

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATION-2021

B.Tech III, V 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.

Section-1 (10 questions, 2 Marks each)

- Q1. What is molecular clock hypothesis? (2 marks)
- Q2. What are molecular fossils? (2 marks)
- Q3. What is meant by a monophyletic group? (2 Marks)
- Q4. Define polytomy(2 Marks)
- Q5. What is the significance of outgroup in a phylogenetic tree?
- Q6. Give some differences between phylogram and cladogram. (2 Marks)
- Q7. What is homoplasy effect?(2 Marks)
- Q8. What are advantages of Kimura substitution model? (2 Marks)
- Q9. What are OTUs?
- Q10. In neighbor joining, how will you define the distance of each taxon from a composite taxon? (2 Marks)

Section-2 (3 questions, 3 Marks each)

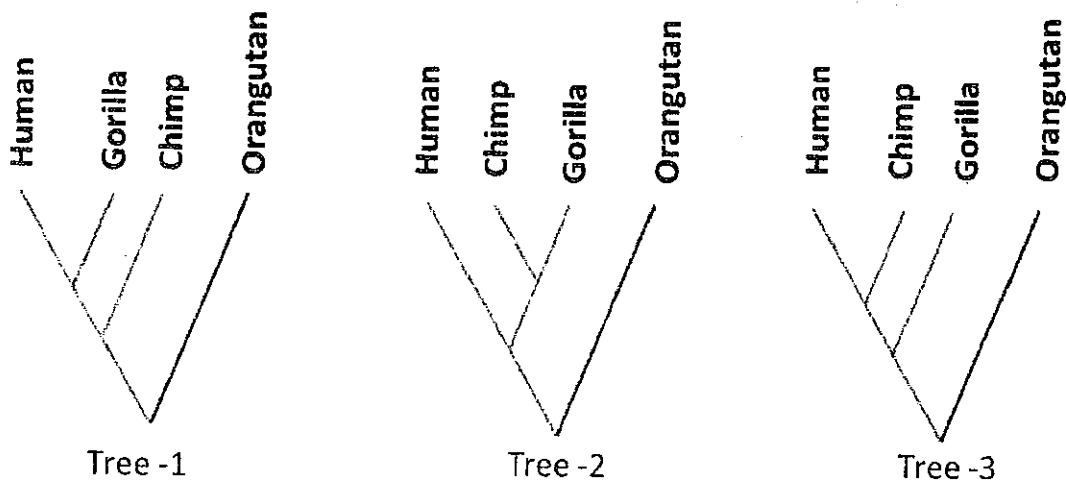
- Q11. Calculate the branch length of taxon A and taxon B in a UPGMA cluster if their evolutionary distance is 18. (3 Marks)
- Q12. In reference to a phylogenetic tree, define the following(3 Marks)

- a) Node
- b) Taxa
- c) Branches

Q13. If the distance between taxon A and taxon B is 10, find the R-value and R-transformed value for A and B. (3Marks)

Section-3 (1 question, 6 Mark)

Q14. Find out the most parsimonious tree using given multiple sequence alignment. (6Marks)



Multiple sequence alignment

Human T T A G C T A C T
 Chimp C T A G C T C C C
 Gorilla C T G G C C A C T
 Orangutan C T G G A C C C T