JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

Make-up Examination-Nov-2025

COURSE CODE (CREDITS): 25B11B1312 (3) 13 MI)BTII2

MAX. MARKS: 25

COURSE NAME: Advanced Bioinformatics

COURSE INSTRUCTORS: Dr. Shikha Mittal

MAX. TIME: 1 Hour 30 Minutes

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

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

Q.No	Qı	estion		Marks
Q1	What do understand by Phred score in a fastq file? What is the minimum requirement of Phred score to start further downstream analysis? For a sequence, if Phred score is 30, what will be the percentage inaccuracy?			(4)
Q2	Now-a-days next generation sequencing is widely used in multiple fields of biosciences. Describe in detail the fields in which next generation sequencing is used.			(4)
Q3	Write in short — a. Can you explain what FASTQ format files are b. Difference between single value and multi-valued attributes c. Notations used in E-R model d. Composite and component attributes e. Difference between DDL and DML			(5)
Q4.	Table: EMPLOYEE EmpID EmpNa 101 Riya 102 Aman 103 Suresh 104 Meena a. List names of employees wor b. Find the total salary of all em c. Display the names of employe	D1 D2 D1 D3 king in departingloyees. ees who earn r	more than 35000.	(4)
Q5	d. Display all employees sorted by salary in descending order Briefly explain the different types of keys used in database management systems.			(4)
Q6	What is the difference between file system and DBMS?			(4)