changes in evaluations very close or equal to zero, due to either no new progeny or relatively few in the recent data. After aligning the evaluation scales, changes in evaluations for the validation test bulls, who have all their progeny in the recent data, are equivalent to contrasts of evaluation changes for validation bulls relative to previous generations of proven bulls who have expected changes of 0.

Average changes in evaluation between reduced and full data will now have an expectation of 0 for any group of bulls, after the scales are aligned. A new user option to output base-adjusted evaluations from reduced data, for all or selected traits, can also be used to help isolate reasons for detected biases in the evaluations of any traits failing the GEBV test.

Besides the application of the official GEBV test, the software also allows users to choose different validation targets for further internal research.

A Bootstrapping approach has been implemented to replace the previous t-test for bias in validation slopes, addressing technical concerns that the t-test was not valid, because validation bulls are genetically related, and the validation model residuals are correlated.

The overall validation result, which combines results from either a PASS or FAIL across several sub-tests, will present the following value: PASS, hiSE (i.e. high Standard Error) or FAIL. An overall PASS requires a PASS for the different slope tests plus either a PASS or hiSE for the accuracy test. A result of fail for either the combination of different slope tests or the accuracy test causes an overall FAIL. The new reporting of hiSE indicates too little data to conclusively prove PASS or FAIL in some traits and populations.

The improved GEBVtest has been distributed by Interbull Centre as the official genomic validation tool since August 2024.

Next steps

Interbull Centre will focus on improving the current trend test III for conventional validation in order to make it more robust towards detecting genomic pre-selection bias in the conventional evaluation and more flexible to handle a significant reduction in the number or proven bulls as a consequence of genomic selectiom.

References:

Sullivan, P.G. 2023. Updated Interbull software for genomic validation tests. Interbull Bulletin 58, p.7-16.

VanRaden, P.M. 2021. Improved genomic validation including extra regressions. Interbull bulletin 56: 65-69.

Mäntysaari, E., Liu, Z and VanRaden P. 2010. Interbull Validation Test for Genomic Evaluations. Interbull Bulletin 41, p. 17-21.

Definitions:

1. EBV - Estimated Breeding Value (conventional national evaluations of the trait, free of genomic information, which are submitted to Interbull to be used in MACE evaluations)
2. DGV - Direct Estimated Genomic Value (genomic evaluations based on SNP prediction equations)
3. GEBV - Genomically Enhanced Estimated Breeding Value (evaluations that combine EBV and DGV)
4. GREL - Genomic reliability of the bull's GEBV
5. EDC - Effective Daughter Contribution
6. MACE - Multiple Trait Across Country Evaluation
7. PA - Parent Average
8. NGEC - National Genetic Evaluation Centre
9. GEBVf - The national GEBV of current MACE bulls
10. GEBVr - Genomic evaluation including the genotypes, while using the truncated data (only phenotypes up to 4 years prior to the date of analysis) but including in the analysis all animals present in the current official evaluations used as input to MACE
11. dGEBV – de-regressed GEBV