JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATIONS APRIL-2025

M.Tech-II Semester (BT)

COURSE CODE (CREDITS): 14M11BT213 (3) MAX. MARKS: 25

COURSE NAME: FUNCTIONAL GENOMICS

COURSE INSTRUCTOR: DR JATA SHANKAR MAX. TIME: 1 Hour and 30 minutes

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 with an example how the identification and discovery of SNPs led to the creation of a marker to differentiate between healthy and diseased individuals considering TP53	3
Q2	Describe how the genes of the patients affect the effectiveness of the medication 'Gefitinib'. Explain the pharmacokinetics and pharmacodynamics factors/ terms.	3
Q3	Explain the principle of Restriction Fragment Length Polymorphism (RFLP). Describe the steps involved in conducting an RFLP analysis and discuss its significance in distinguishing homozygous, heterozygous and homozygous mutant disease alleles.	3
Q4.	Describe the concepts of sequence alignment and mapping in genomics. Explain the sequence alignment techniques, including global and local alignment, and discuss their applications. Additionally, elaborate on the importance of sequence mapping in genomics and how it facilitates genome assembly, variant detection, and functional annotation.	3
Q5	What are the main genomics data retrieved from the human genome project, which is a scientific landmark? What is a repeating element in the genome, and is there a need for it? Estimate gene density using the number of genes and genome size?	4
Q6	Describe the mechanism and methodology of Serial Analysis of Gene Expression. How SAGE helps to identify the expression pattern of two different cell types	4
Q7	Define a. Phred score b. Transcriptome c. Transcript d. Transcription e. Alternate splicing	5