One *Moo-ve* Closer: Single-Step Genomic Predictions for Crossbred Holstein and Jersey Cattle Using Metafounders

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Experience with Single-Step I

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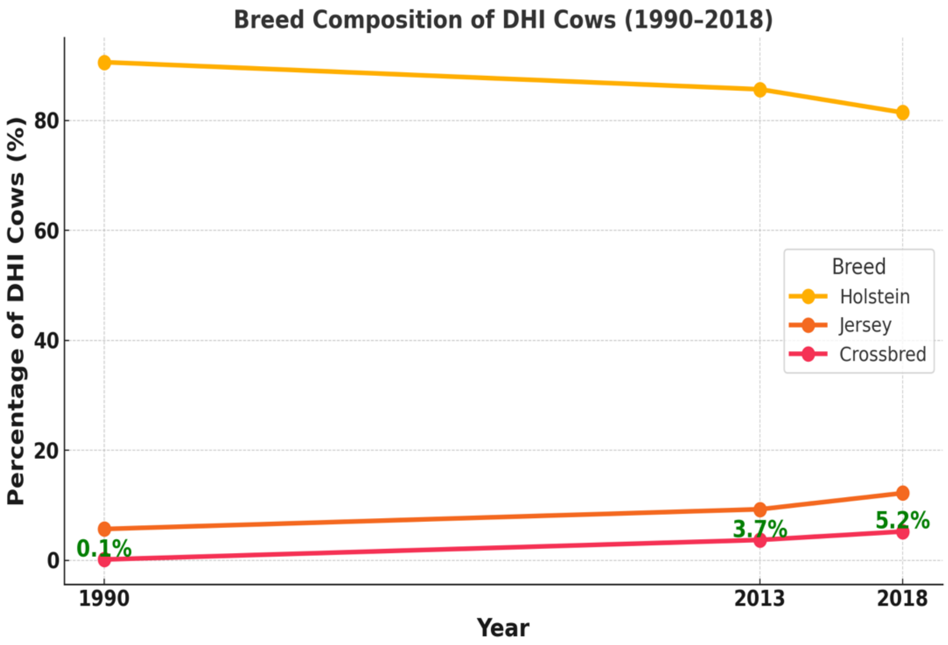
Background

Why Crossbreds Matter

Guinan et al., 2019

- Dairy crossbreds are becoming increasingly popular
- Commercial genomic evaluation is usually separated by breed
- Growing interest in combined purebred and crossbred evaluation



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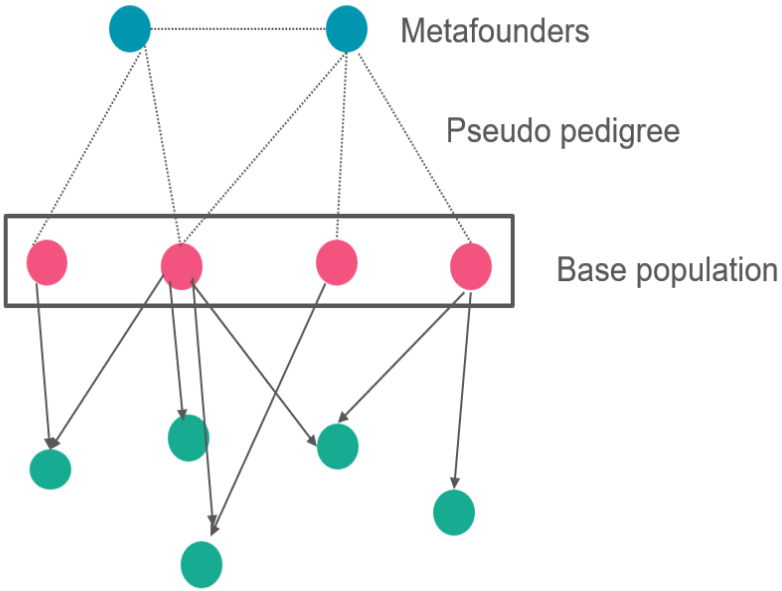
Background

Single-Step Genomic Evaluation

- Joint evaluation of genotyped and ungenotyped animals
- Critical assumption: A and G must refer to the same base population
- **Pedigree missingness:** Biased estimations of breeding values
- **Unknown Parent Groups (UPGs) => Unrelated**



Thompson (1979), Quaas (1988), Kennedy (1991), Legarra et al., (2015)

Aim

Develop and **validate** an ssGBLUP model for a multibreed population composed of Holstein, Jersey, and their crossbreds

This involved the use of metafounders to model genetic differences caused by **breed, sex** and **year of birth**.

Data

Number of Records (2000-2022)

Group	**Phenotypes**		**Genotyped animals**
	N	Cows	**(ssGBLUP only)**
Holstein	20,166,782	7,298,374	1,905,292
Jersey	2,868,461	996,353	181,379
CROSS	701,732	266,259	50,938
Total	23,736,975	8,560,986	2,137,609

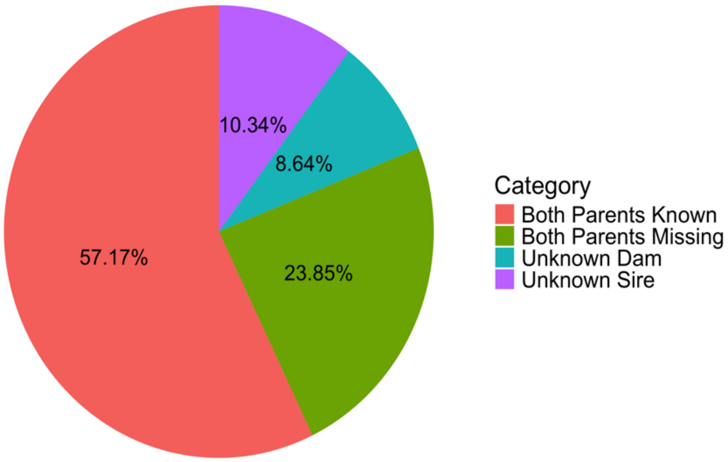
Trait	**h2**
Milk Yield(MY)	0.35
Fat Yield (FY)	0.29
Protein Yield(PY)	0.31
Somatic Cell Count(SCS)	0.13
Daughter Pregnancy rate (DPR)	0.07

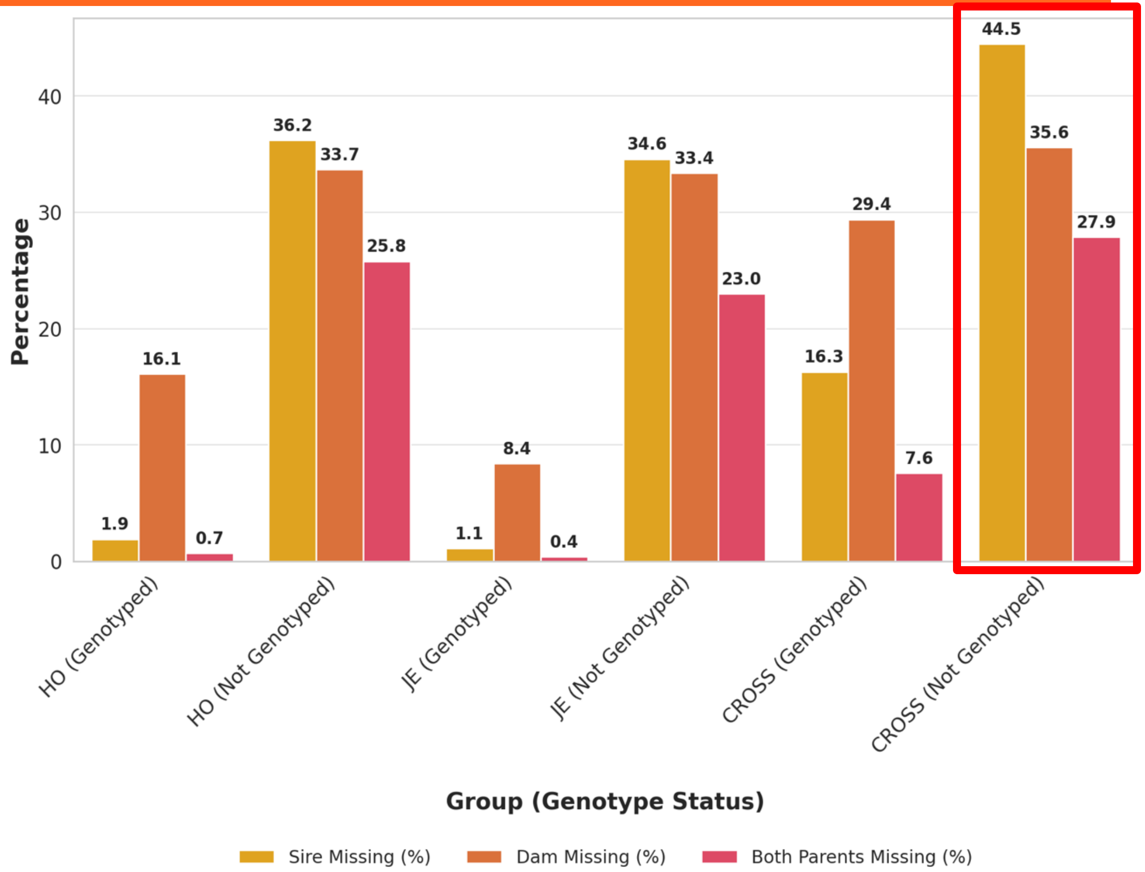
DairyComp 305, PC Dart, and DHI Plus (Vukasinovic et al., 2017)

Data

Pedigree

27 million animals…





Materials and Methods I

Metafounder Definitions

4 Metafounders (Γ4) (ssGLUP_4MF)

- Breed: Holstein (HO), Jersey (JE), Crossbred (CROSS), Unknown

24 Metafounders (Γ24) (ssGLUP_24MF)

- Breed: Holstein (HO), Jersey (JE), Unknown
- Sex
- Year of Birth: ≤2000, 2001–2005, 2006–2010, ≥2011

32 Metafounders (Γ32) (ssGLUP_32MF)

- Breed: Holstein (HO), Jersey (JE), Crossbred (CROSS), Unknown
- Sex
- Year of Birth: ≤2000, 2001–2005, 2006–2010, ≥2011

ssGBLUP_NOMF

Gammaf90 (Aguilar & Misztal, 2008)

Materials and Methods II

Model

A 5-trait repeatability model was applied to:

- a **complete dataset** with phenotypes of cows born from 2000 until 2022
- a **reduced dataset** with phenotypes of cows born from 2000 up until 2018

Effects in the model=> herd x management, age group, parity, inbreeding, heterosis, herd x sire, animal, PE, residual

Algorithm for Proven Young: random core size of 30,000

BLUP90IOD20MP1 (Tsuruta et al., 2001)

Materials and Methods III

Validation animals

- **Cows** = genotyped females born in 2019-2022 with no phenotypes in the reduced dataset
    - **HO:** 96,265 **JE:** 26,436 **CROSS:** **136**

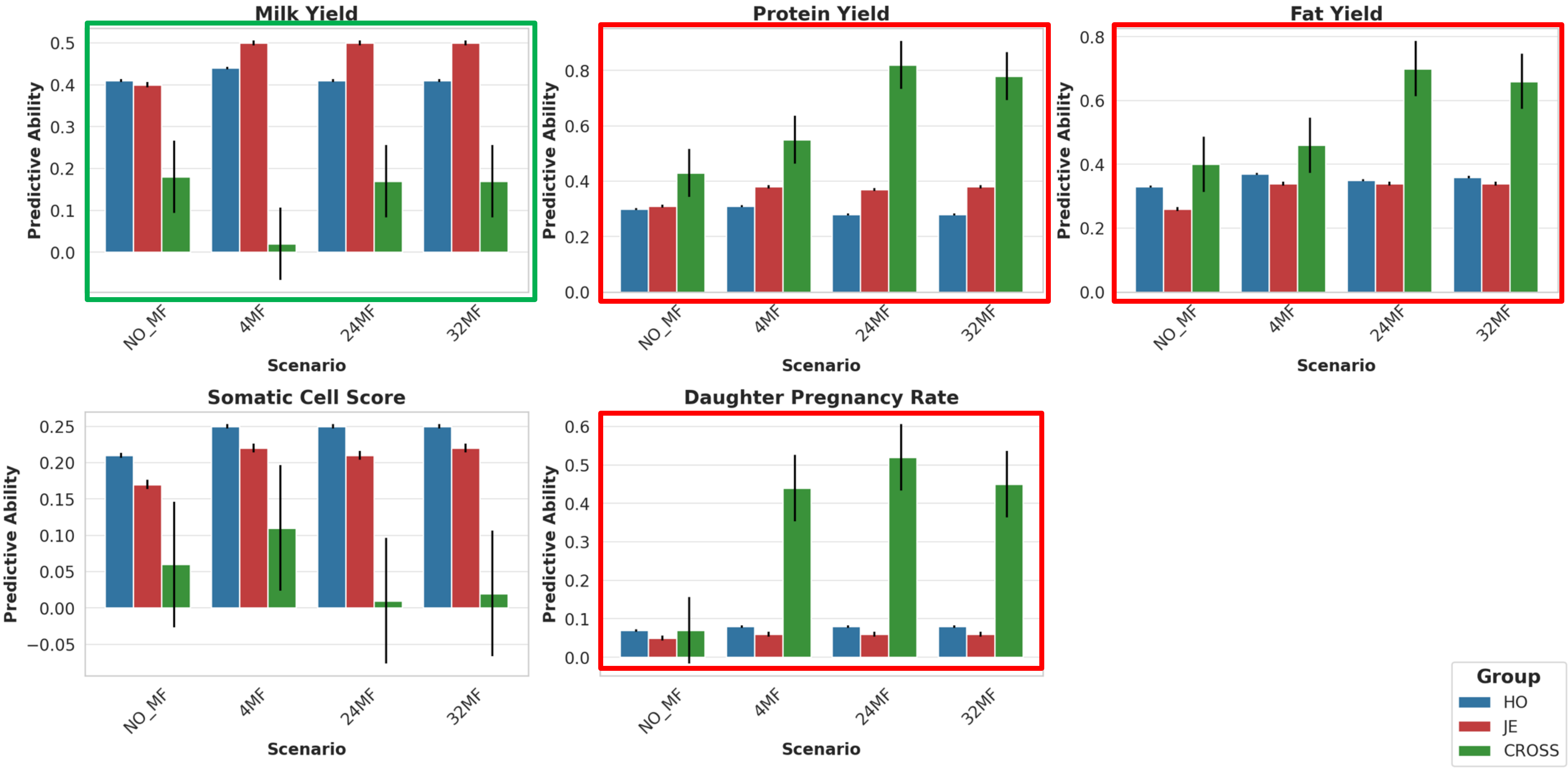
- **Metrics**
    - **Predictability:** Pearson correlation between adjusted y and (G)EBV
    - **Inflation (Slope):** Regression of adjusted y on (G)EBV
    - **Stability:** Pearson correlation between G(EBV)complete, G(EBV)reduced

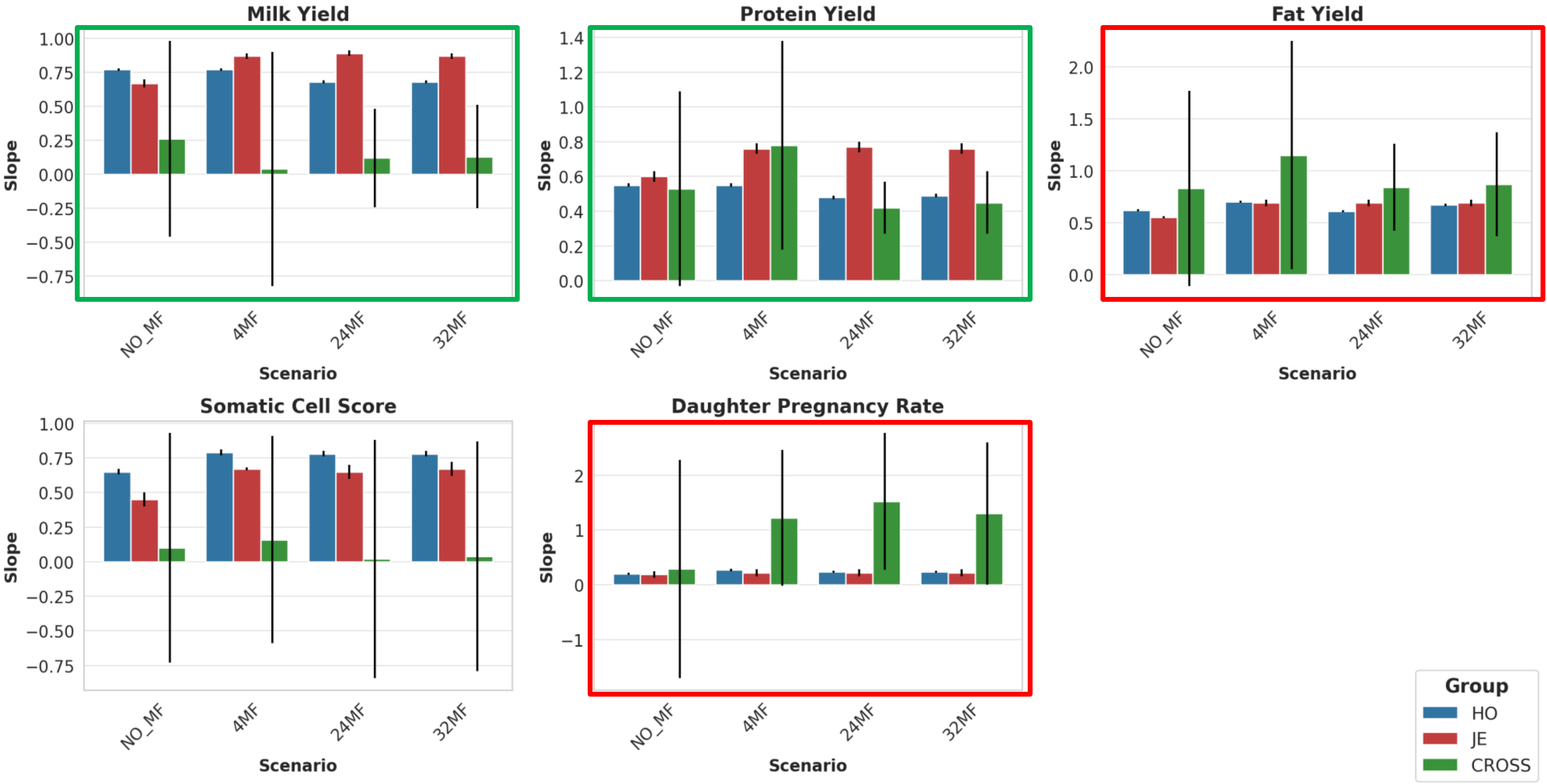
Results

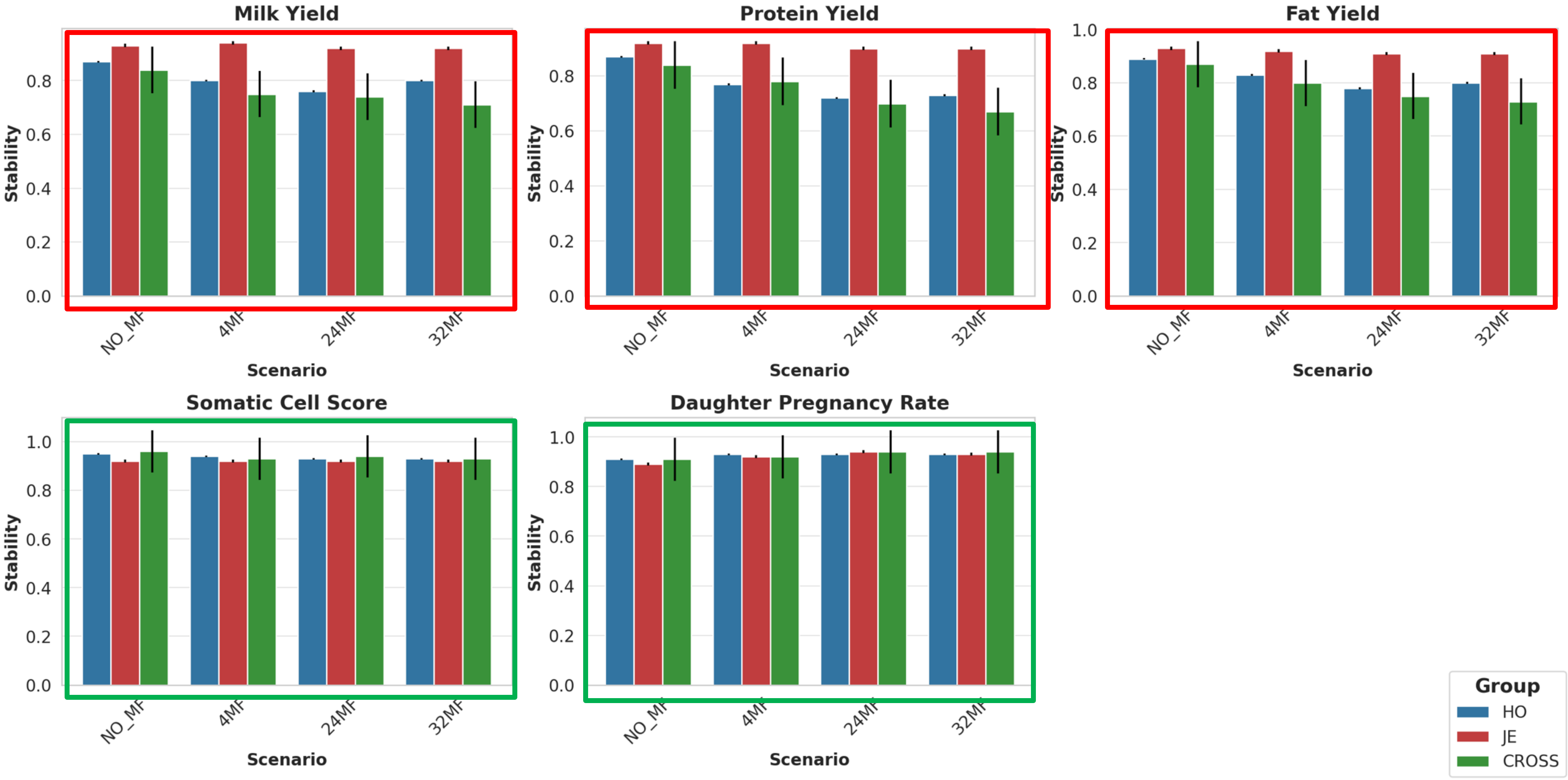
Diagonal and Off-Diagonal Elements

Matrix	Mean	Minimum	Maximum
A_{22}	1.004	1.000	1.286
G	1.004	0.779	1.453
$A\ \Gamma_{4,22}$	1.324	1.266	1.551
$G\ \Gamma_{4}$	1.320	1.121	1.568
$A\ \Gamma_{24,22}$	1.306	1.008	1.504
$G\ \Gamma_{24}$	1.319	1.120	1.568
$A\ \Gamma_{32,22}$	1.306	1.163	1.504
$G\ \Gamma_{32}$	1.319	1.120	1.568

Matrix	Mean	Minimum	Maximum
A_{22}	0.016	0.000	0.666
G	0.016	-0.216	1.015
$A\ \Gamma_{4,22}$	0.613	0.532	1.154
$G\ \Gamma_{4}$	0.632	0.397	1.386
$A\ \Gamma_{24,22}$	0.604	0.385	1.073
$G\ \Gamma_{24}$	0.631	0.395	1.380
$A\ \Gamma_{32,22}$	0.604	0.413	1.073
$G\ \Gamma_{32}$	0.631	0.396	1.380


Milk Yield
Protein Yield
Fat Yield
Somatic Cell Score
Daughter Pregnancy Rate
Predictive Ability
Scenario
NO_MF
4MF
24MF
32MF
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.8
−0.05
0.00
0.05
0.10
0.15
0.20
0.25
Group
HO
JE
CROSS


Milk Yield
Protein Yield
Fat Yield
Somatic Cell Score
Daughter Pregnancy Rate
Slope
Scenario
NO_MF
4MF
24MF
32MF
1.00
0.75
0.50
0.25
0.00
−0.25
−0.50
−0.75
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
2.0
1.5
1.0
0.5
0.0
2
1
0
−1
Group
HO
JE
CROSS


Milk Yield
Protein Yield
Fat Yield
Somatic Cell Score
Daughter Pregnancy Rate
Stability
0.0
0.2
0.4
0.6
0.8
1.0
NO_MF
4MF
24MF
32MF
Scenario
Group
HO
JE
CROSS

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Conclusions

- Increased correlation between **G** and **A**
- Use of metafounders improves predictability and inflation of (G)EBVs for crossbreds and parent breeds
- Predictabilities for crossbred may be impacted by the number of records available
- GEBV inflation may be influenced by heritability and number of records
- 24MF gave the best estimates for this population

Next Steps …..

Acknowledgments

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