

An approach to reduce computing time in multi-trait single-step evaluations*L.H. Maugan, T. Tribout and V. Ducrocq**Université Paris-Saclay, INRAE, AgroParisTech, GABI, Allée de Vilvert, 78350 Jouy-en-Josas, France;**laure-helene.maugan@inrae.fr*

Single-Step (SS) evaluations are planned to replace current genetic and genomic evaluations in France. SS evaluations consider all phenotypic and genotypic information available as well as their pedigree. However, multi-trait (MT) SS evaluations can be very time-consuming, in particular due to complex underlying models leading to slow convergence. An alternative solving strategy consists in running univariate SS evaluations first, in order to provide better starting values for GEBV or SNP effects as well as corrected phenotypes for fixed effects and other complicating features. Then a much simpler multi-trait SS evaluation can be envisioned as a second step. Such a strategy was successfully implemented on a Montbéliarde dataset with about 1.6 million animals with performance on a group of 8 correlated type traits. On the one hand, a multi-trait SS was launched to obtain GEBV of animals for each trait with a stringent convergence criterion. On the other hand, a univariate SS evaluation was first run for each trait and after correction for fixed effects, followed by a simplified multi-trait SS evaluation. GEBV obtained were similar to the ones of a conventional run multi-trait SS but with a strong reduction in overall computing time (by a factor of about 4). The strategy was extended to other situations – with missing performances on some traits or accounting for heterogeneous residual variances.

Fitting the mean of genotyped individuals per breed had limited benefit for single-step evaluations*M.N. Aldridge¹, J. Vandenplas¹, J.M. Henshall², P. Duenk¹, R.J. Hawken³ and M.P.L. Calus¹**¹Wageningen University and Research, Animal Breeding and Genomics, P.O. Box 338, 6700 AH Wageningen, the Netherlands, ²Cobb Vantress Inc., Koorstraat 2, 5831 GH Boxmeer, the Netherlands, ³Cobb Vantress Inc., Siloam Springs, AR 72761-1030, USA; michael.aldridge@wur.nl*

Fitting the mean of genotyped individuals as a fixed regression has been shown to increase accuracy and reduce bias in single-step evaluations. The value of the associated covariate (J-factor) for genotyped animals are equal to -1, and ranges between -2 and zero for ungenotyped relatives. To date the mean of genotyped animals has been considered only in purebred populations, but in crossbred evaluations different breeds have different base populations. Our aim was to determine if there is a benefit to fitting a separate J-factor for each breed. To test this, we used data from a three-way crossbred experiment with 150 sires in the purebred sire line and 5,000 crossbred progeny. For two traits (body weight at 7 or 35 days), the data was filtered for different genotyping rates (100, 75, 50 and 25%). The filtering was either random or selective of the top performing phenotypes. The animal models fitted either one J-factor (across all breeds), three J-factors based on the expected breed proportion (50% for the sire line and 25% for each of the dam lines), or three J-factors calculated with the actual breed proportions derived from genotypes. In total 100 validation replicates with five cross validation folds were performed for each combination of J-factors, genotyping rate, and genotyping selection method. Results indicate there is no difference for sire EBVs, accuracy or bias of prediction when using one or three expected breed J-factors. The correlation of EBVs using actual breed J-factors and one J-factor is between 0.87 and 0.91. The accuracy is marginally higher with actual breed contributions ($\pm 1\%$) and there is no consistent pattern for bias. If there is no selective genotyping we recommend one J-factor be fitted. With selective genotyping, particularly at lower genotyping rates, it may be considered to fit multiple J-factors.