Modeling genetic differences of combined broiler chicken populations in single-step GBLUP

Matias Bermann, Daniela Lourenco, Vivian Breen, Rachel Hawken, Fernando Brito Lopes, and Ignacy Misztal

EAAP – August 2021

UNIVERSITY OF GEORGIA

Background

- Introduction of animals from an external farm is a common practice and should be accounted in the genetic evaluation to avoid bias and lack of accuracy of EBV

- How to model it:
  - Inclusion of an extra fixed effect
  - Genetic groups (UPG)
  - Metafounders
- How to evaluate which is the best approach:
  - Bias and dispersion (inflation)
  - Predictive ability
  - LR-method

Objectives

- Evaluate a multiple trait model with merged lines using a fixed effect, UPG, or metafounders
- Validate each model using predictive ability and LR-method
- Compare predictive ability and LR-method to estimate the accuracy of EBV

Materials and methods

Pedirgree

- 242,413 birds
- 1% of missing parents
- 20 generations
- Selection candidates: animals from the last generation

Genotypes

- 107,216 genotypes
- 60,000 SNP panel
- 47,952 SNP after quality control

Farm of origin

- C1 (own origin):
  - 240,929 from the original farm
  - 828 from an external farm
- C2 (parents' origin):
  - 203,759 both from the original line
  - 18,599 both from an external farm
  - 16,407 crosses.

Traits

Trait	Abbreviation	h^2	Number of records	Focal individuals
Weight	WGT	0.16	74,400 (38,000)	8,600 (3,000)
Carcass yield component 1	CYC1	0.59	15,300 (14,920)	820 (580)
Feed efficiency 1	FE1	0.36	59,500 (28,400)	9,000 (3,000)
Carcass yield component 2	CYC2	0.62	15,200 (14,840)	820 (580)
Feed efficiency 2	FE2	0.24	60,100 (28,500)	8,900 (3,000)

Model 1 (M1)

$$\boldsymbol{y} = \mathbf{X}_1\boldsymbol{\beta} + \mathbf{X}_2\boldsymbol{\gamma} + \mathbf{Z}_1\boldsymbol{\delta} + \mathbf{Z}_2\boldsymbol{u} + \boldsymbol{\epsilon}$$

- $\boldsymbol{y}$ is the vector of records ordered by trait
- $\mathbf{X}_1$, $\mathbf{X}_2$, $\mathbf{Z}_1$, and $\mathbf{Z}_2$ are incidence matrices
- $\boldsymbol{\beta}$ represents the contemporary group effect
- $\boldsymbol{\gamma}$ represents the sex effect
- $\boldsymbol{\alpha}$ represents the grouping in C2

Model 2 (M2)

$$\boldsymbol{y} = \mathbf{X}_1\boldsymbol{\alpha} + \mathbf{X}_2\boldsymbol{\beta} + \mathbf{X}_3\boldsymbol{\gamma} + \mathbf{Z}_1\boldsymbol{\delta} + \mathbf{Z}_2\boldsymbol{u} + \boldsymbol{\epsilon}$$

- $\boldsymbol{\delta} \sim \mathrm{MVN}\left(\mathbf{0}, \mathbf{I}\sigma^2_{pe}\right)$ represents the permanent environmental effect
- $\boldsymbol{u} \sim \mathrm{MVN}(\mathbf{0}, \mathbf{R}_u \otimes \mathbf{H})$ represents the additive genetic effect
- $\boldsymbol{\epsilon} \sim \mathrm{MVN}(\mathbf{0}, \mathbf{R}_e \otimes \mathbf{I})$ is the error vector
- $cov(\boldsymbol{\delta}, \boldsymbol{u}) = cov(\boldsymbol{\delta}, \boldsymbol{\epsilon}) = cov(\boldsymbol{u}, \boldsymbol{\epsilon}) = \mathbf{0}$

Scenarios

Symbol	Modeling of introduction of external animals
$M1_{N}$	None
$M1_{UPG\_INB}$	UPG with inbreeding
$M1_{UPG\_RAN}$	Random UPG
$M1_{MF}$	Metafounders
$M2_{N}$	Extra fixed effect
$M2_{UPG\_INB}$	Extra fixed effect + UPG with inbreeding
$M2_{UPG\_RAN}$	Extra fixed effect + random UPG
$M2_{MF}$	Extra fixed effect + metafounders

Validation

- Bias
- Dispersion
- Accuracy

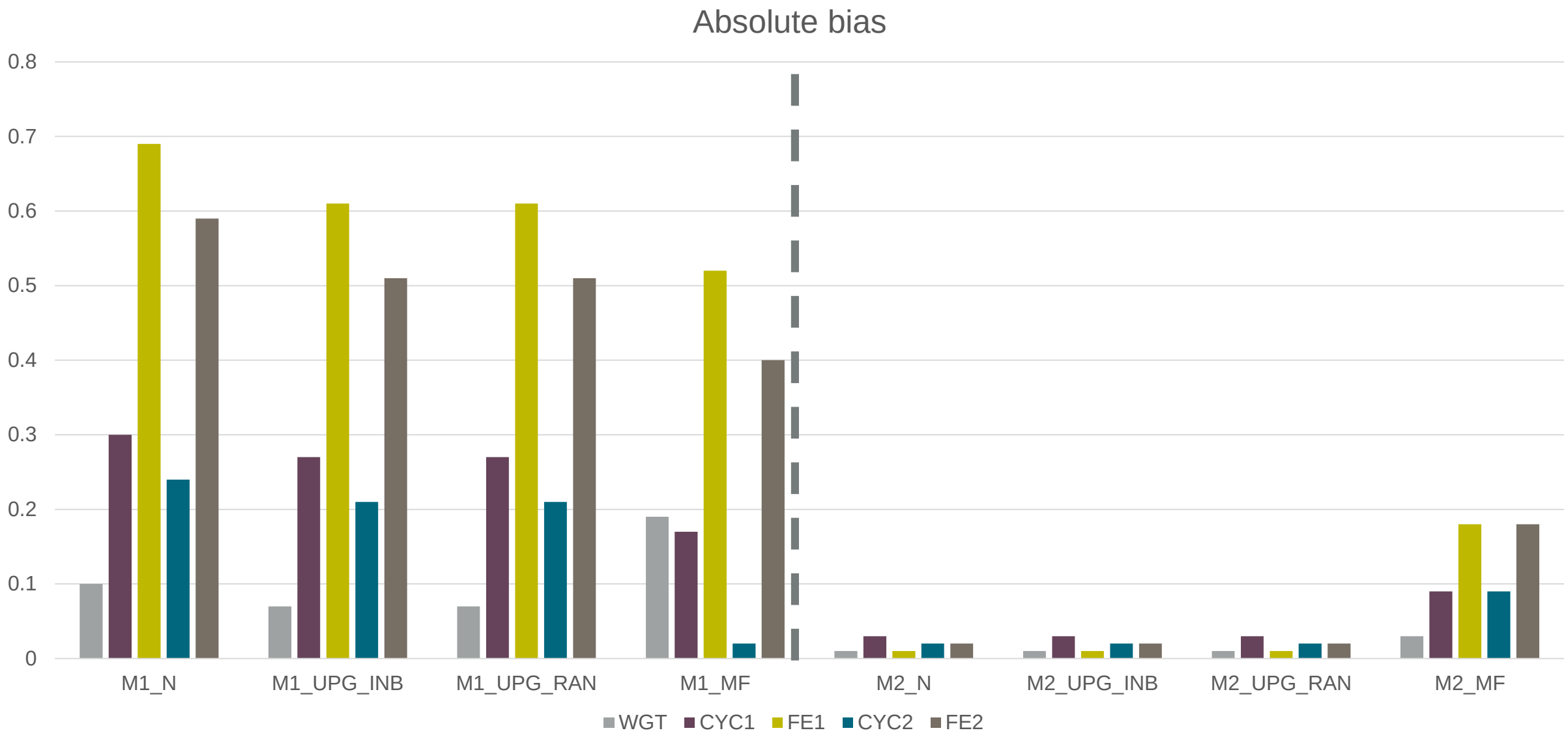
$$\mu_{w,p} = \overline{\hat{\boldsymbol{u}}_p} - \overline{\hat{\boldsymbol{u}}_w}$$

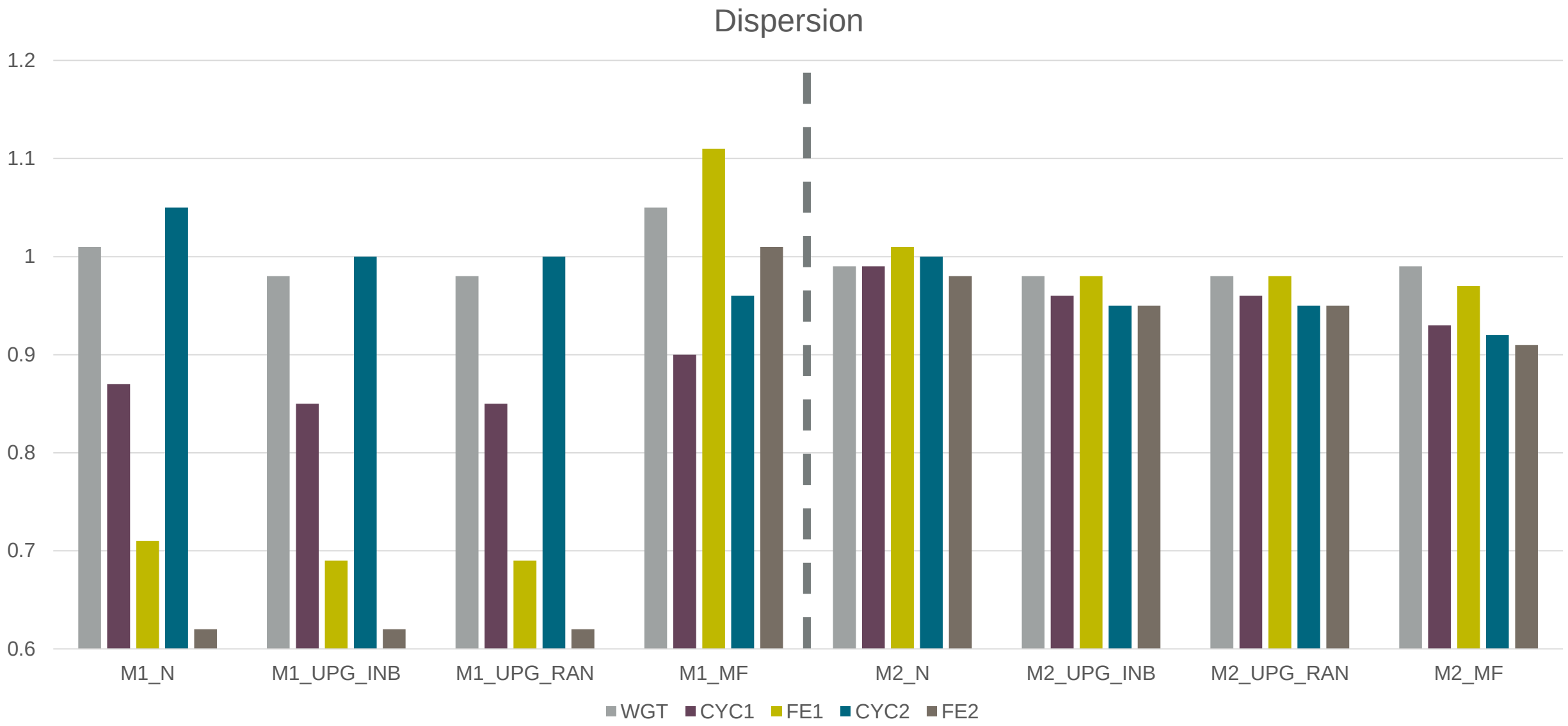
$$b_{w,p} = \frac{cov(\hat{\boldsymbol{u}}_p, \hat{\boldsymbol{u}}_w)}{var(\hat{\boldsymbol{u}}_p)}$$

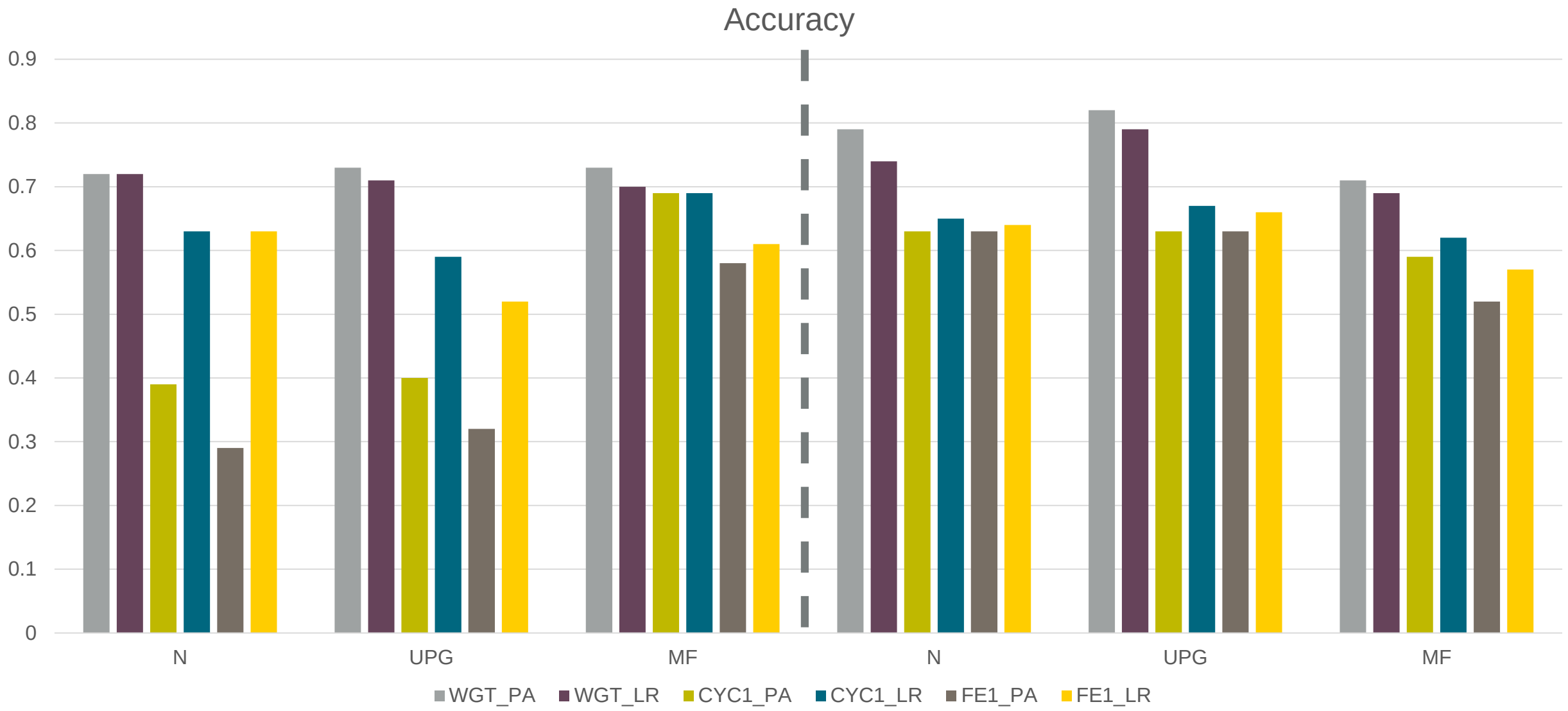
$$\widehat{acc}_{PA} = \frac{corr(\boldsymbol{y}_{adj}, \hat{\boldsymbol{u}})}{\sqrt{h^2}}$$

$$\widehat{acc}_{LR} = \sqrt{\frac{cov(\hat{\boldsymbol{u}}_p, \hat{\boldsymbol{u}}_w)}{(1-\bar{F})\hat{\sigma}_{\boldsymbol{u}}^2}}$$

Results


Absolute bias
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
M1_N
M1_UPG_INB
M1_UPG_RAN
M1_MF
M2_N
M2_UPG_INB
M2_UPG_RAN
M2_MF
WGT
CYC1
FE1
CYC2
FE2


Dispersion
1.2
1.1
1
0.9
0.8
0.7
0.6
M1_N
M1_UPG_INB
M1_UPG_RAN
M1_MF
M2_N
M2_UPG_INB
M2_UPG_RAN
M2_MF
WGT
CYC1
FE1
CYC2
FE2


Accuracy
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
N
UPG
MF
N
UPG
MF
WGT_PA
WGT_LR
CYC1_PA
CYC1_LR
FE1_PA
FE1_LR

Discussion

- M1 was misspecified
- Predictive ability is more sensitive to model specification than LR accuracy
- MF are worst in M2
    - Estimation of the covariance matrix among metafounders
    - Scaling of the genetic variance
    - Unequal distribution of animals in each MF

Conclusion

- The best combination to model the inclusion of external animals is with an extra fixed effect and UPG or metafounders.
- The results obtained with metafounders may be inaccurate when groups to define them are very unbalanced.
- LR-method is a useful tool to validate models and it is preferable than predictive ability.

Questions?

Matias Bermann - mbermann@uga.edu