

Mathematical Models in Biology An Introduction

by Elizebeth Allman and John A. Rhodes

- 4.2.4. a. $\mathcal{P}(A) \approx .05$, $\mathcal{P}(G) \approx .4$, $\mathcal{P}(C) \approx .3$, $\mathcal{P}(T) \approx .25$
b. $\mathcal{P}(\text{purine}) \approx .45$, $\mathcal{P}(\text{pyrimidine}) \approx .55$
c. G , a purine, is the most likely base. This may, at first, appear to contradict part (b) which shows the base is most likely to be a pyrimidine. However, there is no real contradiction: While G is the most likely base, the probability of either a C or T is higher than that of an A or G .

- 4.2.7. a. not mutually exclusive, independent
b. mutually exclusive, dependent
c. not mutually exclusive, dependent

- 4.2.8. Two mutually exclusive events E_1 and E_2 with positive probabilities can not be independent since $0 = \mathcal{P}(E_1 \cap E_2) \neq \mathcal{P}(E_1)\mathcal{P}(E_2) > 0$. More informally, if

the events cannot occur together, then knowing whether one has occurred does give us information as to whether the other has.

- 4.3.1. a. $\{(F, F), (F, M), (M, F), (M, M)\}$, all with probability .25
b. $3/4$
c. $1/2$
d. $2/3$
e. 1
f. No. Knowledge that one child is female effects the likelihood that the youngest child is female, since $1/2 \neq 2/3$. Alternately, $3/4 \neq 1$ shows that knowledge that the youngest child is female affects the likelihood that one child is female.

- 4.3.8. a. $\mathcal{P}(S_0 = A) = .225$, $\mathcal{P}(S_0 = G) = .275$, $\mathcal{P}(S_0 = C) = .275$, $\mathcal{P}(S_0 = T) = .225$, $\mathcal{P}(S_1 = A) = .225$, $\mathcal{P}(S_1 = G) = .3$, $\mathcal{P}(S_1 = C) = .275$, $\mathcal{P}(S_1 = T) = .2$.
 b. No, since $\mathcal{P}(S_1 = i \text{ and } S_0 = j) \neq \mathcal{P}(S_0 = i)\mathcal{P}(S_1 = j)$. For instance, since $\mathcal{P}(S_1 = i \text{ and } S_0 = j) = (1/40)$ (the (j, i) entry of the table), we find $\mathcal{P}(S_1 = A \text{ and } S_0 = A) = 7/40 = .175 \neq (.225)(.225) = .050625$.
 c. Since the sequences are related and mutations are rare, the appearance of a particular base at a site in S_0 means it is highly probable that the same base would appear at the same site in S_1 , i.e. the events $\{S_0 = i\}$ and $\{S_1 = j\}$ are not independent.
- 4.3.9. a. Since there is no relationship between the two sequences, knowing information about one should convey nothing about the other.
 b. All the columns would be the same.
- 4.3.10. a. The formula calculates the conditional probability of a purine occurring in S_2 given a purine occurred in S_0 by accounting for either a purine or a pyrimidine occurring in the intermediate sequence S_1 .
 $\mathcal{P}(S_2 = pur | S_0 = pur) = \mathcal{P}(S_2 = pur | S_1 = pur) \cdot \mathcal{P}(S_1 = pur | S_0 = pur) + \mathcal{P}(S_2 = pyr | S_1 = pyr) \cdot \mathcal{P}(S_1 = pyr | S_0 = pur)$, etc.
 b. $\mathcal{P}(S_2 = pur | S_0 = pur) = .9606$; $\mathcal{P}(S_2 = pyr | S_0 = pur) = .0394$;
 $\mathcal{P}(S_2 = pur | S_0 = pyr) = .0197$; $\mathcal{P}(S_2 = pyr | S_0 = pyr) = .9803$
 c. Note that with the given assumptions

$$\begin{aligned}
 & \mathcal{P}(S_2 = pur | S_1 = pur) \cdot \mathcal{P}(S_1 = pur | S_0 = pur) \\
 &= \mathcal{P}(S_2 = pur | S_1 = pur \text{ and } S_0 = pur) \cdot \mathcal{P}(S_1 = pur | S_0 = pur) \\
 &= \frac{\mathcal{P}(S_2 = pur \text{ and } S_1 = pur \text{ and } S_0 = pur)}{\mathcal{P}(S_1 = pur \text{ and } S_0 = pur)} \cdot \frac{\mathcal{P}(S_1 = pur \text{ and } S_0 = pur)}{\mathcal{P}(S_0 = pur)} \\
 &= \frac{\mathcal{P}(S_2 = pur \text{ and } S_1 = pur \text{ and } S_0 = pur)}{\mathcal{P}(S_0 = pur)}.
 \end{aligned}$$

Similarly,

$$\begin{aligned}
 & \mathcal{P}(S_2 = pur | S_1 = pyr) \cdot \mathcal{P}(S_1 = pyr | S_0 = pur) \\
 &= \frac{\mathcal{P}(S_2 = pur \text{ and } S_1 = pyr \text{ and } S_0 = pur)}{\mathcal{P}(S_0 = pur)}.
 \end{aligned}$$

Therefore

$$\begin{aligned}
 & \mathcal{P}(S_2 = pur | S_1 = pur) \cdot \mathcal{P}(S_1 = pur | S_0 = pur) \\
 & \quad + \mathcal{P}(S_2 = pur | S_1 = pyr) \cdot \mathcal{P}(S_1 = pyr | S_0 = pur) \\
 &= \frac{\mathcal{P}(S_2 = pur, S_1 = pur, S_0 = pur) + \mathcal{P}(S_2 = pur, S_1 = pyr, S_0 = pur)}{\mathcal{P}(S_0 = pur)} \\
 &= \frac{\mathcal{P}(S_2 = pur, S_0 = pur)}{\mathcal{P}(S_0 = pur)} = \mathcal{P}(S_2 = pur | S_0 = pur).
 \end{aligned}$$

- 4.4.1. a. A plot in the forest can be in the state “occupied by an A tree” or the state “occupied by a B tree.”
 b. All the entries are non-negative and the column sums are one.
 c. (1, 1) entry: the conditional probability that a spot which is occupied by an A tree in one year remains occupied by an A tree the next year; (1, 2) entry: the conditional probability that a spot which is occupied by a B tree in one year is occupied by an A tree the next year; (2, 1) entry: the conditional probability that a spot which is occupied by an A tree in one year is occupied by an B tree the next year; (2, 2) entry: the conditional probability that a spot which is occupied by a B tree in one year remains occupied by an B tree the next year
 d. (.01, .99)

- 4.4.4. a. $\alpha = .06$ is faster.
 b. Yes.
 c. The larger the value of α , the more mutation occurs and the quicker any initial vector \mathbf{p}_0 will move towards equilibrium.

- 4.4.8. a. The first theorem applies to M , but the second does not since M has some zero entries. (However, since M^2 has all non-zero entries, you can apply the second theorem to it.)
 b. (.1849, .3946, .2819, .1386)

4.4.9. a. $\mathbf{p}_0 = (.3, .225, .25, .225)$, $M = \begin{pmatrix} .833 & 0 & 0 & .111 \\ .083 & .889 & 0 & 0 \\ 0 & .111 & 1 & .111 \\ .083 & 0 & 0 & .778 \end{pmatrix}$

- b. \mathbf{p}_0 is reasonable close to (.25, .25, .25, .25). M may seem less close to a Jukes-Cantor matrix than you might expect, because of the variation in the off-diagonal entries. One way to estimate α is to average the off-diagonal entries to estimate $\alpha/3$. This gives $\alpha/3 = .0416$, so $\alpha = .1248$.