

**M.Sc. Examination 2018**  
**Semester-III**  
**Computer Science**  
**Course : MCSE-31**  
**(Bioinformatics)**

**Time : 3 Hours**

**Full Marks : 40**

**Questions are of value as indicated in the margin**

Answer Question **No.1** and **any four** from the rest.

1. a) What is central dogma of molecular biology?  
b) What is C-value paradox?  
c) Determine the alignment score for the following global sequence alignment with match score = +1, mismatch score = -1, origination penalty = -2 and length penalty = -1.  
A G A T A G A A A C T G A T A T A T A  
A G - - - A A A A C A G A G T - - - -  
d) What is phylogenetic tree? 4×2=8
2. a) Write down the chemical structures of four nucleotides.  
b) What is degeneracy of genetic code? Is it essential? Justify with an example.  
c) What is ORF? Find different ORFs of the following hypothetical DNA sequence.  
GCTATGTACGATGGATAATCGGTAG 2+3+3=8
3. a) Using the Needleman and Wunsch dynamic programming method, construct the partial alignment score table for the following two sequences.  
TCAGTCGAAG  
TCCGTCG  
Assume the following scoring parameters: match score = +1, mismatch score = 0, gap penalty = -1. What is the optimal global alignment between these sequences?  
b) What is semi-global sequence alignment? How can the dynamic programming method be modified to find semi-global alignment. (4+1)+3=8
4. a) Use UPGMA to reconstruct a phylogenetic tree using the following distance matrix:
- | Species | A  | B  | C  | D |
|---------|----|----|----|---|
| B       | 3  | -  | -  | - |
| C       | 6  | 5  | -  | - |
| D       | 9  | 9  | 10 | - |
| E       | 12 | 11 | 13 | 9 |
- Estimate the branch lengths of the tree. Finally, write the tree in the Newick format.  
b) Briefly explain BLAST sequence alignment search tool. 5+3=8

(2)

5. a) What do you understand by restriction mapping?  
b) Describe the importance of restriction mapping.  
c) Use the branch and bound algorithm to solve Partial Digest Problem for restriction mapping. What is the worst case time complexity of this algorithm.  $2+1+(4+1)=8$
  6. a) Discuss the importance of gene order comparison  
b) Define breakpoint in a permutation.  
c) Define the problem sorting by reversal.  
d) Give an approximation algorithm to solve the problem sorting by reversal with ratio error at most 4.  $1+1+2+4=8$
  7. Write short notes on **any two** :  $2 \times 4 = 8$ 
    - a) Protein structure
    - b) PAM matrix
    - c) Double digest algorithm for restriction mapping
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