Exam Code:0042
Sub. Code: 1007

2054
B.Sc. (Hons.) Bio-Informatics
Fourth Semester
BIN-4003: Computational Methods in Bio-molecular Sequence and Structure Analysis

Time allowed: 3 Hours Max. Marks: 60

NOTE: *Attempt five questions in all, including Question No. I which is compulsory and selecting two questions from each Unit.*

X-X-X

I. Attempt the following:-

(a) Briefly explain Genscan.

(b) Name any two super secondary structures present in RNA.

(c) What is meant by searching by content during gene prediction.

(d) Give full form of GOR and its advantages over Chou Fasman method.

(e) What are the disadvantages of using X-ray crystallography in protein structure determination?

(f) Briefly explain Mfold. (6x2)

UNIT - I

II. a) How are eukaryotic promoters predicted using bioinformatics approaches?

b) Discuss application of DOT plot in RNA structure prediction. (8,4)

III. a) What are the applications of HMM in gene prediction?

b) Briefly explain gene prediction based on searching by signals. (8,4)

IV. a) Discuss any one method of RNA secondary structure prediction based on Ab-initio approach.

b) Write a note on GRAIL. (8,4)

UNIT - II

V. a) Explain principle and application of NMR in protein structure determination.

b) How are protein structures predicted using fold recognition. (8,4)

VI. Write notes on the following:-

a) Neural networks for protein secondary structure prediction

b) Ab-initio approach for tertiary structure prediction of proteins (6,6)

VII. a) How are protein tertiary structure predicted using homology modeling.

b) Write a note on Sfold. (10,2)

X-X-X