

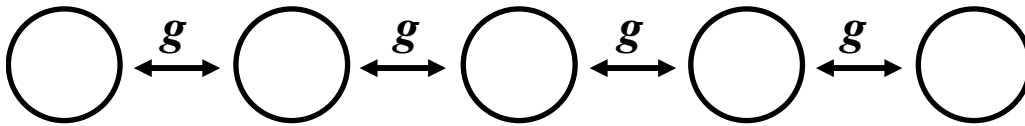
Lab 4: Gene flow and selection

Basic instructions:

For today's lab, the 'selection in a clinal stepping stone' module of Populus will be used. To get to this module, click on 'spatial models' and then on 'selection in a clinal stepping stones'. Set the 'selection regime' to 'gradient'.

Mathematical background:

The mathematical background for today's lab was covered in the lecture 'gene flow and differentiation' and also in the lecture on 'speciation'. It would be helpful to review that material before arriving and to bring a copy of that material with you to lab. This lab will build extra complexity onto this material by considering the interaction between selection and gene flow in linear series of populations connected by gene flow. This scenario is diagrammed below, where each circle represents a population, and each population is connected to its nearest neighbors by gene flow. More specifically, in every generation, each population is composed of a fraction of migrants, g , from its neighboring populations.



In the simulations you will run, the number of populations or 'demes' is fixed at 50. You will, however, be able to change the rate of gene flow between populations, g . In addition, you will be able to change how rapidly selection changes across space. This can be accomplished by changing the parameter, s , which alters genotypic fitnesses in the following manner:

$$W_{AA,i} = 1 - s \left(\frac{i-1}{49} \right)$$

$$W_{Aa,i} = 1 - \frac{s}{2}$$

$$W_{aa,i} = 1 - s \left(\frac{50-i}{49} \right)$$

where i is the deme number (1-49). What this means biologically, is that AA individuals are favored by natural selection in demes 1-25, whereas aa individuals are favored by natural selection in demes 26-50. The parameter, s , determines the magnitude of the differences in genotypic fitness.

Running the simulations:

When this module is first started, Populus plots the fitness of the AA genotype in red, Aa genotype in blue, and the aa genotype in green. Populus also plots the initial allele frequencies in all of the demes in pink. To see what happens as evolution proceeds, press the iteration button. This runs the simulation for a number of generations specified by the 'generations' input box. The iteration button can be pressed repeatedly to step through additional generations. You should continue iterating until equilibrium is reached where allele frequencies no longer change.

Questions:

1. Set the selection parameter, s , equal to .05.
 - A. If the rate of gene flow, g , is set to zero, what is the ultimate fate of the A and a alleles in the various populations/demes?
 - B. In this case, how well adapted are the various populations/demes to their local environments?
 - C. Now set the rate of gene flow, g , to .05. How does this change the ultimate fate of the A and a alleles in the various populations/demes?
 - D. Are the various population/demes now more or less well adapted to their local environments? Why?
2. A team of scientists were interested in exploring the potential for gene flow to inhibit the evolution of insecticide resistance in populations of the European Corn Borer, *Ostrinia nubilalis*. To this end, the scientists established a large scale experiment where fields sprayed with different levels of insecticide were aligned in a linear series. The concentration of insecticide decreased from left to right. Upon measuring the fitness of genotypes that were resistant (AA), partially resistant (Aa) and non-resistant (aa), the scientists established that the fitnesses changed linearly across space such that the parameter s was equal to .2. (Note that the non-resistant populations have a higher fitness in regions where low concentrations of insecticide are sprayed because resistance to insecticide is metabolically costly).
 - A. How much gene flow would there have to be between moth populations before insecticide resistance could be prevented from becoming fixed in population XX?
 - B. Assuming that the scientists found the rate of gene flow between moth populations to be .5, what would the average level of insecticide resistance ultimately evolve to be across all populations? What if the rate of gene flow were .8?

C. What do your answers in part B tell you about the practicality of the scientists plan for managing Corn Borer insecticide resistance? Why?

3. The key to speciation is the elimination of gene flow. One potential mechanism of speciation, parapatric, relies upon spatial variation in selection as a means to reduce gene flow.

A. In the absence of gene flow ($g = 0$), how much selection is required for the two sets of populations to completely diverge in allele frequency, and effectively be on there way to forming two new species?

B. If instead, the rate of gene flow is $g = .05$, how would your answer change?

C. Now imagine a case where individuals initially move freely between populations ($g = .5$). How much selection is now required for the two sets of populations to completely diverge in allele frequency, and effectively be on there way to forming two new species?

D. What does your answer to C indicate about the potential difficulties associated with parapatric speciation?