

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST-3 EXAMINATION-2021

B.Tech. VII Semester

COURSE CODE: 18B11BI313

MAX. MARKS: 35

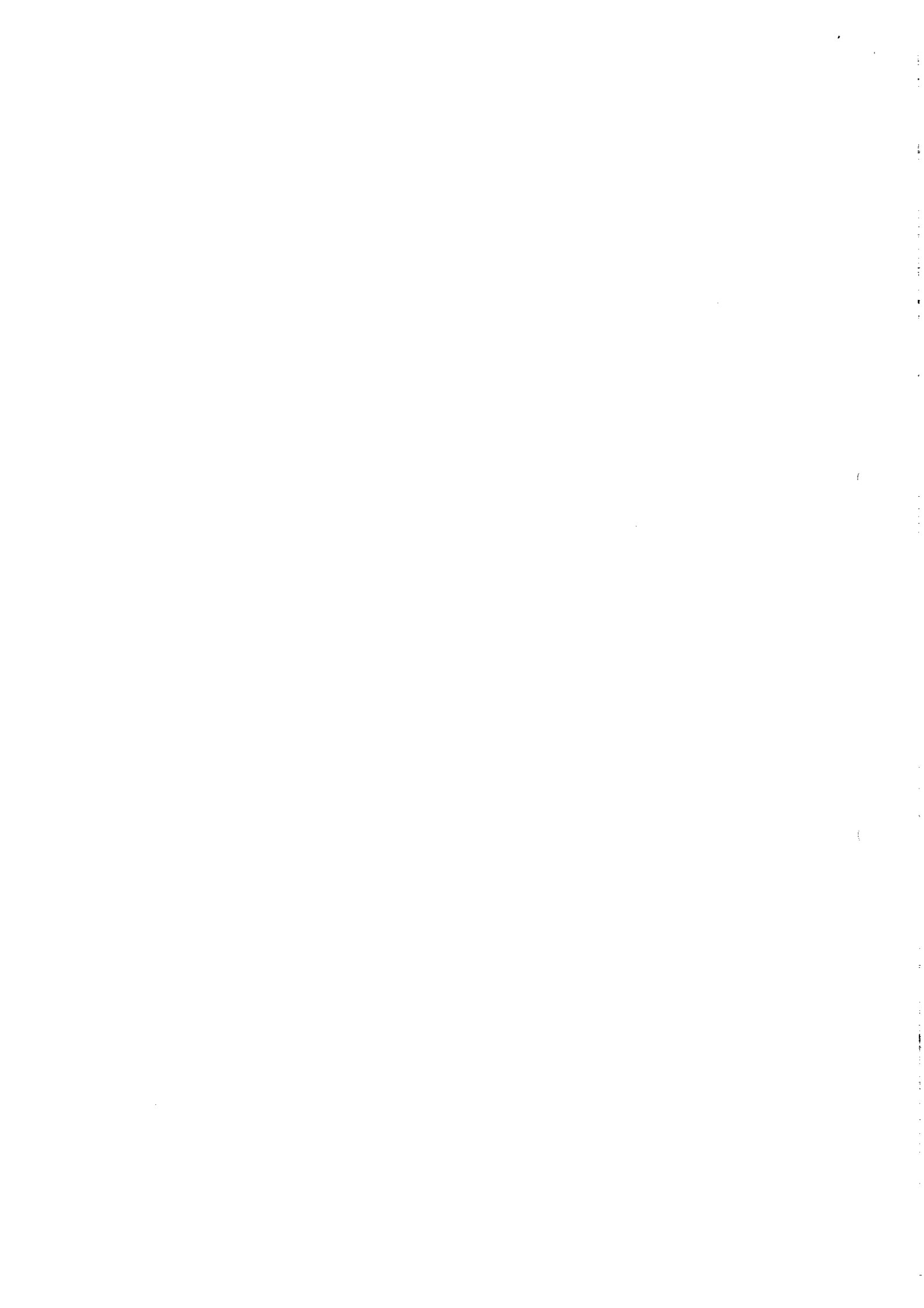
COURSE NAME: Biological Computation

COURSE CREDITS: 04

MAX. TIME: 2 Hours

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

- Q1. The connecting point where two adjacent branches join is called a ___. (1 Mark)
- Q2. The lines in the phylogenetic tree are called ___. (1 Mark)
- Q3. A group of taxa descended from a single common ancestor is defined as a ___ group. (1 Mark)
- Q4. In a phylogenetic tree, can a parent branch split into two or more daughter branches at any given point? Justify your answer. (2 Mark)
- Q5. We can use molecular data to study evolution of a gene. What strategy will you apply to study phylogeny of a species? (3 Marks)
- Q6. To use molecular data to reconstruct evolutionary history requires making a number of reasonable assumptions. Discuss some of these assumptions and significance of molecular data in phylogenetics. (3 Marks)
- Q7. Calculate the R-transformed values for taxon A and taxon B. Given pairwise distances: AB=10, AC=20, AD=40, BC=30, BD=30, CD=20. (3 Marks)
- Q8. Calculate the branch lengths for taxa A and B in a neighbor joining cluster. Given AB distance=10, $r'_A=60$, and $r'_B=70$. (3 Marks)
- Q9. Calculate the number of informative sites in the given alignment. (3 Marks)



Seq 1 **GNVNYKYRYLRHGKLRPFERDISNVPFSPDGKP**
 Seq 2 **GNVNYKYRYLRHGKLRPFERDISNVPFSPDGKP**
 Seq 3 **GNFNYYYRIWRSEKLRPFERDIAHYDYQVGTQF**
 Seq 4 **GNVNYLYRWVRRSKLNPYERDLSNDIYSPGGQS**
 Seq 5 **GNVNYLYRWVRRSKLNPYERDLSNDIYSPGGQS**
 Seq 6 **GNVNYKYRSLRHGKLRPFERDISNVPFSPDGKP**
 Seq 7 **GNVNYLYRFLFRKSNLKPFERDISTEIQAGSTP**

Q10. How will you convert the given multiple sequence alignment into a raw frequency table? (5 Marks)

1 **ATGTCG**
 2 **AAGACT**
 3 **TACTCA**
 4 **CGGAGG**
 5 **AACCTG**

Q11. Build a UPGMA tree for the given pairwise distances? AB=10, AC=20, AD=40, AE=30, BC=30, BD=30, BE=20, CD=20, CE=40, DE=10. (5 Marks)

Q12. Which character will be at the root according to parsimony for the given tree topology? (5 Marks)

