Exam.Code:0040
Sub. Code: 0998

1058

B.Sc. (Hons.) Bio-Informatics
Second Semester
BIN-2006: Introduction to Bioinformatics

Time allowed: 3 Hours Max. Marks: 60

***NOTE**: Attempt five questions in all, including Question No. I which is compulsory and selecting two questions from each Unit.*

x-x-x

I. Attempt the following:-

a) Give full forms of PIR and NCBI.

b) What are the disadvantages of flat file format?

c) Name two softwares for pair wise sequence alignment?

d) Differentiate between clustal W and clustal X

e) What is Gquery?

f) What are HSP and their importance? (6x2)

UNIT – I

II. a) Differentiate between primary and secondary databases giving suitable examples.

b) Discuss Genbank file format. (2x6)

III. a) Compare and contrast SCOP and CATH.

b) What are the uses/applications of the following:-

i) RefSeq
ii) FASTA format
iii) PIR (2x6)

IV. a) Discuss the Uniprot consortium.

b) What are specialized databases? Discuss any two. (2x6)

UNIT- II

V. Differentiate between the following:-

a) PAM and BLOSSUM

b) PSI and PHI BLAST

c) Motif and profile (3x4)

P.T.O.

VI. a) Discuss the steps FASTA algorithm for pairwise sequence alignment, using a suitable example.

b) What are the different types of gap penalties? (2x6)

VII. a) What are the various steps of Clustal procedure?

b) Discuss the various parts of the BLAST output. (2x6)

x-x-x