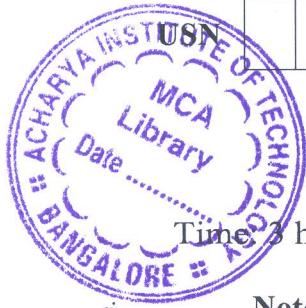


CBCS SCHEME

21BT54



Time: 3 hrs.

Fifth Semester B.E. Degree Examination, June/July 2024 Genomics, Proteomics and Bioinformatics

Max. Marks: 100

Note: Answer any FIVE full questions, choosing ONE full question from each module.

Module-1

- 1 a. Infer on the working mechanism and application of shotgun DNA sequencing. (08 Marks)
b. Write short note on :
i) Types of Polymorphism.
ii) EST Database. (12 Marks)

OR

- 2 a. Appraise on Next generation method in genome sequencing. (10 Marks)
b. Summarize about Genome sequencing and database subscription. (10 Marks)

Module-2

- 3 a. Define Gene variation. Prioritize on SNP and any one SNP detection tool. (10 Marks)
b. Summarize on the usage of Drosophila as a model organism in functional genomic study. (10 Marks)

OR

- 4 a. Infer on DNA chip usage in functional genomics. (08 Marks)
b. Write short note on :
i) RAPD ii) COG. (12 Marks)

Module-3

- 5 a. Interpret about Protein chip and add a note on its types. (12 Marks)
b. Appraise on Yeast – Two – Hybrid Interaction screening. (08 Marks)

OR

- 6 a. Emphasize the application of proteome analysis in Drug development and toxicology. (12 Marks)
b. Discuss on the detection of protein in SDS gel electrophoresis. (08 Marks)

Module-4

- 7 a. Prioritize on PROSITE - PATTERN. (08 Marks)
b. Write short note on :
i) Bootstrap Analysis ii) PHYLIP. (12 Marks)

OR

- 8 a. Give a brief account on Primary Databases with example for Primary Nucleotide Database. (08 Marks)
b. Write short note on :
i) PDB as structural Database
ii) FASTA format. (12 Marks)

Important Note : 1. On completing your answers, compulsorily draw diagonal cross lines on the remaining blank pages.
2. Any revealing of identification, appeal to evaluator and /or equations written eg, $42+8 = 50$, will be treated as malpractice.

Module-5

- 9 a. Infer on Molecular Docking process. Appraise on AUTODOCK tool. (10 Marks)
b. Prioritize on QSAR in Insilico drug design process. (10 Marks)
- OR
- 10 a. Infer on parameters need to be considered while designing a primers and highlight on PRIME – 3 software tool. (12 Marks)
b. Categorize SOPMA and JPRED as a protein prediction tool. (08 Marks)