

This question paper contains 4 printed pages]

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S. No. of Question Paper : 1004

Unique Paper Code : 107455

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Name of the Paper : Bioinformatics [LSPT-409]

Name of the Course : B.Sc. Life Science/B.Sc. (H)

Semester : IV/VI

Duration : 3 Hours

Maximum Marks : 75

(Write your Roll No. on the top immediately on receipt of this question paper.)

Answer section A and B on separate sheets.

Each section is for 37.5 marks.

### Section A

Answer *three* questions including Q. No. 1 which is compulsory.

1. (a) Expand the following (any *four*) :

4×1=4

(i) MIAME

(ii) SAGE

(iii) ChEBI

(iv) GEO

(v) PMC

(vi) NBRF.

(b) Define the following (any *five*) :

5×1=5

(i) SAKURA

(ii) Megablast

(iii) PubMed

P.T.O.

- (iv) Sequin
  - (v) Bank It
  - (vi) Comparative Genomics
  - (vii) RefSeq.
- (c) Differentiate between any *three* of the following : 3×1½=4½
- (i) Composite and Secondary Databases
  - (ii) Entrez and SRS
  - (iii) Metabolic Pathway and Disease Database
  - (iv) PSI-BLAST and RPS-BLAST.
2. (a) How do you define biological database ? Discuss its various features. 6
- (b) What is Swiss-Prot ? Discuss its salient features. 6
3. Write short notes on any *four* of the following : 4×3=12
- (i) LIBRA
  - (ii) UniProt Knowledgebase
  - (iii) INSDC
  - (iv) MMDB
  - (v) TRMBL.
4. (a) Classify the biological databases on the basis of data source and data type. 4
- (b) What is the scope for bioinformatics in biological research ? 6
- (c) How many divisions of nucleotide sequences are present in NCBI and EMBL respectively ? What purpose do they serve ? 2

**Section B**

Answer *three* questions in all including Q. No. 1, which is compulsory.

1. (a) Expand the following (attempt any *five*) : 5×1=5
- (i) PAM
  - (ii) DPA
  - (iii) MSA
  - (iv) SAR
  - (v) GA
  - (vi) HGP
  - (vii) UPGMA.
- (b) Differentiate between any *two* of the following : 2×2=4
- (i) Phylogram and Cladogram
  - (ii) Identity and Similarity
  - (iii) UPGMA and NJ.
- (c) Define any *three* of the following : 3×1½=4½
- (i) Motif
  - (ii) Phylogeny
  - (iii) Bootstrap
  - (iv) Genomics.
2. (a) Distinguish between local and global sequence alignment. 1+2+6+3=12.
- (b) What do you understand by heuristic method of sequence alignment ?
- (c) Discuss various programs used in heuristic method of sequence alignment.
- (d) Briefly state advantages and disadvantages of heuristic method of sequence alignment.

3. (a) What are different scoring matrices ? 2+2+8=12
- (b) Do you need different scoring matrices for alignment of nucleotide and amino acid sequence ? Give reasons to justify your answer.
- (c) Find out the best alignment for given two nucleotide sequences-AGGTCITCATAT and GTCTCATG. provided that the scoring parameters for a match = + 1, a mismatch = 0, and opening gap = - 1.
4. (a) What is the difference between cladistic and phenetic methods of phylogeny ? 3+2+7=12
- (b) Name the distance based method closest to maximum parsimony method in approach.
- (c) Discuss the phenetic methods of phylogeny in detail.
5. Write short notes on any *two* of the following : 6+6=12
- (a) PAM
- (b) PHYLIP
- (c) QSAR.