Exam.Code:0042
Sub. Code: 1007

1059

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) How does homology modeling differ from *ab-mitio* based modeling?

b) What are the limitations of NMR for protein structure determination?

c) What are the different types of RNA and their functions?

d) Define RMSD and give its significance.

e) Briefly explain Shine-Delgamo sequence?

f) Name the secondary structure elements present in proteins? (6x2)

UNIT – I

II. a) What is the importance of HMMs in gene prediction?

b) How are dot matices used in RNA structure prediction? (2x6)

III. a) Discuss comparative approach based method of RNA structure prediction. (6)

b) In gene prediction methods explain the following:-

i) Search by content

ii) Search by signal (2x3)

IV. a) What are the structural features present in eukaryotic genes that help in their prediction?
b) Write notes on the following:-
i) GENSCAN
ii) Glimmer (7,5)

UNIT – II

V. a) Discuss the steps of the PHD program predict protein structures?

b) Give the principle and applications of X-ray crystallography in protein structure determination? (7,5)

VI. a) Explain the steps of the GOR method for protein structure prediction.

b) Compare and contrast threading and fold recognition? (2x6)

VII. a) Discuss the various steps in homology modeling of proteins?

b) Write a note on Vienna RNA package? (10,2)

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