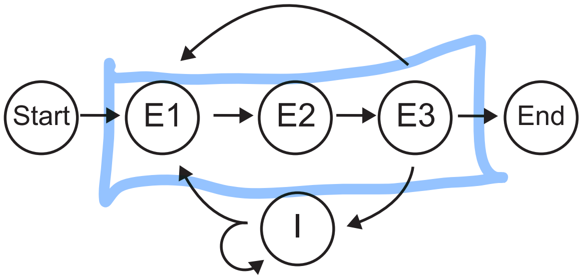
The DNA sequence of a gene determines the amino acid sequence of the protein it produces, with every 3 DNA basepairs coding for one protein amino acid. In eukaryotes, predicting the protein sequence from a gene sequence is not as simple as taking the gene sequence and splitting it into 3's, because of *introns*, stretches of gene sequence that do not code for amino acids. (The regions of DNA in a gene that are not introns are called exons.)

A Markov chain model has been used to detect introns, assuming the 6 states shown in the diagram. The index set here does not represent time, but rather represents basepairs: Each increment is the transition from the previous basepair to the neighboring basepair.



i. Suppose a newly-discovered species has the following properties:

   - The average protein is $L_g = 20000$ amino acids long (i.e., it is 60,000 basepairs long, not counting introns).
   - The average protein-coding gene has $N_I = 10$ introns.
   - The average intron is $L_I = 6000$ basepairs long.

   Write the 6-state Markov transition matrix. The matrix should contain numerical values (e.g., expressed as a fraction or decimal).

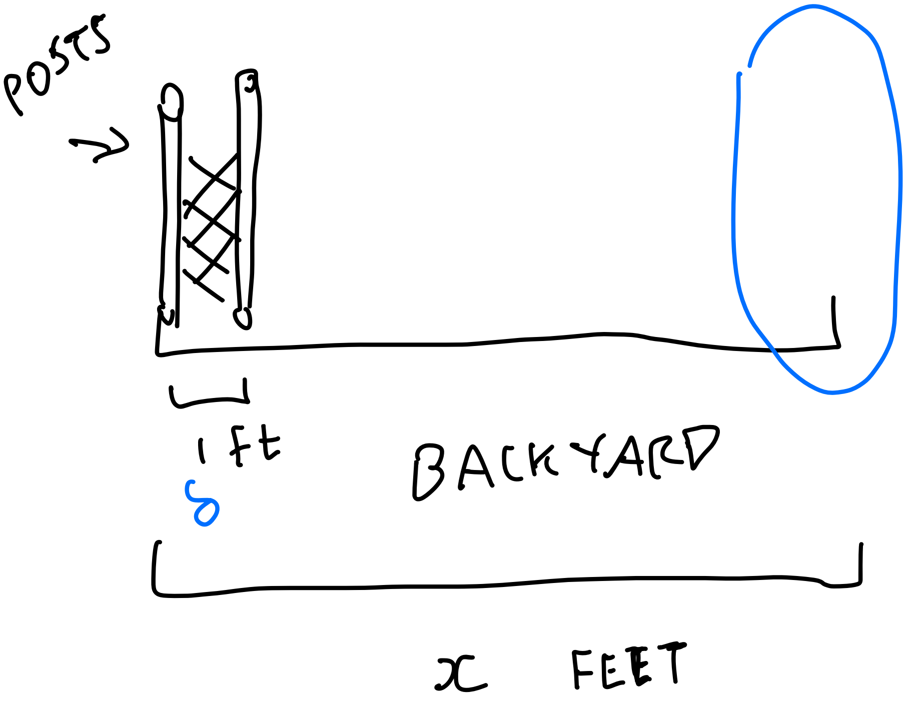
ii. Under the assumptions of this model, what is the average length of a gene, including introns?

START E1 E2 E3 I END

$$M = \begin{array}{c} \left[\begin{array}{cccccc} 0 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & \square & \square & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 1\ 0\ ? \\ 0 & 0 & 0 & \square & \square & 0 \\ 0 & 0 & 0 & \square & 0 & 1 \end{array}\right] \end{array} \begin{array}{l} \cdot\ \text{START} \\ \cdot\ E_1 \\ \cdot\ E_2 \\ \cdot\ E_3 \\ \cdot\ I \\ \cdot\ \text{END} \end{array}$$

6×6

FENCEPOST


POSTS
1 ft
δ
BACKYARD
x FEET