2123
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* <u>*five*</u> *questions in all, including Question No. I which is compulsory and selecting two questions from each Unit.*

x-x-x

I.   Answer briefly

    a) UPGMA

    b) Maximum parsimony

    c) Bootstrapping

    d) Motif

    e) InterPro

    f) PRATT

    g) Protein Family

    h) SMART   (8x1½)

UNIT - I

II.   a) What are Domains? Discuss their different types.

    b) Define sequence profiles and discuss the regular expression profiles.   (2x6)

III. a) Discuss the constructions of PSSM.

    b) Explain any domain database   (2x6)

IV.   a) Write a note on PRATT.

    b) Discuss the applications of PSI-BLAST.   (2x6)

UNIT - II

V.   Write a note on the tree terminologies and topologies in phylogenetic analysis. (12)

VI.   a) Discuss any character based method for phylogenetic tree construction.

    b) Explain the Phylip package for phylogenetic analysis.   (2x6)

VII. a) Discuss the process of Jackkniffing.

    b) Write a note on the Neighbor joining method for tree construction.   (2x6)

x-x-x