

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
B.Tech. (Semester VI), Test 3 (May-June 2016)

Course Code: 10B11BI614

Max. Marks: 35

Course Name: Advanced Algorithms for Bioinformatics

Course Credit: 4

Max. Time: 2:00 Hrs

Attempt all questions. Carrying of mobile phones will be treated as the case of unfair means.

Q. 1. How graph based approaches are different than classical approaches for generating MSA? What is the most beneficial aspect of graph theoretic approaches and for which biological characteristics? Explain POA with an example. [5]

Q.2. Define mathematical/computational properties and applications for following:
(a) Distance (b) Similarity (c) Fragment assembly (d) SP for MSA (e) Entropy [5]

Q.3. Explain how exon chaining is different from spliced alignment algorithm? Write their comparative features and applications with suitable examples. [4]

Q.4. Differentiate between median string and brute-force motif search with an example. Discuss testcode statistics for close homologous sequences. [4]

Q.5. What are various graph based approaches for gene prediction? Define interval graph and its applications for proving a particular property of genome. Also discuss Benzer's experiment. [4]

Q.6. What is LCS? How you solve LCS problem using dynamic programming? Describe with an example. [3]

Q.7. What are RNA secondary structure complexities? Explain approaches used to solve the same with an example. [4]

Q.8. Find out one suitable candidate genome from the given set of fragments: $F = \{ATG, GCG, GTG, CGT, AAT, CAA, GCA, TGC, GGC, TGG\}$. Solve it through Euler's and Hamiltonian path approaches separately. Make the required conversions for the fragments from n to $n-1$. [6]