

MIX: A SOFTWARE FOR CONSTRUCTION OF MULTI-TRAIT SELECTION INDEX

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INTRODUCTION

To improve the overall productivity of animals, selection based on several traits is the most common approach by breeders. The method of index selection is superior to other selection methods, as selection of animals is based on an index combining all available traits on animals. The MIX is designed to construct selection indices in an easy and user-friendly way. It consists of four modules, viz. General Selection Index (SI), Restricted Selection Index (RSI), Partially Restricted Selection Index (PRSI) and Selection Index with Desired Genetic Gain (SIDG). In all modules, complete information regarding the weightage for each trait, variance of the index, variance of the aggregate genotypic value, accuracy and heritability of the index, the response and genetic cost of restriction for each traits and correlated response for all unselected traits would be presented simultaneously.

COMPUTING METHODS

Smith (1936) applied Fisher's (1936) concept of a discriminant function to select for net merit (genetic-economic value) among plant varieties. Hazel (1943) extended Smith's technique to selection for net merit among individual animals. Cunningham *et al.* (1970) presented a simpler solution to the restricted index than the original method of Kempthorne and Nordskog (1959).

General Selection Index. The selection index (I) is defined as: $I = \mathbf{b}'\mathbf{X}$, where \mathbf{b}' is the vector of weighing coefficients for each trait. The net genetic merit (H) of an individual is a function of the breeding value of each trait (g_i) and their relative economic value (a_i) and can be represented as: $\mathbf{H} = \mathbf{G}\mathbf{a}$. The \mathbf{b} is estimated in such a way that the correlation between I and H (r_{IH}) is maximized and are obtained by solving a set of simultaneous equations: $\mathbf{P}\mathbf{b} = \mathbf{G}\mathbf{a}$, where, \mathbf{P} is the phenotypic variance-covariance matrix of X_i , \mathbf{b} is the vector of weighting coefficients, \mathbf{G} is genotypic variance-covariance matrix of g_i and \mathbf{a} is the vector of relative economic values. Hence, $\mathbf{b} = \mathbf{P}^{-1}\mathbf{G}\mathbf{a}$.

Estimates of other parameters are made as follows: variance of index (σ_I^2) = $\mathbf{b}'\mathbf{P}\mathbf{b}$; variance of the aggregate genotype (σ_H^2) = $\mathbf{a}'\mathbf{G}\mathbf{a}$; correlation of I with H (r_{IH}) = σ_I/σ_H ; response in H (ΔH) = $i\sigma_I$, where 'i' is the intensity of selection; response in the i^{th} trait of the index (δG_i) = $\mathbf{g}_i'\mathbf{b}$ (i/σ_I), where \mathbf{g}_i is the i^{th} column vector of \mathbf{G} matrix; correlated response in the j^{th} trait not included in the index (δG_j) = $\mathbf{g}_j'\mathbf{b}$ (i/σ_I), where \mathbf{g}_j is the column vector of the additive genetic covariance of j^{th} trait with traits included in the index; heritability of the index (h_I^2) = $(\mathbf{b}'\mathbf{G}\mathbf{b})/(\mathbf{b}'\mathbf{P}\mathbf{b})$; genetic cost of reduction (%) = $100 \{1 - \sqrt{[(\mathbf{b}'\mathbf{P}\mathbf{b} - b_i^2/w_{ii})/(\mathbf{b}'\mathbf{P}\mathbf{b})]}\}$, where b_i is the weighting coefficients for the i^{th} trait, w_{ii} is the corresponding diagonal elements of \mathbf{P}^{-1} and $\mathbf{b}'\mathbf{P}\mathbf{b}$ is the variance of the index.

Restricted Selection Index. In RSI, the restriction is imposed in one or more traits that are incorporated in aggregate genotypes. The restricted selection index could be constructed after solving the following equations as per Cunningham *et al.* (1970): $\mathbf{P}^*\mathbf{b}^* = \mathbf{G}^*\mathbf{a}^*$. The $(n+1)^{\text{th}}$ column of \mathbf{P}^* consists of the j^{th} column of \mathbf{G} (genetic covariance of the other variances (X_i) with the trait

being restricted, for its first 'n' elements and with a zero in the final position. For getting \mathbf{G}^* , a row of zero is added to the \mathbf{G} matrix equivalent to the restriction of a trait. The \mathbf{a}^* is the vector of the relative economic value in which zero is assigned for the trait to be restricted.

Partially Restricted Selection Index. The theoretical background for PRSI is same as that of RSI (Cunningham *et al.*, 1970). In PRSI, the last element in \mathbf{P}^* is replaced by $(-k/b_d)$, where 'k' is a constant. The estimates of \mathbf{b} and other parameters are same as discussed earlier.

Selection Index with Desired Genetic Gain. The SIDG was constructed according to Yamada *et al.* (1975). They described the index, which attains predetermined breeding goals in minimum number of generations of selection. The breeding goals are defined as ultimate levels of the traits of the interest, expressed as the deviations from present population means. If the intended changes in the means of 'n' traits are by the amount of Q_i ($i = 1, 2, 3, \dots, n$), then \mathbf{Q} is defined as $(n \times 1)$ vector of intended genetic change for 'n' traits. The \mathbf{Q} vector can be represented as: $\mathbf{Q}' = [Q_1, Q_2, \dots, Q_n]$. The weighting coefficients for SIDG can be estimated as: $\mathbf{b} = \mathbf{P}^{-1}\mathbf{G}[\mathbf{G}'\mathbf{P}^{-1}\mathbf{G}]^{-1}\mathbf{Q}$.

USE

The MIX is ideal for teachers, students, researchers as well as practicing animal breeders. MIX can construct four types of indices combining different traits according to the choice of the user. MIX could be used in a variety of circumstances. The module SI could be used for construction of indices combining several traits to obtain the index that would have better accuracy and efficiency. The module RSI or PRSI are usually applied in a selection programme when it is designed to optimise selection for a given aggregate genotype on the condition that no genetic change or a given degree of genetic change would occur in one or more traits. The module SIDG could be used for obtaining maximum benefit from selection index with predetermined genetic goal for each trait particularly in cases where assigning relative economic values for traits is difficult.

AVAILABILITY

The complete package consisting the programme and manual are presently available directly from our institute with the payment of a nominal processing fee. The availability of MIX in the institute web site is under consideration for distributing it freely to scientific community.

COMPUTING ENVIRONMENT

M-MIX is executable in the environment of Windows 95 or later version. The PC users should also have pre-installed macro-enabled MS-Excel 97 or later version. M-MIX is written in Visual Basic. It is very user-friendly and one who has prior knowledge in Animal Breeding could use it effectively without any difficulty.

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