Bio393: Genetic Analysis **Name:**_____
Extra problems!

Question 1:
Circle the correct answer(s).

(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

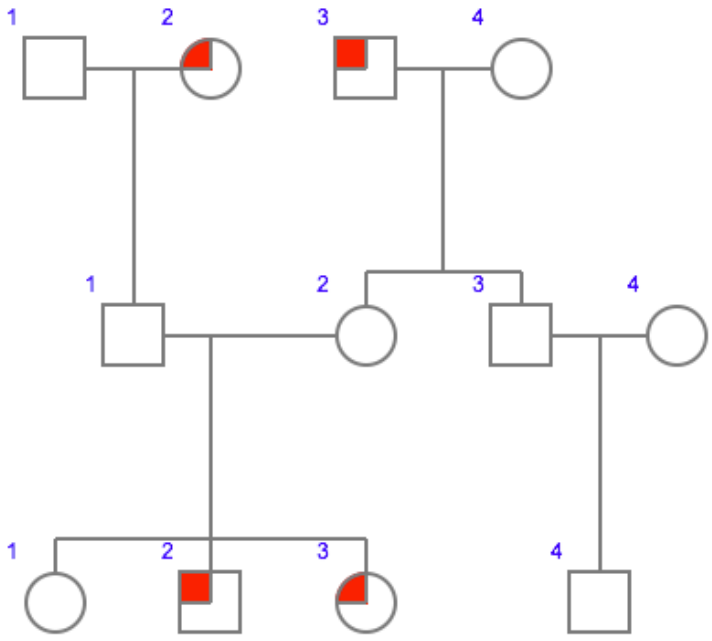
(b) Which type of variant is easiest to map using population-wide analyses?

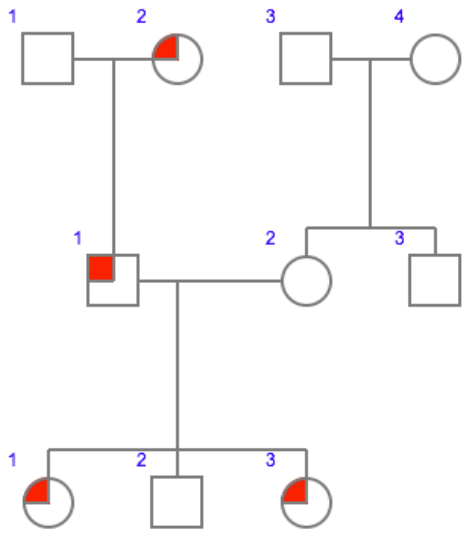
1 - Rare variants with variable penetrance
2 - Common variants with variable penetrance
3 - Rare variants with high penetrance
4 - Common variants with high penetrance

(c) How many individuals need to be sequenced to identify causal variants for Mendelian (single gene) diseases?

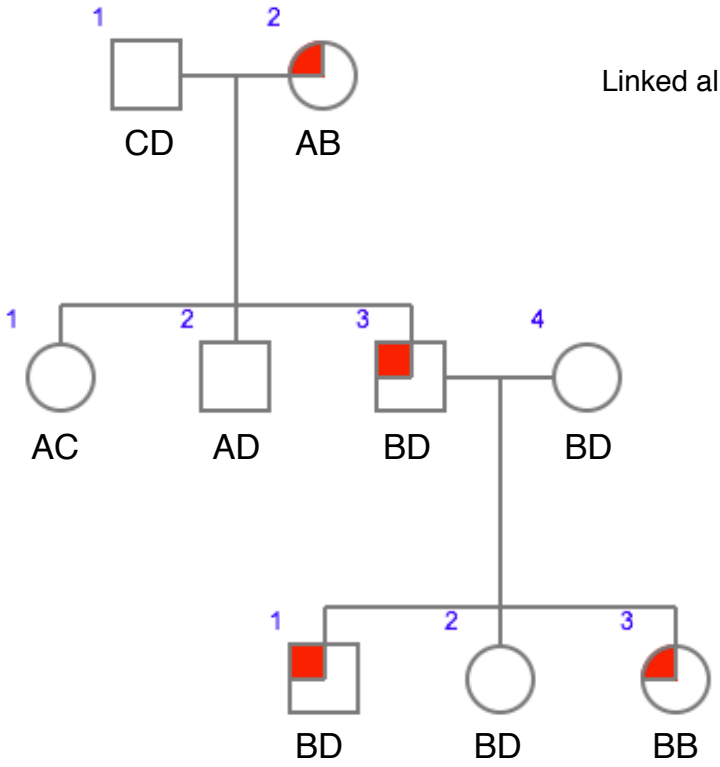
1 - Up to 10
2 - 1000
3 - More than 100,000

Question 2:
For the following two pedigrees, specify the mode of inheritance and explain your rationale. Indicate any ambiguities.





Question 3:
In the following three-generation pedigree, an autosomal dominant disease is thought to be linked to a neutral genetic marker. The marker has four alleles in the population (A, B, C, and D). Please mark the following:
(1) The allele of the marker that could be linked to the disease-causing allele.
(2) Circle the individual(s) where we know the linkage phase.
(3) For every informative individual in generation III, please mark him or her as parental (P) or recombinant (R).



Linked allele: _____