JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATIONS-2023

B. Tech V-Semester (BT)

COURSE CODE (CREDITS): 18B1WBT532 (3) MAX. MARKS: 35

COURSE NAME: COMPARATIVE AND FUNCTIONAL GENOMICS

COURSE INSTRUCTOR: DR. JATA SHANKAR MAX. TIME: 2 Hours

Note: (a) All questions are compulsory.
(b)Marks are indicated against each question in square brackets.
(c) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems

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Q1. How does Pyrosequencing technology fit into the realm of next-generation sequencing, and in comparison to the mechanism and methodology underlying Sanger's DNA sequencing technology? How does Pyrosequencing help analyze the genome wide gene expression analysis transcriptomics study? [5 marks] CO I

Q2.If the frequency of a SNP in a population is 2% and the SNP is linked to cancer. If the population a town is 1 lac, then what is likelihood that people in the town susceptible for Cancer? [5 marks] COII

Q3. In human a common polymorphism involves the substitution of an arginine with a proline at codon 72 in TP53 gene, explain the SNPs and the impact of this SNP on human health in particular to different cancer cases? 5 marks] COII

Q4. Personalized medicine allows the identification of responder and non-responder for target therapies such as lung Cancer, explain with an example you studied? Give your remark on importance of knowing the genetic make-up of an individual's before the treatment? [5 marks] CO III

Q5. How do you proceed to identify the gene expression pattern in drug-resistant *E. coli* in comparison to drug-sensitive *E. coli* using DNA Microarray Technology? In addition illustrate the equation to normalize the microarray data? [5 marks] CO II

Q6. Notes on the following (2.5 marks each) CO II & III

a. Metagenomics

b. Quantitative-RT-PCR

c. Biomarker

d. RNAi