Exercise Set 1

Do at least one of the following three exercises:

- 1. Write a program that simulates the haploid Wright-Fisher model with selection, as described in class. Note that, ultimately, the A allele must sweep to fixation or be lost (i.e., achieve a frequency of q = 0 or 1) in every population.
 - (a) Use your program to estimate the probability (= fraction of replicate simulations) that a new advantageous mutation (i.e., a single copy of the A-type with fitness 1 + s) becomes fixed in a population of size N = 4 when s = 0.1, which represents a substantial selective advantage, and in a population of the same size but for a new mutation with a smaller advantage s = 0.01. How do these compare with the branching process-based approximation P(fixation) = 2s?
 - (b) Can a deleterious mutation sweep to fixation? Use your program to estimate the probability of a new mutation with s = -0.01 sweeping to fixation in a population of size N = 4.
 - (c) Use your program to estimate the probability that a new "neutral" mutation (i.e., one with s = 0) will sweep to fixation. How does this probability compare with those of weakly advantageous (s = 0.01) and weakly deleterious (s = -0.01) mutations?
 - (d) [Optional] Use your program to explore how population size affects fixation probabilities in the different scenarios above. Discuss!
- 2. (*Requires a little background in linear algebra*.) Probabilities of fixation can be computed *exactly* from the binomial transition probabilities, g_{jk} of the Wright-Fisher model with selection. Recall the argument from class: Let u_i be the probability that a population with *i* copies of *A* ultimately becomes fixed for *A*. Note that $u_0 = 0$ (a population with no *A* alleles has no chance of fixation) and $u_N = 1$ (*A* already is fixed). If $i \neq 0$ or *N*, the population will have *j* copies of *A* in the next generation with probability g_{ij} , in which case the probability of fixation would then be u_j . Considering all possible transitions of a population with *i A* alleles leads to (for i = 1, 2, ..., N-1)

(*)
$$u_i = g_{i0}u_0 + g_{i1}u_1 + \dots + g_{i,N-1}u_{N-1} + g_{i,N}u_N = \sum_{k=1}^{N-1} g_{ik}u_k + g_{i,N}u_N$$

where we used $u_0 = 0$ and $u_N = 1$.

Matrix methods can be used to compute all N - 1 of the unknown fixation probabilities. Let the vector of unknown probabilities be $\mathbf{u} = (u_1, u_2, \dots, u_{N-1})^T$. In

addition set $\mathbf{r} = (g_{1,N}, g_{2,N}, \dots, g_{N-1,N})^{\mathsf{T}}$ and let **Q** be a matrix with *ij*th element equal to g_{ij} , with *i* and *j* both ranging from 1 to N - 1. Equation (*) is equivalent to the matrix equation $\mathbf{u} = \mathbf{Q}\mathbf{u} + \mathbf{r}$. This can easily be solved for \mathbf{u} :

$$(**) u = (I - Q)^{-1} r$$
,

where I is the identity matrix of size N-1 and $(I - Q)^{-1}$ is the inverse of the matrix I-Q. The fixation probability of a new mutant A is the first element, u_1 , of **u**. Use (**) to compute the exact probability of fixation for the scenarios described in exercise 1. Discuss!

- 3. Using a branching process approach, we showed in class that the probability *P* of fixation of a new advantageous mutation satisfies $1-P = e^{-(1+s)^{p}}$ and argued that $P \approx 2s$. In this problem, you will develop a better approximation for *P*.
 - (a) Taking the natural log of both sides, the equation defining *P* is equivalent to $\ln(1-P) = -Pe^x$ where $x = \ln(1+s)$. Replace $\ln(1-P)$ and e^x in this equation with their Taylor series in *P* and *x*, respectively.
 - (b) Substitute $P = Ax + Bx^2 + Cx^3 + \cdots$ in the left-hand side of the resulting equation and solve for the coefficients A, B, C, ... by equating coefficients of powers of x on both sides of the equation.
 - (c) Finally, expand $\ln(1+s)$ in a Taylor series and collect terms to find an approximation for *P* that is at least cubic in *s*.
 - (d) Use this approximation to compute P for the scenario described in exercise 1. (Compare this to the "rough" approximation P = 2s.) Discuss!
 - (e) [*Optional*] Compare your answer to (d) with the approximate fixation probability computed via simulation (ex. 1) or the exact probability (ex. 2).