Exam.Code:0441
Sub. Code: 3508

2021
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) S fold
c) Machine learning
d) ORF finder
e) Similarity
f) Functional Cloning
g) GRAIL
h) Hair pin loop in RNA (8x1½)

UNIT – I

II. a) Discuss the first sequenced bacterial genome.
b) Explain positional cloning strategies. (2x6)

III. Elaborate on the traditional routes of gene identification. (12)

UNIT – II

IV. a) Discuss the principle and basis of content based methods for gene identification with two examples.
b) Explain the Hidden Markov model. (8,4)

V. a) Discuss the different types of repeats found in Human genome.
b) Write a note on promoter prediction in prokaryotes. (2x6)

P.T.O.

UNIT – III

VI. a) Discuss the RNA tertiary structures.

b) Elaborate on the role of thermodynamics on RNA secondary structure. (2x6)

VII. Explain two programs for RNA secondary structure prediction. (12)

x-x-x