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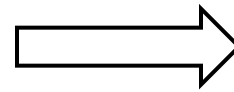
Single-step genomic predictions for yield traits in US Holsteins with UPG and phenotype-pedigree truncation

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A. Cesarani, Y. Masuda, S. Tsuruta, E. Nicolazzi, P. VanRaden, and I. Misztal

Motivation

- Missing pedigree in the US Holstein data
 - ~ 10% sires
 - ~ 20% dams



Biased EBV

- QP-transformation for \mathbf{A}^{-1}

- (Quaas & Pollack, 1981; Westell et al., 1988)

$$\mathbf{A}^* = \begin{bmatrix} \mathbf{A}^{-1} & -\mathbf{A}^{-1}\mathbf{Q} \\ -\mathbf{Q}'\mathbf{A}^{-1} & \mathbf{Q}'\mathbf{A}^{-1}\mathbf{Q} \end{bmatrix}$$

- QP-transformation for \mathbf{H}^{-1} (Misztal et al., 2013)

- Altered QP-transformation for \mathbf{H}^{-1} (Tsuruta et al., 2019)

$$\mathbf{H}^* = \mathbf{A}^* + \begin{bmatrix} 0 & 0 & 0 \\ 0 & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} & -(-\mathbf{A}_{22}^{-1})\mathbf{Q}_2 \\ 0 & -\mathbf{Q}'_2(-\mathbf{A}_{22}^{-1}) & \mathbf{Q}'_2(-\mathbf{A}_{22}^{-1})\mathbf{Q}_2 \end{bmatrix}$$

$$\mathbf{H}^* = \mathbf{A}^* + \begin{bmatrix} 0 & 0 & 0 \\ 0 & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} & -(\mathbf{G}^{-1} - \mathbf{A}_{22}^{-1})\mathbf{Q}_2 \\ 0 & -\mathbf{Q}'_2(\mathbf{G}^{-1} - \mathbf{A}_{22}^{-1}) & \mathbf{Q}'_2(\mathbf{G}^{-1} - \mathbf{A}_{22}^{-1})\mathbf{Q}_2 \end{bmatrix}$$

Motivation

- Matilainen et al. (2016): female fertility traits in Nordic Reds
- Tsuruta et al. (2019): type traits in US Holsteins
- Masuda et al. 2018 (Protein)

Data	UPG	R2	b1
Truncated 2011	Pedigree	0.52	0.78
	Ped. + Genomic	0.32	0.51
	No UPGs	0.50	0.78



UPG poorly estimated
Large number of genotyped
females with missing
pedigree and no phenotypes

- Lourenco et al. (2014): pedigree truncation helped to reduce bias
- due to missingness

Objectives

- Assess bias and reliability of GEBV for bulls and cows in ssGBLUP
 - Milk, Fat, and Protein
 - UPG for \mathbf{A}^{-1} (SS_UPG)
 - UPG for \mathbf{A}^{-1} and \mathbf{A}_{22}^{-1} (SS_UPG2)
- Six phenotype-pedigree truncation scenarios
 - 1980, 1990, or 2000
 - Pedigree depth 2 or 3
- Feasibility of ssGBLUP for dairy evaluations in the US

- US Holstein data up to December 2018

Phenotype cut-off scenario	Records		Genotypes	Animals in pedigree	
	N	Cows		Depth=3	Depth=2
Pheno1980	77.8 M	31.5 M	862 K	40.5 M	39.9 M

Analyses

- QP-transformation for \mathbf{A}^{-1} in \mathbf{H}^{-1}

$$\mathbf{H}_{UPG}^* = \mathbf{A}^* + \begin{bmatrix} 0 & 0 & 0 \\ 0 & \mathbf{G}_{APY}^{-1} - \mathbf{A}_{22}^{-1} & 0 \\ 0 & 0 & 0 \end{bmatrix} \quad \Rightarrow \quad \text{SS_UPG}$$

- Altered QP-transformation for \mathbf{H}^{-1} (Tsuruta et al., 2019)

$$\mathbf{H}_{UPG2}^* = \mathbf{A}^* + \begin{bmatrix} 0 & 0 & 0 \\ 0 & \mathbf{G}_{APY}^{-1} - \mathbf{A}_{22}^{-1} & -(-\mathbf{A}_{22}^{-1})\mathbf{Q}_2 \\ 0 & -\mathbf{Q}_2'(-\mathbf{A}_{22}^{-1}) & \mathbf{Q}_2'(-\mathbf{A}_{22}^{-1})\mathbf{Q}_2 \end{bmatrix} \quad \Rightarrow \quad \text{SS_UPG2}$$

- BLUP90IOD2OMP1 for each phenotype-pedigree truncation scenario
 - APY with 15,000 core animals

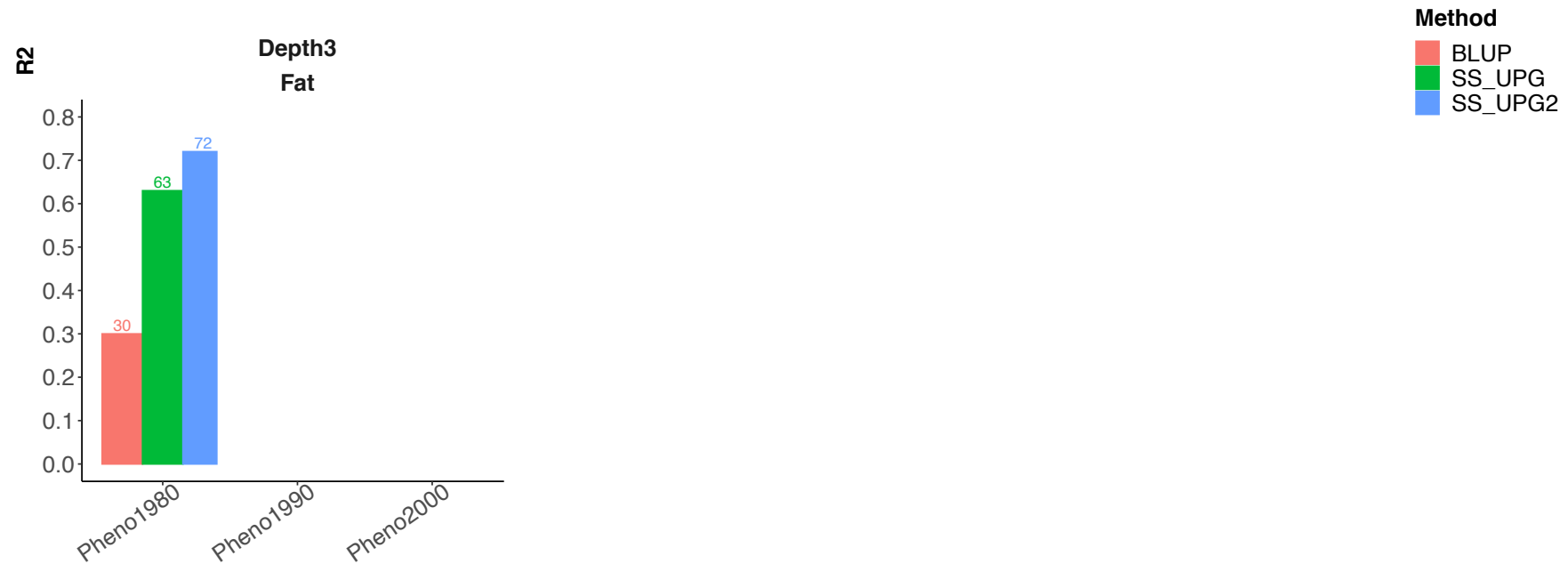
Validation

- Complete data: 2018
- Reduced data: 2014

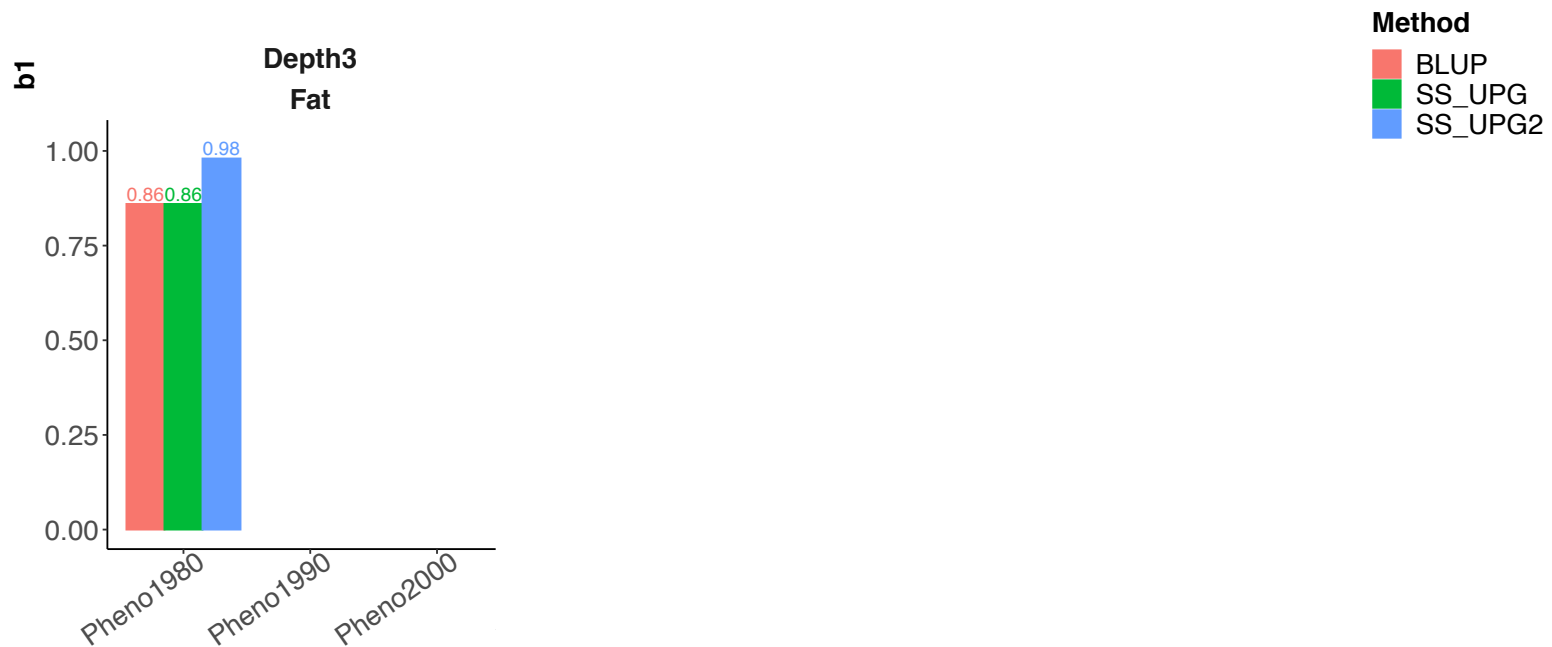
- 2,710 bulls
 - Reliability: $[\text{CORR}(\text{DYD}, (\text{G})\text{EBV})]^2$
 - Dispersion: $\text{DYD} = b_0 + b_1(\text{G})\text{EBV}$

- 381,779 Cows
 - Predictive ability: $\text{CORR}(y_{adj}, (\text{G})\text{EBV})$
 - Dispersion: $y_{adj} = b_0 + b_1(\text{G})\text{EBV}$

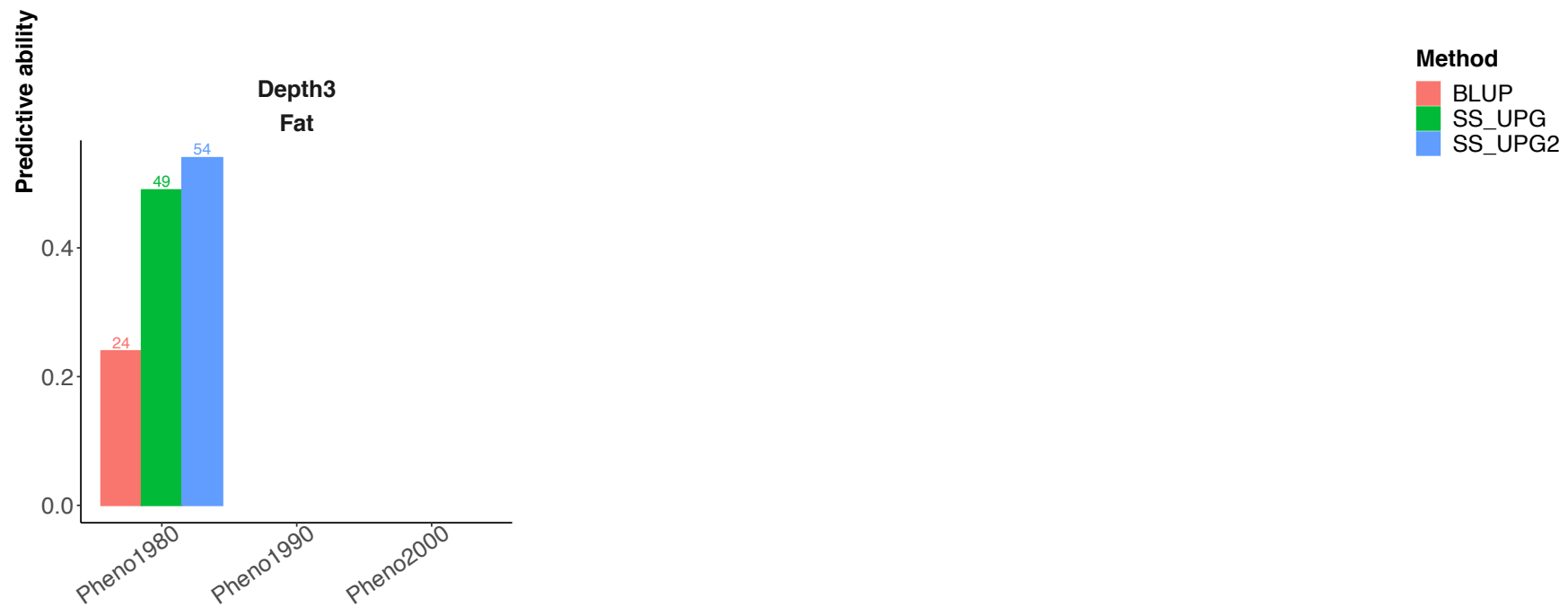
Reliability for bulls



b1 for bulls



Predictive ability for cows

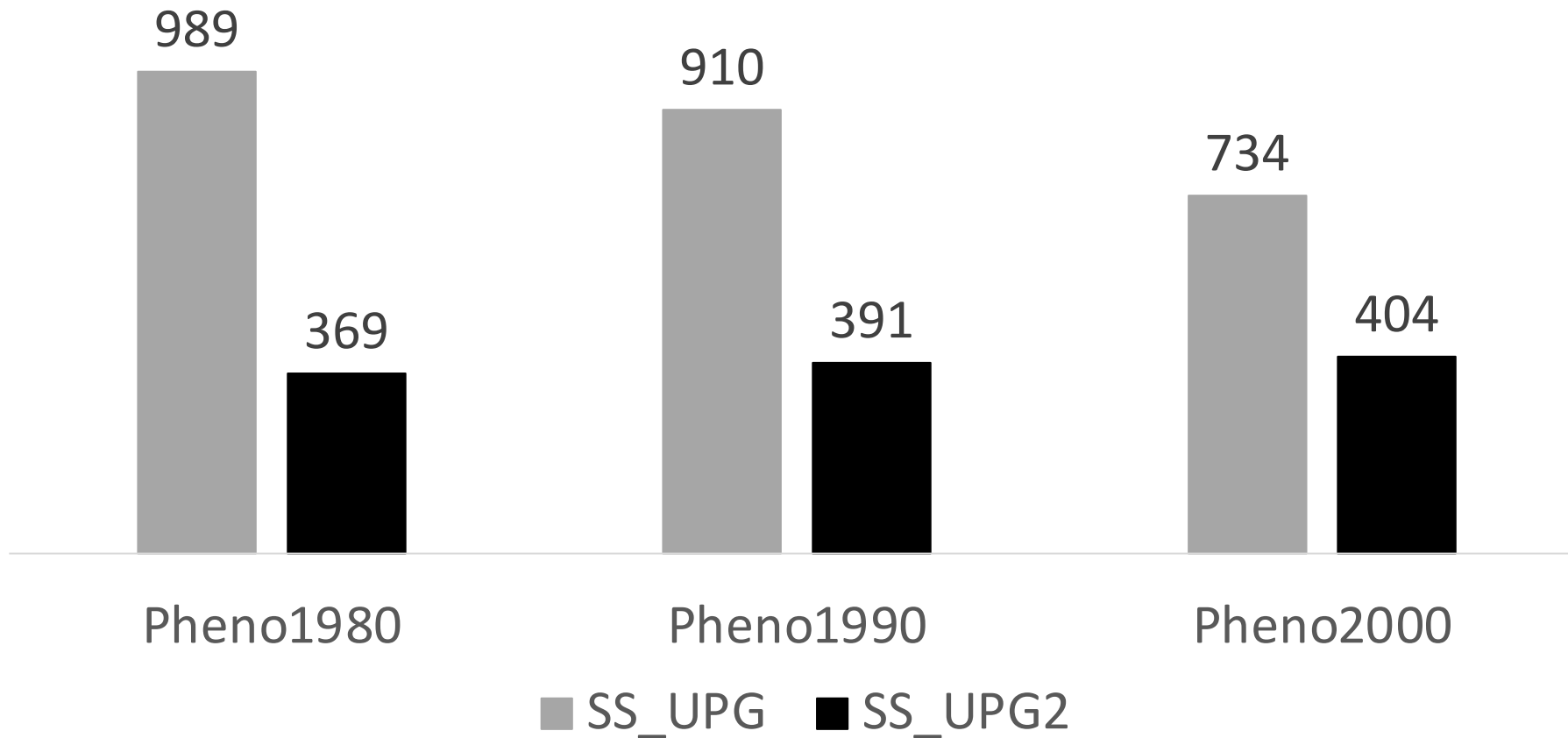


b1 for cows



Rounds to convergence

Pedigree Depth 3



ssGBLUP with many more genotypes

	This study	A. Cesarani (Friday)
Genotypes	862k	3.4M + data
Validation bulls	1,529	1,529
Reliability		
Milk	0.72	0.81
Fat	0.69	0.80
Protein	0.67	0.77

Conclusions

- Genomic predictions for yield traits in US Holsteins using single-step
 - UPG for \mathbf{A}^{-1} and \mathbf{A}_{22}^{-1}
 - Reliable and unbiased
- Removing old generations of pedigree and phenotypes do not compromise predictions for young selection candidates
- Large-scale dairy genomic evaluations are feasible
 - Up to 3.4 Million genotyped animals in less than 3 days
 - Indirect predictions could further reduce computing time

Acknowledgements



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Genomic predictions for yield traits in US Holsteins with unknown parent groups

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