

M.Sc. (Part-I) Semester-I (C.B.C.S. Scheme) Examination

BIOINFORMATICS

(Introduction to Bio-Informatics)

Paper-IV

Time : Three Hours]

[Maximum Marks : 80

Note :— (1) All questions are compulsory and carry equal marks.

(2) Draw well labelled diagrams wherever necessary.

1. Attempt the following :

- (a) Justify "Bioinformatics – A multi disciplinary approach". 4
- (b) Explain scope of Bioinformatics. 4
- (c) Describe role of internet in Bioinformatics. 4
- (d) Give any two biological problems that require computational methods for their solution. 4

OR

- (p) Give any two definitions of Bioinformatics. 4
- (q) Describe the factors which led to emergence of Bioinformatics as a separate discipline. 4
- (r) Enlist any four applications of Bioinformatics. 4
- (s) Historical events of Bioinformatics emergence. 4

2. What is DNA ? Describe in detail different methods of DNA sequencing. 16

OR

Define protein. Explain in detail protein structure determination methods. 16

3. Explain :

- (a) Features of FASTA sequence format. 4
- (b) NCBI as a gateway to Bioinformatics resources. 4
- (c) EMBL as a primary nucleotide sequence database. 4
- (d) Features of PDB format. 4

OR

- (p) Features of Multiple Sequence Format (MSF). 4
- (q) MIPS as a gateway to Bioinformatics. 4
- (r) EST as subsidiary data storage. 4
- (s) Features of FlyBase. 4

4. What is NCBI ? Describe in detail data access, retrieval and submission in NCBI. 16

OR

What is EBI ? Describe in detail data access, retrieval and submission in EBI. 16

5. Attempt the following :

- (a) Define sequence alignment. Give different types of alignment. 4
- (b) Differentiate between sequence similarity and sequence homology. 4
- (c) What is gap penalty ? Describe the role of gap penalty in alignment score. 4
- (d) Explain sequence similarity searching by BLAST. 4

OR

- (p) Give the significance of sequence alignment. 4
- (q) What is sequence homology ? Explain different homologous relationships. 4
- (r) Explain sequence similarity searching by FASTA. 4
- (s) Distinguish between global and local sequence alignment. 4

