

GENE613 - Homework 3

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

Single locus with 2 alleles in 2 population in Hardy-Weinberg equilibrium. Given $f(A) = p_1 = 0,3$ in population 1; and $f(A) = p_2 = 0,4$ in population 2; $a = -2$; $d = 1,5$.

1. Assume a group of migrants $m = 0,12$ from population 2 to population 1.

a) After this migration event, what will be the allele frequencies in each population?

```
> newAlleleFrequencies <- function(p1, p2, m) {  
+   A = ((1 - m) * p1) + (m * p2)  
+   a = 1 - A  
+   return(c(A = A, a = a))  
+ }  
> newAlleleFrequencies(p1 = 0.3, p2 = 0.4, m = 0.12)  
  
      A      a  
0.312 0.688
```

b) Assume random mating in both populations again. What will be the change in means in each population from before to current?

```
> populationMean <- function(p, a, d) {  
+   q <- (1 - p)  
+   return(p^2*a + 2*p*q*d + q^2*-a)  
+ }  
> meansChange <- function(Mnew, M){  
+   Mnew - M  
+ }  
> # Population 1  
> meansChange(Mnew = populationMean(p = 0.312, a = -2, d = 1.5),  
+             M = populationMean(p = 0.3, a = -2, d = 1.5))  
[1] -0.034032  
  
> # Population 2  
> meansChange(Mnew = populationMean(p = 0.4, a = -2, d = 1.5),  
+             M = populationMean(p = 0.4, a = -2, d = 1.5))  
[1] 0
```

c) Put $\Delta = p_2 - p_1$, originally (in terms of a single parameter representing allele frequency) $f(A) = p_1$ and $f(a) = 1 - p_1$ and now $f(A)_{new} = p_1 + m\Delta$, and $f(a)_{new} = 1 - p_1 - m\Delta$. The original genotypic mean was: $M = (2p_1 - 1)a + 2p_1(1 - p_1)d$, and after migration and return to random mating $M_{new} = (2p_1 - 1 + 2m\Delta)a + 2[p_1(1 - p_1) - m\Delta(2p_1 - 1 + m\Delta)]d$. Show algebraically that the change on population mean

is $M_{new} - M = 2m\Delta[a - (2p_1 - 1 + m\Delta)d]$ and confirm that this is correct with allele frequencies as above.

$$\begin{aligned}
 M_{new} &= (2p_1 - 1 + 2m\Delta)a + 2[p_1(1 - p_1) - m\Delta(2p_1 - 1 + m\Delta)]d \\
 &= 2p_1a - a + 2m\Delta a + 2[p_1(1 - p_1) - m\Delta(2p_1 - 1 + m\Delta)]d \\
 &= 2p_1a - a + 2m\Delta a + 2[p_1 - p_1^2 - m\Delta(2p_1 - 1 + m\Delta)]d \\
 &= 2p_1a - a + 2m\Delta a + 2[p_1 - p_1^2 - 2p_1m\Delta - m\Delta + m^2\Delta^2]d \\
 &= 2p_1a - a + 2m\Delta a + 2dp_1 - 2dp_1^2 - 4dp_1m\Delta - 2dm\Delta + 2dm^2\Delta^2
 \end{aligned} \tag{1}$$

$$\begin{aligned}
 M &= (2p_1 - 1)a + 2p_1(1 - p_1)d \\
 &= 2p_1a - a + 2p_1(1 - p_1)d \\
 &= 2p_1a - a + 2dp_1 - 2dp_1^2
 \end{aligned} \tag{2}$$

$$\begin{aligned}
 2m\Delta[a - (2p_1 - 1 + m\Delta)d] &= 2p_1a - a + 2m\Delta a + 2dp_1 - 2dp_1^2 - 4dp_1m\Delta \\
 &\quad - 2dm\Delta + 2dm^2\Delta^2 - [2p_1a - a + 2dp_1 - 2dp_1^2] \\
 2m\Delta[a - (2p_1 - 1 + m\Delta)d] &= 2p_1a - a + 2m\Delta a + 2dp_1 - 2dp_1^2 - 4dp_1m\Delta \\
 &\quad - 2dm\Delta + 2dm^2\Delta^2 - 2p_1a + a - 2dp_1 + 2dp_1^2 \\
 2m\Delta[a - (2p_1 - 1 + m\Delta)d] &= \cancel{2p_1a} - a + 2m\Delta a + 2dp_1 - 2dp_1^2 - 4dp_1m\Delta \\
 &\quad - 2dm\Delta + 2dm^2\Delta^2 - \cancel{2p_1a} + a - 2dp_1 + 2dp_1^2 \\
 2m\Delta[a - (2p_1 - 1 + m\Delta)d] &= \cancel{2p_1a} + 2m\Delta a + 2dp_1 - 2dp_1^2 - 4dp_1m\Delta \\
 &\quad - 2dm\Delta + 2dm^2\Delta^2 - \cancel{2p_1a} - 2dp_1 + 2dp_1^2 \\
 2m\Delta[a - (2p_1 - 1 + m\Delta)d] &= 2m\Delta a + \cancel{2dp_1} - 2dp_1^2 - 4dp_1m\Delta \\
 &\quad - 2dm\Delta + 2dm^2\Delta^2 - \cancel{2dp_1} + 2dp_1^2 \\
 2m\Delta[a - (2p_1 - 1 + m\Delta)d] &= 2m\Delta a - \cancel{2dp_1^2} - 4dp_1m\Delta - 2dm\Delta + 2dm^2\Delta^2 + \cancel{2dp_1^2} \\
 2m\Delta[a - (2p_1 - 1 + m\Delta)d] &= 2m\Delta a - 4dp_1m\Delta - 2dm\Delta + 2dm^2\Delta^2 \\
 2m\Delta[a - (2p_1 - 1 + m\Delta)d] &= 2m\Delta[a - 2dp_1 - d + dm\Delta] \\
 2m\Delta[a - (2p_1 - 1 + m\Delta)d] &= 2m\Delta[a - (2p_1 - 1 + m\Delta)d]
 \end{aligned} \tag{3}$$

```

> p1 <- 0.3
> p2 <- 0.4
> m <- 0.12
> a = -2
> d = 1.5
> delta <- (p2 - p1)
> 2 * m * delta * (a - (2 * p1 - 1 + (m * delta)) * d)
[1] -0.034032

```

- d) Use migration proportions from 0.05 to 0.45 in increments of 0.05 and allele frequency differences between populations (Δ) from 0 to 0.3 in increments of 0.05, develop a matrix of allele frequencies in the receiving population and a matrix of changes in mean of the receiving population after return to random mating. Make both matrices with respect to the initial frequency of the *A* allele in the receiving population, that is, do not make them cumulative. Briefly interpret the results presented in each.

```

> alleleF <- sapply(seq(0.05, 0.45, 0.05), function(mProportion) {
+   sapply(seq(0, 0.3, 0.05), function(alleleDiff) {
+     round(newAlleleFrequencies(
+       p1 = 0.3,

```

```

+       p2 = (0.3 + alleleDiff),
+       m = mProportion
+     )[1], 2)
+   })
+ })
> dimnames(alleleF) <- list(
+   Delta = seq(0, 0.3, 0.05),
+   migrationProportion = seq(0.05, 0.45, 0.05)
+ )
> alleleF
      migrationProportion
Delta 0.05 0.1 0.15 0.2 0.25 0.3 0.35 0.4 0.45
0     0.30 0.30 0.30 0.30 0.30 0.30 0.30 0.30 0.30
0.05 0.30 0.30 0.31 0.31 0.31 0.32 0.32 0.32 0.32
0.1   0.30 0.31 0.32 0.32 0.32 0.33 0.34 0.34 0.34
0.15 0.31 0.32 0.32 0.33 0.34 0.34 0.35 0.36 0.37
0.2   0.31 0.32 0.33 0.34 0.35 0.36 0.37 0.38 0.39
0.25 0.31 0.32 0.34 0.35 0.36 0.38 0.39 0.40 0.41
0.3   0.31 0.33 0.34 0.36 0.38 0.39 0.40 0.42 0.44
> meanChanges <- sapply(seq(0.05, 0.45, 0.05), function(mProportion) {
+   sapply(seq(0, 0.3, 0.05), function(alleleDiff) {
+     originalMean <- populationMean(p = 0.3, a = -2, d = 1.5)
+     newAlleleF <- newAlleleFrequencies(p1 = 0.3,
+                                       p2 = (0.3 + alleleDiff),
+                                       m = mProportion)[1]
+     newMean <- populationMean(p = newAlleleF, a = -2, d = 1.5)
+     round(meansChange(Mnew = newMean, M = originalMean), 2)
+   })
+ })
> dimnames(meanChanges) <- list(
+   Delta = seq(0, 0.3, 0.05),
+   migrationProportion = seq(0.05, 0.45, 0.05)
+ )
> meanChanges
      migrationProportion
Delta 0.05 0.1 0.15 0.2 0.25 0.3 0.35 0.4 0.45
0     0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00
0.05 -0.01 -0.01 -0.02 -0.03 -0.04 -0.04 -0.05 -0.06 -0.06
0.1   -0.01 -0.03 -0.04 -0.06 -0.07 -0.09 -0.10 -0.12 -0.13
0.15  -0.02 -0.04 -0.06 -0.09 -0.11 -0.13 -0.16 -0.18 -0.20
0.2   -0.03 -0.06 -0.09 -0.12 -0.15 -0.18 -0.21 -0.24 -0.28
0.25  -0.04 -0.07 -0.11 -0.15 -0.19 -0.23 -0.27 -0.31 -0.35
0.3   -0.04 -0.09 -0.13 -0.18 -0.23 -0.28 -0.33 -0.38 -0.43

```

Interpretation: The first matrix shows how the frequency of the allele A $f(A)$ change gradually in function of the changes of the Δ parameter and the m proportion. As we can see, the $f(A)$ is more affected in two scenarios, when the Δ is high and the proportion of migrants is also high. The same effect is shown in the second matrix, where the differences in the population mean are shown after a migration event.