

Multi-breed multi-trait single-step genomic predictions for Holstein and Jersey including crossbred animals

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Crossbreeding and genomic predictions

Advantages

- Heterosis
 - Breed Complementarity
 - ↓ Inbreeding
 - ↑ Fertility
 - ↑ Longevity
- Reference population difficult to establish
 - SNP and QTL effects may differ across breeds due to differences in:
 - genetic backgrounds
 - LD between QTL-SNPs
 - environment

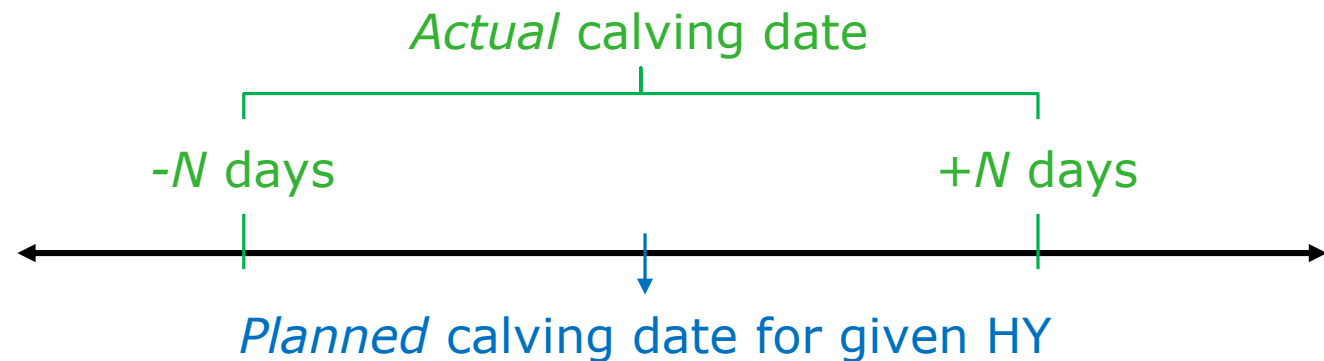
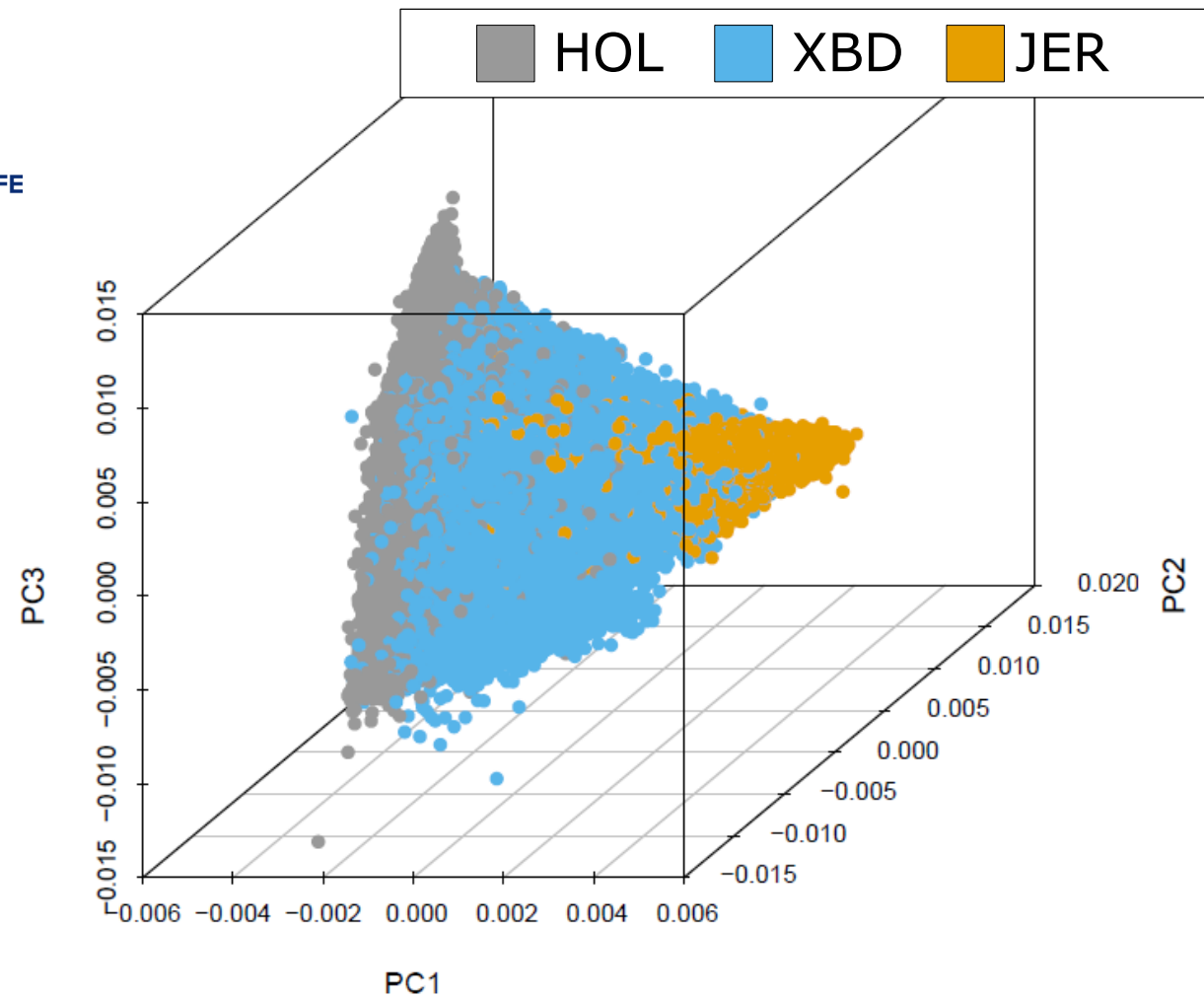
Aim of the study

- Identify the **best** scenario for **multi-breed** single-step evaluations
 - Two purebred populations (PBD)
 - Derived crossbred population (XBD)
- Impact of modelling **missing pedigree information** using genetic groups or meta-founders

Data available



- Pedigree (~1,1 M)
 - Purebred HOL & JER, and XBD
- Genotypes ~127K, 80K SNPs
- Phenotypes
 - Milk yield (~538K) $h^2 = 0.31$
 - CSD (~370K) $h^2 = 0.05$
 - $r_{g \text{ milk, CSD}} = 0.22$



Scenarios

r_g between breeds

- **Single-breed** reference population (**SINGLE_POP**)
 - 3 separate evaluations (with 255 GG)
- **Multi-breed** reference population using :
 - 255 genetic groups : **ALL**
 - 4 genetic groups : **ALL_4GG**
 - 255 metafounders : **ALL_255MF**
 - 4 metafounders : **ALL_4MF**
- **Multi-breed multi-trait** approach (**MBMT**): breeds as traits



Validation

- LR method (Legarra & Reverter, 2018)
- Forward-in-time: whole vs partial dataset
- Cut-off: last 6 years phenotypes removed
- Validation groups, by breed:
 - Cows: with genotyped & phenotype for milk and/or CSD, born after cut-off
 - Bulls: genotyped & ≥ 20 daughters with phenotypes for milk and/or CSD born after cut-off and no daughters with records born before cut-off

Breed	Cows	Bulls
HOL	~ 9K	~ 350
JER	~ 4K	~ 170
XBD	~ 13K	~ 130
<i>Total</i>	~ 27K	~ 650

Software

- GEBVs estimation using ssSNPBLUP
- (pedigree-based) VCE for MTMB scenario: BLUPF90 (gibbs & postgibbs)
- Validation: R functions

MiBLUP



Genetic correlations between traits and breeds

		CSD			Milk		
		HOL	JER	XBD	HOL	JER	XBD
CSD	HOL	0.03 (0.00)					
	JER	0.59 (0.09)	0.04 (0.01)				
	XBD	0.93 (0.03)	0.66 (0.06)	0.03 (0.00)			
Milk	HOL	0.41 (0.05)	-0.02 (0.10)	0.47 (0.05)	0.24 (0.01)		
	JER	0.55 (0.06)	0.24 (0.07)	0.70 (0.06)	0.82 (0.05)	0.27 (0.02)	
	XBD	0.34 (0.04)	-0.03 (0.10)	0.46 (0.04)	0.96 (0.01)	0.87 (0.03)	0.26 (0.01)

Metafounders

- ALL_4MF

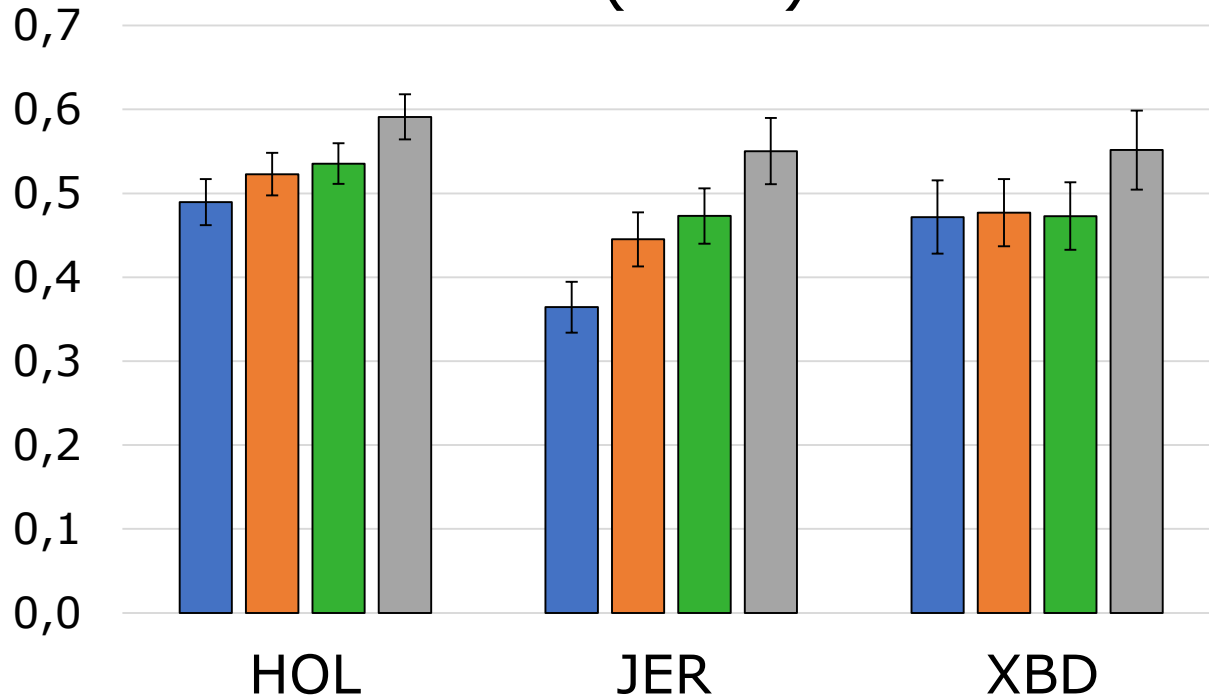
Γ matrix

	HOL	JER	XBD	OTHER
HOL	<i>0.93</i>	0.78	0.83	0.57
JER		<i>0.72</i>	0.75	0.54
XBD			<i>0.78</i>	0.56
OTHER				<i>0.77</i>

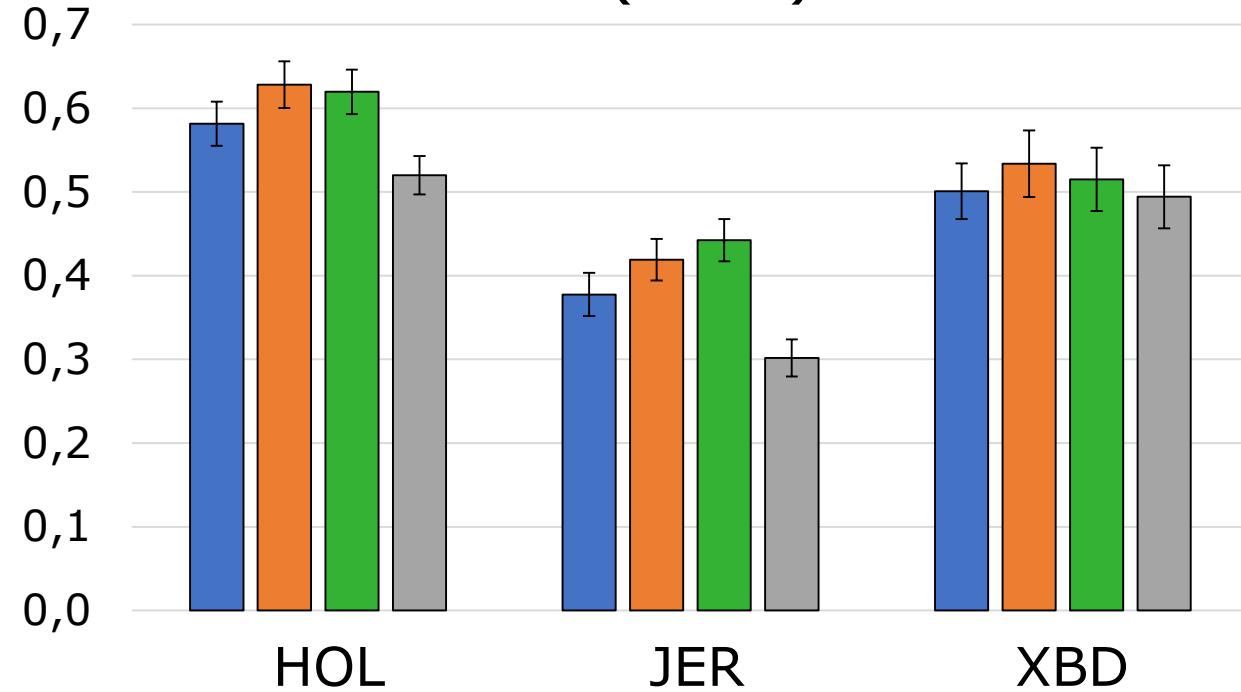
Accuracy partial EBV



Milk (Bulls)



CSD (Bulls)



- **MTMB**: highest accuracy
- **ALL, ALL_4MF**
- **SINGLE_POP**: lowest accuracy

- **ALL, ALL_4MF**: increased accuracy compared to the **SINGLE_POP** (2nd lowest)
- **MTMB**: lowest accuracy

▪ Similar results for cows (smaller SE)

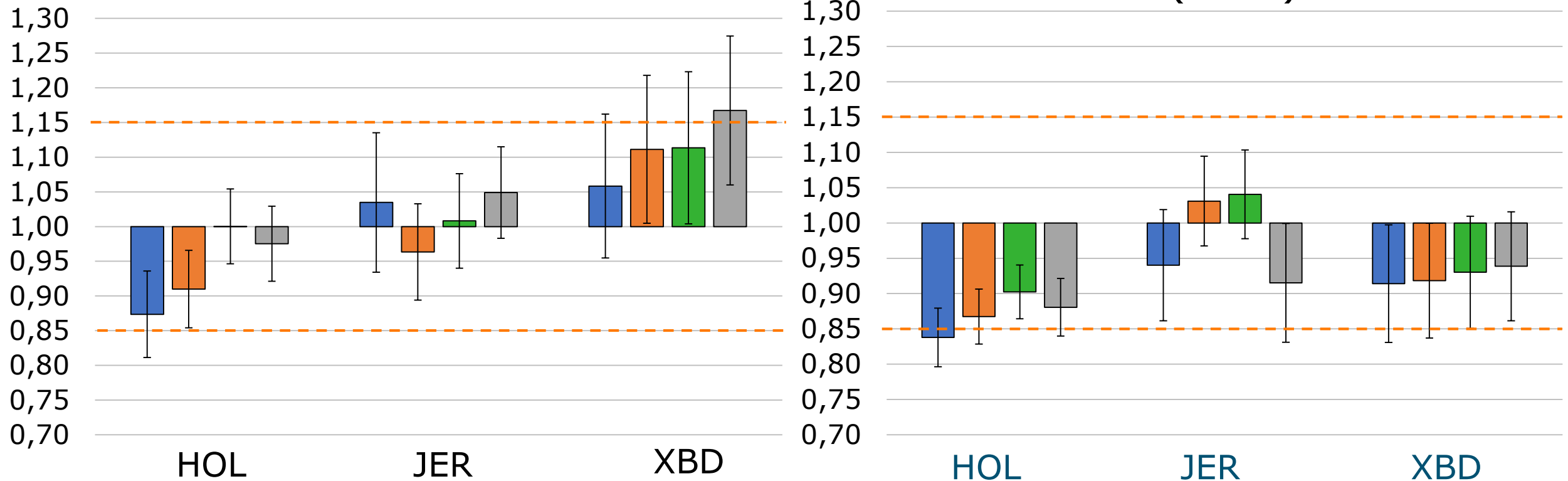
▪ Similar results between: ALL, ALL_255MF, ALL_4GG, ALL_4MF

Dispersion



Milk (Bulls)

CSD (Bulls)



- Overall, **dispersion within ±15%** (except milk-XBD bulls, CSD-HOL bulls)
- Cows have less dispersion and smaller SE
- Milk: both **over/under-dispersion**. CSD: mainly **over-dispersion** (except JER bulls).
- Similar results for **level bias**: overall smaller for Milk (within $\pm 0.05 \sigma_A$) than CSD (within $\pm 0.1 \sigma_A$)

Conclusions

- Benefit of combining data in multi-breed evaluations for PBD and XBD
- Reduce n. GG (similar results with 255 and 4)
- Limited added benefit of using metafounders instead of GG
- MTMB accuracy highest for milk - lowest for CSD
- Further investigations using conformation traits

Acknowledgments



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Thanks for your attention