The test is closed book. You may use a calculator, but you can also leave computations in fractional form, such as $2 \times \frac{3.67}{19}$. You can work in the space provided and also on the back of the same sheet (in which case make it very clear which problem is being worked on). The questions total 100 points. Please write your name on each page.

1. (25 points) A population which has a locus with two alleles ($A$ and $a$) is surveyed. 40 individuals are examined. 10 of these turn out to be $AA$, 30 turn out to be $Aa$, and none are $aa$. Show your work as you answer these questions:

   (i) What is the gene frequency of the $A$ allele in this sample?

   \[
   p_A = \frac{2 \times 10 + 30}{80} = \frac{50}{80} = 0.625
   \]

   (ii) If the population has the same gene frequency, and an offspring generation is produced by random mating, what will be the frequencies of $AA$, $Aa$, and $aa$ genotypes among the newborn offspring?

   \[
   P_{AA} = 0.625^2 = 0.390625
   \]

   \[
   P_{Aa} = 2 \times 0.625 \times 0.375 = 0.46875
   \]

   \[
   P_{aa} = 0.375^2 = 0.140625
   \]

   (iii) Suppose that we know that a new weather pattern has occurred. Because of it, after that newborn stage, but before adulthood, $1/3$ of the $Aa$ individuals die. What will be the expected gene frequency of the $A$ allele be among the surviving adults?

   \[
   p_A = \frac{0.390625 + \frac{1}{2} \times \frac{2}{3} \times 0.46875}{0.390625 + \frac{2}{3} \times 0.46875 + 0.140625} = 0.648148
   \]

   (iv) If the conditions causing that natural selection continue in each subsequent generation, what do we expect to happen to the composition of the population? Why?

   *This is a case of underdominance. The equilibrium gene frequency is 1/2, and the initial gene frequency is greater than 1/2. So we expect it to approach 1, so that the population will ultimately be all $AA$.\*
2. (15 points) Suppose that we have a quantitative character which is a component of fitness, such as litter size. We watch it for a very long time.

(a) If there is genetic variation in this character present at first, will we expect to see changes in the character? Why or why not?

Yes. Unless it also has an effect on some other component of fitness (such as viability). Genetic drift will also cause change of the character in random directions.

(b) In the long run, what will happen to the character? Why?

After a while, genetic variation will be exhausted as loci are fixed by selection and drift. Mutation may introduce new variation. Much of that may be deleterious.

(c) Will there be expected to be genetic variation present in the character at the end of that time? Why or why not?

Yes, but only because of mutation, unless some of the loci involved in the character were overdominant.
3. (30 points) Suppose that females of the Crested Twit (*Parus imaginarius*) arrive at the nesting grounds in pairs, which on average are half-sibs (they had one parent in common). One of them finds a nest site, choosing a good location. The second one decides either to nest in a less favorable site adjacent to that nest, or to nest elsewhere. Suppose that if the two nest near each other, this benefits the viability of the young in the first nest. The average number of offspring raised is, in these two cases:

<table>
<thead>
<tr>
<th>Case</th>
<th>Nest together</th>
<th>Nest apart</th>
</tr>
</thead>
<tbody>
<tr>
<td>First female</td>
<td>8</td>
<td>5</td>
</tr>
<tr>
<td>Second female</td>
<td>3</td>
<td>4</td>
</tr>
</tbody>
</table>

In light of kin selection theory, suppose that there were a behavioral locus allele that had the effect that when present in the second bird, it would make it more likely to choose to nest nearby. Would it increase in the population? Explain why or why not (show any calculations).

Compared to nesting apart, nesting together causes a loss of 1 offspring to the second female, with a gain of 3 offspring to the first female. As they are half sibs, their coefficient of relatedness is 1/4. Using Hamilton’s formula, we have $c = 1$, $r = 1/4$, and $b = 3$. Thus it is not true that $c < r \times b$. So a behavioral locus allele predisposing toward mating together would not be increasing the numbers of copies of it in the population, and would not increase due to kin selection.
4. (30 points) Soon after the rediscovery of Mendel’s work, Mendelian geneticists became aware of mutation. They knew of it mostly in loci where the mutational effects were large visible changes. They tended to view mutation as the main mechanism of evolution, instead of natural selection. They felt that natural selection would be unimportant. They also tended to argue that therefore the resulting changes would be “saltations” (sudden jumps in the phenotype of the species).

(i) Once population geneticists examined this view, what arguments would they be likely to make against this mutationist view ...

... as an explanation for adaptations?

Mutations occur randomly, with effects that are in a random direction with respect to adaptedness. There should be no tendency for a series of random mutations to result in a net adaptation – in fact, most probably the result would be maladaptive. Thus mutationists do not have an explanation for adaptation.

... as a prediction of a saltational pattern of change?

Mutations are instantaneous, discrete changes. But at the population level, the frequency of the newer allele changes more gradually. So even if mutation is the major evolutionary force, does not predict saltations of populations. Mutations also need not be of large effect, but could also be of small effect.

(ii) Discuss ways in which this mutationist view was similar, or different to the punctuated equilibrium theory of 70 years later.

Similar: Saltational (sudden) change.
Little role for within-species natural selection.

Different: Saltation due to drift (under PE) rather than mutation.
Natural selection does occur at the between-species level (PE). Adaptation therefore is expected, due to this (under PE).