Genomic Reliabilities

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An appropriate definition

The first issue discussed was determining an appropriate definition of reliability in the genomic era. The group generally agreed that any measure of genomic reliability should reflect the predictive ability of the model used in estimating genomic breeding values. In other words, it should reflect the likelihood of such evaluations changing as more information becomes available. Secondly, it should reflect the amount of information used in the computation of the genomic evaluations. Thirdly, it should represent the measure of confidence that farmers can place on genomic evaluations.

An additional point which was raised during the discussion was that reliability should reflect the possible genetic change as a result of selection. This was generally not considered important by the group.

Computational methods

National level

It was generally agreed that if there were no computation restriction, Monte Carlo sampling would be the best method to use for computing genomic reliabilities. However, this is not feasible and it is difficult to apply to real data. Broadly the group agreed on two methods:

Cross validation approach

The advantage of this approach is that it gives estimates of realised reliabilities rather than expected values but it has the disadvantage that only one estimate is available for all bulls.

One option presented by a member of the group was to examine the possibility of cross validation being implemented with the bull in question excluded from the sample. The reduction in reliability could then be used to estimate an individual reliability for the bull. This method may suffer from the problem of small sample size.

Prediction error variance through inverse of the left hand side of the MME

This method is currently applied by a number of countries and tends to result in overestimation of the true reliability. However, in order to avoid an upward bias, it is recommended that some form of adjustment using results from the cross validation should be implemented.

Other approximation methods

As a result of difficulties in inverting the left hand side of the MME as the number of genotyped bulls increases, several have implemented methodologies to approximate PEV (*Lui et al.*, 2010 and Wiggans *et al.*, 2010). It was recommended that such approximations should be validated and countries should ensure that the computation of genomic effective daughter contribution (GEDC) from such reliabilities always give a positive value.

General observation

One member of the group commented that it has generally be observed that inclusion of polygenic effects seems in general to avoid the

problem of overestimation of genomic reliabilities using PEV. This underlines the importance of the infinitesimal model even in the current genomic era.

Computing genomic breeding values (GEBV) and their reliabilities

Countries adopt different methods in combining DGV and parent averages (PA) from traditional evaluations to compute GEBV for bulls . While some countries use PA from sire and dam, others use only the sire pedigree. Recently, Mäntysaari and Strandén (2010) proposed a bi-variate analysis of DGV and traditional EBV to compute GEBV. It was pointed out that the use of sire-dam-PA may result in overestimation of GEBV and reliabilities due to preferential treatment of bull dams.

The group agreed in general that countries should be given the freedom on how combination is implemented.

Accounting for pre-selection

One member of the group wanted to know if any other country apart from France accounts for pre-selection on their evaluations and computation of genomic reliabilities. It was indicated that the joint evaluation by Denmark, Finland and Sweden currently apply the one-step approach and therefore accounts for pre-selection. However, the system is working very close to the upper limit in terms of number of equations it can handle. It was concluded that this is an area that will need more attention as more selective genotyping is implemented.

GMACE

It was agreed that in situation such as Intergenomics, the recommendation for the computation of genomic reliabilities as outlined for national centers should also be applicable at the Interbull Centre. However with simple GMACE, there is still overestimation due to pedigree influence. A method to limit the contribution of the genotyped sons to the reliability of genotyped sires should be examined

Multivariate situation

There was a consensus in the group that methods currently used in computing genomic reliabilities could be extended to accommodate multivariate analysis for genomic evaluations. It was pointed that current work on GMACE base on accumulation of information using the approach of Harris and Johnson (1998) accounts for correlated residuals. The method is similar to that of Meyer and Ties(2004) .

Main conclusions

Estimates of genomic reliability should reflect predictive ability of the model. Cross validation and the use of PEV could be used to estimate genomic reliabilities at the national centers. However estimates from PEV should be adjusted by using results from cross validation . Results from approximation methods should ensure that GEDC computed from genomic reliabilties are positive. Cross validation reliabilties for young bulls must be higher than PA reliabilities. These methods recommended for the national centres are applicable as well to Intergenomics at the Interbull centre . Methods recommended above should be adequate for genomics in multivariate setting except for combined linear and non-linear traits

No recommendation was made on how to combine DGV and PA to compute GEBV and their reliabilities; countries should be free to adopted a method they consider suitable. Current framework for computing reliabiites GMACE acounts for correlated residuals.

References

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