

Roll No .....

**MCTA - 301(D)**  
**M.E./M.Tech., III Semester**  
Examination, June 2016  
**Bio Informatics (Elective-I)**

*Time : Three Hours*

*Maximum Marks : 70*

**Note:** Attempt any five questions. All questions carry equal marks.  
Draw neat and clean diagram wherever needed.

1. What is Bioinformatics? Elaborate the concept of bioinformatics. Mention the tools of bioinformatics and enlist its application.
2. a) Discuss the various computational complexity aspects in bioinformatics face in design algorithm.  
b) List the advantages and disadvantages of various computational gene prediction methods.
3. Calculate the dynamic programming matrix and find optimal alignment for sequences GATCCATTA and GTTACA by using Needleman-Wunsch algorithm. Values for Match = +5, Mismatch = -3 and Gap penalty = -4.
4. a) Define sequence alignment and its importance? Differentiate local verse global alignment.  
b) Find the hamming distance and Levenshtein distance of the following sequence:  
GAATTCATTA (first sequence)  
GGATCGA (second sequence)

5. What do you understand by regulatory motifs in DNA? Explain computational techniques in detail to identify these motifs in DNA.
6. What are the different computational methods available for finding minimum energy in protein molecules? Explain first derivative method. How Ramchandran plot helps to find energy?
7. a) What do you mean by machine learning process and discuss the HMM model for profile generation?  
b) What is 5<sup>th</sup> order HMM why it is called so? Which programme uses it?
8. Write short notes on any two:
  - a) Protein folding
  - b) Approximation algorithm for intractability
  - c) Probability and statistics in bioinformatics
  - d) Divide and conquer approach

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