

Results & Discussion

Models fitting a pedigree without genetic groups achieved much faster convergence with less iterations, and, obviously, the pedigree BLUP model converged faster than the SNP-BLUP model when fitting the same pedigree. The difference between both pedigree BLUP scenarios is large. The scenario with genetic groups needed 83 minutes more and 2,007 iterations more to get convergence. Similar situations were observed for the three single-step scenarios. The scenario with genetic groups needed 210 minutes more and 2,353 iterations more to get convergence than scenario without genetic groups, while the scenario with metafounders resulted in an intermediate number of iterations and thus the elapsed time (Table 8).

Table 8: Time and iteration per scenario

Scenario	Wall clock time (min)	Number of iterations
Pedigree BLUP without genetic groups	55	273
Pedigree BLUP with genetic groups	137	2280
ssRRTDM SNP-BLUP without genetic groups	154	949
ssRRTDM SNP-BLUP with genetic groups	372	3302
ssRRTDM SNP-BLUP with metafounders	283	2496

Conclusions

The use of alternatives to missing parents in the form of genetic groups or metafounders markedly improves the validation results. Particular improvements are seen in the single-step random regression SNP-BLUP test-day model, where the use of genetic groups first and then metafounders improved the b_1 , yielded a model with the higher R^2 , and achieved higher correlation between GEBVS obtained from the whole and truncated datasets of validation bulls. The reason for this improvement may be the

large amount of missing pedigree data for individuals born between 2010 and 2019, so the use of genetic groups and metafounders complements the missing information. The downside of using a more sophisticated pedigree architecture is the increased number of iterations and elapsed time until convergence.

References

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