Exam.Code:0441
Sub. Code: 3508

2022
M.Sc. (Bio-Informatics) Third Semester
MBIN-8016: Applications of Computational Biology

Time allowed: 3 Hours

Max. Marks: 60

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

x-x-x

I. Answer the following:-
   a) Which was the first bacterial genome to be sequenced?
   b) Why are genome sequenced?
   c) How are prokaryotic promoters predicted?
   d) Explain computational bias
   e) What is meant by *ab initio?*
   f) Briefly explain content based method for gene prediction
   g) Draw the tertiary structure of tRNA
   h) Enlist the various super secondary structures present in RNA (8x1½)

UNIT - I

II. a) What are the salient features of of Eukaryotic genomes?
   b) How are ORFs detected *in silico?*
   c) What is the relevance of Human Genome Sequencing project? (3x4)

III. Compare and contrast:-
   a) Functional and positional cloning
   b) Glimmer and Grail (8,4)

UNIT - II

IV. a) What are artificial neural networks and how are they used in gene prediction?
   b) How are repeats detected? (8,4)

P.T.O.

V. a) Discuss the signals present in genes that help in their prediction. Give anyone software based on this approach.

b) What are IMMs and their importance in gene prediction? (2x6)

UNIT - III

VI. Write notes on the following:-

a) Mfold

b) RNA secondary structure prediction using comparative approaches (4,8)

VII. a) How is RNA structure predicted using partition function?

b) Write a note on Vienna RNA package. (2x6)

x-x-x