

# Implementation of singlestep for breeding values for Dairy breeds

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## Introduction

*Singlestep is a new method to calculate genomic breeding values. It will gradually replace the current twostep method for all traits with the result of more accurate breeding values. The index for Saved feed is already based on this new type of model and will be followed by type traits in November 2022 and it is in pipeline that more traits will follow the coming years.*

Genetic evaluation is constantly improving due to more knowledge and more computer capacity. In the Nordic countries we have previously used a twostep method for all traits except Saved feed. In the first step traditional breeding values without genomic information are calculated. In the second step these breeding values are combined with genomic information. However, larger computer capacity has made it possible to use the singlestep method where pedigree, phenotypes and genotypes are combined simultaneously. This method has several advantages.

## Higher accuracy – now and in the future

When all information from both genotyped and non-genotyped animals are used simultaneously in the singlestep method it will increase reliability. This is because pedigree, phenotypes, and genotypes will be weighted together in a more optimal way.

The traditional genetic models we are using today as part of the twostep method builds on the assumption that AI bulls and dams of next generation of heifer calves have a genetic level that is equal to parent average. This is not the case after we gradually uses genomic selection more intensive and thereby are able to select the males and females that have got the best genes. The result is that we introduce a bias in our traditional breeding values – a bias that will be even more profound in the future. The bias may have an influence on the genetic trend in the future.

## All information's are used during the AI bull's life

In the present Nordic publication of breeding values for AI bulls, we use all available information, however when a bull gets a high reliability based on own daughters, the genomic information is excluded. When using the singlestep method all information is always used.

## Traits

Singlestep have been used for Saved feed index since 2020.

22 type traits will have singlestep breeding values in Nov2022.

There are calculated a breeding value for each lactation (1.-3.) and a combined breeding value across lactations. Moreover, there is calculated a combined index for Body, Feet&Leg and Udder.

## Model

The model that we use in singlestep evaluation is a singlestep version of a genomic BLUP model (ssGTaBLUP) with partial QP transformation (Quaas and Pollak transformation) and thereby the genetic groups, also called phantom parent groups are included in a computer effective way (Vandenplas, Eding, & Calus, 2021). The pedigree matrix is blended with genomic data.

Inbreeding is included in the model and the genomic relationship matrix is centred and scaled. For type traits a polygenic effect of 30% is used. The allele frequency is unaffected of singlestep and therefor similar to that used for twostep approach. A standard pedigree depth of 3 generations is used.

## Fixed and random effects

The model includes:

- Herd 5-year fixed effect (nh5y1, nh5y2, nh5y3)
- Country month year fixed effect (cmy1, cmy2, cmy3)
- Calving age and 5-year fixed effect (cca1, cca2, cca3)
- Lactation stage week fixed effect (stagew1, stagew2, stagew3)
- Country classifier year (for DNK 2-month) fixed effect (classyr1, classyr2, classyr3)
- Herd year (for DNK half year) random effect (HY1 - HY21)
- Weight of the trait (wrlegs1)
- Residual random effect
- Animal (genetic) random effect

## Genotypes

In the singlestep approach only genotypes from animals born since 2009 are used, since results have shown that use of old genotypes create a bias in the genetic trend.

## Parameters

The parameters used is identical to those used in the twostep approach. The parameters include variance for the random effect of herd year, the genetic variance covariance and the residual variance covariance.

## Weekly and monthly runs

A setup for evaluation for singlestep for monthly and weekly runs have been developed. The monthly and weekly breeding values are calculated based on the SNP solutions from the big evaluations with new phenotypic data.

## Effects on breeding values

We have studied the genetic trend, the correlations and the distribution of differences compared to the current method. Furthermore, we have run a singlestep model on reduced data (removed 4 years of data) and studied the Legarra Reverter regression. Results for all traits are shown in the links in the appendix.

The genetic trend is overall very similar for singlestep and for the official current method both for AI bulls (proven and young) and for females (genotyped and nongenotyped with and without own record).

The correlation by birth year between singlestep breeding value and current official breeding values is overall very high for AI bulls (proven and young) and for females (genotyped and nongenotyped with and without own record). The distribution of differences indicate that few animals have big changed in breeding value when shifting to singlestep, while most animals have very limited changes in breeding value.

The Legarra Reverter regression showed that the b1 value was close to 1 which indicate no bias.

We have also studied for genotyped females getting own record and we found that some cows will increase and some will decrease in breeding value but the overall mean is zero, which we also expect.

The stability of singlestep has been tested by comparing two runs and looked at correlation and distribution of differences, and we found that the singlestep approach is overall stabile between runs. We also checked that bulls overall did not change dramatically in breeding values when going from young to proven bull.

### **Almost no changes for proven AI bulls**

Changes for proven bulls will be minor for all breeds. Ranking within year is almost unchanged, but the trend across years will be a bit steeper. Results shows that the trend will be 1-3 index units larger in the last 7 years depending on breed. This means that around 80% of bulls born since 2010 will change less than 3 index units for udder and only 1-2% of the bulls will change more than 5 index units.

### **Minor changes for unproven AI bulls**

For young unproven AI bulls, there are minor changes. Ranking within year is affected more than for proven bulls and in general, index for udder increases with 1-3 index units compared to twostep evaluation. This means that for RDC and Holstein, 50% of the bulls change less than 3 index units and nearly all other bulls will have indices that are higher (3 or more index units). For all breeds almost no bulls drop more than 2 index units for udder. For Jersey the changes are smaller. Around 60% of the bulls change less than 3 index units for udder and the rest of the bulls will have higher indices (3 or more index units).

### **Almost no changes for non-genotyped females**

For cows and heifers that are not genotyped there are almost no changes for all breeds. Ranking within year is almost unchanged and trend is not affected. This means that around 90% of the animals change less than 3 index units for udder.

### **Minor changes for genotyped females**

For cows and heifers that are genotyped, changes are larger than for non-genotyped females. Ranking within year is affected and in general index for udder increases with 1-2 index units compared to twostep evaluation. This means that 60-80% of the cows and 50-70% of the heifers change less than 3 index units. Most cows and heifers with changes larger than 2 index units have increasing indices for udder, but there are also females that have decreasing indices.

### **Final conclusions**

The singlestep approach fits well with the type traits and the implementation is succeeded in November 2022. Overall the effects on the breeding values are limited and the bias is limited.

Next step will be to develop and implement singlestep approach for more trait groups.

## References

Vandenplas, J., Eding, H., & Calus, M. (March 2021). Technical note: Genetic groups in single-step single nucleotide polymorphism best linear unbiased predictor. *Journal of Dairy Science*, 3, s. 3298-3303.

## Appendix

### Comparison of Singlestep and current evaluation for type traits

Link: [https://projekt.seges.dk/-/media/segesinnovation/maelkeafgiftsfonden/maelkeafgiftsfonden---2022/5514/hd\\_22\\_5514\\_ap1\\_comparison\\_of\\_singlestep\\_and\\_current\\_evaluation\\_for\\_type\\_traits\\_sep.ashx](https://projekt.seges.dk/-/media/segesinnovation/maelkeafgiftsfonden/maelkeafgiftsfonden---2022/5514/hd_22_5514_ap1_comparison_of_singlestep_and_current_evaluation_for_type_traits_sep.ashx)

### Singlestep vs current evaluation for Type traits -with focus on udder

Link: [https://projekt.seges.dk/-/media/segesinnovation/maelkeafgiftsfonden/maelkeafgiftsfonden---2022/5514/hd\\_22\\_5514\\_ap3\\_singlestep\\_type\\_traits\\_presentation\\_19\\_may\\_updated.ashx](https://projekt.seges.dk/-/media/segesinnovation/maelkeafgiftsfonden/maelkeafgiftsfonden---2022/5514/hd_22_5514_ap3_singlestep_type_traits_presentation_19_may_updated.ashx)

### Legarra Reverter regression

Obs page 1-2

Link: [https://projekt.seges.dk/-/media/segesinnovation/maelkeafgiftsfonden/maelkeafgiftsfonden---2022/5514/hd\\_22\\_5514\\_ap1\\_legarra\\_reverter\\_regression\\_v2.ashx](https://projekt.seges.dk/-/media/segesinnovation/maelkeafgiftsfonden/maelkeafgiftsfonden---2022/5514/hd_22_5514_ap1_legarra_reverter_regression_v2.ashx)

### Genotyped females getting a phenotype

Link: [https://projekt.seges.dk/-/media/segesinnovation/maelkeafgiftsfonden/maelkeafgiftsfonden---2022/5514/hd\\_22\\_5514\\_ap1\\_genotyped\\_females\\_getting\\_a\\_phenotype.ashx](https://projekt.seges.dk/-/media/segesinnovation/maelkeafgiftsfonden/maelkeafgiftsfonden---2022/5514/hd_22_5514_ap1_genotyped_females_getting_a_phenotype.ashx)

### Singlestep Type traits - Comparison of May22 and Aug22

Link: [HD\\_22\\_5514\\_AP1\\_Comparison\\_of\\_singlestep\\_May2022\\_and\\_Aug2022.pdf](https://projekt.seges.dk/-/media/segesinnovation/maelkeafgiftsfonden/maelkeafgiftsfonden---2022/5514/hd_22_5514_AP1_Comparison_of_singlestep_May2022_and_Aug2022.pdf)