

2124  
M.Sc. (Bio-Informatics) Third Semester  
MBIN-8016: Applications of Computational Biology

Max. Marks: 60

Time allowed: 3 Hours

**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. Answer briefly:-

- Name the first prokaryotic and eukaryotic genomes that were sequenced?
- Give full form of GLIMMER.
- What are repeat finders?
- Briefly explain homology based method for gene identification.
- What is a pseudoknot in RNA structures?
- Why are RNA structures studied?

(6x2)

UNIT - I

II. a) Differentiate between functional and positional cloning.

b) Discuss Genscan.

(8,4)

III. Write notes on the following:-

- Goals of genome sequencing projects.
- ORF finder
- GRAIL

(3x4)

UNIT - II

IV. a) What is HMM and its application in gene identification.

b) Briefly explain computational bias.

(8,4)

V. a) How are ANN used for gene identification?

b) Differentiate between content and signal based methods of gene identification.

(8,4)

UNIT - III

VI. a) Discuss Ab-initio approach for RNA structure prediction.

b) What is covariation in RNA structures?

(8,4)

VII. a) What is partition function and its importance in RNA structure prediction?

b) How are Dot plots used for RNA structure prediction?

(6,6)

x-x-x