Multiple Trait Selection

Multiple Trait Breeding Objectives

Multiple Trait breeding values

Selection on multiple traits

Predicting multi-trait selection response

Manipulating multi-trait response
Multiple Trait Breeding Objectives

- Animals have many characteristics

» Do we want to improve them all?
Issues with Multiple Trait selection

- We have to spread our selection efforts over several traits
- Not all traits are equally important economically
- Not all traits are equally heritable
- There are correlations between traits
  - Selection for one trait gives also a correlated response for other traits
- How to weight optimally the different traits?
Multiple Trait Selection

- Setting the Breeding Objective
- Defining MT Selection Weights
- Predicting MT Selection Response
- Manipulating MT Selection Response
Introduction to Breeding Objectives

Where do we want to go?

Many possible traits to improve
Many possible traits to record
What is the value of improving different traits?
How do we combine information on different traits to get to where we want to go?
What is a Breeding Objective?

Overall statement about what we want to achieve

e.g.

• Maximise profit

• Minimise costs

• Maximise bad temper and ugliness

• Maximise gross national happiness (Kingdom of Bhutan)
What is an Aggregate Genotype?

A function of genetically controlled traits that contribute value to the breeding objective, that, if maximised (or minimised) will achieve the breeding objective.

\[ H = v_1g_1 + v_2g_2 + v_3g_3 \ldots \text{etc} \]

Where:

- \( v_i \) are **economic weights**
- \( g_i \) are additive genetic values of an individual animal

Note: linearity assumed here (big assumption?)
What is a Selection Index?

A function of genetically controlled phenotypes (or EBV) that if maximised will maximise the aggregate genotype which will achieve the breeding objective.

\[ I = b_1 x_1 + b_2 x_2 + b_3 x_3 \ldots \text{etc} \]

Where \( b_i \) are \textit{selection index weights} and \( x_i \) are the phenotypes (or EBV) of an individual animal.
The Logical Process

Define breeding objective

Develop the aggregate genotype

Develop selection index
Defining an Aggregate Genotype

\[ H = \nu_1g_1 + \nu_2g_2 + \nu_3g_3 \ldots \text{etc} \]

Which traits are included?

- All *genetically controlled* traits that contribute to profit
- Exclude traits that only indirectly associated with profit (e.g., conformation traits)
- Can exclude traits with very little genetic variation (not the same as low heritability)

Note: Not all traits in H may be measured, and there is limited cost associated with including them in H.
Defining an Aggregate Genotype

\[ H = v_1g_1 + v_2g_2 + v_3g_3 \ldots \text{etc} \]

An **economic weight**, \( v_i \), is a partial weight; it is the value of increasing trait \( i \) by one unit when all other traits remain unchanged.

An **economic weight** is the rate of change in profit as the genetic mean of the trait changes, when all other traits remain unchanged.
Selection Index / Selection Criteria Traits

\[ I = b_1 x_1 + b_2 x_2 + b_3 x_3 \ldots \text{etc} \]

Which traits are included?

- Traits that are relatively easy to measure
- Traits that are included in H
- Traits that are correlated with traits in H

Note: These traits require measurement (=cost) so need to do cost-benefit on whether worth while to include them
Selection Index (multiple regression)

\[ EBV_1 = b_1 X_{11} + b_2 X_{12} + \ldots \]
Selection Index Concept

Selection Criteria

- Own performance \( X_{11} \)
- Performance on relatives \( X_{12} \)
- Correlated Trait \( X_{21} \)

Breeding Objective

- Breeding Value \( g_1 \)

Selection Index (multiple regression)

\[
EBV_1 = b_1 X_{11} + b_2 X_{12} + b_3 X_{21} + \ldots
\]

Single trait objective

\( g_1 = \text{breeding value for trait } 1 \)
Selection Index Concept

Selection Criteria \[\rightarrow\] Breeding Objective

<table>
<thead>
<tr>
<th>Selection Criteria</th>
<th>Breeding Objective</th>
</tr>
</thead>
<tbody>
<tr>
<td>Own performance (X_{11})</td>
<td>(H = v_1 g_1 + v_2 g_2)</td>
</tr>
<tr>
<td>Performance on relatives (X_{12})</td>
<td></td>
</tr>
<tr>
<td>Correlated Trait (X_{21})</td>
<td></td>
</tr>
</tbody>
</table>

Selection Index (multiple regression)

\[\text{MTIndex} = b_1 X_{11} + b_2 X_{12} + b_3 X_{21} + \ldots\]
Selection Index Concept

Selection Criteria → Breeding Objective

Own performance $X_{11}$
Performance on relatives $X_{12}$
Correlated Trait $X_{21}$

Breeding Value ($g_1$)

Selection Index (multiple regression)

$EBV_1 = b_1X_{11} + b_2X_{12} + b_3X_{21} + .....$
Selection Index Concept

Selection Criteria

- Own performance $X_{11}$
- Performance on relatives $X_{12}$
- Correlated Trait $X_{21}$

Breeding Objective

Breeding Value $(g_1)$

Breeding Value $(g_2)$

Single trait objective

Selection Index (multiple regression)

$$EBV_2 = b_1X_{11} + b_2X_{12} + b_3X_{21} + \ldots.$$

$g_2 = \text{breeding value for trait 2}$
Selection Index Concept

Phenotypic data $\rightarrow$ Breeding Obj Traits $\rightarrow$ Breeding Obj Overall Merit

$X_{11}, X_{12}$ $\rightarrow$ EBV$_1$ $\rightarrow$ Index

$X_{21}$ $\rightarrow$ EBV$_2$ $\rightarrow$ Index

weights

Selection Index (multiple regression)

Index $= v_1EBV_1 + v_2EBV_2$
Selection Index Concept

Phenotypic data \( \rightarrow \) Breeding Obj Traits \( \rightarrow \) Breeding Obj Overall Merit

Selection Index (multiple regression)

\[
\text{Index} = v_1 \text{EBV}_1 + v_2 \text{EBV}_2
\]

\[
v_1 = v_1 \left[ b_{11}X_{11} + b_{12}X_{12} + b_{13}X_{21} + \ldots \right]
\]

\[
v_2 = v_2 \left[ b_{21}X_{11} + b_{22}X_{12} + b_{23}X_{21} + \ldots \right]
\]

\[
\text{Index} = b_1X_{11} + b_2X_{12} + b_3X_{21} + \ldots
\]
Some formal definitions

Aggregate Genotype / Breeding Goal

\[ H = v_1 g_1 + v_2 g_2 + v_3 g_3 \ldots \text{etc} = v'g \]

\[ \text{Var}(H) = \sigma_H^2 = v'Cv \quad \text{where } C = \text{var}(g) \]

\[ \sigma_H = \text{SD of breeding objective} = \text{SD in profit} \]

\[ \sigma_H \approx \begin{cases} $10 \text{ (sheep)} \\ $30 \text{ (beef)} \\ $50 \text{ (dairy)} \end{cases} \]
Some formal definitions

\[ H = v_1g_1 + v_2g_2 + v_3g_3 \ldots \text{etc} = v'g \]

\[ I = b_1x_1 + b_2x_2 + b_3x_3 \ldots \text{etc} \]

\[ \sigma_I = \text{SD of Index} \]

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

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

where \( P = \text{var}(x) \)

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

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

accuracy = \( \sigma_I/\sigma_H \)

note: \( \sigma_I < \sigma_H \)
Some basic Quantitative Genetic Theory

\[ P = A + E \]

\[ \text{Var}(P) = \text{var}(A) + \text{var}(E) = V_A + V_E \]

\[ \text{cov}(A_i, P_i) = \text{cov}(A_i, A_i) + \text{cov}(A_i, E_i) = V_A \]

\[ \text{cov}(A_i, P_j) = \text{cov}(A_i, A_j) + \text{cov}(A_i, E_j) = a_{ij} V_A \]

\[ \text{cov}(P_i, P_j) = a_{ij} V_A \]

- General Model
- no \text{cov.} between A and E
- if A same animal as P
- \( a_{ij} \) = additive genetic relationship between i and j
- as E’s are uncorrelated if not same animal

Single trait
Some basic Quantitative Genetic Theory

\[ \text{cov}(P_{1i}, P_{2i}) = r_p \sigma_{P1} \sigma_{P2} \]

\[ \text{cov}(P_{1i}, P_{2j}) = a_{ij} r_g \sigma_{g1} \sigma_{g2} \]

Phenotypic covariance as E’s are correlated if same animal

Genetic covariance as E’s are uncorrelated if not same animal

\[ \text{cov}(A_{1i}, P_{2i}) = r_g \sigma_{g1} \sigma_{g2} \]

if \( A_1 \) same animal as \( P_2 \)

\[ \text{cov}(A_{1i}, P_{2j}) = a_{ij} r_g \sigma_{g1} \sigma_{g2} \]

if \( A1 \) not same animal as \( P2 \)

In general, when between traits, replace variance by covariance
Types of correlations

• **Phenotypic correlations**
  – measure association between observed performance
  – Cows that produce more milk tend to have lower fertility

• **Genetic correlations**
  – measure association between breeding values
  – Bulls with daughters that produce more milk tend to have daughters with lower fertility

  – Due to pleiotropy or linkage (may be +ve or –ve)
Types of correlations

- **Phenotypic correlations** \((r_p)\)
  - measure association between observed performance

- **Genetic correlations** \((r_g)\)
  - measure association between breeding values

- **Environmental correlations** \((r_e)\)
  - measure association between random environmental effects

- Recall Variances add up \(V_P = V_A + V_E\)
- Similarly Covariances add up \(\text{Cov}_P = \text{Cov}_A + \text{Cov}_E\)

But correlations do not add up! \(r_p \neq r_A + r_E\)
Selection index with more information sources
(multiple regression)

\( p = \) vector with phenotypes (criteria)

\( g = \) breeding objective (\textit{single trait} BV here)

\[ \text{var}(p) = P = \text{matrix} = \begin{bmatrix}
\text{var}(x_1) & \text{cov}(x_1, x_2) \\
\text{cov}(x_2, x_1) & \text{var}(x_2)
\end{bmatrix} \]

\[ \text{cov}(p,g) = G = \text{vector} = \begin{bmatrix}
\text{cov}(x_1, g) \\
\text{cov}(x_2, g)
\end{bmatrix} \]

weights: \( b = P^{-1}G \)
Selection index with more information sources and with more objective traits (multiple regression)

\[ p = \text{vector with phenotypes (criteria)} \]
\[ H = \text{breeding objective (multiple traits here)} \]
\[ = v_1 g_1 + v_2 g_2 \]
\[ \text{var}(p) = P = \text{matrix} = \begin{bmatrix} \text{var}(x_1) & \text{cov}(x_1, x_2) \\ \text{cov}(x_2, x_1) & \text{var}(x_2) \end{bmatrix} \]
\[ \text{cov}(p, A) = G = \text{matrix} = \begin{bmatrix} \text{cov}(x_1, g_1) & \text{cov}(x_1, g_2) \\ \text{cov}(x_2, g_1) & \text{cov}(x_2, g_2) \end{bmatrix} \]
weights: \[ b = P^{-1}Gv \]
\[ V \text{ are economic values} \]
Back to Selection Index Concept

Information → Evaluation → Choosing

Phenotypic data + Pedigree (+ Genomic) → EBV₁ → v₁
Phenotypic data + Pedigree (+ Genomic) → EBV₂ → v₂
Phenotypic data + Pedigree (+ Genomic) → EBV₃ → v₃

weights

Index

Objective
Limited dispute

Subjective
Room for dispute
Breeding objective traits and selection criteria traits

- Most traits are measured and have value.
- Traits can be measured but have no value themselves.
- Traits can have value but are not measured.

Diagram:
- Measured traits
- Breeding Objective Traits
Predicting genetic change to multiple trait selection

- Single trait selection response
- Correlated response to selection
- Response to multi trait index selection
  - Predicting response per trait
  - How can multiple trait response be manipulated by varying index weights
  - Can we go anywhere we want?
Example

body weight $h^2 = 0.40 \quad \sigma_p = 17 \text{ kg}$

feed intake $h^2 = 0.25 \quad \sigma_p = 2 \text{ kg}$

$r_g = 0.50 \quad r_p = 0.20$
Select on body weight, Objective is body weight

Index = EBV = 0.4\(X_w\)  
Response = 6.80 kg Weight  
Correl. Resp. = 0.32 kg Feed Intake
Breeding Objective

Criteria for selection

Index Weights

Select on body weight + feed intake  
Objective is body weight

Index = $EBV = 0.38X_W + 0.69X_{FI}$

$R_W = 6.93 \text{ kg}$

$R_{FI} = 0.40 \text{ kg}$

We select for bigger eaters, why?
Select on body weight + feed intake  

Objective is feed intake

Index = $EBV = -0.013X_W - 0.23X_{FI}$

Select against bigger animals, why?

$R_W = -5.04 \text{ kg}$

$R_{FI} = -0.55 \text{ kg}$
- Select on body weight + feed intake, Objective is body weight
- Select on body weight, Objective is body weight
- Select on body weight + feed intake, Objective is feed intake
Criteria for selection

\[ W X_1 \]

\[ FI X_2 \]

Index Weights

\[ b_1 \]

\[ b_2 \]

Breeding Objective

\[ W g_1 \]

\[ FI g_2 \]

Economic Weights

\[ 1 \text{ } \$/g \]

\[ -0.5 \text{ } \$/kg \]

Select on body weight + feed intake

Objective is 1.0.BW - 0.5.FI

\[ \text{Index} = \$EBV = 0.38X_W + 0.67X_{FI} \]

\[ R_W = 6.93 \text{ kg} \]

\[ R_{FI} = 0.39 \text{ kg} \]

We still select for bigger eaters, why?
Select on body weight + feed intake

Objective is $1.0 \cdot BW - 0.5 \cdot FI$
Select on body weight + feed intake

Objective is $1.0 \cdot BW - 4 \cdot FI$

Index $= \$EBV = 0.33X_W - 0.22X_{FI}$

Now we select against bigger eaters, why?

But the response is that we get bigger eaters, why?

$R_W = 6.68 \text{ kg}$

$R_{FI} = 0.28 \text{ kg}$
Select on body weight + feed intake  

Objective is 1.0.BW – 4 FI
Breeding Objective

Criteria for selection

W \[ X_1 \]

FI \[ X_2 \]

b_1

b_2

g_1

g_2

Index Weights

Economic Weights

Select on body weight + feed intake

Objective is 1.0.BW – 10 FI

Index = $EBV = 0.25X_W - 1.58X_{FI}$

Now we select more strongly against bigger eaters, why?

R_W = 4.29 kg

R_{FI} = -0.05 kg

But at the expense of less improvement in weight

And the response is that future animals will eat less
Select on body weight + feed intake

Objective is 1.0.BW – 4 FI
Ellipse of all possible outcomes after one round of selection

Iso-economic line for a 1: -10 price ratio
(note that units are not the same on the scales)
Iso-economic line for a 1: -5 price ratio
Iso-economic line for a 1: -1 price ratio
This is a case where both economic values are positive.

The genetic correlation is now favourable.

Note at the direction of selection is quite insensitive to changes in economic values.
Some important points about MT selection

1. The ultimate response of a trait will depend on:

   - choice
   - what has been measured
   - its relative economic weighting
   - accuracy of its EBV
   - correlation with other EBVs

We can control these

 genetic parameters
Some important points

The EBV of a trait can reflect another trait

\[ X_{11} \]

Body Weight

\[ X_{12} \]

Body Weight on relatives

\[ \text{EBV for fertility (g}_2) \]

In this case, selection of \( \text{EBV}_{\text{fertility}} \) will increase fertility, but it will even more increase body weight!

Can predict changes from MT selection using selection index

Need to understand some important MT principles \( \rightarrow \) ellipse
Some important points

The index weight is not always reflecting the response

*Weight can be positive, response can be negative*

The weight does not always reflect the economic value

*Econ Value can be negative, weight can be positive*

Some traits are easier to improve than others

Some traits are easier to improve *jointly* than others
What is this “percent emphasis”

Response per trait in HSI2

Milk Production: 41%
Survival: 30%
Fertility (Fert): 9%
SCS: 9%
Live Weight: 4%
Milking Speed: 3%
Temperament: 4%

Index weights?
Selection response?

e.g. UK: “55% focus on fitness traits” ; “remaining 45% of index covering production”
### Index weight vs Selection response

<table>
<thead>
<tr>
<th></th>
<th>weights</th>
<th>response</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk Kg</td>
<td>0</td>
<td>321</td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>368</td>
</tr>
<tr>
<td>Protein Kg</td>
<td>1</td>
<td>11.0</td>
</tr>
<tr>
<td></td>
<td>0</td>
<td>9.6</td>
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</table>

<table>
<thead>
<tr>
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<th>weights</th>
<th>response</th>
</tr>
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<tbody>
<tr>
<td>Protein Kg</td>
<td>4</td>
<td>9.0</td>
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<tr>
<td></td>
<td>4</td>
<td>11.0</td>
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<tr>
<td>Live Weight Kg</td>
<td>-1</td>
<td>12.5</td>
</tr>
<tr>
<td></td>
<td>0</td>
<td>24.9</td>
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</table>
Case study 1

Dairy: select bulls (50 prog) on

- milk production
- feed intake

<table>
<thead>
<tr>
<th></th>
<th>μ</th>
<th>σ_p</th>
<th>h^2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk (kg/day)</td>
<td>25</td>
<td>2.5</td>
<td>.3</td>
</tr>
<tr>
<td>Feed intake (kg/day)</td>
<td>20</td>
<td>2.0</td>
<td>.2</td>
</tr>
</tbody>
</table>

r_g = .70

r_p = 0.40
Selection for Milk Yield and Feed Intake

<table>
<thead>
<tr>
<th>economic weights</th>
<th>progeny</th>
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<th>response</th>
<th>(4 yrs)</th>
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</thead>
<tbody>
<tr>
<td>milk</td>
<td>feed</td>
<td>milk</td>
<td>feed</td>
<td>milk</td>
</tr>
<tr>
<td>0.2</td>
<td>0</td>
<td>50</td>
<td>-</td>
<td>1.23</td>
</tr>
<tr>
<td>0.2</td>
<td>0</td>
<td>50</td>
<td>50</td>
<td>1.23</td>
</tr>
<tr>
<td>0.2</td>
<td>-0.2</td>
<td>50</td>
<td>-</td>
<td>1.23</td>
</tr>
<tr>
<td>0.2</td>
<td>-0.2</td>
<td>50</td>
<td>50</td>
<td>0.97</td>
</tr>
<tr>
<td>0.2</td>
<td>-0.3</td>
<td>50</td>
<td>-</td>
<td>1.23</td>
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<td>50</td>
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<td>0.52</td>
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<tr>
<td>0.2</td>
<td>-0.3</td>
<td>50</td>
<td>10</td>
<td>0.79</td>
</tr>
</tbody>
</table>

To achieve response for a trait, we need to give it some weight but we also need some data!
Selection for Milk Yield and Feed Intake

<table>
<thead>
<tr>
<th>economic weights</th>
<th>progeny milk</th>
<th>measured milk</th>
<th>response milk</th>
<th>(4 yrs) feed</th>
</tr>
</thead>
<tbody>
<tr>
<td>milk</td>
<td>feed</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>left</td>
<td>0.2</td>
<td>-0.2</td>
<td>50</td>
<td>1.23</td>
</tr>
<tr>
<td>right</td>
<td>0.2</td>
<td>-0.2</td>
<td>50</td>
<td>0.97</td>
</tr>
</tbody>
</table>
Selection for Milk Yield and Feed Intake

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<td>50</td>
</tr>
<tr>
<td>right</td>
<td>0.2</td>
<td>-0.3</td>
<td>50</td>
</tr>
</tbody>
</table>
Case study 2

Dairy: select bulls (50 prog) on

- milk production
- fertility

<table>
<thead>
<tr>
<th></th>
<th>( \mu )</th>
<th>( \sigma_p )</th>
<th>( h^2 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk (kg/lac)</td>
<td>8,000</td>
<td>800</td>
<td>.3</td>
</tr>
<tr>
<td>Fertility(%)</td>
<td>70</td>
<td>46</td>
<td>.03</td>
</tr>
</tbody>
</table>

\[ r_g = -0.25 \quad r_p = -0.1 \]
Selection for milk Yield and Fertility

To achieve response for a trait, we need to give it some weight but we also need some data!
Selection for milk Yield and Fertility

<table>
<thead>
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<th></th>
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<th>measured fertility</th>
<th>response milk</th>
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<td>50</td>
<td>10</td>
<td>391</td>
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<td>50</td>
<td>387</td>
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Selection for milk Yield and Fertility

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<tr>
<td>right</td>
<td>0.2</td>
<td>8</td>
<td>50</td>
<td>50</td>
</tr>
</tbody>
</table>
A challenge

• Assume two traits have a positive economic values

• Why is selection for these traits less sensitive to economic values when they are positively correlated compared to when they are negatively correlated
Unfavourable correlation
Direction is sensitive to econ value changes
This is a case where both economic values are positive.

The genetic correlation is now favourable.

Note at the direction of selection is quite insensitive to changes in economic values.
<table>
<thead>
<tr>
<th>Correlation</th>
<th>Sign of economic weights</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>Equal</td>
</tr>
<tr>
<td></td>
<td>Opposite</td>
</tr>
<tr>
<td>Positive</td>
<td>Favourable (B)</td>
</tr>
<tr>
<td>Negative</td>
<td>Unfavourable (C)</td>
</tr>
<tr>
<td></td>
<td>Favourable (D)</td>
</tr>
</tbody>
</table>
Unfavourable correlation

Not so sensitive to econ value changes if one trait is much more important

Iso-economic line for a 1: -1 price ratio
Selection index with ‘desired gains’

- Rather than
  - determine econ. values >>>> response

- We desire a response >>>> economic values (implicit)

When useful?
Using EBVs as Selection Criteria

1) Define the overall objective (e.g. profit per animal).

2) Develop a linear breeding goal: \( H = v_1 g_1 + v_2 g_2 \ldots + v_n g_n = v'g \)

3) Derive the economic value \((v)\) for each trait in \(H\)

3) Derive a linear index \((l)\) of information sources that maximizes the accuracy of the index with \(H\): \( b = P^{-1}Gv \)
   a. Based on phenotypes: \( I = b_1 x_1 + b_2 x_2 \ldots + b_m x_m = b_x' x \)
   a. Based on EBV: \( I = ^\wedge b_1 g_1 + ^\wedge b_2 g_2 \ldots + ^\wedge b_m g_m = b_{EBV}' g \)

Maximize Response in Overall Objective
Optimize Response in Individual Traits

Slides from Jack Dekkers, WCGALP 2014, Vancouver
**Selection Index Theory**

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

\[ I = b_1^\wedge g_1 + b_2^\wedge g_2 \ldots b_m^\wedge g_m = b_{EBV}'^\wedge g \]

**Optimal Index Weights** (multi-trait EBV): \( b = P^{-1}Gv \)

- if traits in \( I = \) traits in \( H \):
  \[ b_{EBV} = v \]
- if traits in \( I \neq \) traits in \( H \):
  \[ b_{EBV} = b_{gHgI}' v \]
  function of genetic parameters

(Schneeberger et al. 1992)

**Responses to selection:**

- in individual traits:
  \[ S_g = [S_{g_1}, S_{g_2}, \ldots, S_{g_m}] = b_{gHgI}' b_{EBV} G_{EBV}/\sigma_I = v' G_{EBV}/\sigma_I \]
  traits \( I = H \)

**Trait responses depend on:**

- Genetic parameters, economic values
- Variance-covariance matrix of EBV \( = G_{EBV} = \)

\[
\begin{bmatrix}
  r_1^2\sigma_{g_1}^2 \\
  r_2^2\sigma_{g_2}^2 \\
  \vdots \\
  r_m^2\sigma_{g_m}^2
\end{bmatrix}
\]

\( G_{EBV} \) captures the impact of alternate breeding program and phenotyping designs on trait responses – ‘artificial evolution’ (Gibson 1989)

- **EBV covariances**
  - Information
    - phenotypes
    - genomics

\( \sigma_I = b_{EBV}' G_{EBV} b_{EBV} \)
Lost Responses from Uncertainty about Economic Values

TS = traditional selection
\[ r_1 = 0.64 \]
\[ r_2 = 0.43 \]

GS = genomic selection
\[ r_1 = 0.90 \]
\[ r_2 = 0.90 \]

True economic value = 1 for both traits
Lost Responses from Uncertainty about Economic Values

TS = traditional selection  \[ r_1 = 0.64 \quad r_2 = 0.43 \]
GS = genomic selection  \[ r_1 = 0.90 \quad r_2 = 0.90 \]

True economic values = 1 for both traits
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TS = traditional selection

\[ r_1 = 0.64 \]
\[ r_2 = 0.43 \]

GS = genomic selection

\[ r_1 = 0.90 \]
\[ r_2 = 0.90 \]

Assumed economic value trait 1

True economic values = 1 for both traits

% of optimal response

True economic value

Assumed economic value trait 1

- TS \( r_g = +0.5 \)
- GS \( r_g = +0.5 \)
- TS \( r_g = -0.5 \)
- GS \( r_g = -0.5 \)
Breeding Goals and Phenotyping Programs for Multi-Trait Improvement in the Genomics Era

1) Impact of errors in economic values with genomic selection

  • Importance of having accurate economic values is greater with genomic selection

  • Impact of using suboptimal indexes is greater with genomic selection
Use of Genomics to Shape Artificial Evolution

\[ v_1 = v_2 = 1 \]
\[ \sigma_{g1} = \sigma_{g2} \]
\[ r_g = r_p = 0.5 \]

\[ H = g_1 + g_2 \]

<table>
<thead>
<tr>
<th></th>
<th>Trait 1</th>
<th>Trait 2</th>
</tr>
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<tbody>
<tr>
<td>(r_{EBV \ TS})</td>
<td>0.55</td>
<td>0.22</td>
</tr>
<tr>
<td>(r_{EBV \ GS})</td>
<td>0.75</td>
<td>0.75</td>
</tr>
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\[ [S_{g1}, S_{g2}] = b_{EBV}' G_{EBV}/\sigma_l \]
Use of Genomics to Shape Artificial Evolution

\[ v_1 = v_2 = 1 \]
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\[ [S_{g1}, S_{g2}] = b_{EBV} \frac{G_{EBV}}{\sigma_l} \]
\[ v_1 = v_2 = 1 \]
\[ \sigma_{g1} = \sigma_{g2} \]
\[ r_g = r_p = 0.5 \]

\[ H = g_1 + g_2 \]

\[ [S_{g1}, S_{g2}] = b_{EBV} \cdot G_{EBV}/\sigma_I \]

\[ \begin{array}{c|cc}
\text{Trait 1} & \text{Trait 2} \\
\hline
r_{EBV} \text{ TS} & 0.55 & 0.22 \\
r_{EBV} \text{ GS} & 0.75 & 0.75 \\
\hline
\end{array} \]
Use of Genomics to Shape Artificial Evolution

\[ v_1 = v_2 = 1 \]
\[ \sigma_{g1} = \sigma_{g2} \]
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<td>0.22</td>
</tr>
<tr>
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[\( S_{g1}, S_{g2} \) = \( b_{EBV} G_{EBV}/\sigma_l \)]
Use of Genomics to Shape Artificial Evolution

\[
\begin{align*}
\nu_1 &= \nu_2 = 1 \\
\sigma_{g1} &= \sigma_{g2} \\
r_g &= r_p = 0.5
\end{align*}
\]

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</tr>
<tr>
<td>(GS)</td>
<td>TS</td>
<td>GS</td>
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\[
[S_{g1}, S_{g2}] = b_{EBV}' G_{EBV} / \sigma_l
\]
Use of Genomics to Shape Artificial Evolution

\[ v_1 = v_2 = 1 \]
\[ \sigma_{g1} = \sigma_{g2} \]
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\[ [S_{g1}, S_{g2}] = b_{EBV}' G_{EBV}/\sigma_I \]

\[ H = g_1 + g_2 \]
Use of Genomics to Shape Artificial Evolution

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\[ \sigma_{g1} = \sigma_{g2} \]
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<td></td>
</tr>
<tr>
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<td>TS</td>
<td></td>
</tr>
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Use of Genomics to Shape Artificial Evolution

\[ v_1 = v_2 = 1 \]
\[ \sigma_{g1} = \sigma_{g2} \]
\[ r_g = r_p = -0.5 \]

\[
\begin{array}{|c|c|c|c|}
\hline
 & \text{Trait 1} & \text{Trait 2} \\
\hline
r_{EBV} \text{ TS} & 0.55 & 0.22 \\
r_{EBV} \text{ GS} & 0.75 & 0.75 \\
\hline
\text{TBV} & \text{TS} & \text{TS} \\
\text{GS} & \text{TS} & \text{TS} \\
\hline
\end{array}
\]

\[ [S_{g1}, S_{g2}] = b_{EBV}' G_{EBV}/\sigma_l \]
Use of Genomics to Shape Artificial Evolution

\[ v_1 = v_2 = 1 \]
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</tr>
<tr>
<td>( r_{EBV_{GS}} )</td>
<td>0.75</td>
</tr>
</tbody>
</table>

| TBV | TS | TS | GS |
Use of Genomics to Shape Artificial Evolution

\[ v_1 = v_2 = 1 \]
\[ \sigma_{g1} = \sigma_{g2} \]
\[ r_g = r_p = -0.5 \]

\[ H = g_1 + g_2 \]

\[
[S_{g1}, S_{g2}] = b_{EBV}' G_{EBV} / \sigma_I
\]
## Impact of Genomics on Response to Selection

<table>
<thead>
<tr>
<th>Availability and accuracy of GEBV</th>
<th>( r_g = r_p )</th>
<th>Responses to selection</th>
<th>% increase in H</th>
</tr>
</thead>
<tbody>
<tr>
<td>trait 1</td>
<td>trait 2</td>
<td>Trait 1</td>
<td>Trait 2</td>
</tr>
<tr>
<td>---</td>
<td>---</td>
<td>---</td>
<td>---</td>
</tr>
<tr>
<td>-</td>
<td>-</td>
<td>0.56</td>
<td>0.26</td>
</tr>
<tr>
<td>0.75</td>
<td>-</td>
<td>0.74</td>
<td>0.37</td>
</tr>
<tr>
<td>-</td>
<td>0.75</td>
<td>0.58</td>
<td>0.71</td>
</tr>
<tr>
<td>0.75</td>
<td>0.75</td>
<td>0.69</td>
<td>0.68</td>
</tr>
<tr>
<td>-</td>
<td>0.60</td>
<td>0.56</td>
<td>0.55</td>
</tr>
<tr>
<td>-</td>
<td>-</td>
<td>0.51</td>
<td>0.09</td>
</tr>
<tr>
<td>0.75</td>
<td>-</td>
<td>0.71</td>
<td>0.06</td>
</tr>
<tr>
<td>-</td>
<td>0.75</td>
<td>0.32</td>
<td>0.61</td>
</tr>
<tr>
<td>0.75</td>
<td>0.75</td>
<td>0.52</td>
<td>0.54</td>
</tr>
<tr>
<td>-</td>
<td>0.55</td>
<td>0.39</td>
<td>0.39</td>
</tr>
<tr>
<td>-</td>
<td>-</td>
<td>0.51</td>
<td>-0.12</td>
</tr>
<tr>
<td>0.75</td>
<td>-</td>
<td>0.68</td>
<td>-0.23</td>
</tr>
<tr>
<td>-</td>
<td>0.75</td>
<td>0.15</td>
<td>0.42</td>
</tr>
<tr>
<td>0.75</td>
<td>0.75</td>
<td>0.35</td>
<td>0.33</td>
</tr>
<tr>
<td>-</td>
<td>0.43</td>
<td>0.38</td>
<td>0.07</td>
</tr>
</tbody>
</table>

Accuracy of GEBV for trait 2 to achieve the same response in H as having a GEBV for trait 1 with accuracy 0.75.
Using ST EBVs in a multi trait index

The index weights are \[ b = \text{var}(\hat{\alpha})^{-1} \text{cov}(\hat{\alpha}, \alpha) \cdot \mathbf{v}. \]

where \( \alpha \) are the true breeding values of the traits.

\[ \text{var}(\hat{\alpha}) \] is an \( n \) by \( n \) matrix with

- diagonals = \( r_i \cdot \sigma_{a_i}^2 \) where \( \sigma_{a_i}^2 = G(i,i) \)
- off-diagonals = \( r_i \cdot r_j \cdot \sigma_{aij} + 4r_i r_j \cdot (\sigma_{pij} - \frac{1}{4} \sigma_{aij})/n \)
Why are index weights different from economic weights?

Example: Protein Yield $6.00/kg; Feed Intake -$4.00/kg

Feed Intake not measured and not in Breed Obj:

\[
economic\ value\ PY = 6.00 + 0.5 \times (-4.00) = 4.00
\]

Genetic regression

Note: MTEBV, Feed Intake 0.5*ST_EBV_{Protein}

multiple trait BLUP EBVs

\[
Mt\ BLUP\ Index = 6 \times MT_EBV_{Protein} - 4 \times MT_EBV_{FeedIntake}
\]

But not 

Index = 6 \times ST_EBV_{Protein}
Index weights for single trait EBVs depending on EBV accuracies

economic values 6 and -4 and a genetic regression of 0.5

<table>
<thead>
<tr>
<th>EBVAccT1</th>
<th>EBVAccT2</th>
<th>IndWGhtT1</th>
<th>IndWghtT2</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.90</td>
<td>0.00</td>
<td>4.00</td>
<td>NA</td>
</tr>
<tr>
<td>0.90</td>
<td>0.50</td>
<td>4.40</td>
<td>-2.93</td>
</tr>
<tr>
<td>0.90</td>
<td>0.70</td>
<td>4.83</td>
<td>-3.12</td>
</tr>
<tr>
<td>0.90</td>
<td>0.90</td>
<td>5.50</td>
<td>-3.42</td>
</tr>
<tr>
<td>0.95</td>
<td>0.95</td>
<td>5.73</td>
<td>-3.69</td>
</tr>
<tr>
<td>0.99</td>
<td>0.99</td>
<td>5.96</td>
<td>-3.95</td>
</tr>
<tr>
<td>0.999</td>
<td>0.999</td>
<td>5.99</td>
<td>-3.99</td>
</tr>
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</table>
Explaining the Index weights for ST_EBVs

In an index of ST_EBVs an index weight for a trait (say trait 1):

\[ b1 \text{ EV1} + b2 \text{ EV2} \]

where:

\[ b1 \sim r^2_{ST\_EBV1} / r^2_{MT\_EBV1} \]
\[ b2 \sim (1 - r^2_{ST\_EBV2}) \times \text{cov}(A_1,A_2)/\text{var}(A_1) \]

Index weights adjust for correlated response not accounted for by the non-perfect accuracy of a correlated trait
Effect on Response of using incorrect (econ) weights for STEBVs

<table>
<thead>
<tr>
<th>Case</th>
<th>Weight Used</th>
<th>Wght T1</th>
<th>Wght T2</th>
<th>$Resp T1</th>
<th>$Resp T2</th>
<th>Tot $Resp</th>
<th>Rel Resp</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>EV</td>
<td>1.00</td>
<td>2.00</td>
<td>0.36</td>
<td>0.61</td>
<td>0.96</td>
<td>96.5%</td>
</tr>
<tr>
<td>1</td>
<td>IW</td>
<td>1.77</td>
<td>1.76</td>
<td>0.42</td>
<td>0.58</td>
<td>1.00</td>
<td></td>
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STEBV accuracies 0.9 and 0.5 and a genetic correlation of 0.5.
Effect of using incorrect (econ) weights on Selection Response

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<td></td>
</tr>
<tr>
<td>2</td>
<td>EV</td>
<td>1.00</td>
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<td>0.41</td>
<td>0.29</td>
<td>0.71</td>
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<tr>
<td></td>
<td>IW</td>
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<td>0.71</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>EV</td>
<td>1.00</td>
<td>-1.00</td>
<td>0.37</td>
<td>-0.08</td>
<td>0.29</td>
<td>99.2%</td>
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<tr>
<td></td>
<td>IW</td>
<td>0.60</td>
<td>-0.75</td>
<td>0.34</td>
<td>-0.05</td>
<td>0.29</td>
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<td></td>
</tr>
<tr>
<td>4</td>
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<td>IW</td>
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STEBV accuracies 0.9 and 0.5 and a genetic correlation of 0.5.
Effect of using incorrect (econ) weights on Selection Response

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<tr>
<th>Case</th>
<th>Weight Used</th>
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Using ST EBVs Summary

- When using ST EBVs in an index:
  - Index weights are economic weights but adjusted for correlated changes in other traits as far as those are not accounted for by their EBVs.
  - Additional weight is given to traits that are well measured,
  - Includes value of response other breeding objective traits not well measured.
  - Not making this adjustment ignores the value of some correlated changes.
  - Although the overall response is likely to be not affected very much (less than 5%), the weight and response for Production would be higher and the weight and response for Fertility or Fitness would be considerably lower compared to an optimal index.
Summary ST EBVs in index

- When using ST EBVs, best approach is to use index weights, not straight economic weights

- But Index Weights can cause some practical problems
  
  - Some weights maybe hard to explain
  
  - Different bulls might need different weights
  
  - Do not publish weights? Then not easy to calculate your own index