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A simple stepwise procedure of deriving selection index with restrictions*

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Summary. A simplified alternative procedure was derived for computing selection indices with various restrictions. The procedure involved construction of a sub-index for the unrestricted traits by the conventional methods (Smith-Hazel index approach) and construction of a sub-index for the restricted traits based on the restrospective index approach. The two sub-indices were then combined to obtain the desired index which met the prespecified restriction. The formulation is straightforward and easy to compute and does not involve the complicated formula as does the derivation of restricted index by the use of the Lagrange multiplier method. As a consequence of simplification, the proposed procedure is approximate in terms of optimal gain in net merit. The procedure presented can also be extended to derive an index with simultaneous imposition of multiple restrictions. Numerical examples were given to illustrate the use of this alternative approach.

Key words: Stepwise procedure – Restricted index

Introduction

The original concept of the restricted selection index was developed by Kempthorne and Nordskog (1959) to maximize genetic gains in some traits while holding genetic gains of other traits to zero.

Tallis (1962) extended this idea to set the response of some traits to a fixed amount rather than zero. This was called the optimum selection index. The only difference between these two approaches is that the former imposed zero restriction while the latter applied a non-zero constant restriction. Cunningham et al. (1970) presented a simpler solution to the restricted index than the original method of Kempthorne and Nordskog. James (1968) developed a general procedure for constructing a selection index with zero or non-zero restriction. Harville (1975) proposed a procedure of deriving a selection index with proportionality constraints. He claimed that the use of his index would move the means of the component traits farther in the desired direction than would the use of Tallis' index. Niebel and Van Vleck (1983) established a general theory of deriving "single restricted index" and "multiple restricted index" when more than one selection index was used in a population.

Regardless of the nature of the restrictions, the Lagrange multiplier method was used almost exclusively to derive the final index which satisfies the prespecified restriction. While the use of Lagrange multiplier is straightforward to many statisticians, many practitioners in animal breeding are not mathematically oriented and may not fully understand the derivation using a Lagrange multiplier. Therefore, the formula used for application was taken at its face value without regard to its derivation. The purpose of this paper is to show a simple alternative approach to obtain selection indexes with restrictions.

Rationale

Suppose that there are n traits under consideration for simultaneous selection. Of the n traits, we would like to maximize genetic gains in the first t traits and to impose restrictions on the remaining r traits ($r = n - t$). The following simple steps can be taken to derive the restricted index without resort to the use of the Lagrange multiplier technique.

Step 1: Construct a conventional index based on t unrestricted traits in the same way as originally developed by Smith (1936) and Hazel (1943).

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Net merit: $H^\circ = a_1 g_1 + \ldots + a_t g_t$
Index: $I^\circ = b_1 x_1 + \ldots + b_t g_t$
In matrix notation: $H^\circ = \mathbf{g}^{\circ\prime} a^\circ$ and $I^\circ = \mathbf{x}^{\circ\prime} \mathbf{b}^\circ$
Index equation: $P^\circ \mathbf{b}^\circ = G^\circ \mathbf{a}^\circ$
Index coefficients: $\mathbf{b}^\circ = P^{\circ -1} G^\circ \mathbf{a}^\circ$ (1)
Genetic gains in component traits: $\Delta^\circ = G^\circ \mathbf{b}^\circ (i/\sigma_I)$ (2)

Step 2: Construct an index based only on r restricted traits by the retrospective index approach of Dickerson et al. (1954). Detailed descriptions of the retrospective index were given by Allaire and Henderson (1966) and Van Vleck (1979). The index in retrospect can easily be obtained from Expression (2) by dropping (i/σ_I) which is a scalar to the set of equations. That is,

$$\mathbf{b}^* = G^{*-1} \Delta^* \tag{3}$$

The superscript "*" referred to the retrospective index whereas the superscript "°" referred to the unrestricted index. If zero restriction is imposed, this means that Δ^* is a vector of zeros. As a result, $\mathbf{b}^*$ is a null vector as well. Therefore, $\mathbf{b}^*$ will always be set equal to a null vector in the case of zero restriction and there would be no need to do Step 2.

Step 3: Set up the following equations using $\mathbf{b}^\circ$ and $\mathbf{b}^*$ from Steps 1 and 2, respectively.

$$G\,\mathbf{b} = \begin{bmatrix} G^\circ & 0 \\ 0 & G^* \end{bmatrix} \begin{bmatrix} \mathbf{b}^\circ \\ \mathbf{b}^* \end{bmatrix} \tag{4}$$

where the zeros are null matrices of appropriate order. Note that the first matrix on the right-hand side of Expression (4) is a block diagonal matrix. The final index with the desired restriction is then,

$$\mathbf{b} = G^{-1} \begin{bmatrix} G^\circ & 0 \\ 0 & G^* \end{bmatrix} \begin{bmatrix} \mathbf{b}^\circ \\ \mathbf{b}^* \end{bmatrix} \tag{5}$$

where G, G° and G^* are the genetic variance-covariance matrices corresponding to n traits, t unrestricted traits, and r restricted traits, respectively. Expression (4) equates the genetic gains from the final index to genetic gains from Steps 1 and 2, thereby satisfying the restrictions imposed in Step 2. In other words, the derived index would maximize genetic gains in the unrestricted traits subject to the constraints on the restricted traits.

Numerical examples

The phenotypic (P) and genetic (G) variance-covariance matrices and economic weights (**a**) used for this illustration were from the example of Cunningham et al. (1970) as follows:

$$G = \begin{array}{c} \begin{array}{cccc} x_1 & x_2 & x_3 & x_4 \end{array} \\ \begin{bmatrix} 0.0875 & -0.0047 & 0.0887 & 0.2800 \\ -0.0047 & 0.0250 & 0.0000 & 0.2245 \\ 0.0887 & 0.0000 & 9.0000 & 2.8397 \\ 0.2800 & 0.2245 & 2.8397 & 22.4013 \end{bmatrix} \end{array} ; \mathbf{a} = \begin{bmatrix} 2 \\ 22 \\ 1 \\ 0 \end{bmatrix}$$

$$P = \begin{bmatrix} 0.25 & 0.00 & 0.00 & 1.20 \\ 0.00 & 0.25 & 0.00 & 0.80 \\ 0.00 & 0.00 & 36.00 & 14.40 \\ 1.20 & 0.80 & 14.40 & 64.00 \end{bmatrix}$$

Case 1

Suppose that we want to improve x_1, x_2 and x_3 while holding the response of x_4 to zero.

Step 1: Calculate the conventional index using the unrestricted traits (x_1, x_2 and x_3) according to Expression (1)

$$\mathbf{b}^\circ = P^{\circ -1} G^\circ \mathbf{a}^\circ = \begin{bmatrix} 0.6412 \\ 2.1624 \\ 0.2549 \end{bmatrix}$$

Step 2: Since this is zero restriction on a single trait (x_4), $\mathbf{b}^*$ reduces to a scalar of zero and G^* reduces to 22.4013.

Step 3: Obtain the restricted index according to Expression (5).

$$\mathbf{b} = G^{-1} \begin{bmatrix} G^\circ & 0 \\ 0 & G^* \end{bmatrix} \begin{bmatrix} \mathbf{b}^\circ \\ \mathbf{b}^* \end{bmatrix} = \begin{bmatrix} 0.8991 \\ 2.8858 \\ 0.2761 \\ -0.0752 \end{bmatrix}.$$

As a check, genetic gains in component traits resulting from this index (assume i = 1) is,

$$\Delta = \begin{bmatrix} \Delta g_1 \\ \Delta g_2 \\ \Delta g_3 \\ \Delta g_4 \end{bmatrix} = G\,\mathbf{b}/\sigma_I = \begin{bmatrix} 0.0331 \\ 0.0247 \\ 1.1361 \\ 0 \end{bmatrix} \quad \text{and} \quad \Delta H = 1.745\,.$$

Therefore, this procedure does produce a restricted index with zero gain in x_4 as prespecified. In comparison, the restricted index obtained by the method of Kempthorne and Nordskog (1959) or Cunningham et al. (1970) achieved $\Delta g_4 = 0$ and $\Delta H = 1.759$.

It is worth noting that the restricted index in this example included the restricted trait (x_4) as a component trait for selection decision (i.e. $I = b_1 x_1 + b_2 x_2 + b_3 x_3 + b_4 x_4$ with zero restriction on x_4). However, the restricted trait need not be included in the restricted index (i.e. $I = b_1 x_1 + b_2 x_2 + b_3 x_3$ with zero restriction on x_4). Cunningham et al. (1970) used the latter approach to derive the restricted index which yielded $\Delta g_4 = 0$ and $\Delta H = 1.0008$. It is obvious that inclusion of the restricted traits in the restricted index is more efficient than the exclusion of the restricted traits from the restricted index on the basis of ΔH although zero restriction is satisfied either way.

Case 2

To improve genetic gains in x_1 and x_2 while imposing zero gains in x_3 and x_4.

Step 1: Construct unrestricted index based on x_1 and x_2.

$$b^\circ = P^{\circ -1} G^\circ \mathbf{a}^\circ = \begin{bmatrix} 0.25 & 0 \\ 0 & 0.25 \end{bmatrix}^{-1} \begin{bmatrix} 0.0875 & -0.0047 \\ -0.0047 & 0.0250 \end{bmatrix} \begin{bmatrix} 2 \\ 22 \end{bmatrix} = \begin{bmatrix} 0.2864 \\ 2.1624 \end{bmatrix}.$$

Step 2: $\mathbf{b}^*$ is a null vector as this is zero restriction. Note that the elements of G^* could be replaced by zeros in the case of zero restriction.

Table 1. Comparison of Tallis', Harville's and step-wise procedures in deriving selection index with proportionality restrictions ($\Delta g_3 : \Delta g_4 = 2{:}1$)

Procedure	Index weights				Genetic gains in index traits				Gain in net merit	Gain in unrestricted traits
	b_1	b_2	b_3	b_4	Δg_1	Δg_2	Δg_3	Δg_4	$\Delta H = \sum_{i=1}^{4} a_i \Delta g_i$	$\Delta H^\circ = \sum_{i=1}^{2} a_i \Delta g_i$
Tallis	0.4883	2.0638	0.2206	−0.0101	0.0299	0.0282	1.2010	0.6005	1.8819	0.6802
Harville	0.5586	2.0714	0.2639	−0.0076	0.0320	0.0251	1.2721	0.6360	1.8890	0.6162
Stepwise	0.0821	2.1832	0.2235	−0.0066	0.0087	0.0308	1.1689	0.5845	1.8641	0.6950

Step 3: According to Expression (5), the restricted index is

$$\mathbf{b} = G^{-1}\begin{bmatrix} G^\circ & 0 \\ 0 & G^* \end{bmatrix}\begin{bmatrix} \mathbf{b}^\circ \\ \mathbf{b}^* \end{bmatrix} = \begin{bmatrix} 0.3930 \\ 2.4538 \\ 0.0057 \\ -0.0302 \end{bmatrix}.$$

It can be readily verified that the use of this index results in $\Delta' = (\Delta g_1 \Delta g_2 \Delta g_3 \Delta g_4) = (0.0124\ 0.0437\ 0\ 0)$ and $\Delta H = 0.987$ as compared to $\Delta H = 0.991$ obtained from the method of Kempthorne and Nordskog (1959).

Case 3

To improve x_1 and x_2 with the restriction that $\Delta g_3 : \Delta g_4 = 2:1$. This is proportional restriction.

Step 1: Identical to Step 1 in Case 2.

Step 2: Construct a retrospective index based on the restricted traits, x_3 and x_4 according to Expression (3).

$$\mathbf{b}^* = G^{*-1}\Delta^* = \begin{bmatrix} 9.0000 & 2.8397 \\ 2.8397 & 22.4013 \end{bmatrix}^{-1}\begin{bmatrix} 2 \\ 1 \end{bmatrix} = \begin{bmatrix} 0.2168 \\ 0.0172 \end{bmatrix}.$$

Step 3: Set up equations according to Expression (5).

$$\mathbf{b} = G^{-1}\begin{bmatrix} G^\circ & 0 \\ 0 & G^* \end{bmatrix}\begin{bmatrix} \mathbf{b}^\circ \\ \mathbf{b}^* \end{bmatrix}$$

$$= G^{-1}\begin{bmatrix} 0.0875 & -0.0047 & 0 & 0 \\ -0.0047 & 0.0250 & 0 & 0 \\ 0 & 0 & 9.0000 & 2.8397 \\ 0 & 0 & 2.8397 & 22.4013 \end{bmatrix}\begin{bmatrix} 0.2864 \\ 2.1624 \\ 0.2168 \\ 0.0172 \end{bmatrix}$$

$$= \begin{bmatrix} 0.0821 \\ 2.1832 \\ 0.2235 \\ -0.0066 \end{bmatrix}.$$

Comparison of the step-wise procedure with Tallis' and Harville's methods is given in Table 1. The three procedures compared all yielded an index which satisfied the prespecified restriction of $\Delta g_3 : \Delta g_4 = 2:1$. Harville's index fulfilled the goal to maximize ΔH and to change the proportional restricted traits in the desired direction as far as possible. However, the difference in ΔH among the three procedures was minimal. As shown in the last column of Table 1, the stepwise procedure achieved higher genetic gains in the unrestricted traits than Tallis' or Harville's procedure.

It is noteworthy that the proportional restriction does not have to be non-negative. It could be a restriction with negative proportion. For example, we could impose the restriction of $\Delta g_3 : \Delta g_4 = 2 : -1$ instead of $2:1$. The index derived on this basis would not only accomplish the proportional restriction but also ensure that the genetic change in x_4 would be negative. Therefore this method provides a simple means of deriving a restricted index to manipulate genetic changes in some traits in a prespecified sign. This is a sign restriction originally presented by Rao (1962).

Case 4

To impose a linear restriction, say $2\Delta g_3 - 3\Delta g_4 = 0$. This restriction can be rewritten as $\Delta g_3 : \Delta g_4 = 3:2$. Therefore, linear restriction is a variant of proportional restriction. Follow exactly the same procedures as shown in Case 3 with the exception of setting $\Delta^{*\prime} = (3\ 2)$ in Step 2.

Case 5

If there are, say, six traits of interest for selection, one would like to improve x_1 and x_2 subject to two restrictions which are $\Delta g_3 : \Delta g_4 = 2:1$ and $\Delta g_5 = \Delta g_6 = 0$. The index which satisfies these two restrictions can be obtained as follows:

$$\begin{bmatrix} b_1 \\ b_2 \\ b_3 \\ b_4 \\ b_5 \\ b_6 \end{bmatrix} = G^{-1}\begin{bmatrix} G^\circ & 0 & 0 \\ 0 & G^* & 0 \\ 0 & 0 & 0 \end{bmatrix}\begin{bmatrix} \mathbf{b}^\circ \\ \mathbf{b}^* \\ \mathbf{0} \end{bmatrix}.$$

Therefore, this procedure can be extended to derive a restricted index with multiple restrictions such as the simultaneous imposition of proportional and zero restrictions in this case.

Final remarks

The above illustrations have verified that this simplified procedure has led to an index which satisfies the prespecified restrictions. The formulation is straightforward and easy to compute. It does not involve the complicated formulae such as those of Kempthorne and Nordskog (1959); Tallis (1962); James (1968) or Harville (1975). This alternative procedure is only slightly less efficient than the Lagrange multiplier method on the basis of ΔH. In most cases and for practical use, the difference in ΔH is negligible.

In practical applications, this 3-step procedure outlined above has covered the general scheme of index selection. Step 1 alone handles index selection without any restrictions. Step 2 is concerned with index in retrospect. This step can also be used to handle an extreme case of Tallis' optimum selection index to control the relative gains in all traits incorporated in the index (e.g. Pesek and Baker 1969). Steps 1 and 3 could handle index selection with zero restriction. Finally, Steps 1, 2 and 3 deal with index selection with proportional, sign or linear restrictions. It can also be extended to derive an index with multiple restrictions. Each step of the procedure involves simple calculation which results in something meaningful to breeding researchers. Therefore, this stepwise procedure does provide a unified approach to constructing an index with various restrictions.

As a final note, theoretically a restricted index can be derived to meet any restrictions imposed. However, the restrictions must be biologically reasonable. As an example, if two index traits are highly correlated genetically and phenotypically, it would be impractical to improve one trait while restricting the response of the other to zero. Too severe or unreasonable restrictions would also require an unreasonably high selection intensity. Therefore, common sense in biology must prevail prior to constructing any restricted index.

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