

**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) Explain GenBank as a 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