(c) Drug-DNA interactions

(d) Protein Databases

[This· question paper contains 8 printed pages.]

Your Roll No................

Sr. No. of Question Paper : 1262   I

Unique Paper Code   : 2233010010

Name of the Paper   : DSE-10 : Integrative Systems
Biology and Bioinformatics

Name of the Course   : **BSc. (H) Zoology, Theory
Exam, Nov-Dee 2024**

Semester   : Vth, (NEP-UGCF 2022)

Duration : 3 Hours   Maximum Marks : 90

Instructions for Candidates

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

2.   Question No. **1** is compulsory.

3.   Attempt a total of **five** questions, including Q. No. **1**
which is compulsory.

P.T.O.

1. (a) Define the following (**any five**) :–   (1×5=5)

    (i) Evolutionary Distance

    (ii) Log-odds matrix

    (iii) Point Accepted mutation

    (iv) Metabolomics

    (v) Molecular Dynamics

    (vi) Motif

    (vii) PubMed

   (b) Expand the following terms (**any six**) :–

                                 (1×6=6)

    (i) PDB

    (ii) MSA

    (iii) KEGG

    (iv) GOR

5. "Bioinformatics is a multidisciplinary approach with multiple applications and few limiations". Justify the statement with suitable examples.   (15)

6. (a) Describe various steps involved in Protein-Ligand Docking. Name any two softwares used in molecular docking.   (9)

   (b) Enlist Lipinski's rule for chemical compounds to be screened for orally active drugs in humans.   (3)

   (c) ADMET properties of chemicals play vital roles in every stage of drug discovery. Justify the statement.   (3)

7. Write a short note on any **three** of the following :–   (5×3=15)

   (a) Dot Matrix

   (b) Protein tertiary structure prediction methods

(b) Also, explain different databases associated with each omic level with examples, which can be explored to study the biological systems in detail. (9)

(c) Why is it crucial to consider all the different omics levels and their interactions in systems biology to understand biological processes fully? (3)

4. (a) What is a gap penalty? Explain how adjustment of gap penalty as too high or too low affects the sequence alignment. (5)

(b) *"the whole is greater than the sum of its parts"* Explain the significance of this statement in Bioinformatics with suitable examples. (5)

(c) Discuss the major applications of HMM model in bioinformatics. (5)

(v) NDB

(vi) HMM

(vii) TrEMBL

(c) Give an example of the following :– (1×4=4)

(i) Disease Database

(ii) Composite Database

(iii) Small Molecule Database

(iv) Metabolic Pathway Database

(d) State True or False. Justify your answer :

(1×5=5)

(i) Dynamic Programming is slower but more accurate than heuristic methods.

(ii) PAM1 can be used for comparing distantly related sequences.

(iii) GOR predicts structures by analyzing amino acids and nearby residues.

(iv) Similarity and Homology are identical concepts in sequence alignment.

(v) ARSA is a search engine of GenBank.

(e) Differentiate between any **five** of the following :–   (2×5=10)

(i) PAM 250 & BLOSUM 65

(ii) Phylogram and Cladogram

(iii) Rigid and Flexible Molecular docking

(iv) Chou-Fasman and GOR methods of protein secondary structure prediction

(v) Primary and 'Secondary Databases

(vi) Pairwise and Multiple Sequence Alignment

2.   (a) Differentiate between dynamic programming and heuristic methods.   (4)

(b) Explain two heuristic methods using well-labeled diagrams.   (8)

(c) Based on your understanding of dynamic programming, answer the following questions.   (3)

(i) Why are the first row and first column of the SW matrix filled with zeros?

(ii) Why does the traceback step in the SW matrix not start from the lowermost cornered cell?

3.   (a) Explain different omics levels which are commonly studied in bioinformatics.   (3)