Answers, assignment 2, BIOL 434

1. The allele is initially present as a single copy in a population of 24 diploid organisms. So its initial frequency is 1/48. Therefore the probability of fixation is 1/48. The probability of loss is 1 - 1/48 = 47/48 = 0.97917. If the locus is X-linked, there are only 36 alleles in the population, so the probability of fixation is 1/36 and the probability of loss is 35/36.

2. The effective population size is 20 diploids. Therefore the change in F is predicted by

$$(1-F_t)=\left(1-\frac{1}{2N_e}\right)^t(1-F_0)=\left(1-\frac{1}{2(20)}\right)^8(1-F_0)=0.817(1-F_0).$$

So F_8= 0.183 + 0.817 F_0.

3. The populations starts with a single heterozygote that selfs. After one generation, the probabilities of the three possible states of the population are: (0.25, 0.5, 0.25) for two A's, one A, and no A's, respectively. You can get this from basic Mendelian genetics of crossing a heterozygote with itself, or by calculating T_{ij} from a Wright-Fisher model. Using the Wright-Fisher model, we get $T_{1,2}$ = 0.25, $T_{1,1}$ = 0.5, and $T_{1,0}$ = 0.25.

(For example, $T_{1,1}=\binom{2}{1}\left(\frac{1}{2}\right)^1\left(1-\frac{1}{2}\right)^{2-1}=0.5$.)

To get the following generations, you need the rest of the possible transition probabilities: $T_{0,2}$ = 0, $T_{0,1}$ = 0, $T_{0,0}$ = 1, $T_{2,2}$ = 1, $T_{2,1}$ = 0, and $T_{2,0}$ = 0.

The probability of a certain number of copies of the A allele after two generations is then:

$$\Pr\left[x\,copies of\;A\,after\,two\,generations\right]=$$

$$\sum\Pr\left[x\,copies of\;A\,after\,two\,generations\mid y\,copies\,after\,one\,generation\right]\Pr\left[y\,copies\,after\,one\,generatio\right.$$

So, for example:

$$\begin{aligned}&\Pr\left[1\ copy\ of\ \ A\ after\ two\ generations\right]\\&\quad = T_{0,1}\Pr\left[zero\,copies\,after\,one\ gen.\right] + T_{1,1}\Pr\left[one\,copy\ after\,one\ gen.\right] + T_{2,1}\Pr\left[two\,copies\,after\,one\ gen.\right]\\&\quad = (0)(0.25) + (0.5)(0.5) + (0)(0.25)\\&\quad = 0.25\end{aligned}$$

The rest of the answer for generation 2 is (0.375, 0.25, 0.375), and for generation 3 is (0.4375, 0.125, 0.4375). The heterozygotes in this case drop by half per generation, as you would expect because the population size is one diploid individual, so 1/2N = 0.5.