

KATHMANDU UNIVERSITY  
End Semester Examination [C]  
November/December, 2023

Level : B.Tech.  
Year : III  
Time : 2 hrs. 30 mins.

26 NOV 2023  
Course : BIOT 312  
Semester : II  
F. M. : 55

SECTION "B"

(Long answer questions)  
[3Q. × 7 = 21 marks]

Attempt *ANY THREE* questions.

1. Produce a distance tree using clustering with UPGMA. Also indicate branch lengths between OTUs and all internal nodes. [7]

	A	B	C	D	E	F
A	0					
B	5	0				
C	4	7	0			
D	7	10	7	0		
E	6	9	6	5	0	
F	8	11	8	9	8	0

2. Differentiate between shotgun and hierarchal sequencing technique. Explain each of the individual steps behind DNA Sequencing method of Sanger Sequencing. Provide your answer with detailed figures. [7]
3. Explain the three major steps pf dynamic programming in depth? Create a possible alignment for the below provided sequences; considering score for match = 3, mismatch= -1 and gap penalty = -3. [3+4]  
Seq #1: ATCGTACTAG  
Seq #2: ACGTCTAC
4. Explain how genes are predicted in prokaryotes. What features of prokaryotic genes facilitate the prediction process? [4+3]

SECTION "C"

(Short answer questions)  
[6Q. × 4 = 24 marks]

Attempt *ANY SIX* questions.

5. Classify biological databases and provide what kind of information are stored in with examples.
6. Explain how repeats, palindromic, microsatellite and minisatellite regions can be identified by dot plot.
7. Explain how BLOSUM matrix used for protein alignments are created.
8. Explain how operons are predicted in prokaryotes.

9. Explain how multiple sequence alignment is made with progressive alignment method.
10. How does the distance matrix calculation between Jukes-Cantor and Kimura model vary?
11. How protein structure is determined by X-ray crystallography?

SECTION "D"

(Very short answer questions)

[5Q. × 2 =10 marks]

Attempt *ANY FIVE* questions.

12. State the applications of Bioinformatics.
13. Describe how information is stored in FASTQ format.
14. BLAST method of database searching.
15. Differentiate between gene and species phylogeny with an example.
16. What is Hidden Markov Model?
17. Visualize a secondary structure of RNA: GUUUGGUUCAAAAC using a dot plot.