Estimation of heritabilities and genetic correlations in very large datasets using predictivities within and across traits

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Challenge of parameter estimation in genomic era

Potential negative effects of genomic selection

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- Possibly rapidly changing parameters
- Need estimates using complete data including genomic
- Computing issues with REML and Bayesian methods
- Can we estimate parameters without size restriction, generation by generation?

Realized and theoretical accuracies

Realized accuracy

$$acc = corr\left(y - Xb, \hat{u}\right)/h$$

Legarra et al. (2008)

y-Xb - adjusted phenotype

$\hat{u}$ - breeding value obtained without that phenotype

h^2 - heritability

Theoretical accuracy

$$acc = \sqrt{\frac{Nh^2}{Nh^2 + M_e}}$$

Daetwyler et al. (2008)

N – number of genotyped animals with phenotypes

M_e – number of independent chromosome segments

Me ≈ 5k (chickens, pigs), 10k (beef), 15k (Holsteins)

Pocrnic et al. (2017)

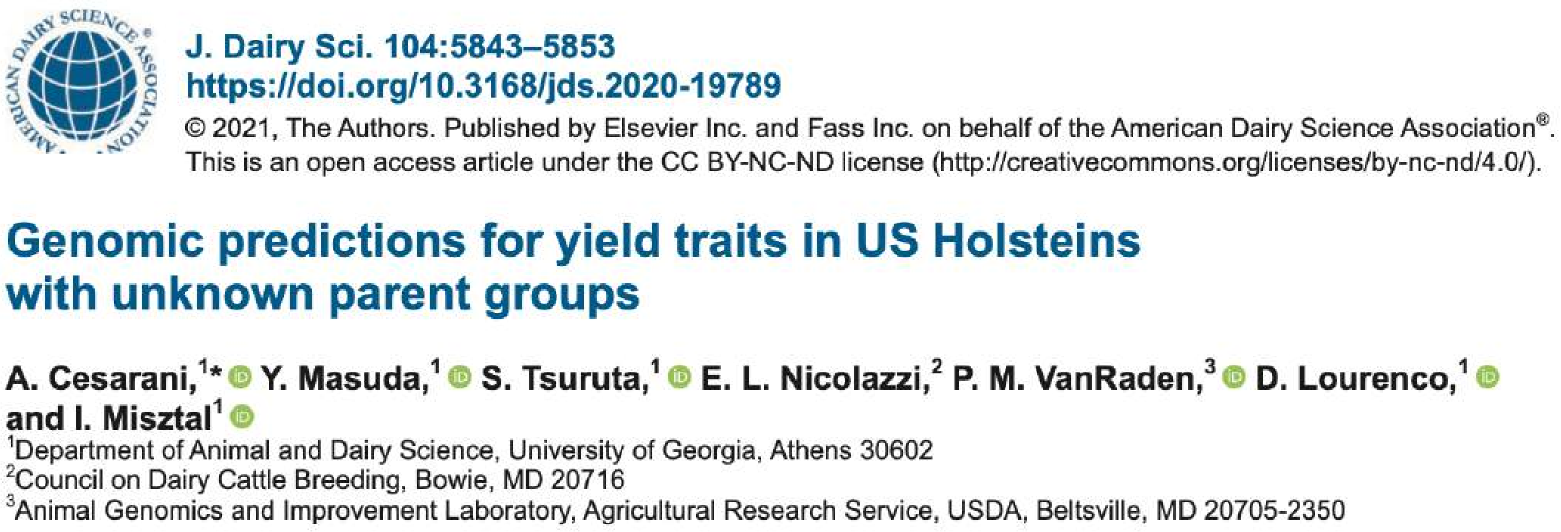
Formula for estimating heritability

$$\widehat{h^2} = \frac{c^2 + \sqrt{c^4 + 4c^2 M_e / N_{ref}}}{2} \mp \frac{3c}{\sqrt{N_{val}}}$$

$$c = corr(y - Xb, \hat{u})$$

N_{ref} – animals in reference population
Me – effective chromosome segments, ~5k in pigs and chicken, ~15k in cattle
N_{val} – number of animals in validation population

Heritabilitv for milk in Holsteins



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

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Reference: 580k   Validation 381k

Starting $h^2 = 0.35$ Me=15k chromosome segments

Predictivity = 0.55

Calculated $h^2 = 0.33$

Formula for genetic correlations

$corr\left(y_i - Xb_i, \widehat{u_j}\right)$ Predictivity of trait i by trait j

$$corr_{ij} = \frac{corr\left(y_i - Xb_i, \widehat{u_j}\right)}{h_i \; acc_j} \mp \frac{1}{h_i \; acc_j \sqrt{N_{val}}}$$

Under correct model: $corr_{ij} = corr_{ji}$

Procedure

- Select reference population, number of genotyped N > 10,000
- Select validation population, number of genotyped $N_{val} > 5000$
- Estimate GEBV with phenotypes of reference population and genotypes of both populations; treat traits uncorrelated
- Calculate predictivities within and across traits
- Recalculate heritabilities $\widehat{h^2} = \frac{c^2+\sqrt{c^4+4c^2 M_e/N}}{2}$
- Recalculate accuracies $acc = corr(y - Xb, \hat{u})/h$
- Calculate genetic correlations $corr_{ij} = \frac{corr(y_i - Xb_i, \widehat{u_j})}{h_i \; acc_j} \pm \frac{1}{h_i \; acc_j \sqrt{N}}$

Data simulation

- y_i^j, u_i^j - phenotype and breeding values of trait i in j-th generation

- Two uncorrelated traits
  - “production” with $h^2 = 0.4$
  - “base fitness” with $h^2 = 0.1$

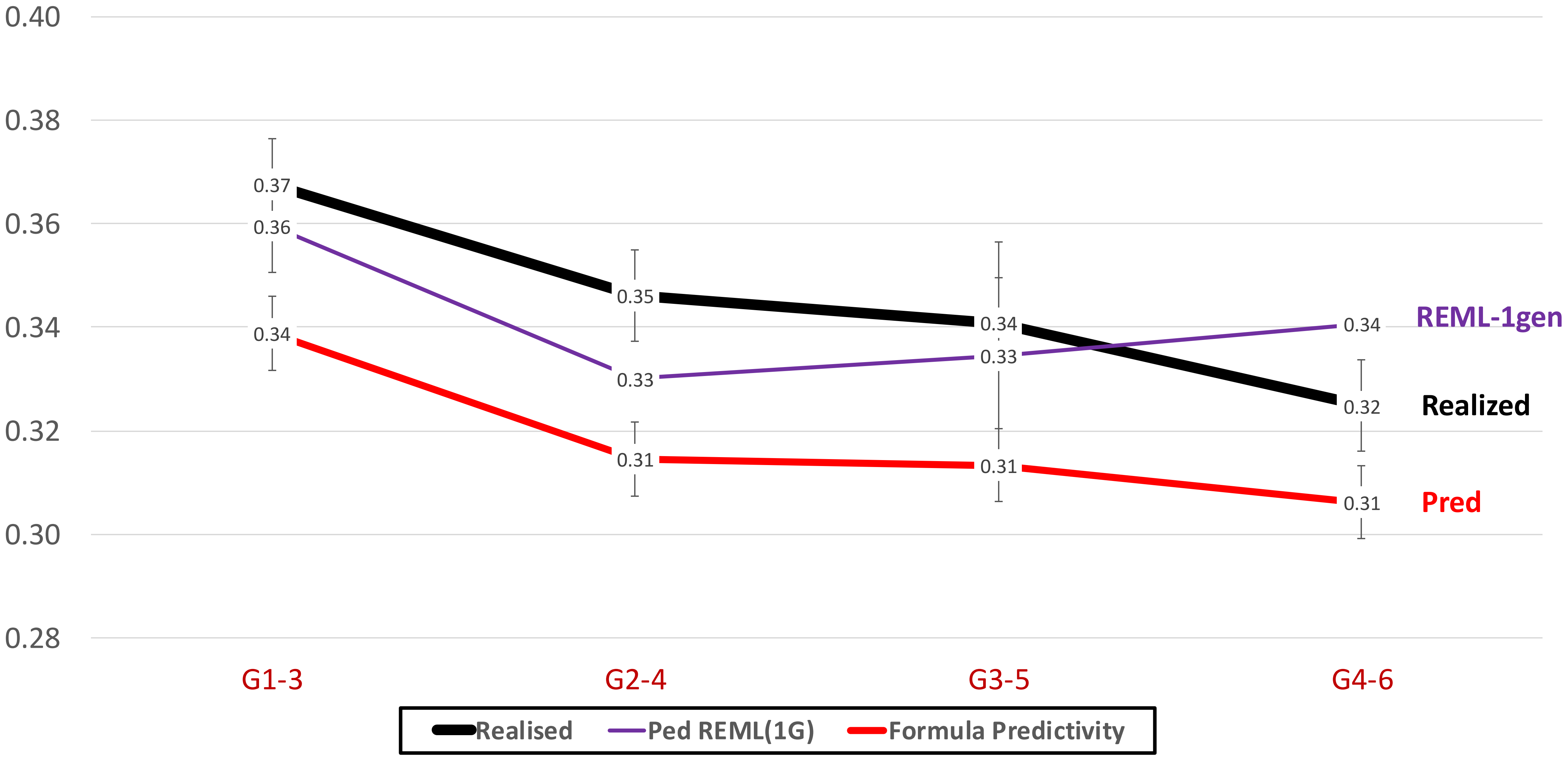
- Evolving fitness trait $u_3^j = \alpha_j \left(u_2^j - \beta u_1^j \overline{(u_1^j - u_1^0)} \right)$
  - α_j - scaling factor so that $var\left(u_3^j\right) = const$
  - β - chosen to change genetic correlation between traits 1 and 3 by about -0.1 each generation.

Data simulation (2)

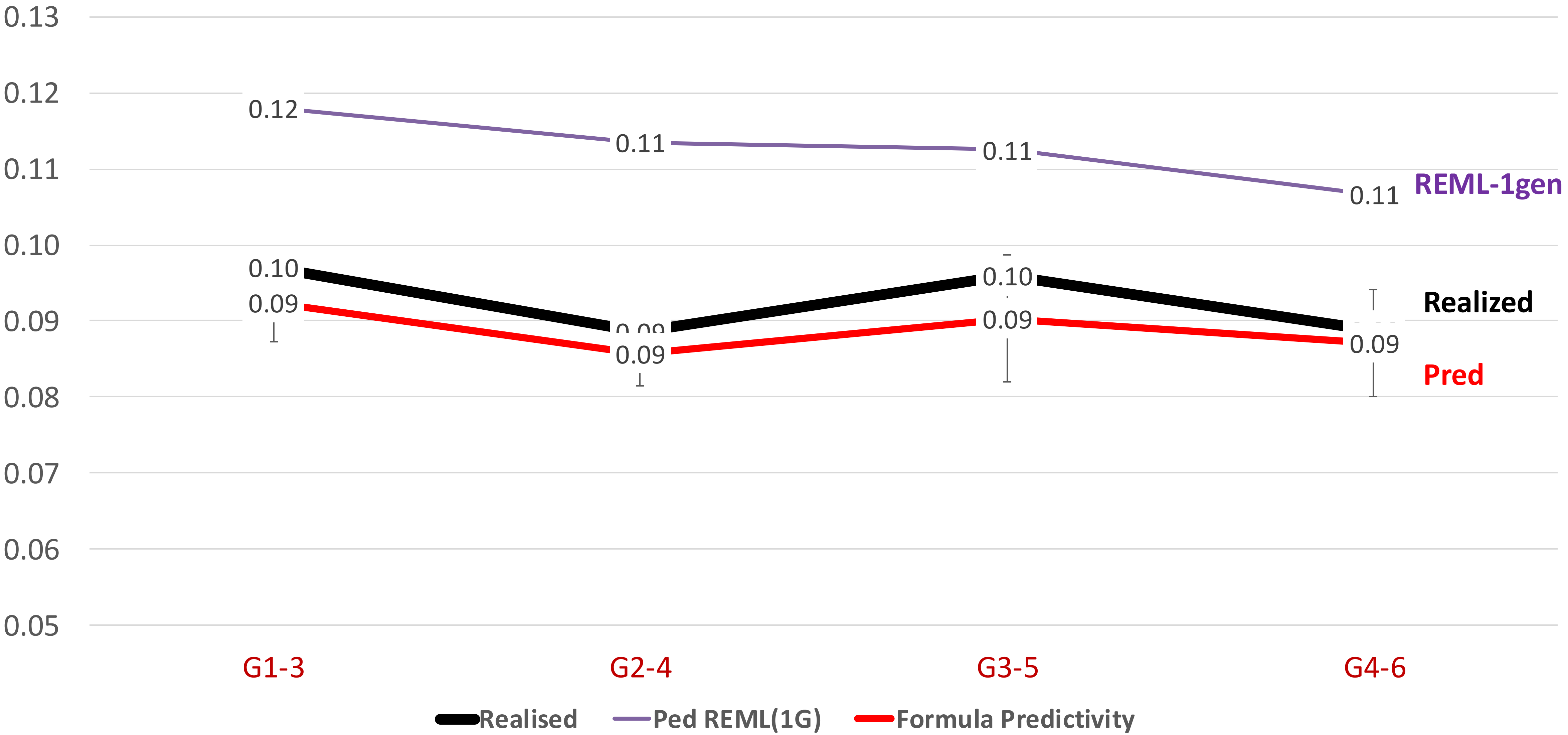
- Simulation by AlphaSim
  - 40k genotyped and phenotyped per generation
  - 6 generations
  - GBLUP selection in each generation
  - Effective population size 50

- Analyzes
  - Realized parameters for each generation
  - Pedigree REML
  - Parameters by predictivity, use 2 reference generations

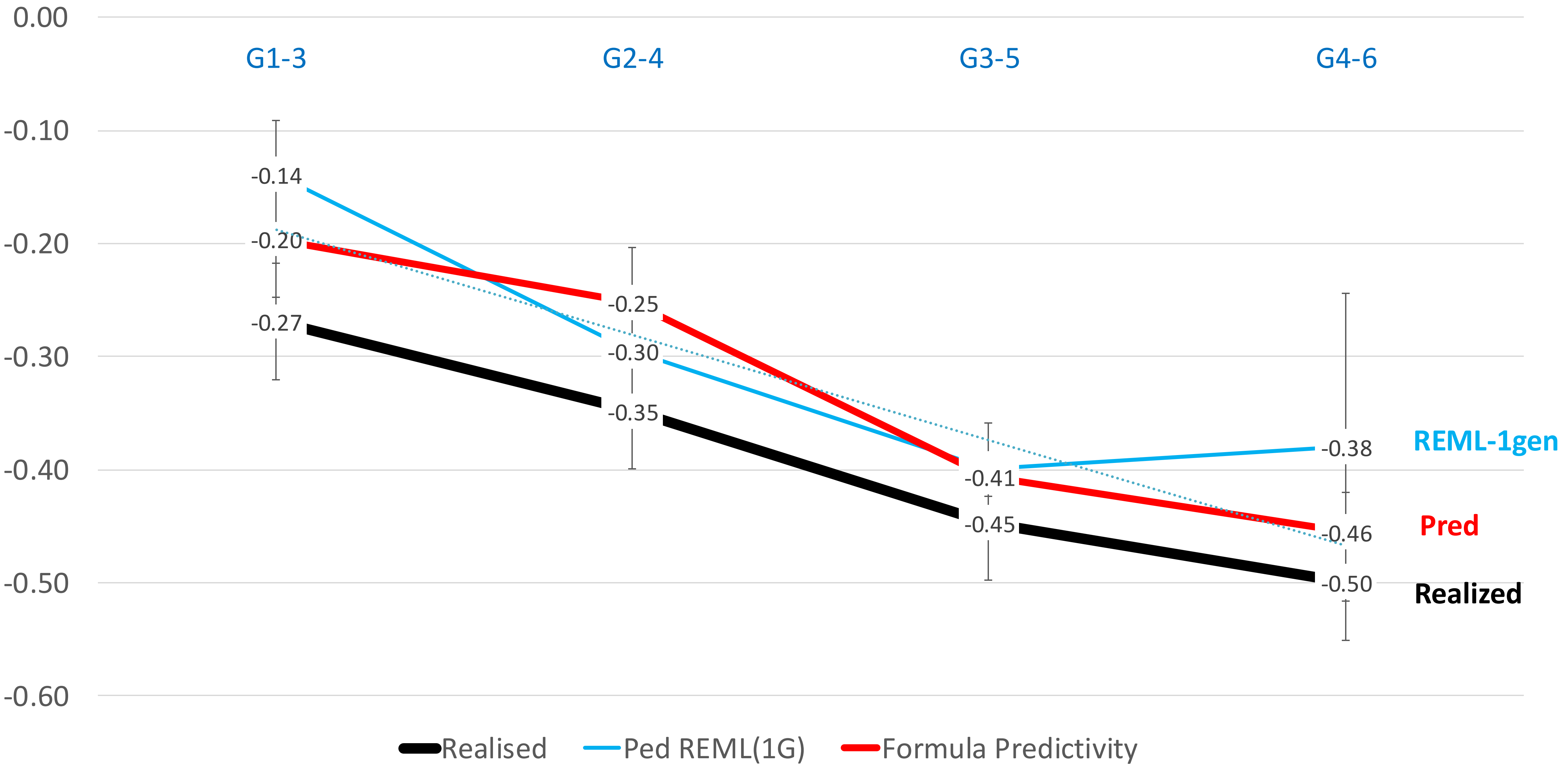
Heritability for "Production" Trait



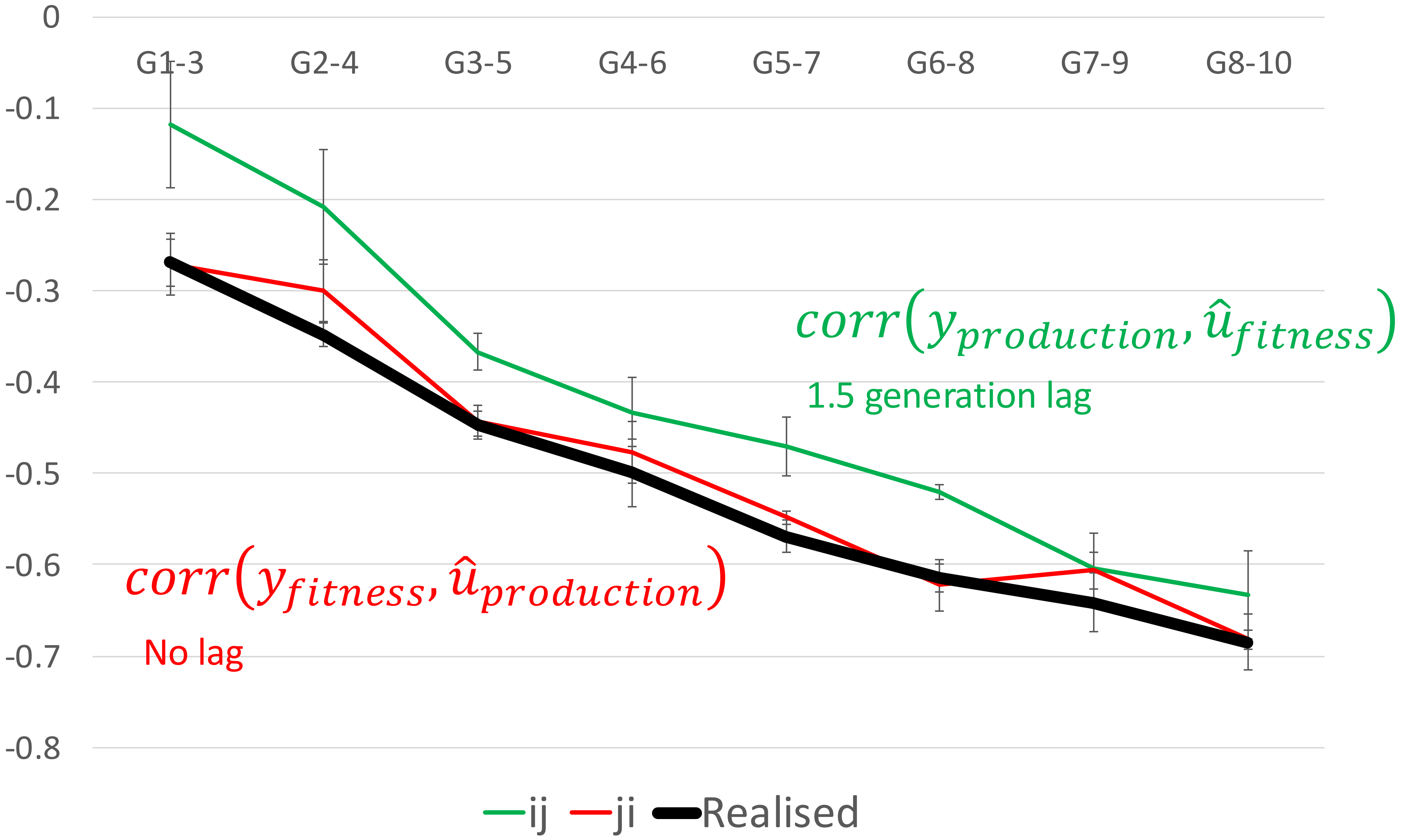
Heritability for “Fitness” Trait



Genetic correlations



Two predictivities: IJ and JI



$corr(y_{production}, \hat{u}_{fitness})$

1.5 generation lag

$corr(y_{fitness}, \hat{u}_{production})$

No lag

Comments

- Results with pedigree REML OK because of simple selection
- Order of genetic correlation important
- Predictivity sensitive to selected genotyping – no problem with current commercial data
- ssGBLUP: use number of both genotyped and phenotyped

Conclusions

- Can estimate heritability from theoretical and realized accuracies
- Can estimate genetic correlations by predictivity across traits
- Any data size and data slice

- Applicable to models where predictivity is applicable

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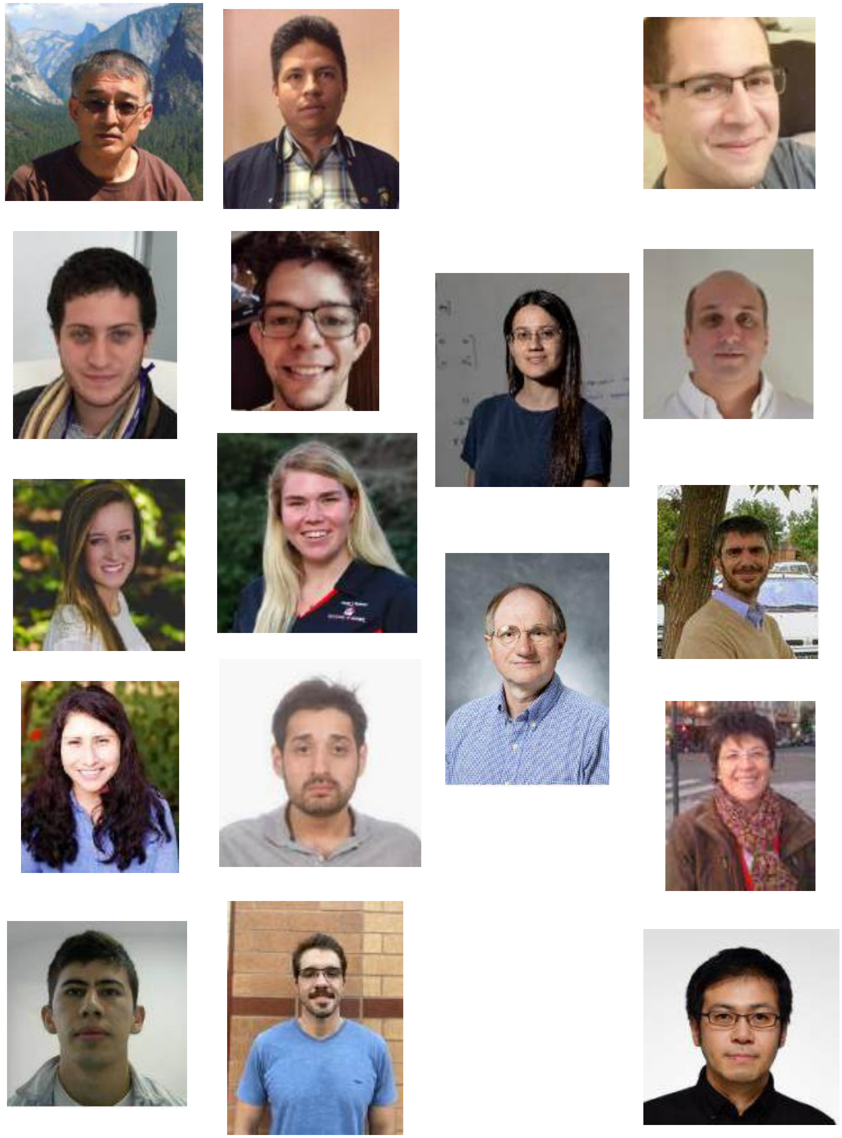
UGA AB&G team



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