Reminders:

- Please put your tutors name on all assignments handed in.

- Please hand in plagiarism declaration forms with your next assignment (if you haven’t already done so)
Practical 2: Part 1

Aim: to understand breeding values at a single locus level

- breeding values are the sum of the average effect of alleles ($\alpha$)
Calculation of expected breeding values as sum of $\alpha$

<table>
<thead>
<tr>
<th>Genotype</th>
<th>$A_2A_2$</th>
<th>$A_1A_2$</th>
<th>$A_1A_1$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Value</td>
<td>280</td>
<td>300</td>
<td>320</td>
</tr>
<tr>
<td>Frequency</td>
<td>0.25</td>
<td>0.50</td>
<td>0.25</td>
</tr>
<tr>
<td>Pop’n mean</td>
<td>300</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genetic value</td>
<td>-20</td>
<td>0</td>
<td>20</td>
</tr>
<tr>
<td>Breeding value</td>
<td>-20</td>
<td>0</td>
<td>20</td>
</tr>
</tbody>
</table>

Average effect ($\alpha$) of $A_1$

$A_1$ allele will meet $A_1$ at frequency $p$ and $A_2$ at frequency $q$

$$A_1A_1 \times p + A_1A_2 \times q = 20 \times 0.5 + 0 \times 0.5 = 10$$

Average effect ($\alpha$) of $A_2$

$A_2$ allele will meet $A_1$ at frequency $p$ and $A_2$ at frequency $q$

$$A_2A_1 \times p + A_2A_2 \times q = 0 \times 0.5 + -20 \times 0.5 = -10$$
Working from previous slide

- **Population mean** = sum of frequency \( \times \) values
  - \( 280 \times 0.25 + 300 \times 0.5 + 320 \times 0.25 = 300 \)

- **Genetic value** = deviation from population mean
  - e.g. \( A2A2 = 280 - 300 = -20 \)

- **Breeding value** = sum of average effect of alleles
  - **Average effect of** \( A1 \)
    - \( A1 \) allele will meet \( A1 \) at frequency \( p \) and \( A2 \) at frequency \( q \)
    - \( A1A1 \times p + A1A2 \times q = 20 \times 0.5 + 0 \times 0.5 = 10 \)

  - **Average effect of** \( A2 \)
    - \( A2 \) allele will meet \( A1 \) at frequency \( p \) and \( A2 \) at frequency \( q \)
    - \( A2A1 \times p + A2A2 \times q = 0 \times 0.5 + -20 \times 0.5 = -10 \)
Breed own animals: single locus example

Steps

- give progeny a random allele from sire
- give progeny a random allele from dam

thus have progeny genotype
and genotypic value

- give progeny a random environmental effect
- determine progeny phenotype
Example

Single locus model where

- $A1A1 = 350 \text{ Kg}$, $A1A2 = 340 \text{ Kg}$, $A2A2 = 300 \text{ Kg}$
- Sires are one of the above genotypes
- Dams have frequency of $A1 = A2 = 0.5$
Transmission of alleles

Simulate allele transmission by tossing a coin

‘heads (H)’ = A1 and ‘tails (T)’ = A2

A1A2 sire x random dams

<table>
<thead>
<tr>
<th>Sire allele</th>
<th>Dam allele</th>
<th>Progeny genotype</th>
<th>Genetic Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>H: A1</td>
<td>H: A1</td>
<td>A1A1</td>
<td>350 Kg</td>
</tr>
<tr>
<td>T: A2</td>
<td>H: A1</td>
<td>A2A1</td>
<td>340 Kg</td>
</tr>
<tr>
<td>T: A2</td>
<td>T: A2</td>
<td>A2A2</td>
<td>300 Kg</td>
</tr>
<tr>
<td>H: A1</td>
<td>T: A2</td>
<td>A1A2</td>
<td>340 Kg</td>
</tr>
</tbody>
</table>
### Environmental effect (E)

Simulate E by tossing a dice

<table>
<thead>
<tr>
<th>Die value</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\sigma$</td>
<td>-2.5</td>
<td>-1.5</td>
<td>-0.5</td>
<td>+0.5</td>
<td>+1.5</td>
<td>+2.5</td>
</tr>
<tr>
<td>If $\sigma=20$</td>
<td>-50</td>
<td>-30</td>
<td>-10</td>
<td>10</td>
<td>30</td>
<td>50</td>
</tr>
</tbody>
</table>
Add genetic and environmental values to get phenotype: $P = G + E$

<table>
<thead>
<tr>
<th>Progeny genotype</th>
<th>Genetic Value</th>
<th>Environment</th>
<th>Phenotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>A1A1</td>
<td>350 Kg</td>
<td>-30 Kg</td>
<td>320 Kg</td>
</tr>
<tr>
<td>A2A1</td>
<td>340 Kg</td>
<td>50 Kg</td>
<td>390 Kg</td>
</tr>
<tr>
<td>A2A2</td>
<td>300 Kg</td>
<td>10 Kg</td>
<td>310 Kg</td>
</tr>
<tr>
<td>A1A2</td>
<td>340 Kg</td>
<td>-30 Kg</td>
<td>310 Kg</td>
</tr>
</tbody>
</table>
Sires breeding value
(realised rather than expected)

- Calculate average of offspring for each sire
  eg A1A1 sire: 345 Kg

- Calculate overall mean
  eg 331.6 Kg

- EBV sire = 2 x (progeny mean - overall mean)
  eg A1A1 sire: 2 x (345 Kg - 331.6 Kg)
Compare EBVs for sires:

- To expected values
- When no environmental effect is assumed
- When an environmental effect is assumed

Realise that:

- EBVs will differ from expected due to random sampling (but we can predict average outcome)
- Degree of randomness is larger when there is environmental effects
GENE351 students only do question 1c.

**Compare EBVs for sires:**
- When frequency of A1 in dams = 0.5
- When frequency of A1 in dams = 0.166

**Realise that:**
- Breeding values depend on the population allele frequency
- Average effect of an allele is greater if the allele is rare
Practical 1: Part 2

Aim: to understand that quantitative traits are controlled by a number of loci

- normal distributions of genetic values are approached when the number of loci is large
- normality is not achieved under some circumstances
Module loci in GENUP

- Draws a histogram of genetic merit (genotypic effects) for animals drawn from a population.

Single locus model: $A_1 = +1$, $A_2 = -1$, $p=0.5$

4 individuals

<table>
<thead>
<tr>
<th>Genotypic effect</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>$A_2A_2$</td>
<td>-2</td>
</tr>
<tr>
<td>$A_1A_2$</td>
<td>0</td>
</tr>
<tr>
<td>$A_1A_1$</td>
<td>2</td>
</tr>
</tbody>
</table>
Module loci in GENUP

Assumptions

- each locus has two alleles
- p (frequency of favourable allele) is the same for each locus
- genetic values for the three genotypes at each locus are the same
Compare:

- Distributions of genotypic effect when allele frequencies are intermediate ($p=q=0.5$) and non-intermediate

Realise that:

- Non-intermediate allele frequencies causes non-normal distributions when the number of loci is small, but less so when the number of loci is large
Compare:

- Distributions of genotypic effects when genotypes do or do not show dominance

Realise that:

- Dominance causes non-normal distributions when the number of loci is small, but less so when the number of loci is large
Problem set 2

- Due Tuesday 12\textsuperscript{th} August
- Try to complete in class