

B.Sc. DEGREE EXAMINATION, APRIL 2022
BRANCH V(a) – PLANT BIOLOGY AND PLANT BIOTECHNOLOGY
FOURTH SEMESTER

COURSE : ELECTIVE
PAPER : INTRODUCTION TO BIOINFORMATICS
TIME : 3 HOURS

MAX. MARKS: 100

SECTION - A

A. ANSWER THE FOLLOWING

18 Marks

I. Choose the correct answer

(1x5=5)

1. Most Bioinformatics programming utilized _____.
a) Program C b) GO c) MATLAB d) PERL
2. Molecular visualization done by using _____ tool.
a) RASMOL b) FDF c) PROSITE d) SOPM
3. The gap scores are typically _____.
a) Positive b) Null c) Negative d) None of the above
4. To identify sequence similarity between the query sequence with the library sequence is
a) PIR b) Insilico Hybridisation c) ESTs d) CATH
5. In the expansion of QSAR, the 'Q' stands for _____.
a) Quantitative b) Qualitative c) Quantify d) Qualify

II. Fill in the blanks:

(1x5=5)

6. A tool for identifying the presence of domain _____.
7. The term Bioinformatics was coined by _____ and _____.
8. Global alignment identify _____ regions.
9. Preclinical phase of drug discovery involves _____ studies.
10. BLAST originally developed and controlled by _____.

III. State True or False

(1x3=3)

11. Genomic databases contain gene level information.
12. All proteins have only motif.
13. tBlastx compares the nucleotide query against the translated nucleotide.

IV. Match the following

(1x5=5)

14. Tertiary structure - Dynamic Programming
15. Secondary database - Sequencing RNA
16. Frederick Sanger - BLOCKS
17. Robert Holley - SWISS-PROT
18. Richard Bellman - Sequencing DNA

V. ANSWER ANY SIX OF THE FOLLOWING QUESTIONS IN 50 WORDS EACH:**(6x3=18)**

19. Conserved region
20. Motif and Domain
21. Global vs Local alignments
22. RE – base cutter
23. Dynamic programming
24. Query sequences
25. Threading
26. Candidate drugs
27. Consensus Sequence

SECTION - B**ANSWER ANY FOUR OF THE FOLLOWING QUESTIONS IN ABOUT 200 WORDS EACH. DRAW DIAGRAMS WHEREVER NECESSARY.****(4x6=24)**

28. List the applications of Bioinformatics.
29. Write short notes on PIR.
30. Discuss about drug toxicity.
31. Explain Multiple Sequence alignment.
32. Write short notes on Structural databases.
33. Illustrate molecular modelling.

SECTION - C**ANSWER ANY TWO OF THE FOLLOWING QUESTIONS IN ABOUT 1000 WORDS EACH. DRAW DIAGRAMS WHEREVER NECESSARY.****(2x20=40)**

34. Give a detailed account on Sequence Similarity Searches.
35. Discuss elaborately on Drug discovery.
36. Give a detailed account on methods for protein structure prediction.
37. Discuss elaborately on various Nucleotide databases.
