

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 4<sup>th</sup> 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)

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(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