

Combining large broiler populations into a single genomic evaluation: Dealing with genetic divergence

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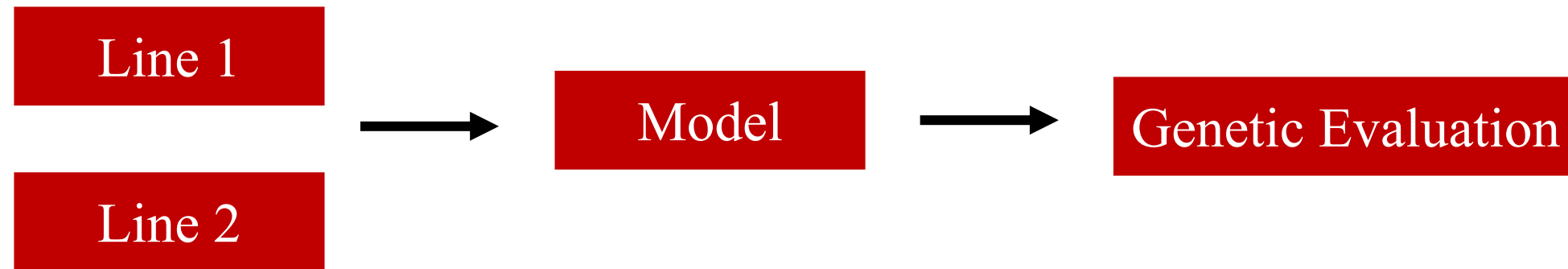
Introduction

- Populations of different genetic background are often combined
 - To simplify the genetic evaluation system
 - When a company buys lines or farms from other companies
- Correctly accounting for genetic and environmental differences is crucial
 - Failure can lead to inaccurate and biased GEBV
 - Compromises selection and genetic gain



Objective

- To combine two divergent broiler populations into a genomic evaluation



- Modeling strategies:
 - Fixed effect accounting for the line of origin
 - Line-specific fixed effects
 - Unknown Parent Groups and Metafounders

Data - Cobb-Vantress, Inc. (Siloam Springs, AR, USA)

Population	Pedigree	Genotypes
Line 1	398k	155k
Line 2	412k	169k
Total	911k	324k

Phenotypes	Body Weight	Carcass Yield	Mortality	Feet Health
Line 1	359k	23k	398k	50k
Line 2	201k	27k	410k	37k
Total	592k	54k	855k	89k

Variance Components Estimation

Multitrait model:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{mpe} + \mathbf{Z}_2\mathbf{a} + \mathbf{e}$$

\mathbf{y} : vector of phenotypes

$\boldsymbol{\beta}$: vector of fixed effects containing contemporary group and sex

\mathbf{mpe} : vector of random maternal permanent environment effect (used only for BW)

\mathbf{a} : vector of additive genetic random effects

\mathbf{e} : vector of random residuals

\mathbf{X} , \mathbf{Z}_1 , and \mathbf{Z}_2 : incidence matrices for the effects in $\boldsymbol{\beta}$, \mathbf{mpe} , and \mathbf{a}

Blupf90 suite of programs



Model and analysis

	<u>Models</u>								
<u>Scenarios</u>	1	2	3						
NO UPG	MTM	MTM + Fixed Effect of Animal Origin	MTM + Sex and CG made Origin specific						
UPG1									
UPG2									
MF1									
MF2									
		<table border="1"> <tr> <td>Sire</td> <td>Dam</td> </tr> <tr> <td>1</td> <td>2</td> </tr> <tr> <td>Level</td> <td>3</td> </tr> </table>	Sire	Dam	1	2	Level	3	
Sire	Dam								
1	2								
Level	3								

single-step GBLUP methodology

Model and analysis

- **NO UPG:** This scenario did not use any unknown parent group (UPG) or metafounder (MF)
- **UPG1:** defined based on the line of origin. The UPGs are from the same sex
- **UPG2:** defined based on sex and line of origin. The UPGs are from different sex
- **MF1/MF2:** same definitions as UPGs but use the metafounders feature

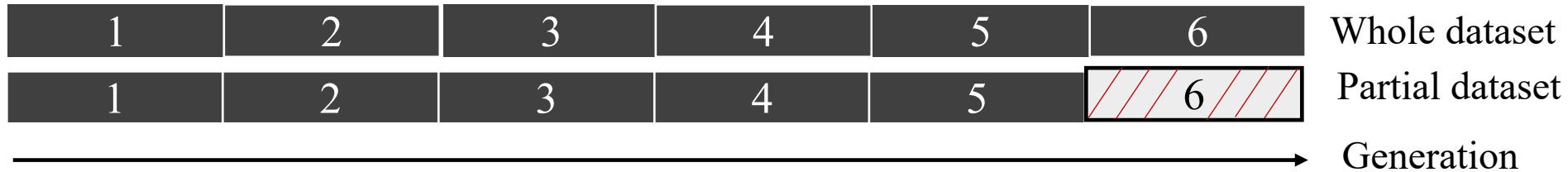
ID	Sire	Dam	Line
2	0	1	1
3	0	0	2
4	2	3	3

ID	Sire	Dam	Line
2	-1	1	1
3	-2	-2	2
4	2	3	3

ID	Sire	Dam	Line
2	-1	1	1
3	-2	-3	2
4	2	3	3

Code	Scenario	
	UPG1/MF1	UPG2/MF2
-1	4,388	2,124
-2	4,264	2,140
-3		2,153
-4		2,235

Validation process – LR Method



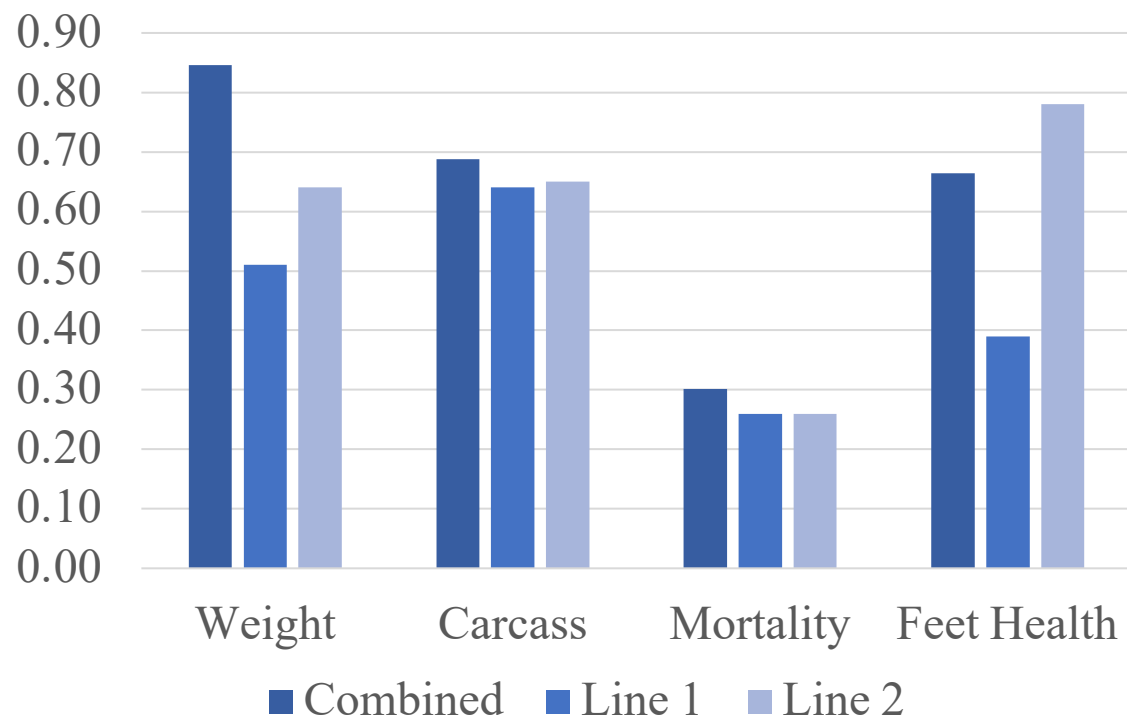
$$\text{Accuracy of prediction: } acc_{LR} = \sqrt{\frac{\text{cov}(\hat{u}_p, \hat{u}_w)}{(1-\bar{F})\sigma_u^2}}$$

$$\text{Bias} = (\hat{u}_p - \hat{u}_w)$$

$$\text{Dispersion: } b_1 = \frac{\text{cov}(\hat{u}_w, \hat{u}_p)}{\text{var}(\hat{u}_p)}$$

Legarra and Reverter, 2018

Results – LR accuracy

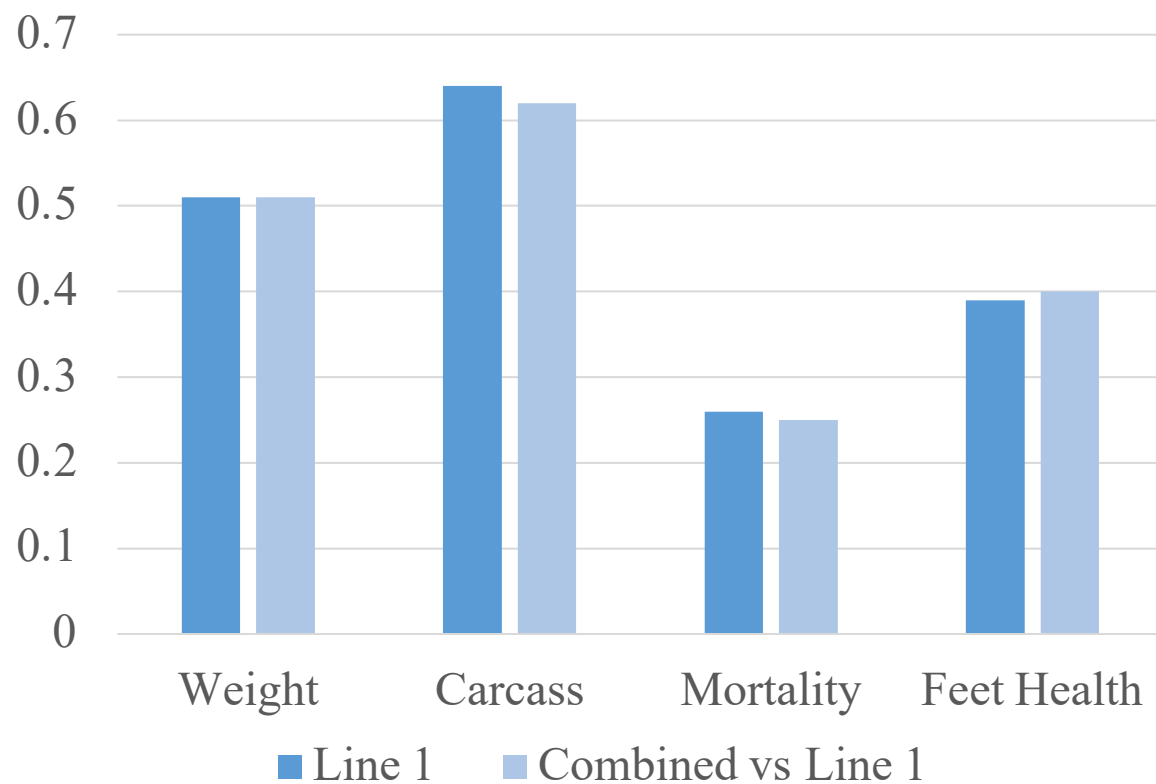


- Increase in accuracy of prediction
- Benefits for the combined evaluation
- Similar accuracies across models/scenarios

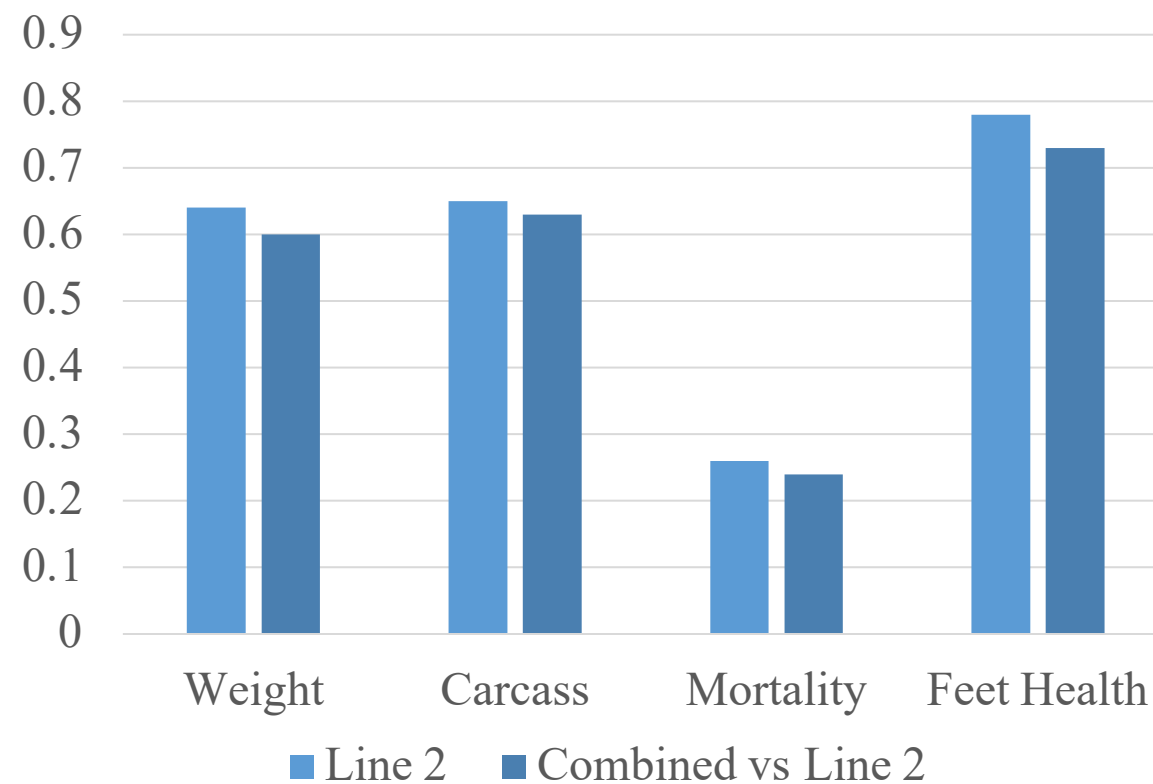
	Body Weight	Carcass Yield	Mortality	Feet Health
Model 2	0.86	0.68	0.30	0.66
Model 3	0.87	0.68	0.28	0.67

Results – LR accuracy

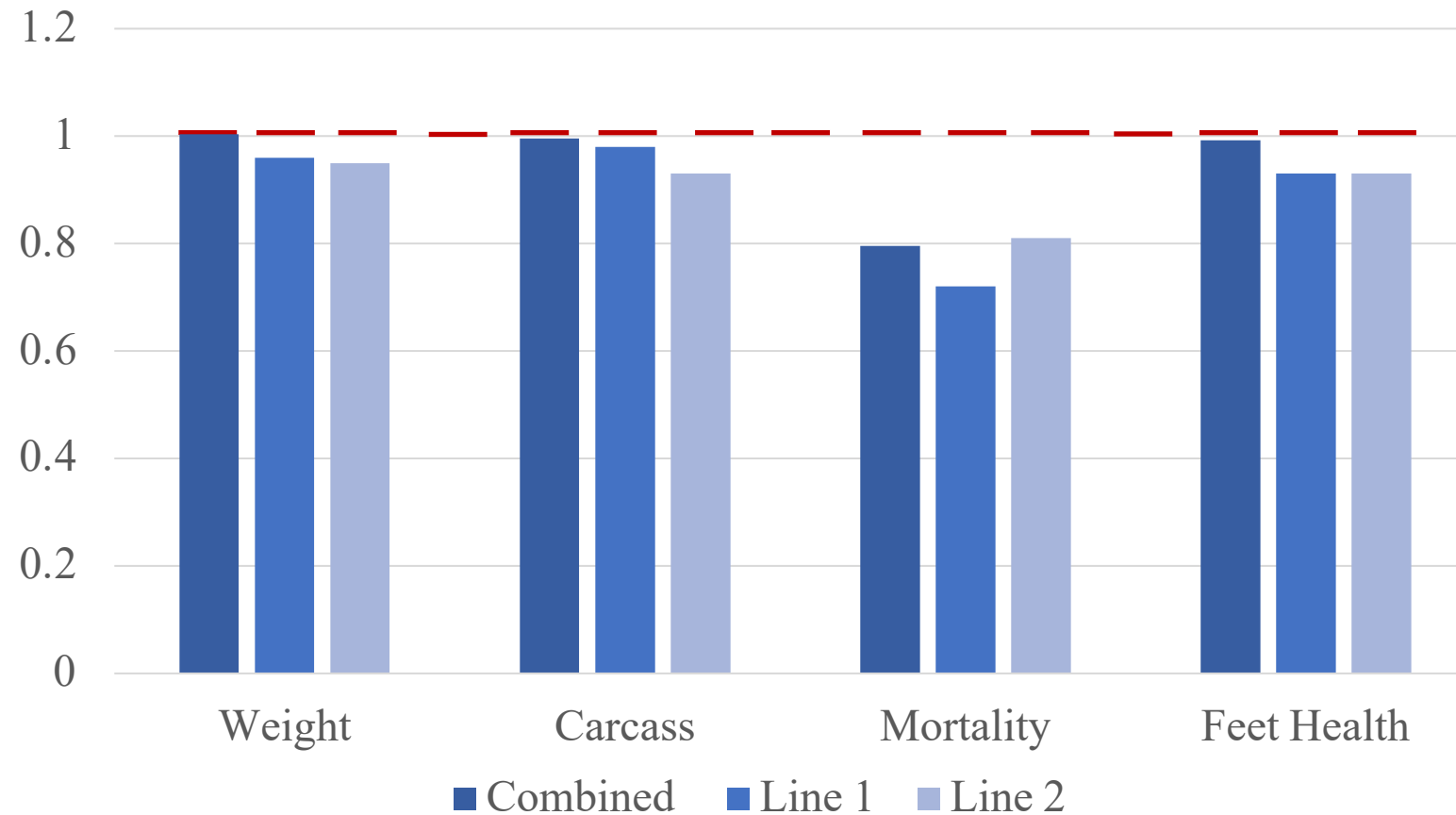
Accuracy of prediction of validation candidates from Line 1



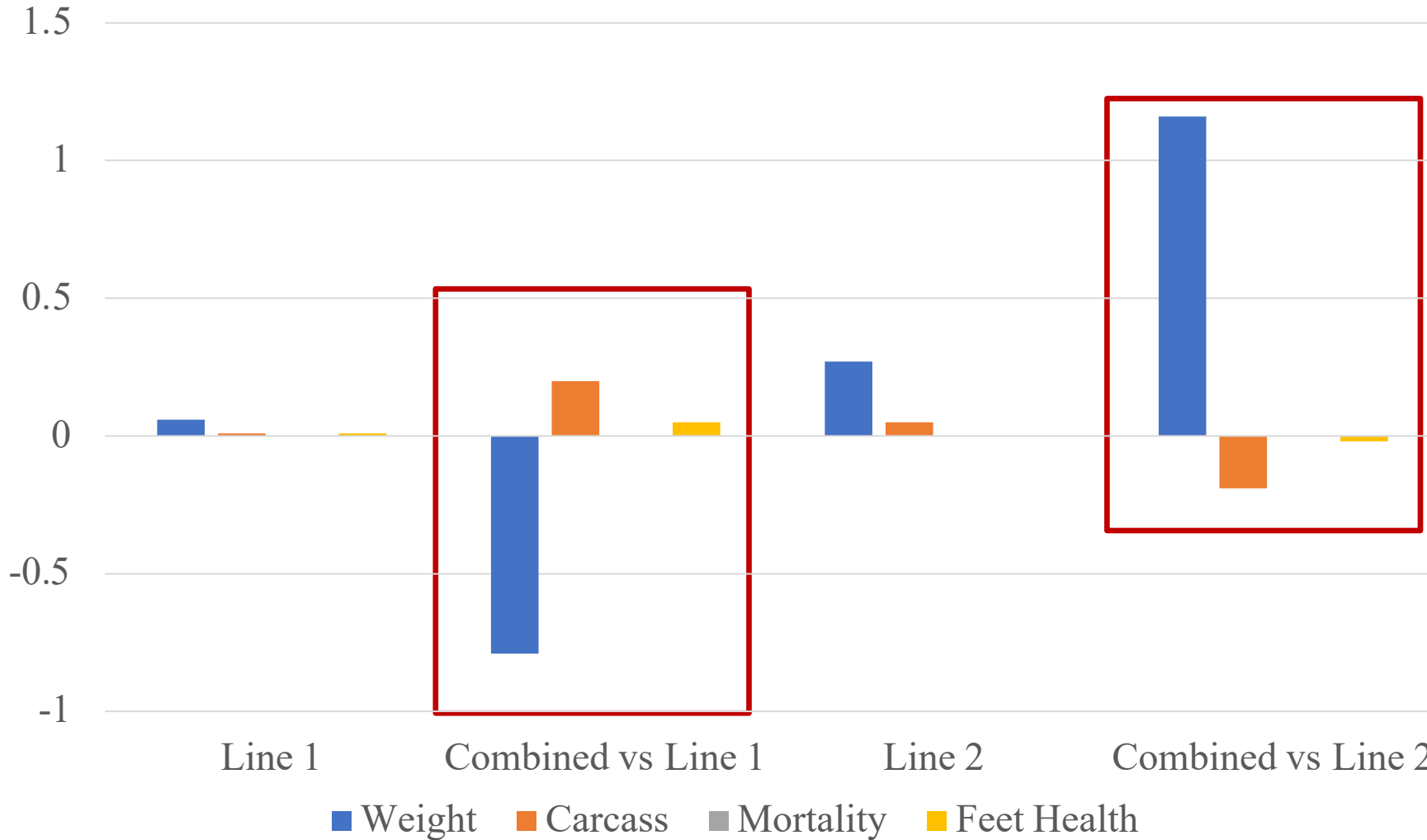
Accuracy of prediction of validation candidates from Line 2



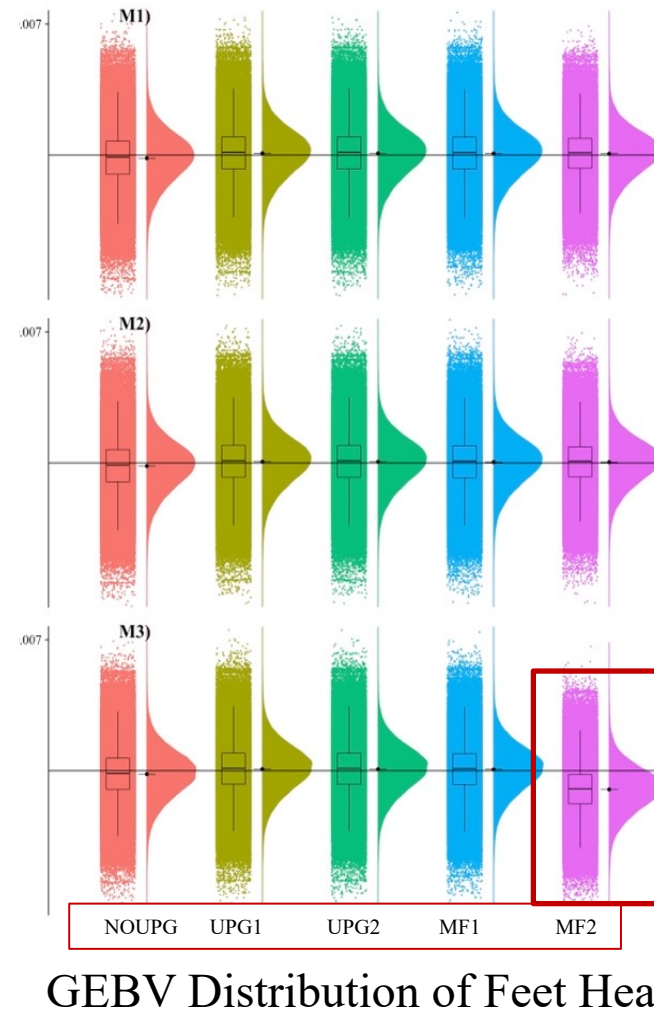
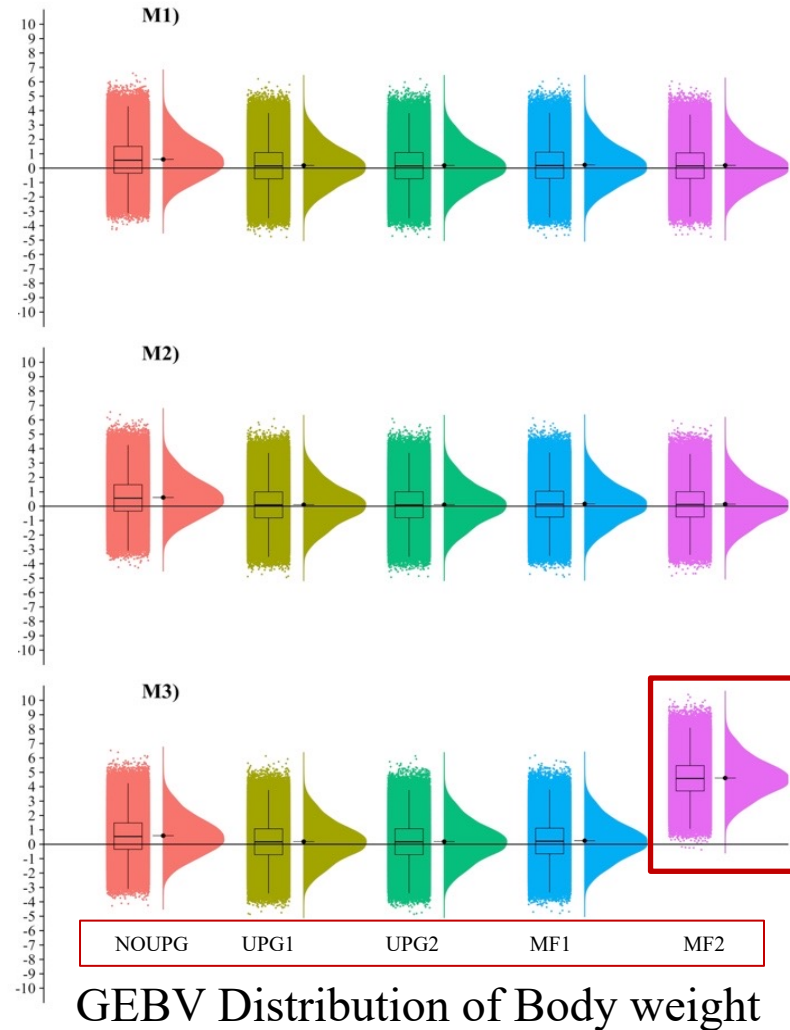
Results – LR Dispersion



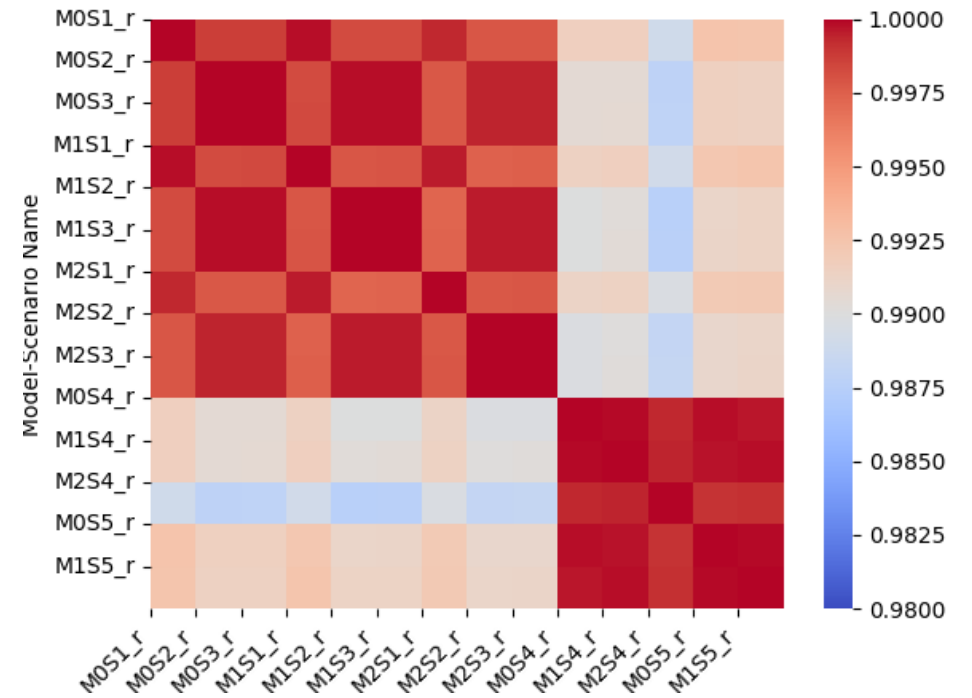
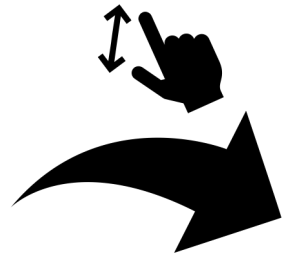
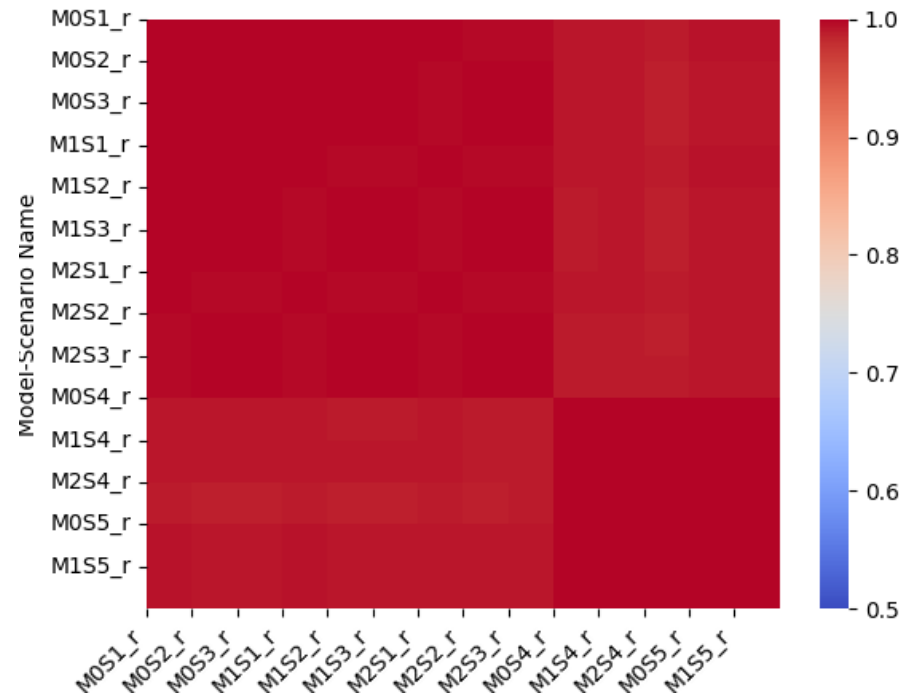
Results – LR bias



Results – Distribution of GEBV



Results – Rank correlation



Conclusions

- Combining lines may benefit genomic evaluations for both populations
 - When differences are properly modeled
- Estimates were less biased when including:
 - Line of origin as fixed effect
 - Unknown parent groups or metafounders
- There may still be differences in scale of GEBV across lines
 - Across-line adjustment is recommended for across-line selection



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Thank you

Questions?