Application of ssGBLUP using random regression models in the Ayrshire and Jersey breeds

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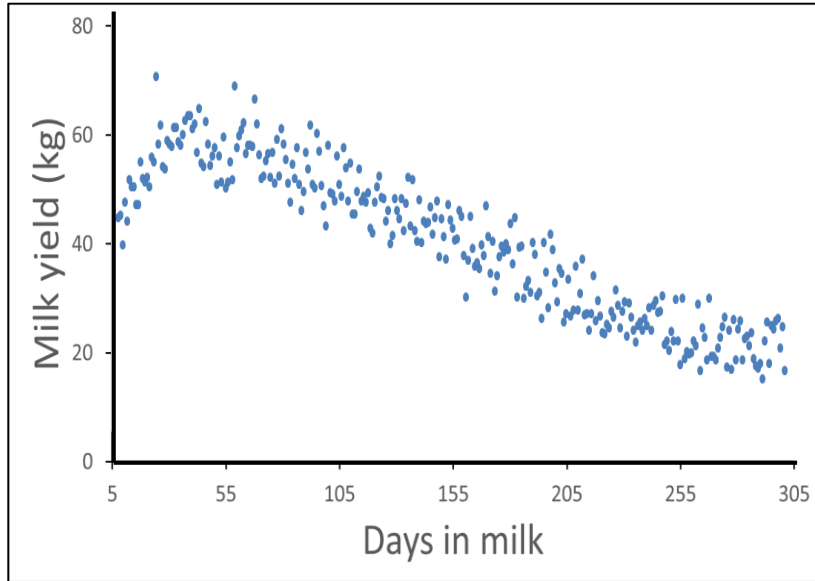[1]Universidade Federal de Viçosa, Brazil; [2]CGIL - University of Guelph, Canada; [3]University of Georgia, USA; [4]Canadian Dairy Network, Canada

Dubrovnik - Croatia

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Introduction

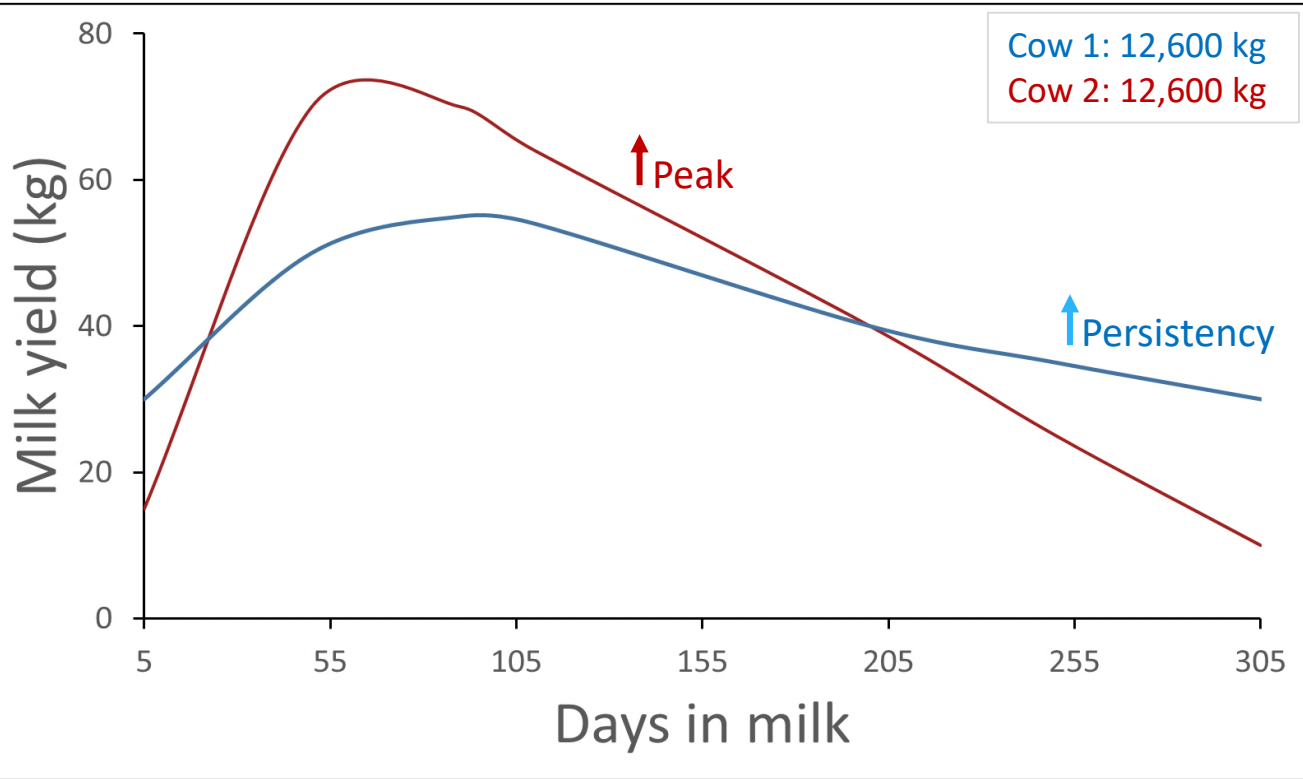## Longitudinal traits and random regression models

ID	DIM	Yield
28673	15	32.5
28673	80	61.0
28673	217	28.8
140782	43	54.3
140782	72	65.4
140782	138	49.7
140782	256	19.2
140782	270	20.1

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wp} + \mathbf{e}$$

Schaeffer and Dekkers (1994),
Schaeffer (2004), Schaeffer (2016)

Introduction

Using random regression models in all steps of multiple-step evaluations does not seem to increase the reliability of genomic predictions

Trait	Ayrshire			Jersey		
	PA	GEBV$_{305}$	GEBV$_{RRM}$	PA	GEBV$_{305}$	GEBV$_{RRM}$
Milk	0.31	0.32	0.30	0.55	0.52	0.46
Fat	0.42	0.41	0.35	0.53	0.48	0.47
Protein	0.41	0.39	0.36	0.59	0.55	0.51

(Oliveira *et al.*, unpublished)

ssGBLUP can lead to more accurate and less biased GEBVs
(Aguilar *et al.*, 2010; Christensen and Lund, 2010)

$$
\begin{bmatrix} \mathbf{X}'\mathbf{X} & \mathbf{X}'\mathbf{Z} \\ \mathbf{Z}'\mathbf{X} & \mathbf{Z}'\mathbf{Z} + \mathbf{H}^{-1}\dfrac{\sigma_e^2}{\sigma_g^2} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{b}} \\ \hat{\mathbf{g}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{y} \\ \mathbf{Z}'\mathbf{y} \end{bmatrix}
$$

$$
\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}
$$

Objectives

1) Investigate the feasibility of applying ssGBLUP to evaluate longitudinal traits using random regression models for the Ayrshire and Jersey breeds
2) Define the most appropriate scaling factors to combine $\mathbf{G}^{-1}$ and $\mathbf{A}_{22}^{-1}$

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & \tau(\alpha\mathbf{G} - \beta\mathbf{A}_{22})^{-1} - \omega\mathbf{A}_{22}^{-1} \end{bmatrix}$$

Material and Methods

	Ayrshire	Jersey
Ped	204,429 animals	157,718 animals
Phen	2,143,941 test-days	1,353,185 test-days
Gen	1,812 animals	1,005 animals
Val	97 bulls	88 bulls
SNPs	38,096 SNPs	34,500 SNPs

Traits:
Milk, fat and protein yield in the first three lactations

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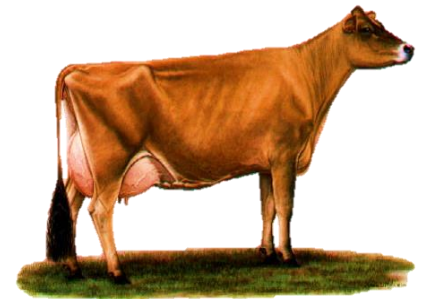
$$y_{ijklr} = HTD_i + \sum_{m=1}^{5}\beta_k z + \sum_{m=1}^{5}\delta_l z + \sum_{m=1}^{5}\alpha_j z + \sum_{m=1}^{5}\rho_j z + e_{ijklr}$$

y_{ijklr} was the phenotype

HTD_i was the fixed herd-test day effect

β_k was the fixed regression for age-parity season of calving

δ_l was the random regression for herd-year of calving

α_j was the random additive genetic regression

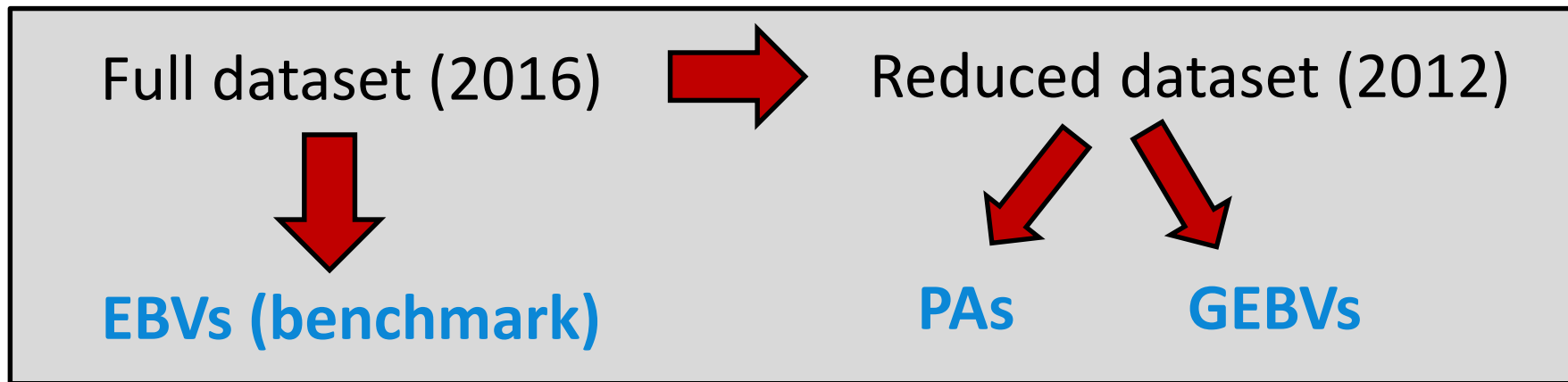ρ_j was the random permanent environmental regression

e_{ijklr} was the residual effect

z were covariates (4th order Legendre polynomials)

To evaluate the reliability and bias of the genomic predictions, a reduced dataset was created from the full dataset

Full dataset (2016) → Reduced dataset (2012)

EBVs (benchmark)   **PAs**   **GEBVs**

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Material and Methods

➢ **BLUP:**

$$\mathrm{E}[\mathbf{y}] = \mathbf{X}\boldsymbol{\beta}$$

$$\mathrm{Var}\begin{bmatrix} \boldsymbol{\delta} \\ \boldsymbol{\alpha} \\ \boldsymbol{\rho} \\ \boldsymbol{e} \end{bmatrix} = \begin{bmatrix} \mathbf{I} \otimes \mathbf{HY}_0 & 0 & 0 & 0 \\ 0 & \mathbf{A} \otimes \mathbf{G}_0 & 0 & 0 \\ 0 & 0 & \mathbf{I} \otimes \mathbf{P}_0 & 0 \\ 0 & 0 & 0 & \mathbf{R} \otimes \mathbf{R}_0 \end{bmatrix}$$

➢ **ssGBLUP:**

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$$\mathrm{Var}\begin{bmatrix} \boldsymbol{\delta} \\ \boldsymbol{\alpha} \\ \boldsymbol{\rho} \\ \boldsymbol{e} \end{bmatrix} = \begin{bmatrix} \mathbf{I} \otimes \mathbf{HY}_0 & 0 & 0 & 0 \\ 0 & \mathbf{H} \otimes \mathbf{G}_0 & 0 & 0 \\ 0 & 0 & \mathbf{I} \otimes \mathbf{P}_0 & 0 \\ 0 & 0 & 0 & \mathbf{R} \otimes \mathbf{R}_0 \end{bmatrix}$$

Material and Methods

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$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & \tau(\mathbf{G} - \mathbf{A}_{22})^{-1} - \omega\mathbf{A}_{22}^{-1} \end{bmatrix}$$

➤ τ = 1.0, 1.5 and 2.0; and ω = 0.6, 0.7, 0.8, 0.9 and 1.0

Validation Reliability and Bias

➤ **Validation reliability:** squared Pearson correlation coefficient

➤ **Scale bias:** regression coefficient estimated using a linear regression

Results and Discussion

Reliability and scale bias in the Ayrshire breed

Lactation	Method	Milk yield	
		Reliability	**Bias**
First	PA	0.32	0.70±0.006
	$\tau_{1.0}\omega_{0.6}$	0.40	0.81±0.006
	$\tau_{1.0}\omega_{1.0}$	0.39	0.64±0.005
	$\tau_{1.5}\omega_{0.6}$	0.40	0.83±0.006
	$\tau_{1.5}\omega_{1.0}$	0.39	0.70±0.005
	$\tau_{2.0}\omega_{0.6}$	0.40	0.85±0.006
	$\tau_{2.0}\omega_{1.0}$	0.39	0.73±0.005

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Results and Discussion

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Results and Discussion

➤ Average reliability for PA and GEBV were:

- 0.42 and 0.46 for the Ayrshire
- 0.44 and 0.57 for the Jersey breed

$$\tau = \omega = 1.0$$

➤ τ and ω had small influence in the validation reliabilities

➤ Less biased regression coefficients were obtained by the ssGBLUP method when compared to PA when τ and ω were used
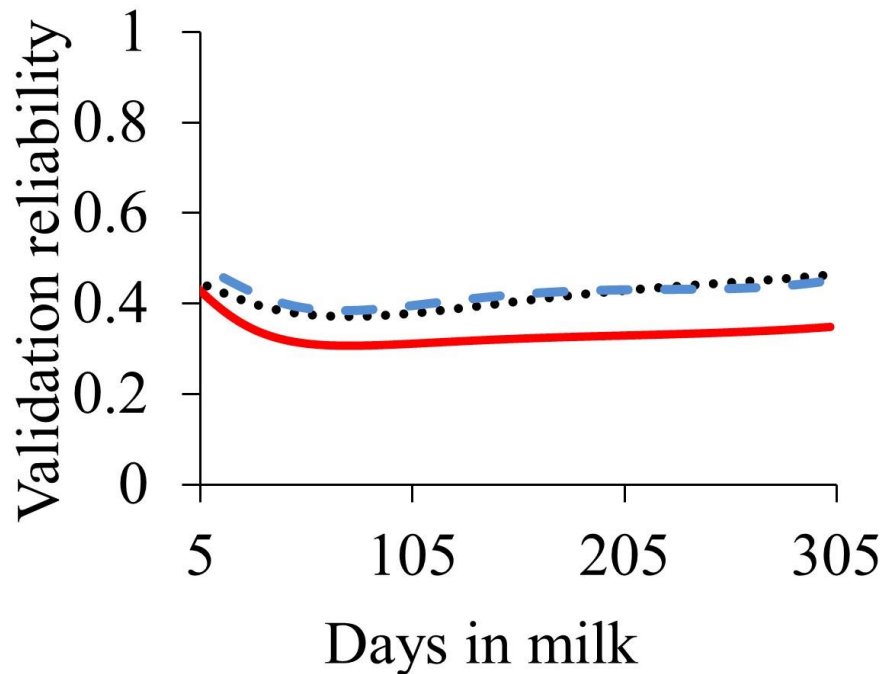
Ayrshire: $\tau = 2.0$ and $\omega = 0.6$
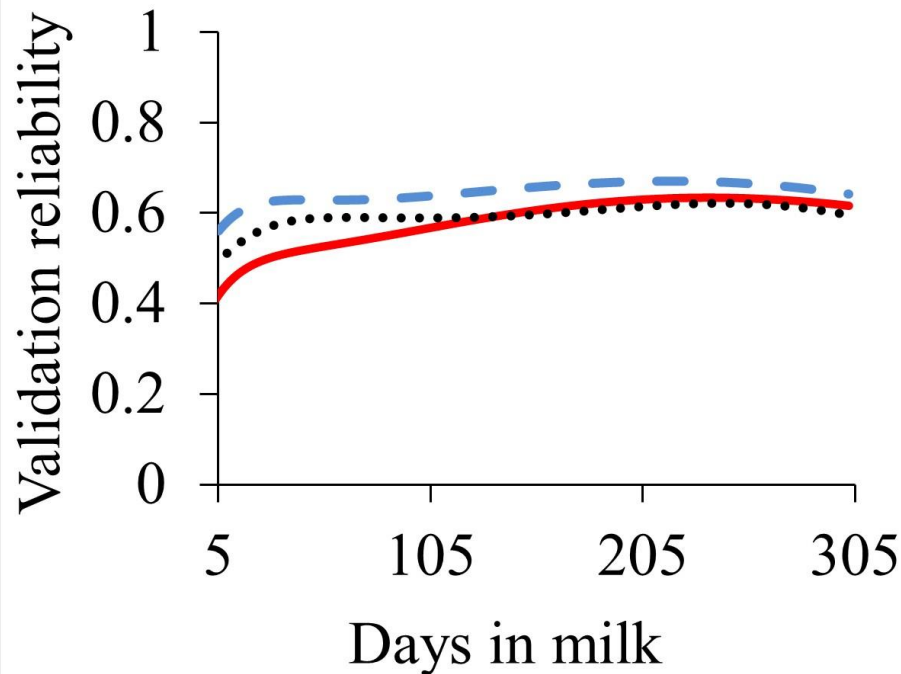**Jersey:** $\tau = 1.5$ and $\omega = 0.9$

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Results and Discussion

Ayrshire

Jersey

Traits: Milk (——), fat (•••), and protein (- -) yields in the first lactation

Conclusions

➢ The use of ssGBLUP based on RRMs is a feasible alternative to implement genomic evaluation for production traits in Ayrshire and Jersey breeds

➢ Scaling factors used to combine $\mathbf{G}^{-1}$ and $\mathbf{A}_{22}^{-1}$ should be carefully chosen

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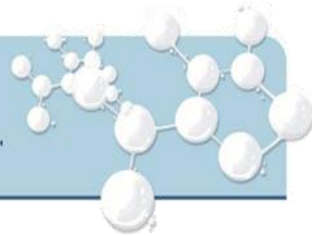EMERGING LEADERS IN THE
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QUESTIONS OR SUGGESTIONS?

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