

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST -2 EXAMINATION- 2025

B.Tech-VIII Semester (BT/BI)

COURSE CODE (CREDITS): 18B1WBI834 (3)

MAX. MARKS: 25

COURSE NAME: NGS Data Analysis & Applications

COURSE INSTRUCTORS: Dr. Shikha Mittal

MAX. TIME: 1 Hour 30 Min

Note: (a) All questions are compulsory.

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

Q.No	Question	CO	Marks
Q1	Describe the methods used for quality control (QC) in sequencing data. Mention at least two tools used for QC	[CO-3]	(04)
Q2	a. Define the FASTQ format. b. What is variant calling? c. Technical and biological replicates d. Sanger and Maxam gilbert sequencing e. Bridge and emulsion PCR	[CO-1, CO-2, CO-3]	(10)
Q3	a. In a FASTQ file, each sequence entry is represented by four lines. If you have a FASTQ file containing 500 sequence entries, how many total lines will the file have? b. Two bases in a sequencing read have Phred scores of 25 and 35. What is the difference in error probabilities between these two bases?	[CO-1, CO-3]	(04)
Q4	What are the key steps involved in <i>denovo</i> assembly?	[CO-3]	(03)
Q5	How did the Human Genome Project help in understanding human genetic variation?	[CO-4]	(04)