News genomic prediction - NAV routine evaluation
3 March 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 18th February 2015. Nordic phenotypic information for the reference population used in the genomic prediction was the same as in the 3rd February 2015 routine evaluation.

News in relation to NAV genomic prediction
Deregressed proofs
NAV has in routine run in the autumn 2014 observed some instability in the DRPs. The problem has been carefully investigated, and the following modifications were introduced for Holstein in February and are introduced in the March run for Jersey and RDC:

- Limitation for outliers with extreme deviations from pedigree index - Bulls deviation from PA > 20 index units set to 20 index units, and cows deviation from PA >15 index units set to 15 index units

The changes have very little impact on the rankings - correlations are about 0.99 between GEBV in February 2015 and March 2015 run.

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