1. UPGMA is one of the oldest methods for the reconstruction of phylogenetic trees. In UPGMA sequences are grouped into clusters as the tree is constructed, each cluster being defined as the set of all descendants of the new node just added. Initially, all sequences are regarded as defining their own cluster. At each stage, the two clusters with the shortest evolutionary distance are combined into a new cluster. The tree is complete when all the sequences belong to the same cluster, whose node is the root of the tree.

The following figure shows the distance matrix for six operational taxonomic units. Give the final tree based on the information of that matrix. Label the operational taxonomic units and the length of each branch. Remember to list all the intermediate distance matrices.

d_{ij}	A	B	C	D	E	F
A	—	6	8	1	2	6
B		—	8	6	6	4
C			—	8	8	8
D				—	2	6
E					—	6

2. The underlying idea of maximum parsimony method is that the best topology is the one requiring the smallest number of changes to explain the observed data. The following figure shows an alignment of four DNA sequences, along with the three possible unrooted topologies for the four sequences. Which tree is the best estimate of the true phylogeny? Explain your result.