1. Consider the following pedigree:

a). What is the pedigree inbreeding coefficient $F$ of the female shown by the solid circle relative to this pedigree?
SIMPLIFY THE PEDIGREE INTO TWO MUTUALLY EXCLUSIVE LOOPS:

\[ F \] IS DEFINED IN TERMS OF PROBABILITY OF IDENTITY BY DESCENT FOR A RANDOMLY CHOSEN AUTOSOMAL LOCUS. THERE ARE 7 MEIOTIC EVENTS IN EACH LOOP CONNECTING THE SOLID CIRCLE FEMALE TO HER COMMON ANCESTORS, AND SINCE WE DON’T CARE WHICH ALLELE SHE GETS, EACH LOOP CONTRIBUTES \( 2^{(\frac{1}{2})^7} = (\frac{1}{2})^6 = 0.015625 \). SINCE THERE ARE TWO LOOPS WITH THE SAME NUMBER OF MEIOTIC EVENTS, \( F = 0.03125 \) (4 POINTS)

b). What is the probability of identity by descent in the female shown by the solid circle of a randomly chosen X-linked locus relative to this pedigree (recall the laws of transmission for an X-linked locus)?

SINCE THE COMMON ANCESTRAL MALE DID NOT PASS ON HIS X CHROMOSOME TO HIS SON, THE PROBABILITY OF I BY D IN THE RIGHT-HAND LOOP IS 0. IN THE COMMON FEMALE ANCESTRAL LOOP, EVERY TRANSMISSION FROM FATHER TO DAUGHTER HAS A PROB. OF 1, WHEREAS TRANSMISSIONS FROM A FEMALE HAVE A PROB. OF \( \frac{1}{2} \). THERE ARE 5 TRANSMISSIONS IN THIS LOOP WITH \( p = \frac{1}{2} \) AND TWO WITH \( p = 1 \), AND SINCE WE DON’T CARE WHICH ALLELE SHE GETS, THE MATERNAL LOOP CONTRIBUTES \( 2^{(\frac{1}{2})^5} = (\frac{1}{2})^4 = 0.0625 \) (4 POINTS)

2. Given the following allele frequencies for an autosomal locus with two alleles (A and a, with \( p \) being the frequency of A) and inbreeding coefficients (measured as a deviation from Hardy–Weinberg proportions in all problems in this set), calculate the genotype frequencies.

<table>
<thead>
<tr>
<th></th>
<th>AA</th>
<th>Aa</th>
<th>aa</th>
</tr>
</thead>
<tbody>
<tr>
<td>a.</td>
<td>0.784</td>
<td>0.032</td>
<td>0.184</td>
</tr>
<tr>
<td>b.</td>
<td>0.469</td>
<td>0.462</td>
<td>0.069</td>
</tr>
<tr>
<td>c.</td>
<td>0.574</td>
<td>0.252</td>
<td>0.174</td>
</tr>
<tr>
<td>d.</td>
<td>0.040</td>
<td>0.720</td>
<td>0.240</td>
</tr>
</tbody>
</table>

2 POINTS

3. Estimate the value of \( f \) for each population given the following genotype numbers.

Genotypes
4. Suppose two populations are polymorphic at an autosomal locus with two alleles, $A$ and $a$. Suppose population 1 has $p=0.25$ (the frequency of $A$), and population 2 has $p=0.8$. Both populations avoid inbreeding with $f=0.2$.

a. Suppose you sample 1000 people from population 1 and 1000 people from population 2. What are the expected genotype numbers within each population given $f$, and what are expected sums for genotype numbers in your combined sample?

<table>
<thead>
<tr>
<th></th>
<th>AA</th>
<th>Aa</th>
<th>aa</th>
<th>total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Exp freq 1</td>
<td>0.025</td>
<td>0.45</td>
<td>0.525</td>
<td>1</td>
</tr>
<tr>
<td>Exp num 1</td>
<td>25</td>
<td>450</td>
<td>525</td>
<td>1000</td>
</tr>
<tr>
<td>Exp freq 2</td>
<td>0.608</td>
<td>0.384</td>
<td>0.008</td>
<td>1</td>
</tr>
<tr>
<td>Exp num 2</td>
<td>608</td>
<td>384</td>
<td>8</td>
<td>1000</td>
</tr>
<tr>
<td>Exp num sample</td>
<td>633</td>
<td>834</td>
<td>533</td>
<td>2000</td>
</tr>
</tbody>
</table>

3 POINTS

b. What is the $f$ in your combined expected sample? $F = 0.164$ 2 POINTS

c. Suppose that you did not know that the combined sample had been drawn from two distinct populations but rather thought that the combined sample was from a single deme with a single system of mating for this locus. What would you conclude about the system of mating of the sample that you mistakenly regard as a deme for this locus?

The positive $f$ from part b implies either inbreeding or assortative mating. (2 POINTS)

5. All mating pairs in a population are scored at two unlinked, autosomal loci, each with two alleles, and each associated with distinct phenotypes for every genotype, with the following results for each locus:

<table>
<thead>
<tr>
<th>Locus 1 Mates</th>
<th>Freq</th>
<th>Locus 2 Mates</th>
<th>Freq.</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA x AA</td>
<td>0.48</td>
<td>BB x BB</td>
<td>0</td>
</tr>
<tr>
<td>AA x Aa and Aa x AA</td>
<td>0</td>
<td>BB x Bb and Bb x BB</td>
<td>0.1364</td>
</tr>
<tr>
<td>AA x aa and aa x AA</td>
<td>0</td>
<td>BB x bb and bb x BB</td>
<td>0.0455</td>
</tr>
<tr>
<td>Aa x Aa</td>
<td>0.24</td>
<td>Bb x Bb</td>
<td>0</td>
</tr>
<tr>
<td>Aa x aa and aa x Aa</td>
<td>0</td>
<td>Bb x bb and bb x Bb</td>
<td>0.8182</td>
</tr>
<tr>
<td>aa x aa</td>
<td>0.28</td>
<td>bb x bb</td>
<td>0</td>
</tr>
</tbody>
</table>

a. What do you conclude about system of mating for these loci?

The two loci obviously have different systems of mating. Locus 1 shows 100% assortative mating; locus 2 shows 100% disassortative mating. The results cannot be explained by inbreeding or avoidance of inbreeding since they affect all loci. 4 POINTS.

b. What are the equilibrium genotype frequencies for locus 1 if the observed system of mating is continued?
For locus 1, equilibrium frequencies are 0.6 for $AA$; 0 for $Aa$; and 0.4 for $aa$ (equation 3.4). 3 POINTS

c. What are the genotype frequencies for locus 2 in the offspring produced by the mating types shown above?

Using Figure 3.8, $G'_{BB} = \frac{1}{2}(0.1364) = 0.0682$; $G'_{Bb} = \frac{1}{2}(0.1364) + 0.0455 + \frac{1}{2}(0.8182) = 0.5227$; $G'_{bb} = \frac{1}{2}(0.8182) = 0.4091$ 3 POINTS