

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 _____.

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(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) Tendencia

(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

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

(i) What is EST ?

(ii) What is RDBMS ?

(iii) What is genome ?

(iv) What is sequence alignment ?

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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 microarray 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