

**B.Sc. (Part-III) Semester-V Examination****5S : 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) \_\_\_\_\_ is an information retrieval system of NCBI.

(ii) \_\_\_\_\_ is a protein information resource database.

(iii) The FASTA format of sequence begins with \_\_\_\_\_ symbol.

(iv) GenBank is maintained by \_\_\_\_\_. 2

(b) Choose the correct alternative :

(i) All are nucleotide sequences databases except :

(a) Swiss-Prot

(b) EMBL

(c) DDBJ

(d) GenBank

(ii) Phylogenetic relationship can be shown by :

(a) Dendrogram

(b) GenBank

(c) Data tool

(d) Tendrogram

(iii) BLAST program is used for :

(a) DNA sequencing

(b) Sequence alignment

(c) Basic sequence searching

(d) DNA barcoding

(iv) Which of the following is protein tertiary structure prediction method ?

(a) BLAST

(b) SRS

(c) Homology modeling

(d) HMM 2

(c) Answer in **one** sentence each :

(i) What is EST ?

(ii) What is RDBMS ?

(iii) What is genome ?

(iv) What is sequence alignment ? 4

2. (a) What is database ? Types of databases. 4

(b) Describe the enzyme database. 4

(c) Describe Data management and Architecture. 4

**OR**

- (d) Describe misc. database. 4
- (e) What is data security ? 4
- (f) Explain database design. 4
3. (a) Explain GenBank as a database. 4
- (b) What are the limitations of computer analysis ? 4
- (c) Describe transcription. 4

**OR**

- (d) Describe structural organizations of genome. 4
- (e) Describe STS. 4
- (f) Describe Genome databases. 4
4. (a) Explain BLAST tool and its types. 12

**OR**

- (b) Explain protein translation and genetic code. 12
5. (a) Describe protein sequence database. 4
- (b) Describe protein structure database. 4
- (c) Describe GenBank file format. 4

**OR**

- (d) Describe restriction maps. 4
- (e) Explain SRS features. 4
- (f) Describe GenBank libraries. 4
6. (a) Explain structural level of proteins. 12

**OR**

- (b) Explain protein tertiary structure prediction methods. 12
7. (a) Explain HMM application in sequence alignment. 4
- (b) Explain features of Bioperl. 4
- (c) What is sequence Homology ? 4

**OR**

- (d) Write applications of HMM in structure prediction. 4
- (e) Describe parsing of BLAST output. 4
- (f) Describe BLAST string matching in Bioperl. 4