

2054
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. 1 which is compulsory and selecting two questions from each Unit.

x-x-x

I. Answer the following:-

- (a) Give full forms of CATH and PIR.
- (b) Name any two sequence formats.
- (c) What is G-query?
- (d) Differentiate between Clustal X and Clustal W.
- (e) Define Sum of Pairs.
- (f) Differentiate between affine and general gap penalty.

(6x2)

UNIT - I

II. a) Discuss the Uniport consortium.

b) Briefly explain FASTA format.

(8,4)

III. Differentiate between the following:-

a) Primary and secondary databases

b) CATH and SCOP

(2x6)

IV. Give the applications of the following:-

a) SWISS prot

b) PDB

c) NCBI resource

(3x4)

UNIT - II

V. Differentiate between the following:-

a) Pair wise alignment and multiple sequence alignment

b) BLAST and FASTA

(2x6)

(2)

- VI. a) Discuss the BLAST alongwith taking a suitable example.
b) What is 'safe-zone' and its importance in alignments. (8,4)
- VII. Differentiate between the following:-
a) Motif and profile giving suitable examples
b) PAM and BLOSUM (2x6)

x-x-x