JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- 2023

M.Tech-1 Semester (BT)

COURSE CODE (CREDITS): 13M11BT112 (3) MAX. MARKS: 25

COURSE NAME: Advanced Bioinformatics

COURSE INSTRUCTORS: Dr. Raj Kumar MAX. TIME: 1 Hour 30 Minutes

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Note: *(a)All questions are compulsory.*

(b)Marks are indicated against each question in square brackets.

(c) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems

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Q1. Write down a R-programming code to create given data frames. Combine the given data frames using bind() function? [3]

Data Frame -1

Gene	*ID*	*Common Name*
ATR	231	ATR serine-threonine kinase
BAK1	278	BCL2-antagonist 1
BAX	119	BCL2-associated X protein

Data Frame -2

Gene	*ID*	*Common Name*
BCL2	69	B-cell lymphoma 2
BDNF	191	Brain-derived neurotrophic factor
BLM	68	RecQ helicase-like

Q2. Describe the principle of chain termination using dideoxynucleotides. [3]

Q3. Give a brief overview of a typical NGS data analysis pipeline. [3]

Q4. Describe the following steps involved in performing quality control analysis on NGS data: [2 × 4]

a) Per base sequence quality
b) Per sequence quality scores
c) Per sequence GC content
d) Base calling

Q5. Give a brief account of SRA accession types. [2]

Q6. What is the Phred quality score scale, and how does it relate to NGS quality scores? [2]

Q7. What is the significance of the Q30 quality score in NGS data, and why is it often used as a benchmark for data quality? [2]

Q8. Discuss fundamental approaches to genome assembly. [2]