JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
T3 EXAMINATION-MAY 2018
B.Tech (Bioinformatics) VI Semester

COURSE CODE: 10B11BI614   MAX.MARKS: 35

COURSE NAME: Advanced Algorithms for Bioinformatics

MAX. TIME: **2 Hrs**

COURSE CREDITS: 4

Note: All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means. Marks are indicated in square brackets. Calculator is allowed.

1. What is MSA and how it is useful for biological sequence analysis? Discuss recent developments in MSA technologies. (CO-2, 3)   [2]

2. Explain how Greedy approach is different from basic profile based search for motif finding. Discuss Entropy based approach for MSA. (CO-1, 2)   [1.5*2=3]

3. Compare 2D vs 3D MSA. Discuss how dynamic programming can be used for MSA. Also discuss its complexities. (CO-2, 3)   [3]

4. What was Benzer's experiment and what did he proved through that experiment? (CO- 3)
                                                                               [2]

5. Differentiate between Euler's and Hamiltonian problems. Solve any problem of fragment assembly through both approaches and provide complexity analysis also. (CO- 2, 3)   [3]

6. What are iterative refinements for MSA? Discuss Berger and Munsen algorithm for the refinements. (CO- 3)   [3]

7. Solve MSA for the following set of sequences through STAR alignment procedure: (ATTGCCATT / ACTGACC /ATCTTCTT / ATGGCCATT / ATCCAATTTT) (CO- 3) [4]

8. Describe following: (a) Icosian game (b) Algorithm Complexities (c) Interval Graph (d) Konigsberg Bridge Problem (e) gene Prediction Methods (CO- 1, 2, 3)   [1*5=5]

9. Differentiate between following: (a) Finiteness and effectiveness of an algorithm (b) Edit and hamming distance (c) Quick sort and Bubble sort (d) pattern matching and motif finding (e) Brute force and Median string search methods. (CO- 1, 2, 3)   [1*5=5]

10. Draw MSA for the following sequences through SOP method. Use scoring system as :

match =1, mismatch =0, gap = -1. (CO- 3)   [5]