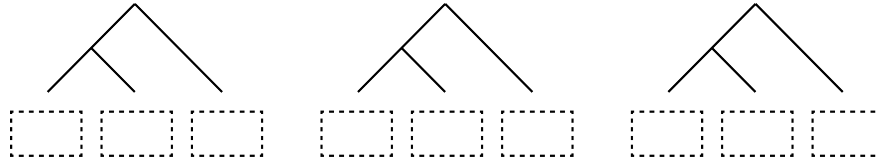


## 9 Exercises – Phylogenetic tree

### 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.

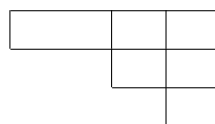
	A	B	C	D
A	0	2	7	7
B		0	5	9
C			0	8
D				0

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

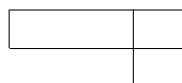
$$d_{(\alpha\beta),\gamma} = \frac{d_{\alpha,\gamma} + d_{\beta,\gamma}}{2}$$

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

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



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



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

(d) Fill the distances of the reconstructed tree.

	A	B	C	D
A	0			
B		0		
C			0	
D				0

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

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