

Outline MT Selection

- Properties of EBVs
- Single Trait Selection Index
- Multiple Trait Selection Index
 - Predicting Response
 - Manipulating Response
 - MT Index and MTBLUP selection
 - Increased Accuracy from MT Selection
 - Effect of Incorrect Parameters
 - Other Issues

Selection Criteria



Breeding Objective

Own performance X_1

Performance on relatives X_2

Correlated Traits X_n

Breeding Value (s)

Selection Index (multiple regression)

$$EBV = \text{Index} = b_1X_1 + b_2X_2 + b_3X_3 + \dots + b_nX_n$$

Finding the optimal index weights

Regression of A on X_i

$$\text{Regression coefficient} = \frac{\text{cov}(X_i, A)}{\text{var}(X_i)}$$

Examples:

$$X_1 = \text{Own Performance} \quad \mathbf{b} = h^2$$

$X_1 = \text{Dam Performance}$

$$\mathbf{b} = \frac{\frac{1}{2}V_A}{V_A + V_E} = \frac{1}{2}h^2$$

Finding the optimal index weights

Regression of A on X_i

$$\text{Regression coefficient} = \frac{\text{cov}(X_i, A)}{\text{var}(X_i)}$$

Examples:

$X_1 =$ Own Performance

$$\frac{V_A}{V_A + V_E} = h^2$$

$X_1 =$ Dam Performance

$$\mathbf{b} = \frac{\frac{1}{2}V_A}{V_A + V_E} = \frac{1}{2}h^2$$

Progeny Testing

$$\hat{A} = b_1 P_1$$

P_1 = Mean of n progeny

b_1 = Index Weight

= “heritability of progeny test

See also
GEST325

Note, algebra
is to
illustrate not
to learn

b_1 depends on the number of progeny
and on the heritability

$$b_1 = \frac{\frac{1}{2}V_A}{\frac{1}{4}V_A + (V_P - \frac{1}{4}V_A)/n} = \frac{2n}{n + 4/h^2 - 1} = \frac{2n}{n + \frac{4-h^2}{h^2}}$$

Some basic QG: variances

$$X = A + E$$

$$\text{Var}(X) = \text{var}(A) + \text{var}(E) = V_A + V_E$$

(no cov. Between A,E)

$$\text{var}(\text{mean}) = \text{common variance} + \text{specific}/n$$

X_1 = Mean of n Full Sibs

$$\text{var}(X) = \frac{1}{2}V_A + V_{ce} + \frac{(\frac{1}{2}V_A + V_{te})}{n}$$

Some basic QG covariances

$$X = A + E$$

$$\text{cov}(X_1, A) = \text{cov}(A, A) + \text{cov}(E, A) = V_A$$

$$\text{cov}(X_1, X_2) = a_{ij} V_A \quad \dots\dots\dots \text{if relatives}$$

$$\text{cov}(X_1, \bar{X}_2) = \frac{1}{n} \text{cov}(X_1, \sum_{i=1}^n X_{2i}) = \frac{1}{n} \sum_{i=1}^n \text{cov}(X_1, X_{2i}) = \text{cov}(X_1, X_{2i})$$

Finding the optimal index weights

Selection Index (multiple regression)

$$EBV = \text{Index} = b_1X_1 + b_2X_2 + b_3X_3 + \dots + b_nX_n$$

Regression of A on X; $X' = [X_1, X_2, \dots, X_n]$

$$\frac{\text{cov}(X, A)}{\text{var}(X)} = \text{var}(X)^{-1} \text{cov}(X, A) = P^{-1}G$$

$$P = \text{var}(X)$$

$$G = \text{cov}(X, A)$$

Selection index with more information sources (multiple regression)

X = vector with phenotypes (“ P_i values” = sel. criteria)

A = True breeding Value

$$\text{var}(X) = P = \text{matrix} = \begin{bmatrix} \text{var}(X_1) & \text{cov}(X_1, X_2) \\ \text{cov}(X_2, X_1) & \text{var}(X_2) \end{bmatrix}$$

$$\text{cov}(X, A) = G = \text{vector} = \begin{bmatrix} \text{cov}(X_1, A) \\ \text{cov}(X_2, A) \end{bmatrix}$$

Opt. weights: $b = P^{-1}G$ = “cov/var_X” (single trait Sel Index eqn: $Pb = G$)

**Example: X_1 = weight for own phenotype
 X_2 = mean of n full sibs**

	n=3		n=10	
h^2	b_1	b_2	b_1	b_2
0.10	0.09	0.12	0.08	0.32
0.30	0.26	0.26	0.22	0.49
0.50	0.43	0.29	0.38	0.48
0.70	0.62	0.24	0.57	0.36

- **Own performance more important with high heritability
and smaller amount of family info**
- **Otherwise, family information more important**

Accuracy of selection index

r_{IA} = correlation between Index and A

$$= \frac{\text{cov}(I,A)}{\sigma_I \sigma_A} = \frac{\sigma_I^2}{\sigma_I \sigma_A} = \frac{\sigma_I}{\sigma_A} = \sqrt{(b'Pb/V_A)}$$

because $\text{cov}(I,A) = \text{cov}(bX,A) = b' \text{cov}(X,A)$

$$\begin{aligned} &= b'G = b'Pb = b' \text{var}(X)b \\ &= \text{var}(bX) \\ &= \text{var}(I) \end{aligned}$$

Note: I = EBV = sel. criterion

A = BV = Objective

→ $r_{IA} = \text{sqrt}(\text{var}(\text{EBV}) / V_A) = \text{accuracy} = \text{correlation}$

Summary of this lecture

- Selection Index Theory can be used to work out weights and accuracy for a given set of information about an particular EBV
- Quantitative Genetic Theory and matrices (P, G) are used to work out such index weights (b) and accuracies
- In Genetic Evaluation we use BLUP where this all occurs ‘automatically’
- Selection Index Theory still useful to predict what happens
 - Accuracy for a given amount of information
 - Importance of own vs family information for given situations