BRAINWARE UNIVERSITY

Term End Examination 2023
Programme – B.Tech.(CSE)-AIML-2022/B.Tech.(CSE)-DS-2022/B.Tech.(RA)-2022
Course Name – Biology for Engineers
Course Code - BSCM203/BSCD203/BSCR203
(Semester II)

Full Marks : 30 **Time : 1:30 Hours**

[The figure in the margin indicates full marks. Candidates are required to give their answers in their own words as far as practicable.]

Group-A
(Multiple Choice Type Question) 1 x 5=5

1. *Choose the correct alternative from the following :*

(i) Damage and errors in DNA cause_____
a) Cloning b) Variation
c) Totipotency d) Mutation

(ii) The most appropriate diagram for representing spatial-series data is:
a) Bar-diagram b) Histogram
c) Line-diagram d) Column-diagram

(iii) There are different categories of biological organisms. A data set on various organisms would be best represented using which of the following diagrams?
a) Line-diagram b) Bar-diagram
c) Pie chart d) Histogram

(iv) Types of molecular databases are
a) Primary Database b) Derivative Database
c) Both a and b d) None of these

(v) Which of the following cell organelles does not contain DNA?
a) Chloroplast b) Lysosomes
c) Nucleus d) Mitochondria

(vi) Which of the following cell organelles is absent in animal cells and present in a plant cell?
a) Mitochondria b) Cytoplasm
c) Vacuoles d) Nucleus

(vii) which of the following cell organelle is known as powerhouse of the cell?
a) Mitochondria b) Nucleus
c) Endoplasm reticulum d) Lysosomes

Group-B

(Short Answer Type Questions) 3 x 5=15

2. Elucidate the essential fatty acids. (3)
3. Define line diagram with examples. (3)
4. Explain skewness. (3)
5. Write a short note on National Center for Biotechnology Information. (3)
6. Construct the double helical structure of DNA. (3)

OR

Complete the classification of RNA. (3)

Group-C

(Long Answer Type Questions) 5 x 2=10

7. Explain the steps of DNA replication. (5)
8. Calculate the relative alignment having the highest score with the given two string sequence #1 and sequence #2. (scoring system= match=(+1), mismatch=(-1), Gap=(-3) Seq#1: GAATTCAGTTA Seq#2: GGATCGA (5)

OR

Compute the median of the following grouped frequency distribution: *Class: 10-19 20-29 30-39 40-49 50-57* *Freq.: 23 46 62 51 33* (5)

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