

**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) \_\_\_\_\_ A database of current sequence map of the human genome.
- (ii) Phylogenetic relationship can be shown by \_\_\_\_\_.
- (iii) Flybase is a database for \_\_\_\_\_.
- (iv) E.coli model organism database is \_\_\_\_\_.

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(b) Choose the correct alternative :

(i) Which of the following is a protein structure database ?

- (a) GenBank
- (b) Swiss-Prot
- (c) DDBJ
- (d) PDB

(ii) STAG is a text based search centre of :

- (a) DDBJ
- (b) GenBank
- (c) PIR
- (d) EMBL

(iii) Which of the following is the search and retrieval tool of NCBI ?

- (a) SAKURA
- (b) SRS
- (c) Seqin
- (d) Entrez

(iv) Which of the following is a metabolic database ?

- (a) PIR
- (b) PDB
- (c) KEGG
- (d) OMIM

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

- (i) What is repositories ?
- (ii) What is algorithms ?
- (iii) What is homology ?
- (iv) What is Insilico analysis ?

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2. (a) Describe the enzyme database. 4  
 (b) Describe the microarray database. 4  
 (c) Describe the architecture of data management. 4  
**OR**
- (p) Describe the types of database. 4  
 (q) Describe the importance of database. 4  
 (r) Describe data warehousing. 4
3. (a) Describe the structural organization of human genome. 4  
 (b) Insilico analysis of primary structures of nucleic acid sequence. 4  
 (c) Describe the program to store DNA fragments. 4  
**OR**
- (p) Describe the EST as a repositorie. 4  
 (q) Describe the DNA to RNA sequence databank. 4  
 (r) Describe the GenBank features. 4
4. Describe the Hashes data structures and algorithms for Biology. 12  
**OR**  
 Describe the BLAST and features of FASTA format sequence. 12
5. (a) Describe the SwissProt. 4  
 (b) Describe the GenBank files. 4  
 (c) Explain the Separating sequerences. 4  
**OR**
- (p) Describe protein sequence data bank SRS. 4  
 (q) Explain the restriction map. 4  
 (r) Explain parsing annotations indexing. 4
6. Describe the Protein Tertiary Structure Prediction Methods. 12  
**OR**  
 Describe the Insilico prediction of secondary structures of Protein. 12
7. (a) Application of HMM. 4  
 (b) Describe HMMSTR. 4  
 (c) Describe use of BLAST in homology. 4  
**OR**
- (p) BLAST output files. 4  
 (q) Describe HMMER. 4  
 (r) Describe parsing of BLAST output. 4