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JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATIONS- 2026

B.Tech-VIII Semester (BT/BI)

COURSE CODE (CREDITS): 18B1WBI834 **MAX MARKS: 25**

COURSE NAME: NGS data Analysis & Applications

COURSE INSTRUCTOR: 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

(c) Use of calculator is not allowed

Q.No	**Question**	**CO**	**Marks**
Q1.	**a.** Gene A expression: Control = 50 Treatment = 200 Calculate Fold change **b.** If a dataset contains 10 million reads and 9 million pass quality filtering, calculate: Percentage of high-quality reads **c.** @SEQ_ID ATGCATGC + IIIIIIII What does "IIIIIIII" represent?	[III]	(6)
Q2.	Compare de novo assembly and reference-based assembly in terms of: i. Accuracy ii. Computational requirements iii. Applications	[I, III]	(3)
Q3.	What is N50? How is it used to evaluate genome assembly quality?	[IV]	(2)
Q4.	You are given sequencing data of a novel organism with no reference genome. Explain how you would assemble its genome and validate the results with the help of a flow diagram.	[II]	(4)
Q5.	Explain the role of the Human Genome Project in disease diagnosis and treatment.	[IV]	(4)

Q6.	Differentiate between – **a.** SAM and Bam format **b.** First generation and second-generation sequencing techniques **c.** Technical and Biological replicates	[II, III]	(6)