

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY WAKNAGHAT

MID SEMESTER EXAMINATION-2015

B.Tech VI SEMESTER

COURSE CODE: 10B11BI614

MAX MARKS: 30

COURSE NAME: Advanced Algorithms for Bioinformatics

MAX TIME: 2 hrs

COURSE CREDITS: 4

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**Note: All questions are compulsory**

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**Section A**

**[Marks: 6]**

**Q1.** Answer each of the following in brief with a suitable example: [0.5 X 4= 2]

- i. What are five criteria to be satisfied by all algorithms while designing?
- ii. Explain arrow preference in dynamic programming for pair wise alignment.
- iii. Differentiate between Hamming and Levenshtein distances.
- iv. Discuss various kinds of complexities for algorithms.

**Q2.** Explain each of the following with supporting examples: [1X 4]

- i. What is test code statistics?
- ii. Design architecture of 3D alignment cell for DP in MSA.
- iii. What is STAR alignment?
- iv. Explain Greedy approach for MSA.

**Section B**

**[Marks: 9]**

**Q1.** Describe in detail all the mathematical properties of distance and similarity functions along with their summary of properties. [3]

**Q2.** Generate alignment for FASTA through lookup table and offset vector for the following set of sequences: A= ARHARFYAAQI and B = HARFYVID. [3]

**Q3.** Explain semi-global alignment with a suitable example using two nucleotide sequences of your choice along with arbitrary scoring system. Fill matrix and generate final alignment through it. [3]

**Section C**

**[Marks: 15]**

**Q1.** Write DP algorithm for LCS problem along with PrintLCS pseudocode. Fill matrix and find out LCS for given two sequences: TAGTCTA and ATACGT. [5]

**Q2.** Explain exon-chaining algorithm for gene prediction along with its pseudocode. Solve the exon-chaining for the following set of data: (11,15,6) (10,16,12) (13,17,4) (1,6,4) (3,7,4) (2,4,3) (9,12,5) (5,8,5) and (14,18,4). [5]

**Q3.** What is sum of pair's method? How it is different from progressive and iterative methods for MSA? Explain any one algorithm for iterative refinement method? [5]