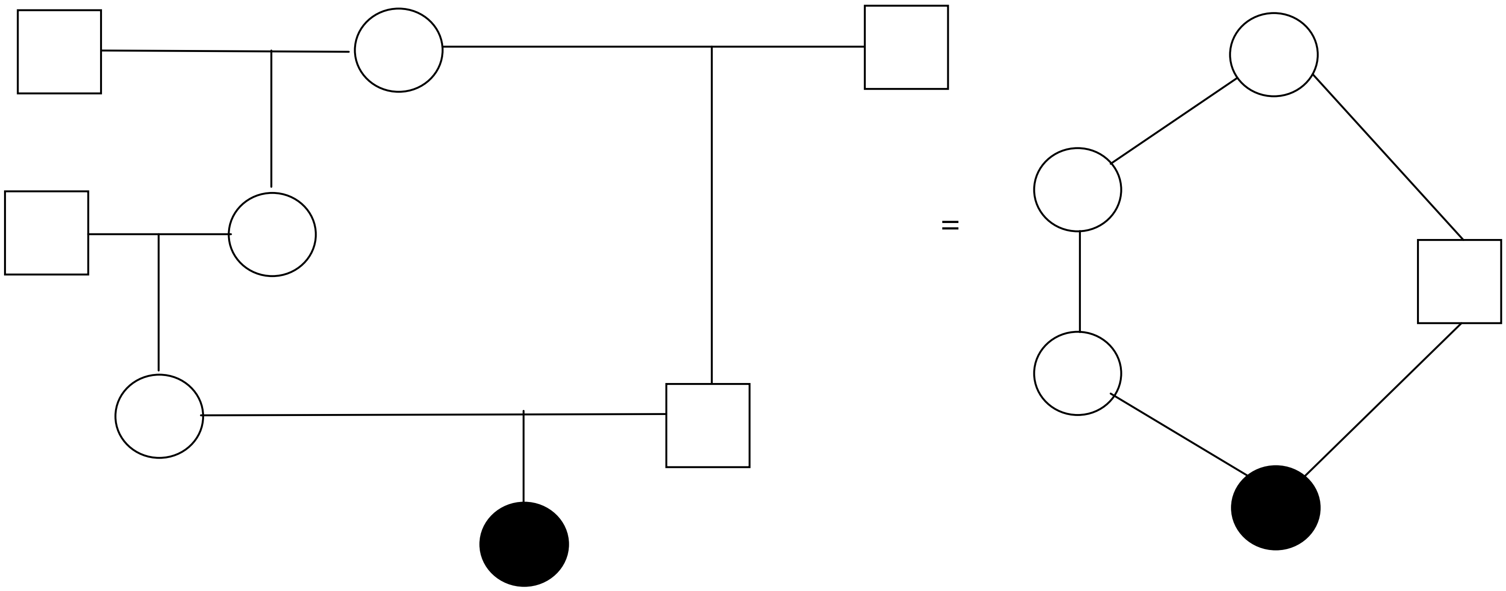
Problem Set 2, Bio 4181: Due Sept. 17, 2009

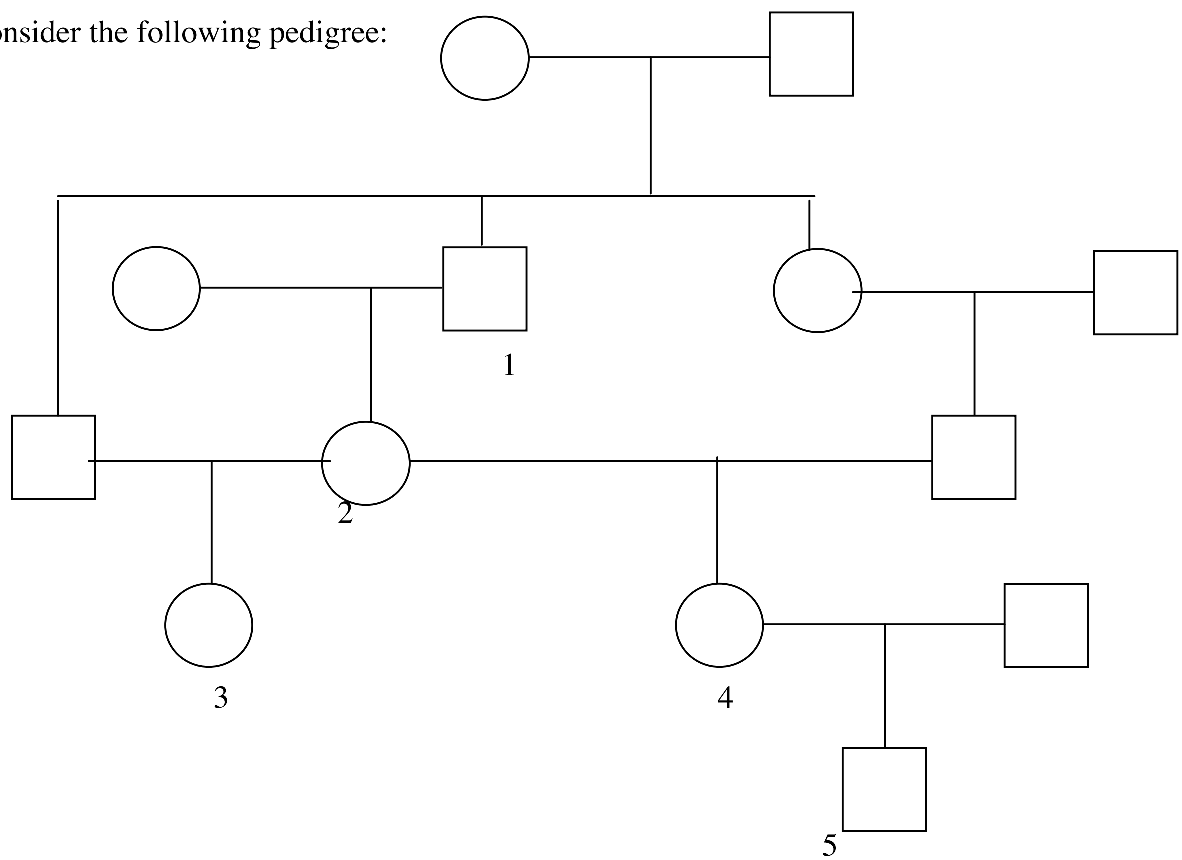
1. Consider the following pedigree:



a). What is the pedigree inbreeding coefficient F of the female shown by the solid circle relative to this pedigree? **2 pts. From the simplified pedigree, $F = (0.5)^4 = 0.0625$**

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? **3pts. From the simplified pedigree, $F = (0.5)^3 = 0.125$**

2. Consider the following pedigree:



Indicate which of the numbered individuals are inbred in the sense that $F > 0$ based on the information in the pedigree. **5pts. 3 and 4 have $F > 0$, all the others have $F = 0$.**

3. The incidence of an autosomal recessive genetic disease in a population is 1.2%. The frequency of the disease allele in the gene pool is 0.05. What is *f* for this population? **2 pts. use the equation 0.012 = p^2+pqf with p=0.05 and solve for f = 0.2**

4. 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. **4 pts.**

	AA	**Aa**	**aa**
a. $p = 0.8, f = -0.2$	**.608**	**.384**	**.008**
b. $p = 0.2, f = 0.1$	**.195**	**.210**	**.595**
c. $p = 0.4, f = -0.3$	**.088**	**.624**	**.288**
d. $p = 0.1, f = 0.9$	**.091**	**.018**	**.891**

5. Consider the following three populations. For each population, estimate the value of *f* given the following genotype numbers. **3 pts.** **All 3 populations are in HW and f = 0 in each case.**

Genotypes	*AA*	*Aa*	*aa*
a.	25	50	25
b.	8	64	128
c.	49	42	9

Now assume that an investigator pooled all three samples together and regarded them as a single population. Estimate the value of *f* for the pooled sample and test the null hypothesis that *f* = 0 and use a p-level of 0.05 to accept or reject the null hypothesis. **6 pts.**

For the pooled population:

Genotype	AA	Aa	aa	Total	
Numbers	82	156	162	400	
Genotype Freq.	0.205	0.390	0.405	1	**1 pt**
Alleles	A	a			
Allele Freq.	0.400	0.600		1	**1 pt**
Inbreeding coef.	0.1875				**1 pt**
Genotype	AA	Aa	aa	SUM	Probability
H.W. Freq.	0.160	0.480	0.360	1	**1 pt**
Exp.	64.000	192.000	144.000	400.000	
(o-e)2/e	5.0625	6.75	2.25	14.0625	0.000176835
				1 pt	**reject 1 pt.**

6. A population has variation at two loci, each with two alleles (A and a; B and b) with a recombination frequency of 0.2 between the loci. The genotype frequencies are as follows:

Genotypes	*AB/AB*	*AB/Ab*	*AB/aB*	*AB/ab*	*Ab/Ab*	*Ab/aB*	*aB/aB*	*Ab/ab*	*aB/ab*	*ab/ab*
freq.	0.25	0.1	0.1	0.3	0.01	0.02	0.01	0.06	0.06	0.09

Assume now that each capital letter allele contributes +2 to a phenotype and each small letter allele contributes 0 to a phenotype, with the total phenotypic value determined by the sum of these numbers over both alleles and both loci. Assume further that there is 100% assortative mating. What are the equilibrium genotype frequencies? **5 pts.**

Although the phenotypic scale is different, the above results in the same phenotypically distinct categories and mating types as the example in the text shown in Table 3.4. Therefore, the equilibria are those given in Table

3.5. (2 pts). All we need are the allele frequencies: p_A= 0.6 and p_B = .6 (2 pts), so from Table 3.5 the equilibrium genotype freq. of AB/AB is 0.6, the equilibrium frequency of ab/ab is 0.4, and all other frequencies are 0 (1 pt).