Some basic Quantitative Genetic Theory

Single trait

$P = A + E$ → General Model

$Var(P) = var(A) + var(E) = V_A + V_E$ no cov. between A and E

$cov(A_i,P_i) = cov(A_i, A_i) + cov(A_i, E_i) = V_A$ if A same animal as P

$cov(A_i,P_i) = cov(A_j, A_i) + cov(A_j, E_i) = a_{ij}V_A$ aij = additive genetic relationship between i and j

$cov(P_i, P_j) = a_{ij}V_A$ as E's are uncorrelated if not same animal

Some more basic Quantitative Genetics theory

Calculating weights when using information based on a mean of n individuals

	n Full Sibs	n Half Sibs	n progeny
Var(mean P) = $\left(t+\frac{1-t}{n}\right)\sigma_p^2$	$t_{FS} = ½ h^2 + c^2$	$t_{HS} = ¼ h^2$	$t_{FS} = ¼ h^2$
Cov(mean P, A) = $a_{ij}\sigma_a^2$	$a_{ij} = ½$	$a_{ij} = ¼$	$a_{ij} = ½$

a_{ij} = genetic relationship between members of group and a target individual BV (A)

Some basic Quantitative Genetic Theory

Multi trait

$\mathrm{cov}(P_{1i}, P_{2i}) = r_p \sigma_{P1} \sigma_{P2}$

phenotypic covariance as

E’s are correlated if same animal

$\mathrm{cov}(P_{1i}, P_{2j}) = a_{ij} r_g \sigma_{g1} \sigma_{g2}$

genetic covariance as

E’s are uncorrelated if not same animal

$\mathrm{cov}(A_{1i}, P_{2i}) = r_g \sigma_{g1} \sigma_{g2}$ if A_1 same animal as P_2

$\mathrm{cov}(A_{1i}, P_{2j}) = a_{ij} r_g \sigma_{g1} \sigma_{g2}$ if A1 not same animal as P2

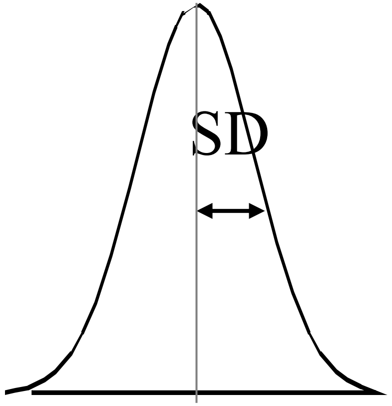
In general,
when between traits, replace variance by covariance

Some formal definitions

$H = v_1g_1 + v_2g_2 + v_3g_3......etc = v'g$

$I = b_1x_1 + b_2x_2 + b_3x_3......etc$

σ_I = SD of Index



SD of $index

$\mathrm{Var}(H) = \sigma_H^2 = v'Cv$

$\mathrm{Var}(I) = b'Pb$

where $P = \mathrm{var}(x)$

$\mathrm{cov}(x,g) = G$

$b = P^{-1}Gv$

G = matrix

V = econ val

accuracy = σ_I / σ_H

note: $\sigma_I < \sigma_H$

Selection index with more information sources (multiple regression)

x = vector with phenotypes (criteria)

g = breeding objective (single trait BV here)

var(*x*) = P = matrix = $\begin{bmatrix} \mathrm{var}(x_1) & \mathrm{cov}(x_1, x_2) \\ \mathrm{cov}(x_2, x_1) & \mathrm{var}(x_2) \end{bmatrix}$

cov(*x*,g) = G = vector = $\begin{bmatrix} cov(x_1, g) \\ cov(x_2, g) \end{bmatrix}$

weights: $b = P^{-1}G$

Selection index with more information sources and with more objective traits (multiple regression)

x = vector with phenotypes (criteria)

H = breeding objective (multiple traits here)

= $v_1 g_1 + v_2 g_2$

var(x) = P = matrix = $\begin{bmatrix} \mathrm{var}(x_1) & \mathrm{cov}(x_1, x_2) \\ \mathrm{cov}(x_2, x_1) & \mathrm{var}(x_2) \end{bmatrix}$

cov(x,A) = G = matrix = $\begin{bmatrix} cov(x_1, g_1) & cov(x_1, g_2) \\ cov(x_2, g_1) & cov(x_2, g_2) \end{bmatrix}$

weights: $b = P^{-1}Gv$

V are economic values

Predicting Selection Response

- Total Response to selection (in \$\$)

$$R = i.r_{IH}.\sigma_H = i.\sigma_I$$

in \$\$ if MT Index

- Response for each trait (in trait units)

$$\delta g_i = b_{gi,I}\, R \quad = \frac{cov(g_{i,}\ b'x)}{\sigma^2_I}\, i.\sigma_I = i.b'G_i/\sigma_I$$

$G_i = cov(g_{i,}x) = i^{th}$ column of G

Regression of g_i on Index

See also mtindex.xls