

This question paper contains 4 printed pages]

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S. No. of Question Paper : 8555

Unique Paper Code : 216/223/558

Name of the Paper : LSPT 409 : Bioinformatics

Name of the Course : B.Sc. (Hons.) Botany III Year

Semester : V

Duration : 3 Hours

Maximum Marks : 75

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

Attempt five questions in all,

including Question No. 1 which is compulsory.

1. (a) Expand the following (Attempt any five) :

$5 \times \frac{1}{2} = 2\frac{1}{2}$

(i) PHYLIP

(ii) BLAST

(iii) PIR

(iv) PAM

(v) SCOP

(vi) ADMET

(vii) QSAR

(viii) ICGEB

(b) Define the following terms (Any ten) :

$10 \times 1 = 10$

(i) SAKURA

(ii) UniProt

P.T.O.

(iii) Molecular docking

(iv) Pubmed

(v) MSA

(vi) Spidey

(vii) Bootstrap

(viii) ORF

(ix) Scoring matrix

(x) Cladogram

(xi) PDB

(c) Match the following :

$5 \times \frac{1}{2} = 2\frac{1}{2}$

**Column A**

**Column B**

- |  |                       |
|--|-----------------------|
| (1) The server that provides data about quaternary structure of protein                            | (a) Protein modelling |
| (2) A database that deals with structure classification  | (b) Swiss-Prot        |
| (3) A database which is a result of collaboration between EBI and SIB                              | (c) SCOP              |
| (4) A web based sequence submission tool available on NCBI   | (d) CATH              |
| (5) A database that classifies protein 3D structure in a hierarchical scheme of structural classes | (e) OMIA              |
|  | (f) BankIT            |
|  | (g) PDB               |

2. Differentiate between any *five* : 5×3=15
- (i) PAM and BLOSUM scoring matrix
  - (ii) Orthologous and Paralogous sequences
  - (iii) Primary and Secondary databases
  - (iv) MATCHBOX and CINEMA
  - (v) Gene bank and FASTA file format
  - (vi) Rooted and Unrooted phylogenetic trees
  - (vii) Global and local sequence alignment
3. Write short notes on any *three* of the following : 3×5=15
- (i) Clustal W
  - (ii) In Silico drug designing
  - (iii) Molecular clock
  - (iv) Swiss-Prot
  - (v) Microbial Genome Application
4. (a) What is a biological database? What are its features and ways in which it can be classified?
- (b) What is NCBI? Mention briefly the various tools available at NCBI. Discuss the organization of databases at NCBI. 7½+7½=15

5. (a) Discuss the different statistical methods used to verify robustness of obtained phylogenetic trees.
- (b) Draw a comparison between the following methods :  
Neighbour- Joining, Maximum Parsimony, and Maximum Likelihood.  $7\frac{1}{2}+7\frac{1}{2}=15$
6. (a) Discuss SAR and QSAR techniques and their role in computer aided drug designing.
- (b) What do you mean by genetically modified crops? Give an account of role of computational biology in crop improvement.  $7\frac{1}{2}+7\frac{1}{2}=15$