

S.NO: 6923

P16MBE4A

**(For Candidates admitted from 2016-2021 Batch)
M.Sc. Degree Examination, November 2023.
Microbiology- Elective
BIOINFORMATICS AND BIOSTATISTICS**

Time : 3 hours

Maximum : 75 marks

SECTION A - (10 x 2 = 20)

Answer ALL questions

1. What is Bioinformatics?
2. What is HGP (Human genome project) and when it started?
3. Define the basic differences between UNIX and Linux operating systems.
4. Describe the principles behind BLAST and FASTA algorithms in sequence comparison.
5. Define term database.
6. Define GOR method.
7. What is the role of Chou-Fasman method in secondary structure prediction in proteins.
8. Define Phylogenetic tree.
9. What is RASMOL?
10. Define Variance.

SECTION B - (5 x 5 = 25)

Answer ALL questions, choosing either (a) or (b) in each.

11. a. Discuss the importance of biological databases in genomics research. Highlight the specific functions of NCBI, EMBL, and DDBJ.

(OR)

- b. Discuss the methods involved in protein modelling briefly with examples.

12. a. Describe the principles and processes involved in genome sequence comparison.

(OR)

- b. Explain the significance of visualizing protein structures. How does RASMOL aid in this process?

13. a. Compare and contrast BLAST and FASTA algorithms in sequence alignment. Provide examples of their application.

(OR)

- b. Evaluate the role of protein databases in understanding the structure-function relationship of proteins.

14. a) Analyse the relevance of pairwise sequence comparison in understanding genetic relationships.

(OR)

- b) Compare the Protein Data Bank with Swissprot-PIR, SCOP, and CATH in terms of their scope and content.
15. a) Explain the significance of multiple sequence alignments in evolutionary studies. How does Phylip contribute to this area?

(OR)

- b) Elaborate GOR method for predicting protein secondary structures. Highlight their differences and applications.

SECTION C - (3 x 10 = 30)

Answer any THREE questions

16. Discuss the practical applications of genomics in personalized medicine, considering the role of databases and sequence comparisons.
17. Analyze the impact of proteomics on drug discovery and development, emphasizing the importance of structural predictions and databases.
18. Conduct a comparative study of variance and standard deviation as measures of dispersion. Provide examples from biological datasets.
19. Explore the significance of probability distributions in biostatistics, focusing on Poisson, Binomial, and Normal distributions. Provide real-world instances where these distributions are applicable in biological studies.
20. Critically evaluate the role of hypothesis testing in biological research, citing examples where hypothesis testing techniques such as chi-square, t-test, and ANOVA are utilized.
