

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATIONS-2022

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. Human genome project is the landmark in the science, what are the outcomes of the genome projects? What is repetitive element in the genome; do find any application of it? [3.5 marks]
- Q2. The cancerous tissue contain heterogeneous cells with respect expression or unique drug response, Illumina sequencing could distinguish the expression of these cells, write the strategy for sequencing approach? [2.5 marks]
- Q3. If you have given a nucleotide sequence (1000b), the possible ORF is six, make schematic presentation to decipher six possible reading frames from a 1000b sequence read? [2.5 marks]
- Q4. How variation in the genome leads to the development biomarker such RFLP or RAPD? How does it helps to distinguish the various genomic DNA, explain? [2.5 marks]
- Q5 Genomics of model organism is important, state a model organism applicable to functional genomics studies for neurological diseases or cancer and why? [2.5 marks]
- Q6. Write on pyrosequencing? And how it influences the genomics studies? [2.5 marks]
- Q7. What is purpose of mapping of sequence/ reads to the reference genome and how it helps to identify the open read frame? [3 marks]
- Q8. In genomics, assigning coding and non-coding sequence in the genome project is important task? What basic strategies you would construct to distinguish prokaryotic vs eukaryotic genes? [3 marks]
- Q9. Gene density varies significantly in the genome starting prokaryotic to eukaryotic system. The approximate no. of genes in *S. cerevisiae* eukaryotic genome is around 6000; calculate the gene density? [3 marks]