

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST-2 EXAMINATIONS-2023

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 30 Min

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*Note: All questions are compulsory. Marks are indicated against each question in square brackets.*

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- Q1. How identification/ discovery of SNP lead to a development marker to distinguish diseases vs healthy, explain with example? [2.5 marks] CO II
- Q2. Human genome project is the landmark in the science, what are the major genomics data recovered from the genome projects? What is repetitive element in the genome; do find any application of it? [2.5 marks] CO I
- Q3. Where do you find the application of 16SrRNA and ITS in genomics studies? [2.5 marks] CO I
- Q4. When the nucleotide sequences in a chromosome from two random people are compared, give the relevance with respect to SNPs in the same chromosome likely to be inherited together in healthy vs disease condition? [2.5 marks] [2.5 marks] CO II
- Q5 Over-expression of EGFR is linked to cancer; explain, how the response of Gefinitib drug varies among the patients? [2.5 marks] CO II
- Q6. Write on Metagenomics? What is purpose of functional-based metagenomics and sequence-based metagenomics that influence the metagenomics studies? [2.5 marks] CO II
- Q7. What is personalized microbiome and how Machine learning finds its application in personalized microbiome? [2.5 marks] CO II
- Q8. What are the major characteristics of an ideal biomarker; define the quantitative and qualitative assessment in a reference to the biomarker? [2.5 marks] CO II
- Q9. Gene density varies significantly in the genome starting prokaryotic to eukaryotic system. The approximate no. of genes in *human* eukaryotic genome is around 20,000; calculate the gene density? [2.5 marks] CO I
- Q10. Application of VNTR and RFLP [2.5 marks] CO II