1115

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. 1 which is compulsory and selecting atleast one question from each Unit.*

x-x-x

I. Attempt the following:-

a) Which was the first prokaryotic genome to be sequenced?

b) What is meant by Compositional Bias?

c) What is Repeat Finder?

d) Name program used for gene findings in eukaryotes.

e) Which program is used for predicting genes in microbes?

f) Name various experimental methods to identify gene coding sequences.

g) Name a software based on homology based method for gene prediction.

h) What is a hair pin loop in RNA?   (8x1½)

UNIT – I

II.   Write a note on any two of the following:-
   a) ORF Finder
   b) Genmark
   c) Grail   (2x6)

III. Differentiate between the experimental and *Insilico* methods of gene identification.
                                                                    (12)

UNIT – II

IV.   a) Explain any two machine learning methods in detail.

      b) What is a Hidden Markov model?   (2x6)

V.   a) Write a note on Promoter analysis.

      b) How are content based methods used for gene prediction? Give examples. (12)

UNIT- III

VI.   a) What are the tertiary structures found in RNA?

      b) Explain the RNA secondary structure thermodynamics.   (2x6)

VII. a) What is the basis for RNA secondary structure prediction in Vienna RNA package?

      b) Write a note on RNA fold.   (2x6)

x-x-x