JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATIONS- 2025

M.Tech-I Semester (BT)

COURSE CODE (CREDITS): 13M11BT112 **MAX. MARKS: 35**

COURSE NAME: Advanced bioinformatics

COURSE INSTRUCTORS: 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

Q.No	Question	Marks
Q1	Explain the different data types in R with examples. How are vectors, lists, and data frames different from each other?	(5)
Q2	Discuss the importance of quality control in NGS data. Explain parameters like Phred score, GC content, duplication rate, and adapter contamination.	(4)
Q3	Explain in brief – **A.** FASTQ format **B.** Applications of bioinformatics in translational medicine **C.** Notations used in E-R model **D.** Difference between SAM and BAM format **E.** Micrioarrays	(10)
Q4	Explain the workflow of 16S rRNA metagenomics—from sample collection to taxonomic assignment. Include tools (QIIME2, DADA2).	(4)
Q5	Explain how to interpret a VCF file. Describe major fields like CHROM, POS, REF, ALT, QUAL, INFO, and FORMAT.	(3)
Q6	a. OTU counts in a sample: OTU1=300, OTU2=150, OTU3=50. Compute relative abundances (%) for each b. Transition/transversion: Given 200 SNPs where 120 are transitions (Ti) and 80 are transversions (Tv). Compute Ti/Tv ratio.	(4)
Q7	Consider the following tables: BOOK(BookID, Title, AuthorID, PublisherID) AUTHOR(AuthorID, AuthorName, Country) PUBLISHER(PublisherID, PublisherName, City) **a.** List all books written by authors from 'India'. **b.** Find the number of books published by each publisher. **c.** Retrieve details of authors who have written more than 3 books. **d.** Find books whose title contains the word 'Genomics'. **e.** List authors who have never published any book.	(5)