

B.Sc. DEGREE EXAMINATION, APRIL 2024
BRANCH V(a) – PLANT BIOLOGY AND PLANT BIOTECHNOLOGY
FOURTH SEMESTER

COURSE : ELECTIVE
PAPER : INTRODUCTION TO BIOINFORMATICS
SUBJECT CODE : 19BT/ME/BI45
TIME : 3 HOURS MAX. MARKS: 100

SECTION – A

A. ANSWER THE FOLLOWING

18 Marks

I. Choose the correct answer

(5 x 1 = 5)

- Identify the first completed and published gene sequence ?
 - T4 phage
 - Lambda phage
 - M13 phage
 - ΦX174
- Which of the following tool is used for motif identification ?
 - BLAST
 - PROSPECT
 - COPIA
 - PATTERN HUNTER
- Who established the first Bioinformatics database ?
 - J D Watson
 - Margaret Dayoff
 - Frederic Sanger
 - Pauline Hogeweg
- Which if the following is a nucleotide sequence database ?
 - EMBL
 - SWISS PROT
 - PROSITE
 - TREMBL
- Identify the compound that has desirable properties to become a drug ?
 - Lead
 - Fit Drug
 - Target
 - Fit compound

II. Fill in the blanks

(5 x 1 = 5)

- _____ is the process of finding the relative location of genes on a chromosome.
- _____ coined the term Bioinformatics.
- Process of finding new medicines using genetic research is _____.
- GenBank is maintained by _____.
- Virtual high-throughput screening allows one to identify _____ from a large collection of compound libraries.

III. State True or False

(4 x 1 = 4)

- Algorithms are used for solving problems using computer software.
- Gene annotation is used to predict the function of a gene.
- RASMOL is a program used to visualize proteins and nucleic acids.
- GALAXY is web based platform for biomedical research.

IV. Match the following**(4 x 1 = 4)**

- | | |
|---------------------------------|------------------|
| 15. Multiple Sequence Alignment | k-tuple |
| 16. FASTA | Needleman-Wunsch |
| 17. Global alignment | CLUSTALW |
| 18. Local alignment | Smith-Waterman |

V. ANSWER ANY SIX OF THE FOLLOWING QUESTIONS IN 50 WORDS EACH:**(6 x 3 = 18)**

19. Hydrophobicity profile
20. CDD
21. Gap penalty
22. FASTA
23. OMIM
24. Scoring matrix
25. Homology modelling
26. Hamming distance
27. Phylogenetic tree

SECTION - B

ANSWER ANY FOUR OF THE FOLLOWING QUESTIONS IN ABOUT 200 WORDS EACH. DRAW DIAGRAMS WHEREVER NECESSARY.

(4 x 6 = 24)

28. Identify the aim, scope and research areas in bioinformatics.
29. List the salient features of Swiss-Prot and PIR.
30. Elaborate QSAR.
31. Differentiate between global and local alignment.
32. Explain the Chou-Fasman method for protein secondary structure prediction.
33. Describe how bioinformatics is applied in crop improvement.

SECTION - C

ANSWER ANY TWO OF THE FOLLOWING QUESTIONS IN ABOUT 1000 WORDS EACH. DRAW DIAGRAMS WHEREVER NECESSARY.

(2 x 20 = 40)

34. Elaborate the important biological sequence databases.
35. List the uses of ORF finder, RE base cutter and PubChem.
36. Write an essay on multiple sequence alignment using CLUSTALW.
37. Discuss the role of structural bioinformatics in drug discovery.
