2055
M.Sc. (Bio-Informatics) Second Semester
MBIN-8008: Sequence Bio-Informatics and Software Tools

Time allowed: 3 Hours   Max. Marks: 60

NOTE: *Attempt* <u>*five*</u> *questions in all, including Question No. I which is compulsory and selecting atleast one question from each Unit.*

x-x-x

I.   Attempt briefly:-

    a) PAUP

    b) Clustal X

    c) PSSM

    d) Identity

    e) UPGA

    f) Orthologues

    g) Nucleotide substitution

    h) Neighbour joining method   (8x1½)

UNIT - I

II.   a) How is Gquery use for sequence retrieval?

    b) Discuss the GenBank flatfile format.   (2x6)

III. Write notes on:-

    a) SWISSPROT

    b) GenBank

    c) UNIPROT   (12)

UNIT - II

IV.   a) How is Dotplot used for sequence alignment?

    b) Write a note on the Needleman and Wunsch algorithm.   (2x6)

V.   a) Discuss the algorithm and application of BLAST.

    b) Elaborate on Homology and similarity with reference to evolutionary relationship.

                                           (2x6)

P.T.O.

UNIT - III

VI.   a) Explain the bootstrapping evaluation method for phylogenetic analysis.

        b) Discuss the terminology of phylogenetic trees.   (2x6)

VII.   Describe the character based methods for phylogenetic estimation.   (12)

x-x-x