1. (13 points) Do Exercise (not Problem) 4 in Chapter 1:
   Suppose there are two populations that have genotype frequencies
   
   \[
   \begin{array}{c|ccc}
   & AA & Aa & aa \\
   \hline
   \text{Pop. 1} & 0.64 & 0.32 & 0.04 \\
   \text{Pop. 2} & 0.09 & 0.42 & 0.49 \\
   \end{array}
   \]

   If a researcher draws a sample, thinking it is coming from a single population, but it
   is actually composed of individuals two-thirds of whom came from population 1, and
   one-third from population 2,

   (i) If these individuals are simply collected together, but have no time to interbreed,
       what will the genotype frequencies in the sample expected to be?

   (ii) What will the gene frequencies be expected to be in that sample?

   (iii) If we mistakenly assume that the sample is from a random-mating population, and
       use the sample gene frequency, what proportion of heterozygotes will we expect to
       see?

2. (12 points) Suppose that there is a microsatellite locus \( \text{[It actually doesn’t matter whether you understand what that is, except to say that alleles with different copy numbers can be distinguished]} \). There are four alleles, one called 18, one called 19, one called 20, and
   one a deletion. If an individual has (say) both alleles 19 and 20, we can see that there
   is a 19/20 heterozygote. But if it has (say) allele 19 and the deletion, we cannot tell
   that from a homozygote for allele 19. We can of course tell the homozygote for the
   deletion from the others. If the gene frequencies for these four alleles are 0.20, 0.30,
   0.20, and 0.30, what will be the different classes that we will see, and what will be their
   genotype frequencies, if the population follows the assumptions of the Hardy-Weinberg
   calculation?