REDUCING INDEX SIZE USING OPTIMIZATION: A FOCUS ON SIMPLICITY

SANTOS, M.G.[1]; BOCK, M. J.[2]; LIMA, A.R.[1]; MARTINS, T.F.[1]; ROCHA, R. F. B[3]; COBUCI, J. A[4]; SILVA, M. V. G. B.[5]; GUIMARAES, S. E. F.[6]

[1]Phd Student in Animal Science, Departamento de Zootecnia, Universidade Federal de Viçosa, email: mateus.g.santos@ufv.br; [2]Master's Student in Animal Science, Departamento de Zootecnia, Universidade Federal de Viçosa;
[3]Postdoctoral Research in Animal Science, Departamento de Zootecnia, Universidade Federal de Viçosa; [4]Full professor, Departamento de Zootecnia, Universidade Federal do Rio Grande do Sul;
[5]Reasercher, Embrapa Gado de Leite;
[6]Full professor, Departamento de Zootecnia, Universidade Federal de Viçosa.

The selection index plays a major role in multi-trait scenarios, allowing for different selection pressures, such as positive, negative, and null. While it is easy to use, especially with empirical weights, an n-trait problem can arise where the index consists mainly of traits without significant correlated response (CR). This study aims to optimize the simplest combination of traits to maximize the index for eight simulated traits. The simulation in AlphaSimR involved 5,000 animals and 29 chromosomes based on the bovine genome. Eight traits were simulated with a fixed phenotypic variance of 1000, and heritabilities were set from 0.05 to 0.40 in 0.05 increments. CR was calculated as $CR = i\sigma_i$, where $\sigma_i^2 = \boldsymbol{X}'\boldsymbol{V}^{-}\boldsymbol{1c}$ with c representing covariances between the target trait's additive value and auxiliary traits, and V as the matrix of phenotypic variances and covariances. Direct selection (DS) response was obtained by multiplying each trait's square root of heritability by its additive genetic variance. The ratio (RA) was calculated by dividing CR by the DS response. Twenty minimal importance points (IP), ranging from 0.00 to 0.20 in 0.01 increments, were used to minimize trait numbers in the index. Traits were added only if they increased the RA beyond the IP threshold. A local search was applied to maximize CR with the fewest traits, the final index was calculated using equal weights, and the Spearman correlation (SC) with the target estimated breeding value was calculated to assess re-raking. CR decreased as heritability increased, with RA ranging from 1.00 to 1.55 (excluding cases where the RA was equal to 1.00, indicating no index was used), and the average ratio for all traits is 1.17. For traits with heritabilities above 0.15, the minimal importance breakdown marked the point where CR provided no advantage over DS; this point depended on the arrangement of genetic and phenotypic covariances within the target and auxiliary traits and approximately 1.06. The SC ranged from 0.30 to 1.00, with lower values observed when an importance of 0.00 was used; in this case, the mean SC was 0.46. In cases where SC was different from 1.00 (indicating that an index was used), the mean was 0.55. The results show that RA is inversely proportional to the target trait's heritability, with the indices proving to be more advantageous for traits with lower heritability. Each trait has a breakdown point that marks the minimal importance value that can be used to minimize the index size. With a lower importance value, SC decreases significantly, indicating that a large index can be inefficient. This approach can be applied to real breeding populations.

Key-Words: local search, correlated response, spearman correlation