

Unique Paper Code (UPC) : 32537501
Name of the Paper : Bioinformatics
Name of the Course : B.Sc. (Hons.) Microbiology
Semester : 5
Duration : 4 hours including time taken for downloading question paper and uploading answer sheets
Maximum marks : 75

On first page, please write the following details:

1. Date and time of examination (DD/MM/YYYY, Hours:Min)
2. Examination Roll Number
3. Name of the Program, i.e. B.Sc. (H) Microbiology
4. Semester
5. Unique Paper Code (UPC)
6. Title of the Paper
7. Name of the College
8. Email ID of the student
9. Mobile Number of the student

SET 1

Attempt any **four** questions. **All** questions carry equal marks. Supplement your answers with self-explanatory diagrams/flowcharts, wherever applicable. Please answer on A4 size sheets and mark the page number at the top of each page.

Q1: Describe the role of the following in detail : INSDC, Primer-BLAST, molecular markers, SRS, PROCHECK, Gene ontology. (18.75 marks)

Q2: Write short notes on the following: Uni-Prot, ORF Finder, salient features of viral genome, RDBMS, CADD. (18.75 marks)

Q3: Differentiate between the following (**any four**): Global and Local Sequence Alignment, Genomics and Proteomics, Secondary and Tertiary structure of proteins, Cladistic and Phenetic methods of phylogeny, PAM and BLOSUM. (18.75 marks)

Q4: What are biological databases? Describe the features of a biological database. Comment on the contribution of Margaret Dayhoff in development of biological databases. Explain in detail about the genome databases and metabolic databases by giving two examples of each of these databases. What are the advantages of encrypted data transfer? (18.75 marks)

Q5: Is it possible to predict the structure and function of a protein from sequence information? Justify and discuss the methods in detail. What is the role of BLAST search in this process? Write the significance of motif, domain and hydrophobic pockets? Differentiate between secondary and tertiary structure of the proteins in terms of types of bonds formed and the atoms involved? (18.75 marks)

Q6: Name the two categories of file formats based on the data type. Explain any one file format in detail. What is the difference between FASTA and FASTQ files? Explain the significance of sequence alignment in phylogenetic analysis. What are the advantages and disadvantages of maximum parsimony method of tree construction? Construct a UPGMA phylogenetic tree using the following distance matrix and also calculate the branch lengths for all the branches. (18.75 marks)

	A	B	C	D
B	2	-	-	
C	4	4	-	
D	8	8	6	
E	12	12	8	8