Printed Pages: 3 | 688 | NBT502

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

Paper ID : 154502   Roll No.[ ][ ][ ][ ][ ][ ][ ][ ][ ]

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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(i) What is the template structure?

(i) What is the use of Jmol program?

Section-B

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

(10×5=50)

2. Perfom 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 and BlOSUM can be used in database similarty serach? Explain.

4. What is the role of multiple sequence aligment? 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 structrue elements.

7. Define RMSD. Discuss the uses of RASMOL program.

8. Explain the rational drug design approach.

9. What are the various file formats?

Section-C

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

(2×15=30)

10. Explain the concept of dendogram. Descuss 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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