

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- October 2017

M.Tech (BT)

COURSE CODE: 13M11BT112

MAX. MARKS: 25

COURSE NAME: ADVANCED BIOINFORMATICS

COURSE CREDITS: 03

MAX. TIME: 1H 30 MIN

Q1. Each question carries 2 marks. Answer any three.

(2x3=6)

- i. Motifs are key elements for interactions and also present in different protein families. What is a motif and how is it being identified (explain with examples)? How are the motifs identified?
- ii. How are the PROSITE patterns determined and identified? How are these patterns used to identify proteins from same family?
- iii. What are the major differences between UPGMA and neighbor joining (NJ) methods and discuss the major advantages of the latter (NJ) one? Take any rooted tree with five OTUs and provide its Newick's format?
- iv. What is a scoring scheme of an alignment and how does it decide the alignment? Why do you start traceback step from the maximum score in local pairwise alignment?

Q2. Each question carries 3 marks. Answer any three.

(3x3=9)

- i. From a highly conserved region, how do you determine PSSM? Instead of representing composition as PSSM, why do you calculate odd ratio as PSSM? (2+1)
- ii. Suppose you are provided with 30 diverse sequences (Operational taxonomic units; OTUs), out of many phylogenetic inferring methods which methods should be preferred and why? Why is it important to infer phylogenetic tree using many methods? (2.5+0.5)
- iii. Suppose you are provided MSA of four sequences, how do you infer phylogenetic tree using maximum likelihood (ML) methods?
- iv. Why do you calculate robustness of a predicted tree (explain with examples)? Suppose you infer NJ, maximum parsimony and ML trees, how do you determine their robustness using bootstrap method? (1+2)

Q3. Each question carries 5 marks.

(2x5=10)

- i. Suppose you have 4 OTUs, provide all phylogenetic rooted tree constructed from these OTUs? As number of OTUs increases, the inferring of MP and ML trees becomes difficult. How do you implement branch and bound method to identify optimal trees? Can this approach (branch and bound) be implementable for unrooted tree and how (explain with example)? (2+2+1)
- ii. Pairwise distances among 4 OTUs are given below. Use transformed distance and neighbor relation method to infer phylogenetic tree? Make a comparison among trees determined using two different approaches? (2.5+1.5+1)

OTU	A	B	C
B	13		
C	26	29	
D	18	21	26