

2022  
B.A./B.Sc. (General) Third Semester  
Bio-Informatics  
Paper - V (BNE-3001): Sequence Analysis

Time allowed: 3 Hours

Max. Marks: 67

**NOTE:** Attempt five questions in all, including Question No. I which is compulsory and selecting two questions from each Unit

x-x-x

I. Answer the following briefly:-

- a) What is consensus sequence?
- b) Significant BLAST Z score
- c) Define indels.
- d) Tree of life & its uses
- e) BLOSUM 62
- f) Cladogram
- g) What is called as low information content region?
- h) High scoring pair
- i) Molecular homoplasy
- j) Clustal W

(10x1½)

UNIT - I

- II. a) Write a note on DOT matrix and its application.  
b) Differentiate between progressive Vs iterative methods of MSA. (7,6)
- III. a) Discuss different uses of multiple sequence alignments.  
b) Discuss dynamic programming methods & its significance. (7,6)
- IV. a) How BLAST algorithm works?  
b) Discuss scoring functions and its uses. (7,6)
- V. a) Write a note on Gap penalty.  
b) What is significance of sequence alignments? (7,6)

P.T.O.

(2)

UNIT - II

- VI. Discuss overview of tree of life and what are three domain of life. (13)
- VII. a) What is taxonomic identification?  
b) Discuss about Binomial Nomenclature. (7,6)
- VIII. a) What are Taxonomic descriptions and its signification in classification?  
b) What is Ernst Haeckels recapitulation theory? (7,6)
- IX. a) Differentiate between Rooted and unrooted tree.  
b) Discuss Bootstrapping & its applications. (7,6)

x-x-x

C4KNOWLEDGESEEKERS