Exercises for 12/5

Write out your answers and make two copies, one to keep and one to turn in at the beginning of class.

1. At a Cold Spring Harbor symposium on organelle genes, I heard an argument over the identification of amino acids required for targetting a mitochondrial protein. Two different labs were studying the problem; while they agreed on the identity of some essential amino acids in the leader, each group had identified one or two additional amino acids as essential while the other group said they were not essential. Someone in the audience pointed out that one group used human cells while the other group used rat cells. Was one group necessarily wrong about the essential amino acids?

2. Jane and Joe are graduate students working in different laboratories but by chance are working on the same problem: sequencing the *blue* gene that controls the synthesis of pigment in the fur of the Australian blue monkey. Each of them gets tissue samples from monkeys in zoos, makes a clone bank, and isolates and sequences the gene. Each presents a poster at the annual Midwest Blue Gene meeting. As Jane looks at Joe's poster, she realizes that their sequences are not identical. In the 3 kb gene there are 2 base pair differences and one indel (one sequence has an extra base due to an insertion, or to a deletion in the other one). Jane and Joe both sequenced each part of their genes at least once on each strand. Did Jane screw up the sequencing, or Joe, or both, or neither?

3. In what sense is it correct, and in what sense is it incorrect, to say that *the* genome of Drosophila (or yeast, or Caenorhabditis, or ...) has been sequenced? (We are ignoring the fact that no eukaryotic genome sequence is 100% complete.)

4. Consider the imaginary electrophoresis data in which the frequencies of the AdhF and S alleles are 0.4 and 0.6, respectively. What would be the frequencies of the three different genotypes, F/F, F/S, and S/S, in a population that is:
(1) random mating
(2) inbred

5. Imagine that the mutation rate in humans suddenly went to zero, so no new mutations occurred.
(1) What would happen to allelic diversity in the human population?
(2) What would happen to genotypic diversity in the human population?