Exam.Code:0440
Sub. Code: 3498

1058

M.Sc. (Bio-Informatics) Second Semester
MBIN-8008: Sequenc 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) Why PAM 250 matrix is preferred evolutionary relationship?

b) Discuss PSSM.

c) What is the opening gap penalty?

d) What is PIR?

e) Define scoring matrix.

f) What is gene duplication?

g) What is a global alignment?

h) What is a rooted tree? (8x1½)

UNIT – I

II. a) What are nucleotide databases and their significance?
b) What is Uniport and discuss their role. (2x6)

III. a) Discuss the role of sequence retrieval tools.
b) Discuss "GenBank flat file format". (2x6)

UNIT – II

IV. a) Discuss Dot pot and its significance.
b) Discuss development Blossom scoring matrices. (2x6)

V. a) Discuss MSA and its role in creating motifs database.
b) Discuss BLAST and it significance? (2x6)

UNIT – III

VI. a) What is phylogenetic analysis and how it helps to understand biology.

b) Discuss Maximum likelihood method it applications. (2x6)

VII. a) Write a note for computer tools used for Phylogenetic analysis.

VIII. b) Discuss Bootstrapping evaluation method. (2x6)

x-x-x