Deterministic Models for EBV
Jack Dekkers

Accuracy of Selection
The Breeder’s Equation for Response to Selection:
\[ \Delta G = i \, r \, \sigma_g \]

- \( i \) = selection intensity
- \( \sigma_g \) = genetic St. Deviation
- \( r \) = accuracy of selection
  - = corr(selection criterion, true breeding value)
  - = accuracy of EBV for single trait selection
  - or of total merit index for multi-trait selection

- maximize to increase gain
- need to be able to model accuracy to be able to predict genetic gain and to determine the value of information

EBV = unbiased estimate of BV

Data recording
- Phenotypic records
  - phenotype
  - management group
  - age, sex, etc.
- Pedigree records
  - animal id
  - sire id
  - dam id
- Marker genotypes

Central data base

Statistical Analysis
- Animal model BLUP
- Genomic evaluation models
- Total Merit Indexes

EBV + accuracy

Use for selection

Methods to Model Accuracy of EBV
1) EBV from own records
   - simple regression
2) EBV from records on a single type of relatives
   - simple regression
3) EBV from multiple sources of information
   - multiple regression - selection index
4) EBV from BLUP animal model

All derivations assume records are perfectly adjusted for systematic environmental effects (herd, season, sex, age, etc.)

Animal model EBV

Linear regression theory:

Model: \[ y = a + b_{yx} x + e \]
Prediction: \[ \hat{y}_i = \bar{y} + b_{yx}(x_i - \bar{x}) \]

Regression coefficient: \[ b_{yx} = \frac{\sigma_y}{\sigma_x} = r_{xy} \frac{\sigma_y}{\sigma_x} \]

Accuracy of prediction: \[ r_{xy} = \frac{\sigma_{xy}}{\sqrt{\sigma_y^2 \sigma_x^2}} \]
1) EBV from own records ($x$)

\[ \hat{g}_i = b_{g,x} x_i = b_{g,x} \text{(phenotype of individual)} \]

\[ b_{g,x} = \frac{\sigma_{g|x}^2}{\sigma^2_p} = \frac{\sigma_{g|x}^2}{\sigma^2_g + \sigma^2_e} = \frac{\sigma^2_g}{\sigma^2_p} = h^2 \]

\[ \hat{g}_i = h^2 x_i \]

Accuracy = \( r = r_{g,g^*} = \frac{\sigma_{g|x}^2}{\sigma^2_g \sigma_h^2 x_i} = h \)

---

1) EBV from own records - simple regression

\[ g \]

\[ h^2 = .3 \]

\[ +150 \]

\[ +500 \]

\[ 0 \]

\[ \text{Phenotype } x \]

---

1) EBV from own records

Effect of Heritability on Accuracy

\[ \text{Accuracy} \quad r = h \]

\[ 0 \]

\[ 1 \]

\[ 0 \]

\[ 0.1 \]

\[ 0.2 \]

\[ 0.3 \]

\[ 0.4 \]

\[ 0.5 \]

\[ 0.6 \]

\[ 0.7 \]

\[ 0.8 \]

\[ 0.9 \]

\[ 1 \]

\[ 0 \]

\[ 0.1 \]

\[ 0.2 \]

\[ 0.3 \]

\[ 0.4 \]

\[ 0.5 \]

\[ 0.6 \]

\[ 0.7 \]

\[ 0.8 \]

\[ 0.9 \]

\[ 1 \]

\[ 0 \]

\[ 0.1 \]

\[ 0.2 \]

\[ 0.3 \]

\[ 0.4 \]

\[ 0.5 \]

\[ 0.6 \]

\[ 0.7 \]

\[ 0.8 \]

\[ 0.9 \]

\[ 1 \]

\[ 0 \]

\[ 0.1 \]

\[ 0.2 \]

\[ 0.3 \]

\[ 0.4 \]

\[ 0.5 \]

\[ 0.6 \]

\[ 0.7 \]

\[ 0.8 \]

\[ 0.9 \]

\[ 1 \]
EBV based on the Mean of Two or more Phenotypic Records

Definition of Repeatability
Repeated records on same individual: \( x = g + pe + te \)

- \( pe \) = permanent environment effect
- \( te \) = temporary environment effect

Repeatability, \( t \) = prop. of total phenotypic variance that is due to permanent effects (envir. + genetic)

\[
t = \frac{\sigma_g^2 + \sigma_{pe}^2}{\sigma_p^2} \quad \text{or} \quad t = \frac{\sigma_g^2 + \sigma_{pe}^2}{\sigma_p^2 + \sigma_{pe}^2 + \sigma_{te}^2}
\]

Cow \( i \) has two lactation records, \( x_{i1} \) and \( x_{i2} \)

\[
x_{i1} = g_i + pe_i + te_{i1}
\]

\[
x_{i2} = g_i + pe_i + te_{i2}
\]

Correlation between records on an individual is

\[
r_{x_{i1}x_{i2}} = \frac{\sigma_{x_{i1}x_{i2}}}{\sqrt{\sigma_{x_{i1}}^2 \sigma_{x_{i2}}^2}}
\]

and

\[
\sigma_{x_{i1}x_{i2}} = \sigma_{(g_i + pe_i + te_{i1}, g_i + pe_i + te_{i2})} = \sigma_g^2 + \sigma_{pe}^2
\]

Hence,

\[
r_{x_{i1}x_{i2}} = t
\]

EBV from Repeated Records on a Single Trait
Select on mean of \( m \) records: \( \hat{g}_i = b_{g.x} \bar{x}_i \) where \( \bar{x}_i = \frac{\sum_{j=1}^{m} x_{ij}}{m} = \frac{\sum_{j=1}^{m} (g_i + pe_i + te_{ij})}{m} \)

Then,

\[
b_{g.x} = \frac{\sigma_{g.x}}{\sigma_{x}^2}
\]

The variance of \( \bar{x}_i \) is:

\[
\sigma_{\bar{x}_i}^2 = \sigma_g^2 + \sigma_{pe}^2 + \frac{\sigma_{te}^2}{m} = t\sigma_p^2 + \frac{(1-t)\sigma_p^2}{m} = \frac{(mt+1-t)\sigma_p^2}{m}
\]

The covariance is: \( \sigma_{g,\bar{x}} = \sigma_g^2 \)

Thus,

\[
b_{g.x} = \frac{m\sigma_g^2}{\sigma_p^2((m-1)t+1)} = \frac{mh^2}{(m-1)t+1}
\]

Accuracy is:

\[
r = \sqrt{\frac{mh^2}{(m-1)t+1} \sigma_g^2} = \sqrt{\frac{mh^2}{(m-1)t+1}}
\]
2) EBV from One Type of Relatives’ Records

1 record on \( m \) relatives of individual \( i \)

\[ a_{ij} = \text{additive genetic relationship of each relative with individual } i. \]

\[ a_{jj'} = \text{additive genetic relationship among relatives with records} \]

\[ x_g|b = \frac{\sum_{j=1}^{m} x_{ij}}{m} \]

Then,

\[ b_g|x = \frac{\sigma_g}{\sigma^2_x} \]

\[ t = \text{(intra-class) correlation} \] between phenotypic records on \( j \) and \( j' \):

\[ t = r_{xi,j} = \frac{\sigma_{xij}}{\sigma^2_p} = \frac{\sigma_{gij} + e_{ij} + e_{ij'}}{\sigma^2_p} = \frac{(a_{ij} \cdot \sigma^2_g + c^2 \cdot \sigma^2_p)}{\sigma^2_p} = a_{ij} \cdot h^2 + c^2 \]

\[ c^2 = \text{common environment correlation} \] between records \( c^2 = \sigma_{eij}^2 / \sigma^2_p \)

**Variance** of mean of \( m \) records with intra-class correlation \( t \):

\[ \sigma^2_x = \text{Var}\left( \sum_{j=1}^{m} x_{ij} / m \right) = \frac{m \sigma^2_p + m(m-1)t \sigma^2_p}{m^2} = \frac{1 + (m-1)t}{m} \frac{\sigma^2_p}{\sigma^2_p} \]

The **covariance** is:

\[ \sigma_{g,x} = a_{ij} \sigma^2_g \]

Thus,

\[ b_g|x = \frac{ma_{ij} \sigma^2_g}{\sigma^2_p ((m-1)t + 1)} = \frac{mh^2}{(m-1)t + 1} \]

**Accuracy** of selection:

\[ r = a_{ij} \sqrt{\frac{mh^2}{(m-1)t + 1}} \]

For repeated own records \( a_{ij} = 1 \) and \( t \) = repeatability
2) EBV from single relative record

Effect of degree of relationship

- Effect of heritability on progeny test accuracy
- Effect of # records and relationship

* each from a different dam

Average $P^* = +125$

$h^2 = 0.3$  $a_{ij} = 0.5$
$a_{ij} = 0.25$  $t = (0.25)(3) = 0.75$

$b = 0.24$

$g = (0.69)(+125) = +30.6$

$r = 0.49$
Selection index theory: combining information from a variety of sources to obtain the most accurate predictor of genetic merit.

Two separate types of selection indexes:
1) **economic selection index**: predict genetic merit for overall economic value
2) **family selection index**: predict genetic merit for a single trait.
**Selection Index theory**

**Breeding objective** - maximize improvement of economic merit.

**Aggregate genotype or breeding goal**

\[ H = v_1g_1 + v_2g_2 + \ldots + v_ng_n = v'g \]

\[ v' = [v_1, v_2, \ldots, v_n] \quad \text{v}_i \text{ is economic weight for trait } i \]

\[ g' = [g_1, g_2, \ldots, g_n] \quad \text{g}_i \text{ is true breeding value for trait } i \]

**Selection index**

\[ I = b_1x_1 + b_2x_2 + \ldots + b_mx_m = b'x \]

\[ b' = [b_1, b_2, \ldots, b_m] \quad \text{vector of index weights} \]

\[ x' = [x_1, x_2, \ldots, x_m] \quad \text{vector of records} \]

Estimate \( b_i \), such that:

- selection on \( I \) maximizes response in \( H \)
- \( r_{I,H} \) is maximized
- prediction error variance = \( \text{Var}(H-I) \) minimized

**Family selection index**:

\[ H = g \]

\[ I = g = b_1x_1 + b_2x_2 + \ldots + b_mx_m \]

**Derivation of index coefficients**

Find index weights such that \( \text{Var}(H-I) \) is minimized

\[ E(H-I)^2 = E[I - H)'(I - H)] = E[(I - H)'(I - H)]' = E[(b'x - v'g)(x'b - g'v)] = E[(b'xx' - b'xg' - v'gx'b + v'gg'v)] \]

\[ E(b'xx'b) = Var(b'x) = Var(I) = b'Var(x)b = b'Pb \]

\[ P = \text{Var}(x) \]

\[ G = \text{Cov}(x,g) \]

\[ C = \text{Var}(g) \]

\[ G = m \times m \text{ matrix of phenotypic covariances among the observations in I} \]

\[ G = m \times n \text{ matrix of genetic covariances among } m \text{ observations in I and the } n \text{ traits in H} \]

\[ C = n \times n \text{ matrix of genetic covariances among the } n \text{ traits in H} \]

To find index weights, minimize

\[ M = b'Pb - 2b'Gv + v'Cv \]

\( \Rightarrow \) set first derivative =0

\[ \frac{\delta M}{\delta b} = 0 = 2Pb - 2Gv + 0 \Rightarrow \quad Pb = Gv \]

\( \Rightarrow \) Optimal index weights found from \( b = P^{-1}Gv \) = **SELECTION INDEX EQUATIONS**
Accuracy of the index

\[ r_{HI} = \frac{\sigma_{HI}}{\sigma_I \sigma_H} \]

\[ \sigma_I^2 = \text{Var}(I) = b'Pb \]

\[ \sigma_H^2 = \text{Var}(H) = v'Cv \]

\[ \sigma_{HI} = \text{Cov}(H,I) = b'Gv \]

For the optimal index:

\[ b_{HI} = 1 = \frac{\sigma_{HI}}{\sigma_I^2} \Rightarrow \sigma_{HI} = \sigma_I^2 \]

and

\[ Pb = Gv \Rightarrow b'Pb = b'Gv \]

\[ \Rightarrow r_{HI} = \frac{\sigma_I}{\sigma_H} = \sqrt{\frac{b'Pb}{v'Cv}} = \frac{\sigma_{HI}}{\sigma_H} = \sqrt{\frac{b'Gv}{v'Cv}} \]

Accuracy for Family Selection Indexes

\[ H = g \]

\[ v = [1] \]

\[ \sigma_H^2 = \sigma_g^2 \]

\[ b = P^{-1}Gv \Rightarrow b = P^{-1}G \]

\[ r_{HI} = r_{g,\bar{g}} = \sqrt{\frac{b'G}{\sigma_g^2}} \]

Example Index of individual record and full-sib mean performance

\[ x_1 = \text{individual's performance} \]

\[ x_2 = \text{mean performance of that individual's 5 full sibs} \]

\[ h^2 = 0.5 \]

\[ I = g = b_1x_1 + b_2x_2 \]

\[ P = \begin{bmatrix} \sigma_{x_1} & \sigma_{x_2} \\ \sigma_{x_2} & \sigma_x^2 \end{bmatrix} \]

\[ G = \begin{bmatrix} \sigma_{xg}^2 \\ \sigma_{xg}^2 \end{bmatrix} \]

\[ P = \begin{bmatrix} 1 & \frac{1}{2}h^2 \\ \frac{1}{2}h^2 & \frac{1+(m-1)\frac{1}{2}h^2}{m} \end{bmatrix} \]

\[ \sigma_p^2 = \begin{bmatrix} 1 & 0.25 \\ 0.25 & 0.4 \end{bmatrix} \]

\[ G = \begin{bmatrix} h^2 \\ \frac{1}{2}h^2 \end{bmatrix} \sigma_p^2 = \begin{bmatrix} .5 \\ .25 \end{bmatrix} \sigma_p^2 \]

\[ b = P^{-1}G = \begin{bmatrix} 1 & 0.25 \\ 0.25 & 0.4 \end{bmatrix}^{-1} \begin{bmatrix} .5 \\ .25 \end{bmatrix} = \begin{bmatrix} .4074 \\ .3704 \end{bmatrix} \]

\[ I = g = 0.4074x_1 + 0.3704x_2 \]

\[ r_{HI} = r_{g,\bar{g}} = \sqrt{\frac{b'G}{\sigma_g^2}} = \sqrt{\frac{\begin{bmatrix} .4074 \\ .3704 \end{bmatrix} \begin{bmatrix} .5 \\ .25 \end{bmatrix} \sigma_p^2}{0.5 \sigma_p^2}} = 0.77 \]

By adding the mean of 5 full sibs the accuracy of evaluation is increased from 0.71 to 0.77, i.e. by 8.9%.
Correlation between relatives: Correlation between index values of two relatives, \( i \) and \( j \),

\[
t_{ij} = \text{corr}(I_i, I_j) = \text{corr}(b'x_i, b'x_j) = \frac{b'\text{cov}(x_i, x_j)b}{b'Pb} = \frac{b'Rb}{b'Pb}
\]

\( R = m \times m \) matrix with covariances between information sources on the relatives

Summary of selection index formulae for any index and for the optimum index

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Any Index</th>
<th>Optimal Index</th>
</tr>
</thead>
<tbody>
<tr>
<td>Index weights</td>
<td>( b )</td>
<td>Arbitrary</td>
</tr>
<tr>
<td>Index variance</td>
<td>( \sigma_i^2 )</td>
<td>( b'Pb )</td>
</tr>
<tr>
<td>Breeding goal var.</td>
<td>( \sigma_H^2 )</td>
<td>( v'Cv )</td>
</tr>
<tr>
<td>Goal-index covar.</td>
<td>( \sigma_{HI} )</td>
<td>( b'Gv )</td>
</tr>
<tr>
<td>Accuracy</td>
<td>( r_{HI} )</td>
<td>( \sqrt{b'Pb} \langle \frac{b'Gv}{v'Cv} \rangle )</td>
</tr>
</tbody>
</table>

General equations to derive elements of selection index matrices

\( m = \) number of records within a group
\( c^2 = \) common environment component
\( \sigma_{pk} = \) phenotypic standard deviation of trait \( k \)
\( \sigma_{gk} = \) genetic standard deviation of trait \( k \)
\( r_{pl} = \) phenotypic correlation between traits \( k \) and \( l \)
\( r_{gkl} = \) genetic correlation between traits \( k \) and \( l \)
\( a = \) genetic relationship within a group
\( a_{ij} = \) relationship between groups \( i \) and \( j \)
\( a_{hj} = \) additive genetic relationship between individual in breeding goal \( (h) \) and individuals in group \( j \)

P-matrix
diagonal:
- Variance of \( m \) records of a given type
  \[
  \frac{1 + (m - 1)t}{m} \sigma_p^2 = \sigma_p^2 \quad (\text{for } m = 1)
  \]
  \( t = \) repeatability for repeated records
  \( t = ah^2 + c^2 \) for multiple individuals

off-diagonal:
- Covariance between mean of \( m \) records on different traits \( (k \) and \( l \)) for same group:
  \[
  \frac{r_{pl} \sigma_{p_k} \sigma_{p_l} + (m - 1)a_{rl} \sigma_{g_k} \sigma_{g_l}}{m} = r_{gkl} \sigma_{g_k} \sigma_{g_l} \quad (\text{for } m = 1)
  \]
- Covariance between (mean of) record(s) on same trait \( k \) for different groups \( (i \) and \( j)\):
  \[
  (a_{ij} h_k^2 + c_k^2) \sigma_{p_k}^2
  \]
- Between records on different traits \( (k \) and \( l) \) in different groups \( (i \) and \( j)\):
  \[
  a_{ij} r_{gk} \sigma_{g_k} \sigma_{g_l}
  \]
G-matrix
- Covariance of the genetic value for trait $k$ on the breeding goal animal ($h$) with records on trait $l$ for group $j$
  \[ a_{hl} r_{kl} \sigma_{gk} \sigma_{gl} \] (if $k=l$)

C-matrix
- diagonal: Variance of genetic value for trait $k$
  \[ \sigma_{gk}^2 \]
- off-diagonal: Covariance between genetic values for traits $k$ and $l$ on breeding goal animal
  \[ r_{kl} \sigma_{gk} \sigma_{gl} \]

4) Selection Index and Animal Model BLUP – Pseudo BLUP EBV

Two approaches to modeling Animal model BLUP EBV using selection index:
1) Selection index based on relatives providing the greatest amount of information
2) Pseudo-BLUP: Selection index that includes parental EBV as sources of information, along with records on the individual itself, collateral relatives, and progeny.

Information sources:
- $x_i$ = animal’s own record,
- $x_{fs}$ = average of $n-1$ full sibs
- $x_{hs}$ = average of $(m-1)n$ half sibs
- $\hat{g}_s$ = EBV of the sire
- $\hat{g}_d$ = EBV of the dam
- $\bar{g}_m$ = average EBV of $(m-1)$ mates of the sire that produced the half sibs

Pseudo BLUP EBV =
\[ I_i = \hat{g}_i = b_1 x_i + b_2 x_{fs} + b_3 x_{hs} + b_4 \hat{g}_s + b_5 \hat{g}_d + b_6 \bar{g}_m \]

\[
P = \begin{bmatrix}
\sigma_{x_i}^2 & \sigma_{x_i x_{fs}} & \sigma_{x_i x_{hs}} & \sigma_{x_i \hat{g}_s} & \sigma_{x_i \hat{g}_d} & \sigma_{x_i \bar{g}_m} \\
\sigma_{x_{fs}}^2 & \sigma_{x_{fs} x_{fs}} & \sigma_{x_{fs} x_{hs}} & \sigma_{x_{fs} \hat{g}_s} & \sigma_{x_{fs} \hat{g}_d} & \sigma_{x_{fs} \bar{g}_m} \\
\sigma_{x_{hs}}^2 & \sigma_{x_{hs} x_{hs}} & \sigma_{x_{hs} \hat{g}_s} & \sigma_{x_{hs} \hat{g}_d} & \sigma_{x_{hs} \bar{g}_m} \\
\sigma_{\hat{g}_s}^2 & \sigma_{\hat{g}_s \hat{g}_s} & \sigma_{\hat{g}_s \hat{g}_d} & \sigma_{\hat{g}_s \bar{g}_m} \\
\sigma_{\hat{g}_d}^2 & \sigma_{\hat{g}_d \hat{g}_s} & \sigma_{\hat{g}_d \hat{g}_d} & \sigma_{\hat{g}_d \bar{g}_m} \\
\sigma_{\bar{g}_m}^2 & \sigma_{\bar{g}_m \hat{g}_s} & \sigma_{\bar{g}_m \hat{g}_d} & \sigma_{\bar{g}_m \bar{g}_m} \\
\end{bmatrix}
\]
\[
P = \begin{bmatrix}
1 & \frac{1}{2} h^2 + c^2 & \frac{1}{4} h^2 & \frac{1}{2} r_s^2 h^2 & \frac{1}{2} r_d^2 h^2 & 0 \\
\frac{1}{n-1} & \frac{1}{4} h^2 & \frac{1}{2} r_s^2 h^2 & \frac{1}{2} r_d^2 h^2 & 0 & 0 \\
\frac{1}{n-1} & \frac{1}{4} h^2 + \frac{1}{4} h^2 + c^2 & \frac{1}{2} r_s^2 h^2 + \frac{1}{m-1} h^2 - c^2 & \frac{1}{2} r_d^2 h^2 & 0 & 0 \\
0 & 0 & r_s^2 h^2 & 0 & 0 & 0 \\
0 & 0 & 0 & r_d^2 h^2 & 0 & 0 \\
\end{bmatrix}
\]

\[G = \begin{bmatrix}
\sigma_{g_i x_i} & \sigma_{g_i x_{f_i}} & \sigma_{g_i x_{h_s}} & \sigma_{g_i \hat{g}_s} & \sigma_{g_i \hat{g}_d} & \sigma_{g_i \hat{g}_m}
\end{bmatrix}
\]

\[G = \begin{bmatrix}
h^2 & \frac{1}{2} h^2 & \frac{1}{4} h^2 & \frac{1}{2} r_s^2 h^2 & \frac{1}{2} r_d^2 h^2 & 0
\end{bmatrix} \sigma_p^2
\]

\[b = P^{-1}G \]

\[r_{g,\hat{g}} = \sqrt{b' P b / \sigma_g^2}
\]

With

\[x_{hs} = \left( \sum_{k=1}^{m-1} \sum_{l=1}^{n} \frac{x_{kl}}{n} \right) / (m-1)
\]

Where

\[x_{kl} = \frac{1}{2} g_s + \frac{1}{2} g_{d_k} + g_{ms_{kl}} + c_{kl} + e_{kl}
\]

Thus

\[x_{hs} = \frac{1}{2} g_s + \frac{1}{2} \frac{\sum_{k=1}^{m-1} (g_{d_k} + c_k)}{m-1} + \frac{\sum_{k=1}^{m-1} \sum_{l=1}^{n} (g_{ms_{kl}} + e_{kl})}{n(m-1)}
\]

And

\[\sigma_{x_{hs}}^2 = \frac{1}{4} \sigma_g^2 + \frac{1}{4} \sigma_g^2 + \frac{c^2}{m-1} + \frac{1}{2} \sigma_g^2 + \sigma_c^2 + \frac{1}{2} \sigma_g^2
\]

Also,

\[\sigma_g^2 = r_{g,\hat{g}} \sigma_g^2
\]

And

\[\sigma_{x_{h_s} \hat{g}_s} = \sigma \left( \frac{1}{2} g_s + \frac{1}{2} g_d + g_{m_{kl}} + e_{i,\hat{g}_s} \right) = \sigma \left( \frac{1}{2} \hat{g}_s, \hat{g}_s \right) = \frac{1}{2} \sigma g_s \hat{g}_s = \frac{1}{2} r_s^2 \sigma_g^2
\]
Iterative Procedure to Compute Accuracy of EBV

Building-up pedigree information

\[ \text{EBVI} = b^* [x_i, x_{fa}, x_{fs}, \text{EBV}_{\text{Dam}}, \text{EBV}_{\text{Sire}}, \text{EBV}_{\text{Mates}}]' \]
\[ b = P^{-1}G \quad r_{\text{EBV}} = \sqrt{b'Pb/\sigma_g^2} \]

1) Set accuracy of \( \text{EBV}_{\text{Sire}} = \text{EBV}_{\text{Dam}} = \text{EBV}_{\text{Mates}} = h \) (own record)
2) Set up index \((P, G)\) and derive accuracy \( r_{\text{EBVI}} = \sqrt{b'Pb/\sigma_g} \)
3) Set accuracy of \( \text{EBV}_{\text{Sire}} = \text{EBV}_{\text{Dam}} = \text{EBV}_{\text{Mates}} \) equal to \( r_{\text{EBV}} \)
4) Repeat steps 2 and 3 until accuracy converges

Needs adaptation if selection after progeny

Example

<table>
<thead>
<tr>
<th>Iteration</th>
<th>Accuracy</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0.688</td>
</tr>
<tr>
<td>1</td>
<td>0.702</td>
</tr>
<tr>
<td>2</td>
<td>0.704</td>
</tr>
<tr>
<td>3</td>
<td>0.706</td>
</tr>
<tr>
<td>4</td>
<td>0.708</td>
</tr>
<tr>
<td>5</td>
<td>0.710</td>
</tr>
<tr>
<td>6</td>
<td>0.712</td>
</tr>
<tr>
<td>7</td>
<td>0.714</td>
</tr>
</tbody>
</table>

Iteration builds pedigree info

Some general properties of EBV

Unbiased:
\[ E(g_i | \hat{g}_i) = \hat{g}_i \]

\( \Rightarrow \) selection on \( \hat{g} \) maximizes \( E(g) \) for the group of selected individuals

Regression of true on EBV = 1:
\[ b_{g,\hat{g}} = 1 \]

Accuracy of EBV:
\[ r = r_{g,\hat{g}} = b_{g,\hat{g}} \frac{\sigma_{\hat{g}}}{\sigma_g} = \frac{\sigma_{\hat{g}}}{\sigma_g} \]

Covariance between true and EBV:
\[ \sigma_{g,\hat{g}} = r_{g,\hat{g}} \sigma_g \sigma_{\hat{g}} = \sigma_{\hat{g}}^2 \]

Variance of EBV:
\[ \sigma_{\hat{g}}^2 = r^2 \sigma_g^2 \]

\( \Rightarrow \) BLUPEBV.XLS

\( \Rightarrow \) SELACTION growth sigp=.25 h2 = 0.25 own + 5 FS SIP_r = 0.7698
Effect of Accuracy on Distribution of EBV

**High accuracy**

Distribution of EBV

\[ \xi_{EBV} = r \xi_g \]

**Low accuracy**

Distribution of EBV

\[ \xi_{EBV} = r \xi_g \]

Prediction error:

\[ \varepsilon_i = g_i - \hat{g}_i \]

Variance of prediction errors:

\[ \sigma_{\varepsilon}^2 = \sigma_g^2 + \sigma^2 - 2 \sigma_g \sigma_{\hat{g}} \]

\[ = (1 - r^2) \sigma_g^2 \]

Note that

\[ \sigma_g^2 = \sigma_{\hat{g}}^2 + \sigma_{\varepsilon}^2 \]

Covariance between EBV and prediction errors:

\[ \sigma_{\varepsilon,\hat{g}} = \sigma_{\varepsilon,\hat{g}} = 0 \]

Dist’n of true BV given EBV:

\[ g_i | \hat{g}_i \sim N(\hat{g}_i, (1 - r^2) \sigma_g^2) \]

Dist’n prediction errors:

\[ \varepsilon_i \sim N(0, (1 - r^2) \sigma_g^2) \]
Effect of Accuracy on Distribution of True BV for animals with a given $\hat{BV}$

Low accuracy
Distribution of true BV

High accuracy
Distribution of true BV

$\sigma^2 = (1-r^2)\sigma_g^2$