

# Using theoretical and realized accuracies to estimate changes in heritabilities and genetic correlations

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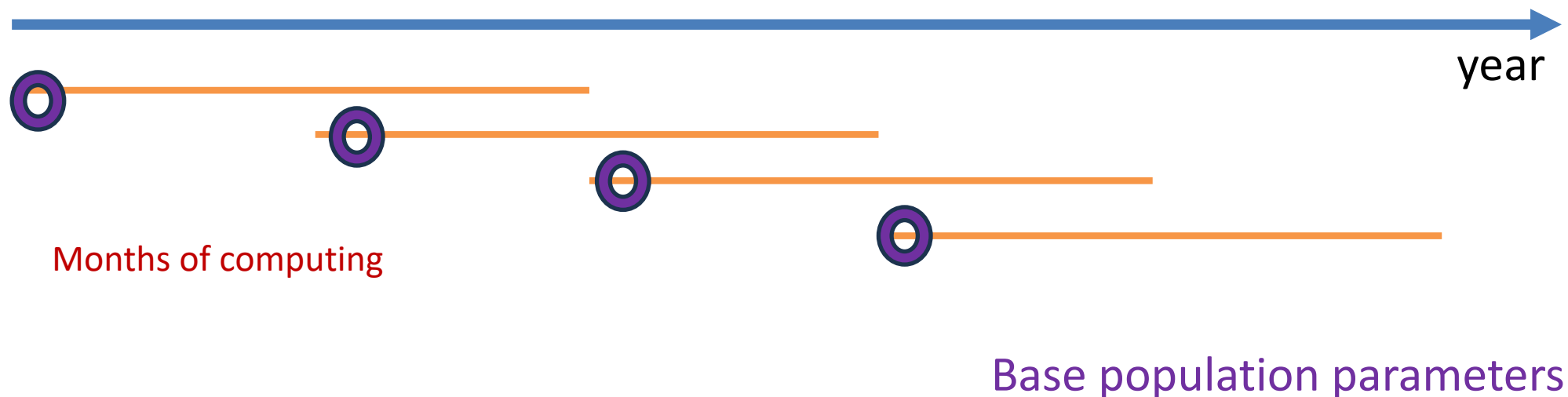
# Changes under genomic selection

- Under selection:
  - Heritabilities decline
  - Antagonistic correlations intensify
- Accelerated changes under genomic selection
  - heritability halved for growth, negative correlations almost doubled (Hidalgo et al, 2019)
- With wrong parameters
  - Selection index inaccurate
  - Genetic gain not as expected
  - Possible deterioration of fitness traits
- How to estimate parameter change for last generation/year with commercial data sets?

# How to estimate parameter change by generation?

- If REML/Gibbs sampling
  - Base population parameters
  - Impossible computations with too many genotypes
  - Biases with too few generations (Cesarani et al., 2019)

Data sampling in Hidalgo et al.(2019)



# Requirements for new estimation

- All data including genomic
- Parameters by last generation/ year
- Reasonable computing cost



Hours of computing

Last generation parameters

# Realized and theoretical accuracies

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

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

$M_e \approx 5k$  (chickens, pigs),  $10k$  (beef),  $15k$  (Holsteins)  
Pocrnic et al. (2017)

# Derivations of realized accuracies

$$acc = corr(u, \hat{u}) = \frac{cov(u, \hat{u})}{\sqrt{\sigma_u^2 \sigma_{\hat{u}}^2}} \quad y = Xb + u + e, \quad y - Xb = u + e$$

$$corr(y - Xb, \hat{u}) = \frac{cov(u + e, \hat{u})}{\sqrt{\sigma_p^2 \sigma_{\hat{u}}^2}} = \frac{cov(u, \hat{u})}{\sqrt{\sigma_p^2 \sigma_{\hat{u}}^2}} = \frac{cov(u, \hat{u})}{\sqrt{\frac{\sigma_u^2}{\sigma_u^2} \sigma_p^2 \sigma_{\hat{u}}^2}} = \frac{cov(u, \hat{u})}{\sqrt{\frac{\sigma_p^2}{\sigma_u^2} \sigma_u^2 \sigma_{\hat{u}}^2}}$$

$$= \frac{cov(u, \hat{u})}{\sqrt{\frac{1}{h^2} \sigma_u^2 \sigma_{\hat{u}}^2}} = acc \ h$$

# Pig data set

150k records on growth ( $h^2=0.21$ )

25k records on fitness ( $h^2=0.05$ )

53k genotyped animals



Hollifield et al., 2021

Theoretical accuracy

$$\sqrt{\frac{\text{growth} \cdot 53k}{\text{growth} \cdot 53k + 5k}} = 0.83$$

$$\sqrt{\frac{\text{fitness} \cdot 25k}{\text{fitness} \cdot 25k + 5k}} = 0.44$$

Realized accuracy

0.82

0.41

# Broiler chicken data set

820k phenotypes for growth

$$h^2=0.3$$

150k genotyped

Theoretical accuracy  $\sqrt{\frac{150k * 0.3}{150k * 0.3 + 5k}} = 0.94$

Realized accuracy 0.58

Both accuracy same 0.89 if  $h^2 = 0.13$

Company was using 0.14! (Breen, 2022)



Hidalgo et al., 2021



# Formulas for estimating heritability

$$\widehat{h^2}: \sqrt{\frac{Nh^2}{Nh^2 + M_e}} = \text{corr}(y - Xb, \hat{u})/h$$

$$\widehat{h^2} = \frac{c^2 + \sqrt{c^4 + 4c^2 M_e/N}}{2}, c = \text{corr}(y - Xb, \hat{u})$$

$$SE(\widehat{h^2}) \approx \frac{1}{\sqrt{N_{val}}} \left[ c + \frac{2c^2 + \frac{4M_e}{N}}{\sqrt{c^2 + \frac{4M_e}{N}}} \right] \widehat{h^2} \approx \frac{3c}{\sqrt{N_{val}}}$$

N – # animals in reference    N<sub>val</sub> – number of animals in validation

# Heritability for milk in Holsteins



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

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# animals with phenotypes and genotypes	580k
# animals with validation	381k
Assumed $M_e$	15k
Initial $h^2$	0.35
Predictivity	0.55
Calculated $h^2$	0.33

# Predictivity with large populations

$$acc = corr(y - Xb, \hat{u})/h < 1$$

$$h^2 > [corr(y - Xb, \hat{u})]^2$$

If  $corr(y - Xb, \hat{u}) = 0.55$  then  $h^2 > 0.30$

# How to estimate genetic correlations?

Predictivity for trait i

$$\text{corr}(y_i - Xb_i, \hat{u}_i) = \text{acc}_i h_i$$

What is predictivity from trait i to trait j?

$$\text{corr}(y_i - Xb_i, \hat{u}_j) = ?$$

.....  
.....

$$\text{corr}(y_i - Xb_i, \hat{u}_j) = \text{acc}_j \text{corr}_{ij} h_i$$

$$\text{corr}_{ij} = \frac{\text{corr}(y_i - Xb_i, \hat{u}_j)}{h_i \text{acc}_j}$$

$$SD(\text{corr}_{ij}) \approx \frac{1}{h_i \text{acc}_j \sqrt{N_{val}}}$$

# Test by simulation

	Trait 1	Trait 2
<b>Validation population</b>	10k	10k
<b>Heritability</b>	0.3	0.2
<b>Correlation</b>		-0.5
<b>Accuracy</b>	0.8	0.3

## Estimate

$\text{corr}_{12}$

$-0.50 \pm 0.06$

$\text{corr}_{21}$

$-0.50 \pm 0.03$

# Procedure

- Select reference population, number of genotyped  $N > 10,000$
- Select validation population, number of genotyped  $N_{\text{val}} > 5000$
- 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 
$$acc = \text{corr}(y - Xb, \widehat{u}) / h$$

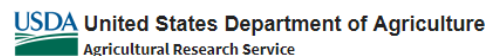
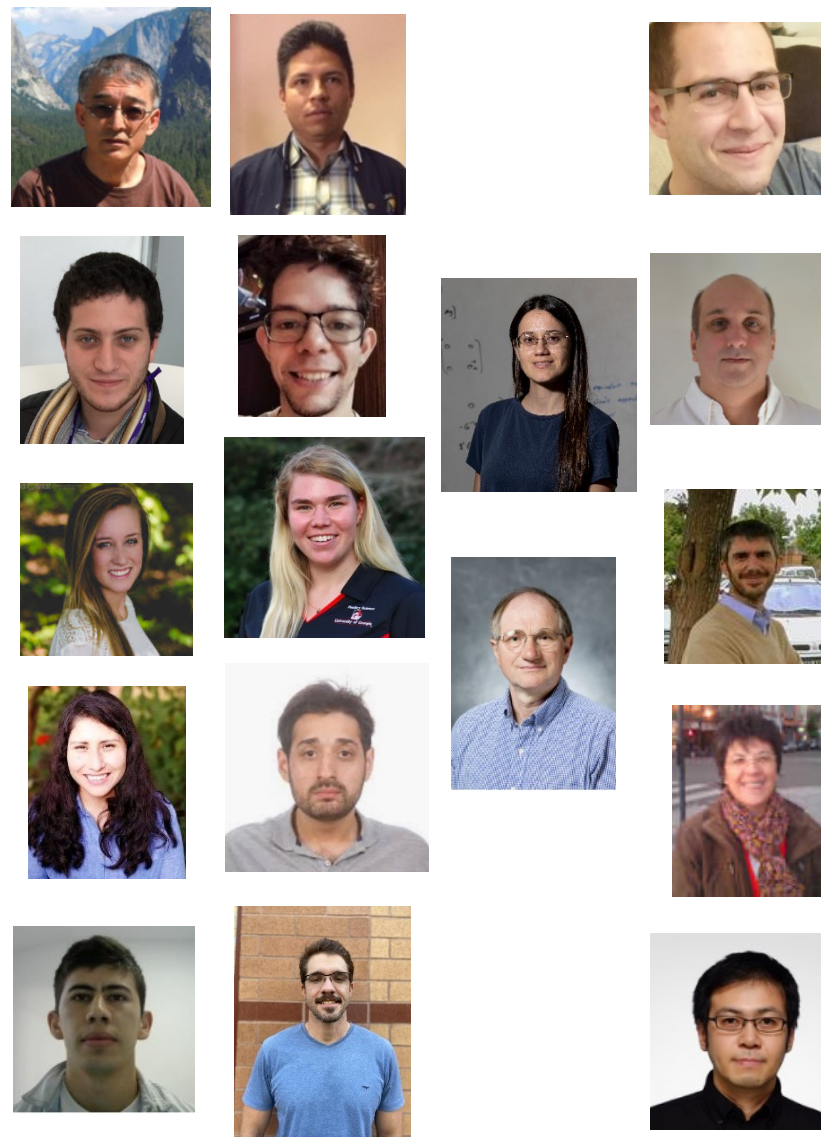
- Calculate genetic correlations 
$$\text{corr}_{ij} = \frac{\text{corr}(y_i - Xb_i, \widehat{u}_j)}{h_i \text{acc}_j} \pm \frac{1}{h_i \text{acc}_j \sqrt{N}}$$

– Select correlation with smaller SE

# Conclusions

- Estimate of heritability from theoretical and realized accuracies
- Estimate of genetic correlations by predictivity across traits
- Any data size and data slice
- Low standard errors with large reference and validation populations

# UGA AB&G team



Warmwater Aquaculture Research Unit



Cool and Cold Water Aquaculture Research

