

B.Tech (Biotechnology) V Semester

Course Code: 10B11BT511

MAX. MARKS: 25

Course Name: Introduction to Bioinformatics

Course Credits: 03

MAX. TIME: 1.5 Hr

Note: All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means.

1. Explain the limitations of the progressive approach to Multiple Sequence alignment. How are these overcome using iterative approach? (2+2)
2. Explain the different type of dotplots along with its pros and cons. (2+2)
3. Explain what are sequence logos and why is it used. (2)
4. How many rooted and unrooted trees are possible for 6 OTUs? (2+2)
5. Why are rRNA sequences used for phylogenetic reconstruction? (3)
6. Get the phylogenetic tree using UPGMA method for the following distance matrix. State the disadvantages of UPGMA method. (6+2)

	A	B	C	D	E
A	0				
B	20	0			
C	60	50	0		
D	100	90	40	0	
E	90	80	50	30	0