JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST-3 EXAMINATIONS-2024

M. Tech-II Semester (BT)

COURSE CODE (CREDITS): 14M11BT213 (3) MAX. MARKS: 35

COURSE NAME: FUNCTIONAL GENOMICS

COURSE INSTRUCTORS: 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

---

Q1. What is Gene Chip? What are the important features of gene Chip making it a successful tool in whole genome expression profiling? CO II [3]

Q2. How to quantify and identify the transcripts from lung cancer cells in comparison to the normal cells using DNA Microarray Technology? Give the details of the normalization step associated with it. CO II [3]

Q3. What is sequence-based and function-based metagenomics? What are biological pumps and their role in maintaining the carbon cycle in the environment? CO III [3]

Q4. How do best describe the role of 16SRNA in metagenomics? What do understand by unculturable microorganisms and the term pipeline in the analyses of the metagenomics projects? CO II [3]

Q5. Explain the role of the genetic makeup of a cancer patient while treating with an anticancer drug gefitinib. Describe the difference between pharmacogenomics and pharmacodynamics factors. CO III [3]

Q6. Explain the efficacy of the drugs such as warfarin, codeine, and omeprazole depending on the genotype of the individuals. Describe the terms responder & non-responder in the pharmacogenomics. CO III [3]

Q7. Discuss the comparative genomics considering an example, gene/gene function with species and across the species. CO I [3]

Q8. Describe the next-generation sequencing technology (NGS) mechanism and compare it with Sanger's sequencing. CO I [4]

Q2. Notes on; CO I & II [Each 2]

a. Define Probe
b. Heat Map and K-Mean
c. Haplotype
d. Model organism *Saccharomyces cerevisiae*
e. Central Dogma