

**CS/2051**  
**BIOINFORMATICS–DSE-4-BHB-31**  
**(Semester–VI)**

Time : Three Hours]

[Maximum Marks : 74

**Note** : The paper consists of three Section A, B and C. Section A and B have four questions and each question from Section A and Section B will carry 11 marks. Candidates are required to do *two* questions from each Section A and B. Section C is compulsory consisting of 15 short answer type questions of 2 marks each.

**SECTION–A**

- I. What is sequence information source? Explain its role in the field of bioinformatics. (11)
- II. Write short notes on the following :
  - (a) UNIGENE. (6)
  - (b) ENTREZ. (5)
- III. What is Swissprot? Explain its features and application. (11)
- IV. Describe the problems that occur while obtaining bioinformatics related data from PCR and Mass spectroscopy. (11)

## SECTION-B

- V. Write short notes on the following :
- (a) Sequence and phylogeny analysis. (6)
  - (b) Pairwise alignment. (5)
- VI. What is Blast? Explain different types of Blast and their applications. (11)
- VII. Write notes on the following :
- (a) Genome annotation. (6)
  - (b) SRS. (5)
- VIII. What are gene identification tools? Explain with suitable examples. (11)

## SECTION-C

- IX. (a) EMBL.
- (b) PDB.
  - (c) TREMBL.
  - (d) Protein information source.
  - (e) Chromatograms.
  - (f) Open reading frames.
  - (g) Microarrays.
  - (h) Multiple sequence alignment.

- (i) Phylogenetic analysis.
  - (j) Blots.
  - (k) GENBANK.
  - (l) Mutation matrices.
  - (m) Restriction digestion.
  - (n) FASTA.
  - (o) BLASTn. (15×2=30)
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