Single-step genomic selection: accommodating several key issues

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Overview

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- **Genomic selection**

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- Motivating Example

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- **Complexities**

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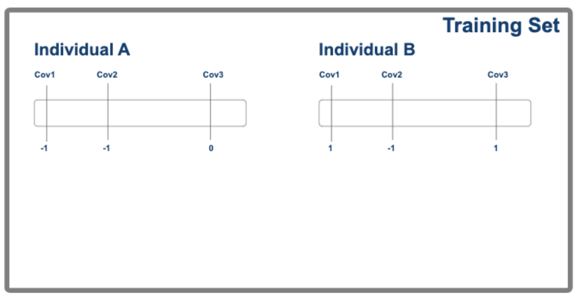
    - These estimated relationships are then used to predict the performance of a set of test individuals

Genomic Selection



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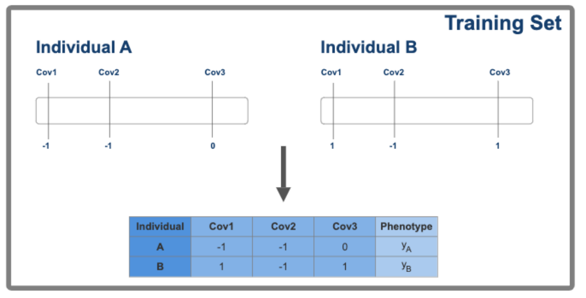

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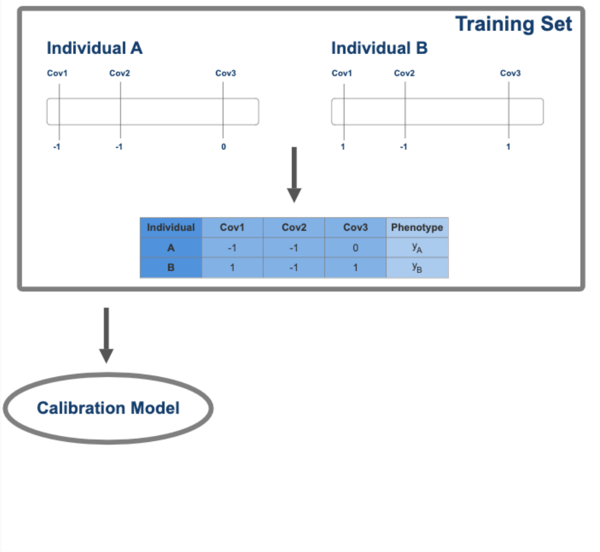

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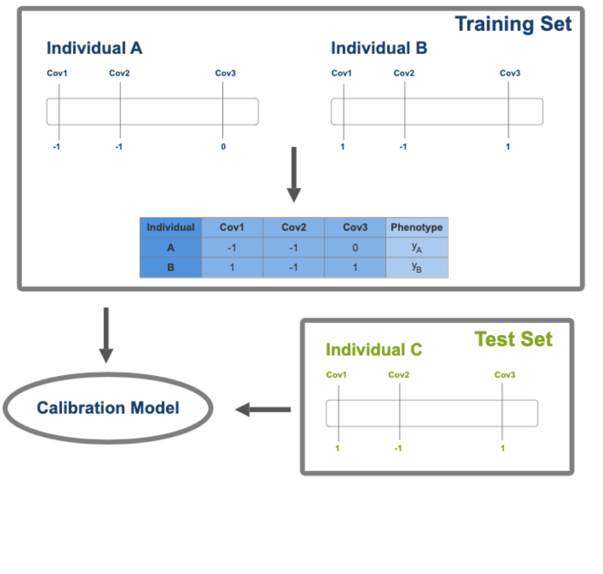

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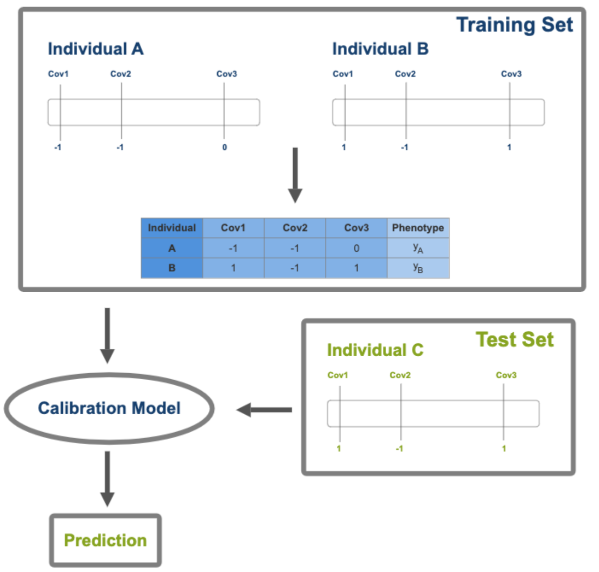

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- For the additive VE effects $\mathbf{u}_a$, covariance between varieties is also modelled via a known relationship matrix denoted $\mathbf{G}$

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- The matrix formed via ancestral records is denoted **A** and known as the numerator relationship matrix (NRM) (Oakey et al. [2007])

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- ψ_a is a diagonal matrix with the site specific variances ψ_{a_i} on the diagonals

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- The final model fit included $k_a = 2$ additive and $k_e = 1$ non-additive factors

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- Several strategies exist to overcome this complexity however the method we have used is a blending of the **K** and **A** relationship matrices

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- The added parameter λ controls the weighting from the two sources of relatedness, with genomic information dominating when $\lambda \approx 1$ and pedigree information dominating when $\lambda \approx 0$

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- However this can be shown graphically through profiling on the parameter of interest (λ) and assessing the residual log-likelihood under a range of values for this parameter

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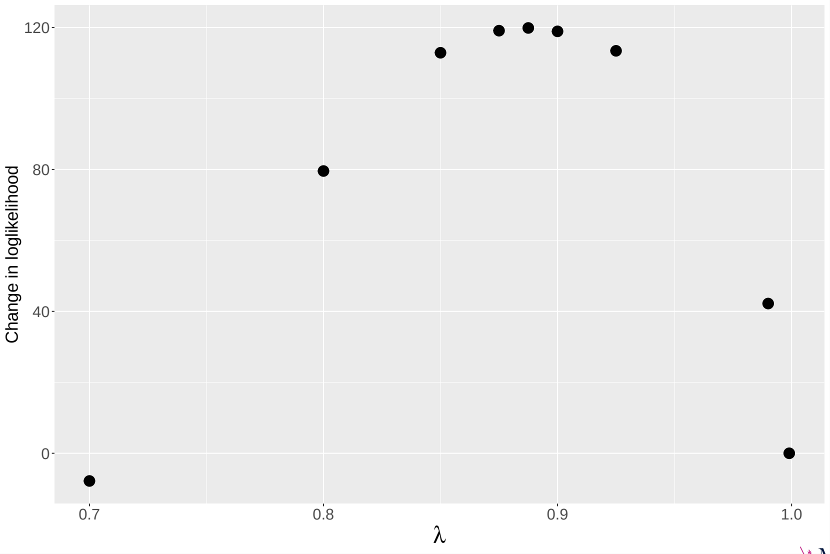

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$$\tilde{\mathbf{f}}_{a_2} = (\mathbf{G}_{21}\mathbf{G}_{11}^{-1} \otimes \mathbf{I}_{k_a})\tilde{\mathbf{f}}_{a_1}$$

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- However many complexities arise in implementation, a few of which have been explored here, specifically singularities in the GRM ($\mathbf{K}$)
- Combining both ancestral and genomic relationship matrices both overcomes this issue
- Finally DWReml (Butler, pers comm) can handle the high computational demand when fitting complex single-step factor models which include genetic relatedness such as the motivating example

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