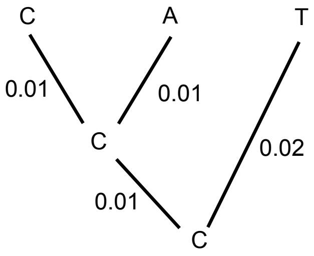
Exercise 1: A thumbtack has a certain probability p to land with the pin pointing up when you toss it.

(a) You toss the thumbtack 10 times. Plot as a function of p the probability that in exactly 6 of the 10 tosses the pin points up.

(b) You tossed the thumbtack 100 times. Sixty times the pin pointed up and 40 times it pointed down. Plot the likelihood function of p.

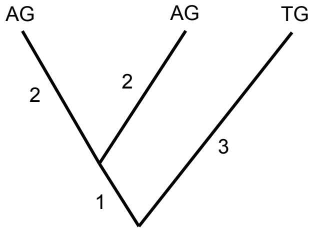
Exercise 2: The labels at the branches of this tree are probabilities that the nucleotide in the daughter node is a different from that in the mother node. If the nucleotide is different in the daughter node, each of the three possible nucleotides has a probability of 1/3. Assume that the nucleotide in the root has been drawn according to the uniform distribtion, that is, each nucleotide type with probability 1/4. Calculate the probability that this process leads to the shown nucleotides.



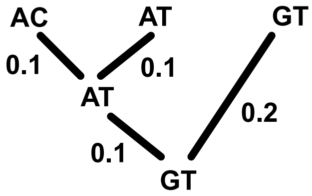
Exercise 3: The labels at the branches are branch lengths ℓ with the following property: If the nucleotide in the mother node is x and y is a different nucleotide ($y \neq x$), then the probability that the nucleotide in the daughter node is y (in the same alignment position) can be calculated with the formula

$$\frac{1}{4} \cdot \left(1 - e^{-\ell/80}\right).$$

Assume that two sequence positions evolved independently along the tree according to this model, with each position starting in the root with a random nucleotide according to the uniform distribution. Calculate the probability that this process leads to the sequences that are shown at the tipps of the tree.



Exercise 4: Calculate the probability for this sequence data set according to the Jukes-Cantor model, given the tree for the following cases:



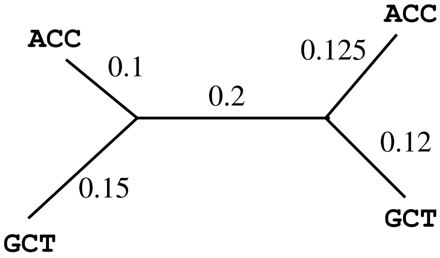
(a) The rate of events in which a nucleotides forgets its type and is replaced by a nucleotide randomly drawn from $\{$A,C,G,T$\}$ is 0.5 for each site.

(b) The rate of actual mutations in which a nucleotides change their type is 0.5 for each site.

(c) If x is the current nucleotide and y is any of the three other nucleotides, then the rate at which x is changed into y is 0.5 for each site.

(d) Now assume that the sequences at the internal nodes are unknown and apply the Felsenstein pruning algorithm to calculate the likelihood of the tree for the given data at the three tips of the tree. For this, assume that the rate of events in which a nucleotides forgets its type and is replaced by a nucleotide randomly drawn from $\{$A,C,G,T$\}$ is 0.5 for each site.

Exercise 5: Compute the likelihood of the following tree given the sequences that are labeled to its tips in a sequence evolution model with uniform base frequencies, transversion rate 0.0 and transition rate 0.3.



Exercise 6: Let $X_1, X_2, X_3, \ldots$ be a Markov chain on a state space $\mathcal{Z} = \{a, b, c\}$ with the following matrix of transition probabilities $P_{y \to z} = \Pr(X_{n+1} = z \mid X_n = y)$:

$$P = \begin{pmatrix} P_{a\to a} & P_{a\to b} & P_{a\to c} \\ P_{b\to a} & P_{b\to b} & P_{b\to c} \\ P_{c\to a} & P_{c\to b} & P_{c\to c} \end{pmatrix} = \begin{pmatrix} 0.5 & 0.2 & 0.3 \\ 0.3 & 0.4 & 0.3 \\ 0.4 & 0.1 & 0.5 \end{pmatrix}$$

(a) Calculate the equilibrium distribution of this Markov chain.

(b) Will this Markov chain converge against its stationary distribution?

(c) Is this Markov chain reversible?