

ON THE EFFICIENCY OF THE NEW GENETIC SELECTION INDEX

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Abstract

A new genetic selection index was proposed by the author in [1] for the case of unknown $E(\underline{Y})$. Here, the efficiency of this index is compared with the index for known $E(\underline{Y})$.

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1. Introduction

Consider the genetic model

$$\underline{Y} = X\underline{\beta} + Z\underline{u} + \underline{e}; \quad \begin{pmatrix} \underline{e} \\ \underline{u} \end{pmatrix} \sim N \left[\begin{matrix} 0 \\ 0 \end{matrix}, \begin{pmatrix} E & 0 \\ 0 & G \end{pmatrix} \right] . \quad \text{--- (1)}$$

Suppose we want to predict a linear combination of the 'genetic' components of the model, say $\underline{L}'\underline{u}$. When $\underline{\beta}$ is known the best predictor for $\underline{L}'\underline{u}$ is given by $\underline{L}'\hat{\underline{u}}_{(1)}$ where

$$\hat{\underline{u}}_{(1)} = GZ'A^{-1}(\underline{Y} - X\underline{\beta}) \quad \text{--- (2)}$$

and

$$A = ZGZ' + E .$$

A new selection index $\hat{\underline{u}}_{(2)}$ was proposed in [1], viz.

$$\hat{\underline{u}}_{(2)} = GZ'P'(PAP')^{-1}P\underline{Y} \quad \text{--- (3)}$$

where

$$P = (I - X(X'A^{-1}X)^{-1}X'A^{-1})$$

and hence a predictor of $\underline{L}'\underline{u}$ is $\underline{L}'\hat{\underline{u}}_{(2)}$.

We shall now show that even when $\underline{\beta}$ is known, (3) can be used and still achieve at least the same efficiency as (2) in terms of variances of the predicted values.

2. The efficiency

For any \underline{l} , we have

$$V(\underline{l}'\hat{\underline{u}}_{(1)}) = \underline{l}'GZ'A^{-1}ZG\underline{l} \quad \text{--- (4)}$$

$$V(\underline{l}'\hat{\underline{u}}_{(2)}) = \underline{l}'GZ'P'(PAP')^{-1}PZG\underline{l} \quad \text{--- (5)}$$

and

$$\begin{aligned} \text{Cov}(\underline{l}'\hat{\underline{u}}_{(1)}, \underline{l}'\hat{\underline{u}}_{(2)}) &= \underline{l}'GZ'A^{-1}AP'(PAP')^{-1}ZG\underline{l} \\ &= \underline{l}'GZ'P'(PAP')^{-1}ZG\underline{l} \\ &= V(\underline{l}'\hat{\underline{u}}_{(2)}) \end{aligned} \quad \text{--- (6)}$$

$$\begin{aligned} \therefore [V(\underline{l}'\hat{\underline{u}}_{(2)})]^2 &= [\text{Cov}(\underline{l}'\hat{\underline{u}}_{(1)}, \underline{l}'\hat{\underline{u}}_{(2)})]^2 \\ &\leq V(\underline{l}'\hat{\underline{u}}_{(1)}) \cdot V(\underline{l}'\hat{\underline{u}}_{(2)}) \end{aligned} \quad \text{--- (7)}$$

Since $V(\underline{l}'\hat{\underline{u}}_{(2)}) \geq 0$, (7) gives

$$V(\underline{l}'\hat{\underline{u}}_{(2)}) \leq V(\underline{l}'\hat{\underline{u}}_{(1)}) \quad \text{for all } \underline{l} .$$

Thus $\underline{l}'\hat{\underline{u}}_{(2)}$ is a more efficient predictor of $\underline{l}'\underline{u}$ than $\underline{l}'\hat{\underline{u}}_{(1)}$ in general. It is easy to see that, when $\underline{\beta}$ is known, $V(\underline{l}'\hat{\underline{u}}_{(1)}) = V(\underline{l}'\hat{\underline{u}}_{(2)})$ since $\underline{l}'\hat{\underline{u}}_{(1)}$ is the minimum variance predictor in that case. The generalization to the case, where

$V\begin{pmatrix} \underline{e} \\ \underline{u} \end{pmatrix} = \begin{pmatrix} E & C \\ C & G \end{pmatrix}$; $C \neq 0$ is straightforward.

Reference

[1] Nair, R. C. [1974] A note on the genetic selection index. BU-539-M in the Biometrics Unit Mimeo Series, Cornell University.