Homework no. 8

Due Wednesday, March 2

Get the simulation program PopG which is accessible from a link on the course web site. There are versions that run on Windows, on Mac OS X, and on Linux. Do the following computer simulations using it, and report to me the results.

1. Suppose that we have a locus with the geometric fitness pattern:

<table>
<thead>
<tr>
<th>Genotype</th>
<th>AA</th>
<th>Aa</th>
<th>aa</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fitness</td>
<td>1.1025</td>
<td>1.05</td>
<td>1</td>
</tr>
</tbody>
</table>

In a population of size $N = 1000$, if we start from a single copy of the $A$ allele, what is the probability of fixation of $A$? To find this, start with the appropriate initial gene frequency (careful! people often get this number wrong) and have no mutation of migration. Run a large number of replicate populations. Report to me what starting gene frequencies you used. Run the program until all populations have fixed $A$ or lost it – the numbers will be on the right side of the graph of gene frequencies. Report the number of replicates run and the number of those that fixed for $A$ (not just the fraction). If you do more than one run for these parameter values you can just add up the numerators and denominators. I do not need to see the actual graphs.

2. Now try a dominant case with fitnesses 1.05 : 1.05 : 1. Report the same numbers. How much influence does the fitness of $AA$ appear to have?

3. Try both of these cases with a smaller population size ($N = 100$) and the appropriate initial gene frequency to correspond to having a single copy of $A$ in the initial population. Does the population size have much effect?

4. Finally, find in Chapter VII some formulas that predict some of these results. How well do they correspond to what you found in your simulation?