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Session 01 Theatre 1

The single step: genomic evaluation for all

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Due to complexity of real populations, there is a long tradition in animal breeding to consider all data simultaneously. This has lead to optimal theoretical solutions: the mixed model equations, the (inverse of) the numerator relationship matrix, multiple trait evaluations. In genomic evaluations, not all animals in a population are genotyped. This leads to use of pseudo-data (DYDs), which are uncertain, correlated, and sometimes hard to define. It has been also shown that after implantation of genomic selection, pedigree-based genetic evaluations (and DYD's) will be biased, unless genomic information is included in the estimation. However, this is essentially a missing data problem: genotypes are lost. Missing data problems can be solved by 'imputation' (data augmentation). Use of linkage (disequilibrium) analysis to impute is still very challenging in a general pedigree beyond one or two generations. However, under mild assumptions (no major genes), relationships serve to predict genotypes, and thus a linear model can be implemented by using a modified relationship matrix, H, whose inverse is $H^{-1} = A^{-1} + [0\ 0;\ 0\ G^{-1}-A_{22}^{-1}]$, where G is a genomic relationship matrix. BLUP equations can be used at a low computational cost (number of SNPs x number of individuals). Beyond unexpected – but statistically and genetically sound – features (i.e. negative relationships), main problems of the method are: (1) what is the effect of selection? (2) how to deal with genes of large effect? The effect of selection is akin to drift, increasing overall relationships, changing the genetic base and creating bias. A correction based on Wright's F_{st} removes this bias for pedigree-based selection. As for major genes, more credit can be given in G to SNPs of 'large' effect; or, a hierarchical model can be written to consider all unknowns and a non-linear method for SNPs effects. These remain open questions.

Session 01 Theatre 2

Comparison of different methods to calculate genomic predictions – results from SNP-BLUP, G-BLUP and one-step H-BLUP

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Genomic selection has become an attractive approach to estimate breeding values because it allows breeders to select animals early in life. Several strategies to use genomic data in genomic evaluations have been proposed. The aim of this study was to compare different approaches to predict genomic breeding values. After edits the data consisted of 6145 genotyped Nordic Red breed bulls with 37996 SNP markers. Two different phenotypic data for production and mastitis traits were used in the analyses. First, deregressed proofs (DRP) and variance components were calculated for the milk, protein, fat and mastitis using the estimated breeding values (EBV) from 2005. Genomic breeding values were calculated using different BLUP models: marker SNP-BLUP, genomic breeding value G-BLUP and one-step approach H-BLUP. EBV data from 2010 was used for the validations. Of genotyped bulls, the reference bulls had EBVs in the 2005 and in the 2010 data, and the candidate bulls had index only in the 2010 data. Interbull protocol was used in the comparison of DGV's and model validation. For the candidate bulls, SNP BLUP and G-BLUP gave the same DGV's (e.g. correlation of DGV's between SNP-BLUP and G-BLUP for protein was 0.999) but there was a difference to DGV's from H-BLUP (correlations of SNP-BLUP to G-BLUP and H-BLUP were about 0.96). For all the traits, SNP-BLUP and G-BLUP got the same validation reliabilities R^2, but for H-BLUP they were slightly better. For example for protein, R^2 was 13% higher in H-BLUP than in SNP-BLUP or G-BLUP. Therefore, there seems to be slight advantage of using H-BLUP instead of other genomic evaluation models.

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