Exam.Code:0441
Sub. Code: 3508

2123

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) Give full forms of ORF and GRAIL.

b) What is genome annotation?

c) Briefly explain computational bias.

d) What are the structural features present in promoters on which insilico identification tools are based?

e) Draw well labelled diagram of secondary structure of tRNA.

f) Explain covariation in RNA structures. (6x2)

UNIT - I

II. a) Discuss any one traditional route for gene identification.

b) What are ORF finders and their applications? (8,4)

III. Write notes on the following:-

a) Goals of gene sequencing project

b) Genscan

c) Grail (3x4)

UNIT - II

IV. a) How are ANNs used in gene prediction?

b) What are repeat finders and their applications? (8,4)

V. a) Discuss signal based method for gene prediction.

b) How are Markov model used in gene prediction? (2x6)

UNIT - III

VI. a) What are the secondary structure elements and higher levels of structure present in RNA? Include relevant figures.

b) Compare and contrast Mfold and RNA fold. (2x6)

VII. a) Discuss partition function and its application in RNA structure prediction.

b) How is DOT plot used in RNA secondary structure prediction? (2x6)

x-x-x