

## Approximating individual animal reliabilities in single-step genomic model

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Calculation of individual animal reliabilities of genomic breeding values from single-step genomic BLUP (ssGBLUP) requires elements in the inverse of the coefficient matrix of the mixed model equations (MME). The inversion is often computationally unfeasible due to the large size of the MME. We used a simple approximation. Approximate reliabilities for the genotyped animals were computed using weighted SNP-BLUP/GBLUP (wSNP/GBLUP) where the weights were effective record contributions (ERC). The ERC for the genotyped animals were calculated using reversed reliability approximation from an animal model without genomic information. The method was tested with a dataset including about 20,000 genotyped animals from Finnish Red dairy cattle population with 136,593 pedigree animals. Correlation (MSE) between the reliabilities from the correct ssGBLUP and the wSNP/GBLUP was 0.988 (0.0003). The regression coefficient (slope) and intercept of reliabilities from ssGBLUP on wSNP/GBLUP were 0.93 and 0.04, respectively. Correlation between the reliabilities in ssGBLUP and animal model (without genomics) was 0.945. Both the slope and the intercept of the ssGBLUP on the animal model reliability indicated increased reliability due to genomic information. The method can be extended for non-genotyped animals by blending the increased genomic information in animal model. Preliminary results suggest that the wSNP/GBLUP and blending can be used to approximate ssGBLUP reliabilities for all animals even for large data sets.