

Exam. Code: 5014
Sub. Code: 11891

2056

Bachelor of Science (FYUP)-Fourth Semester
Bioinformatics

Paper: Computational Methods for Gene and RNA Structure Analysis
(Common with B.Sc. Bio-Informatics 4th Semester FYUP)

Time allowed: 3 Hours

Max. Marks: 60

NOTE: Attempt five questions in all, including Question No. 1 which is compulsory and selecting one question from each Unit.

x-x-x

I. Answer briefly:-

- a) Grail
- b) Discriminant Analysis in gene prediction
- c) Homology based gene prediction
- d) HMM
- e) SiRNA
- f) Vienna RNA package

(6x2)

UNIT - I

- II. (a) Describe the role of promoters and enhancers in gene regulation.
(b) Explain untranslated regions and their importance in gene expression. (2x6)
- III. a) What are reading frames? Explain how frame shifts affect protein synthesis.
b) Discuss the identification and importance of Open Reading Frames in genome annotation. (2x6)
- IV. a) Explain Artificial Neural Networks in gene prediction.
b) Describe performance evaluation of gene prediction methods, including sensitivity and specificity. (2x6)

UNIT - II

- V. a) Compare promoter structures in prokaryotes and eukaryotes.
b) Explain phylogenetic foot printing in promoter prediction. (2x6)

P.T.O.



(2)

- VI. a) Describe RNA secondary structure and its biological significance.
b) Discuss Mfoldtool used for RNA secondary structure prediction. (2x6)
- VII. a) Explain the role of miRNA in gene silencing mechanisms.
b) Describe comparative methods used in RNA structure prediction with suitable examples. (2x6)

x-x-x