Exam.Code:0440
Sub. Code: 3498

1059

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) Give the full form of DDBJ and PIR.

b) What is GQuery?

c) What are the various disadvantages of a flat file format?

d) Differentiate between Paralogues and Orthologues.

e) Briefly explain a motif taking a suitable example.

f) What is PSI-BLAST?

g) Calculate the number of rooted trees for four taxa.

h) Briefly discuss any bioinformatics software for phylogenetic analysis. (8x1½)

UNIT – I

II. a) Discuss the Uniprot Consortium.

b) Differentiate between primary and secondary databases giving suitable examples. (8,4)

III. a) Discuss one DNA and RNA sequence databases and give their uses.

b) What are the various parts of the GenBank flat file? (8,4)

UNIT – II

IV. Differentiate between the following:-

a) BLAST and FASTA (4)

b) PAM and BLOSUM (4)

c) Global and local alignments (2)

d) Clustal W and Clustal X (2)

P.T.O.

V. a) What are the various steps of the FASTA algorithm?

b) What is the importance of the following:-

i) Multiple sequence alignment.

ii) PSSM (6,6)

UNIT – III

VI. a) What is Bootstrapping and how does it differ from Jackknifing?

b) Discuss the importance of the following in phylogentic analysis:-

i) Occam's razor

ii) Molecular clock hypothesis (6,6)

VII. a) Discuss UPGA method for Phylogentic analysis.

b) Differentiate between the following:-

i) Phylogram and Cladogram

ii) Distance based and character based methods of phylogentic analysis. (6,6)

x-x-x