VETERINARY

Genomic Best Linear Unbiased Prediction

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Introduction

- Genomic best linear unbiased prediction (gBLUP) utilizes genomic relationships to estimate variance components, genomic heritability, and genetic merit.
- A genomic relationship matrix is employed, incorporating DNA marker information and capturing covariance between individuals based on genomic similarity and pedigree information.
- gBLUP utilizes a mixed model framework to estimate genetic values, considering both marker information and relationships between individuals.
- More accurate predictions of genetic merit can be achieved using gBLUP.
- gBLUP is advantageous in that it can make predictions for individuals with limited pedigree information, making it particularly useful in genomic selection.
- By leveraging genetic information from markers across the entire genome, gBLUP enables more precise predictions of an individual's genetic potential, leading to improved breeding strategies and selection outcomes.

Realized versus expected relationship matrix

- With G, we estimate this realized relationship matrix (VanRaden, 2008)
- A is a matrix of expected relationships

E(G)= A

Fixed Model: y = Xb + e $\hat{b} = (X'X)^{-1}$ Xy Random Model: y = Zu + e $\hat{u} = (Z'Z + \lambda A^{-1})^{-1} Zy$ - where A = Relationships Matrix and $\lambda = \frac{V_E}{V_A}$ We say that \hat{u} is BLP of u. u is the vector of TBV's and \hat{u} is the vector of EBV's Mixed Model: y = Xb + Zu + e= fixed effects + breeding values + residual Mixed Model Equations:

Where,

Methods

y = Observational matrix of traits

b = is a vector of fixed effects

u = is a vector of random effects

- X = Design matrix for fixed effect
- Z = Incidence matrix for random effect

$$\begin{pmatrix} \hat{b} \\ \hat{u} \end{pmatrix} = \begin{pmatrix} X'X & X'Z \\ Z'X & Z'Z + \lambda A^{-1} \end{pmatrix}^{-1} \begin{pmatrix} X'y \\ Z'y \end{pmatrix}$$

- ✓ Solutions for the fixed effect:
- ✓ β= (X^{*}X)⁻¹(X^{*}Y)
- ✓ Solutions for the random part
- $\checkmark \hat{u} = (Z'Z + \lambda A^{-1})^{-1}Z'Y$
- ✓ The mixed model is a mixture of a fixed and a random model.

- ✓ Both fixed effects (eg. The mean effect and the year effects) and random effects (usually animals' breeding values) are fitted in the same model and estimated simultaneously in the same analysis.
- ✓ When I use pedigree /BLUP

(\hat{b})	(X'X)	X'Z	$^{-1}(X'y)$
$\left \hat{u} \right =$	Z'X	$Z'Z + \lambda A^{-1}$	(Z'y)

✓ When I use genomic data /GBLUP

(\hat{b})	(X'X)	X'Z	$^{-1}(X'y)$
$\left(\hat{u}\right) =$	Z'X	$Z'Z + \lambda$ G ⁻¹	(Z'y)

Advantages

- In populations without pedigree recording, genomic relationships provide a reliable and well-defined measure of relatedness.
- When using >50K SNP chips, genomic relationships are comparable to pedigree relationships but offer greater precision.
- The specific formula for calculating genomic relationships may vary depending on the intended interpretation, but the results remain largely consistent.
- In cases where a combination of pedigree and molecular relationships is desired, further considerations and adjustments may be necessary to account for both sources of information.