AS–1469

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) EMBL is primary ________ sequence database.

(ii) Two sequences are said to be homologous if they have common _______.

(iii) EST stands for expression sequence _______.

(iv) The PDB is a crystallographic database for the three dimensional _______ data. 2

(B) Choose the correct alternative :

(i) GenBank and SWISS PROT are examples of :

(A) Primary database (B) Secondary database

(C) Composite database (D) None of these

(ii) Which is data retrieving tool ?

(A) EMBL (B) PHD

(C) BLAST (D) ENTRE2

(iii) Which of the following is database search utility tool ?

(A) PRINT (B) PDB

(C) BLAST (D) PIR

(iv) HMM stands for :

(A) Hindusthan Motor Machine (B) Hidden Marcov Model

(C) Hidden Marcov Machine (D) Hindusthan Marcov Model 2

(C) Answer in **ONE** sentence each :

(i) What is FASTA ?

(ii) Define Sequence Alignment.

(iii) What is Database ?

(iv) What is EST ? 4

2. (a) Describe data management. 4

(b) Define biodiversity. Explain biodiversity database. 4

(c) Explain data abstraction. 4

OR

(p) Define Microarray. Explain microarray database. 4

(q) Describe DBMS as a database design. 4

(r) Explain the importance of database. 4

3. Describe any three tools used for in silico analysis of nucleotide sequences. 12

OR

Explain genomic database repositories like EST and STS in detail. 12

4. (a) Explain characteristics of genetic code. 4

(b) Describe BLAST-2. 4

(c) Explain the features of FASTA format sequence. 4

OR

(p) Write the algorithm for translating DNA into protein sequence. 4

(q) Describe FASTA as database similarity search tool. 4

(r) Describe Hashes data structure. 4

5. What are biological databanks ? Explain the features of any two primary protein sequence databanks. 12

OR

What is GenBank ? Describe GenBank annotation and its indexing with DBM in detail. 12

6. (a) Describe secondary structures of protein. 4

(b) Explain Homology modeling. 4

(c) Explain features of PDB file. 4

OR

(p) Describe fold recognition method. 4

(q) Explain any two tools used for in silico analysis of primary structure of proteins. 4

(r) Describe Ab initio method of structure prediction. 4

7. (a) What is HMM ? Describe its role in sequence alignment. 4

(b) Describe HMMER. 4

(c) Explain parsing of BLAST output in biopearl. 4

OR

(p) Explain role of HMM in structure prediction. 4

(q) Describe HMMSTR. 4

(r) Explain BLAST output in short. 4