News genomic prediction - NAV routine evaluation
15 March 2012

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 2nd March 2012. Interbull information from December 2011. Nordic phenotypic information used in the genomic prediction was the same as in the 2nd February 2012 routine evaluation.

News in relation to NAV genomic prediction
New genetic parameters are used in the genomic prediction. Until March 2012 estimated genomic variances based on the deregressed proofs have been used. In the 15th March run the same genetic parameters (NAV parameters) as used in the routine run with phenotypic data are used. The correlations between GEBVs from a model with NAV parameters and one with the estimated ones are in general very high. The lowest correlations are found for Jersey for birth and calving traits where the genomic variances have been estimated with the highest standard error.

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