Abstract no.: 23556

Abstract title: Efficient computations for single-step genomic evaluation

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Preferred presentation: Theatre

Preferred session: 49: Free communications

Abstract text:

Genomic evaluations by single-step BLUP (ssGBLUP) allow combining genomic and pedigree information. Inclusion of genomic information requires dense matrices of size number of genotyped animals in the coefficient matrix of mixed model equations (MME). Because rest of the coefficient matrix in MME is very sparse, computations due to the dense matrices start to dominate computing time as number of genotyped animals increase. ssGBLUP has two dense inverse matrices for genotyped animals: genomic and pedigree based relationship matrix. We present an approach for solving ssGBLUP where these dense matrices will be replaced by computationally less demanding steps. For the inverse of pedigree relationship matrix of genotyped animals, the matrix is not explicitly build but required computations are made by a matrix equivalent formula. We present three approaches: iteration on pedigree (IOP), iteration in memory (IM), and cholmod (CM). For the inverse of the genomic relationship matrix, the appr oximate method of proven and young (APY) approach through matrix decompositions is formulated. These approaches were tested on a joint Nordic fertility evaluation for Holstein. Genomic data totaled 81,031 genotyped animals including bulls from the Eurogenomics collaboration . The pedigree had 9.73 million animals of which 7.5 million had fertility record. The fertility model had 11 traits. ssGBLUP were solved by preconjugate gradient (PCG) iteration. According to the results, computing time per iteration was 1.04 min. by regular ssGBLUP, 1.44 min. by IOP, 1.22 min by IM, and 1.06 min. by CM. When APY using 10,000 (20,000) animals in the core was used, the computing times were 0.86 (1.00) min. for IOP, 0.57 (0.74) min. for IM, and 0.46 (0.60) min for CM. Thus, ssGBLUP computations can be reduced by using a combination of approximate and direct computing approaches.