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Total Number of Pages : 01

B.Tech
PIT8J001

8th Semester Regular Examination 2018-19
ALGORITHM FOR BIOINFORMATICS

BRANCH : IT

Max Marks : 100

Time : 3 Hours

Q.CODE : F004

Answer Question No.1 (Part-1) which is compulsory, any EIGHT from Part-II and any TWO from Part-III.

The figures in the right hand margin indicate marks.

Part- I

Q1 Only Short Answer Type Questions (Answer All-10) (2 x 10)

- a) What is Cystic fibrosis. Explain it.
- b) Explain CFTR Protein.
- c) What is platelet-derived growth factor (PDGF)
- d) Find the prefix computation of the string 'XYXRXY'
- e) What is approximate string matching? Explain with example.
- f) State topological ordering of Directed Acyclic Graph.
- g) Give at least four examples of how graphs are used in modelling.
- h) What is UniGene? Give an example.
- i) Define Euler circuit and Euler path in an undirected graph.
- j) What is bioinformatics? Explain the importance of bioinformatics?

Part- II

Q2 Only Focused-Short Answer Type Questions- (Answer Any Eight out of Twelve) (6 x 8)

- a) Find the edit distance between strings 'XYZ' and 'ABC'
- b) What is Change problem? Write procedure/Algorithm for change problem based dynamics Programming.
- c) Find motifs in a set of DNA sequences suing a dynamic programming approach
- d) Explain Manhattan Tourist Problem. Write the algorithm for Manhattan Tourist Problem based on recursive function.
- e) Explain GenBank? What is the importance of specialized genomic resources?
- f) Compare perfect Phylogeny Problem and small Parsimony Problem.
- g) Explain the Hamiltonian path problem in DNA sequencing. Explain through example.
- h) Explain Central Dogma of Molecular biology with neat diagram. What is the various ways to express gene?
- i) What is the problem with using clustal to do pairwise alignment?
- j) Explain hierarchical clustering. Describe the difference between K- means and hierarchical clustering
- k) Explain CLIQUE algorithm using DNA computing techniques
- l) Explain Protein identification via Database Search.

Part-III

Only Long Answer Type Questions (Answer Any Two out of Four)

- Q3** What is Longest Common Subsequences? Write the procedure for find the LCS. Determine an LCS of <1,0,0,1,0,1,0,1> and <0,1,0,1,1,0,1,1,0> **(16)**
- Q4** Write about BLAST (Basic Local Alignment Search Tool). Explain the Needleman and Wunsch algorithm for global alignment. **(16)**
- Q5** Define Multiple sequence alignment? What is the goal of Multiple sequence alignment? Explain simultaneous methods and progressive methods for multiple alignments? **(16)**
- Q6** What is Hidden Markov Models? Explain forward and Backward (Viterbi) algorithm. **(16)**