Exam.Code:0440
Sub. Code: 3498

2054

M.Sc. (Bio-Informatics) Second Semester

MBIN-8008: Sequence Bio-Informatics and Software Tools

Time allowed: 3 Hours
Max. Marks: 60

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

x-x-x

I. Attempt the following:-

a) FASTA

b) Clustal W

c) PAUP

d) BLASTx

e) Motifs

f) Cladogram

g) Orthologues

h) PAM matrix

(8x1½)

UNIT - I

II. a) Explain the features and applications of SWISSPROT.

b) Discuss any Sequence retrieval tool?

(2x6)

III. a) Explain the Genbank flatfile format.

b) Write short note on:

i) UNIPROT

ii) DDBJ

(4,8)

UNIT - II

IV. a) Discuss the Smith waterman algorithm. Explain the significance of the same.

b) Explain the applications of PSSM.

(8,4)

V. a) Elaborate on the concept and algorithm of BLAST. Discuss its applications.

b) Write a note on the notion of homology.

(7,5)

P.T.O.

UNIT - III

VI. a) Explain the evolutionary change in nucleotide sequence rates and its significance.

b) Elaborate on any distance based method for phylogenetic analysis. (2x6)

VII. a) Explain the terminology of Phylogenetic trees.

b) Discuss the Boostrapping evaluation method. (2x6)

x-x-x