



RR-0868

Third Year B. Sc. Examination
March / April – 2010
Microbial Genomics & Bioinformatics
(Microbiology CAN Course) (IDS)

Time : 3 Hours]

[Total Marks : 70

Instructions :

(1)

नीचे दृष्टावेक निशानीवाणी विगतो उत्तरवही पर अवश्य कभवी. Fillup strictly the details of signs on your answer book.	Seat No. :
Name of the Examination :	<input type="text"/>
<input type="text" value="T.Y. B.Sc."/>	<input type="text"/>
Name of the Subject :	<input type="text"/>
<input type="text" value="MICROBIAL GENOMICS & BIOINFORMATICS"/>	<input type="text"/>
Subject Code No. : <input type="text" value="0"/> <input type="text" value="8"/> <input type="text" value="6"/> <input type="text" value="8"/>	<input type="text"/>
Section No. (1, 2,.....) : <input type="text" value="NIL"/>	
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) Phylogenetic trees
 - (c) Motifs and their prediction
 - (d) Future of genomics
 - (e) Network computers.
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