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Reg. No. : ....

Name : ....

Fourth Semester M.Sc. Degree Examination, July 2024

Botany

BO 241 : BIOINFORMATICS AND BIOPHYSICS

(2019 Admission Onwards)

Time : 3 Hours Max. Marks : 75

I. Answer the following questions.

1. Define *Entrez.*

2. Distinguish between *TBLASTX* and *TBLASTN.*

3. Give two examples for pathway databases.

4. Expand CHARMM.

5. Name any two programs for protein ligand docking.

6. How will you explain the high boiling and melting points of water and hydrogen fluoride (HF)?

7. Define coupled reactions.

8. Distinguish between equivalent and effective doses of radiations.

9. Define *Retention time.*

10. Write down the role of TEMED and APS in SDS-PAGE.

(10 × 1 = 10 Marks)

P.T.O.

II. Answer the following questions in not more than **50** words.

11. (a) Comment on Rigid and flexible docking approaches.

OR

(b) Differentiate between Maximum parsimony and maximum likelihood methods of tree construction.

12. (a) Comment on the BLAST output format.

OR

(b) Explain the Needleman-Wunsch Algorithm.

13. (a) Describe the role of PSI- BLAST. Mention its advantages over traditional BLAST.

OR

(b) Differentiate between polar and non- polar covalent bonds.

14. (a) Describe the two types of preparative ultracentrifugation.

OR

(b) Explain the principle of gas chromatography.

15. (a) Explain the factors affecting rate of migration of DNA through agarose gels.

OR

(b) Explain the basic principle of mass spectroscopy.

(5 × 2 = 10 Marks)

III. Answer the following questions in not more than **150** words.

16. (a) Discuss the principles and applications of IR spectroscopy.

OR

(b) Explain the principle of confocal microscopy.

17. (a) Explain the basic instrumentation of NMR spectrometer. Add a note on the solvents used in NMR.

OR

(b) Explain the techniques of visualization of gels in agarose and polyacrylamide gel electrophoresis.

18. (a) Describe the principles and major components of affinity chromatography.

OR

(b) Explain the important hydrodynamic properties of aqueous solutions.

19. (a) Write a note on secondary or derived Protein Sequence Databases with suitable examples.

OR

(b) Discuss the significance of virtual screening in *in* silico drug designing.

20. (a) Discuss the major steps in the process of homology modeling.

OR

(b) List out the differences between PAM and BLOSUM matrices.

21. (a) Write a note on publically available databases for comparative genomics.

OR

(b) Give the fundamental concepts behind systems biology.

22. (a) Define functional genomics. Describe the major study areas under functional genomics.

OR

(b) Explain the dot matrix method of sequence alignment. Mention the web servers available for this method.

(7 × 5 = 35 Marks)

IV. Answer the following questions in not more than **250** words.

23. (a) Give a detailed account on the secondary and tertiary structure prediction of proteins.

OR

(b) Write an essay on the applications of bioinformatics in 'multi-omics' research.

24. (a) Give a detailed account on the applications of tracer techniques in biology.

OR

(b) Describe the different types and techniques of chromatographic separations.

(2 × 10 = 20 Marks)
