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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 briefly:-

a) Markov Chain

b) Repeat Finders

c) Machine learning

d) Homolgy

e) Similarity

f) Positional Cloning

g) Content based method

h) RNA polymerase   (8x1½)

UNIT – I

II. a) Discuss the goals of the Human Genome Sequencing project.

b) Explain two traditional routes of gene identification.   (2x6)

III. Write notes on:-

a) ORF Finder

b) Grail

c) Genscan   (3x4)

UNIT – II

IV. a) Discuss the signal based methods for gene identification with two examples.

b) Explain the artificial neural network based gene prediction softwares.   (2x6)

V.   a) What is the significance of Compositional Bias? Give examples of such regions.

b) Discuss promoter analysis in prokaryotes.   (2x6)

P.T.O.

UNIT – III

VI.   Discuss the RNA secondary and tertiary structures.   (12)

VII.   a) Explain the thermodynamics of RNA secondary structure.

        b) Write a note on S fold and Vienna RNA package.   (5,7)

x-x-x