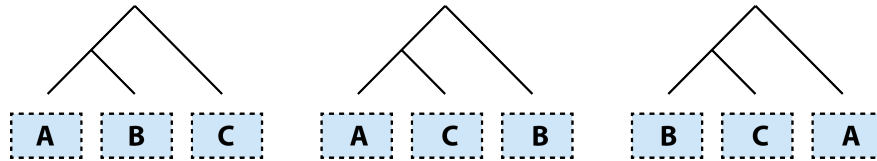


9 Exercise solutions – Phylogenetic tree

1. Tree topology

A rooted phylogenetic tree can have three topologically different trees when m is 3.

(a) Fill the labels A, B, or C to satisfy three topologically distinct trees.



2. UPGMA

UPGMA is an unweighted version of PGMA (pair-group method using arithmetic mean) for reconstructing a phylogenetic tree. Pairwise sequence alignments are used to calculate the distances among four sequences A, B, C, and D.

| | A | B | C | D |
|---|---|---|---|---|
| A | 0 | 2 | 7 | 7 |
| B | | 0 | 5 | 9 |
| C | | | 0 | 8 |
| D | | | | 0 |

Below are two examples of the distance calculation that can be used for UPGMA.

$$d_{(\alpha\beta),\gamma} = \frac{d_{\alpha,\gamma} + d_{\beta,\gamma}}{2}$$

$$d_{(\alpha\beta\gamma),\delta} = \frac{d_{\alpha,\delta} + d_{\beta,\gamma} + d_{\delta,\gamma}}{3}$$

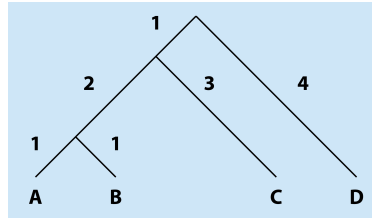
(a) Identify the first internal node and update the distance matrix.

| | (AB) | C | D |
|------|------|---|---|
| (AB) | 0 | 6 | 8 |
| C | | 0 | 8 |
| D | | | 0 |

(b) Identify the second internal node and update the distance matrix accordingly.

| | (ABC) | D |
|-------|-------|---|
| (ABC) | 0 | 8 |
| D | | 0 |

(c) Reconstruct a rooted tree from the calculated distances.



(d) Reconstruct a rooted tree by using UPGMA.

| | A | B | C | D |
|---|---|---|---|---|
| A | 0 | 2 | 6 | 8 |
| B | | 0 | 6 | 8 |
| C | | | 0 | 8 |
| D | | | | 0 |

(e) Calculated the Cavalli-Sforza and Edwards criterion.

$$\sum_{i,j} (M_{i,j} - d_{i,j})^2$$

Solution:

$$\sum_{i,j} (M_{i,j} - d_{i,j})^2 = 2((5 - 6)^2 + (8 - 6)^2 + (5 - 6)^2) = 12$$