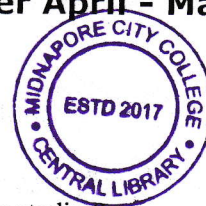


The West Bengal University of Health Sciences
B.Sc. in Medical Microbiology 5th Semester April - May, 2024
Examination

Subject : Bioinformatics



Time : 2 hrs.

Full Marks : 50

Attempt all questions

1. Tick the correct answer :

10 x 1

- a) What is the purpose of virtual screening in ligand-protein interaction studies?
 - i) To synthesize new ligands.
 - ii) To identify potential drug candidates.
 - iii) To perform laboratory experiments.
 - iv) To analyze gene expression.
- b) Which programming language is commonly used for developing tools for data retrieval and analysis in bioinformatics?
 - i) Python.
 - ii) HTML.
 - iii) MATLAB.
 - iv) Ruby.
- c) Which of the following best describes a ligand?
 - i) A protein that binds to DNA.
 - ii) A small molecule that binds to a receptor protein.
 - iii) A type of enzyme that catalyzes chemical reactions.
 - iv) A structural component of the cell membrane.
- d) Which bioinformatics database is commonly used for storing information about ligands and their interactions with proteins?
 - i) GenBank.
 - ii) UniProt.
 - iii) Protein Data Bank (PDB).
 - iv) BLAST.
- e) What is the role of computational algorithms in bioinformatics?
 - i) To perform laboratory experiments.
 - ii) To analyze and interpret biological data.
 - iii) To design new organisms.
 - iv) To synthesize chemicals.
- f) Which of the following is NOT a common biological database?
 - i) PubMed.
 - ii) NCBI.
 - iii) Swiss-Prot.
 - iv) BLAST.
- g) What is the primary purpose of data retrieval in bioinformatics?
 - i) To generate new data.
 - ii) To analyze existing data.
 - iii) To validate experimental results.
 - iv) To design new algorithms.
- h) What is the primary role of ligand-protein interactions in biological systems?
 - i) To stabilize the structure of proteins.
 - ii) To regulate gene expression.
 - iii) To facilitate cell division.
 - iv) To mediate cellular signaling and biochemical processes.
- i) How can bioinformatics aid in the design of novel ligands with improved binding affinity?
 - i) By analyzing sequence motifs.
 - ii) By predicting ligand-protein interactions.
 - iii) By conducting high-throughput screening.
 - iv) By studying protein expression levels.
- j) Which scoring scheme is commonly used in sequence alignment algorithms?
 - i) BLOSUM matrix.
 - ii) PAM matrix.
 - iii) Smith-Waterman matrix.
 - iv) Dynamic programming matrix.

2. Answer **any four** of the following questions :

4 x 2

- a) What is genome annotation?
- b) Define genomics.
- c) What is pharmagetics?
- d) What is molecular modeling?
- e) What is auto dock?
- f) What is integrative bioinformatics?

3. Answer **any four** of the following questions :

4 x 4

- a) Describe the major sub-disciplines of bioinformatics.
- b) How do you analyze any DNA sequence by using bioinformatics?
- c) Differentiate between gene and genome.
- d) Name any four protein databases and their importance.
- e) What are the purposes of database searching in bioinformatics?
- f) What does CDS stand for? What is the difference between the gene and the CDS?

4. Answer **any two** of the following questions :

2 x 8

- a) Discuss any one sequence submission tool. Differentiate between similarity and homology. 5+3
- b) Write short notes on : i) dot-plot matrix. ii) Docking. 4+4
- c) Differentiate between local and global alignment. State the application of docking. 4+4