

Homework 8
due Wednesday March 1, 2017

Do these problems, and email the results (if you can, in a PDF or else in Word .DOC or .DOCX format. PDF is best as I cannot read some .docx files. From recent versions of Microsoft Word you can save to PDF format using the Save As menu item.) Like all of the weekly homeworks this one totals 25 points and is due at the end of that day (at midnight).

1. (13 points) Suppose that we have a species that mates monogamously, so that the N individuals in each generation are randomly paired into $N/2$ pairs. Unlike the Wright-Fisher model, each pair then produces exactly 2 offspring that survive to adulthood. What will be the effective population size? *Hint: You will need to follow two quantities – the probability h_t of non-IBD of the two copies in an individual, and the probability k_t of non-IBD of two copies that are in different individuals. Work out the equations that give h_{t+1} and k_{t+1} in terms of h_t and k_t . You will need to be able to work out, looking backward from the offspring to the generation that produced it, what the probability is that, given that one offspring came from a particular pair of parents, that particular one of the remaining offspring came from that same pair of parents.* Once you have these equations, look at the formulas for effective population size with varying offspring number. Do these seem to give you the same result?

2. (12 points) **(i)** Use the genetic simulation program PopG or some equivalent program to simulate the outcome of genetic drift and selection in a diploid locus which has fitnesses 1.21 : 1 : 1 for genotypes AA , Aa and aa in a population of size 1000 individuals. What is the fixation probability of the A allele if it starts out with just one copy in the population? (*Be careful, that is not a gene frequency of 1/1000*). Simulate many populations, for long enough that all of them go to fixation or loss of the allele. Report to me how many populations in all were simulated, and in how many of those A fixed. I will be combining the results across the class.
(ii) How do those results compare with the case where there is some favorable effect of allele A in the heterozygote, namely fitnesses of 1.21 : 1.1 : 1 ? For that case report how many populations were run and in how many of them A fixed.
(iii) Looking ahead in the book, in section VII.8, find fixation probability formulas for these two cases, and show the fixation probabilities that these predict. Do they seem to agree with your simulations? Are the fixation probabilities much affected by the selection in the heterozygotes?