

# Livestock Breeding and Genomics - Solution 4

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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
$\alpha$	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  $A$ .

Genotypes	Numbers
$A_1A_1$	24
$A_1A_2$	53
$A_2A_2$	23

- Compute the genotype frequencies
- Compute the allele frequencies
- Compute the population mean  $\mu$  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

- Compute the genotype frequencies

```
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
```

- Compute the allele frequencies

```
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  $\mu$  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.

```
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
```