

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATIONS- 2026

B.Tech-VIII Semester (BT/BI)

COURSE CODE (CREDITS): 18B1WBI834(3)

MAX MARKS: 35

COURSE NAME: NGS data Analysis & Applications

COURSE INSTRUCTOR: Dr. Shikha Mittal

MAX. TIME: 2 Hours

Note: (a) All questions are compulsory.

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

(c) Use of calculator is not allowed

Q.No	Question	CO	Marks
Q1	You collected soil samples and want to study microbial diversity. a. Which sequencing approach will you choose (amplicon vs shotgun) and why? b. Your metagenomic data shows many unclassified reads. What could be the reasons and how will you improve classification? c. Your metagenomic assembly is highly fragmented. What strategies can improve assembly quality?	IV	(6)
Q2	Compare different NGS platforms (Illumina, PacBio, Nanopore) in terms of read length, accuracy, and applications.	II	(3)
Q3	a. If a sequencer generates 200 million reads with 100 bp length. What is total data generated? b. Find Q-score Error, probability = 0.01 c. Calculate Mapping efficiency: Total reads = 50 million Mapped reads = 45 million	III	(6)
Q4	Compare whole genome sequencing (WGS) and whole exome sequencing (WES). Highlight advantages and limitations.	III, IV	(4)
Q5	a. Difference between amplicon sequencing and shotgun metagenomics. b. Explain steps involved in metagenomic analysis.	IV	(4)
Q6	You are given sequencing data from a cancer study. Explain how you would identify mutations and interpret their biological significance.	III	(4)
Q7	Briefly explain - a. Mapping or Alignment b. Difference between First and second generation of sequencing c. Purpose of N50 value d. Differential gene expression	II, IV	(8)