

GENE613 - Homework 2

Daniel Osorio - dcosoriorh@tamu.edu
 Department of Veterinary Integrative Biosciences
 Texas A&M University

1. Assume there are n alleles at given locus. Given $\frac{n(n+1)}{2}$ different possible genotypes and $\frac{n(n-1)}{2}$ heterozygotes, prove algebraically that there are n homozygotes.

$$\begin{aligned}
 n &= \frac{n(n+1)}{2} - \frac{n(n-1)}{2} \\
 n &= \frac{n}{2}(n+1 - n+1) \\
 n &= \frac{2n}{2} \\
 n &= n
 \end{aligned}
 \tag{1}$$

2. The Booroola (B) gene influences fecundity (offspring number) in some populations (Australian) of Merino sheep. For two flocks, all individuals were genotyped and the average litter sizes for females of the different genotypes were determined.

	bb	Bb	BB
Population 1	668	100	232
Population 2	9030	936	34
Mean litter size	1.48	2.17	2.66

- a) Calculate the allele and genotype frequencies and population means at this locus.

```

> alleleFrequencies <- function(genotypes){
+   BB <- genotypes[[3]]
+   Bb <- genotypes[[2]]
+   bb <- genotypes[[1]]
+   B <- (BB + 0.5 * Bb) / sum(genotypes)
+   b <- (bb + 0.5 * Bb) / sum(genotypes)
+   return(c(B=B, b=b))
+ }
> t(apply(boorola, 1, alleleFrequencies))

           B           b
Population 1 0.2820 0.7180
Population 2 0.0502 0.9498

> genotypeFrequencies <- function(genotypes){
+   genotypes / sum(genotypes)
+ }
> t(apply(boorola, 1, genotypeFrequencies))

```

```

          bb      Bb      BB
Population 1 0.668 0.1000 0.2320
Population 2 0.903 0.0936 0.0034

> populationMean <- function(genotypes, phenotypes){
+   centeredPhenotypes <- phenotypes - mean(phenotypes[c(1,3)])
+   sum(genotypeFrequencies(genotypes) * centeredPhenotypes)
+ }
> apply(boorola, 1, function(genotypes){populationMean(
+   genotypes = genotypes,
+   phenotypes = c(1.48,2.17,2.66))
+ })

```

```

Population 1 Population 2
-0.247240    -0.521404

```

b) For population 2, calculate:

- average effects of alleles,

```

> allelesAverageEffect <- function(genotypes, phenotypes){
+   gValue <- phenotypes - mean(phenotypes[c(1, 3)])
+   names(gValue) <- c("-a", "d", "a")
+   alleles <- alleleFrequencies(genotypes)
+   names(alleles) <- c("p", "q")
+   B = (alleles[["q"]] *
+   (gValue[["a"]] + (gValue[["d"]] *
+   (alleles[["q"]] - alleles[["p"]]))))
+   b = (-alleles[["p"]] *
+   (gValue[["a"]] + (gValue[["d"]] *
+   (alleles[["q"]] - alleles[["p"]]))))
+   return(c(B = B, b = b))
+ }
> allelesAverageEffect(genotypes = c(bb=9030, Bb=936, BB=34),
+   phenotypes = c(bb=1.48, Bb=2.17, BB=2.66))
          B          b
0.64582601 -0.03413399

```

- average effect of an allele substitution,

```

> substitutionAverageEffect <- function(genotypes, phenotypes) {
+   gValue <- phenotypes - mean(phenotypes[c(1, 3)])
+   names(gValue) <- c("-a", "d", "a")
+   alleles <- alleleFrequencies(genotypes)
+   names(alleles) <- c("p", "q")
+   sAE <- (gValue[["a"]] +
+   (gValue[["d"]] * (alleles[["q"]] - alleles[["p"]])))
+   return(sAE)
+ }
> substitutionAverageEffect(
+   genotypes = c(bb = 9030, Bb = 936, BB = 34),
+   phenotypes = c(bb = 1.48, Bb = 2.17, BB = 2.66)
+ )
[1] 0.67996

```

- breeding values,

```

> breedingValues <- function(genotypes, phenotypes) {
+   alphas <- allelesAverageEffect(genotypes = genotypes,
+                                   phenotypes = phenotypes)
+   BB = 2 * alphas[[1]]
+   Bb = sum(alphas)
+   bb = 2 * alphas[[2]]
+   return(c(BB = BB, Bb = Bb, bb = bb))
+ }
> breedingValues(
+ genotypes = c(bb = 9030, Bb = 936, BB = 34),
+ phenotypes = c(bb = 1.48, Bb = 2.17, BB = 2.66)
+ )

```

```

          BB          Bb          bb
1.29165202 0.61169202 -0.06826798

```

■ dominance deviations,

```

> dominanceDeviations <- function(genotypes, phenotypes){
+   gValue <- phenotypes - mean(phenotypes[c(1, 3)])
+   names(gValue) <- c("-a", "d", "a")
+   alleles <- alleleFrequencies(genotypes)
+   names(alleles) <- c("p", "q")
+   BB = -2 * (alleles[["q"]] ^ 2) * gValue[["d"]]
+   Bb = 2 * alleles[["p"]] * alleles[["q"]] * gValue[["d"]]
+   bb = -2 * (alleles[["p"]] ^ 2) * gValue[["d"]]
+   return(cbind(BB = BB, Bb = Bb, bb = bb))
+ }
> dominanceDeviations(
+ genotypes = c(bb = 9030, Bb = 936, BB = 34),
+ phenotypes = c(bb = 1.48, Bb = 2.17, BB = 2.66)
+ )

```

```

          BB          Bb          bb
[1,] -0.180424 0.009535992 -0.000504008

```

■ breeding value variance,

```

> breedingValueVariance <- function(genotypes, phenotypes){
+   alleles <- alleleFrequencies(genotypes)
+   names(alleles) <- c("p", "q")
+   alphas <- allelesAverageEffect(genotypes = genotypes,
+                                   phenotypes = phenotypes)
+   alpha <- (alphas[[1]] - alphas[[2]])
+   vA <- 2 * prod(alleles) * (alpha ^ 2)
+   return(vA)
+ }
> breedingValueVariance(
+ genotypes = c(bb = 9030, Bb = 936, BB = 34),
+ phenotypes = c(bb = 1.48, Bb = 2.17, BB = 2.66)
+ )
[1] 0.04408924

```

■ dominance variance and

```

> dominanceVariance <- function(genotypes, phenotypes){
+   alleles <- alleleFrequencies(genotypes)

```

```

+   names(alleles) <- c("p", "q")
+   gValue <- phenotypes - mean(phenotypes[c(1, 3)])
+   names(gValue) <- c("-a", "d", "a")
+   alphas <- allelesAverageEffect(genotypes = genotypes,
+   phenotypes = phenotypes)
+   alpha <- (alphas[[1]] - alphas[[2]])
+   dV <- (2 * prod(alleles) * gValue[["d"]]) ^ 2
+   return(dV)
+ }
> dominanceVariance(
+ genotypes = c(bb = 9030, Bb = 936, BB = 34),
+ phenotypes = c(bb = 1.48, Bb = 2.17, BB = 2.66)
+ )
[1] 9.093514e-05

```

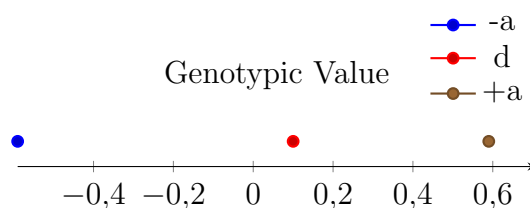
■ genetic variance.

```

> geneticVariance <- function(genotypes, phenotypes){
+   gV <- breedingValueVariance(
+     genotypes = c(bb = 9030, Bb = 936, BB = 34),
+     phenotypes = c(bb = 1.48, Bb = 2.17, BB = 2.66)
+   ) + dominanceVariance(
+     genotypes = c(bb = 9030, Bb = 936, BB = 34),
+     phenotypes = c(bb = 1.48, Bb = 2.17, BB = 2.66)
+   )
+   return(gV)
+ }
> geneticVariance(
+ genotypes = c(bb = 9030, Bb = 936, BB = 34),
+ phenotypes = c(bb = 1.48, Bb = 2.17, BB = 2.66)
+ )
[1] 0.04418017

```

c) What kind of genetic action appears to be responsible at this locus?



There appears that the genetic action responsible at this locus is an incomplete dominance associated to the B allele.

d) By random mating with each of the populations a new generation within each of the population above is created. Predict the allele and genotype frequencies and means.

```

> onePopulationRandomMating <- function(genotypes, phenotypes) {
+   alleles <- alleleFrequencies(genotypes)
+   BB <- alleles[["B"]]^2
+   Bb <- 2*prod(alleles)
+   bb <- alleles[["b"]]^2
+   popMean <- populationMean(c(bb, Bb, BB), phenotypes)
+   return(c(

```

```

+   alleles,
+   BB = BB,
+   Bb = Bb,
+   bb = bb,
+   popMean = popMean
+ ))
+ }
> apply(boorola, 1, function(genotypes) {
+   onePopulationRandomMating(genotypes = genotypes,
+   phenotypes = c(bb = 1.48,
+   Bb = 2.17,
+   BB = 2.66))
+ })

```

	Population 1	Population 2
B	0.2820000	0.05020000
b	0.7180000	0.94980000
BB	0.0795240	0.00252004
Bb	0.4049520	0.09535992
bb	0.5155240	0.90212004
popMean	-0.2167448	-0.52122801

- e) A 3rd population results from randomly crossing individuals of population 1 with those in population 2. Predict allele and genotype frequencies and means.

```

> twoPopulationsRandomMating <-
+   function(p1Genotypes, p2Genotypes, phenotypes) {
+     p1Alleles <- alleleFrequencies(p1Genotypes)
+     p2Alleles <- alleleFrequencies(p2Genotypes)
+     punnet <- outer(p1Alleles, p2Alleles, "*")
+     BB <- punnet["B", "B"]
+     Bb <- punnet["B", "b"] + punnet["b", "B"]
+     bb <- punnet["b", "b"]
+     newGenotypesF <- c(bb, Bb, BB)
+     newAlleleF <- alleleFrequencies(c(bb, Bb, BB))
+     popMean <- populationMean(newGenotypesF, phenotypes = phenotypes)
+     c(newAlleleF, c(BB = BB, Bb = Bb, bb = bb), popMean = popMean)
+   }
> twoPopulationsRandomMating(
+   p1Genotypes = boorola[1, ],
+   p2Genotypes = boorola[2, ],
+   phenotypes = c(bb = 1.48,
+   Bb = 2.17,
+   BB = 2.66)
+ )

```

	B	b	BB	Bb	bb	popMean
	0.1661000	0.8339000	0.0141564	0.3038872	0.6819564	-0.3636133

- f) By random mating within the 3rd population a new generation is created. Predict allele and genotype frequencies and means.

```

> onePopulationRandomMating(
+   genotypes = c(bb = 0.6819564,

```

```
+           Bb = 0.3038872,  
+           BB = 0.0141564),  
+   phenotypes = c(bb = 1.48,  
+   Bb = 2.17,  
+   BB = 2.66)  
+   )
```

	B	b	BB	Bb	bb	popMean
	0.16610000	0.83390000	0.02758921	0.27702158	0.69538921	-0.36629984