(c) Explain PSI – BLAST algorithm steps. 5

(d) Explain phenetic and cladistic approach of phylogenetic analysis. 5

OR

(p) Describe molecular clock hypothesis. 5

(q) Explain distance method of phylogenetic analysis. 5

(r) What is EMBOSS ? Explain features of EMBOSS. 5

(s) Define phylogenetic tree. Explain types of trees. 5

5. Define secondary structure of protein. Describe any two methods of secondary structure prediction.

OR

What is tertiary structure of protein ? Describe homology modelling and ab – initio method of structure prediction. 20

AQ – 1053

Third Semester M. Sc. (Part–II) Examination

BIOTECHNOLOGY

3 BTB 3

Paper – XI

Biostatistics and Bioinformatics

P. Pages : 4

Time : Three Hours] [Max. Marks : 100

Note : (1) All questions are compulsory and carry equal marks.
(2) Draw well labelled diagram wherever necessary.

1. Find the mean, mode, median, variance and standard deviation of following data

Height in cms	70 - 75	75 - 80	80 - 85	85 - 90	90 - 95	95 - 100	100 - 105	105 - 110	110 - 115
No. of Children	3	4	7	7	15	9	6	6	3

OR

What is probability ? Give laws of probability and calculate the probability of a card drawn at random from any ordinary pack of cards is

(i) A black card.

(ii) A Jack.

(iii) A Club.

(iv) A king of club.

(v) One of the court cards (Jack or Queen or King). 20

2. Explain :—

(a) Methods of deposition of data to databases. 5

(b) Explain primary protein sequence database with an example. 5

(c) NCBI as bioinformatics resource. 5

(d) Derived databases with an example. 5

OR

(p) EBI as bioinformatics resource. 5

(q) Retrival system at NCBI. 5

(r) Viral genome databases. 5

(s) EST as repository for high throughput genomic sequences. 5

3. Attempt :—

(a) What are scoring matrices ? Give their limitations. 5

(b) Define sequence alignment. Give its type and significance. 5

(c) Explain steps of FASTA algorithm. 5

(d) Define MSA. Give progressive alignment approach used for MSA. 5

OR

(p) Define Homology. Explain different homologous relationships with an example. 5

(q) Describe steps of Smith – Watermann algorithm. 5

(r) Explain basic BLAST programs. 5

(s) Features of FASTA format of sequence. 5

4. Attempt the following :—

(a) Define comparative genomics. Describe role of synteny in comparative genomics. 5

(b) What is ExPasy ? Describe any one tool for protein sequence analysis at ExPasy. 5