A method for partitioning trends in genetic mean and variance to understand/improve breeding practices

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Introduction and Motivation

- Dissecting genetic trends is essential for identifying key breeding actions and optimising breeding programmes.
- Managing the genetic variance in breeding programmes is essential to ensure the sustainable selection and long-term genetic gain and prevent inbreeding depression.
- Genetic values are assumed to be multivariate and normally distributed $\boldsymbol{a} \sim N\left(\boldsymbol{0}, \sigma_a^2 \boldsymbol{A}\right)$
- Decomposition: $\sigma_a^2 \boldsymbol{A} = \boldsymbol{T}\boldsymbol{W}\boldsymbol{T}^T\sigma_a^2 \rightarrow$ we can then transform the additive genetic value as: $\boldsymbol{a} = \boldsymbol{T}\boldsymbol{w}$, with $\boldsymbol{w} \sim N\left(\boldsymbol{0}, \sigma_a^2 \boldsymbol{W}\right)$
- Suppose any set $\boldsymbol{P}_1 + \boldsymbol{P}_2 + \boldsymbol{P}_3 + \ldots + \boldsymbol{P}_m = \boldsymbol{I}$, thus: $\boldsymbol{a} = \boldsymbol{T}\left(\boldsymbol{P}_1 + \boldsymbol{P}_2 + \boldsymbol{P}_3 + \ldots + \boldsymbol{P}_m\right)\boldsymbol{w} = \boldsymbol{T}_1\boldsymbol{w} + \boldsymbol{T}_2\boldsymbol{w} + \boldsymbol{T}_3\boldsymbol{w} + \ldots + \boldsymbol{T}_m\boldsymbol{w}$
- Aim: extend the method of [1] to i) partition the genetic variance and integrate the method into `AlphaPart` [2] R package, and ii) apply the partitioning methods to breeding values estimated by posterior sampling [3].

Methods

- As $\widehat{\boldsymbol{a}} = \boldsymbol{T}\widehat{\boldsymbol{w}}$, then $\widehat{\boldsymbol{w}} = \boldsymbol{T}^{-1}\widehat{\boldsymbol{a}}$. Consequently,

$$\begin{aligned}\widehat{\boldsymbol{a}} &= \boldsymbol{T}_1\boldsymbol{T}^{-1}\widehat{\boldsymbol{a}} + \boldsymbol{T}_2\boldsymbol{T}^{-1}\widehat{\boldsymbol{a}} + \boldsymbol{T}_3\boldsymbol{T}^{-1}\widehat{\boldsymbol{a}} + \ldots + \boldsymbol{T}_m\boldsymbol{T}^{-1}\widehat{\boldsymbol{a}} \\ &= \widehat{\boldsymbol{a}}_1 + \widehat{\boldsymbol{a}}_2 + \widehat{\boldsymbol{a}}_3 + \ldots + \widehat{\boldsymbol{a}}_m \end{aligned} \quad (1)$$

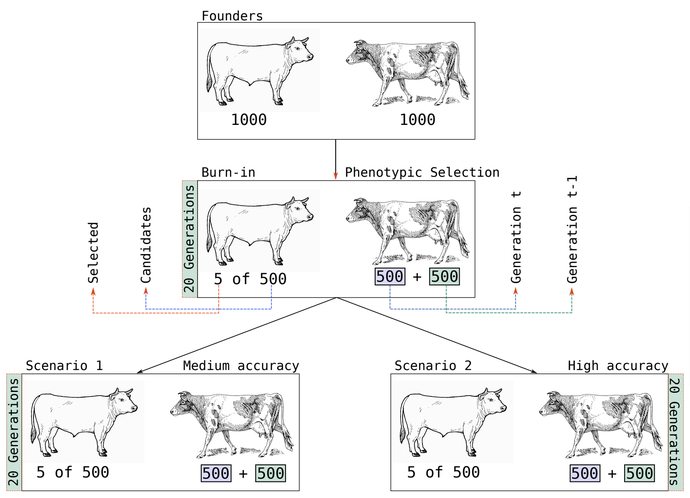
where $\boldsymbol{a}_i$, $i = 1, 2, ..., m$, is a part of the breeding value that can be assigned to the group i.

We extend the partitioning method to analyse the contribution of groups to genetic variance:

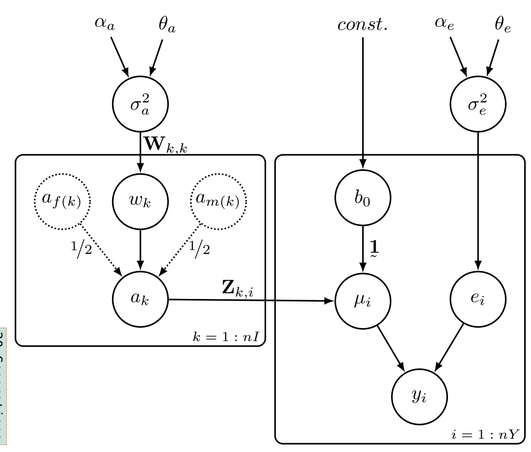
$$Var(\boldsymbol{a}) = Var\left[\left(\boldsymbol{T}_1, \boldsymbol{T}_2, \ldots, \boldsymbol{T}_p\right)\boldsymbol{w}\right] = \sum_{j=1}^{p} Var\left(\boldsymbol{T}_j\boldsymbol{w}\right) + 2\sum_{j=1}^{p-1}\sum_{j'=j+1}^{p} Cov\left(\boldsymbol{T}_j\boldsymbol{w}, \boldsymbol{T}_{j'}\boldsymbol{w}\right),$$

$$= \left(\sum_{j=1}^{p}\boldsymbol{A}_j + 2\sum_{j=1}^{p-1}\sum_{j'=j+1}^{p}\boldsymbol{A}_{j,j'}\right)\sigma_a^2, \quad (2)$$

Simulation and Statistical Model



(a) Breeding Programme



(b) Model

Full Bayesian approach:

$$p\left(b_0\right) \propto \text{const.},$$
$$p\left(\tau_a = 1/\sigma_a^2\right) \propto \tau_a^{\alpha_a - 1}\exp\left(-\theta_a\tau_a\right), \text{ for } \tau_a > 0,\ \alpha_a \geq 0,\ \theta_a \geq 0$$
$$p\left(\tau_e = 1/\sigma_e^2\right) \propto \tau_e^{\alpha_e - 1}\exp\left(-\theta_e\tau_e\right), \text{ for } \tau_e > 0,\ \alpha_e \geq 0,\ \theta_e \geq 0.$$

- We used Markov Chain Monte Carlo (MCMC) to generate samples from the posterior distribution using Gibbs sampler algorithm

$$p\left(b_0, \boldsymbol{a}, \sigma_a^2, \sigma_e^2 | \boldsymbol{y}\right) \propto p\left(\boldsymbol{y} | b_0, \boldsymbol{a}, \sigma_e^2\right) p\left(b_0\right) p\left(\boldsymbol{a} | \boldsymbol{A}, \sigma_a^2\right) p\left(\sigma_a^2\right) p\left(\sigma_e^2\right).$$

References

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[3] Sorensen, D., Fernando, R., Gianola, D.: Inferring the trajectory of genetic variance in the course of artificial selection. **Genetical Research** 77(1), 83–94 (2001). doi:10.1017/S0016672300004845.

Conclusion

- Help breeders and researchers to better understand the genetic gain and variance dynamics in specific breeding programmes
- Method is not limited to working with true breeding values and we can asses the uncertainty of the contributions by drawing samples from the posterior distribution of breeding values
- We should not consider the contribution of different groups in isolation but should perform a holistic analysis and partition of the observed genetic variance instead

Results and Discussion

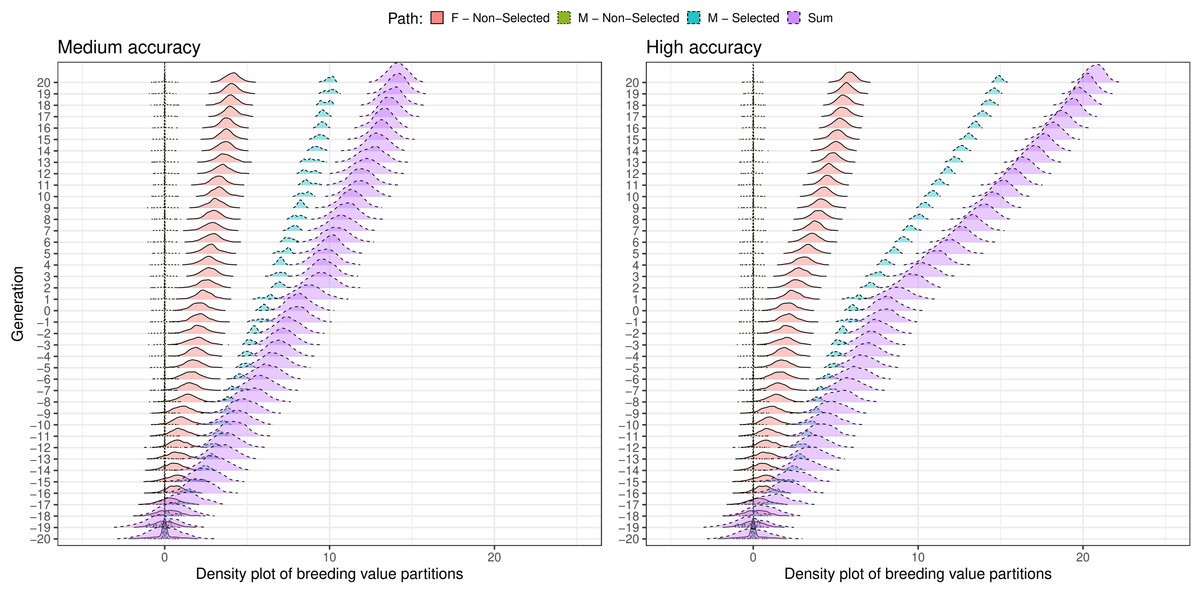

Figure 2: Distribution of breeding value partitions by sex and selection status (selected males (M(S)), non-selected males (M(N)), and females (F)) over generations for medium-accuracy scenario

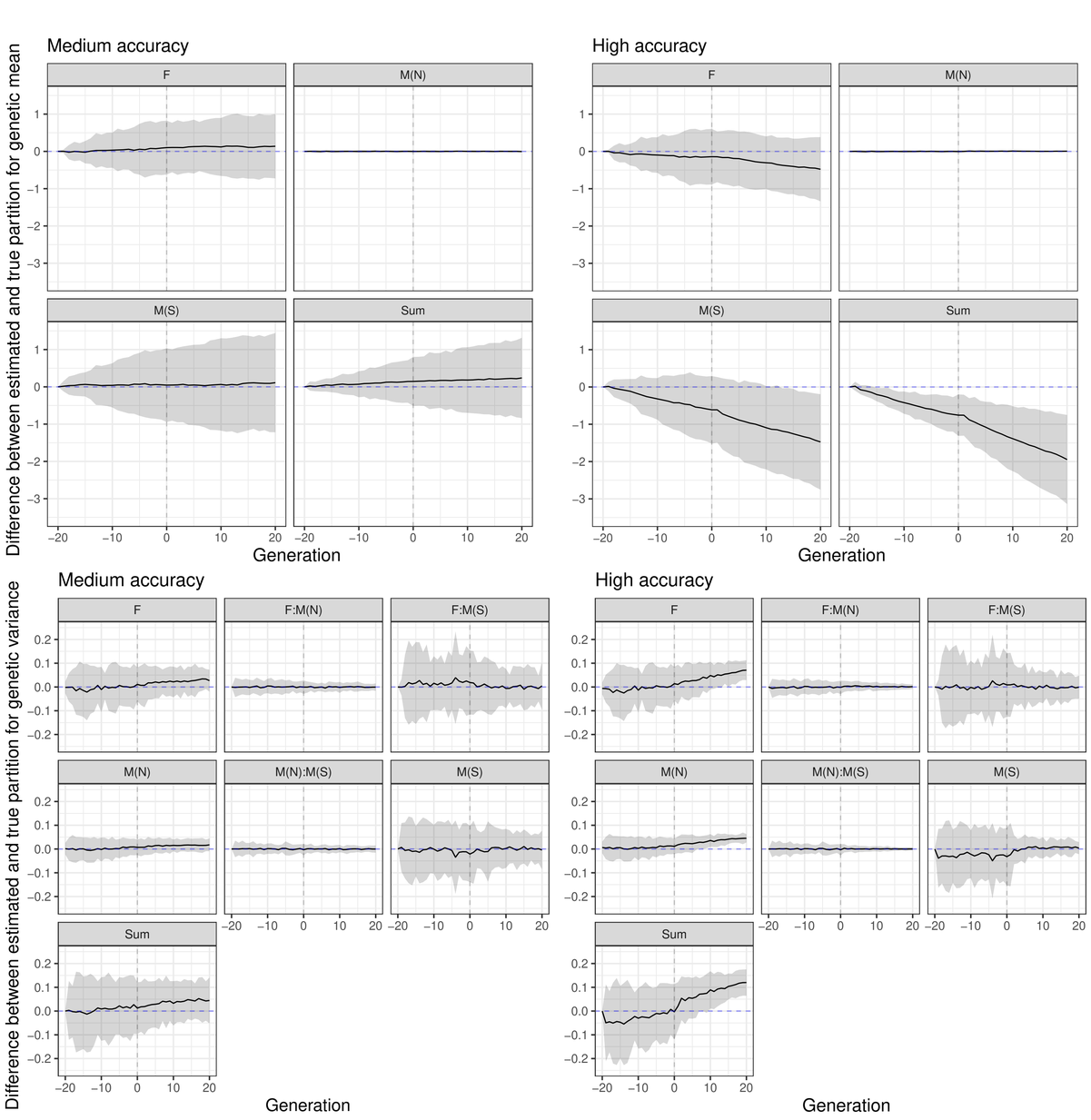

Figure 3: Distribution of the difference between true and estimated contributions for the genetic mean and variance over generations by gender (male (M) and female (F)) and status (selected males (S) and non-selected males (N)) considering 30 simulations replicate

- Extend the methodology to use genomic models to overcome the systematic bias shown in the high accuracy scenario

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