Hardy-Weinberg equilibrium

1. If you have not used AlleleA1 before, play with it for a bit to see how it works. Then restore all parameters to their default settings. The default settings encompass initial frequencies of 0.5 for both alleles, and the assumptions of no selection, no mutation, no migration, no genetic drift, and random mating. Run the simulation to verify that under these conditions the allele frequencies do not change. Try different values for the starting frequency of allele A1. Does your experimentation verify that any starting frequencies for A1 and A2 are in equilibrium so long as there is no selection, no mutation, no migration, and no drift?

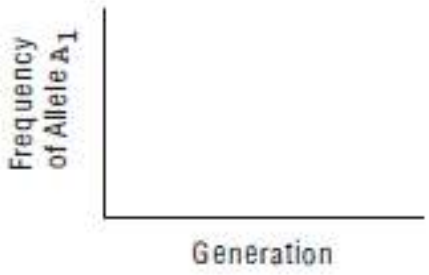
Migration as a mechanism of evolution

2. AlleleA1 uses the one-island model of migration described on pages 234-237 of the text. The simulation tracks the frequency of allele A1 in an island population. The parameter called Fraction of migrants each generation determines the number of individuals that move from the mainland to the island every generation, as a fraction of the island population. For example, setting the parameter to 0.1 means that each generation ten percent of the individuals in the island population are new arrivals from the mainland. The parameter called Frequency of A1 in the source pop'n determines the frequency of allele A1 on the mainland (and thus among each generation's migrants).

a) Click on the Reset button to restore all parameters to their default values. Predict what will happen when you set the fraction of migrants each generation to 0.01 and the frequency of A1 in the source population to 0.8. Then set the parameters to these values and run the simulation. If your prediction was not correct, try to explain the difference between what you expected and what actually happened.

Prediction:

What actually happened:



Explanation:

b) Leave the frequency of A1 in the source population at 0.8, and try setting the fraction of migrants each generation to 0.05, then 0.1.

c) Try several different values for the both the fraction of migrants and the frequency of allele A1 in the source population.

d) Based on your experiences in parts a, b, and c, summarize what migration from the mainland does to the frequency of A1 on the island. How long does it take for migration to exert its influence? How effective is migration as a mechanism of evolution?

Migration and selection

3. Imagine that allele A1 is deleterious for individuals living on the island, such that the fitnesses of genotypes A1A1, A1A2, and A2A2 are 0.9, 0.95, and 1.

a) If there is no migration, what is the frequency of A1 after 500 generations? Why?

b) In accord with what you saw in part a, set the starting frequency of A1 to 0. Remember that this is the frequency in the island population. Now imagine that although it is deleterious on the island, allele A1 is beneficial on the mainland, such that A1 is fixed in the source population (that is, its frequency is equal to 1). What is the island frequency of A1 after 500 generations if the fraction of migrants each generation is 0.0001? 0.001? 0.01? 0.1?

Fraction of migrants	Ending frequency of A_1
0.0001	
0.001	
0.01	
0.1	

c) In the scenario you investigated in part b, how high does the migration rate have to be for migration to overwhelm selection in controlling the frequency of A1 on the island? If selection against A1 on the island were stronger than we assumed in this example, would migration be less likely to overwhelm it

Genetic drift as a mechanism of evolution

5. We have so far used AlleleA1 to simulate evolution in populations of infinite size. In reality, of course, populations are finite. Is evolution in finite populations different from evolution in infinite populations? Return all parameters to their default settings. Set the number of generations to 15 (use the popup menu to the right of the graph's horizontal axis). Now play with populations of finite size. For example, set the population size to 10 or 20 individuals and run the simulation several times. What happens? Why? Does the same thing happen every time? Why or why not?

6. How much does genetic drift change with population size? Return all parameters to their default settings. Set the number of generations to 100. Set the graph line mode to multiple, and the graph line color to auto. Now investigate the power of genetic drift at different population sizes:

a) Set the population size to 4 and run the simulation several times.
b) Clear the graph. Set the population size to 40 and run the simulation several times.
c) Clear the graph. Set the population size to 400 and run the simulation several times.
d) Why are the results different for populations of different sizes?

7. Conservation biologists generally consider genetic diversity to be a good thing. That is, populations are more likely to escape extinction if there are several alleles present for each gene.
a) What does drift do to the genetic diversity in a population as the population nears extinction?

b) Reset all parameters to their default values. Note that the starting frequencies for alleles A_1 and A_2 are 0.5. Roughly how big does the population have to be for the chances to be reasonably good that both alleles will persist for 500 generations?

The random fixation of alleles

8. You have seen that when genetic drift is the only evolutionary force at work in a population—when there is no selection, no mutation, and no migration—the frequencies of alleles in the population wander between 0 and 1. If we track a particular allele for long enough, its frequency will eventually hit one boundary or the other. That is, sooner or later the allele will drift to loss or fixation. Investigate the effect of an allele's initial frequency on the probability that its ultimate fate will be fixation versus loss.

a) Reset all parameters to their default values, and set the population size to 100. Pick an initial frequency for A1, and set the starting frequency parameter in AlleleA1 accordingly. Then run the simulation 100 times. Record your results in the grid below. There are 100 squares in the grid. If A1 drifts to fixation in a particular run, write a 1 in one of the squares on the grid. If A1 drifts to loss, write a 0 in one of the squares. If a run ends with A1 still at a frequency between 0 and 1, disregard the run and continue with the experiment. After 100 runs in which A1 drifted to fixation or loss, count the 1's on your grid to determine the percentage of runs in which A1 drifted to fixation.

Starting frequency of allele A_1: ___

Final frequencies for 100 runs:

Percentage of runs in which allele A_1 drifted to fixation: ___

b) Repeat the experiment you performed in part a, but use a starting frequency for A1 that is substantially different from the one you used before. Record your results in the grid below.

Starting frequency of allele A_1: ___

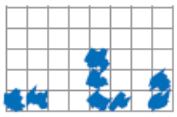
Final frequencies for 100 runs:

Percentage of runs in which allele A_1 drifted to fixation: ___

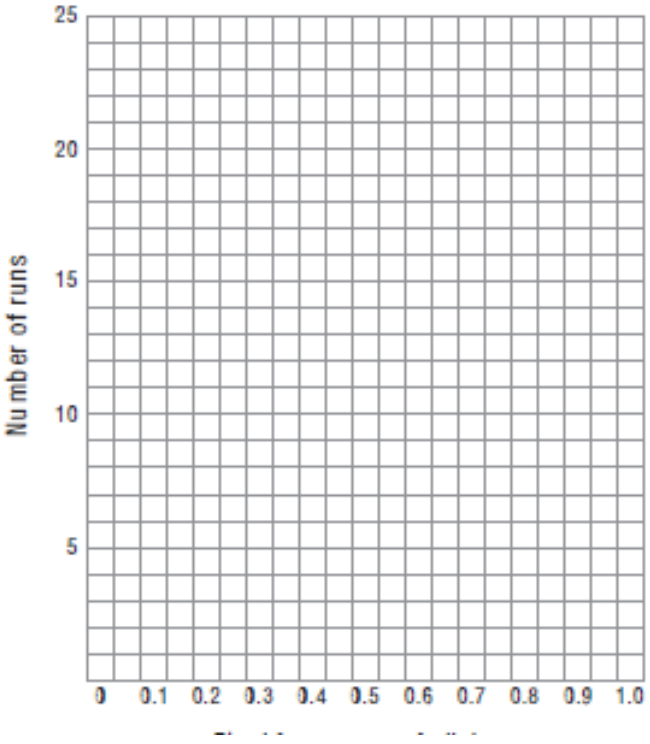
c) Based on your experiments in parts a and b, can you use the starting frequency of an allele to predict the probability that the allele will eventually drift to fixation?

9. Peter Buri (1956) followed the frequency of the bw75 allele for 19 generations in 107 populations of fruit flies. Buri maintained each population at a size of just 16 individuals, which caused the populations to evolve rapidly by genetic drift. Use AlleleA1 to simulate Buri's experiment.

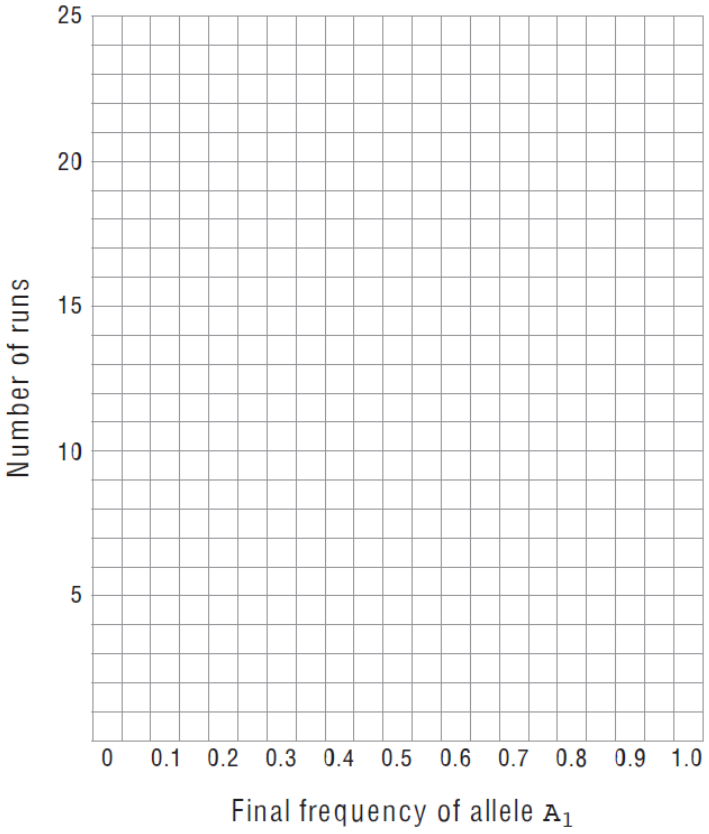
a) Reset all parameters to their default values, then set the population size to 16 and the number of generations to 20. Run the simulation 50 times. After each run, round the final frequency of A1 to the nearest 0.05, and fill in a box on the grid at right above the resulting value. As the number of runs you have completed grows, stack the filled boxes on top of each other so that they form a histogram, like this:



After completing 50 runs, compare your histogram to the one from generation 19 of Buri's experiment, at the bottom of Figure 7.16 on page 250. How well did your simulated experiment "predict" the results of Buri's actual experiment? Can you explain the difference between the shape of your graph and the shape of Buri's?



b) Now set the population size to 9, and run the simulation another 50 times. Record your results on the graph at right just as you did in part a. Again compare your histogram to the one from generation 19 of Buri's experiment. Does the shape of your second graph match Buri's more closely than your first graph did?



c) What does it mean to say that although the actual population size in Buri's experiment was 16 individuals, the effective population size was approximately 9? What evidence do you have to support this claim?

Drift and selection

10. Consider the fate of a rare allele in a small population.
a) Reset all parameters to their default values, then set the starting frequency of A_1 to 0.005 and the population size to 100. Run the simulation several times. What usually happens? Why?

b) Now make the rare allele beneficial (and dominant) by setting the fitnesses of genotypes A_1A_1, A_1A_2, and A_2A_2 to 1.1, 1.1, and 1.0. Run the simulation several times. What usually happens? Why?

c) How strong does selection in favor of the rare dominant allele have to be before the allele has a reasonable chance of becoming fixed in the population instead of lost?

d) How strong would selection have to be if the rare allele were recessive instead of dominant?

Drift, mutation, and selection

11. How big must a population be before a mildly advantageous allele will become fixed as rapidly as it would in a population of infinite size? Restore all parameters to their default values. Set the starting frequency of A_1 to zero, and both mutation rates to 0.00001. Make A_1 beneficial by setting the fitnesses of genotypes A_1A_1, A_1A_2, and A_2A_2 to 1.04, 1.02, and 1. Set the number of generations to 1000.

a) Set the graph line color to black, and run the simulation once with the population size set to infinite. How long does it take for allele A_1 to be created by mutation and carried by natural selection to fixation?

b) Now set the graph line mode to multiple, the graph line color to red, and the population size to 10. Run the simulation several times. What typically happens?

c) Set the graph line color to orange and the population size to 100. Run the simulation several times. What typically happens?

d) Set the graph line color to green and the population size to 1000. Run the simulation several times. What typically happens?

e) Finally, set the graph line color to blue and the population size to 10000. Run the simulation two or three times. What typically happens?

f) How large does a population have to be before a mildly advangateous allele will become fixed as rapidly as it would in a population of infinite size? How strongly does the answer depend on the strength of selection and the mutation rate?

Drift, selection, migration, and genetic diversity

12. In question 7, we noted that conservation biologists consider genetic diversity to be a good thing, and found that genetic drift can reduce genetic diversity and potentially hasten the extinction of small populations. We now revisit these issues by investigating a particular scenario in more detail. Imagine that allele A_1 is maintained in a population by heterozygote advantage, with the fitnesses of genotypes A_1A_1, A_1A_2, and A_2A_2 equal to 0.2, 1.0, and 0.8.

a) What is the equilibrium frequency of A_1 in an ideal population? (You can answer this question either by using the formula derived in Box 6.7 on pages 208-209, or by using AlleleA1.)

b) Once the frequency of allele A_1 has reached its equilibrium value, what are the frequencies of the three genotypes? (You can answer this question either by using the Hardy-Weinberg equilibrium principle, or by using AlleleA1.)

c) Once the frequency of allele A_1 has reached its equilibrium value, what is the mean fitness of the population? (To calculate the mean fitness, multiply the fitness of each genotype by its frequency, then sum the results; see Box 6.3 on page 194).

d) Using AlleleA1, first reset all parameters to their default values. Then set the starting frequency of A_1 to 0.2, the fitnesses of A_1A_1, A_1A_2, and A_2A_2 to 0.2, 1.0, and 0.8, and the population size to 20. Run the simulation several times. What usually happens?

e) After A_1 has been lost due to genetic drift, what is the mean fitness of the population? By how much has drift reduced the mean fitness? If this effect were multiplied across several loci, could drift substantially increase the chance that our small population will go extinct? Why or why not?

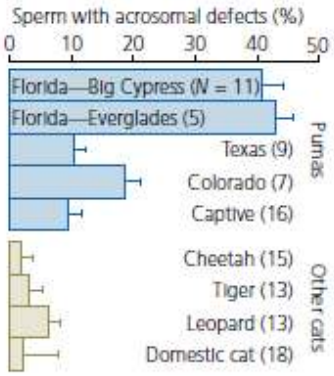
f) Use AlleleA1 to investigate the effect of introducing a single migrant individual into our small population each generation, where the migrant comes from a large population in which the frequency of A_1 is 0.2. (What value for the *Fraction of migrants each generation* parameter reflects a single individual joining a population of 20?) Could the introduction of migrants maintain enough genetic diversity in the population to ameliorate the effects of genetic drift? Compare the scenario you have investigated in this question to the case of the Florida panther discussed at the beginning and end of Chapter 7.

Florida's state animal was on the verge of extinction. The Florida panther (*Puma concolor coryi*) once ranged across southeastern North America from Louisiana to South Carolina and as far north as Tennessee. By 1995, however, the big cat had seen its confines shrink, due to habitat loss and hunting, to a pair of tiny and dwindling patches of swampland in Florida's southern tip (Johnson et al. 2010). Scarcely two dozen individuals remained (McBride et al. 2008).

To make matters worse, the surviving panthers were suffering poor health (Roelke et al. 1993). They showed high rates of heart defects, undescended testes, skeletal malformations, infectious and parasitic diseases, and, as documented at right, sperm abnormalities associated with infertility. Exposure to environmental toxins may have contributed to some of these problems, but the primary causes appeared to be genetic.

Wildlife managers decided that intervention offered the best hope of saving the Florida panther (see Johnson et al. 2010). Their diagnosis of the panther's underlying problem, and the treatment they prescribed, involves three population genetics phenomena introduced earlier (in Chapter 6) but not discussed in depth: migration, genetic drift, and nonrandom mating.

Among other health problems, the Florida panther had high rates of defective sperm compared to other *Puma* populations and other cats. Bars show mean ± se. Photo by Rodney Cammauf, NPS; graph from Roelke et al. (1993).



7.5 Conservation Genetics of the Florida Panther

We opened this chapter with the case of the Florida panther, a once abundant big cat that in the mid-1990s appeared to be destined for extinction. Like a great many other vulnerable and endangered species, the panther's worst enemies are humans with plows, bulldozers, and guns. Yet habitat loss and hunting are not the panther's only problem.

The cat was placed under the protection of the State of Florida in 1958 and listed as endangered by the federal government in 1967 (Pimm et al. 2006). In the 1980s, after a time during which the panther was thought to be extinct, government and citizen groups sought to aid the panther's recovery by protecting additional habitat, changing the way its prey are managed, and building highway underpasses to reduce road deaths (Culver et al. 2008; Johnson et al. 2010). Nonetheless, the panther's population size hovered at less than three dozen from the mid-1989s to the mid-1990s. Something else was now threatening the survival of the Florida panther, but what?

Our discussion of migration, genetic drift, and nonrandom mating has given us the tools to understand the likely answer. Human activity did two things to the panther. First, it directly reduced the size of the cat's population. Second, it isolated the cat from other puma populations that it is closely related to—and that it once interbred with.

A small population with little or no gene flow is precisely the place where genetic drift is most influential. And genetic drift results in random fixation and declining heterozygosity. If some of the alleles that become fixed are deleterious recessives, then the average fitness of individuals will be reduced. A reduction in fitness due to genetic drift is reminiscent of inbreeding depression. In fact, it is inbreeding depression. Reduced heterozygosity due to drift and increased homozygosity due to inbreeding are two sides of the same coin. In a small population all individuals are related, and there is no choice but to mate with kin.

Michael Lynch and Wilfried Gabriel (1990) have proposed that an accumulation of deleterious recessives (a phenomenon known as genetic load) can lead to the extinction of small populations. They noted that when exposure of deleterious mutations produces a reduction in population size, the effectiveness of drift is increased. The speed and proportion of deleterious mutations going to fixation subsequently increases, which further decreases population size. Lynch and Gabriel termed this synergistic interaction between mutation, population size, and drift a "mutational meltdown."

A loss of allelic diversity under genetic drift appears to have caused inbreeding depression in Florida panthers.

The Florida panther appeared to be trapped in just such a scenario. As the population dwindled, the cats began to display conditions we mentioned in the introduction—heart defects, low sperm counts, and susceptibility to infection—that looked like symptoms of inbreeding depression. This inbreeding depression reduced individual reproductive success and caused the remnant population to

continue its decline. The continued decline in population size led to even more drift, which led to worse inbreeding depression, and so on. The cats had fallen into an "extinction vortex" (see Soulé and Mills 1998).

To test this hypothesis, Carlos Driscoll and colleagues (2002) assessed the genetic diversity of Florida panthers relative to other puma populations and other species of cats at several different kinds of loci. Figure 7.40 shows a typical result. Florida panthers have substantially lower heterozygosity than other populations or species of cat.

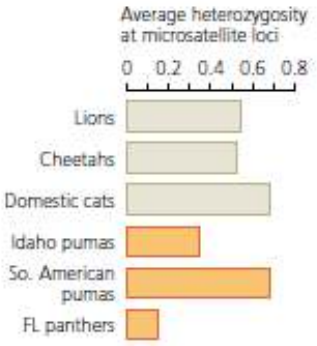


Figure 7.40 Genetic variation in Florida panthers relative to other puma populations and other cats Drawn from data in Driscoll et al. (2002).

Philip Hedrick and colleagues (Culver et al. 2008) compared the genetic variation of present-day Florida panthers to that of museum specimens collected in the 1890s. Although their sample sizes were small, their results were consistent with Driscoll's. Present-day panthers have microsatellite heterozygosities roughly a third of those shown by museum specimens.

Hedrick and colleagues solved Sewall Wright's equation for the decline in heterozygosity across generations for N_e plugged in the heterozygosities from 1890 and today along with generation times ranging from 4 to 6 years, and calculated how small the effective population size must be to reduce heterozygosity by two-thirds over the course of a century. The answer was fewer than 10. If the bottleneck in the Florida panther's population size was shorter and more recent, the breeding population may at one point have consisted of just two individuals.

In sum, consistent with the extinction vortex hypothesis, the Florida panther is genetically depauperate compared to both its own ancestral population and other present-day populations.

The final test of the extinction vortex hypothesis was to use it to develop a conservation strategy. If the problem for the Florida panther is reduced genetic diversity, then the solution is gene flow. Migrants from other populations should bring with them the alleles that have been lost in Florida. Reintroduction of these lost alleles should reverse the effects of drift and eliminate inbreeding depression. Natural migration of panthers into Florida ceased long ago. But in 1995, managers trapped eight Texas pumas and released them in southern Florida.

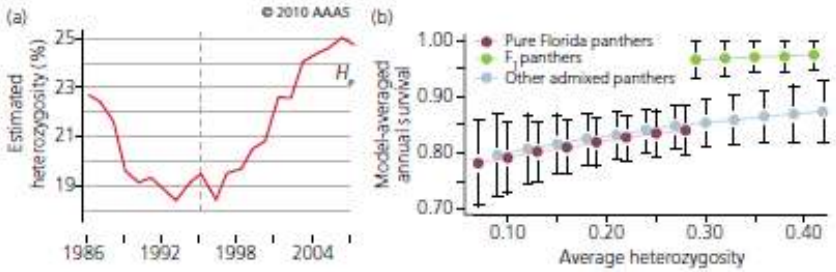


Figure 7.41 Genetic restoration of the Florida panther (a) Heterozygosity has increased since the introduction of Texas pumas. (b) So, as a result, has survival. From Johnson et al. (2010) and Benson et al. (2011).

The plan seems to be working. Warren Johnson and colleagues (2010) report that the Texas and Florida panthers are interbreeding, and that heterozygosity is rising (Figure 7.41a). John Benson and colleagues (2011) report that higher heterozygosity has led to improved survival (Figure 7.41b). And the population has risen to over 100 cats. The Florida panther is not completely back in the woods yet, but its chances of avoiding extinction have improved.

Arranged migration of panthers from Texas to Florida appears to be replenishing the allelic diversity of the Florida population and alleviating inbreeding depression.

Literature Cited

Buri, P. 1956. Gene frequency in small populations of mutant *Drosophila*. *Evolution* 10:367–402.

King, R.B., and R. Lawson. 1995. Color-pattern variation in Lake Erie water snakes: The role of gene flow. *Evolution* 49:885–896.