

M.Sc. (Part-I) Semester-II (CBCS Scheme) Examination

BIOINFORMATICS

(Techniques in Bioinformatics)

Paper-VIII

Time : Three Hours]

[Maximum Marks : 80

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

(2) Draw suitable diagram wherever necessary.

1. Describe :

- | | |
|--|---|
| (a) Features of Genbank. | 4 |
| (b) DSSP. | 4 |
| (c) INTERPRO as a composite database. | 4 |
| (d) GSS as a repository for genomic sequences. | 4 |

OR

- | | |
|----------------------------------|---|
| (p) Features of PIR. | 4 |
| (q) PRINTS. | 4 |
| (r) BLOCK as a derived database. | 4 |
| (s) KEGG. | 4 |

2. Explain :

- | | |
|--|---|
| (a) PSI-BLAST algorithm. | 4 |
| (b) Searching sequence pattern by scanprosite. | 4 |
| (c) HMMer role in profile analysis. | 4 |
| (d) Identification of SNPs. | 4 |

OR

- (p) Rules used for derivation of sequence pattern in prosite. 4
 (q) Role of OMIM database in identification of disease genes. 4
 (r) SNP arrays. 4
 (s) Integrated genomic maps. 4
3. What is gene ? Explain the structure of prokaryotic and eukaryotic genes and describe the methods used for prediction of prokaryotic gene structure. 16

OR

- What is CpG island ? Explain its role in gene prediction and describe any one tool used for CpG island analysis. 16
4. Describe in detail role of caps. tails and genome duplication in genome rearrangement. 16

OR

- Explain in detail role of Breakpoint graphs, permutation and sorting reversals in genome rearrangement. 16
5. Describe :
- (a) Gene Expression Omnibus. 4
 (b) SAGE database. 4
 (c) Sequence based clustering. 4
 (d) Normalization of microarray data. 4

OR

- (p) Array Express. 4
 (q) Microarray database. 4
 (r) Character based clustering. 4
 (s) Understanding of microarray data. 4