News genomic prediction - NAV routine evaluation
15 December 2011

The latest NAV routine genomic prediction took place as scheduled. NAV carried out genomic prediction for Holstein, RDC and Jersey:

Data used in genomic prediction
Genotypes were extracted from the joint Nordic SNP data base 30th November 2011. Interbull information from December 2011. Nordic phenotypic information used in the genomic prediction was the same as in the 2nd November 2011 routine evaluation.

News in relation to NAV genomic prediction
About 3000 genotyped NRF bulls are included in the RDC reference population. By adding the NRF bulls to the RDC reference population the reliabilities increase by 1-2% and we do see some reranking of animals with genomic information included in EBVs. The correlations between GEBVs for bulls being candidates in both the 2nd November run and 15th December run are between 0.96 and 1.00. The correlations are lowest for traits where we have most information about NRF bulls on NAV scale from Interbull – production traits and mastitis. In practice it means we see some reranking among genotyped animals due to inclusion of the NRF bulls in the reference population.

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