Session 28 Theatre 8

Accuracy of genome-assisted breeding values for German Holstein Friesian bulls

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Linkage disequilibrium (LD) due to historic mutation events affects accuracy of genome-assisted breeding values (GEBVs), persistence of accuracy over generations without further phenotyping, the potential to reduce breeding costs, effective selection intensity and inbreeding. The objective of this study was to analyze how additive-genetic relationships affect accuracy of GEBVs and to estimate accuracy due to LD from historic mutations using real cattle data from 773 German Holstein bulls. These bulls were genotyped for 54K SNPs and daughter yield deviations were available for milk, fat and protein yield of the first and second lactation of their daughters. GEBVs were estimated with Ridge-Regression BLUP (RR-BLUP) which models each SNP with identical prior variance and BayesB which fits only a small number of SNPs in each iteration of the MCMC-algorithm and allows for different prior variances of SNP effects. To analyze the effect of genetic relationships on accuracy and to estimate accuracy due to LD from historic mutations, bulls were assorted to training and validation data sets such that the maximum additive-genetic relationship between bulls in both sets was 0.25, 0.125, and 0.0625. For most traits, accuracy of GEBVs ranged between 0.5 and 0.6 for a relationship of 0.25. Accuracy declined substantially with decreasing additive-genetic relationship between training and validation set, where the amount of decline varied between traits. RR-BLUP tended to have lower accuracies and higher decline than BayesB, where the accuracy of some traits obtained by RR-BLUP was close to zero for a genetic relationship of 0.0625. In conclusion, although standard errors were high, a large part of the accuracy of GEBVs resulted from information other than LD due to historic mutations which is unfavorable for effective selection intensity, inbreeding and persistence of accuracy over generations, meaning that a reduction of performance testing can not be recommended with the statistical methods used in this study.

Session 28 Theatre 9

Multi-trait genomic selection: comparison of methods

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Genomic selection is becoming common practice in animal breeding. It uses genome-wide dense marker maps, to accurately predict the genetic ability of animals, without the need to record phenotypic performance from the animal itself or from close relatives. Therefore, it is particularly beneficial for selection of traits that are difficult or expensive to measure. Without genomic selection, selection depends on predictor traits in multi-trait breeding value estimation. To get the benefit of recording of predictor traits in genomic selection, our objective is to develop a multi-trait genomic selection method. Four different multi-trait models are considered: 1) a model with a traditional pedigree based relationship matrix, 2) a model where the traditional pedigree based relationship matrix is replaced by a genomic relationship matrix based on markers, 3) a model that both includes polygenic effects related through pedigree information and SNP effects without considering the covariance between traits when estimating the SNP effects, and 4) the same as model 3, with considering the covariance between traits when estimating the SNP effects. The second model assumes equal contribution of each SNP to the total additive genetic (co)variance, while model 3 and 4 allow unequal contributions per SNP. Those 4 models will be compared for 2 simulated traits, having a genetic correlation of 0.2, 0.5 or 0.8 between them. Scenarios are included where some animals have phenotypes for one trait, but not for the other.