JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATIONS-2026

M.Tech-II Semester (BT)

COURSE CODE (CREDITS): 14M11BT213 (3) MAX. MARKS: 15

COURSE NAME: FUNCTIONAL GENOMICS

COURSE INSTRUCTOR: DR JATA SHANKAR 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

Q. No.	Question	Marks
Q1	Calculate the percentage of the genome that encodes proteins if the total genome size is 3 billion base pairs and the protein-coding region is approximately 50 Mb	2.5
Q2	Explain the highly repeated sequences, moderately repeated sequences, and unique sequences of the human genome. Describe the Human Genome Project and discuss how the functional reference genome data reflect the complexity of the human genome.	2.5
Q3	Describe the splicing vs alternative splicing events occurring in cells. Give two examples of genes that are known to produce multiple isoforms	2.5
Q4	If the Phred quality score is 30 for Sample A and 40 for Sample B, each with a sequencing length of 1 billion base pairs, determine the error rate in Sample A and Sample B.	2.5
Q5	Describe the concept of orthologous genes and explain the orthologs of a few selected genes across different model organisms	2.5
Q6	What is single-cell sequencing? Illustrate its mechanism (a labelled schematic diagram for the mechanism) and discuss the major applications of single-cell sequencing	2.5

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