BIOLOGY 4DD3 Problem Set 1

1. Extremophiles are organisms that live in conditions that are extreme in some respect relative to the conditions in which most organisms that inhabit Earth are found. For instance, the thermophilic bacterium *Thermus aquaticus* can live in hot springs (the DNA polymerase taq that is used in Polymerase Chain Reactions is extracted from this organism). Please state whether the genome for *Thermus aquaticus* should be A-T rich, G-C rich, or comprise equivalent proportions for each pair.

2. Please list all 'standard nucleotide' pairings for RNA, enumerating the hydrogen bonds that are involved in each.

3. If the sense strand for a particular DNA molecule contained a short segment comprising the nitrogenous bases (in order) ACGTACGTACGTACGT, then please deduce the nitrogenous bases (in order) comprising the corresponding segment in the pre-mRNA that would be produced.

4. Please read the paragraph that begins with the words "The universal genetic code …" on page 24 in the textbook and identify a technical error therein.

5. Please propose an explanation for how a correlation could exist between Okazaki fragment size and replication rate.

6. If any nucleotide in a sequence were to change into each among its three counterparts without bias, then please predict the proportion among all nucleotide changes in that sequence that would be (a) transitions and (b) transversions.

These proportions may be utilised as a null hypothesis for studying molecular evolution. Please consider the graph that was presented during lecture session 5 (in the frame that contains the title "NEUTRAL THEORY"), which concerns sequences for a gene that was collected from influenza viruses from 1968 until 1988 and (c) state whether nucleotide changes transpired without bias. In so doing, please assume that the gene initially was argenine rich, specifically with the codon AGG, and nucleotide changes occurred only at the third position.

7. Please use equation 2.2 in the textbook to verify equations 2.7 and 2.9, which represent dominance and under- & overdominance scenarios.

8. Please (a) state whether and (b) explain why you agree or disagree with the statement that is presented in paragraph 1 on page 41 in the textbook: "When a population consists of individuals that do not differ from one another in … traits [related to reproductive success], it is not subject to natural selection."

9. Please (a) state whether and (b) explain why you agree or disagree with the statement: "A change in allele frequencies from generation to generation indicates that selection is operating."

10. Codominant selection regimes may be represented by the algebraic scenario

A_1A_1	A_1A_2	A_2A_2
1	1 + s	1 + 2s

Suppose that s = 0.01.
(a) Please describe relative fitnesses for the three genotypes.
(b) Please explain why selection is inefficient (*i.e.*, allele frequencies change slowly), when the frequency for allele A2 is low (hint: you might compare genotype frequencies when the frequency for allele A2 is 0.01 and 0.5).

11. Consider a population comprising 5 individuals containing the heterozygous genotype A_1A_2, as described on pages 50-51 in the textbook. The textbook authors claim that the probability that one allele is lost in the first generation is 0.1%. Please show how to use equation 2.11 in the textbook to calculate the 0.1% for a population comprising 5 individuals containing the heterozygous genotype A_1A_2.

12. Please show that the values for heterozygosity h and average heterozygosity H for the sequences in Figure 2.8a and 2.8b are the same. Please use equation 2.30 to reproduce the values for nucleotide diversity $\prod$ for the two sequences that are reported on page 59 in the textbook.