RR-0868-R/100

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Third Year B. Sc. Examination

March / April – 2010

Microbial Genomics & Bioinformatics

(Microbiology CAN Course) (IDS)

Time : **3** Hours] [Total Marks : **70**

Instructions :

(1)

નીચે દર્શાવેલ ☛ નિશાનીવાળી વિગતો ઉત્તરવહી પર અવશ્ય લખવી.
Fillup strictly the details of ☛ signs on your answer book.
Name of the Examination :
☛ **T.Y. B.Sc.**
Name of the Subject :
☛ **MICROBIAL GENOMICS & BIOINFORMATICS**
☛ Subject Code No. : **0 8 6 8** ☛ Section No. (1, 2,.....) : **NIL**

Seat No. : ☐☐☐☐☐☐

Student's Signature

(2) Figures to the right indicate full marks of the question.

(3) All questions are compulsory.

1 Give specific answers for each of the following : **14**

(a) Define: Bioinformatics and Genomics

(b) Enlist four chemicals used in Maxam's method of sequencing.

(c) Give names of first bacterial and first viral genome sequenced.

(d) Enlist ideal characters of a database.

(e) Give few examples of PBD viewers.

(f) What was ARPANET? What is its significance?

(g) What do you mean by mainframe computers? What are its general uses?

2 Justify / Comment on any **three** of the following : **15**

(a) Computers are also present in laboratory as embedded systems.

(b) Two dimensional electrophoresis is a coretechnique of proteomics.

(c) FASTA format is one of the most common ways of representing nucleotide sequence.

(d) ENTREZ is a common system to search sequences in many databases.

(e) DOT-PLOT is one of the simplest ways of pairwise alignment.

3 Explain and compare different popular tools of multiple sequence alignment. **10**

OR

3 Explain dideoxynucleotide method of DNA sequencing. **10**

4 Attempt any two of the following in detail : **16**

(a) Describe the development of bioinformatics in India.

(b) Describe secondary structure of protein and its prediction using bioinformatics.

(c) Explain the process of photolithography in detail with appropriate diagram.

(d) Explain history, working and use of Blast algorithm.

5 Write short notes on any three of the following : **15**

(a) Spotted DNA arrays

(b) Phylogenic trees

(c) Motifs and their prediction

(d) Future of genomics

(e) Network computers.
