1. Given $S_1 = \text{CCGT GTTTCA}$, $S_2 = \text{GTGGCCA}$, $S_3 = \text{GTCCGCGCGGG}$, and $S_4 = \text{CGT CCCAGT T T}$, perform the center star alignment computation using the following score function, $s(a, b) = 0$ if $a = b$, $s(a, b) = 1$ if $a \neq b$, and $s(a, -) = s(-, b) = 1$. Write down the center sequence and the intermediate alignments.

2. Given four species $\{A, B, C, D\}$ with a distance defined as: $d(A, B) = 10$, $d(A, C) = 13$, $d(A, D) = 18$, $d(B, C) = 6$, $d(B, D) = 13$, $d(C, D) = 12$. Use the neighbour-joining algorithm to produce the evolutionary tree of $\{A, B, C, D\}$.

3. Let $T$ be a labelled binary phylogenetic tree with $n \geq 3$ leaves, prove that there are $\prod_{j=3}^{n} (2j - 5)$ different trees.

4. In UPGMA clustering algorithm, the distance between two clusters $C_i$ and $C_j$ can be defined as the average distance between pair of objects from each cluster:

$$d_{ij} = \frac{1}{|C_i||C_j|} \sum_{p \in C_i, q \in C_j} d_{pq}.$$ 

Prove that if $C_k$ is the union of $C_i$ and $C_j$ and if $C_l$ is any other cluster, then

$$d_{kl} = \frac{d_{il}|C_i| + d_{jl}|C_j|}{|C_i| + |C_j|}.$$ 

5. The consensus model of multiple alignment is a special case of tree alignment. Simplify the 2 approximation tree alignment algorithm proof to show a 2 approximation consensus multiple alignment algorithm proof.

6. (optional) Show that, in UPGMA algorithm, a node is always lies above its child nodes.