

# Improving the efficiency of heritability estimation with genomic information – Method R

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**Animal Breeding and  
Genetics Group**

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# Why is VCE expensive?



- REML (Patterson and Thompson, 1971)
  - Requires inversion of the LHS of MME
  - Becomes too expensive or unattainable
- Bayesian via Gibbs sampling
  - Costly with GS → dense MME matrices
- APY (Miszta et al., 2014)
  - Limited success in REML (Junqueira et al., 2022)

# Change in VCE over time



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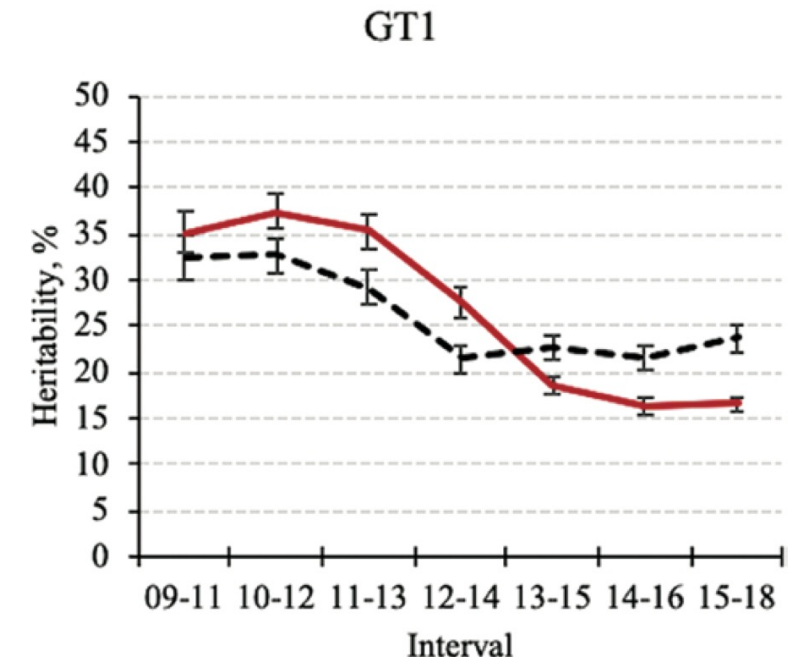
## ANIMAL GENETICS AND GENOMICS

### Changes in genetic parameters for fitness and growth traits in pigs under genomic selection

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- Selection decreases heritability over time
- Reason for routine VCE updates
- Heritability may be different with genomics



# Objectives



- Compare heritability estimation with genomic information using AIREML and Method R
- Reduce computing expense of heritability estimation with large genomic models

$$E[b_{w,p}] = \frac{E[\hat{\mathbf{u}}_w' \hat{\mathbf{u}}_p]}{E[\hat{\mathbf{u}}_p' \hat{\mathbf{u}}_p]} = 1$$

$b_1 > 1$  : heritability underestimated

$b_1 < 1$  : heritability overestimated

# Materials and Methods



- QMSim - 10 non-overlapping generations, 5,000 animals each
- $h^2 = 0.3$ , all genotyped at 50k SNP
- External genomic selection by GBLUP
  - $\mathbf{y} = \mathbf{u} + \mathbf{e}; \text{Var} \begin{bmatrix} \mathbf{u} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{G}\sigma_a^2 & 0 \\ 0 & \mathbf{I}\sigma_e^2 \end{bmatrix}$
- Replacement ratios:
  - Sires = 0.9
  - Dams = 0.4

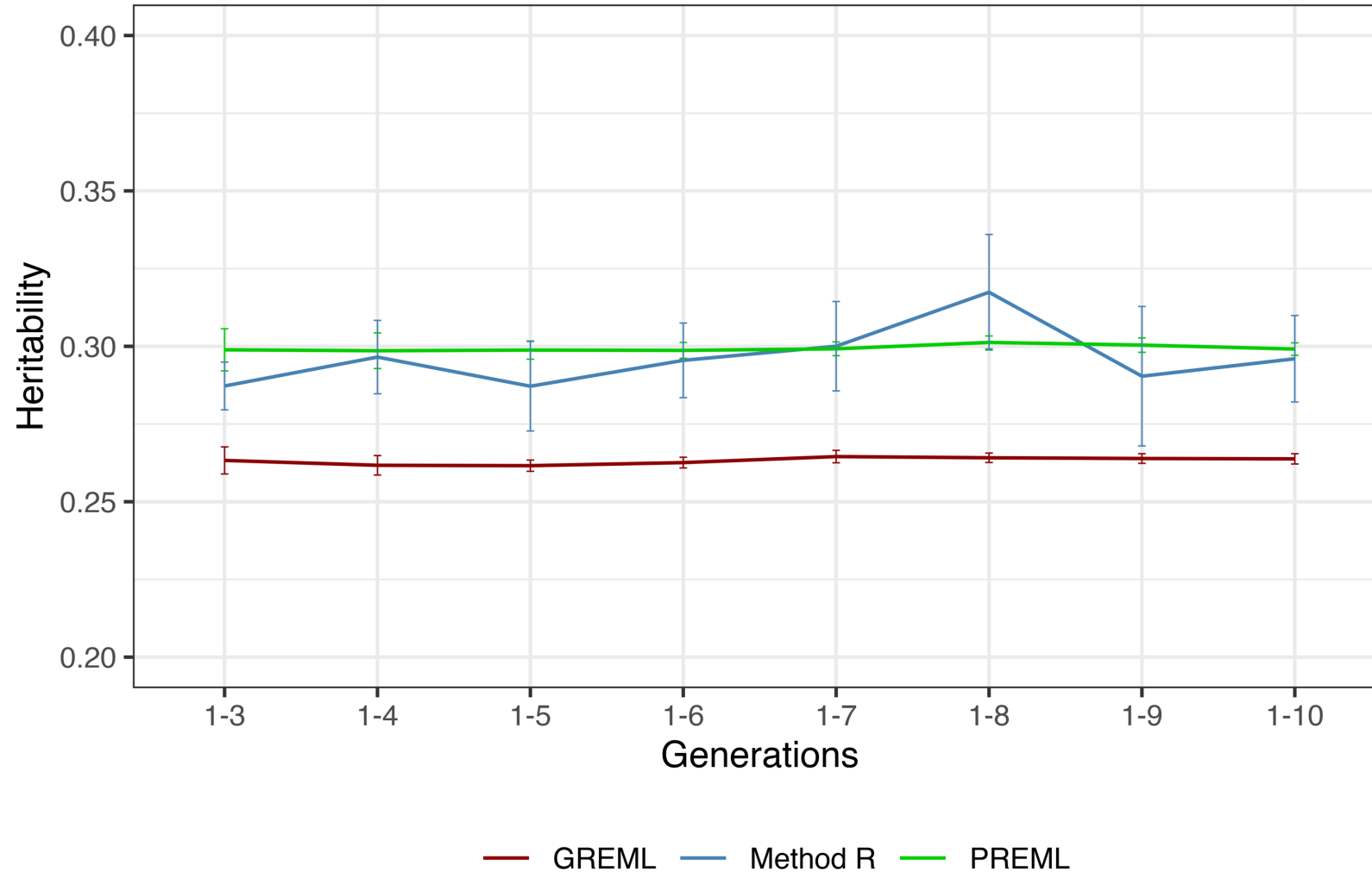
# Heritability Estimation

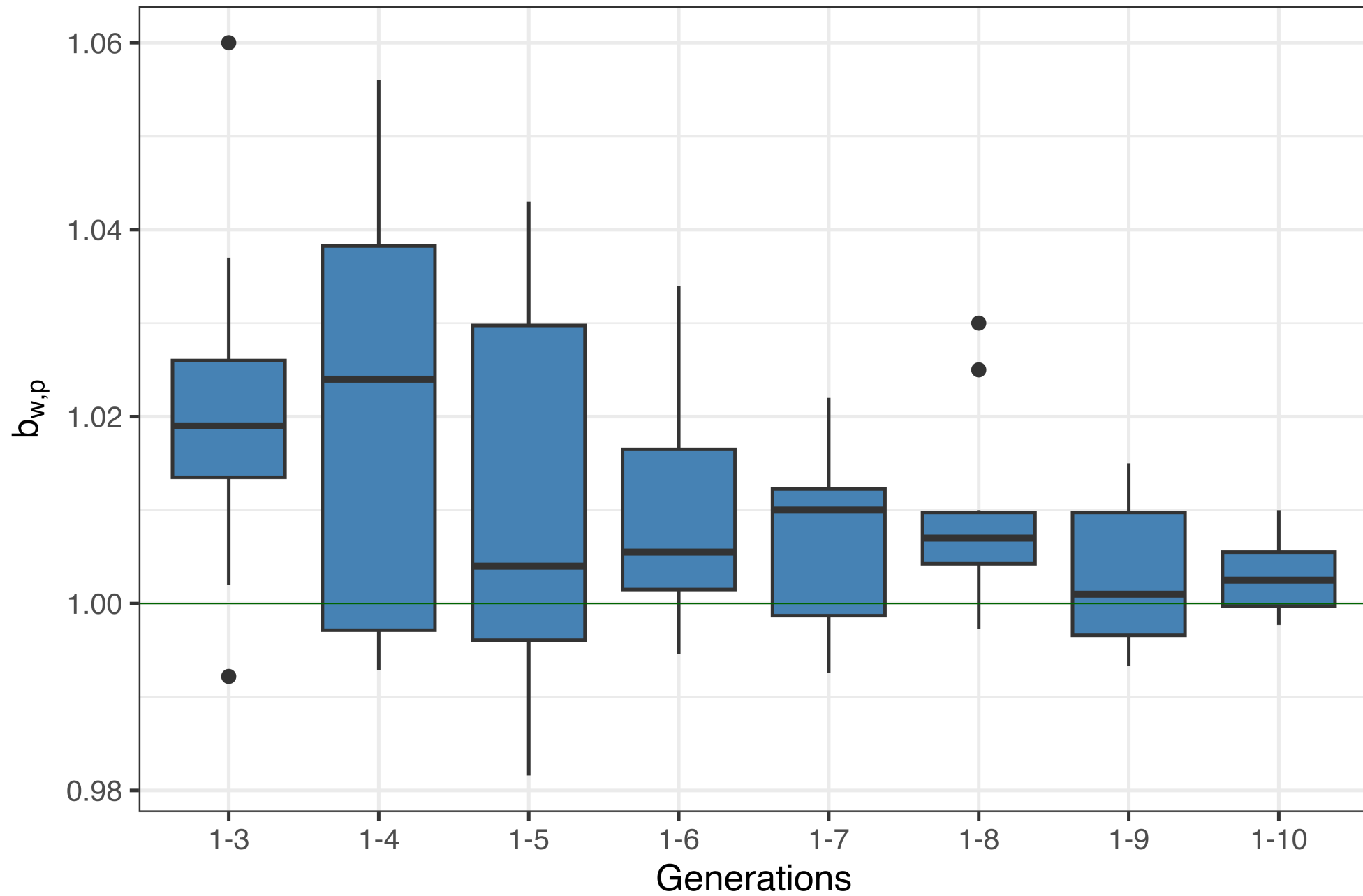


- Method R
  - Partial dataset: most recent generation removed
  - $\lambda = \frac{\sigma_e^2 + (\sigma_a^2 - x)}{x}$ 
    - $x = 1.5, 2.0, 2.5, 3.0, 3.5, \text{ or } 4.0$
    - $\sigma_e^2$  and  $\sigma_a^2$  from GREML
- AIREML (blupf90+; Misztal et al., 2014)
  - GBLUP and PBLUP model

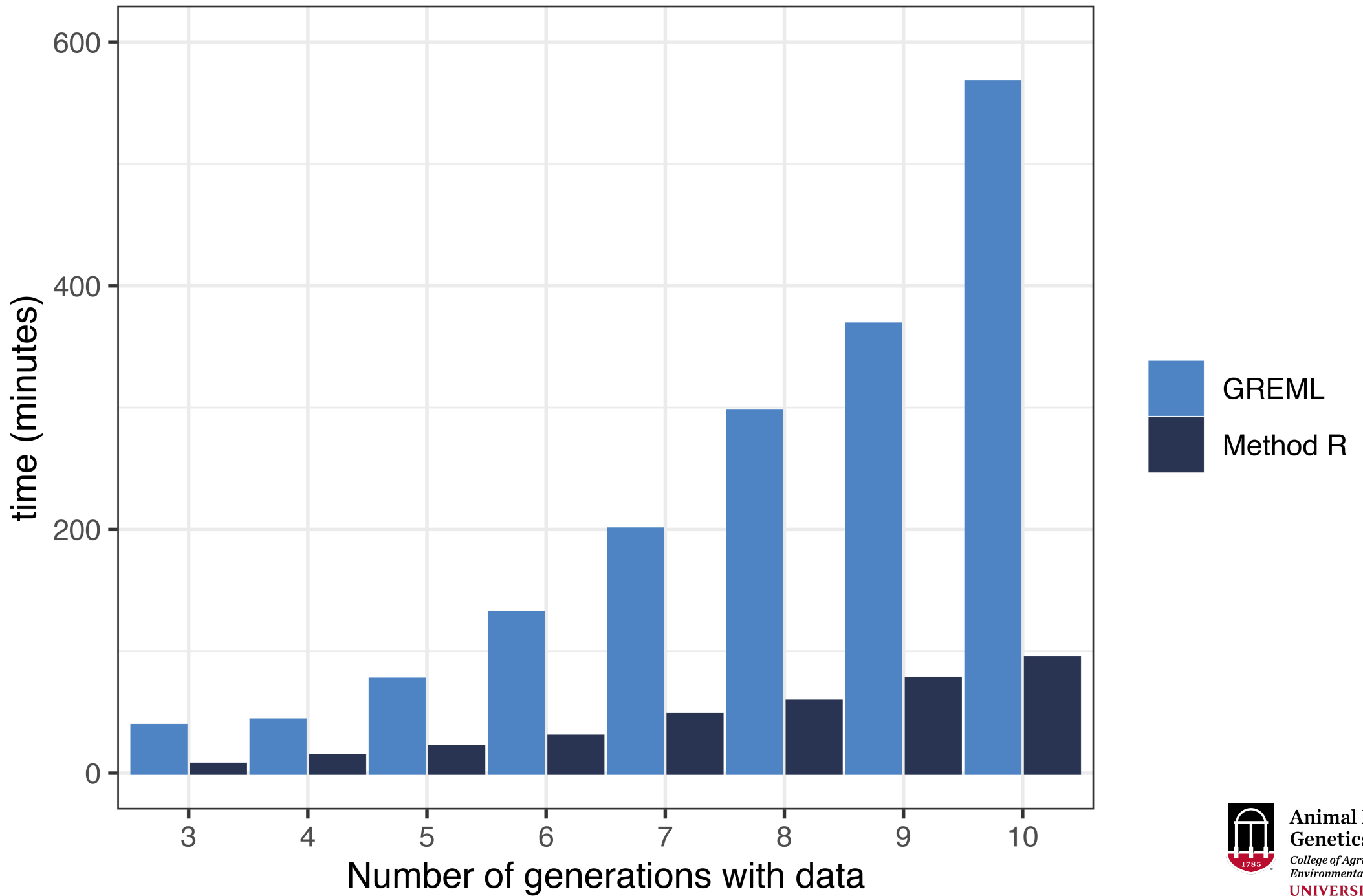
- $$\begin{bmatrix} \mathbf{X}'\mathbf{X} & \mathbf{X}'\mathbf{Z} \\ \mathbf{Z}'\mathbf{X} & \mathbf{Z}'\mathbf{Z} + \lambda\mathbf{G}^{-1} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}} \\ \hat{\mathbf{u}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{y} \\ \mathbf{Z}'\mathbf{y} \end{bmatrix}$$
- $$\text{Var} \begin{bmatrix} \mathbf{u} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{G}\sigma_a^2 & 0 \\ 0 & \mathbf{I}\sigma_e^2 \end{bmatrix}$$
- $$b_1 = \frac{\hat{\mathbf{u}}_w' \hat{\mathbf{u}}_p}{\hat{\mathbf{u}}_p' \hat{\mathbf{u}}_p} = 1$$

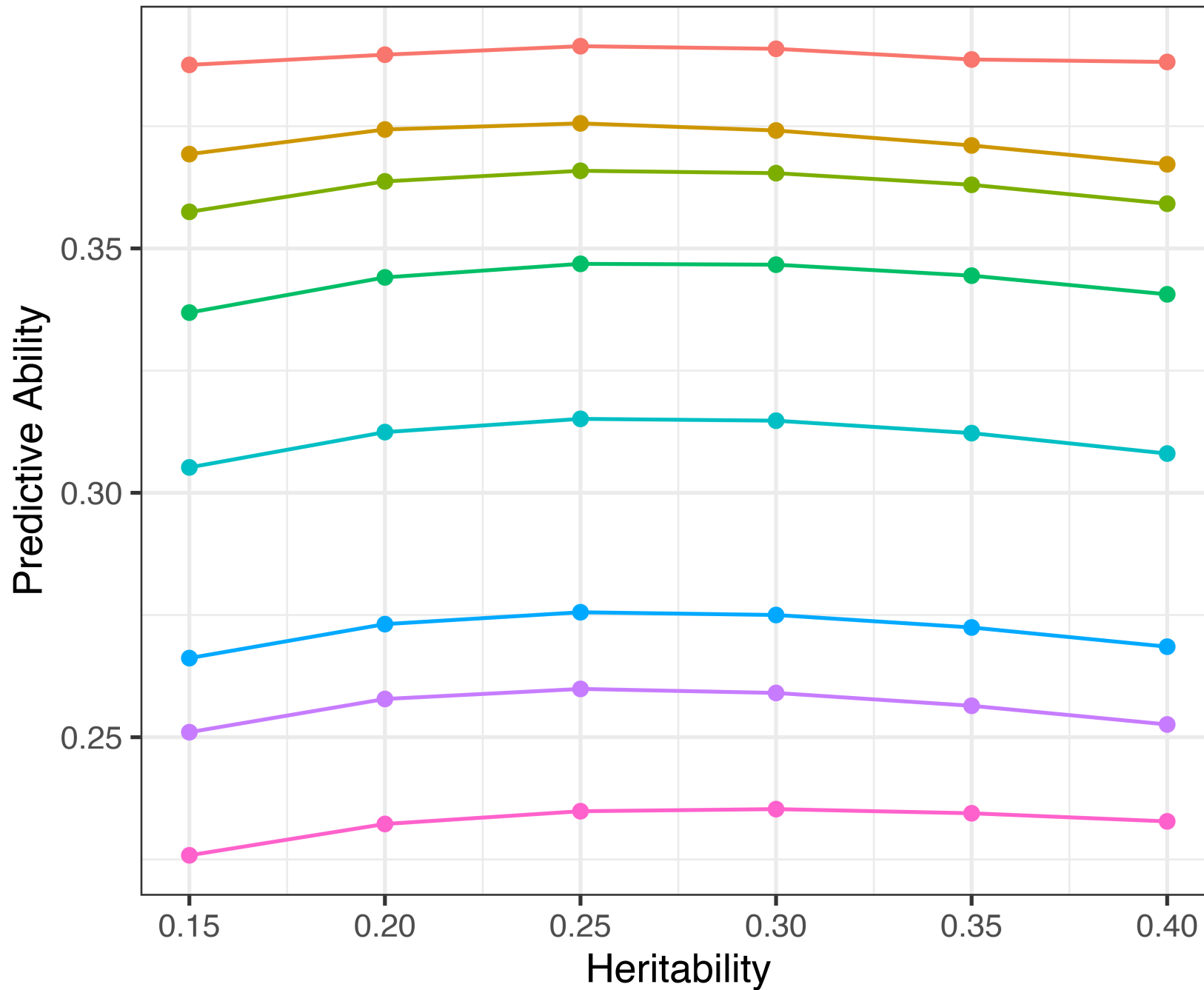
# Results











### Generations

- 1-10
- 1-9
- 1-8
- 1-7
- 1-6
- 1-5
- 1-4
- 1-3



# Conclusions



- Method R: short computing time and relatively low expense
- Estimates are not as precise as GREML
- More research needed in:
  - Real populations
  - Multiple-trait models
  - Additional random effects

Thank You!

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