AU–277

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

BIO-INFORMATICS

(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. Define Bioinformatics. Describe in detail history, scope, emergence and applications of Bioinformatics. 16

OR

Do Biologists need computers ? Describe biological problems that require computational methods for their solution and explain role of internet in Bioinformatics. 16

2. Attempt the following :

(a) Describe dideoxy method of sequencing. 4

(b) Explain Expressed Sequence Tags. 4

(c) Give protein structure determination methods. 4

(d) How is biological information stored ? Describe different forms of biological information. 4

OR

(p) Describe Genomic survey sequences. 4

(q) Explain automated DNA sequencing. 4

(r) Define cDNA. What kind of information can be obtained from cDNA library ? 4

(s) How to collect gene expression data ? 4

3. Attempt the following :

(a) Features of NBRF/PIR sequence format. 4

(b) GOLD as a gateway to Bioinformatics. 4

(c) DDBJ as a primary sequence database. Explain. 4

(d) Describe the features of PDB. 4

OR

(p) Explain GSSs as subsidiary data storage. 4

(q) Describe important features of OMIM. 4

(r) Explain UniGene as a gateway to Bioinformatics. 4

(s) Give annotations of SWISS-PROT. 4

4. What is Eutrez ? Describe in detail features of Eutrez and explain role of Boolean operators in searching. 16

OR

What is SRS ? Describe in detail features of SRS and explain role of adjacent searching and phrase searching in SRS. 16

5. Attempt :

(a) What is similarity searching ? Give algorithms used for similarity searching. 4

(b) How are alignment scores calculated ? 4

(c) Give the significance of sequence alignment. 4

(d) Is similarity synonymous to homology ? Explain. 4

OR

(p) Explain global and local sequence alignment. 4

(q) Describe GOP and GEP. 4

(r) Explain sequence similarity searching by BLAST. 4

(s) Describe measurement of sequence similarity. 4