Bio393: Biomedical Genetics **Name:**_____
Problem Set #5
Due on Friday, May 10, 5 PM

Question 1:
Circle the correct answer.

(a) Which type of variant is easiest to map using family-based analyses?

1 - Rare variants with variable penetrance
2 - Common variants with variable penetrance
3 - Rare variants with high penetrance
4 - Common variants with high penetrance

(b) Which type of variant is easiest to map using population-wide analyses?

1 - Rare variants with variable penetrance
2 - Common variants with variable penetrance
3 - Rare variants with high penetrance
4 - Common variants with high penetrance

Question 2:
Genetic loci with large phenotypic effects are usually rare across populations.

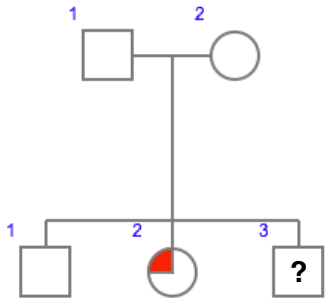
(a) Provide an explanation for why.

(b) The variants that cause age-related macular degeneration have reached intermediate frequency in the human population. How do you think that large-effect variants (like those alleles) reach intermediate frequencies in humans?

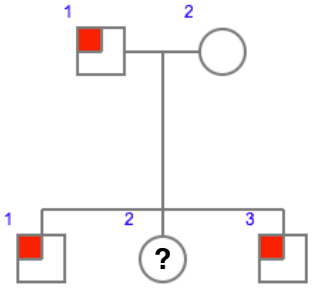
Question 3:
Recurring behavioral disorders were observed in some male members of a large pedigree extending over several generations. The males were mildly mentally retarded and, especially when under stress, were prone to repeated acts of aggression, including sex offenses, attempted murder, and arson. An X-linked gene, MAO, coding for the enzyme monoamine oxidase, which participates in the breakdown of neurotransmitters, was found to be defective in the affected men in this pedigree. Other researchers found abnormal levels of monoamine oxidase in some unrelated men with similar behavioral issues, even though the MAO gene was not defective in these cases. Does this evidence support the hypothesis that defective monoamine oxidase is responsible for the behavioral disorder? Please explain your answer.

Question 4:
Each of the families below exhibits a different, extremely rare genetic disorder. Individuals expressing the trait (the disorder) are indicated by symbols with red sections. Assume that no new mutations have arisen in any of the individuals shown. Consider the following possible modes of inheritance: (i) X-linked recessive with complete penetrance, (ii) autosomal recessive with complete penetrance, (iii) autosomal recessive with 70% penetrance, (iv) autosomal dominant with complete penetrance, (v) autosomal dominant with 70% penetrance. For each pedigree state which, if any, of these five modes of inheritance are not possible. For the modes of inheritance that are possible, calculate the probability that the individual indicated by a "?" is affected.

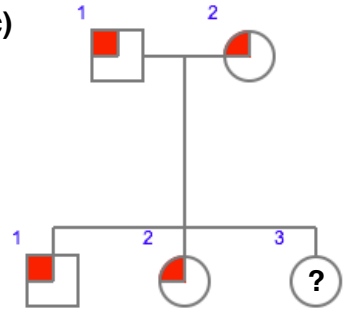
(a)



(b)



(c)



(d)