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INTRODUCTION

- Which accuracy can be reached for genomic predictions in French Charolais beef cattle according to :
 - ▶ markers density (54 K vs 777 K genotypes)
 - ▶ statistical model (GBLUP vs Bayes π) ?
- What is the gain in accuracy when doubling the training set of the reference population?

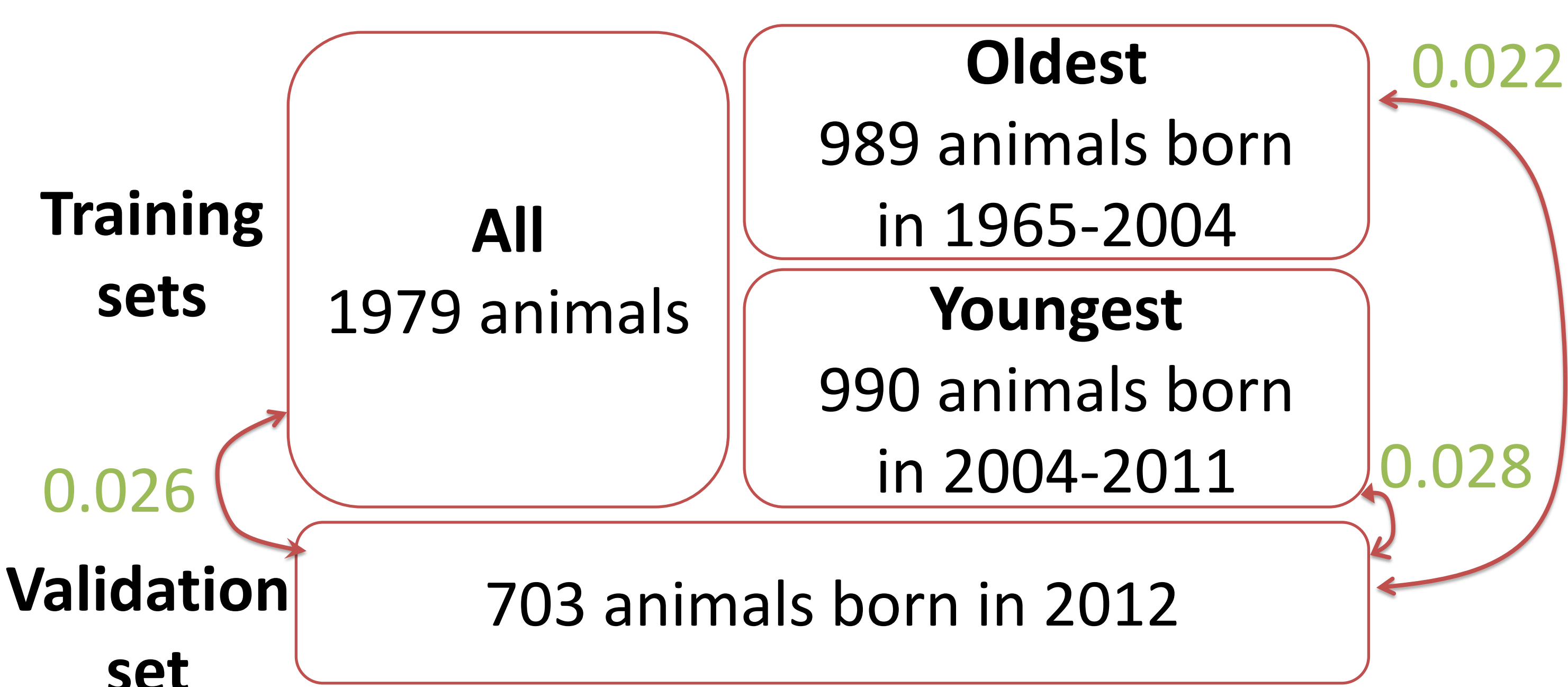
MATERIALS AND METHODS

Data

- 777K genotypes for 664 bulls (Illumina Beadchip)
- 54K genotypes for 2 018 bulls and cows
- 777K imputed genotypes from 54K ones with Beagle
- Estimated Breeding values (EBV) and their accuracies from a BLUP-animal model for birth and weaning traits recorded in French Charolais selection nucleus
=> total number of animals: 2 682

Reference population and tested scenarii

Number of animals *and* average kinship coefficient



- ▶ 3 different training sets:
All animals, 50% Oldest, 50% Youngest

Statistical methods

- Performances : weighted deregressed EBV (DEBV)
- Model : Genomic Values (GV) estimated by GBLUP or Bayes π (GS3 software)
- Accuracy = Correlation (GV, DEBV) / $\sqrt{h^2}$
estimated for the validation population

RESULTS

Accuracy for GBLUP predictions*

Training set	Youngest	Oldest	All animals	
	777 K		54 K	
Birth weight	0.36	0.25	0.33	0.40
Birth condition	0.11	0.21	0.25	0.21
Weaning weight	0.36	0.32	0.42	0.45
Muscular development	0.22	0.17	0.34	0.38
Skeletal development	0.20	0.14	0.26	0.31
Average accuracy	0.25	0.22	0.32	0.35

Accuracy for Bayes π predictions*

Training set	Youngest	Oldest	All animals	
	777 K		54 K	
Birth weight	0.37	0.35	0.42	0.36
Birth condition	0.15	0.32	0.34	0.29
Weaning weight	0.37	0.35	0.45	0.43
Muscular development	0.37	0.41	0.52	0.55
Skeletal development	0.17	0.22	0.27	0.25
Average accuracy	0.28	0.33	0.40	0.37

*Standard-deviation of 0.04 for all traits

CONCLUSION

- Highest accuracy observed for Bayes π with 777K
- Increasing marker density
 - ▶ improves accuracy obtained with Bayes π
 - ▶ decreases accuracy obtained with GBLUP
- Doubling the size of the training set
 - ▶ increases the average accuracy by 20% to 48%

