Some formulas you might find helpful:

\[ \text{Freq}(AA) = p^2(1 - F) + pF \]
\[ \text{Freq}(Aa) = 2pq(1 - F) \]
\[ \text{Freq}(aa) = q^2(1 - F) + qF \]

\[ D = p_{11}p_{22} - p_{11}p_{22} \]
\[ I = \frac{\sum x_i y_i}{(\sum x_i^2)(\sum y_i^2)^{1/2}} \]

\[ H_t = H_0(1 - 1/2N) + q \mu \]
\[ F_t = 1 - (1 - 1/2N)^{1/4} \]
\[ F_t = \frac{1}{4N_e m + 1} \]

1. (40 pts) How much genetic variation is there within human populations, and why is it present? (Your answer must be \leq 500 words)

2. (25 pts) A particularly bloody murder has occurred and a suspect identified. A bloody glove is found at the home of a suspect, and DNA analysis reveals that the genotype of the blood is sp1 25/30 – the same as that of the victim.

   The DNA analysis works by identifying the alleles present (named 20, 25, 30, etc) at each of several potential loci (named sp1–sp4). Assume linkage equilibrium.

   a) Using data in the table below, calculate the probability that the blood on this glove came from a randomly-selected person.

   b) Suppose now that further analysis revealed that the blood on the glove was also sp2 20/35, sp3 35/40, sp4 40/40. What is the probability now?

<table>
<thead>
<tr>
<th>Allele</th>
<th>sp1</th>
<th>sp2</th>
<th>sp3</th>
<th>sp4</th>
</tr>
</thead>
<tbody>
<tr>
<td>20</td>
<td>0.10</td>
<td>0.10</td>
<td>0.30</td>
<td>0.40</td>
</tr>
<tr>
<td>25</td>
<td>0.10</td>
<td>0.40</td>
<td>0.40</td>
<td>0.10</td>
</tr>
<tr>
<td>30</td>
<td>0.10</td>
<td>0.40</td>
<td>0.25</td>
<td>0.30</td>
</tr>
<tr>
<td>35</td>
<td>0.60</td>
<td>0.05</td>
<td>0.10</td>
<td>0.10</td>
</tr>
<tr>
<td>40</td>
<td>0.10</td>
<td>0.05</td>
<td>0.05</td>
<td>0.10</td>
</tr>
</tbody>
</table>
25% of the Control (not HLA-Bw53 positive) human population shown develops severe malaria. Severe malaria is lethal 20% of the time. Also assume that there is no difference for the risk of developing severe malaria between heterozygotes and homozygotes for the HLA-Bw53 allele, and that no other components of fitness are involved for selection at this locus.

a) Calculate the relative fitnesses and selection coefficients for this locus.

b) What is the expected equilibrium frequency of the HLA-Bw53 allele in West Africa?

c) What is the expected change in allele frequency, over 1 generation, for a population in Gambians where the frequency of individuals who test positive for the HLA-Bw53 antigen is 25%?
3. Shown below is the pedigree of some chimpanzees in the LA county zoo. Assume that Anabel and Bruce are unrelated and not inbred in the pedigree below:
   a) What are the inbreeding coefficients of Cara, Dante and Ernst?
   b) Assume there is a recessive allele that causes a genetic disease; the frequency of afflicted individuals is 1/900 (the same as cystic fibrosis). Then what is the probability that Cara would be affected by this disease? Dante? Ernst?

4. [Note, this can be a hard problem, depending on the detail you provide. So I suggest that you work on it last.]

   Suppose that each allele at a locus in humans confers resistance to one strain, and only one strain, of AIDS. Initially the AIDS virus is all one strain and the human population is polymorphic – 95% susceptible and 5% resistance [About like the proportions of Windows and Macintosh PCs]. Both the humans and the AIDS virus are capable of mutating.
   a) Describe selection at this locus in humans.
   b) What is the equilibrium level of polymorphism – i.e. How many alleles and at what frequency?