

PRACTICE PROBLEMS 5

Answers

1. (a) $H = 1 - [(0.5)^2 + (0.5)^2] = 0.50$ or $2 \times 0.5 \times 0.5 = 0.5$
(b) $H = 0.0198$
(c) $H = 0.80$
(d) $H = 0.187$

The largest value of expected heterozygosity is reached when there are many alleles of similar frequencies. When one allele is in great excess, H is low.

2. (a) $f(c^1) = [309 + (24/2) + (1/2) + (1/2)]/335 = 0.9612$

$$f(c^2) = (1/2)/335 = 0.0015$$

$$f(c^3) = (1/2)/335 = 0.0015$$

$$f(c^4) = (24/2)/335 = 0.0358$$

$$\text{Check: } 0.9612 + 0.0358 + 0.0015 + 0.0015 = 1$$

(b) $H = 0.0748$

(c) Observed heterozygosity is $(24+1+1)/335 = 0.078$, very close to H , suggesting that the population is random mating.

3.

- (a) $1 - 0.001$. With no additional information about the second codon and the role played by the amino acid for which it codes, our best guess is that diversity at that codon is representative of diversity in the gene as a whole.
(b) 1, because this is part of the invariant ATG start codon.

4.

- (a) 0, because all mutations in a pseudogene are neutral.
(b) 1, or nearly so, because the mutants can grow whereas the wild type fitness is 0 or nearly 0.
(c) > -1 and < 0 . The answer is not 0; you can tell that the mutation is detrimental because bacteria normally live in the absence of antibiotic but never become entirely resistant as they would if resistance mutations were neutral and occasionally would be fixed by drift.

5. (a) = (b) $<$, because zoo populations of animals are small and small populations are forced to inbreed.

6. Using $H = 4Neu/(1 + 4Neu)$:

- (a) 0.1667 (b) 0.9524 (c) 0.9995 (d) The last two values are *much* larger than are observed in real life; the first value of Ne is more likely.

7.

- (a) This question can be understood as asking the probability that out of 20 offspring from a cross of A a X A A, what is the probability that none of the offspring will get the mutant allele? The probability that any one offspring will get it is $1/2$, so the answer is $(1/2)^{20} = 9.54 \times 10^{-7}$.
- (b) The probability of fixation is $1/2N = 1/100$, and the probability of loss is $1 - 0.01 = 0.99$.

8.

- (a) No, mutation rates are similar for all sites in a gene, because the factors that cause mutations (replication errors, mutagens) are the same regardless of the function of a site.
- (b) No, synonymous and nonsynonymous refer only to coding sequences.
- (c) No, promoters aren't transcribed.
- (d) Yes; functionally important sequences are difficult to change without bad effect, so an especially large fraction of mutations are detrimental instead of neutral.