## 2016

# M.Sc.

# 2nd Semester Examination

#### **MICROBIOLOGY**

PAPER-MCB-204

Full Marks: 40

Time: 2 Hours

The figures in the right-hand margin indicate full marks.

Candidates are required to give their answers in their own words as far as practicable.

Illustrate the answers wherever necessary.

Answer any two questions from each group.

# Group - A

[Marks : 20]

Answer any two questions.

1. (a) What is programming languages? Differentiate between system programme and Application programme.

(Turn Over)

- (b) How is the Switch User option different from the Log
  Off option?
- (c) Write the shortcut key combination used for navigating—
  - (i) Used to select all the content of MS-Word documents.
  - (ii) Used the save the documents.
  - (iii) Open a existing document.

(2+3)+2+3

- 2. (a) What is an operating system? Briefly describe features of any one desktop operating system.
  - (b) What are the different types of the image format used in computer system?
  - (c) (i) Convert decimal number "5" into binary number.
    - (ii) What is information.

(2+3)+2+3

3. Write short notes on:

 $4\times2\frac{1}{2}$ 

- (a) Storage divice & their types;
- (b) CPU;
- (c) RAM;
- (d) Generation of computer.

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(Continued)

# Group - B

[Marks: 20]

- 4. (a) How bioinformatics solve the biological problems at molecular level and how it is helpfull in modern research?
  - (b) How phylogram is more advantageous than cladogram?
  - (c) Write the utility of ligard-protein interaction analysis through bioinformatics in medical science.
  - (d) What are the popular languages in Bioinformatics?
    4+2+3+1
- 5. (a) What do you understand by pairwise sequence alignment? What is the utility? Distinguish between global and local sequence alignment. Explain with examples.
  2+1+2
  - (b) What is gap opening penulty and gap extension penalty? Write its significance in sequence alignment.

2+1

(c) State the utilities of conserved domain motif and signature sequences in protein functional similarity.

6. (a) Write the short note of any three of the following:

3×2

- (i) Biological Database;
- (ii) BLAST;
- (iii) FASTA;
- (iv) Molecular phylogeny;
- (v) Genome annotation.
- (b) (i) Describe the features and importance of NCBI.
  - (ii) Explain in detail about DB and MMDB.

(2+2)