Use of information from relatives

Gene351 only. Lecture 9
Introduction
EBVs and TBVs

- EBVs are estimates of the true breeding values (TBVs), which cannot be observed directly.

- The closer the EBV is to the true breeding value, the greater the response.
Sources of information

- Thus far EBVs have been determined from one source of information: own phenotype, as $EBV_i = h^2P$

- But in general we have other sources of information, such as information from relatives.
Why use additional information sources

Using additional sources of information, such as information from relatives in addition to own phenotype, results in a more accurate EBV and thus an increase in response.
Different selection strategies
Example: Which 4 ‘best’ animals would you select?

<table>
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<th>C</th>
<th>D</th>
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Mean
Mass selection: select on high phenotype
(utilizes own phenotype as information source)

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Mean
Family selection: select all from best family
(utilizes family mean as information source)

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<th>C</th>
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<tr>
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<td>8</td>
<td>6</td>
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</table>

- Family A: 13, 10, 8, 5
Within family selection: select best animals within each family (utilizes an individual's deviation from their family mean as the information source).

<table>
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<tr>
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<tbody>
<tr>
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Within family selection: select best animals within each family (utilizes an individual's deviation from their family mean as the information source).
Note:

Phenotype = family mean + within family deviation

\[ P = P_f + P_w \]
Summary: different selection strategies

Individual or mass selection
- select based on high phenotype
- utilizes own phenotype as information source

Family selection
- select all animals from the best family
- utilized family mean as information source

Within family selection
- select the best animal from each family
- utilizes deviation from family mean as info source
Factors affecting the relative importance of the different information sources
Use of information sources

Rather than use one information source in preference to another, the different information sources are weighted or valued.

In this course you don’t need to know how to determine the weights of the different information sources, but you do need to understand the factors influencing these weights (as described on the next few slides).
Factors affecting the importance of the information sources

- Heritability
  - more weight on own phenotype if higher \( h^2 \)
  - with high \( h^2 \) a large proportion of phenotype (P) is due to breeding value (A), and it makes sense to place a high weight on the animal's own phenotype

- Consider \( h^2 = 1 \). In this case all of P is A and own phenotype is the only information source required
Factors affecting the importance of the information sources

- Family size
  - more weight on family mean for larger families
  - with a larger family, environmental effects are averaged out, and the family mean is a more truer representation of the genetic value of the family
Factors affecting the importance of the information sources

- Type of family
  - more weight on full sib family mean than half-sib family mean, as full sibs are genetically more related than half-sibs
  
  - complication: full sibs have common environmental effect ($V_{EC}$) due to having the same mother which can be ‘confused’ with a genetic effect
Selection indexes using information from relatives
Selection index

The different sources of information are weighted into a selection index

\[ EBV = b_1 P + b_2 P_f \]

- Weight
  - Own performance
- Weight
  - Family performance
There can be many information sources

- own performance
- mean performance of full sibs
- mean performance of half sibs
- performance of sire and/or dam
- performance of progeny

\[ \text{EBV} = b_1P + b_2P_2 + b_3P_3 + \ldots \ldots b_nP_n \]
Index weights

Index weights (b)

- combine information from different sources

- are regression coefficients (multiple regression)
  - taking into account the relationships between information sources & the relationship between these sources and breeding value

- recall that when using own phenotype $h^2$ is a regression coefficient (regression of $A$ on $P$ is equal to $h^2$)
Selection index weights: example

\( b_1 \) = weight for own phenotype, \( b_2 \) = weight for mean of full sibs

<table>
<thead>
<tr>
<th>( h^2 )</th>
<th>( b_1 )</th>
<th>( b_2 )</th>
<th>( b_1 )</th>
<th>( b_2 )</th>
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<tr>
<td>( h^2 = 0.10 )</td>
<td>0.09</td>
<td>0.12</td>
<td>0.08</td>
<td>0.32</td>
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<tr>
<td>( h^2 = 0.70 )</td>
<td>0.62</td>
<td>0.24</td>
<td>0.57</td>
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Observe that ...

- Index weights are higher with higher heritability
- Higher heritability $\rightarrow$ more weight on own information
- Larger family $\rightarrow$ more weight on family mean
And note that ...

- Under high heritability selection on such an index is similar to phenotypic selection

- Under low heritability selection on such an index is more like family selection, which leads to higher inbreeding
Response using a selection index
Response using a selection index

More information

More accuracy

More response

Selection accuracy: 
correlation between true and estimated breeding value
Selection on own phenotypes

\[ R = i \ h^2 \ \sigma_p \]

\[ R = i \ h \ \sigma_A \]

Selection on a selection index

\[ R = i \ r_{IA} \ \sigma_A \]

Accuracy of MASS selection

Accuracy of index selection
Examples of accuracies

\[ h^2 = 0.1 \quad h^2 = 0.3 \]

- own information
- mean of 10 half sib
- mean of 1000 half-sibs
- mean of 1000 full-sibs
- mean of 100 progeny

\[ equal \ to \ \sqrt{h^2} \]

\[ max \ is \ \sqrt{0.25} = 0.5 \]

\[ max \ is \ \sqrt{0.5} = 0.71 \]

\[ max \ approaches \ 1.0 \]
Progeny testing
Progeny testing

- Progeny testing is the most accurate way to determine an animal's EBV

- Progeny testing can give accuracies approaching 1.0 (if sufficient progeny are tested)
Progeny testing

$$\text{EBV}_{PT} = b_1 P_1$$

- $P_1$ is the mean of $n$ progeny

- $b_1$ is the index weight, and depends on number of progeny and $h^2$

\[
b_1 = \frac{2n}{n + \alpha} \quad \alpha = \frac{4 - h^2}{h^2}\]
Using progeny testing to predict future progeny performance

- If
  \[ EBV_{PT\text{sire}} = \frac{2n}{n+\alpha} P_1 \]

- Performance of future progeny is
  \[ \hat{G}_{FutureProgeny} = 0.5\left(\frac{2n}{n+\alpha}\right) P_1 = \frac{n}{n+a} P_1 \]

Heritability of progeny test: \( h^2_{PT} \)
Example

- Herd annual lactation mean = 2000 Kg
- Bull had 20 daughters, mean = 2500 Kg
- $h^2 = 0.25$, $\alpha = 15$

\[
EBV_{PTsire} = \frac{2n}{n + \alpha} P_1 = \frac{2 \times 20}{20 + 15} \times 500 = 571 Kg
\]

\[
\hat{G}_{FutureProgeny} = \frac{n}{n + a} P_1 = \frac{20}{20 + 15} \times 500 = 286 Kg
\]
Concept

Observed progeny mean

Regress by $h_{PT}^2$

True or future progeny mean
Accuracy of progeny tests

- For EBV = h^2P accuracy is sqrt(h^2) = h

- For progeny testing heritability is n/ (n+a) and accuracy is sqrt(n/ (n+a))

- Example, n=100, trait h^2=0.5, accuracy = 0.995

\[
 r_{AA} = \sqrt{\frac{n}{n+a}} = \sqrt{\frac{n}{n + \frac{4 - h^2}{h^2}}} = \sqrt{\frac{100}{100 + \frac{4 - 0.5}{0.5}}} = 0.995
\]
# Examining accuracies

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<th>Progeny test</th>
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<td>n=5</td>
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<tr>
<td>$h^2=0.1$</td>
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<tr>
<td>$h^2=0.7$</td>
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Note that ...

- The lower the heritability, the greater the progeny group size required to reach a certain accuracy.

- At high heriabilities, accuracies relating to EBVs based on own performance are more competitive.
## Accuracies are important in marketing

### Analysis Date Friday, 15 June 2001

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<th>Whit</th>
<th>Pennut</th>
<th>Ywat</th>
<th>Pat</th>
<th>Pernd</th>
<th>Carcase +</th>
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Factors influencing the decision to progeny test or not

- **For**
  - higher accuracies are obtained (esp low $h^2$)
  - can market proven sires
  - necessary for sex-limited traits e.g. dairy

- **Against**
  - increases general interval (L)
  - as few animals are tested, selection intensity (i) can decrease
  - cost