Registration No : | | | | | | | | | | |

Total Number of Pages : 01 **B.Tech**
PCS8J001

8th Semester Regular Examination 2018-19
ALGORITHM FOR BIOINFORMATICS
BRANCH : CSE
Max Marks : 100
Time : 3 Hours
Q.CODE : F003

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 Phylogenny 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 Morkov Models? Explain forward and Backward (Viterbi) algorithm. **(16)**