CHAPTER 7 Answers to Problems

Problem 7.1. The effect of 10% of southern elephant seal bulls doing all of the breeding can be estimated using expression 7.2. Let's examine the case of a local population that consists of 50 males and 50 females. If all individuals had equal probability of reproducing, then the effective population size would be 100:

$$N_e = \frac{4 N_f N_m}{N_f + N_m} = \frac{4(50)(50)}{50 + 50} = 100$$

However, if only 10% of all bulls participated in the mating (0.10 x 50 = 5), then

$$N_e = \frac{4(50)(5)}{50 + 5} = 18.2$$

Thus, the N_e of population in which only 10% of the males breed would be reduced 82% to approximately 18% (18.2/100) that of a population in which all males participate in the mating. We would get the same proportional effect (that is, an 82% reduction in N_e) no matter what size population we considered in cases where only 10% of the males breed.

Problem 7.3. We can solve this problem using expression 7.9:

$$N_e = \frac{t}{\Sigma(\frac{1}{N_i})}$$

It will take 10 generations of doubling in size before the population size reaches 1,000.

$$N_e = \frac{t}{\Sigma(\frac{1}{N_i})} = \frac{10}{(\frac{1}{2} + \frac{1}{4} + \frac{1}{8} + \frac{1}{16} + \frac{1}{32} + \frac{1}{64} + \frac{1}{128} + \frac{1}{256} + \frac{1}{512} + \frac{1}{1024})} = \frac{10}{(1023 / 1024)} = 10.01$$

We can substitute this value for N_e (i.e., 10.01) into expression 6.7 to estimate what proportion of the original heterozygosity we expect to retain after 10 generations:

$$h_t = \left(1 - \frac{1}{2N}\right)^t h_o = (1 - \frac{1}{2(10.01)})^{10} = 0.599$$

Thus, we expect to lose approximately 40% of the heterozygosity because of this bottleneck.

We would get very near the same answer if we considered just the first 5 generations after the bottleneck because most of the heterozygosity is lost when the population size is small (<50).

$$N_e = \frac{t}{\Sigma(\dfrac{1}{N_i})} = \frac{5}{(\dfrac{1}{2} + \dfrac{1}{4} + \dfrac{1}{8} + \dfrac{1}{16} + \dfrac{1}{32})} = \frac{5}{(31/32)} = 5.16$$

$$h_t = \left(1 - \frac{1}{2N}\right)^t h_o = (1 - \frac{1}{2(5.16)})^5 = 0.601$$

Problem 7.4. We could screen all of the individuals at a locus to minimize allele frequency change from generation to generation. However, this would be true for only one locus. That is, Mendelian segregation will still occur at the rest of the genome.

We can eliminate Mendelian segregation potentially in captivity by subdividing our population into many inbred lines that are nearly completely homozygous. However, results with inbred lines of mice and other species show that many of these inbred lines will be lost due to the severe inbreeding depression associated with such small population size. See Chapter 14.

Problem 7.6. One-half of the genes in the post-clearcut population will be from the lone maternal tree. Therefore, the frequency of the A_1 and A_2 alleles will each be 0.25. We expect (0.25) x (0.25) = 0.0625 of the individuals in the post-clearcut population to be homozygous A_1A_1, and simililarly 0.0625 of the individuals in the post-clearcut population to be homozygous A_2A_2. Thus, 01.25 of the post-clearcut population to be homozygous.

Problem 7.8. Two.