News genomic prediction - NAV routine evaluation
1 September 2015

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 19th August 2015. INTERBULL information from August 2015 and national information from 11th August run were included in the genomic prediction.

News in relation to NAV genomic prediction

NAV has introduced two technical changes to make the routine genomic prediction procedures faster. The changes are introduced in order to prepare for weekly genomic prediction:

- Starting September 1st. Fimpute is also used in RDC instead of the software program Beagle. Beagle is a very time consuming program and cannot be used in weekly genomic prediction. Fimpute is significant faster, and the differences in GEBV predicted from Fimpute or Beagle genotypes are very limited – correlations are over 0.99. The software program Fimpute has routinely been used for imputation in Holstein and Jersey for a long time.
- The solving algorithm used in the genomic prediction program has been changed from the so-called GBLUP to SNP-BLUP. The SNP-BLUP procedure is significant faster. The correlations between GEBVs predicted with SNP BLUP and GBLUP are over 0.999, only exception is temperament, other diseases and calving traits in Jersey, where extra information from genomic information is very limited. For these traits the correlations are 0.95-0.97.

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