**NAME:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Student #\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**NAME:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Student #\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**NAME:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Student #\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**Problem Set # 4 – Due Fri., Nov. 1**

This is the fouth of six problem sets that will count towards your final grade. The problem set is due **at the start of lecture** on Friday, Nov 1. You may work in groups of up to three people (and are encouraged to do so). Please hand in one assignment per group with up to three names listed. Late assignments will be penalized 20% per day or part thereof. **Staple multiple pages together** –no paper clips or folded corners as sheets inevitably get lost. **Show your work.** Incorrect answers with some correct work will receive part marks; correct answers with no work might not receive full marks.

1. Assume a large population is subdivided into smaller subpopulations within which mating is random. Drift occurs over a number of generations, yielding an *FST* of 1/16. Now suppose that a first-cousin mating takes place in one of the subpopulations. a) What is the probability of identity by descent (*f* = *FIS*) in the offspring of this mating caused by the inbreeding alone (i.e. assume the ancestors are not themselves inbred)? b) What is the total probability of IBD (*FIT*) in this offspring including that arising from inbreeding and drift?

2. A population geneticist is interested in whether populations of garter snakes are genetically structured by a road that passes through their habitat. To address this, she estimates allele frequencies for a biallelic locus from each of 6 subpopulations (3 on either side of the road), yielding the following results:

West of road: p = 0.15, 0.4, and 0.05

East of road: p = 0.02, 0.1, and 0.6

a) Calculate *FSR*, *FRT*, and *FST*. Be careful of rounding errors propagating; carry through several significant figures in intermediate calculations.

b) Summarize what your results imply about population structuring including the effect, if any, of the road.

3. Selander and Yang (1969) estimated FST for subpopulations of wild mice trapped from four different chicken coops in California. Average FST across several loci was 0.12.

a) Assuming no migration between coops, how long would it take genetic drift to produce this level of divergence if the subpopulations are of size N=100 individuals?

b) Assuming the observed FST is an equilibrium between divergence due to genetic drift and homogenizing effects of gene flow (i.e. migration), estimate the absolute number of migrants per generation that would produce this level of population structure under the island model.

4. a) What is the effective size of a herd of dairy cows that includes 96 cows (i.e. females) and 4 bulls (i.e. males)?

b) In some human populations, the widespread use of birth control together with a desire to have only a small number (often two) children, can increase the effective population size above the census size. It does this by reducing the variance among families in the number of offspring (*k*) below the Poisson expectation of the mean number of offspring (which would be 2 in a population of constant size). Using data from a Japanese population in the 1920’s, Imaizumi et al. (1970) estimated var(*k*) to be 1.09. What is the ratio of the effective relative to the census size in this population? Hint: you need to rearrange this equation to solve for the requested ratio: .

5. a) Calculate *F*IS, *F*ST, and *F*IT for two subpopulations with the following observed genotype counts:

|  |  |  |
| --- | --- | --- |
| Genotype | Subpopulation 1 | Subpopulation 2 |
| *AA* | 410 | 1240 |
| *Aa* | 380 | 220 |
| *aa* | 210 | 40 |

b) Briefly interpret your fixation indices above in terms of what they imply about the causes of any reduced heterozygosity.

6. Consider a new mutation present in a single copy in a random mating population of constant size *N* = 50.

a) What is the probably that this allele drifts to a frequency of 0.03 in the next generation?

b) What is the probability that the allele eventually fixes by drift (assuming it is currently at a frequency of 0.03)?

c) For cases in which the allele is eventually lost by drift, how long will this take on average (assuming the starting frequency is *p* = 0.03)?

d) For cases in which the mutation eventually fixes by drift, how long will this take on average (again assuming the starting frequency is *p* = 0.03)?

e) In once sentence, explain why the times above differ the way they do.