JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATION- 2026

M.Tech-I Semester (BT)

COURSE CODE (CREDITS): 12M11BT112(3) **MAX. MARKS: 15**

COURSE NAME: Advanced Bioinformatics

COURSE INSTRUCTOR: Dr. Shikha Mittal **MAX. TIME: 1 Hour**

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	Marks
Q1	Two samples have the same number of reads, but Sample A has an average quality score of Q35 and Sample B has Q20. Which sample is generally more reliable for downstream analysis? Why?	(2)
Q2	**a.** What information is encoded in the four lines of a FASTQ record? **b.** What is the difference between a biological replicate and a technical replicate? **c.** Where does FastQC fit into an RNA-seq pipeline, and what information does it provide?	(6)
Q3	Explain RNA-Seq pipeline for denovo and reference based assembly using flowchart.	(4)
Q4	The following de Bruijn graph was generated from a set of reads: AT → TT → TG → GC → CA → AC → CT TT → TC → CG → GA → AC **a.** What is the purpose of constructing this graph during de novo assembly? **b.** Reconstruct the sequence using the selected path. **c.** Explain how this graph would eventually contribute to formation of a contig.	(3)