

2012

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. 1 which is compulsory and selecting two questions from each Unit.

x-x-x

I. Attempt the following:-

- a) Protein Domain
- b) Profile
- c) Phylip package
- d) Jackknifing
- e) UnRooted tree
- f) Cladogram
- g) PRATT
- h) Translocation

(8x1½)

UNIT - I

- II. a) Differentiate between pattern and profile.
- b) How is a sequence pattern different from sequence profile? Give example. (2x6)
- III. a) How is PSI-BLAST used for profile based database search?
- b) Discuss the regular expression (Prosite-type) profile. (2x6)
- IV. a) Write a note on CDD.
- b) Explain InterPro as a tool for searching patterns. (2x6)

UNIT - II

- V. Write a note on phylogenetic tree terminology and topologies. (12)
- VI. a) Discuss the different distance based methods.
- b) Explain the two character based methods for phylogenetic tree construction. (2x6)
- VII. a) Discuss the process of Bootstrapping.
- b) Write a note on the MEGA package. (2x6)

x-x-x