

COMPARISON OF *GBLUP* AND *CGBLUP* POWER OF QTL DETECTION USING THEIR MARKER ESTIMATED EFFECTS

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INTRODUCTION

Since the early work of Meuwissen *et al.* (2001), researchers have proposed different methods of computing genomic breeding values (GBLUP). Those models are most often based on the simultaneous estimation of SNP marker effects a (Gianola *et al.*, 2006). Jahan Bakhshi (2013) proposed a chromosomal genomic model (CGBLUP) in which animal records can be incorporated for separate chromosomal models. Chromosomal models used for making a multivariate analysis that can benefit numerator relationship matrix directly for chromosomal level. However overall estimated marker effects were used primarily for estimating individuals BV but this marker effect used for QTL detection. The objective of this study was comparison of marker effects estimated by conventional GBLUP and CGBLUP for power of QTL detection on genome.

MATERIAL AND METHODS

Stochastic simulation was used in this study. Simulation includes two steps like Meuwissen *et al.* (2001). A procedure as Jahan Bakhshi (2013) was used to simulate a genome consisting 500 bi-allelic genes and 10000 biallelic markers evenly distributed on 10 chromosomes and average linkage disequilibrium of $r^2=0.2$ as a source population. Population size increased to 100000 dams and 500 active sires. Gene effect were sampled from a normal distribution to meet desired trait parameters. Pseudo records were simulated by adding an error component (prediction error) to true breeding values according to $N \sim (0, \frac{1-r^2}{r^2} VarBv)$, in which $r^2 = 0.95$ is reliability of estimated breeding values of sires (CEBV). Two methods GBLUP (Model 1) and CGBLUP model (2) were used to estimate marker effects. Gauss Sidel Iteration with 10-5 convergence criteria was used to estimate marker effects.

$$\hat{g} = (\hat{Z}Z + I\alpha)^{-1}\hat{Z}Y \quad (1.1) \quad \alpha = \frac{\sigma_{PE}^2}{\sigma_g^2} \quad \sigma_g^2 = \frac{\sigma_{BV}^2}{n} \quad (1.2) \quad \hat{a}_i = Z_i\hat{g} \quad (1.3)$$

$$(2.2) \quad (2.1)$$

$$\begin{bmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_{nc} \\ Y_{nc+1} \\ Y_{nc+2} \end{bmatrix} = \begin{bmatrix} Z_1 & 0 & \dots & 0 \\ 0 & Z_2 & \dots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \dots & Z_n \\ Z_1 & Z_2 & \dots & Z_n \\ 0 & 0 & \dots & 0 \end{bmatrix} u + \begin{bmatrix} 0 & W_2 & \dots & W_n \\ W_1 & 0 & \dots & W_n \\ \vdots & \vdots & \ddots & \vdots \\ W_1 & W_2 & \dots & 0 \\ 0 & 0 & \dots & 0 \\ W_1 & W_2 & \dots & W_n \end{bmatrix} g + \begin{bmatrix} e_1 \\ e_2 \\ \vdots \\ e_n \\ e_{(n+1)} \\ e_{(n+2)} \end{bmatrix} \quad Y = Z_f u + W_f g + e_f$$

$$(2.4) \quad (2.3)$$

$$Var(Y_c) = Z_c A \hat{Z}_c \sigma_{u_c}^2 + \sum_{\substack{\hat{c}=1 \\ \hat{c} \neq c}}^{nc} W_{\hat{c}} I W_{\hat{c}} \sigma_{g_{\hat{c}}}^2 + I \sigma_e^2$$

$$(2.6)$$

$$\begin{bmatrix} \hat{Z}_f Z_f + A_f^{-1} \alpha_c & Z_f \hat{W}_f \\ \hat{W}_f Z_f & \hat{W}_f W_f + I \alpha_g \end{bmatrix} \begin{bmatrix} \hat{u} \\ \hat{g} \end{bmatrix} = \begin{bmatrix} \hat{Z}_f Y \\ \hat{W}_f Y \end{bmatrix}$$

$$(2.5)$$

$$A_f^{-1} = \begin{bmatrix} A^{-1} & 0 & \dots & 0 \\ 0 & A^{-1} & & 0 \\ \vdots & & \ddots & \vdots \\ 0 & 0 & \dots & A^{-1} \end{bmatrix}$$

$$\alpha_c = \frac{\sigma_e^2}{\sigma_u^2} \quad \alpha_g = \frac{\sigma_e^2}{\sigma_a^2/m} \quad \sigma_u^2 = \sigma_a^2/n$$

RESULTS

in order to prepare statistical comparison, marker effects were standardized for average and standard deviation of all estimated effects of related model. For all of the QTLs with weak, intermediate and high contribution of traits variance, number of markers meet estimation of over 3 were considerably superior for CGBLUP. Results indicate that CGBLUP can detect QTLs more efficiently than GBLUP.

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