

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST-2 EXAMINATION- October -2017

B. Tech Bioinformatics (3rd Semester)

COURSE CODE: 10B11BI311

MAX. MARKS: 25

COURSE NAME: BIOLOGICAL COMPUTATIONS

COURSE CREDITS: 04

MAX. TIME: 1 HR 30 MIN

Q1: Each question carries 1 mark. Answer any three. (1x3=3)

- i. How do you use local alignment (Smith-Waterman method) for database searching?
- ii. Prosite patterns are used as signature for protein family. How are these patterns identified and how do you use them to identify similar proteins in a database?
- iii. How do you determine whether a pairwise alignment is correct or not (explain with examples)?
- iv. Why neighbor-joining (NJ) method is considered to produce the most robust tree?

Q2: Each question carries 2 marks. (2x3=6)

- i. MSA software uses dynamic programming to carry out multiple sequence alignment. How does this software determine optimal alignments? What is the limitation of this software? (1.5+0.5)
- ii. Discuss the advantages of evolutionary profile over the average one? How does it identify sequences of a family with a particular pattern?
- iii. How do you determine robustness of an inferred phylogenetic tree? How do you determine robustness of a tree inferred using NJ approach? (0.5+1.5)

Q3: Each question carries 4 marks. (4x4=16)

- i. What is the principle of progressive method used to determine multiple sequence alignment? How does ClustalW carry out multiple sequence alignment (MSA)? How does this software incorporate scoring and other parameters to determine optimal alignments? (1.0+0.5+2.5)
- ii. Helix-loop-helix motif is present in different protein families. How do you determine this motif using profile score method when you have ten sequences?
- iii. Discuss the limitations of maximum parsimony (MP) method as compared to maximum likelihood (ML)? Take a hypothetical site of MSA and explain how do you infer phylogenetic tree using ML method? (1+3)
- iv. Pairwise distance among 4 OTUs is given below. Use NJ method to infer phylogenetic tree?

| | A | B | C |
|---|----|----|----|
| B | 18 | | |
| C | 13 | 21 | |
| D | 26 | 26 | 29 |