



Differential handling of missing parents in genetic evaluation of dairy cattle using single step test day SNP-BLUP model

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Purpose of the study

- Pedigree impact on validation results
- Differences in time and iteration
- Differences in validation results across scenarios



Model

$$y = Xh + Wf + Vp + Vu + e$$



y – cow's test day fat yield records in the first 3 lactation

h – fixed effects of herd-test-date-parity-milking-frequency

f – fixed lactation curve effects, modeled as regression on DIM using the Wilmink function

p –permanent environmental effects

u –additive genetic effects or breeding values

e –random residuals



Scenarios

- Pedigree BLUP without genetic groups
- Pedigree BLUP with genetic groups
- Single-step SNP BLUP Multiple-Lactation random regression test day model (ssRRTDM) without genetic groups
- ssRRTDM with genetic groups
- ssRRTDM with metafounders



Genetic groups

- Genetic groups created based on country of origin, birth of year and sex

Country	Year of birth	Male	Female
	< 1960	-99	-99
POL	1960-1969	-1	-2
USA/CAN	1960-1969	-3	-4
OTHERS	1960-1969	-5	-6
POL	1970-1979	-7	-8
USA/CAN	1970-1979	-9	-10
OTHERS	1970-1979	-11	-12
POL	1980-1989	-13	-14
USA/CAN	1980-1989	-15	-16
OTHERS	1980-1989	-17	-18
POL	1990-1999	-19	-20
USA/CAN	1990-1999	-21	-22
OTHERS	1990-1999	-23	-24
POL	2000-2009	-25	-26
USA/CAN	2000-2009	-27	-28
OTHERS	2000-2009	-29	-30
POL	2010-2019	-31	-32
USA/CAN	2010-2019	-33	-34
OTHERS	2010-2019	-35	-36
POL	2020-now	-37	-38
USA/CAN	2020-now	-39	-40
OTHERS	2020-now	-41	-42



Materials



	Sex	Number of animals	Number of records	
Phenotype data (fat yield) $h^2=0.29$	Cows	3,701,610	Full data set	63,484,231
			Truncated data set	58,441,242
Genotype data	Cows	113,171	182,143	
	Bulls	68,972		
Pedigree data	Cows	4,418,710	4,513,226	
	Bulls	94,516		

- Polish national evaluation April 2024, without MACE



Results



815 validation bulls:

- sires of cows that were removed for validation
- having more than 20 daughters
- born between 2015-2019



Results

- Pedigree BLUP without genetic groups

Bulls	b_0	b_1	R^2	corr.
1 st lactation	-21.928	0.984	0.420	0.648
2 nd lactation	-26.448	1.045	0.444	0.667
3 rd lactation	-31.238	1.092	0.448	0.670
Total EBV (0.5*1 st , 0.3* 2 nd , 0.2*3 rd)	-8.471	1.030	0.435	0.660

- Pedigree BLUP with genetic groups

Bulls	b_0	b_1	R^2	corr.
1 st lactation	-23.766	0.969	0.473	0.688
2 nd lactation	-29.896	1.024	0.492	0.702
3 rd lactation	-33.439	1.060	0.492	0.701
Total EBV (0.5*1 st , 0.3* 2 nd , 0.2*3 rd)	-9.304	1.009	0.485	0.696



Results

- ssRRTDM without genetic groups

Bulls	b_0	b_1	R^2	corr.
1 st lactation	-30.391	0.818	0.441	0.664
2 nd lactation	-30.428	0.809	0.457	0.676
3 rd lactation	-27.911	0.823	0.467	0.684
Total EBV (0.5*1 st , 0.3* 2 nd , 0.2*3 rd)	-9.990	0.815	0.450	0.67

- ssRRTDM with genetic groups

Bulls	b_0	b_1	R^2	corr.
1 st lactation	-19.690	0.934	0.621	0.788
2 nd lactation	-18.783	0.907	0.613	0.783
3 rd lactation	-16.873	0.907	0.614	0.784
Total EBV (0.5*1 st , 0.3* 2 nd , 0.2*3 rd)	-6.285	0.919	0.617	0.785



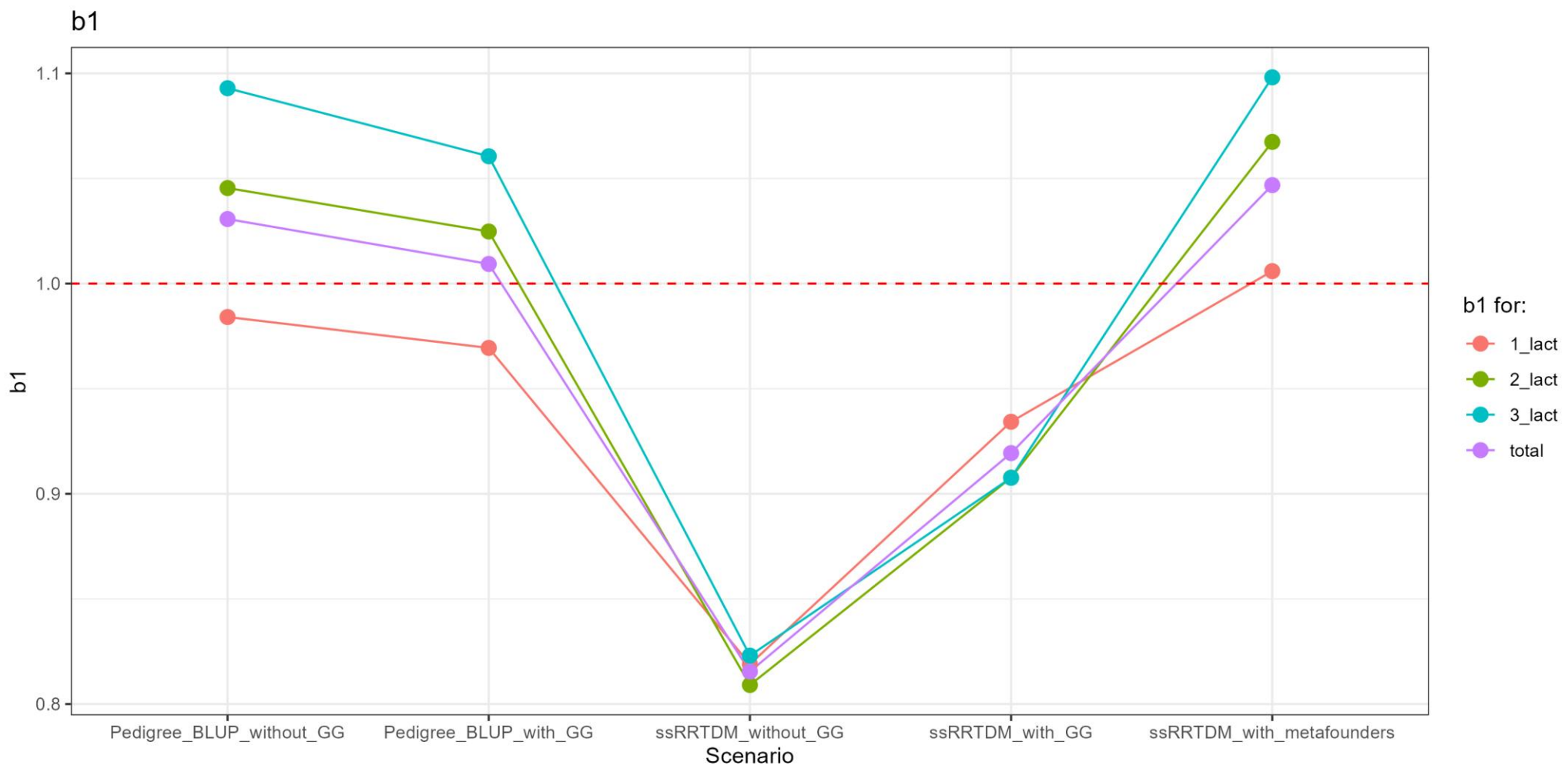
Results

- ssRRTDM with metafounders

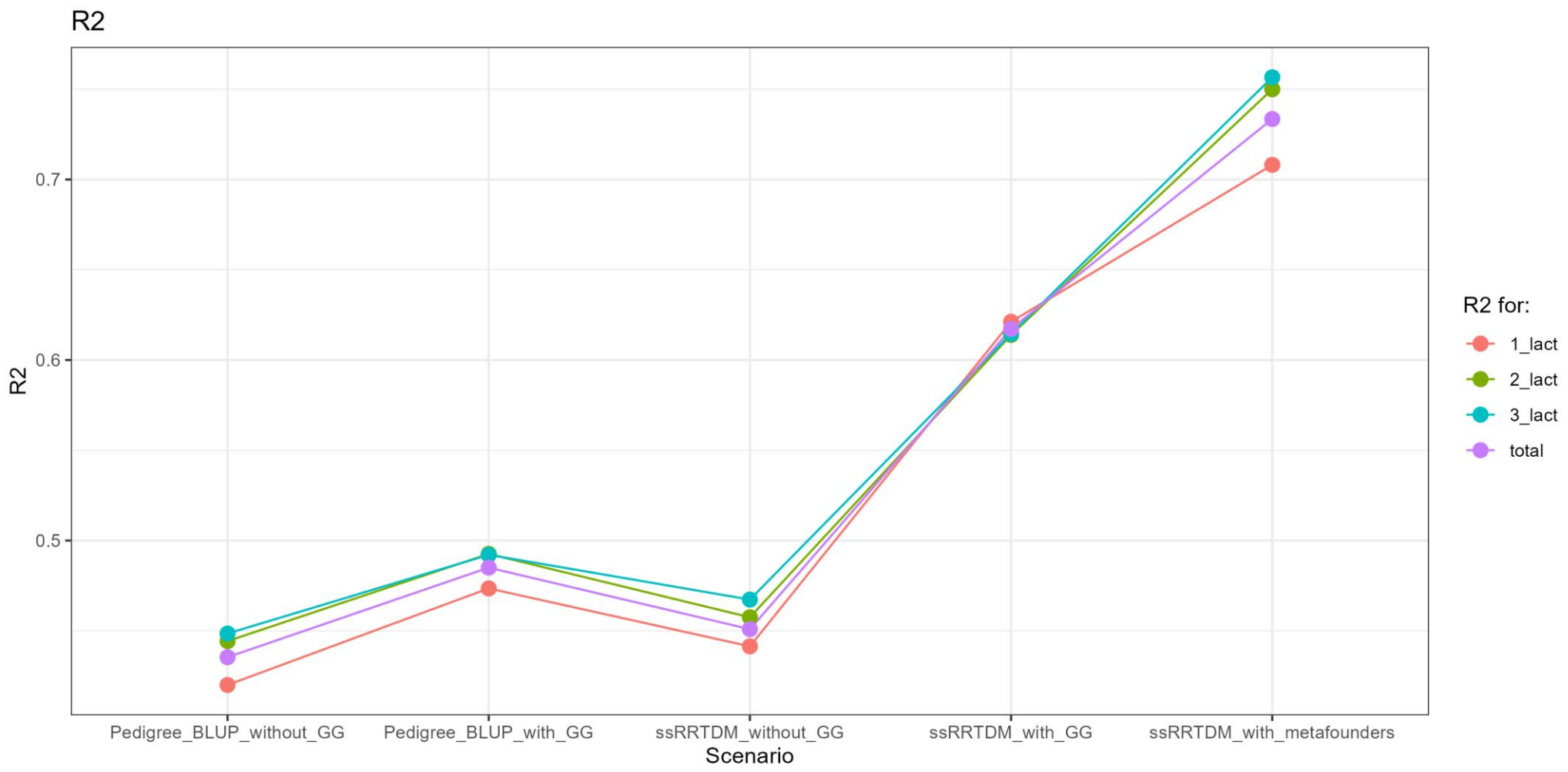
Bulls	b_0	b_1	R^2	corr.
1 st lactation	-19.655	1.005	0.708	0.841
2 nd lactation	-30.137	1.067	0.750	0.866
3 rd lactation	-35.647	1.098	0.756	0.869
Total EBV (0.5*1 st , 0.3* 2 nd , 0.2*3 rd)	-8.774	1.046	0.733	0.856



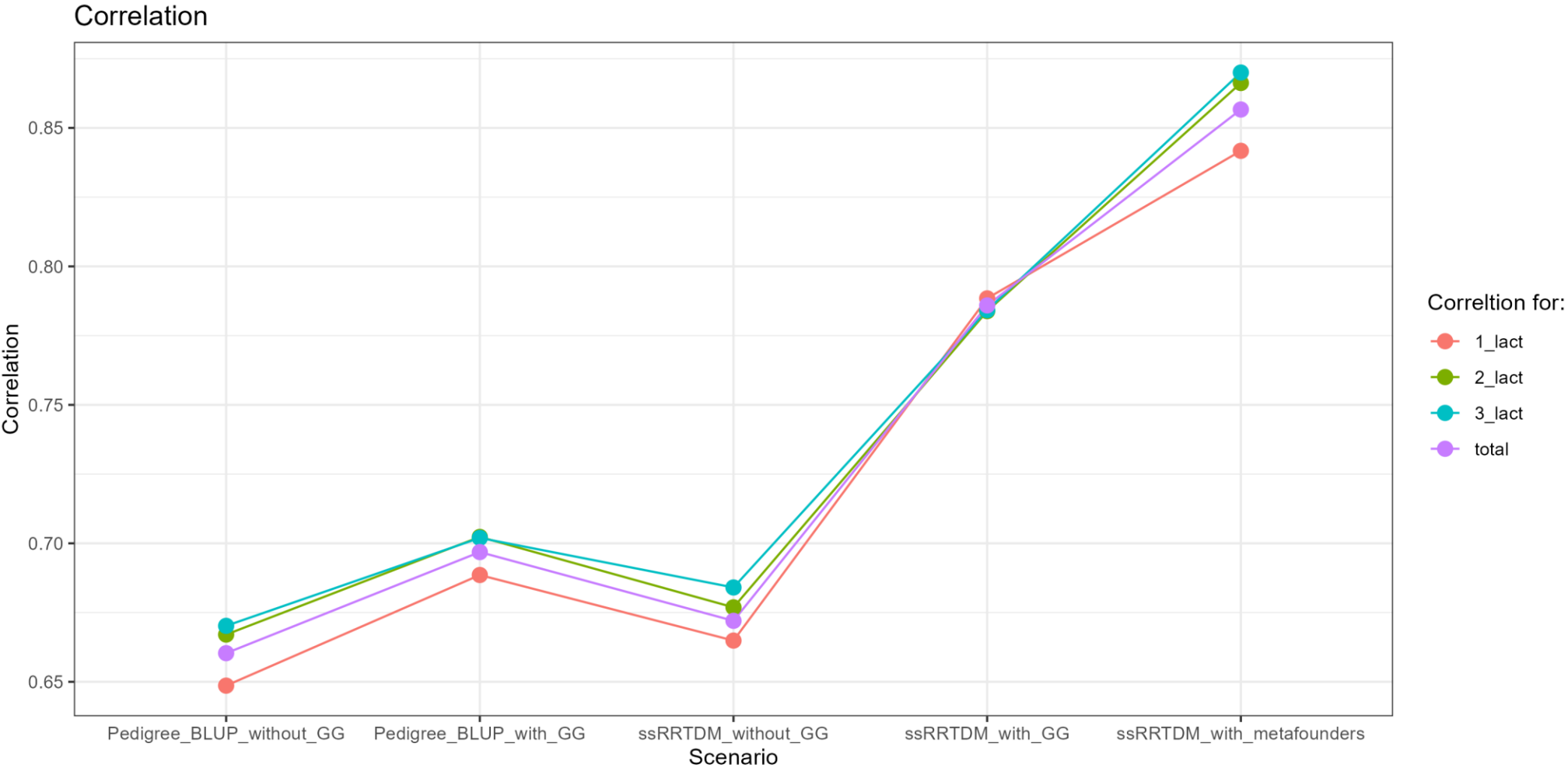
Results



Results



Results



Time and iteration



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

MiXBLUP 3.0



Conclusions

- The use of genetic groups and metafounders improves validation results
- When using genetic groups and metafounders, we observe an increase in correlation between individuals, improvement in R^2 , expected b_1 value
- When using genetic groups and metafounders, the number of iterations increases, and the model runtime extends



Thank You!



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