1. Suppose we have a population 5 made up of type A and type B individuals. Let i be the number of type A individuals. Suppose in each time step the probability of the number of A's increasing by 1 is $\frac{1}{3}$, and the probability of the number decreasing by 1 is $\frac{2}{3}$. In addition, assume if we ever reach a state with 0 A's or 5 A's then no further changes happen. If we start with 1 A and 4 B's what is the probability we end up with 5 A's? If we start with 4 A's and 1 B, what is the probability we end up with 0 A's?

2. In the maximum parsimony method we build a phylogenetic tree for a number of different taxa by comparing bases at each site of the aligned sequences. We only need to consider sites where at least two different bases occur at least twice. These sites are called informative sites. For example, with 5 sequences, the following site with bases A,A,G,G,C is informative, but the site with bases A,G,G,G,C is not. Draw 3 different trees with 5 taxa and convince yourself that the first site can have trees with different parsimony numbers, but that the parsimony number for the second site will always be 2.

3. Given the five aligned sequences corresponding to five different taxa

$$S1: \quad AGCTGACGTTAACCG$$
$$S2: \quad GGCTGAACTTAACTG$$
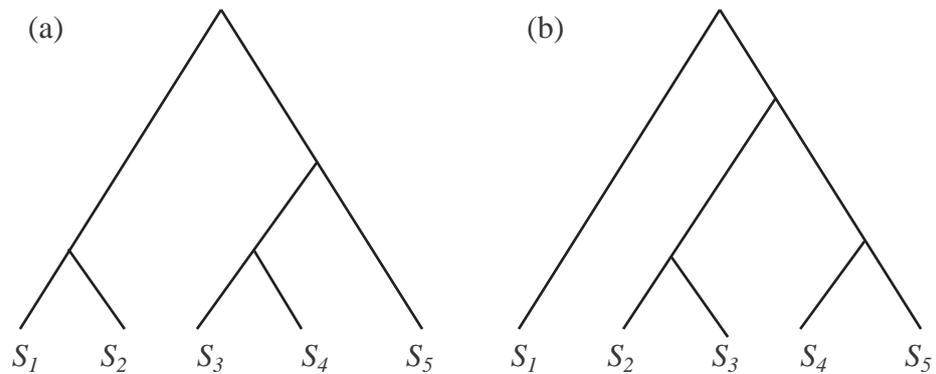$$S3: \quad ATATCAGCCGCACCG$$
$$S4: \quad ATATTAGCCTCACCG$$
$$S5: \quad AGATTAGTGTTACCG$$

(a) Circle all the informative sites

(b) Of the informative sites, how many give distinct information about the parsimony of a tree? (ie how many distinct patterns are there?)

(c) Using only informative sites determine which of the trees below is most parsimonious.

(e) Find the parsimony number for one other tree.

(f) Explain why no tree could have a parsimony number less than 8.

4. Use the average distance method (UPGMA) to determine the phylogenetic tree for the five taxa listed in the phylogenetic distance table below

	A	B	C	D	E
A		0.4	0.2	0.7	0.3
B			0.6	0.4	0.4
C				0.5	0.5
D					0.3