

$$1a. P(AGG) = \left(\frac{1}{4}\right)\left(\frac{1}{4}\right)\left(\frac{1}{4}\right)$$

$$P(AGG) = \frac{1}{64}$$

$$b. P(GAT) = \left(\frac{1}{4}\right)\left(\frac{1}{4}\right)\left(\frac{1}{4}\right)$$

$$P(GAT) = \frac{1}{64}$$

$$c. P(A|GAA) = \frac{P(A, GAA)}{P(GAA)}$$

$$= \frac{P(A) \cdot P(GAA)}{P(GAA)}$$

$$= \frac{P(GAA)}{P(GAA)}$$

$$= \left(\frac{1}{4}\right)\left(\frac{1}{16}\right)$$

$$= \left(\frac{1}{64}\right)$$

$$P(A|GAA) = \frac{1}{4}$$

$$2a. P(AGG) = \left(\frac{2}{8}\right)\left(\frac{2}{7}\right)\left(\frac{1}{6}\right)$$

$$P(AGG) = \frac{1}{84}$$

$$b. P(GAT) = \left(\frac{2}{8}\right)\left(\frac{2}{7}\right)\left(\frac{2}{6}\right)$$

$$P(GAT) = \frac{1}{42}$$

$$c. P(A|GAA) = \frac{P(A, GAA)}{P(GAA)}$$

$$P(GAA) = \frac{2}{8} \cdot \frac{2}{7} \cdot \frac{1}{6}$$

$$P(A|GAA) = \frac{0}{\left(\frac{1}{84}\right)}$$

$$d. P(G|GAA) = \frac{P(G, GAA)}{P(GAA)}$$

$$= \frac{\left(\frac{2}{8}\right)\left(\frac{1}{84}\right)}{\frac{1}{84}}$$

$$P(G|GAA) = \frac{1}{5}$$

3a. The DNA polymerase used in amplifying the DNA could have incorporated the wrong complementary nucleotide. In this case a G was added instead of an A when building the reverse complementary strand in sequencing.

- b. d_1 is more likely to show up as an error b/c the error occurs at the last nucleotide base whereas in d_2 , it's likely a SNP. There is likely a desynchronization of the terminators in d_1 b/c if it happened in d_2 , the downstream nucleotides would be incorrect too.