

[This question paper contains 6 printed pages.]

Your Roll No.....

Sr. No. of Question Paper : 8374 HC
Unique Paper Code : 32537501
Name of the Paper : Bioinformatics
Name of the Course : Microbiology : Discipline Specific
Elective for Honours
Semester : V
Duration : 3 Hours Maximum Marks : 75

Instructions for Candidates

1. Write your Roll No. on the top immediately on receipt of this question paper.
 2. Attempt five questions in all.
 3. All questions carry equal marks.
 4. Attempt all parts of a question together.
 5. Question one is compulsory.
1. (a) Match the following :
- | | |
|------------------------------------|------|
| (i) Secondary structure prediction | PAM |
| (ii) Protein structure validation | EMBL |

8374

2

- | | |
|-----------------------|------------------------|
| (iii) Pattern | SCP |
| (iv) Tree evaluation | 2D gel electrophoresis |
| (v) Distance method | System biology |
| (vi) Proteomics | PROCHECK |
| (vii) Webin | Neighbor joining |
| (viii) Cell designer | Jackknife |
| (ix) Margaret Dayhoff | PSI-PRED |
| (x) Encrypted data | PROSITE |

 $(\frac{1}{2} \times 10 = 5)$

(b) Expand the following abbreviations :

TCP/IP, ANSI, DDBJ, KEGG, CATH

 $(1 \times 5 = 5)$

(c) Name one biological database for the following :

- (i) Literature
- (ii) Chemical
- (iii) Enzymes
- (iv) Disease
- (v) Nucleotide

 $(1 \times 5 = 5)$

8374

3

2. Write short notes (Any five) :

- (a) Gap penalty
- (b) Hydrophobic pockets
- (c) SWISS-PROT
- (d) Phylogenetic markers
- (e) RDBMS
- (f) BankIT

 $(3 \times 5 = 15)$

3. (a) Align following two sequences using dot matrix analysis.

GGTAGCTAGCGA

CGTAGCATAGGA

(3)

(b) Calculate score for the following aligned sequences using affine gap penalty.

(3)

GATGACCTGATATTAC

GA__CCTGA__TT_C

For: Match = (+3); Mismatch = (0); Gap opening penalty
d = (-6); Gap extension penalty e = (-1)

(c) Define Uniprot and describe its layers. (1+3)

(d) Explain the concept of energy minimization. Why is Ramachandran's plot important in studying the secondary structure? (2+3)

4. (a) Write the advantages of SFTP over FTP. (2)

(b) Elaborate any two techniques used in proteomics. (4)

(c) Define system biology and give its applications. (4)

(d) Construct a phylogenetic tree using UPGMA method for the following matrix. (5)

	W	X	Y	Z
W	0			
X	9	0		
Y	8	10	0	
Z	13	15	12	0

5. (a) Define the role of INSDC. (2)

(b) Write the various features of genomic organization of *E. coli*. (3)

(c) Define BLOSUM. Calculate the BLOSUM matrix for the following sequences :

Sequence 1 : AAI

Sequence 2 : SAL

Sequence 3 : TAL (1+4)

(d) Differentiate between the following (Any two) :

(i) Flat file database and Relational database format

(ii) Maximum Parsimony and Neighbour Joining methods of tree construction

(iii) Genomics and Transcriptomics (2.5×2=5)

(a) Define the followings (Any five) :

Molecular clock, MALDI, Accession number, Foreign key, Motif, Log odds ratio, Paralogous gene. (1×5=5)

(b) How do you predict the 3D structure of proteins by Homology Modelling? (5)

- (c) Define biological databases, list the types and describe the databases associated with structural annotation of protein sequences.

(1+2+2=5)