Exam.Code:0042
Sub. Code: 1007

2053

B.Sc. (Hons.) Bio-Informatics

Fourth Semester

BIN-4002: 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) What are the signals present in genes that help in their prediction?

(b) Give full form of GRAIL and briefly explain it.

(c) Draw a well-labelled diagram of secondary structure of tRNA.

(d) What are the disadvantages of GOR for protein structure prediction?

(e) Define R-factor.

(f) What is role of GROMACS in protein structure prediction? (6x2)

UNIT - I

II. a) What are HMMs and their role in gene prediction?

b) Briefly explain the various types of RNA structures. (8,4)

III. Write notes on the following:-

a) Ab initio approach for RNA secondary structure prediction

b) Genscan (8,4)

IV. a) How are genes predicted using homology based approach.

b) Briefly explain the concept of promoter. (8,4)

UNIT - II

V. a) Discuss principle and applications of NMR in protein structure determination.

b) What are advantages of GOR over Chau Fasman method for protein secondary structure prediction? (8,4)

VI. a) Discuss protein tertiary structure prediction using homology modeling.

b) Name any two ab initio softwares / tools for protein tertiary structure prediction. (8,4)

VII. a) How is GOR used for protein structure prediction?

b) Explain protein structure prediction using threading approach. (8,4)

x-x-x