

Printed Pages: 3

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NBT502

(Following Paper ID and Roll No. to be filled in your Answer Book)

Paper ID : 154502

Roll No.

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**B.Tech.**

**(SEM. V) THEORY EXAM. 2015-16**

**BIO-INFORMATICS-I**

**[Time:3 hours]**

**[Total Marks:100]**

**Section-A**

1. Attempt **all** parts. All parts carry equal marks. Write answer of each part in short. (2x10=20)

- (a) Define homology.
- (b) What is regular expression?
- (c) Define the protein domain.
- (d) Define pairwise alignment.
- (e) What is ClustalW?
- (f) What is PHI-BLAST?
- (g) Define phylogeny.
- (h) Define alpha helix.

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(1)

P.T.O.

- (i) What is the template structure?
- (j) What is the use of Jmol program?

**Section-B**

**Note :** Attempt any five questions from this section.  
(10x5=50)

- 2. Perform an optimal global alignment for the DNA sequences GAATTC and GATTA using dynamic programming (scoring: +2 for a match, -1 for a mismatch, and 2 for a linear gap penalty).
- 3. How do PAM<sub>1</sub> and BLOSUM can be used in database similarity search? Explain.
- 4. What is the role of multiple sequence alignment? Explain the ClustalW program.
- 5. Define the tertiary structure of a protein? Discuss the method of homology modeling.
- 6. Explain the Chou-Fasman method for analysis of protein secondary structure elements.
- 7. Define RMSD. Discuss the uses of RASMOl program.
- 8. Explain the rational drug design approach.
- 9. What are the various file formats?

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**Section-C**

**Note :** Attempt any two questions from this section.

(2x15=30)

- 10. Explain the concept of dendrogram. Discuss the UPGMA method for phylogenetic tree construction.
- 11. Write short notes on:
  - i) IEDB
  - ii) EMBL
- 12. What do you mean by protein structure visualization? Describe recently developed tools available for visualization and analysis of protein structures.

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