1 Relative fitnesses

W_{11}	W_{12}	W_{22}
1	1.1	1.21
1	$(1+S)$	$(1+S)^2$

$\Downarrow$

$S = 0.1$

$\text{freq}(A_1) = P_1 = 0.4 \leftarrow p(0)$

$q(0) = 0.6$

$\Rightarrow$ Looks like multiplicative selection
  $\hookrightarrow$ Which is equivalent to selection in haploids,

Thus

$$p(t) = \frac{p(0)\,\exp\{st\}}{q(0) + p(0)\,\exp\{st\}}$$

$$\boxed{p(10) = \frac{0.4\,e^{(0.1 \cdot 10)}}{0.6 + 0.4\,e^{(0.1 \cdot 10)}} = 0.64}$$

2. Let

u_1 be the fixation prob. in pop 1 w/ size n

u_2 be the fixation prob. in pop 2 w/ size $4n$

Let a new mutation arise with $p = \frac{1}{2N}$

$$\frac{u_1}{u_2} = \frac{\dfrac{1 - \exp\{-2s\}}{1 - \exp\{-4ns\}}}{\dfrac{1 - \exp\{-\frac{1}{2}s\}}{1 - \exp\{-16ns\}}}$$

However, this exact solution is hard to interpret. We can use the approximation.

$|Ns| \ll 1, \quad u_1\left(\frac{1}{2N}\right) \approx \frac{1}{2N}$

$|Ns| \gg 1, \quad u_2\left(\frac{1}{2N}\right) \approx 2s$

since $4n \gg n$,

$$\frac{u_1}{u_2} \approx \frac{\frac{1}{2n}}{2s} = \frac{1}{4ns}$$

The mutation is more likely to fix in the larger population w/ size $4n$, because a smaller pop. size leaves mutations much more subject to drift, in which even a beneficial mutation could be lost.

3. What affects π in a region of the genome?

① <u>Strong selection</u> in a region of the genome can <u>lower π</u>, because a strong selective sweep will reduce genetic diversity around a site as it carries neutral polymorphisms w/ it.

② <u>Mutation rate</u> in a region of the genome can affect π. Higher than average mutation rates increases π, as molecular diversity increases, while low mutation rates have the opposite effect.

③ <u>Recombination rate in a particular region — large amounts of recombination will increase π</u> b/c many changes are being made to the genome.

4.   a) Pop 1 (big N)   b) Pop 2 (small N)   c) Pop 1 + Pop 2

site   site   site
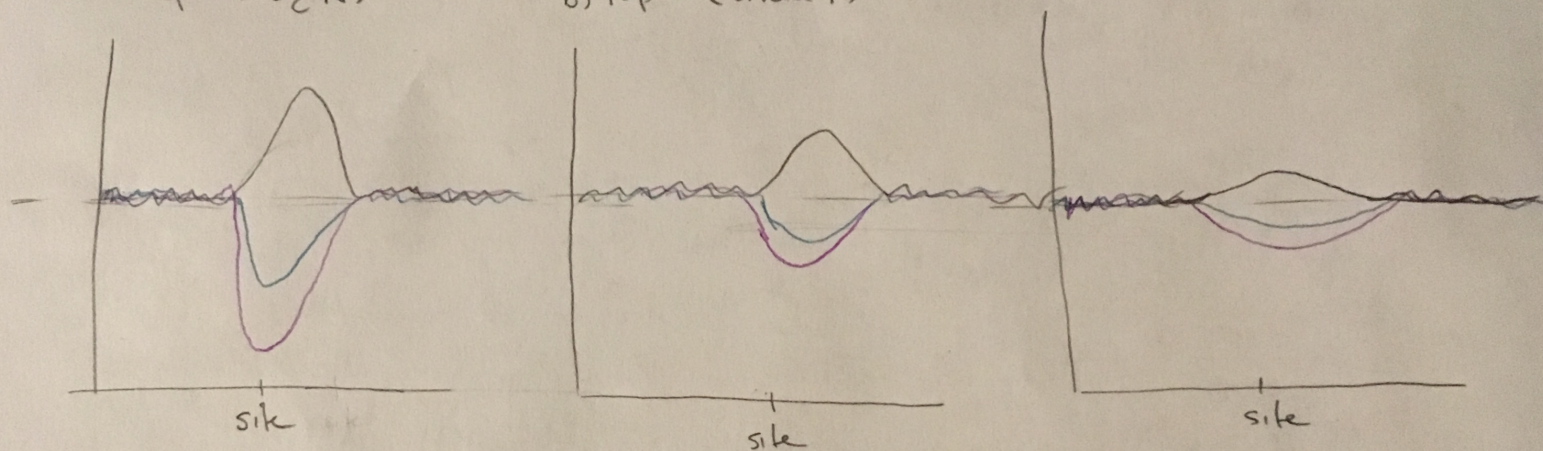
🟦 = π   🟪 = Tajima's D   ⬛ = LD

Basically, smaller pop size should make signals of selection less apparent

5. Performed GWAS and over ½ genome under selection.

① You may not have accounted for <u>population structure</u> ⇒ occurs when the trait you're looking at is already somehow correlated with non-genetic factors (i.e., Russian + Russian drinkers), to solve <u>use population as a covariate</u>.

② Your trait might be under <u>omnigenic</u> selection ⇒ occurs when most of the genome affects a trait at a low level, we can test it by looking at a plot of p-values vs. effect size to see the distribution of effects across the genome ⇒ would be likely for a complex trait (coral stress?).

③ You <u>may not have accounted for linkage disequilibrium</u> ⇒ likely when a trait is under polygenic selection, but you did not account for linked sites in close proximity to selected site ⇒ fix using "LD clumping"