2022

M.Sc.

2nd Semester Examination

MICROBIOLOGY

PAPER—203

Full Marks : 50

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.

UNIT-203.1 BIOMATHEMATICS

Group - A

Answer any *two* questions. 2×2

1. Define simple random sampling.

2. Compare histogram and frequency polygon.

3. 18% of a group of 80 men and 16% of a group of 120 women were found to be diabetic. Find the mean percentage of diabetics for both the groups combined.

4. What is maximum yield coefficient in bacterial fermentation?

Group – B

Answer any *two* questions. 2×4

5. Explain qualitative and quantitative data with example. What is continuous variable? 3+1

6. Determine the median of the following frequency distribution of body weight (kg) of human.

Class:	51-53	54-56	57-59	60-62	63-65
Frequency:	7	14	25	12	8

7. Explain the Monod kinetics of bacterial growth with equation.

8. Why t-test is performed? Explain null hypothesis and alternative hypothesis in t-test. 1+3

Group - C

Answer any *one* question. 1×8

9. The body weight (gram) of 8 male mice and 8 female mice are given below. Perform t-test and find out whether or not mean body weights of male mice are significantly higher than female mice? [given data: $t_{0.01(14)} = 2.624$]

body weight (gram) of male mice : 50, 58, 61, 55, 59, 57, 54, 64

body weight (gram) of female mice: 49, 51, 52, 57, 55, 52, 53, 48

10. Determine the mean, standard deviation and variance of the following distribution of height (cm) of human:

Class:	156-160	161-165	166-170	171-175	176-180
Frequency:	5	13	26	11	5

3+3+2

UNIT–203.2 BIOINFORMATICS

Group – A

Answer any *two* questions. 2×2

1. What is BLAST?

2. What is the difference between global and local alignment?

3. What do you mean by substitution matrix?

4. Name a protein sequence database and a protein 3D structure database.

Group – B

Answer any *two* questions. 2×4

5. What is gap opening and gap extension penalty? What is the importance of gap in sequence alignment? 2+2

6. What is molecular docking in drug discovery? Write the basics steps involved in ligand-protein docking? 2+2

7. Write a short note on PAM. In a protein of 436 amino acid, 38 amino acids are changed in course of evolution – calculate the change in PAM unit. 2+2

8. Which method is used for pairwise alignment? What is accession number? What is the importance of accession number? 1+1+2

Group – C

Answer any *one* question. 1×8

9. 'Protein sequences are more important than DNA sequence' – Justify. What is identity and similarity? 6+2

10. Align the following sequences and calculate the score (match score = 2, mismatch score = 0, gap opening penalty = 11, gap extension penalty = 1)

Sequence 1: ATGACTAAGTTCTGCTACGCAAAGGTCG GTACTGCGCATTAGGATTAG

Sequence 2: ATGACTTTCTGCTACGCAAAGGTCGG TACTGCGCATTAGAATTCG

[Internal Assessment – 10 Marks]

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