

## Tutorial - 2

1. What is a phylogenetic tree?
2. What do the root, leaves, branches, and branch lengths represent in a phylogenetic tree?
3. What is the difference between rooted tree and unrooted tree in phylogenetic trees?
4. State the additive property and four-point condition in phylogeny.
5. What are the key characteristics of distance matrix methods in phylogenetics
6. Describe the UPGMA algorithm.
7. Describe the steps involved in constructing a phylogenetic tree using the UPGMA method.
8. Explain the UPGMA (Unweighted Pair Group Method with Arithmetic Mean) algorithm for constructing phylogenetic trees.
9. Use UPGMA method  
Given the following distance matrix for four species (A, B, C, and D), calculate the UPGMA tree and provide the detailed steps involved in the calculation.

	A	B	C	D
A	0	5	9	2
B	5	0	10	6
C	9	10	0	3
D	2	6	3	0

10. What are the characteristics of the UPGMA method?
11. Describe neighbour-joining algorithm
12. Differences between UPGMA and neighbour-joining algorithms.

13. Build the tree from the following distance matrix between species A, B, C, and D using the neighbor-joining algorithm.

	A	B	C	D
A	0	6	7	5
B		0	10	9
C			0	6
D				0

14. What are the advantages and disadvantages of the Neighbor-Joining algorithm?