BOX 8.1 Simulating Trajectories

It is often useful to do computer simulations of population genetic processes in order to better visualize what happens. Many of the figures in this chapter are based on results from a simulation program that models selection and genetic drift in a population of *N* diploid individuals. The simulations assume the Wright–Fisher model described in Chapter 2. There are two alleles, *A* and *a* in a population of *N* diploid individuals. At the start of a generation, the frequency of *A* is f_A. The allele frequency is then changed to f'_A, given by the last equation in Box 7.3, because of genotypic differences in viability:

$$f'_A = f_A \frac{v_{AA} f_A + v_{Aa}(1-f_A)}{v_{AA} f_A^2 + 2v_{Aa} f_A (1-f_A) + v_{aa}(1-f_A)^2}$$

Then genetic drift is simulated by having the computer choose 2*N* gametes randomly, each of which has a probability f'_A of being an *A* and a probability of $1-f'_A$ *of*being an *a*. This is done for each gamete by generating a random number, *x*, that has a uniform distribution between 0 and 1. If $x < f'_A$, the gamete has an *A* and if $x \geq f'_A$ the gamete has an *a*. Then the program counts the number of *A* gametes to determine f_A in the next generation.

Each replicate simulation generates the trajectory of an allele. Then the selection and genetic drift steps are alternated until f_A reaches 0 or 1. After that, a new replicate is started and the process continues until a specified number of trajectories has been generated.