GLOBAL EDITION

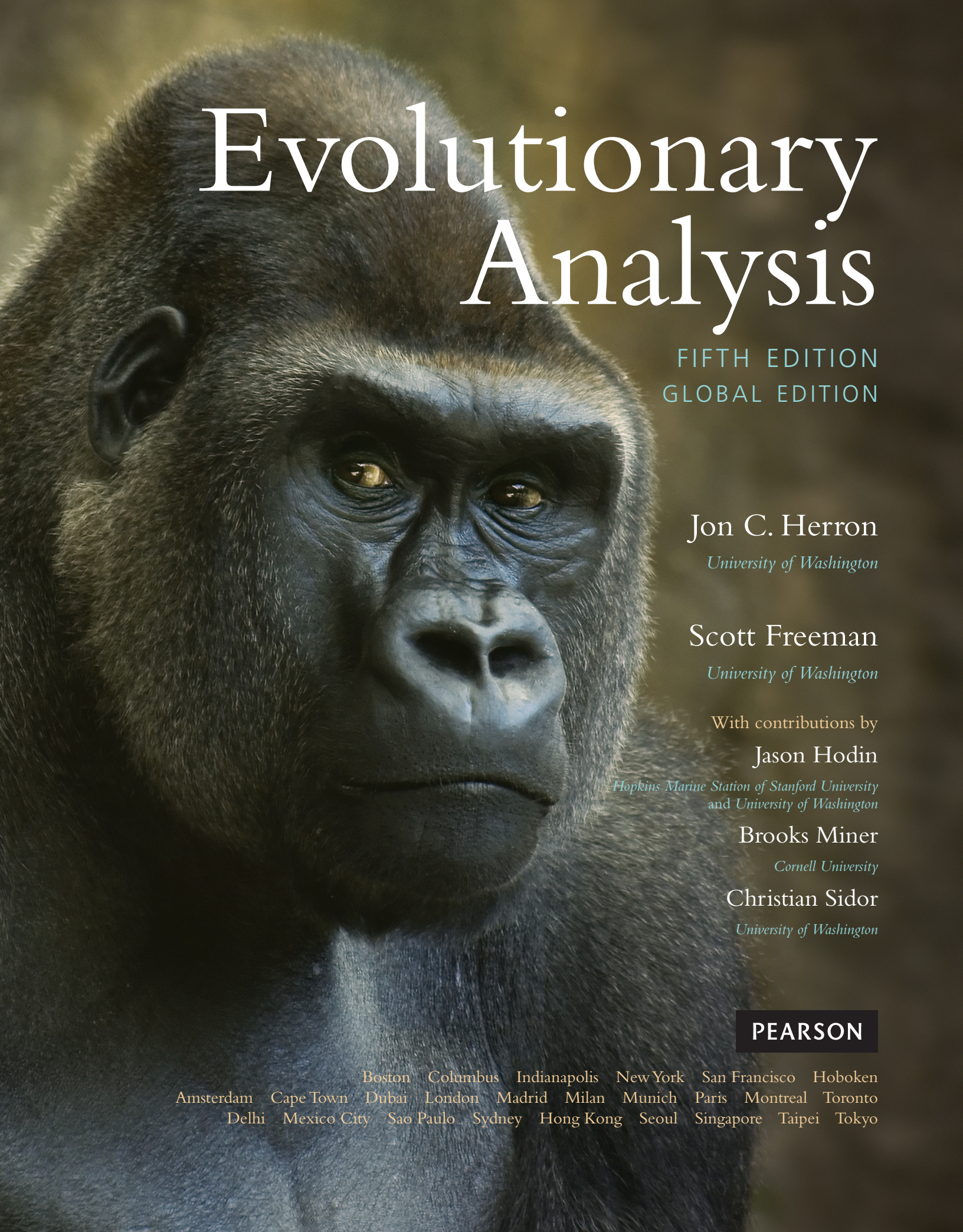
Evolutionary Analysis

FIFTH EDITION

Jon C. Herron • Scott Freeman

ALWAYS LEARNING

PEARSON



Evolutionary Analysis

FIFTH EDITION
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plotted on the same scale. The height of each bar represents the frequency of a particular allele.

The Australian populations appear in orange. Each harbors numerous alleles, all of them at fairly low frequency. The populations from Vanuatu, Fiji, Samoa, the Cook Islands, the Society Islands, and the Marquesas appear in purple. They harbor fewer alleles, some of them at higher frequency. The populations from Hawaii, the remotest of the islands the researchers sampled, harbor just two or three alleles each, one of them at high frequency.

The overall pattern across all seven loci was the same. The cricket populations from Hawaii carried significantly less allelic diversity than those from Oceania. The populations from Oceania, in turn, harbored significantly less allelic diversity than those from Australia. This pattern is consistent with dispersal aboard Polynesian boats, and with genetic drift in the form of the founder effect.

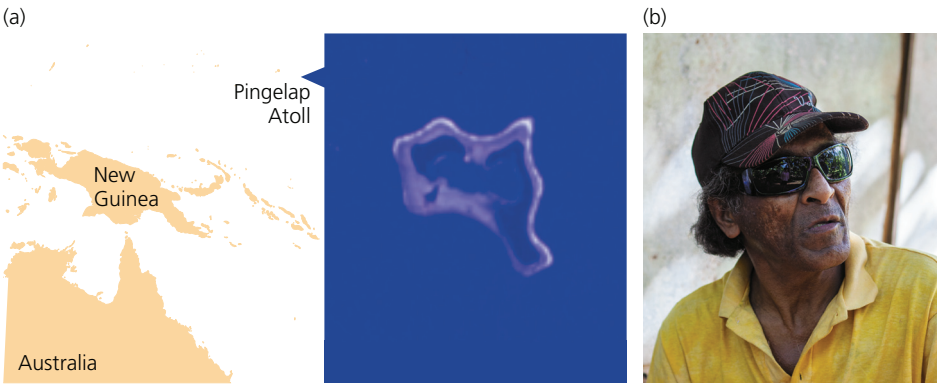

Figure 7.13 Founder effect in a human population
(a) Pingelap Atoll, photographed from the space shuttle *Challenger* in 1984. Image courtesy of NASA Headquarters. (b) A Pingelapese achromat wearing sunglasses to protect his light-sensitive eyes. Photo by John Amato.

Founder effects are often seen in genetically isolated human populations. For example, the Pingelapese people of the Eastern Caroline Islands, located about 2,700 miles southwest of Hawaii, are descended from 20 survivors of a typhoon and subsequent famine that devastated Pingelap Atoll, shown in Figure 7.13a, in about 1775 (Sheffield 2000). Among the survivors was a heterozygous carrier of a recessive loss-of-function allele of the *CNGB3* gene (Sundin et al. 2000). This gene, located on chromosome eight, encodes one component of a protein crucial to the function of cone cells, the photoreceptors in the retina that give us color vision. We know this survivor was a carrier because four generations after the typhoon, homozygotes for the mutant allele began to appear among his descendants. These individuals have achromatopsia, a condition characterized by complete color blindness, extreme sensitivity to light, and poor visual acuity (Figure 7.13b). Achromatopsia is rare in most populations, affecting less than 1 person in 20,000 (Winick et al. 1999). Among today's 3,000 Pingelapese, however, about 1 in 20 are achromats.

When a new population is founded by a small number of individuals, it is likely that chance alone will cause the allele frequencies in the new population to be different from those in the source population. This is the founder effect.

The high frequency of the achromatopsia allele among the Pingelapese is probably not due to any selective advantage it confers on either heterozygotes or homozygotes. Instead, the high frequency of the allele is simply due to chance. Sampling error by the typhoon, a founder effect, left the allele at a frequency of at least 2.5%. Further genetic drift in subsequent generations carried it still higher, to its current frequency of more than 20%.

Our examples from Polynesian crickets and the Pingelapese illustrate not only the founder effect, but the cumulative nature of genetic drift. In the next section we consider the cumulative consequences of genetic drift in more detail.

Random Fixation of Alleles and Loss of Heterozygosity

We have seen that genetic drift can change allele frequencies in a single generation, and that drift is even more powerful as a mechanism of evolution when its effects are compounded over many generations. We can further investigate the cumulative effects of genetic drift with the same physical model we have used before: closing our eyes and picking gametes from a paper gene pool. Our starting point will be the gene pool in **Figure 7.14a**, with alleles A_1 and A_2 at frequencies of 0.6 and 0.4. We will call the parents who produced this gene pool generation zero. As we did before, we now blindly select gametes to simulate the production of 10 zygotes by random mating. This time, the allele frequencies among the newly formed zygotes turn out to be 0.5 for A_1 and 0.5 for A_2. We will call these zygotes generation one. The reader's own results will likely vary.

To continue the simulation for another generation, we need to set up a new gene pool, with alleles A_1 and A_2 at frequencies of 0.5 and 0.5 (Figure 7.14b). Drawing gametes from this gene pool, we get the zygotes for generation two. Generation two's allele frequencies happen to be 0.4 for A_1 and 0.6 for A_2.

We now set up a gene pool with alleles A_1 and A_2 at frequencies of 0.4 and 0.6 (Figure 7.14c) and draw zygotes to make generation three. Generation three's allele frequencies are 0.45 for A_1 and 0.55 for A_2.

Now we need a gene pool with alleles A_1 and A_2 at frequencies of 0.45 and 0.55, and so on. The advantage of using a computer to simulate drawing gametes from gene pools is rapidly becoming apparent. We can have the computer run the simulation for us generation after generation for as long as we like, then plot graphs tracing the frequency of allele A_1 over time.

Graphs in **Figure 7.15a**, b, and c show the results of 100 successive generations of genetic drift in simulated populations of different sizes. Each graph tracks allele frequencies in eight populations. Every population starts with allele frequencies of 0.5 for A_1 and 0.5 for A_2. The populations tracked in graph (a) have just 4 individuals each, the populations tracked in graph (b) have 40 individuals each, and the populations tracked in graph (c) have 400 individuals each. Three patterns are evident:

1. Because the fluctuations in allele frequency from one generation to the next are caused by random sampling error, every population follows a unique evolutionary path.
2. Genetic drift has a more rapid and dramatic effect on allele frequencies in small populations than in large populations.
3. Given sufficient time, genetic drift can produce substantial changes in allele frequencies even in populations that are fairly large.

Note that if genetic drift is the only evolutionary mechanism at work in a population—if there is no selection, no mutation, and no migration—then sampling error causes allele frequencies to wander between 0 and 1. This wandering is particularly apparent in the population whose evolution is highlighted in the graph in Figure 7.15b. During the first 25 generations, allele A_1's frequency rose from 0.5 to over 0.9. Between generations 25 and 40 it dropped back to 0.5. Between generations 40 and 80 the frequency bounced between 0.5 and 0.8. Then the frequency of A_1 dropped precipitously, so that by generation 85 it hit 0 and A_1 disappeared from the population altogether. The wandering of allele frequencies produces two important and related effects: (1) Eventually alleles drift to fixation or loss, and (2) the frequency of heterozygotes declines.

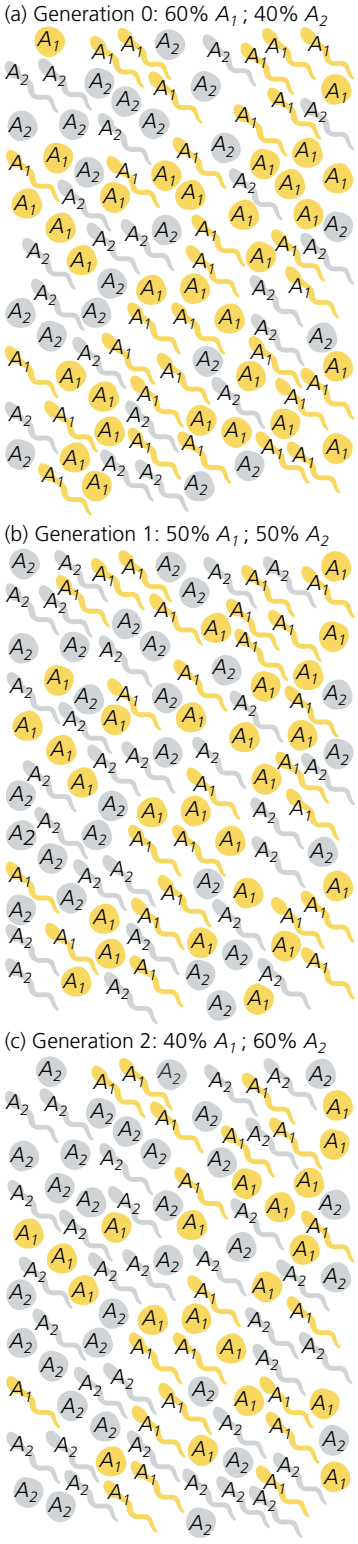

Figure 7.14 Modeling the cumulative effects of drift The gametes that make each generation's zygotes are drawn, with sampling error, from the previous generation's gene pool.

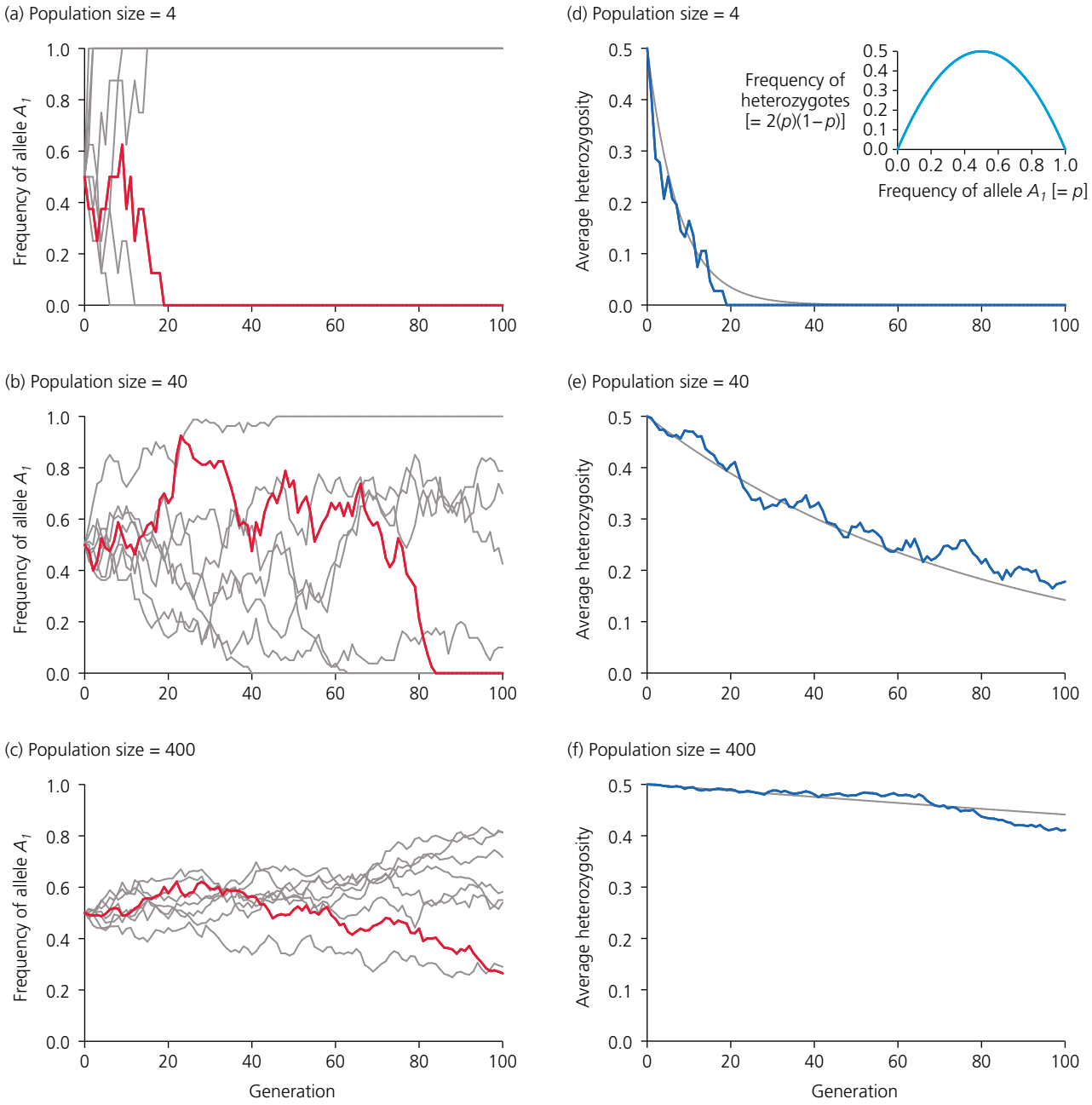

Figure 7.15 Simulations of genetic drift in populations of different sizes Plots (a), (b), and (c) show the frequency of allele A_1 across 100 generations. Eight populations are tracked in each plot, one of them highlighted in red. Plots (d), (e), and (f) show the average frequency of heterozygotes over 100 generations in the same sets of simulated populations. The gray curves represent the rate of decline predicted by theory. The inset in plot (d) shows the frequency of heterozygotes in a population in Hardy–Weinberg equilibrium, calculated as 2 (*p*)(1-*p*), where *p* is the frequency of allele A_1. Collectively, the graphs in this figure show that (1) genetic drift leads to random fixation of alleles and loss of heterozygosity; and (2) drift is a more potent mechanism of evolution in small populations.

Random Fixation of Alleles

As any allele drifts between frequencies of 0 and 1.0, sooner or later it will meet an inevitable fate: Its frequency will hit one boundary or the other. If the allele's frequency hits 0, then the allele is lost forever (unless it is reintroduced by mutation or migration). If the allele's frequency hits 1, then the allele is said to be

COMPUTING CONSEQUENCES 7.3

The probability that a given allele will be the one that drifts to fixation

Sewall Wright (1931) developed a detailed theory of genetic drift. Among many other results, he showed that the probability that a given allele will be the one that drifts to fixation is equal to that allele's initial frequency. Wright's model of genetic drift is beyond the scope of this book, but we can provide an intuitive explanation of fixation probabilities.

Imagine a population of N individuals. This population contains a total of $2N$ gene copies. Imagine that every one of these gene copies is a unique allele. Assume that drift is the only mechanism of evolution at work.

At some point in the future, one of the $2N$ alleles will drift to fixation, and all the others will be lost. Each allele must have an equal chance of being the one that drifts to fixation; that is what we meant when we assumed that drift is the only mechanism of evolution at work. So we have $2N$ alleles, each with an equal probability of becoming fixed. Each allele's chance must therefore be $\frac{1}{2N}$.

Now imagine that instead of each allele being unique, there are x copies of allele A_1, y copies of allele A_2, and z copies of allele A_3. Each copy of allele A_1 has a $\frac{1}{2N}$ chance of being the one that drifts to fixation. Therefore, the overall probability that a copy of allele A_1 will be the allele that drifts to fixation is

$$x \times \frac{1}{2N} = \frac{x}{2N}$$

Likewise, the probability that the allele that drifts to fixation will be a copy of A_2 is $\frac{y}{2N}$, and the probability that a copy of allele A_3 will be the allele that drifts to fixation is $\frac{z}{2N}$.

Notice that $\frac{x}{2N}$, $\frac{y}{2N}$, and $\frac{z}{2N}$ are also the initial frequencies of A_1, A_2, and A_3 in the population. We have shown that the probability that a given allele will be the one that drifts to fixation is equal to that allele's initial frequency.

fixed, also forever. Among the eight populations tracked in Figure 7.15a, allele A_1 drifted to fixation in five and to loss in three. Among the populations tracked in Figure 7.15b, A_1 drifted to fixation in one and loss in three. It is just a matter of time before A_1 will become fixed or lost in the other populations as well. As some alleles drift to fixation and others to loss, the allelic diversity in a population falls.

Now imagine a finite population where several alleles are present at a particular locus: A_1, A_2, A_3, A_4, and so on. If genetic drift is the only evolutionary mechanism at work, then eventually one of the alleles will drift to fixation. At the same moment one allele becomes fixed, the last of the others will be lost.

We would like to be able to predict which alleles will meet which fate. We cannot do so with certainty, but we can give odds. Sewall Wright (1931) proved that the probability that any given allele in a population will be the one that drifts to fixation is equal to that allele's initial frequency (see **Computing Consequences 7.3**). If, for example, we start with a finite population in which A_1 is at a frequency of 0.73, and A_2 is at a frequency of 0.27, there is a 73% chance that the allele that drifts to fixation will be A_1 and a 27% chance that it will be A_2.

Under genetic drift, every population follows a unique evolutionary path. Genetic drift is rapid in small populations and slow in large populations. If genetic drift is the only evolutionary process at work, eventually one allele will drift to a frequency of 1 (that is, to fixation) and all other alleles will be lost.

Loss of Heterozygosity

As allele frequencies in a finite population drift toward fixation or loss, the frequency of heterozygotes decreases. Graphs (d), (e), and (f) in Figure 7.15 show the decline in the frequency of heterozygotes in our simulated populations.

To see why the frequency of heterozygotes declines, look at the inset in graph (d). The inset plots the frequency of heterozygotes in a random mating population

as a function of p, the frequency of allele A_1. Random mating allows us to calculate the frequency of heterozygotes as $2(p)(1 - p)$. The frequency of heterozygotes has its highest value, 0.5, when A_1 is at frequency 0.5. As the frequency of A_1 drops toward 0 or rises toward 1, the frequency of heterozygotes falls. If the frequency of A_1 reaches 0 or 1, the frequency of heterozygotes falls to 0.

Now look at graphs (a), (b), and (c). In any given generation, the frequency of A_1 may move toward or away from 0.5 in any particular population (so long as A_1 has not already been fixed or lost). Thus the frequency of heterozygotes in any particular population may rise or fall. But the overall trend across all populations is for allele frequencies to drift away from intermediate values and toward 0 or 1. So the average frequency of heterozygotes, across populations, should tend to fall.

Finally, look at graphs (d), (e), and (f). In each graph, the blue line tracks the frequency of heterozygotes averaged across the eight populations. The frequency of heterozygotes indeed tends to fall, rapidly in small populations and slowly in large populations. Eventually one allele or the other will become fixed in every population, and the average frequency of heterozygotes will fall to 0.

The frequency of heterozygotes in a population is sometimes called its **heterozygosity.** We would like to be able to predict just how fast the heterozygosity of finite populations can be expected to decline. Sewall Wright (1931) showed that, averaged across many populations, heterozygosity obeys the relationship

As alleles drift to fixation or loss, the frequency of heterozygotes in the population declines.

$$H_{g+1} = H_g\left[1 - \tfrac{1}{2N}\right]$$

where H_{g+1} is the heterozygosity in the next generation, H_g is the heterozygosity in this generation, and N is the number of individuals in the population. The value of $\left[1 - \frac{1}{2N}\right]$ is always between $\frac{1}{2}$ and 1, so the expected frequency of heterozygotes in the next generation is always less than the frequency of heterozygotes in this generation. In Figure 7.15, the gray curves in graphs (d), (e), and (f) show the declines in heterozygosity predicted by Wright's equation.

We can assess the differentiation among a set of populations due to genetic drift by calculating F_{ST}, a statistic we mentioned earlier. It is defined as follows:

$$F_{ST} = \frac{H_T - H_S}{H_T}$$

where H_T is the expected heterozygosity under Hardy–Weinberg equilibirum in a total population created by combining all of our separate populations, and H_S is the average across separate populations (also known as subpopulations) in their expected heterozygosities. At the start of the simulation depicted in graph (a), F_{ST} is zero, because both H_T and H_S are 0.5. By the end, F_{ST} is 1, because—with all subpopulations fixed—H_S is 0. F_{ST} is sometimes called the **fixation index.**

To appreciate just one implication of the inevitable loss of heterozygosity in finite populations, imagine you are managing a captive population of an endangered species. Suppose there are just 50 breeding adults in zoos around the world. Even if you could transport adults or semen to accomplish random mating, you would still see a loss in heterozygosity of 1% every generation due to genetic drift.

An Experiment on Random Fixation and Loss of Heterozygosity

Our discussion of random fixation and heterozygosity loss has so far been based on simulated populations and mathematical equations. Peter Buri (1956) studied these phenomena empirically, in laboratory populations of the fruit fly *Drosophila melanogaster*. Adopting an approach used earlier by Kerr and Wright (1954), Buri

established 107 populations of flies, each with eight females and eight males. All the founders were heterozygotes for an eye-color gene called *brown*. They all had the genotype bw^{75}/bw. Thus, in all 107 populations, the initial frequency of the bw^{75} allele was 0.5. Buri maintained these populations for 19 generations. For every population in every generation, Buri kept the population size at 16 by picking eight females and eight males at random to be the breeders for the next generation.

What results would we predict? If neither allele bw^{75} nor allele *bw* confers a selective advantage, we expect the frequency of allele bw^{75} to wander at random by genetic drift in every population. Nineteen generations should be enough, in populations of 16 individuals, for many populations to become fixed for one allele or the other. Because allele bw^{75} has an initial frequency of 0.5, we expect it to be lost about as often as it becomes fixed. As bw^{75} is drifting toward fixation or loss in each population, we expect the average heterozygosity across all populations to decline. The rate of decline should follow Wright's equation, given in the previous section.

Buri's results confirm these predictions. Each small graph in **Figure 7.16** is a histogram summarizing the allele frequencies in all 107 populations in a particular generation. The horizontal axis represents the frequency of the bw^{75} allele, and the vertical axis represents the number of populations showing each frequency. The frequency of bw^{75} was 0.5 in all populations in generation zero, which is not shown in the figure. After one generation of genetic drift, most populations still had an allele frequency near 0.5, although one had an allele frequency as low as 0.22 and another had an allele frequency as high as 0.69. As the frequency of bw^{75} rose in some populations and fell in others, the distribution of allele frequencies rapidly spread out. In generation four, the frequency of bw^{75} hit 1 in a population for the first time. In generation six, the frequency of bw^{75} hit 0 in a population for the first time. As the allele frequency reached 0 or 1 in ever more populations, the distribution of frequencies became U-shaped. By the end of the experiment, bw^{75} had been lost in 30 populations and had become fixed in 28. The 30:28 ratio of losses to fixations is very close to the 1:1 ratio we would predict under genetic drift. During Buri's experiment there was dramatic evolution in nearly all 107 of the fruit fly populations, but natural selection had nothing to do with it.

The genetic properties of *brown* were such that Buri could identify all three genotypes from their phenotypes. Thus Buri was able to directly assess the frequency of heterozygotes in each population. All the founding flies

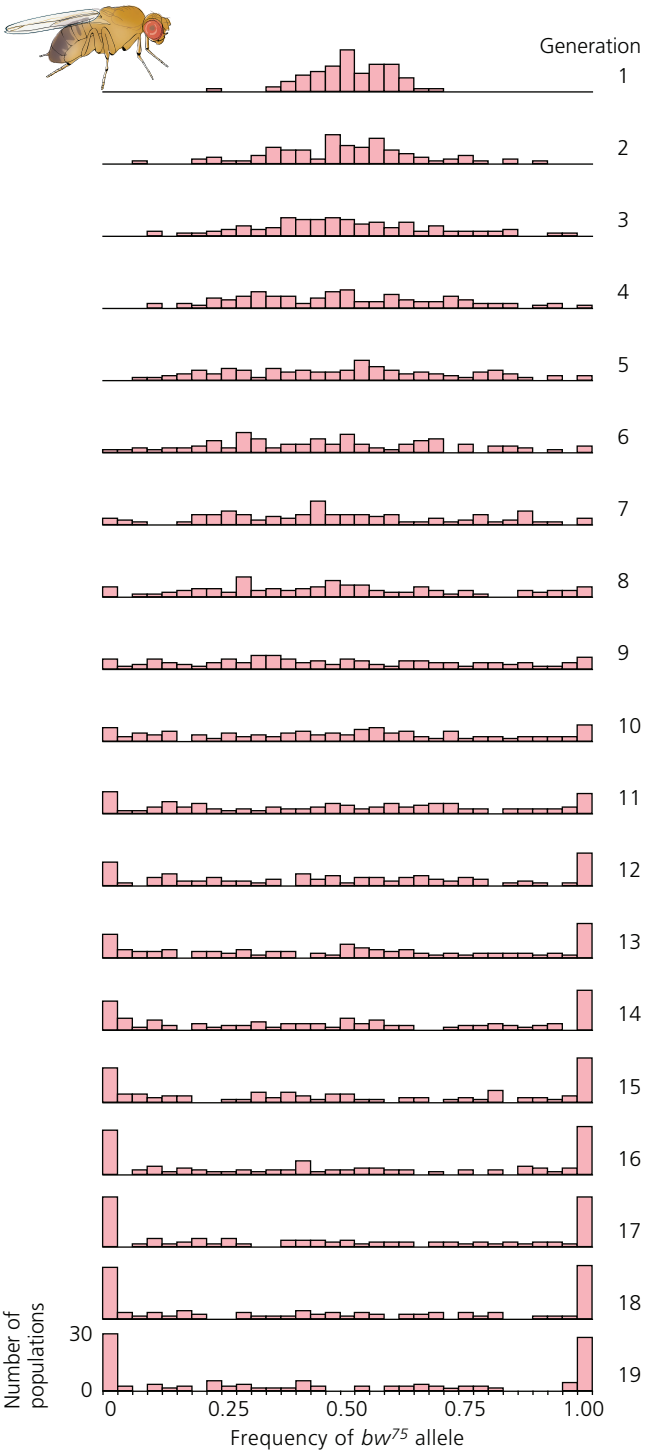

Figure 7.16 Drift in 107 populations of 16 flies Each histogram summarizes allele frequencies in all 107 populations in a particular generation. The horizontal axis represents the frequency of the bw^{75} allele; the vertical axis represents the number of populations showing each frequency. The frequency of bw^{75} was 0.5 in all populations in generation zero (not shown). By generation 19, bw^{75} had been lost from 30 populations, and fixed at a frequency of 100% in 28 populations. From data in Buri (1956), after Ayala and Kiger (1984).