

Practice Thought Question/ Problem Answers for Week 4

- 1) We don't expect a difference, since mutations are not generally more likely to occur when organisms "need" them. If the mutation DID arise, it'd be more likely to spread in the population with droughts, but that spread is by natural selection-- there should be no difference in mutation RATE.
- 2) 7. It seems like it should be 6, but think of it like this-- you have 0-6 "increase" alleles possible. That's 7 possibilities, since 0 is included. The distribution should resemble a normal one since there are many combinations that would increase pH by 3, but only one each (aabbcc or AABBCC) that would increase pH by 0 or 6.
- 3) Mutations from A to "anything but A". Presumably that would be the sum of three mutation rates: A-> C, A-> G, and A-> T.
- 4) Many reasons. There may be a stretch that has low recombination, so the center isn't exactly where the gene is. The estimate of the peak may be off since there are two nearby genes contributing to variation in height, and the plot is incorrectly inferring these as one gene with a big effect (remember the example with the "T" marker). Many others.
- 5) GWAS studies do tend to have greater precision than family pedigree analyses, but that does not mean the pedigree analysis was wrong. If the mutation causing breast cancer is abundant in the family but rare in the population, you'd expect to be able to map it in the family but not via GWAS.