

2022
M. Sc. (Biotechnology) Third Semester
MBIO-305: Advances in Genomics and Proteomics

Time allowed: 3 Hours

Max. Marks: 80

NOTE: Attempt five questions in all, including Question No. 1 which is compulsory and selecting one question from each Unit.

x-x-x

1. Write short notes on the following:-

- a) What are neural networks?
- b) Explain Bridge PCR.
- c) What kind of database Ensembl is?
- d) What are the genetic basis of drug response in different individuals?
- e) What is repeatmasker?
- f) How can you digest the protein?
- g) Explain MUMMER.
- h) Phylogenetic footprinting
- i) Role of SDS in Protein gel electrophoresis.
- j) How the gene tags such as HIS-tag, FLAG -tag are added to genes? (10x1.6)

Unit I

- 2 (a) How the large scale genome sequencing and analysis will help in understanding complex traits in higher organisms? give examples.
- (b) Discuss any two homology based methods of gene prediction from genome in eukaryotes?
- 3 (a) Why the genome sequencing coupled with transcriptome is beneficial for identification of gene and gene structures?
- (b) What are protein microarrays? Explain its principle and methodology.

8 x 2 = 16

Unit II

- 4 (a) What do you understand by pharmacogenomics and personalized medicine?
- (b) Explain BLASTZ and AVID in details.
- 5 (a) UCSC is one of genome repertoire, Discuss its features and how you can access data from UCSC?
- (b) What is comparative genomics? How this can lead to evolution studies.

8 x 2 = 16

P.T.O.

(2)

Unit III

- 6 (a) How can you isolate and study the proteome of cell?
(b) What is SAGE and why it is not a very popular method of expression analysis compared to other available methods?
- 7 (a) How the yeast one and two hybrid system helps in studying the protein interactions?
(b) Explain the principle and working 2DE of proteins? 8 x 2=16

Unit IV

- 8 (a) Explain STRING and GRID databases?
(b) What is chromatin immunoprecipitation helps in genome wide interaction studies?
- 9 (a) How the proteome analysis helps in drug designing?
(b) What is phylogenetic profiling? 8 x 2=16

X-X-X