JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- 2024

B.Tech-III Semester (BI)
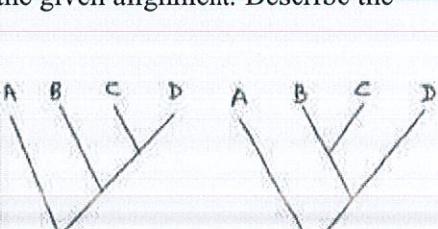
COURSE CODE (CREDITS): 18B11BI313 (4)   MAX. MARKS: 25

COURSE NAME: Biological Computation   MAX. TIME: 1 Hour 30 Minutes

COURSE INSTRUCTORS: Dr. Raj Kumar, Dr. Tiratha Raj Singh

Note: (a) *All questions are compulsory.*

(b) *The candidate is allowed to make Suitable numeric assumptions wherever required*

for solving problems

Q.No	Question	CO	Marks
Q1	What is dynamic programming (DP)? Realize the DP algorithms for pairwise alignment with an example and its description.	3	4
Q2	Align the given two sequences A = "ATGCTGCAG" and B = "ATGCCAG" for the scoring system as match = +1, mismatch = 0, gap penalty = -1 using DP.	3	6
Q3	Tree topology summarizes the patterns of evolutionary relatedness among a group of species independent of the branch lengths of a phylogenetic tree. Can you explain the difference between rooted and unrooted phylogenetic trees in terms of their topology?	4	3
Q4	Interpret the provided multiple sequence alignment and briefly summarize your inferences. S.scrofa NTELPAPLSYFQNAQKSEDNHVSNNVSSQNDSREPHEHSIEPRRRGNSESLSNGGAQGNS 60 B.taurus NTELPAPLSYFQNAQKSEDNHLSNTVRSQNDSREPHEHGNEPRRRGNTESVSNGRAPSSS 60 H.sapiens NTELPAPLSYFQNAQKSEDNHLSNTVRSQNDHREROEH-NDRRSLGHPEPLSNGRPQGNS 59 M.musculus NTEIPAPLSYFQNAQKSEDSHSSSAIRSQNDSQERQQQ-NDRQRLDNPEPISNGRPQSNS 59 ***:************::**:.* *. ; ****.:**::: :*: .:.*.:*** .…*	3, 5	3
Q5.	Find the most parsimonious tree for the given alignment. Describe the steps involved. 1 2 3 4 5 6 7 8 9 10 A - A T G G A T T T C G B - A T G G C G T T C G C - G C G G A G T T C G D - G C G G C G T T T G	4	5

Q6.	Calculate the phylogenetic tree for the given matrix, based on a distance based method that uses molecular clock hypothesis.	4,5	4

	A	B	C	D
A	0			
B	3	0		
C	5	4	0	
D	7	1	2	0