

Livestock Breeding and Genomics - Solution 2

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Problem 1: Breeding Values For a Monogenic Trait

We assume that the absorption of cholesterol is determined by a certain enzyme. The level of enzyme production is determined by a single bi-allelic locus E . The genotype frequencies and the genotypic values for the two dairy cattle populations **Original Braunvieh** and **Brown Swiss** are given in the following table.

Variable	Original Braunvieh	Brown Swiss
$f(E_1E_1)$	0.0625	0.01
$f(E_1E_2)$	0.3750	0.18
$f(E_2E_2)$	0.5625	0.90
a	15.0000	29.00
d	3.0000	0.00

Hints

- Assume that allele E_1 is the allele with the positive effect on the enzyme level
- Assume that the Hardy-Weinberg Equilibrium holds in both populations

Your Task

Compute the breeding values for all three genotypes in both populations.

Solution

The breeding values are computed as shown in the following table.

Genotype	Breeding Value
E_1E_1	$BV_{11} = 2q\alpha$
E_1E_2	$BV_{12} = (q - p)\alpha$
E_2E_2	$BV_{22} = -2p\alpha$

with $\alpha = a + (q - p)d$. The values for a and d are given in the task and the allele frequencies p and q can be computed from the given genotype frequencies.

$$p = f(E_1) = f(E_1E_1) + \frac{1}{2}f(E_1E_2)$$

and $q = 1 - p$

For the two populations we get

Variable	Original Braunvieh	Brown Swiss
p	0.25	0.1
q	0.75	0.9
α	16.50	29.0

The breeding values for the two breeds are given in the following table

Genotype	Breeding Value	Original Braunvieh	Brown Swiss
E_1E_1	BV_{11}	24.75	52.2
E_1E_2	BV_{12}	8.25	23.2
E_2E_2	BV_{22}	-8.25	-5.8

Problem 2: Quantitative Genetics

In a population the following numbers of genotypes were counted for a given genetic locus called A .

```
dfGenotypeFreq <- data.frame(Genotypes = c("$A_1A_1$", "$A_1A_2$", "$A_2A_2$"),
                             Numbers = c(24, 53, 23),
                             stringsAsFactors = FALSE)
knitr::kable(dfGenotypeFreq)
```

Genotypes	Numbers
A_1A_1	24
A_1A_2	53
A_2A_2	23

a) Compute the genotype frequencies

Solution

```
nTotNrInd <- sum(dfGenotypeFreq$Numbers)
vGenoTypeFreq <- dfGenotypeFreq$Numbers / nTotNrInd
cat(paste("genotype-frequency", dfGenotypeFreq$Genotypes[1]), ": ", vGenoTypeFreq[1])
## genotype-frequency $A_1A_1$ : 0.24
cat(paste("genotype-frequency", dfGenotypeFreq$Genotypes[2]), ": ", vGenoTypeFreq[2])
## genotype-frequency $A_1A_2$ : 0.53
cat(paste("genotype-frequency", dfGenotypeFreq$Genotypes[3]), ": ", vGenoTypeFreq[3])
## genotype-frequency $A_2A_2$ : 0.23
```

b) Compute the allele frequencies

Solution

```
vGenFreqP <- vGenoTypeFreq[1] + 0.5*vGenoTypeFreq[2]
vGenFreqQ <- vGenoTypeFreq[3] + 0.5*vGenoTypeFreq[2]
cat("allele frequency for A1: ", vGenFreqP)
```

```
## allele frequency for A1: 0.505
```

```
cat("allele frequency for A2: ", vGenFreqQ)
```

```
## allele frequency for A2: 0.495
```

c) Compute the population mean μ under the following assumptions

- the difference between the genotypic values of the homozygous genotypes is 20 and
- the genotypic value of the heterozygous genotype is 2.

Solution

```
nDeltaHom <- 20
### # additive value A
nAddValue <- nDeltaHom / 2
nDom <- 2
### # population mean
nMu <- (vGenFreqP-vGenFreqQ) * nAddValue + 2 * vGenFreqP * vGenFreqQ * nDom
cat("Population mean: ", nMu, "\n")
```

```
## Population mean: 1.0999
```