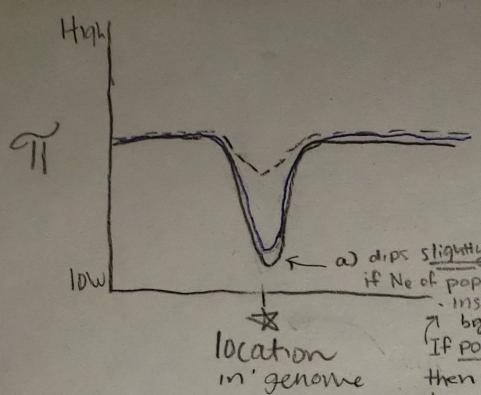
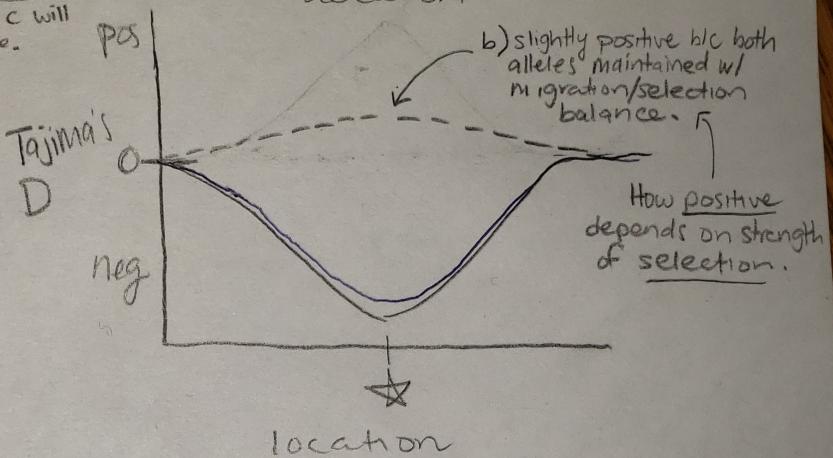
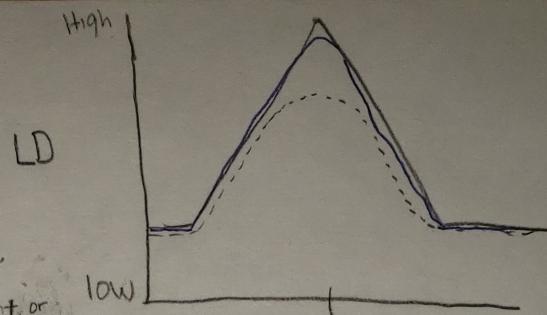


(4)



a) dips slightly lower,  
if  $N_e$  of pop2 is not  
insignificant or  
1 bg's.  
If pop2 swamped,  
then a & c will  
be ~same.



— = a) Sample of  $N$  inds. from  
pop #1

--- = b) Sample  $N$  inds from  
pop #2

— = c) Sampled  $N/2$  for each  
pop at random

★ = locus under selection

(5) > First of all, you probably need a larger sample size. Sample/  
sequence more individuals & reanalyze.

> Secondly, GWAS works best for single gene traits. Polygenic traits  
are trickier. If this is the case, try calculating the Polygenic  
Score (effect sizes of all SNPs)

> Linkage disequilibrium can also screw stuff up. (Choose best SNPs,  
remove LD & repeat)

Pop Gen Midterm  
Part B  
Evelyn Abbott  
3/13/2020

$$P_1 = 0.40 \Delta P_1 = 0.02$$

$$P_2 = 0.42 \Delta P_2 = 0.02$$

$$P_3 = 0.44 \Delta P_3 = 0.02$$

$$P_4 = 0.46 \Delta P_4 = 0.02$$

$$P_5 = 0.48 \Delta P_5 = 0.02$$

$$P_6 = 0.50 \Delta P_6 = 0.02$$

$$P_7 = 0.52 \Delta P_7 = 0.02$$

$$P_8 = 0.54 \Delta P_8 = 0.02$$

$$P_9 = 0.56 \Delta P_9 = 0.02$$

$$P_9 + \Delta P_9 = 0.56 + 0.02 = 0.58$$

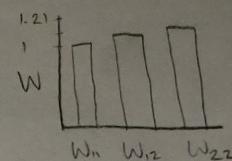
$$W_{11} \quad W_{12} \quad W_{22}$$

$$\frac{1}{(1+s)^2} \quad \frac{1-s}{(1+s)} \quad \frac{1}{1+s}$$

$$A_1: P_1 = 0.4$$

$$* \text{plug into eqn} * \quad q_1 = 0.6 = (1 - 0.4)$$

$$s = 0.1$$



$$\Delta P_1 = \frac{0.1}{1 + (0.1)(0.4)} (0.4)(0.6)$$

could also use  $\Delta P \approx 3pq$ , but used this to be precise

$$P_{10} = 0.58$$

redo w/  $\Delta P = 3pq$

$$(2) \quad W_{11} \quad W_{12} \quad W_{22} \\ (1+s)^2 \quad (1+s) \quad 1$$

$$\text{Pop1 } N_e = n$$

$$\text{Pop2 } N_e = 4n$$

$$U \approx \frac{1 - \exp\{-2s\}}{1 - \exp\{-4Ns\}}$$

↑  
Prob  
fixation  
of new  
mutation

↑  
 $n^2$   
 $4n$

Ratio (to be precise)

$$\frac{1 - \exp\{-2s\}}{1 - \exp\{-4Ns\}} : \frac{1 - \exp\{-2s\}}{1 - \exp\{-16ns\}}$$

$$\text{pop1} : \text{pop2}$$

If the mutation is NEW, the probability of fixation is greater in the small population because the initial frequency is higher.

- ③ 1. Selection at that region will reduce diversity by purging (usually deleterious) new variants. Neutral regions will, in contrast, have higher  $\pi$ .
2. Recombination: areas with reduced recombination will also have reduced  $\pi$ .
3. Linkage disequilibrium: neutral sites may be linked/associated w/ sites under selection and have reduced  $\pi$ , despite not being under selection themselves.