

1129

B.Sc. (Hons.) Bio-Informatics

Third Semester

BIN-3002: Computational Methods in Bio-molecular Sequence and Phylogenetic Analysis

Time allowed: 3 Hours

Max. Marks: 60

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 briefly:-

- a) Cladogram
- b) SMART
- c) Pattern
- d) PRATT
- e) Homology
- f) Paralogous
- g) InterPro
- h) Unrooted tree

(8x1½)

UNIT – I

- II. a) Differentiate between Pattern and Profile.
b) Define Motif and describe the different types of motifs. (2x6)
- III. Explain the construction and uses of PSSM. (12)
- IV. a) Write short notes on:-
 - i) ProDom
 - ii) Pfam
b) What is CDD? Explain the applications of this database. (2x6)

UNIT – II

- V. Explain the neighbor joining method for phylogenetic analysis. (12)
- VI. a) Discuss the significance of Phylip package in phylogenetic analysis.
b) With the help of an example demonstrate the UPGMA method of tree construction. (2x6)

P.T.O.

(2)

VII. Write notes on:-

- a) Bootstrapping
- b) Jackknifing
- c) Jukes Cantor Model

(12)

x-x-x