Original article

Restricted multistage selection indices

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Summary – Multistage selection index is an important extension to single stage selection index for genetic improvement of multiple traits. Recently, a multistage selection procedure, referred to as selection index updating, has been developed. This procedure combines several desired aspects of independent culling and selection index. In this study, we directly extend selection index updating to cases of restricted multistage selection indices by imposing restrictions for solving index coefficients. The resulting indices restrict genetic changes to zero or to some proportion in the chosen characters or linear functions of characters. As such, it makes multistage selection indices more flexible. The possibility of imposing restrictions on different stages is also discussed. A numerical example is given to illustrate the calculation of restricted multistage selection indices.

independent culling / multistage selection / restricted selection index / sequential selection

Résumé – **Index contraints dans la sélection à étapes.** *L'index de sélection à plusieurs étapes est une extension importante de l'index de sélection à une seule étape. Récemment, Xu et Muir ont développé une procédure de sélection à plusieurs étapes appelée index de sélection avec mise à jour. Cette procédure combine plusieurs aspects intéressants de la sélection sur index et de la sélection à niveaux indépendants. Dans cette étude, nous étendons directement la mise à jour des index de sélection au cas d'index de sélection à plusieurs étapes en imposant des restrictions pour trouver les coefficients des index. Les index correspondants contraignent les progrès génétiques à être nuls ou à être dans des rapports donnés pour des caractères ou des combinaisons de caractères. De la sorte, les index de sélection multiétapes sont plus souples. La possibilité d'imposer des restrictions à différentes étapes est aussi discutée. Un exemple numérique est donné pour illustrer le calcul des index de sélection multiétapes contraints.*

sélection à niveaux indépendants / sélection multiétapes / index de sélection contraint / sélection séquentielle

INTRODUCTION

The genetic merit of a plant or an animal is often defined as a function of several traits, and is predicted by an index that combines information on its own and relatives' measurements. Smith (1936) and Hazel (1943) presented a linear index

that maximizes the improvement of an overall genetic value for all traits. Later, Kempthorne and Nordskog (1959) introduced the idea of restricted selection index, which holds certain characters constant while allowing other characters to increase freely. Tallis (1962) and Harville (1975) extended this idea to the case where some traits can be changed by amounts proportional to a predetermined selection goal. Rao (1962) presented a method for computing an index to improve one trait while requiring changes in other traits to be in specific directions. James (1968) showed how restrictions could simultaneously be imposed on the genetic results of selection and on the index weighting factors. The theory of restricted selection indexes was further extended by Niebel and Van Vleck (1982). They introduced fixed and proportional restrictions when more than one selection index is used in a population. A detailed review of restricted selection indices was given by Brascamp (1984).

When traits have a developmental sequence in ontogeny or there is a large difference in the cost of measuring various traits, independent culling or multistage index selection for multiple trait genetic improvements is the most efficient procedure with respect to cost saving owing to the possibility of early culling (Young and Weiler, 1960; Young, 1964; Namkoong, 1970; Cunningham, 1975; Ducrocq and Colleau, 1989; Norell et al, 1991). In most cases, the extension of these developments for independent culling selection to the case of selecting combination of traits at each stage is straightforward. Recently, Xu and Muir (1991, 1992) developed a multistage selection procedure, referred to as selection index updating, that combines several desired aspects of independent culling and selection index. Use of selection index updating allows breeders to determine the optimum truncation points for the maximization of genetic gain in aggregate breeding value, economic return in terms of genetic gain per unit cost, or profit.

In all multistage selection procedures presented by those authors, the selection goal was to improve all characters without restrictions. However, a breeder may be interested in increasing the overall genetic gain with restrictions that certain traits remain constant or change in a predetermined amount. For instance, a poultry breeder may feel that mean egg size should be kept at a constant intermediate level while using a multistage selection index to maximize overall economic value. The breeder may manage this based on body weight and egg weight measured at the first stage, and production at the second stage. Hence, a two-stage restricted selection index may arise in practice. The purpose of the present note is to extend restricted single stage selection indices to the case of restricted multistage selection indices.

THEORY

In subsequent derivations the assumptions and notation will be similar to those of Xu and Muir (1992). For convenience, the relevant notation is summarized below:

$\mathbf{y}$ = an $n \times 1$ vector of phenotypic values of n traits with elements y_i,

$\mathbf{g}$ = a $k \times 1$ vector of genetic values of k traits to be improved with elements g_i,

$\mathbf{w}$ = a $k \times 1$ vector of economic weights with elements w_j,

Z = $\mathbf{b}^T \mathbf{y}$, selection index, where the superscript T denotes matrix transposition,

$H = \mathbf{w}^T \mathbf{g}$, the aggregate breeding value,
$\mathbf{P} = \text{Var}(\mathbf{y})$, an $n \times n$ phenotypic variance–covariance matrix,
$\mathbf{G} = \text{Cov}(\mathbf{y}, \mathbf{g}^T)$, an $n \times k$ genetic covariance matrix, and
$\mathbf{G}_r = $ an $n \times r$ matrix corresponding to the r columns (restrictions) of $\mathbf{G}$.

Suppose that n traits are to be selected in m stages ($m < n$). The phenotypic values of n traits, $\mathbf{y}$, can be partitioned into m subvectors, $\mathbf{y}_1$, $\mathbf{y}_2 \ldots \mathbf{y}_m$. For example, if there are four traits to be selected in three stages, y_1 and y_2 are measured in the first stage, y_3 is obtained in the second stage, and y_4 is measured in the third stage, then $\mathbf{y} = [y_1 \ y_2 \ y_3 \ y_4]^T$, $\mathbf{y}_1 = [y_1 \ y_2]^T$, $\mathbf{y}_2 = [y_1 \ y_2 \ y_3]^T$, and $\mathbf{y}_3 = [y_1 \ y_2 \ y_3 \ y_4]^T$. For simplicity, vector $\mathbf{n} = \{n_1, n_2, \ldots, n_m\}$ represents the number of traits measured up to stage m, where n_i denotes the number of traits measured up to the ith stage. Let $\mathbf{z} = [Z_1 \ Z_2 \ Z_3]^T$ be a 3×1 vector of the updated selection indices defined by Xu and Muir (1992), then the indices for the above example are

$$\mathbf{z} = \mathbf{B}^T \mathbf{y} \qquad [1]$$

where

$$\mathbf{B} = \begin{bmatrix} b_{11} & b_{12} & b_{13} \\ b_{21} & b_{22} & b_{23} \\ 0 & b_{32} & b_{33} \\ 0 & 0 & b_{43} \end{bmatrix}$$

is a 4×3 matrix with the ith column, $\mathbf{b}_i$, representing the weights for the selection indices at the ith stage. Thus, the selection index at the ith stage is

$$Z_i = \mathbf{b}_i^T \mathbf{y}_i, \ i = 1, 2, \ldots, m \qquad [2]$$

According to $\mathbf{y}_1, \mathbf{y}_2, \ldots, \mathbf{y}_m, \mathbf{P}$ and $\mathbf{G}$ can be correspondingly partitioned as:

$$\mathbf{P} = \begin{bmatrix} \mathbf{P}_{11} & \mathbf{P}_{12} & \cdots & \mathbf{P}_{1m} \\ \mathbf{P}_{21} & \mathbf{P}_{22} & \cdots & \mathbf{P}_{2m} \\ & \vdots & & \vdots \\ \mathbf{P}_{m1} & \mathbf{P}_{m2} & \cdots & \mathbf{P}_{mm} \end{bmatrix} \quad \text{and} \quad \mathbf{G} = \begin{bmatrix} \mathbf{G}_1 \\ \mathbf{G}_2 \\ \vdots \\ \mathbf{G}_m \end{bmatrix} \qquad [3]$$

Let $\mathbf{Q}$ be a submatrix of $\mathbf{P}$ and $\mathbf{A}$ be a submatrix of $\mathbf{G}$, ie, $\mathbf{Q}_{ij} = [\mathbf{P}]_{i x j}$ and $\mathbf{A}_i = [\mathbf{G}]_i$ for $i, j = 1, 2, \ldots, m$. Note that $[\mathbf{G}]_i$ differs from $\mathbf{G}_r$ defined before. Selection response based on an index that maximizes the economic values of selected individuals is proportional to ρ_{ZH} (Kempthorne and Nordskog, 1959), the correlation between index (Z_i) values and genetic merits ($H = \mathbf{w}^T \mathbf{g}$), that is

$$\rho_{ZH}^2 = \frac{\text{Cov}^2(Z_i, H)}{\sigma_Z^2 \sigma_H^2} = \frac{(\mathbf{w}^T \mathbf{A}_i^T \mathbf{b}_i)^2}{\mathbf{b}^T \mathbf{Q}_{ii} \mathbf{b}_i \mathbf{w}^T \mathbf{A} \mathbf{w}} \qquad [4]$$

where $\mathbf{A}$ is the covariance matrix of genetic values of k traits. The $\mathbf{b}_i$s are found such that ρ_{ZH} is a maximum or equivalently

$$E[(\mathbf{b}_i^T \mathbf{y}_i - \mathbf{w}^T \mathbf{g})^T (\mathbf{b}_i^T \mathbf{y}_i - \mathbf{w}^T \mathbf{g})] \qquad [5]$$

is a minimum subject to the restrictions

$$\mathrm{Cov}(\mathbf{g}_r, Z_i) = \mathbf{G}_r^T \mathbf{b}_i = \mathbf{k}_r \tag{6}$$

$$\mathrm{Cov}(Z_i, \mathbf{z}_{(i-1)}) = \mathbf{b}_i^T \mathbf{Q}_{i(i-1)} \mathbf{B}_{(i-1)} = \mathbf{0} \tag{7}$$

where $\mathbf{g}_r$ is a $r \times 1$ vector of genetic values for r restricted traits, $\mathbf{k}_r$ is a $r \times 1$ vector of desired values, $\mathbf{z}_{(i-1)} = [Z_1, \ldots, Z_{(i-1)}]$ is a vector of selection indices, and $\mathbf{B}_{(i-1)}$ is a submatrix of B that contains index coefficients up to stage $i - 1$. To insure there exists a solution, it has to be that $r < n_i$, ie, the number of restrictions at a given stage should be less than the number of characters at the same stage. The first restriction [6] constrains some characters to be changed in predetermined amounts (Tallis, 1962). The second restriction [7], requiring that indices at different stages are independent, insures the existence of an exact solution for truncation points without resorting to multiple integration (Xu and Muir, 1991, 1992).

After introducing Lagrange multipliers of λ and τ (λ is an r vector and τ is an $m - 1$ vector), the optimum $\mathbf{b}_i$ is found by minimizing the following quantity with respect to $\mathbf{b}_i$:

$$\mathbf{T} = \mathbf{b}_i^T \mathbf{Q}_{ii} \mathbf{b}_i - 2\mathbf{b}_i^T \mathbf{A}_i \mathbf{w} + \mathbf{w}^T \mathbf{A} \mathbf{w} - 2\lambda^T(\mathbf{G}_r \mathbf{b}_i - \mathbf{k}_r) - 2\tau^T(\mathbf{b}_i^T \mathbf{Q}_{i(i-1)} \mathbf{B}_{(i-1)}) \tag{8}$$

Vector differentiation gives

$$\partial \mathbf{T}/\partial \mathbf{b}_i = 2\mathbf{b}_i^T \mathbf{Q}_{ii} - 2\mathbf{w}^T \mathbf{A}_i - 2\lambda^T \mathbf{G}_r - 2\tau^T \mathbf{B}_{(i-1)}^T \mathbf{Q}_{(i-1)i} = \mathbf{0} \tag{9}$$

or

$$\mathbf{b}_i = \mathbf{Q}_{ii}^{-1}(\mathbf{G}_r^T \lambda + \mathbf{R}_{i(i-1)}^T \tau + \mathbf{w}^T \mathbf{A}_i) \tag{10}$$

where $\mathbf{R}_{i(i-1)} = \mathbf{B}_{(i-1)}^T \mathbf{Q}_{(i-1)i}$. From constraints [6] and [7], we obtain

$$\mathbf{G}_r \mathbf{Q}_{ii}^{-1}(\mathbf{G}_r^T \lambda + \mathbf{R}_{i(i-1)}^T \tau + \mathbf{w}^T \mathbf{A}_i) - \mathbf{k}_r = \mathbf{0} \tag{11a}$$

$$\mathbf{R}_{(i-1)i} \mathbf{Q}_{ii}^{-1}(\mathbf{G}_r^T \lambda + \mathbf{R}_{i(i-1)}^T \tau + \mathbf{w}^T \mathbf{A}_i) = \mathbf{0} \tag{11b}$$

where $\mathbf{R}_{(i-1)i} = \mathbf{Q}_{i(i-1)} \mathbf{B}_{(i-1)} = \mathbf{R}_{i(i-1)}^T$. After solving equations [11a, b] for λ and τ and substituting them into [10], we have

$$\mathbf{b}_i = \{(\mathbf{I} - \mathbf{Q}_{ii}^{-1}\mathbf{M}_i)[\mathbf{I} - \mathbf{Q}_{ii}^{-1}\mathbf{G}_r^T \mathbf{H}_i^{-1}\mathbf{G}_r(\mathbf{I} - \mathbf{Q}_{ii}^{-1}\mathbf{M}_i)]\}\mathbf{Q}_{ii}^{-1}\mathbf{A}_i \mathbf{w}$$
$$+ (\mathbf{I} - \mathbf{Q}_{ii}^{-1}\mathbf{M}_i \mathbf{Q}_{ii}^{-1})\mathbf{G}_r^T \mathbf{H}_i^{-1}\mathbf{k}_r \tag{12}$$

where $\mathbf{I}$ is an identity matrix with the same dimension as $\mathbf{Q}_{ii}$, and

$$\mathbf{M}_i = \mathbf{R}_{i(i-1)}[\mathbf{R}_{(i-1)i}\mathbf{Q}_{ii}^{-1}\mathbf{R}_{i(i-1)}]^{-1}\mathbf{R}_{(i-1)i}$$

and

$$\mathbf{H}_i = \mathbf{G}_r \mathbf{Q}_{ii}^{-1}\mathbf{G}_r^T - \mathbf{G}_r \mathbf{Q}_{ii}^{-1}\mathbf{M}_i \mathbf{Q}_{ii}^{-1}\mathbf{G}_r^T \tag{13}$$

Equation [12] is the solution for coefficients for a restricted multistage selection index. It has a form similar to the optimal single stage selection index of Tallis (1962). Note that when $\mathbf{k}_r = \mathbf{0}$, the above expression reduces to:

$$\mathbf{b}_i = \{(\mathbf{I} - \mathbf{Q}_{ii}^{-1}\mathbf{M}_i)[\mathbf{I} - \mathbf{Q}_{ii}^{-1}\mathbf{G}_r^T \mathbf{H}_i^{-1}\mathbf{G}_r(\mathbf{I} - \mathbf{Q}_{ii}^{-1}\mathbf{M}_i)]\}\mathbf{Q}_{ii}^{-1}\mathbf{A}_i \mathbf{w} \tag{14}$$

This is similar to the restricted single stage selection index of Kempthorne and Nordskog (1959). When $r = 0$, ie, $\mathbf{G}_r = \mathbf{0}$, equation [14] gives the ordinary unrestricted multistage selection index presented by Xu and Muir (1992)

$$\mathbf{b}_i = (\mathbf{I} - \mathbf{Q}_{ii}^{-1}\mathbf{M}_i)\mathbf{Q}_{ii}^{-1}\mathbf{A}_i\mathbf{w} \qquad [15]$$

Let Δz_i be the coefficient of standardized selection intensity for the ith selection index and $\Delta z = [\Delta z_1 \dots \Delta z_i \dots \Delta z_m]$, then the vector of genetic gains, $\Delta\mathbf{G}$, is predicted by

$$\Delta\mathbf{G} = [\Delta G_1 \dots \Delta G_k]^T = \mathbf{G}^T\mathbf{B}\Delta\mathbf{z} \qquad [16]$$

where ΔG_i, the ith element of $\Delta\mathbf{G}$, is the genetic gain of the ith trait. The total genetic change in aggregate breeding value is

$$\Delta H = \sum_{i=1}^{m} \mathbf{w}\mathbf{A}_i^T\mathbf{b}_i\Delta z_i \qquad [17]$$

where $\mathbf{w}$ are the economic values of the traits, and the $\mathbf{A}_i$ is defined as before.

Note that equation [17] provides the linear relationship between ΔH and $\Delta\mathbf{z}$, but does not indicate how to select the optimal set of $\Delta\mathbf{z}$ so that ΔH is maximized. Let u_i be the truncation point corresponding to selection intensity Δz_i and $q_i = 1 - \Phi(u_i)$ be the proportion selected for the ith index, where Φ is the cumulative distribution function of the standard normal distribution. The interrelationship among Δz_i, u_i and q_i is

$$\Delta z_i = \frac{\exp\left\{-\frac{1}{2}u_i^2\right\}}{q_i\sqrt{2\pi}} \qquad [18]$$

Substituting equation [18] into [17] and using Newton's method, the optimum ΔH can be found by maximizing ΔH with respect to $\mathbf{u} = [u_1 \; u_2 \dots u_m]^T$ under the constraint

$$\prod_{j=1}^{m} q_j = p \qquad [19]$$

where p is a predetermined total proportion selected (Xu and Muir, 1992; Xu et al, 1995).

NUMERICAL EXAMPLE

Data from a classical example of index selection given by Hazel (1943) and Cunningham (1975) are used to illustrate the computation of restricted multistage selection indices. The information used in a swine selection scheme comprises the five traits: pig's own market weight (y_1), pig's own market score (y_2), productivity of dam (y_3), average market weight of pig and littermates (y_4), and average market score of pig and littermates (y_5). Only the first three traits are assumed to be economically important (by Hazel, 1943; Cunningham, 1975). The economic weights

are $\mathbf{w} = [1/3, 1, 2]$. The estimated phenotypic and genotypic variance–covariance matrices for the five traits are:

$$
\begin{array}{ccccc}
y_1 & y_2 & y_3 & y_4 & y_5
\end{array}
$$

$$
\mathbf{P} = \begin{bmatrix}
1015.0596 & 93.5066 & -7.4323 & 457.9949 & 41.2218 \\
93.5066 & 22.8484 & -3.7634 & 41.2218 & 8.2985 \\
-7.4323 & -3.7634 & 94.4784 & -7.4323 & -3.7634 \\
457.9949 & 41.2218 & -7.4323 & 457.9949 & 41.2218 \\
41.2218 & 8.2985 & -3.7634 & 41.2218 & 8.2985
\end{bmatrix}
$$

and

$$
\mathbf{G} = \begin{bmatrix}
302.5893 & 13.5093 & 0.0 \\
13.5093 & 2.2391 & 0.0 \\
0.0 & 0.0 & 7.6339 \\
181.5536 & 8.1056 & 0.0 \\
8.1056 & 1.3435 & 0.0
\end{bmatrix}
$$

The overall proportion selected is set to $p = 6\%$, having a standardized selection differential, $\Delta z = 1.98538$.

A three-stage selection is performed with y_1 and y_2 selected at the first stage, y_3 at the second stage, and y_4 and y_5 at the third stage. This selection procedure is simply denoted as $\mathbf{n} = \{2, 3, 5\}$. We now assume that the selection goal is to keep y_2 constant or change at a desired level, while allowing y_1 and y_3 to increase without constraints. The unrestricted three-stage selection has index coefficients that are determined by equation [15], ie,

$$
\begin{array}{ccc}
\mathbf{b}_1 & \mathbf{b}_2 & \mathbf{b}_3
\end{array}
$$

$$
\begin{bmatrix}
0.03681 & -0.00130 & -0.03259 \\
-0.07149 & 0.02234 & 0.05703 \\
0 & 0.10328 & -0.00092 \\
0 & 0 & 0.07540 \\
0 & 0 & -0.16477
\end{bmatrix}
$$

A multidimensional Newton's iterative equation system is used to search for the optimal truncation points (u_is) (Xu and Muir, 1992). The sets of truncation points (u_i), standardized selection differentials (Δz_i), and the proportions selected in each stage (q_i) are:

$$
\begin{aligned}
\mathbf{u} &= [1.34806 \quad -0.66292 \quad -1.31152]^T \\
\Delta \mathbf{z} &= [1.81045 \quad 0.42911 \quad 0.18650]^T \\
\mathbf{q} &= [0.08882 \quad 0.74631 \quad 0.90516]^T
\end{aligned}
$$

The gains for three traits predicted from this index are $\Delta \mathbf{G} = [18.98569 \quad 0.63881 \quad 0.33699]^T$ and the aggregate economic value is $\Delta H = 7.64128$.

Assume now that we want to maximize the response from selection with the restriction of no change ($k_{y2} = 0$) in attribute y_2, where the subscript y_2 is used to denote the corresponding values for the second trait (y_2) and the same thereafter. For this case, $\mathbf{G}_{y2} = [13.5093 \quad 2.2391 \quad 0.0000 \quad 8.1056 \quad 1.3435]^T$. That is, $\mathbf{G}_{y2}$ consists of the second column of $\mathbf{G}$. The restricted index coefficients computed from equation [14] are:

$$
\begin{array}{ccc}
\mathbf{b}_1 & \mathbf{b}_2 & \mathbf{b}_3 \\
\left[\begin{array}{ccc}
0.03731 & -0.00219 & -0.02355 \\
-0.22509 & 0.01322 & 0.19453 \\
0 & 0.10306 & -0.00904 \\
0 & 0 & 0.07086 \\
0 & 0 & -0.51489
\end{array}\right]
\end{array}
$$

Using the same sets of u_is, Δz_is and q_is as those obtained from the unrestricted selection indices, we obtain genetic gains, $\Delta \mathbf{G} = [15.5069 \quad 0.0000 \quad 0.3247]^T$, and aggregate economic value, $\Delta H = 5.81835$. Therefore, selection on restricted multistage indices should result in zero gain in y_2 as expected. As a further check, it can be verified that $\mathrm{Cov}(g_{y2}, Z_i) = \mathbf{G}_{y2}^T \mathbf{b}_2 = 0$, when $k_{y2} = 0$.

As a final example, we demonstrate an index that maximizes economic gain while allowing y_2 to reach a predetermined value (Tallis, 1962, 1968). Let $\mathrm{Cov}(g_{y2}, Z_i) = -0.2$. Then the restricted selection procedure has index coefficients,

$$
\begin{array}{ccc}
\mathbf{b}_1 & \mathbf{b}_2 & \mathbf{b}_3 \\
\left[\begin{array}{ccc}
0.03493 & -0.03098 & -0.00026 \\
-0.24292 & -0.00440 & 0.00099 \\
0 & 0.00027 & -0.00647 \\
0 & 0 & -0.04539 \\
0 & 0 & 0.01312
\end{array}\right]
\end{array}
$$

with $\Delta \mathbf{G} = [7.58025 \quad -0.38624 \quad -0.00831]^T$ and $\Delta H = 2.12386$.

A summary of genetic gains and aggregate breeding values from single- or multistage selection with or without restrictions is shown in table I. The genetic gain from one-stage selection is used as a standard for comparing the two- or three-stage selection procedure. The unrestricted two-stage selection presented here is the same as Cunningham's selection procedure 4 except that the actual truncation point in the first stage selection is predetermined in Cunningham's procedure 4($u = 1.2338$) with a proportion selected on I_1 of 38% and is optimized in selection index updating ($u = 1.5091$) with a proportion selected on Z_1 of 6.56%. This leads to the aggregate breeding value of 8.0773 in this note and of 7.8675 presented by Cunningham (1975).

For a given stage, the index is computed from $Z_i = \mathbf{b}_i^T \mathbf{y}_i$. As selection stages advance, more and more information is incorporated into the index. In practice, it is necessary that restrictions on some characters should be incorporated into the index at a later stage when the trait measurements become available. This problem is solved by modifying $\mathbf{G}_r$ and $\mathbf{k}_r$ of equation [12] for each stage of selection since

the index is derived with $\text{Cov}(Z_i, Z_j) = 0$ for $i \neq j$. For example, suppose we desired no genetic changes for y_2 and y_3 in a three-stage selection with $\mathbf{n} = \{2, 4, 5\}$. Thus, the constraint on y_2 would begin at the first stage and would begin on y_3 at the second stage. Under such a selection procedure, the restricted selection indices give genetic gains of $\Delta\mathbf{G} = [15.28095 \ \ 0.0000 \ \ 0.0000]^T$ whereas the unrestricted selection indices produce genetic gains of $\Delta\mathbf{G} = [18.90569 \ \ 0.65909 \ \ 0.41079]^T$. From this it can be seen that selection on restricted multistage indices where restrictions are incorporated into index at different stages results in zero gains as expected.

DISCUSSION

There are a number of practical situations to which the techniques of the previous sections could be applied. For example, in the selection of dual-purpose bulls for use in artificial insemination, the bulls are first selected using information from their parents; they are subsequently screened for their own performance, and finally selected on the basis of a progeny test of their daughters. In that case, selection can be regarded as a stochastic process in continuous time. For practical and economic reasons the selection is performed in several stages in such situations (Cunningham, 1975; Niebel and Van Vleck, 1982; Norell et al, 1991; Xu et al, 1995).

When selection uses all information collected from a number of traits performed in several stages, the selection objective usually remains constant. That is, we are interested in the quantity associated with primary product. In some situations, certain growth patterns may be more economical, or otherwise more desirable, than others. For instance, in the example given by Tallis (1968) one desirable characteristic in fat lamb production is rapid and early increase in body weight. On the other hand, if the body weight increases too much, some production and marketing problems may arise. Hence, selection is a process to use available information to push breeds towards the optimum growth pattern (Tallis, 1968; Harville, 1975; Niebel and Van Vleck, 1982). The technique of restricted selection index is justified as a means to achieve a prespecified selection goal (Lin, 1989).

The procedure given here either restricts genetic changes to zero or to proportional changes in chosen characters or linear functions of characters. In this note, the restrictions are achieved by calculating $\mathbf{b}_i$ under certain constraints and are unrelated to economic weighting factors. The restrictions also might be achieved by modifying economic weighting factors (James, 1968; Lin, 1989).

The effect of restricted multistage selection indices is similar to restricted single stage selection indices. For instance, the restriction is obviously achieved at the expense of total aggregate genetic gain as compared with unrestricted indices (table I). Selection on restricted multistage indices produces an even lower gain than that on restricted single stage index. This is similar to cases of unrestricted selection where the multistage selection index would result in less genetic gain than the single stage selection index owing to early culling (Xu and Muir, 1991). However, reduction in genetic gains, as one referee pointed out, is not necessarily coupled with restricted index selection. Because economic weights in the numerical example are assumed to be known, then one of the traits was restricted to a less optimum level. As such, genetic gain for the restricted index is significantly less than that obtained with the optimum index (table I). Nevertheless, in many situations

Table I. Summary of genetic gains from single and multistage index selection with or without restrictions.

	One-stage			Two-stage[a]			Three-stage[b]		
	Unrestricted	y_2 constant	$k_{y_2} = -0.2$[c]	Unrestricted	y_2 constant	$k_{y_2} = -0.2$[c]	Unrestricted	y_2 constant	$k_{y_2} = -0.2$[c]
ΔG_1	19.59159	16.22407	14.91993	18.72241	14.56913	10.54723	18.98569	15.50687	7.58025
ΔG_2	0.65907	0.00000	−0.11826	0.64225	0.00000	−0.20161	0.63881	0.00000	−0.38624
ΔG_3	0.58324	0.60913	0.58750	0.59714	0.68777	0.68102	0.33699	0.32472	−0.00831
ΔH	8.35601	6.62622	6.02999	8.07728	6.23187	4.67614	7.64129	5.81835	2.12386

[a]$\mathbf{n} = \{3, 5\}$; [b]$\mathbf{n} = \{2, 3, 5\}$; [c]$\text{Cov}(g_{y2}, Z_i) = k_{y2}$.

knowledge of economic values is vague, especially over the long term (Pešek and Baker, 1969; Niebel and Van Vleck, 1982; Itoh and Yamada, 1988a, b). Under these circumstances, it may be more efficient to give relative values or to assign predetermined amounts of genetic gains to the traits (Tallis, 1962; Itoh and Yamada, 1988a, b).

The coefficients for the restricted index presented in this note are found so that the correlation between Z_i and H at each stage is maximum with constraints $\text{Cov}(Z_i, Z_j) = 0$ for $i \neq j$. An index constructed in that manner will have explicitly determined solutions for the truncation points. However, genetic gain will be somewhat less than that obtained without constraints (Xu and Muir, 1992). But Xu and Muir (1991) also showed that under certain conditions the efficiency of restricted multistage index selection may greatly exceed that of conventional multistage selection because the latter dose not incorporate information from previous stages of selection into the current stage. Owing to computational advantages over best linear unbiased prediction (BLUP) under selection models, this procedure can be used to effectively design performance testing and selection programs that will optimize profit in commercial breeding (Xu et al, 1995). For situations with phenotypic variances and covariances, heritabilities, economic values, and costs of measurement known, the breeder can investigate many options relative to choices of traits and stages with respect to maximizing either total economic value of genetic change or profit.

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