AV–1803

B.Sc. Part–III Semester–V Examination
BIOINFORMATICS
(Methods in Bioinformatics)

Time : Three Hours] [Maximum Marks : 80

Note.:— (1) All questions are compulsory.

(2) Draw well labelled diagram wherever necessary.

1. (A) Fill in the blanks :

(i) BLAST stands for _______.

(ii) Sequence format for the BLAST program is the _______ format.

(iii) PDB is the database of protein _______.

(iv) NCBI stands for _______. 2

(B) Choose correct alternatives :

(i) Bank and Sequin are sequence submission tools in :

(a) DDBJ (b) PDB

(c) NCBI (d) EMBL

(ii) Which of the following is the first biological database ?

(a) GenBank

(b) DDBJ

(c) Atlas of protein sequence and structure

(d) OMIM

(iii) GenBank is maintained by :

(a) EBI (b) NIG

(c) NCBI (d) SIB

(iv) All are nucleotide sequence database except.

(a) Swiss-prot (b) EMBL

(c) DDBJ (d) GenBank 2

(C) Answer in one sentence each :

(i) What is PDB ?

(ii) What is BLAST-2 ?

(iii) What is RDBMS ?

(iv) What is data warehousing ? 4

2. (a) Describe importance of data. 4

(b) Describe Data Models. 4

(c) Describe Data Security. 4

OR

(p) Explain Test databases. 4

(q) Describe Biodiversity database. 4

(r) Describe the RDBMS as a database design. 4

3. (a) Describe the genomic databases repositories like EST. 4

(b) Describe Transcription Sequence Bank. 4

(c) Describe the features of GenBank. 4

OR

(p) Explain the limitation of computation analysis. 4

(q) Describe the genomic databases repositories like STS. 4

(r) Explain the program to store DNA sequence. 4

4. (a) Describe the Hashes data structure. 4

(b) Describe BLAST. 4

(c) Describe the characteristics of genetic code. 4

OR

(p) Describe DNA sequence in FASTA format. 4

(q) Describe program for simulation for DNA mutation. 4

(r) Discuss BLAST-2. 4

5. (a) What is the GenBank files ? 4

(b) Describe the separation sequences and annotation. 4

(c) Explain the features of Swiss-prot databank. 4

OR

(p) Describe the SRS as retrieval system. 4

(q) Describe GenBank libraries. 4

(r) What is the PDB Database ? 4

6. Describe the in silico analysis of primary structure of protein and its comparison with tertiary structure. 12

OR

Describe the fold recognition and Ab initio method of tertiary protein structure prediction. 12

7. Describe the role of HMM in sequence alignment and explain features of HMMSTR. 12

OR

Describe the BLAST output files and explain parsing of BLAST output data in Bioperl. 12