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JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATIONS April 2019

B.Tech (Biotechnology) 3<sup>rd</sup> year

Course Code: 10B11BT611

MAX. MARKS: 35

Course Name: Comparative and Functional Genomics

Course Credits: 04

MAX. 1.5 hrs

*Note: All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means. Marks are indicated in square brackets against each question*

Q1. What are the applications of screening SNPs in the genome and how it helps in the personalized medicine? 2.5 COIII

Q2 For whole genome expression analysis DNA microarrays are used; what are the important characteristics of DNA microarray? 2.5 Marks COII

Q3. What are different types of DNA microarrays? Discuss the features of these microarrays? 2.5 COII

Q4. What is the genome size of *Homo sapiens* and how many genes encoding proteins are present? 2.5 COI

Q5. How SNPs are differentiated from point mutation? What is the frequency of SNP in the genome when you consider the similar population and diverse populations? How SNP are introduced in the genome and how do you screen SNPs (different methods) from the give sequence and out of those which one you considered the most reliable method? 5 (COII)

Q6. Sequencing by reverse termination is gaining importance, write the steps involved in it including its application, and represent the methods in diagrammatic flow? 5 COI

Q7. If you are provided with oligo-nucleotide based mouse genome DNA chips? Present the strategies to identify the differentially expressed genes from cancerous and non-cancerous mouse model? Also, discuss the normalization equation applied to remove systemic and technical biases? 5 COII