

Roll No.

Total No. of Questions : 13]

[Total No. of Pages : 02

J-3742[S-1606]

[2037]

M.Sc. (BI) (Semester - 2nd)

BIO - INFORMATICS (M.Sc. (BI) - 201)

Time : 03 Hours

Maximum Marks : 75

Instruction to Candidates:

- 1) Section - A is **compulsory**.
- 2) Attempt any **Nine** questions from Section - B.

Section - A

Q1)

(15×2 = 30)

- a) Write briefly about data retrieval tools.
- b) Differentiate between genomics and proteomics.
- c) What do you know about yeast - 2 - hybrid system?
- d) Explain the term (i) Homologus (ii) Orthologus.
- e) Constitute a profile HMM (Hidden Markov Model) for finding genes.
- f) Differentiate between pair-wise sequence alignment and multiple sequence alignment.
- g) Write briefly about protein databases.
- h) Explain the use of sequence pattern.
- i) Differentiate between Local and Global alignment.
- j) Draw a comparison between BLAST and FASTA.
- k) What are the advantages of phylogenetic analysis?
- l) Write a short note on NMR spectroscopy.
- m) How will you construct a phylogenetic tree?
- n) Write briefly about Dynamic Programming Method.
- o) Write a short note on (i) String (ii) Gap penalty.

P.T.O.

Section - B

(9 x 5 = 45)

- Q2)** Compare between PAM matrices and BLOSUM matrices.
- Q3)** Define the terms
- (a) Deletion
 - (b) Xenologus
 - (c) Insertion
 - (d) Transcription
 - (e) Translation.
- Q4)** Write briefly about Neural networking. Give its significance.
- Q5)** Give a flow chart for protein structure prediction.
- Q6)** Explain briefly about Genetic Maps versus Physical Maps.
- Q7)** Differentiate between structural and functional annotation.
- Q8)** Write short note on
- (a) Monte Carlo Simulations
 - (b) Molecular Dynamic Simulations
- Q9)** Explain the significance of
- (a) Motifs
 - (b) Patterns.
- Q10)** Explain abinitio approach for protein prediction.
- Q11)** Write short note on
- (a) Protein sequence databases
 - (b) Genetic databases.
- Q12)** Write briefly about SCOP. Give its significance.
- Q13)** Discuss advantages and limitations of using HMM (Hidden Markov Model) for prediction of genes.

