

Test-Day single-step genomic evaluation using APY algorithm

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Number of genotyped animals is increasing rapidly in dairy cattle creating computational challenges for genomic evaluation. The APY algorithm for core and young animals is one approach to overcome the computational challenges. We compared the single-step BLUP (ssGBLUP) using APY algorithm and regular ssGBLUP for the joint Nordic Red dairy cattle (RDC) evaluations for milk, protein, and fat using test-day model. We used test-day (TD) data containing ca. 4 million cows with 90 million records. There were 56017 genotyped RDC animals of which 27095 had either records or offspring in the full TD data. We tested different sets of core animals in APY to study how it affects the solutions. For the validation, four latest years of observations were removed from the TD data. The reduced data was used to solve GEBVs and EBVs for all animals in the pedigree and the full data was used to solve current EBVs and GEBVs for testing purpose. Deregressed proofs for 305 d milk, protein and fat yields were used for a posteriori validation. According to the results, the TD ssGBLUP model gives considerably higher validation reliabilities (r^2) than TD model without genomic information, e.g., for milk ssGBLUP r^2 was 0.46 and EBV r^2 was 0.36. No significant differences were found in validation reliability between the regular and APY TD ssGBLUP models. Also the GEBVs from the full TD model were 0.999 the same with the different ssGBLUP. With sufficiently large core group (more than 10000 animals) also correlation between GEBVs for the young animals is over 0.99. Thus, the use of APY algorithm is feasible and can overcome some of the computational problems.