

PBG 200A Notes

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1 Questions from the Notes - my answers in

Question 6 A)

$$\frac{\mathbb{P}[G|W]\mathbb{P}[W]}{\mathbb{P}[G]} \quad (1)$$

where $\mathbb{P}[G|W] = \mathbb{P}[AA|W]\mathbb{P}[bb|W]$ and $\mathbb{P}[G] = \mathbb{P}[G|W]\mathbb{P}[W] + \mathbb{P}[G|E]\mathbb{P}[E]$
B)

something for now - fill in later (2)

Question 7 A) Use

$$p_A = p_{AB} + p_{Ab}p_B = p_{AB} + p_{aB} \quad (3)$$

and eq. 21

B) Just average each frequency since they are combined in equal proportions. Final answer is $D = 0.1225$.

2 Recombination and Linkage Disequilibrium (LD)

A haplotype is a combination of alleles on a chromosome. Let r = the recombination fraction probability of an odd number of crossovers occur between our markers $0 < r < \frac{1}{2}$. Define the expected frequency (expected if independent) of each of the possible haplotypes as p_{AB} , p_{aB} , etc. Then we find covariance (deviation from independence) as $D_{AB} = p_{AB} - p_A p_B$, etc. The algebra simplifies to

$$D_{AB} = -D_{Ab} \quad D_{AB} = D_{ab} \quad D_{Ab} = D_{aB} \quad (4)$$

In a large randomly mating population,

$$D_t = (1 - r)^t D_0 \quad (5)$$

This is because $D_{AB} = p_{AB} - p_A p_B$. In the next generation (notation D' , p'), we have $p'_{AB} = (1 - r)p_{AB} + r p_A p_B$. Thus

$$\Delta p_{AB} = p'_{AB} - p_{AB} = -r p_{AB} + r p_A p_B = -r D \quad (6)$$

Thus

$$D_{t+1} = (1 - r) D_t \quad (7)$$

If $r \ll 1$, then $1 - r \approx e^{-r}$. Thus

$$D_t \approx e^{-rt} D_0. \quad (8)$$

3 What creates LD?

- Mutational origin
- Genetic drift (and hitchhiking)
- epistatic selection

- assortive mating
 - inbreeding
 - population structure and admixture
 - assortative mating by phenotype

Mixing two populations with no LD but with different allele frequencies will cause LD.

4 Evolution by Genetic Drift

Evolution *by genetic drift* is a change in allele frequency because individuals carry the allele by chance produce more or less offspring in any given generation (in sexual populations).

- Genetic drift can affect selected alleles but only if they are very weakly selected (except when they are rare)
- A neutral allele is an allele with no effect on fitness as compared to other alleles at the same locus