

4.2. An Introduction to Probability

- 4.2.1. a-c. Answers may vary.
 d. Generally, the estimates from experiments with more flips should be better, though that is not always the case.
- 4.2.2. a. $(\frac{1}{2})^{10} = .0009765625$
 b. $(\frac{1}{2})^{10} = .0009765625$
 c. People tend to believe (falsely) that a string of ten tails is less likely than any particular run of heads and tails such as that in part (a).
- 4.2.3. a. $p_A \approx .4$, $p_G \approx .6$, $p_C \approx 0$, $p_T \approx 0$
 b. $p_A \approx .4$, $p_G \approx .3$, $p_C \approx .1$, $p_T \approx .2$
 c. $p_A \approx .4$, $p_G \approx .2$, $p_C \approx .25$, $p_T \approx .15$
 d. There are more *G*'s at the beginning of the sequence and more *C*'s towards the end. The *A*'s and *T*'s are more evenly distributed.
- 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*.
- 4.2.5. a. (F, F, F) , (M, F, F) , (F, M, F) , (F, F, M) , (F, M, M) , (M, F, M) , (M, M, F) , (M, M, M) , all with probability $(1/2)^3 = .125$
 b. $\{(F, F, F), (F, M, F), (F, F, M), (F, M, M)\}$, $4(.125) = .5$
 c. $\{(F, M, M), (M, F, M), (M, M, F)\}$, $3(.125) = .375$
 d. 'the family is either all male or has at least two daughters', $\{(F, F, F), (M, F, F), (F, M, F), (F, F, M), (M, M, M)\}$, $5(.125) = .625$
 e. $\{(F, F, F), (M, F, F), (F, M, F), (F, F, M), (M, M, F), (F, M, M), (M, F, M)\}$, $7(.125) = .875$
- 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.
- 4.2.12. a. $\mathcal{P}(\text{change, no change}) + \mathcal{P}(\text{no change, change}) = .02955$
 b. $(\text{no change, no change, nochange})$; $(\text{change, change, no change})$; $(\text{change no change, change})$; $(\text{no change, change, change})$
 c. $4(.985)(.015)^2 = .0008865$

6.1.3. a. $\mathcal{P}(\text{tall wrinkled-seed}) = \mathcal{P}(\text{tall})\mathcal{P}(\text{wrinkled-seed})$. But

$$\begin{aligned}\mathcal{P}(\text{tall}) &= 1 - \mathcal{P}(\text{dwarf}) = 1 - \mathcal{P}(dd) \\ &= 1 - \mathcal{P}(d \text{ from first parent})\mathcal{P}(d \text{ from second parent}) \\ &= 1 - (1/2)(1) = 1/2,\end{aligned}$$

$$\begin{aligned}\mathcal{P}(\text{wrinkled-seed}) &= \mathcal{P}(ww) \\ &= \mathcal{P}(w \text{ from first parent})\mathcal{P}(w \text{ from second parent}) \\ &= (1/2)(1/2) = 1/4.\end{aligned}$$

Therefore $\mathcal{P}(\text{tall wrinkled-seed}) = (1/2)(1/4) = 1/8$.

b. Using the calculations in part (a),

$$\begin{aligned}\mathcal{P}(\text{tall round-seed}) &= \mathcal{P}(\text{tall})\mathcal{P}(\text{round-seed}) \\ &= \mathcal{P}(\text{tall})(1 - \mathcal{P}(\text{wrinkled-seed})) \\ &= (1/2)(1 - 1/4) = 3/8.\end{aligned}$$

6.1.4. a. Since the probability of having the allele is $1/31$ for the male and also $1/31$ for the female, assuming these are independent the probability is $(1/31)^2 \approx .00104$.

b. Since the child must inherit the recessive allele from each parent, the probability is $(1/2)(1/2) = 1/4$.

c. $(1/31)^2(1/4) \approx .0002601$.

6.1.5. a. Four - ABC , aBC , AbC , and abc .

b. 9 genotypes are possible: $AABBCC$, $AaBBCC$, $aaBBCC$, $AABbCC$, $AaBbCC$, $aaBbCC$, $AAbbCC$, $AabbCC$, $aabbCC$. 4 phenotypes are possible: the offspring could have the dominant or recessive phenotype from either of the first two genes, but must have the dominant phenotype from the third.

6.1.7. a. $AA \times aa$ dominant:recessive=1:0; $Aa \times aa$ dominant:recessive=1:1; $aa \times aa$ dominant:recessive=0:1.

b. $DdwwYY$

c. Crossing with a homozygous recessive allows all parental alleles to manifest themselves in phenotypes of the progeny, whereas crossing with a homozygous dominant would result only in progeny of the dominant phenotypes. Quantitatively, the ratios in part (a) are all different, so the parental phenotype can be distinguished, while for a cross with a homozygous dominant, all ratios would be dominant:recessive=1:0. The parental phenotype has no effect.

6.1.10. The cross is $Y^l y \times Y^l y$. Embryo genotype ratios will be $Y^l Y^l : Y^l y : yy = 1:2:1$, but only the last two genotypes will be born. Thus the viable progeny will have genotypes $Y^l y$ or yy , with respective phenotypes yellow and agouti, in proportions $2/3$ and $1/3$.

6.1.12. a. The trait is dominant. If it were recessive, all children of the parents would exhibit brachydactyly. The parents must each be heterozygotes, since one child has normal length fingers. The child with normal length fingers is a homozygous recessive. The child with short fingers is either homozygous dominant or heterozygous.

b. The probability that one child has normal fingers is $1/4$, and since the two children's phenotypes are independent, the probability that both have normal length fingers is $(1/4)^2 = 1/16$.