

[This question paper contains 4 printed pages.]

Sr. No. of Question Paper : 1559 C Roll No.....

Unique Paper Code : 107455

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

Name of the Paper : Bioinformatics (LSPT-409)

Semester : IV

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 Section A and Section B on separate sheets.
3. Each Section is for 37.5 marks.

**SECTION A**

*Question 1 is compulsory.*

*Attempt a total of 3 questions in Section A including Q. 1.*

1. (a) Give an example for **any five** of the following :
  - (i) Derived database
  - (ii) Composite database
  - (iii) Enzyme database
  - (iv) Disease database
  - (v) Microarray database
  - (vi) Literature database
  - (vii) Chemical database (5)
- (b) Expand **any five** of the following acronyms :
  - (i) DDBJ
  - (ii) PDB

*P.T.O.*

- (iii) KEGG
  - (iv) TOPS
  - (v) PIR
  - (vi) INSDC
  - (vii) NMR
  - (viii) GSS
  - (ix) STS
  - (x) MetaCyc (0.5×5=2.5)
2. Write short notes on **any three** of the following :
- (i) Sequence Retrieval System (SRS)
  - (ii) Swiss-Prot
  - (iii) BLAST
  - (iv) DDBJ
  - (v) Nucleotide database (5×3=15)
3. Comment on the following :
- (a) Role of NCBI in bioinformatics
  - (b) Spidey
  - (c) Functions of LIBRA
  - (d) Characteristic features of PIR
  - (e) PubChem
  - (f) ePCR (3×5=15)
4. (a) Differentiate between (**any two**) of the following :
- (i) Bank IT and Webin
  - (ii) Primary database and secondary database
  - (iii) UniGene and HomoloGene (3×2=6)

- (b) Represent the organization of different categories of Protein Information Resource (PIR). (9)

### SECTION B

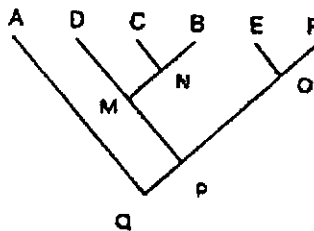
*Attempt three questions in Section B.*

*Question No. 1 is compulsory.*

1. (a) Define the following :
- (i) Bit score
  - (ii) Paraphyletic clade
  - (iii) Signature sequence
  - (iv) K-tuple
  - (v) Phylogeny
  - (vi) Consensus sequence (1×6=6)
- (b) Difference between the following (**any three**) :
- (i) Smith-Waterman and Needleman-Wunsch algorithm
  - (ii) Paralogous and Xenologous sequence
  - (iii) Homology and Similarity
  - (iv) Progressive and Iterative alignment (2×3=6)
- (c) What does the following symbol indicate in a sequence alignment ?
- (i) \* (star)
  - (ii) · (dot)
  - (iii) : (Colon) (½×3=1½)
2. (a) What is BLOSUM matrix ?
- (b) What is the principle of BLOSUM matrix ?
- (c) Discuss the advantages and disadvantages of BLOSUM matrix in sequence alignment.

- (d) When would you use BLOSUM45 and BLOSUM62 matrix in sequence alignment and why? (1+4+4+3=12)

3. (a) Define phylogenetic tree?  
 (b) What is distance based method of phylogenetic tree construction?  
 (c) How UPGMA is different from Neighbour joining method of tree construction?  
 (d) Look at the tree given here and answer the following questions.



- (i) Which of the taxa forms monophyletic clade?  
 (ii) Why it is called a monophyletic clade?  
 (iii) Which is the most recent common ancestor of taxa C, B, D and E? (1+2+6+3=12)
4. (a) Bioinformatics is an amalgamation of different fields. Justify the statement.  
 (b) Discuss the role of bioinformatics in the field of agriculture and medicine. (4+8=12)
5. Write short notes on **any three** of the following :
- (i) Dynamic Programming Algorithm (DPA)  
 (ii) Maximum likelihood method  
 (iii) Microbial genome applications  
 (iv) Molecular markers (3×4=12)