Problem Set #5

Solutions

1) 12.5% of individuals are homozygous in a population at equilibrium between drift and mutation in the infinite alleles model. If the effective population size is 2,000, what value of μ, the mutation rate to neutral alleles, does this imply? Give one reason why this estimate may be unreliable.

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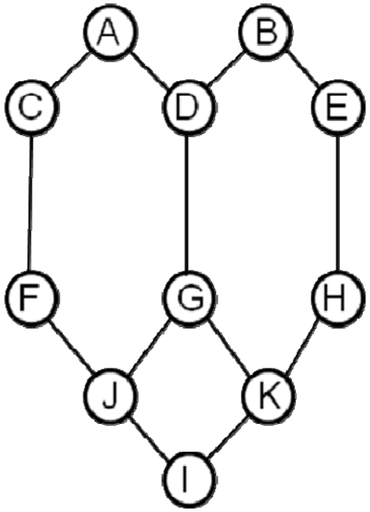
$G = 1/(4N\mu+1)$
$0.125 = 1/(8{,}000\mu + 1)$
$8{,}000\mu + 1 = 8$
$8{,}000\mu = 7$ so $\mu = 8.75\text{x}10^{-4}$

This estimate may be unreliable because:
-effective population size is difficult to estimate and the value used may not be correct
-it assumes mutation-selection balance which takes a long time to reach (mutation rates are low)
-it assumes no selection (i.e. segregating alleles are neutral)
-it assumes no migration
-it assumes every mutation creates a new allele (infinite-alleles model)

2a) Calculate the inbreeding coefficient of individual I, assuming none of the common ancestors are themselves inbred.

b) By what percentage is heterozygosity reduced in individual I compared to that expected in the absence of inbreeding?



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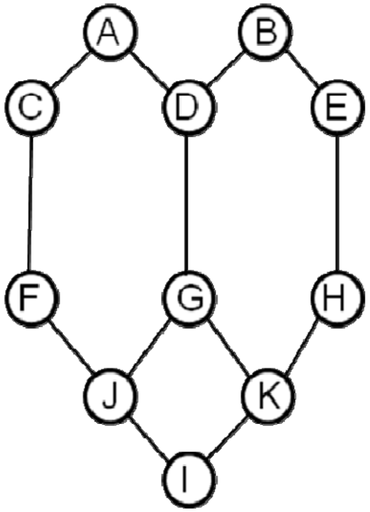

a) Path: JFC**A**DGK = $\frac{1}{2}^7$ = 0.007813
Path: JGD**B**EHK = $\frac{1}{2}^7$ = 0.007813
Path: J**G**K = = $\frac{1}{2}^3$ = 0.125

Total : f = 0.140625 = 0.141

b) By 14.1% .

3. Consider a single locus with two alleles, A1 and A2, at frequencies 0.5 each, in a population in which the inbreeding is occurring. What value of the inbreeding coefficient, *f*, would result in genotypes frequencies of A1A1 = A1A2 = A2A2 = 1/3?

3. Consider a single locus with two alleles, A1 and A2, at frequencies 0.5 each, in a population in which the inbreeding is occurring. What value of the inbreeding coefficient, *f*, would result in genotypes frequencies of A1A1 = A1A2 = A2A2 = 1/3?

$2pq(1 - f) = 1/3$
$2(0.5)(0.5)(1 - f) = 1/3$
$0.5(1 - f) = 1/3$
$1 - f = 2/3$
$f = 1 – 2/3$
$f = 1/3$

Or

$p^2 + pqf = 1/3$ OR $q^2 + pqf = 1/3$
$0.25 + 0.25f = 1/3$
$0.25(1 + f) = 1/3$
$1 + f = 4/3$
$f = 1/3$

4. Using the same approach we employed for determining the values of *h* that would cause inbreeding depression under the dominance hypothesis, calculate the values of *k* in the fitness set below that would cause inbreeding depression under the overdominance hypothesis. Hint: like for the dominance hypothesis, you want to express $\text{w\_bar}_{\text{inbreeding}}$ as $\text{w\_bar}_{\text{random mating}}$ + other stuff.

Genotype	AA	Aa	aa
Fitness	1	$1+k$	1

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Genotype	AA	Aa	aa
Fitness	1	1+*k*	1

In general: $\text{w\_bar}_{\text{random mating}} = p^2 + 2pq(1 + k) + q^2$

With inbreeding: $\text{w\_bar}_{\text{inbreeding}} = p^2 + pqf + 2pq(1 + k)(1-f) + q^2 + pqf$

Simplifying: $\text{w\_bar}_{\text{inbreeding}} = p^2 + pqf + 2pq(1+k) - 2pqf(1 + k) + q^2 + pqf$

$\text{w\_bar}_{\text{inbreeding}} = \text{w\_bar}_{\text{random mating}} + pqf - 2pqf(1 + k) + pqf$

$\text{w\_bar}_{\text{inbreeding}} = \text{w\_bar}_{\text{random mating}} + pqf(1 - 2(1 + k) + 1)$

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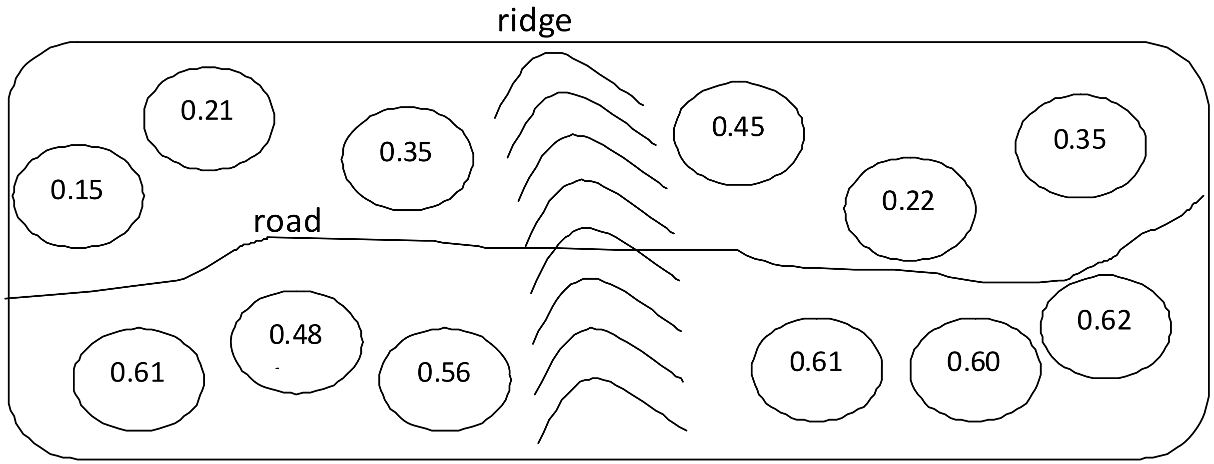
pqf will always be positive, so for $\text{w\_bar}_{\text{inbreeding}}$ to be < $\text{w\_bar}_{\text{random mating}}$ (which means inbreeding depression occurs), $1 - 2(1 + k) + 1 < 0$, or simplifying: $-2k < 0$
so ***k* > 0**

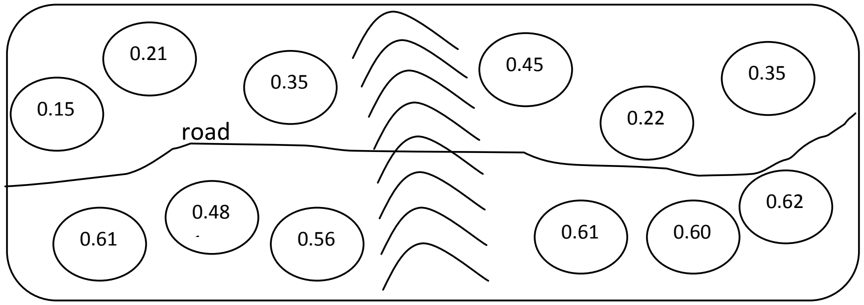
(note that when you divide by -2, the inequality changes direction).

5. A meadow in the Alps in southern Germany is home to the red-listed snail *Helix pomatia* (known as escargot in French cooking). In an attempt to understand the role of landscape features in structuring this population, conservation biologists estimated allele frequency in 12 subpopulations as diagrammed below:



A road passes through the meadow in one direction and a ridge bisects the meadow perpendicular to this. Assuming random mating within each subpopulation, does this population seem to be structured more strongly by the road or the ridge? Hint: to answer this, you will need to calculate FSR, FRT, and FST for two scenarios in which the subpopulations are groups into two regions on either side of the road or on either side of the ridge.

Road:



					Expected		**Expected**
Region		**Observed p**	H	p_{region}	H_{region}	p_{total}	H_{total}
Above road	1	0.21	0.3318	0.28833	0.41039	0.434167	0.491332
	2	0.15	0.255				
	3	0.35	0.455				
	4	0.45	0.495				
	5	0.22	0.3432				
	6	0.35	0.455				
Below road	1	0.61	0.4758	0.58	0.4872		
	2	0.48	0.4992				
	3	0.56	0.4928				
	4	0.61	0.4758				
	5	0.62	0.4712				
	6	0.60	0.48				
			H_S=0.4358		H_R=0.448795		H_T=0.491332

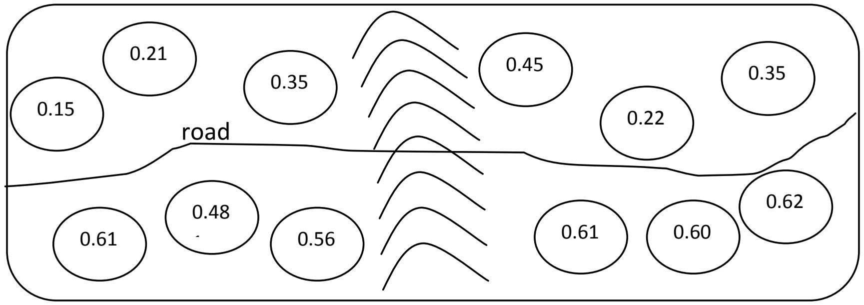
$F_{SR} = (H_R - H_S)/H_R = 0.0289$

$F_{RT} = (H_T - H_R)/H_T = 0.0866$

$F_{ST} = (H_T - H_S)/H_T = 0.1130$

The road therefore accounts for a substantial portion of the total variance in allele frequency among subpopulations

Ridge:



					Expected		**Expected**
Region		**Observed p**	H	p_{region}	H_{region}	p_{total}	H_{total}
Left of ridge	1	0.21	0.3318	0.3933	0.4772	0.434167	0.491332
	2	0.15	0.255				
	3	0.35	0.455				
	4	0.61	0.4758				
	5	0.48	0.4992				
	6	0.56	0.4928				
Right of ridge	1	0.45	0.495	0.475	0.49875		
	2	0.22	0.3432				
	3	0.35	0.455				
	4	0.61	0.4758				
	5	0.62	0.4712				
	6	0.60	0.48				
			H_S=0.4358		H_R=0.4880		H_T=0.491332

$F_{SR} = (H_R - H_S)/H_R = 0.1070$

$F_{RT} = (H_T - H_R)/H_T = 0.0068$

$F_{ST} = (H_T - H_S)/H_T = 0.1130$

The ridge accounts for only a small portion of the total variance in allele frequency among subpopulations.

6. Suppose a large population is subdivided into smaller subpopulations within which mating is random. Genetic drift takes place until the probability of identity by descent in the subpopulations is 1/16. Now suppose that a first cousin mating takes place in one of the subpopulations so that the offspring have an inbreeding coefficient, relative to the subpopulation, of F_{IS} = 1/16. What is the total probability of identity by descent in these inbred offspring, F_{IT}?

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$(1 - F_{IS})\ (1 - F_{ST}) \ = \ (1 - F_{IT})$

$(1 - 1/16)(1 - 1/16) = 1 - F_{IT}$

$15/16*15/16 = 1 - F_{IT}$

$F_{IT} = 1 - 15/16*15/16 \quad = 0.121$